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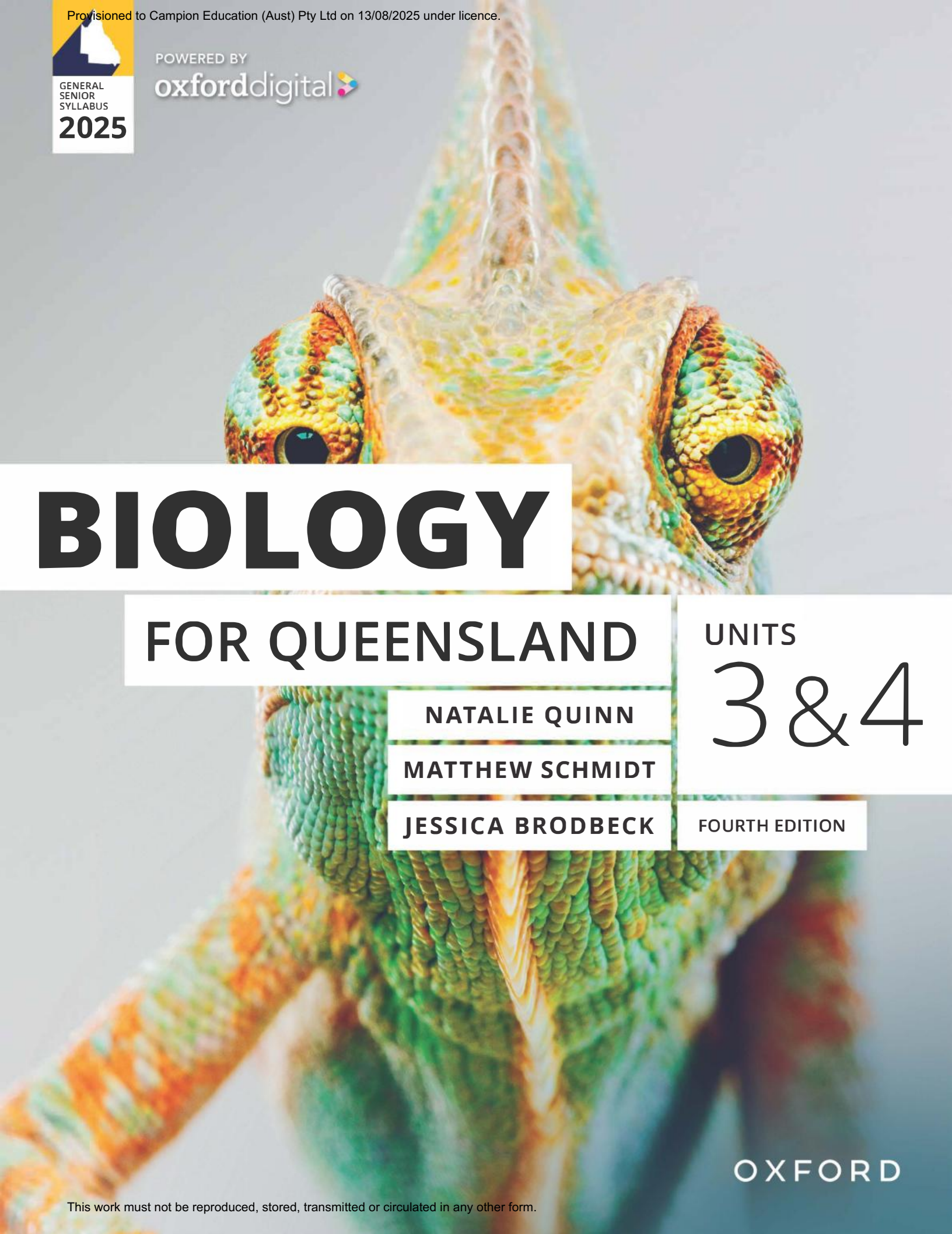

BIOLOGY

FOR QUEENSLAND

UNITS 3&4

NATALIE QUINN
MATTHEW SCHMIDT
JESSICA BRODBECK

FOURTH EDITION

OXFORD

GENERAL SENIOR SYLLABUS 2025

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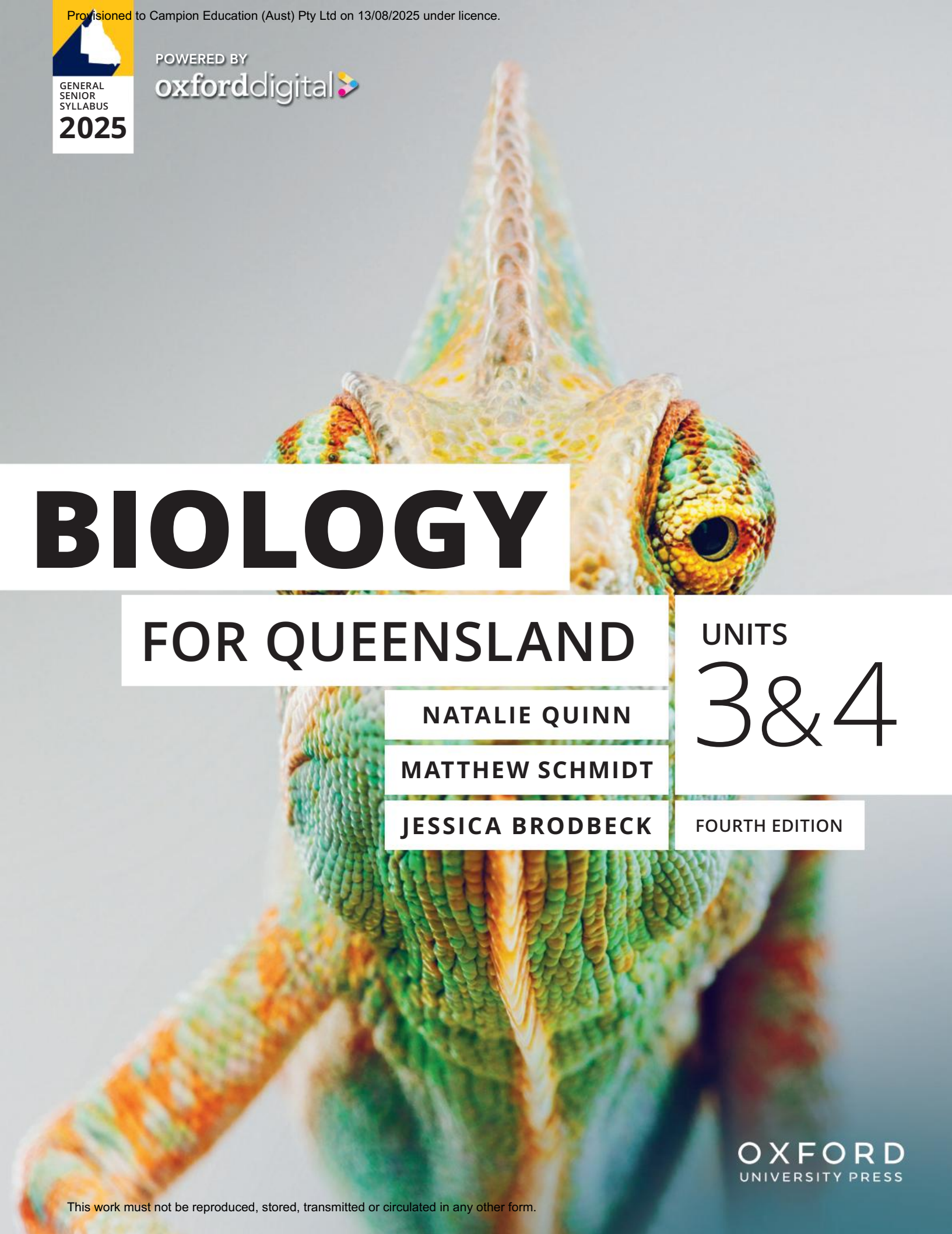

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Warning to First Nations Australians
Aboriginal and Torres Strait Islander peoples are advised that this publication may include images or names of people now deceased.

Contents

Lessons available on Oxford Digital.

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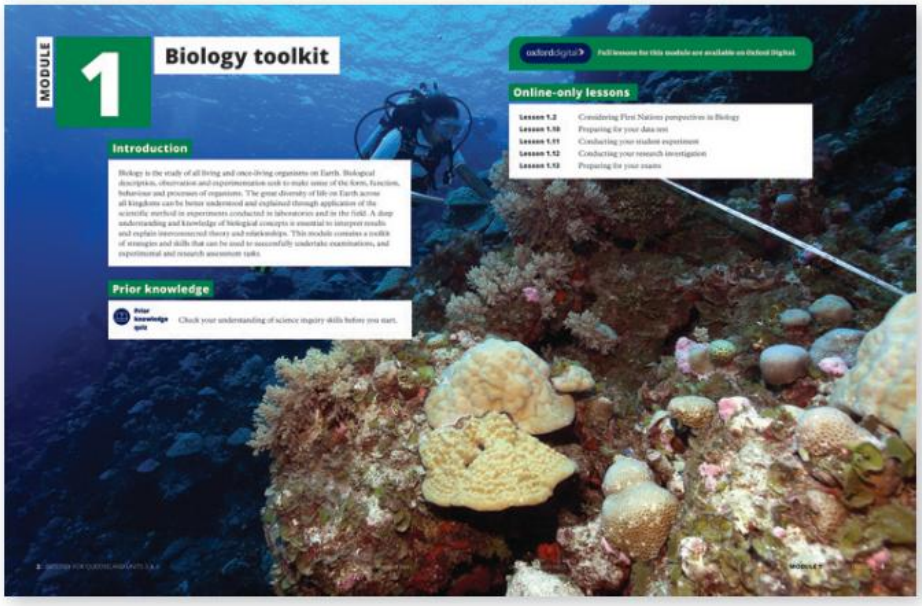
Introducing *Biology for Queensland Units 3 & 4* (Fourth edition)

Congratulations on choosing *Biology for Queensland Units 3 & 4* as part of your studies this year!

Biology for Queensland Units 3 & 4 has been purpose-written to meet the requirements of the QCAA Biology 2025 General senior syllabus. It includes a range of flexible print and digital products to suit your school and incorporates a wide variety of features designed to make learning fun, purposeful and accessible for all students!

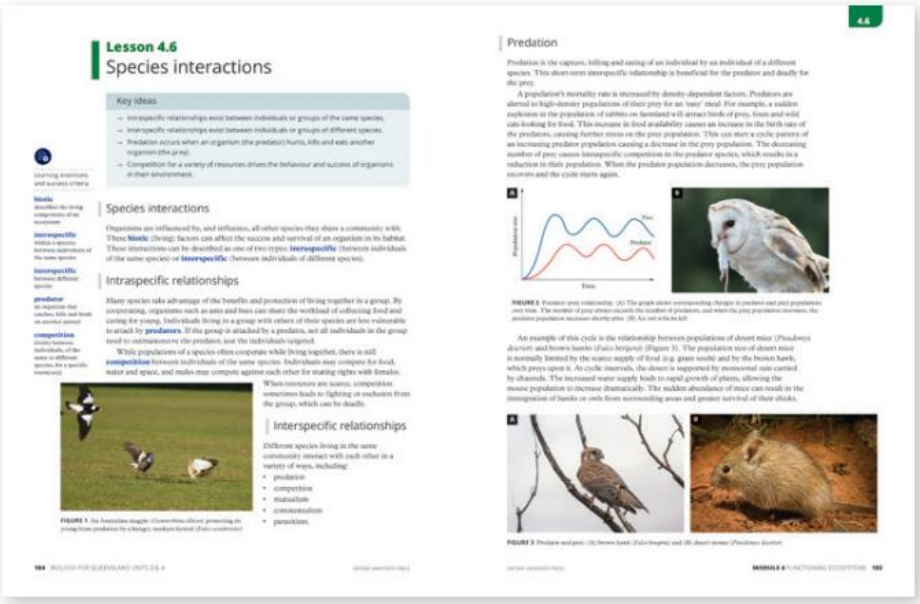
Key features of the Student Books

The Biology toolkit module provides an overview of the syllabus, student-friendly guidance for every science inquiry skill and tips for success on assessment tasks



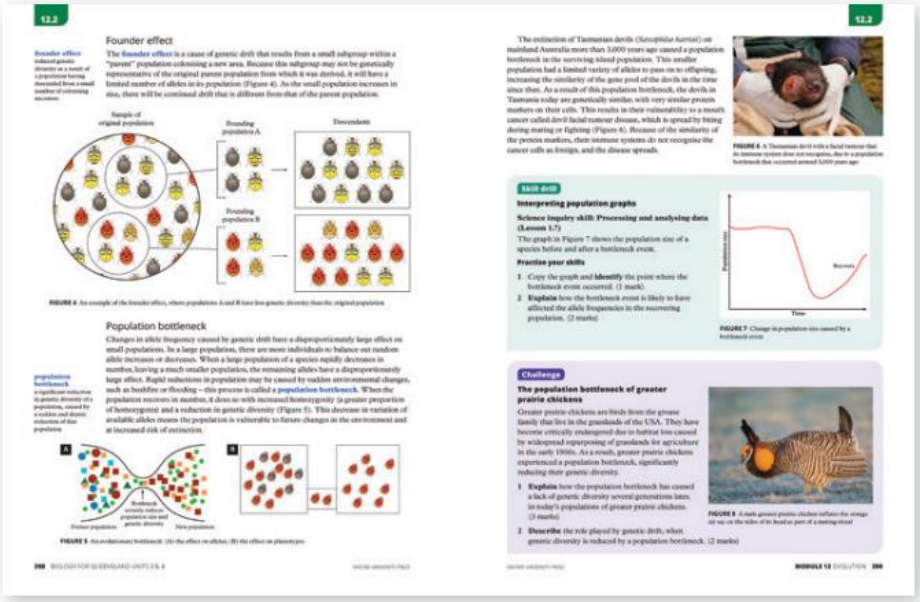
Each module begins with a module opener that includes:

- QCAA subject matter
- reference to a supporting prior knowledge quiz that assesses and informs student understanding of pre-requisite concepts
- a list of practical lessons that support science inquiry.



Each lesson includes:

- **learning intentions and success criteria**
- clearly structured content written in clear, concise language
- definitions for all key terms on the page
- engaging, relevant and informative images and illustrations
- a range of tips and features designed to bring course content to life including **study tips**, **worked examples**, **skill drills** and examples of **real-world science applications**
- references to supporting **digital resources**
- **Check your learning** activities organised according to **Marzano and Kendall's taxonomy** and incorporating **cognitive verbs**.



Each module contains a range of practical activities designed to meet the requirements of science understanding and science inquiry subject matter and develop science inquiry skills.

Find out more

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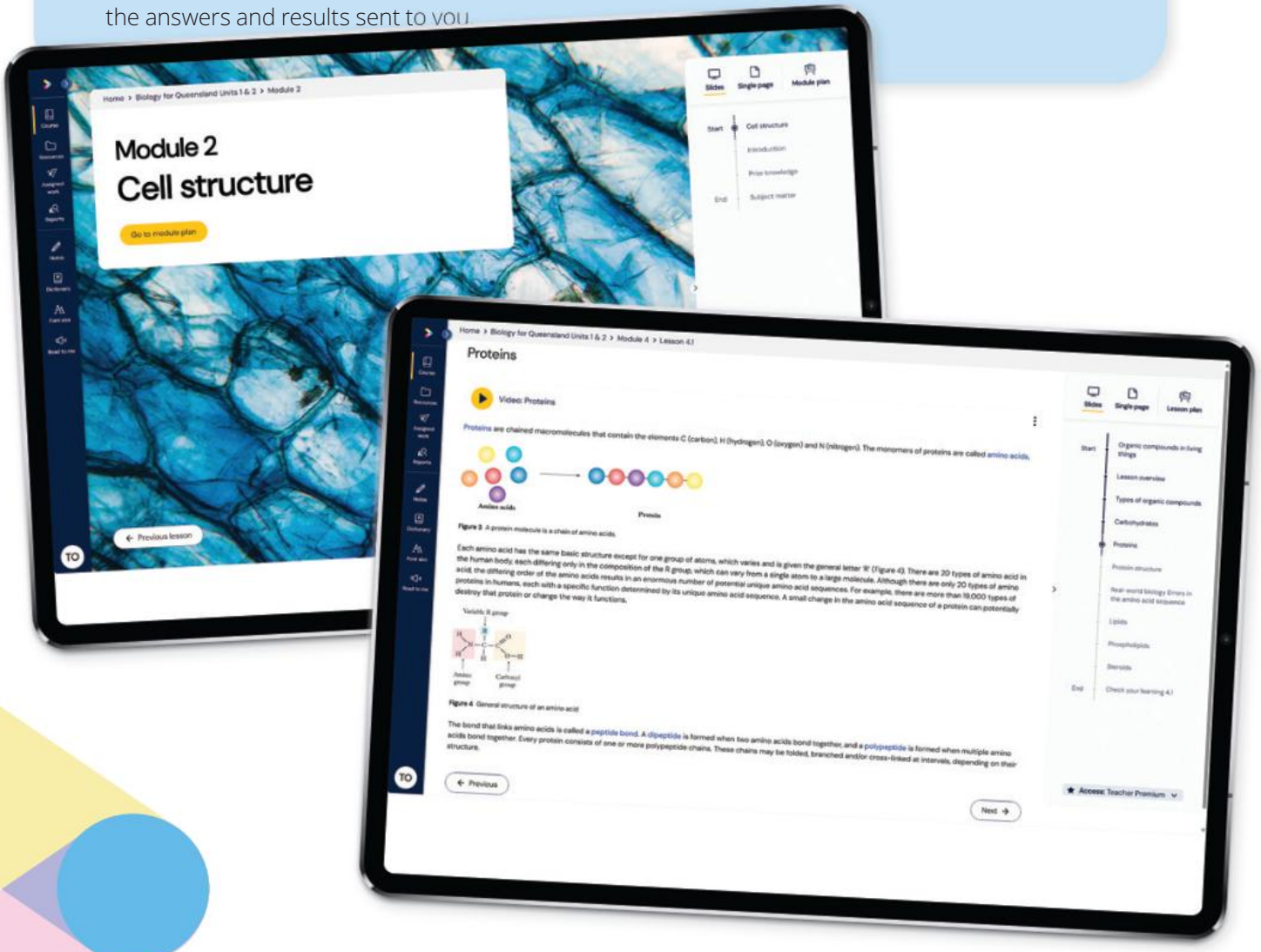

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Meet the authors & reviewers

Natalie Quinn

Author

Natalie Quinn began her career as a terrestrial ecologist before moving into secondary education and is now Head of Department (Science) for Education Queensland. She has completed a Master of Education, conducted scientific research, and has 11 years' experience teaching Biology, Chemistry, and Psychology in a variety of state and independent schools across Queensland. Natalie is the author of *Oxford Study Buddy for Biology* and is a QCAA Subject Matter Expert for Biology and Earth and Environmental Sciences.

Matthew Schmidt

Author

Matthew Schmidt has been teaching for 10 years, including senior Biology since 2018. Holding a Bachelor of Marine Studies and a Graduate Diploma of Education, his main areas of interests within biology are ecology and aquatic organisms. A passionate science teacher, Matthew has experience teaching 7–10 Science, Science in Practice and Aquatic Practices as well as senior Biology.

Jessica Brodbeck

Author

Jessica Brodbeck has been teaching senior Biology, Science, and Mathematics since 2018, and has been a Year Coordinator for six years, and acting Head of Mathematics and Science. She completed her Bachelor of Science, majoring in Immunology and Parasitology, before completing her Graduate Diploma in Education (Secondary). She implemented the 2019 Senior Syllabus within her school, and has since worked as a QCAA assessor, endorser, and confirmer since its introduction, as well as a senior Biology private tutor.

Tony Fraser

Reviewer

Tony Fraser is an accomplished educator with nearly three decades of experience in teaching, having served in various Catholic and independent schools on the Gold Coast and Brisbane. Over the past 15 years, he has held the position of Science Head of Department at three different Catholic colleges. Currently, Tony is the Science Curriculum Leader at Mt Maria College, Mitchelton. He has also contributed to the broader educational community as the Brisbane North Biology District Panel Chair and has been a QCAA assessor since the introduction of the new syllabuses in 2019.

Robyn Flexman

Reviewer

Robyn Flexman holds a Bachelor of Science in Biology. She has taught science and biology for over 20 years in various schools across Queensland, including five years as Head of Department. She has held positions with the QCAA, including Biology District Panel Chair and Biology State Panelist, and is currently an accredited assessor for Endorsement and External Assessments. Robyn was awarded the Peter Doherty Award for Excellence in Science Teaching.

Bernice Zaro

First Nations reviewer

Bernice is a proud Aboriginal and Torres Strait Islander Woman with a strong passion for educational greatness through culturally-inclusive learning. Bernice identifies with parents who are Traditionally connected to Aboriginal Communities of South East Queensland and Mer in Torres Strait Islands (Murray Island), and she is inspired to share and learn continuously. Bernice, and her husband Aicey Zaro, a recognised traditional artist, has been educating schools and communities through Cultural Awareness art workshops for more than 15 years during their time managing the Zaro Cultural Gallery in the Burdekin region. Bernice has a passion for learning through her ongoing studies in Community Development, Child Wellbeing, Cultural Diversity and also sharing personal experiences through family, community and business, which inspire her to take on new opportunities.

We would also like to acknowledge and thank Lorraine Huxley and Margaret Walter for their contributions.

MODULE 1

Biology toolkit

Introduction

Biology is the study of all living and once-living organisms on Earth. Biological description, observation and experimentation seek to make sense of the form, function, behaviour and processes of organisms. The great diversity of life on Earth across all kingdoms can be better understood and explained through application of the scientific method in experiments conducted in laboratories and in the field. A deep understanding and knowledge of biological concepts is essential to interpret results and explain interconnected theory and relationships. This module contains a toolkit of strategies and skills that can be used to successfully undertake examinations, and experimental and research assessment tasks.

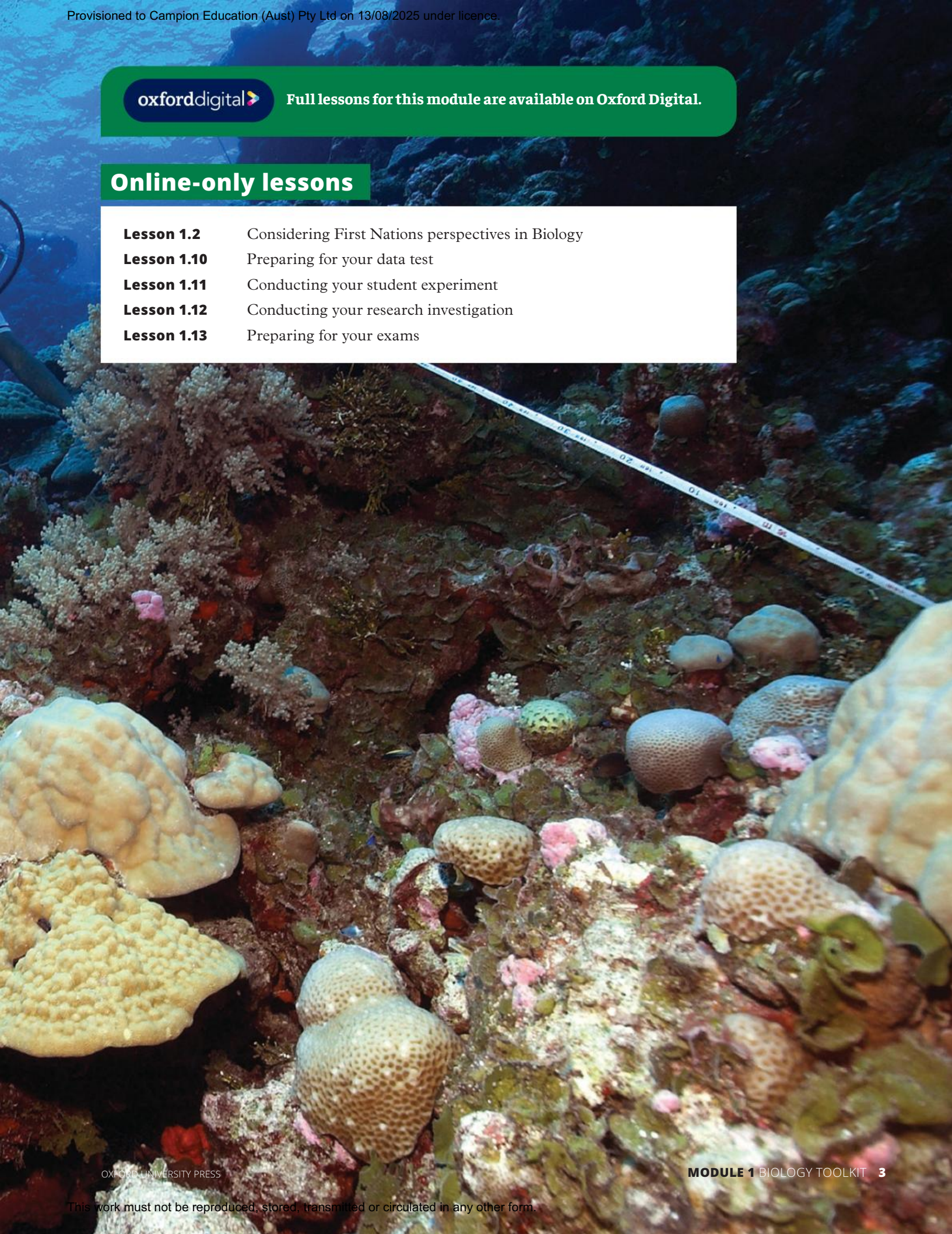
Prior knowledge

Prior knowledge quiz Check your understanding of science inquiry skills before you start.

oxforddigital **Full lessons for this module are available on Oxford Digital.**

Online-only lessons

Lesson 1.2	Considering First Nations perspectives in Biology
Lesson 1.10	Preparing for your data test
Lesson 1.11	Conducting your student experiment
Lesson 1.12	Conducting your research investigation
Lesson 1.13	Preparing for your exams



Lesson 1.1
Studying QCE Biology

Key ideas

- → Biology is the study of living organisms.
- → Studying Biology can lead to a diverse range of career pathways.
- → QCE Biology is divided into units and topics.
- → The science inquiry skills and their application are important for success in QCE Biology.

Learning intentions and success criteria

Rationale

Biology aims to develop students':

- sense of wonder and curiosity about life
- respect for all living things and the environment
- understanding of how biological systems interact and are interrelated, the flow of matter and energy through and between these systems, and the processes by which they persist and change
- understanding of major biological concepts, theories and models related to biological systems at all scales, from subcellular processes to ecosystem dynamics
- appreciation of how biological knowledge has developed over time and continues to develop; how scientists use biology in a wide range of applications; and how biological knowledge influences society in local, regional and global contexts
- ability to plan and carry out fieldwork, laboratory and other research investigations, including the collection and analysis of qualitative and quantitative data and the interpretation of evidence
- ability to use sound, evidence-based arguments creatively and analytically when evaluating claims and applying biological knowledge
- ability to communicate biological understanding, findings, arguments and conclusions using appropriate representations, modes and genres.

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024.

What is biology?

biology
the study of all living and once-living organisms on Earth

Biology is the study of living and once-living organisms. Biologists are concerned with the types of organisms that exist on Earth and how they operate individually, in interactions with other organisms and with their non-living environment. Biology is such a vast field of study that individual researchers tend to specialise in only a small aspect. Further specialisation occurs within each of these broad branches.

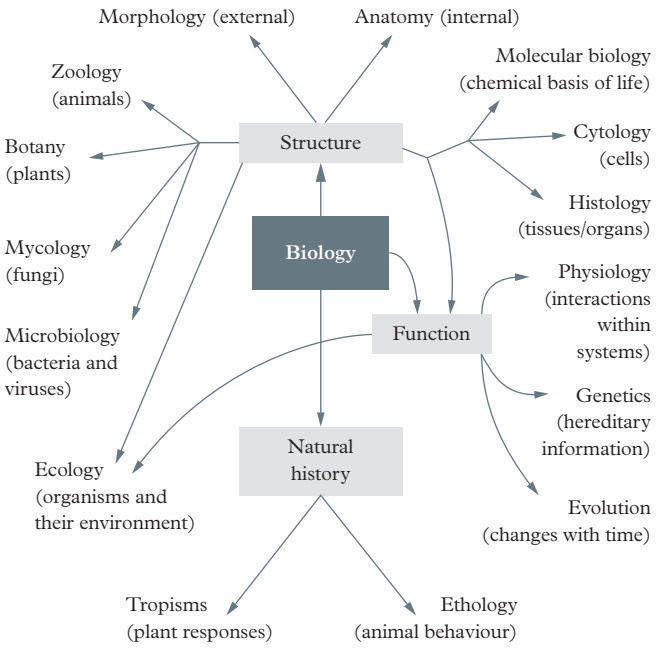


FIGURE 1 Major branches in the study of biology

Studying Biology can lead to a variety of career options in areas such as health sciences, environmental sciences and education. Health sciences cover a wide range of jobs including nursing, dentistry, medicine, pharmacy, physiotherapy, occupational therapy and veterinary science. Opportunities to work in environmental sciences include fields such as marine science, conservation, soil science, water quality, ecology, fisheries and agriculture. Many biologists work in research and education as lecturers, teachers and laboratory scientists.

FIGURE 2 Studying Biology can lead to careers in a range of fields, including (A) medicine, (B) ecology and (C) education.

Structure of the QCE Biology course

Studying QCE Biology provides you with the opportunity to engage in a range of inquiry tasks and develop science inquiry skills. You will develop an understanding of biodiversity and the interconnectedness of life as well as heredity and continuity of life.

The structure of the QCE Biology course is laid out in the Biology General Senior Syllabus. The course consists of four units. Units 1 and 2 are completed in the first year of the QCE Biology course and Units 3 and 4 in the second year. Each unit is divided into topics and each topic can include science understanding, science as a human endeavour and science inquiry subject matter. You should be familiar with these categories of understanding from your studies in years 7 to 10.

An overview of the QCE Biology units is shown in Figure 3, and Units 3 and 4 are summarised in Table 1.

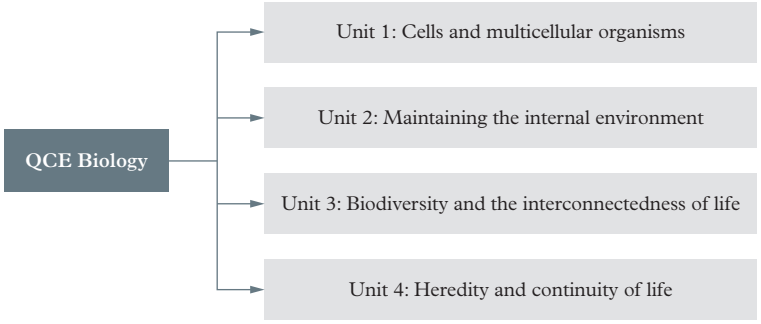


FIGURE 3 The structure of the QCE Biology course

FIGURE 4 Studying QCE Biology will provide you with the opportunity to develop your science inquiry skills.

TABLE 1 Topics in Units 3 and 4 Biology

Unit 3 Biodiversity and the interconnectedness of life	
Topic	**Description**
1. Biodiversity and populations	In this topic you will learn about: • genetic, species and ecosystem diversity • the biological species concept and its limitations • major taxa in the Linnaean system of biological classification and its use in classifying and naming species • identifying and classifying organisms using dichotomous keys • estimating population size using the Lincoln index • using species richness, evenness, percentage cover, percentage frequency, and Simpson's diversity index to measure diversity • sampling methods (random, systematic, stratified), sampling techniques (quadrats, line transects, belt-transects, capture-recapture) • strategies to minimise bias • abiotic and biotic factors that influence distribution and abundance of species in an ecosystem • how habitat influences distribution (uniform, random, clumped) of a species and, therefore, the reliability of sampling • interpreting experimental data to learn how abiotic factors affect the distribution, abundance and/or biodiversity of species in an ecosystem

Topic	Description
	• classifying and naming ecosystems using Specht's classification system and the Holdridge life zone classification scheme • different modes of population growth including exponential and logistic growth • reproductive strategies and growth curves of *K*- and *r*-strategists • calculating population growth rate and change using birth, death, immigration and emigration data.
2. Functioning ecosystems and succession	In this topic you will learn about: • the transfer and transformation of energy as it flows through the ecosystem • food chains, energy flow diagrams and ecological pyramids • transfer and transformation of matter (water, carbon, nitrogen) as it cycles through ecosystems • species interactions including predation, competition, mutualism, commensalism and parasitism • ecological niches and competitive exclusion • keystone species and the role they play in maintaining community structures • analysis of food webs and population data to identify keystone species, infer species interactions and predict outcomes of removing species from ecosystems • overexploitation, habitat destruction, monocultures and pollution, and how they affect community structure and ecosystem functioning • the effect of climate, biotic changes and abiotic changes on carrying capacity of an ecosystem • ecological succession, including primary and secondary succession • pioneer species and the features that make them effective colonisers • successional change in ecosystems • comparing ecosystems across spatial and temporal scales.

Unit 4 Heredity and continuity of life	
Topic	**Description**
1. Genetics and heredity	In this topic you will learn about: • the structure and function of DNA, genes and chromosomes in prokaryotes and eukaryotes • DNA replication • how errors in DNA replication and damage to DNA can lead to frameshift mutations • meiosis (crossing over, independent assortment, random fertilisation) • how errors in meiosis can cause chromosomal abnormalities • genetic disorders in human karyotypes identified through ploidy changes • protein synthesis (transcription and translation) • the effect of point and frameshift mutations on polypeptides using the genetic code • how gene expression is regulated in response to environmental signals and how these allow for cell differentiation • how HOX transcription factors regulate morphology • dominant, recessive, autosomal, sex-linked, polygenic and multiple allele inheritance • patterns of inheritance and using histograms, pedigrees and Punnett squares to predict genotypes and phenotypes • recombinant DNA and restriction enzymes • PCR and gel electrophoresis • interpreting DNA profiles.

Topic	Description
2. Continuity of life on Earth	In this topic you will learn about: • microevolution and macroevolution • mutation, gene flow and genetic drift as processes of microevolutionary change • natural selection (stabilising, directional, disruptive) • how to calculate allele frequencies from genotype data • divergent, convergent, parallel evolution and coevolution • allopatric, sympatric and parapatric speciation • why populations with reduced genetic diversity face increased risk of extinction • comparative genomics • cladograms, phylograms and molecular sequencing as tools for inferring species relatedness • evolutionary radiation and mass extinctions.

Source: Adapted from *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Assessment in QCE Biology

In Units 3 and 4, schools develop three assessments using the assessment specifications and conditions provided by the syllabus.

Many schools assess students studying Units 1 and 2 as they would students studying Units 3 and 4. This means that you will likely have completed assessment in the same format required of you this year.

TABLE 2 Units 3 and 4 assessments

Unit and assessment type	Assessment description	Assessment objectives
Unit 3 Biodiversity and the interconnectedness of life: Data test	Students respond to items using qualitative data and/or quantitative data derived from practicals, activities or case studies from Unit 3.	• Apply understanding of concepts in Unit 3 to given algebraic, visual or graphical representations of scientific relationships and data to determine unknown scientific quantities or features • Analyse data about concepts in Unit 3 to identify trends, patterns, relationships, limitations or uncertainty in data sets • Interpret evidence about concepts in Unit 3 to draw conclusions based on analysis of data sets
Unit 3 Biodiversity and the interconnectedness of life: Student experiment	Students modify (i.e. refine, extend or redirect) an experiment relevant to Unit 3 subject matter to address their own research question.	• Describe ideas and experimental findings about subject matter in Unit 3 • Apply understanding of subject matter in Unit 3 to modify experimental methodologies and process data • Analyse experimental data about subject matter in Unit 3 • Interpret experimental evidence about subject matter in Unit 3 • Evaluate experimental processes and conclusions about subject matter in Unit 3 • Investigate phenomena associated with subject matter in Unit 3

Unit and assessment type	Assessment description	Assessment objectives
Unit 4 Heredity and continuity of life: Research investigation	Students gather evidence related to a research question to evaluate a claim relevant to Unit 4 subject matter. This assessment provides opportunities to assess science inquiry skills and science as a human endeavour (SHE) subject matter.	• Describe ideas and findings about subject matter in Unit 4 • Apply understanding of subject matter in Unit 4 to develop research questions • Analyse research data about subject matter in Unit 4 • Interpret research evidence about subject matter in Unit 4 • Evaluate research processes, claims and conclusions about subject matter in Unit 4 • Investigate phenomena associated with subject matter in Unit 4
Units 3 and 4 external examination	An examination that consists of two papers. Each paper consists of a number of questions related to Units 3 and 4.	• Describe ideas and findings about subject matter from Units 3 and 4. • Apply understanding of subject matter from Units 3 and 4. • Analyse data about subject matter from Units 3 and 4. • Interpret evidence about subject matter from Units 3 and 4.

Source: Adapted from *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

You can use Lesson 1.10 Preparing for your data test, Lesson 1.11 Conducting your student experiment, Lesson 1.12 Conducting your research investigation and Lesson 1.13 Preparing for your exams to guide you through these assessments. Note that Science as a human endeavour content will not be directly assessed in your examinations.

Science inquiry skills

In addition to developing your science understanding in Biology (which will be covered in Modules 2 to 13), the QCE course requires you to develop and apply a range of science inquiry skills. These skills are specified in the QCE Biology General Senior Syllabus and are listed at the beginning of each lesson in this module. This module will help you develop these skills.

The science inquiry skills are applicable to all areas of study in Units 1 to 4 of the QCE Biology course. They are especially important for preparing and planning for your data test, student experiment and research investigation assessment tasks.

Check your learning 1.1

Check your learning 1.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the term "biology". (1 mark)

2 **Identify** three careers that are possible after studying Biology. (3 marks)

Analytical processes

3 **Distinguish** between the data test, the student experiment and the research investigation. (3 marks)

Lesson 1.2
Considering First Nations perspectives in Biology

Key ideas

→ First Nations peoples are the traditional custodians of the land we now know as Australia.

→ First Nations peoples have longstanding scientific knowledge.

→ Correctly acknowledging cultural and/or language groups, rejecting deficit discourse, avoiding Eurocentrism and critically evaluating sources of information can help you to respectfully engage with First Nations perspectives in QCE Biology.

Learning intentions and success criteria

Science inquiry skills

This lesson provides support for the following science inquiry skills:

- identify and implement strategies to manage risks, ethics and environmental impact, e.g.
  - cultural guidelines, protocols for working with the knowledges of First Nations peoples.

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Lesson 1.3
Understanding the scientific method

Key ideas

→ A hypothesis is a statement that attempts to answer a question raised by observations and can be tested by experimentation.

→ The scientific method is a way of testing a hypothesis through controlled experimentation.

Learning intentions and success criteria

Science inquiry skills

This lesson provides support for the following science inquiry skills:

- identify, research and construct questions for investigation.
- propose hypotheses and/or predict possible outcomes.

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

The scientific method

Biology is classified as a natural science. The word "science" is derived from Latin and means *to know*. Therefore the study of biology is an attempt to understand the natural world, of which we are part. All investigations begin with observations, such as:

The leaf is green.

which lead to questions, such as:

Why is the leaf green?

and seeking answers.

Like other disciplines, such as philosophy and art, science has its own method to verify the answer to the question. This is called the **scientific method**.

The basis of science is accurate observations, which are recorded as data. For example:

Dewdrop spiders are found in the webs of golden orb spiders. Orb spiders kill and ingest the body contents of living things trapped in their webs. The silk of golden orb spiders is particularly thick and strong. Golden orb spiders are large. Dewdrop spiders are very small.

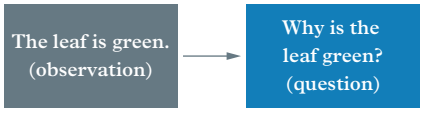


FIGURE 1 Observations lead to questions.

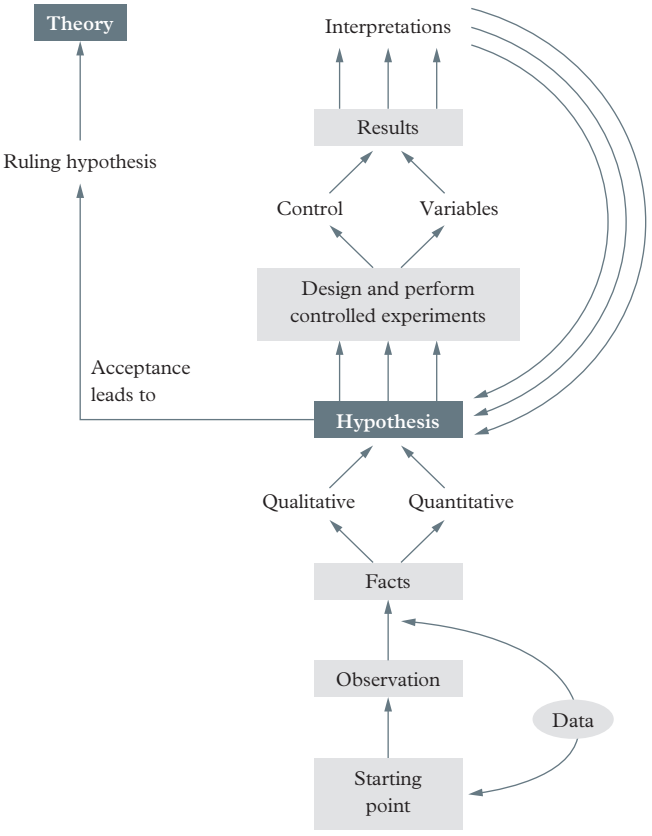


FIGURE 2 Steps in the scientific method

scientific method the testing of hypotheses by controlled experimentation

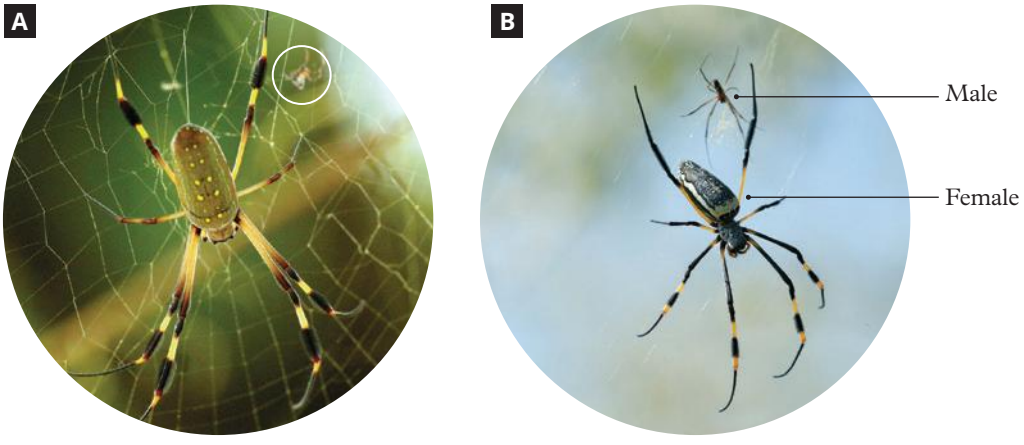


FIGURE 3 (A) A golden orb spider and a dewdrop spider share a web. (B) Male and female golden orb spiders

data
quantitative or qualitative information; facts and statistics

qualitative
descriptive

quantitative
measured

fact
information that has been verified by observation or experimentation

Data may be **qualitative** (descriptive) or **quantitative** (measured and represented by a numerical unit). After repeated observations have been verified, preferably by different people, an observation becomes accepted as **fact**. Observations usually need to be interpreted (logical reasoning), and this leads to question-asking.

TABLE 1 Types of data

Data	Definition	Example
Quantitative	Numerical (measured)	Leaf length
Qualitative	Descriptive (describes a characteristic)	Leaf colour
Objective	Measured according to an identified criterion	Leaf colour using defined special charts, reproducible by others
Subjective	Based on a researcher's opinion	Leaf colour based on researcher's judgement

Questions and hypotheses

Asking the right question is a key step in the scientific method. For example:

> Are dewdrop spiders too small for the golden orb spider to detect? If spiders larger than dewdrop spiders are placed in the webs of golden orb spiders, will they be captured?

The essential requirement for the right question is that it is testable. *Why* and *how* questions cannot be tested; *what if* questions can. Questions lead to hypotheses.

hypothesis
a statement that attempts to answer questions raised by observations and can be tested by experimentation

The **hypothesis** is a statement that attempts to answer the question(s) raised from observation(s). This explanation is then tested by experimentation. For example:

> It is hypothesised that the introduction of spiders slightly larger than the dewdrop spider to golden orb webs in the D'Aguilar Forest Park, during the spring–summer season of 2024, will result in their being captured and eaten by the golden orb spider.

This detailed hypothesis:

- sets limits on the problem to be solved, by specifying
  - the species under study
  - the area involved
  - the effects to be studied
  - the time period over which the question is to be investigated
- points the way to the solution of the question
- leads to the prediction of new information.

alternative hypothesis
a hypothesis that predicts an effect or relationship between variables

null hypothesis
a hypothesis that predicts no effect or no relationship between variables

This hypothesis predicts that the independent variable will affect the dependent variable in some way – this type of hypothesis is known as an **alternative hypothesis**. A **null hypothesis** predicts that the independent variable will have no effect on the dependent variable – it contradicts the alternative hypothesis. In this case, the null hypothesis would be:

> It is hypothesised that the introduction of spiders slightly larger than the dewdrop spider to golden orb webs in the D'Aguilar Forest Park, during the spring–summer season of 2024, will not result in their being captured and eaten by the golden orb spider.

working hypothesis
the most successful hypothesis of a particular investigation

The scientific method is unique in that it tests hypotheses by experimentation. If the experimental evidence for the proposed hypothesis is not supported by the evidence, or if it is inconclusive (there is no clear evidence either for or against), then further hypotheses are suggested. The hypothesis that has the most reproducible evidence is termed the **working hypothesis**.

When an experiment compares the results of two parallel tests that are identical in all but one respect, this is known as a **controlled experiment**. It provides a standard of comparison – a basis for assessing the outcomes of experimental tests. In an **experimental test**, the variation, or **experimental variable**, is altered in a way that is known by the experimenter. Only one variable is changed at a time. Therefore, a different experimental group is set up for each variable to be tested. It is assumed that the changes in the variable factor are the cause of any new effects observed in the experimental test.

controlled experiment
an experiment in which a control group or standard acts as a reference for the experimental group, in which only one variable is different from that in the control group

experimental test
an experiment in which a single variable is compared with that of a control group

experimental variable
the single factor under investigation in a controlled experiment; also known as an independent variable

Variables

A variable is a quantity or quality that can be different at different times or places. Each experiment has two variables: the **independent variable** (IV) is deliberately changed by the researcher; the **dependent variable** (DV) is the property that is measured in response to the changes in the IV (i.e. the changes observed in the DV *depend* on the deliberately altered condition of the experiment). **Controlled variables** are variables that have been kept consistent to ensure that any change to the DV can be solely attributed to the changes in the IV. For example, if a researcher was testing the effect of a fertiliser on plant growth, the IV would be treatment with fertiliser, the DV would be plant growth measured in centimetres, and the controlled variables would include plant pot size, soil type, exposure to light, and amount of water given to each plant.

independent variable
the variable that is changed or controlled in a scientific experiment

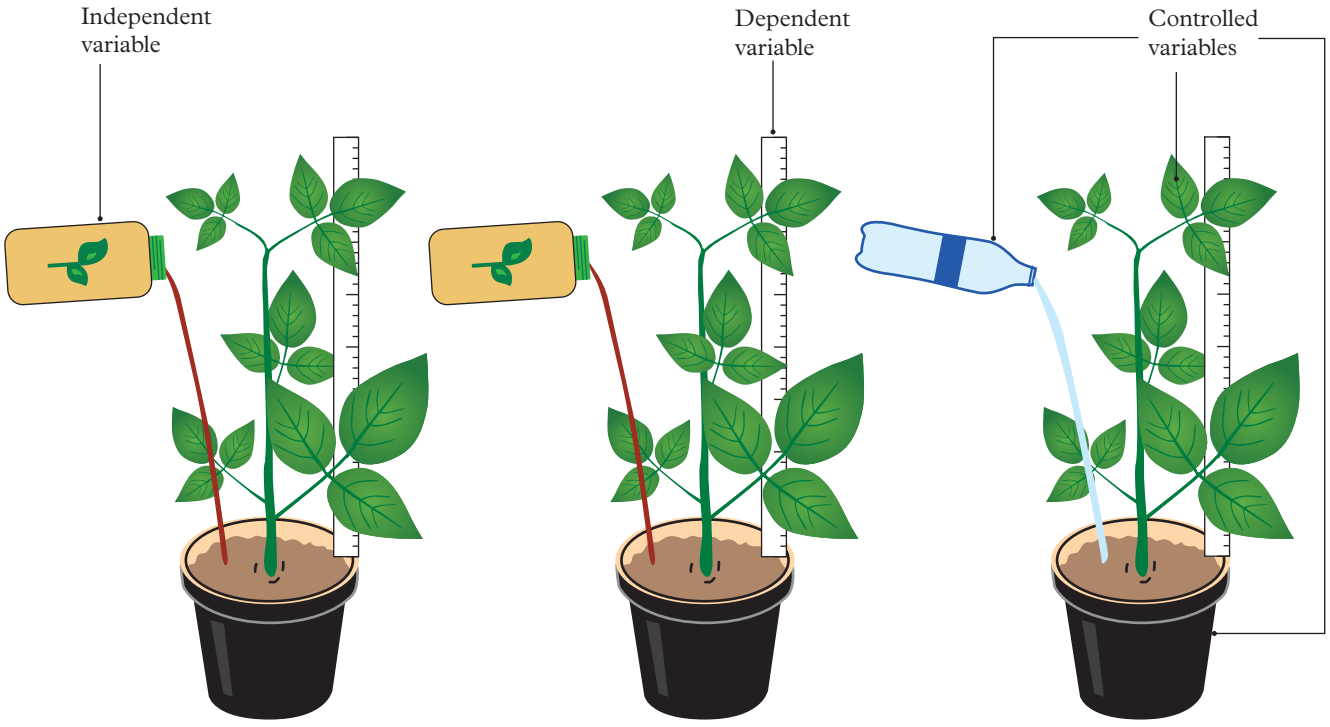


FIGURE 4 When testing the effect of fertiliser on plant growth, the IV would be treatment with fertiliser, the DV would be plant growth, and the controlled variables would include plant pot size, soil type, exposure to light and amount of water given.

dependent variable
a variable whose value is dependent on another variable

controlled variable
a variable that is kept constant by the experimenter to negate any effects it may have on the dependent variable

Development of theories

scientific law
a scientific theory that has been continually upheld by experimentation; a statement based on repeated experimental observations

prediction
forecast of a future event based on similar known events

scientific theory
a well-substantiated explanation of some aspect of the natural world, based on a body of facts that have been repeatedly confirmed through observation and experiment

Repetition of the sequence (observation – hypothesis – experiment) in a number of situations gradually allows broad generalisations to be made. It is important, therefore, that scientists report the details of their experiments fully, so that others can repeat them and validate their findings. These accumulated generalisations enable a **scientific law** to be developed – this law describes the supported observations that have been made, but it does not explain why or how they occur. The scientific law can be used to make **predictions** (or forecasts) about an *unknown*. A **scientific theory** provides an explanation for the observed, reproducible scientific law. In science, theories are never considered absolute, because further discoveries can lead to more accurate ways of observing, testing or interpreting information.

This account of the steps in the scientific method is not a rigid formula. Other factors can play a role in scientific discoveries. Accident, assumptions, prejudice and emotions all play a part in science and should not be overlooked. The fact remains, however, that science is a logical method of considering problems, following a pattern of reasoning characterised by observation, questions, formation of hypotheses, controlled experiments and prediction.

Check your learning 1.3

Check your learning 1.3: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Explain** why scientists prefer not to use the word "prove". (1 mark)
2 **Define** the term "controlled variable". (1 mark)
3 **Define** the terms "hypothesis", "working hypothesis" and "theory". (3 marks)

Analytical processes

4 **Contrast** quantitative and qualitative data. (1 mark)
5 **Distinguish** between a scientific theory and a scientific law. (1 mark)

Knowledge utilisation

6 **Design** a simple concept map that explains the scientific method. (3 marks)
7 **Design** an experiment to test a whether a plant grows best in no sunlight, partial sunlight or direct sunlight. (4 marks)
8 **Generate** an alternative hypothesis and null hypothesis for each of the following scenarios.
   a A researcher is investigating whether a brand of handwash is effective in killing a bacterial species. (2 marks)
   b A researcher is investigating whether an increase in temperature will increase the rate of a reaction. (2 marks)

Lesson 1.4
Planning investigations

Key ideas

→ Primary data is data you collect yourself; secondary data is data collected by someone else.

→ There are many types of investigations you can run to collect data.

Science inquiry skills

Learning intentions and success criteria

This lesson provides support for the following science inquiry skills:

- design investigations, including the procedure/s to be followed, the materials required, and the type and amount of primary and/or secondary data required to obtain valid and reliable evidence, e.g.
  - distinguish between different types of investigations: descriptive, comparative, correlational, experimental, case studies
  - consider replicates, sample size, number of data points and quality of sources
  - identify the types of errors, extraneous variables or confounding factors that are likely to influence results and implement strategies to minimise systematic and random error.

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Investigation types

There are many types of investigations that can be used to answer a research question. You might run an investigation that generates **primary data**, which is data you collect yourself. Or your investigation might use **secondary data**, which is data that has been collected by someone else. Regardless of whether you are working with primary or secondary data, it is important to document all the steps you take in your investigation and all the materials and sources you use to help answer your research question. The procedures and materials you use will vary according to the type of investigation you run.

primary data
data collected by the researcher from their own experiment designed to answer the specific research question

secondary data
secondhand data obtained from other sources

Certain investigation types are better suited to address specific types of research and research questions. In QCE Biology you can run a range of investigations, including:

- descriptive investigations
- comparative investigations
- correlational investigations
- experimental investigations
- case studies.

Descriptive investigations

descriptive investigation
an investigation that aims to describe the characteristics of a phenomenon

A **descriptive investigation** is one that collects qualitative and/or quantitative information that can be used to help describe a phenomenon. Descriptive investigations do not address research questions that focus on "why" something occurs; rather, they help address questions that focus on "what" something is. For example, "What is the average length of a diamond python?" or "What happens to a dried eucalyptus leaf when it is burnt?" These investigations provide information that can be used to help better understand a variable of interest. A hypothesis is not required for this type of investigation.

FIGURE 1 Descriptive investigations help address questions that focus on "what" something is. For example, "What is the average length of a diamond python?"

Comparative investigations

comparative investigation
an investigation that compares two or more conditions to identify similarities and/or differences

correlational investigation
an investigation that is run to determine whether a statistical relationship exists between two variables

correlation
the relationship between two variables

causation
a cause–effect relationship in which a change in one variable directly results in change in another variable

A **comparative investigation** involves collecting data on different factors (e.g. organisms, objects, traits) under different conditions to identify similarities and/or differences. For example, "Which species of birds perform courtship dances?" or "Which bacterial species are able to survive without oxygen?" Comparative investigations are often conducted by collecting data from natural settings; however, in some instances a researcher may need to manipulate conditions to draw comparisons between the variables of interest. A control group is typically not included.

Correlational investigations

A **correlational investigation** is one that investigates whether a relationship exists between two variables without the researcher manipulating variables. For example, a researcher may be interested to see if there is a relationship between shoe size and height. They collect data on the heights of people and their shoe size, then plot each data point to determine whether a trend exists. You will learn more about how to plot data for correlational investigations in Lesson 1.7. It is important to note that, even if a relationship is shown between two variables (**correlation**), this does not establish whether one variable is causing the change in the other variable (**causation**).

Experimental investigations

An **experimental investigation** is one that determines whether a cause-and-effect relationship exists between two variables. There is always at least one independent variable, a dependent variable and a control. For example, consider a researcher investigating the effect of a nitrogen-rich fertiliser (independent variable) on the growth rate (dependent variable) of a tomato plant. Their research question is, "Does nitrogen-rich soil affect the growth rate of tomato plants?" The researcher sets up two conditions of the experiment: one plant that grows in standard potting mix (the control), and one plant that grows in potting mix that has the nitrogen-rich fertiliser added. All variables apart from the independent variable are kept constant and the growth of both plants is measured regularly. Due to the experimental set-up, if the researcher finds that the nitrogen-rich plant grew taller and faster, they can attribute this change to the independent variable alone and thereby establish a causal relationship between the nitrogen fertiliser and plant growth.

experimental investigation
an investigation that involves manipulating one or more variables to determine whether this results in a change in another variable

FIGURE 2 Testing the effect of a nitrogen-rich fertiliser on tomato plant growth is an example of an experimental investigation.

Case studies

A **case study** is an investigation that analyses a specific individual, group or event in detail to explore or better understand a biological concept. This type of investigation often focuses on better understanding "why", "what" or "how" something occurs. It can involve the collection of qualitative and/or quantitative data through observations, interviews or literature review. Data is collected, analysed and interpreted to identify patterns, similarities or mechanisms about the research subject. This often includes comparing data from the case study against the scientific literature or other similar case studies. An example of a case study in biology would be investigating the occurrence of a rare gene mutation in an individual.

case study
a detailed investigation that focuses on a specific individual, group or occurrence to better understand it

Designing valid and reliable investigations

When designing your investigation, it is important that you take measures to ensure your results are truly representative of what you intended to investigate, and that your results are sound enough to address your research question. Two concepts to consider when designing investigations are validity and reliability.

Validity

A good experiment is one that has been designed to produce useful information clearly related to the hypothesis and typical of the species under investigation. **Validity** is a measure of how appropriately an investigation has measured what it set out to measure. If the experiment provides data that refers directly to the hypothesis, then it is considered a valid experiment. For example, an experiment that tests whether eating chocolate causes an increased number of pimples would not be valid unless all other food choices, exercise programs and face-cleaning regimens were also controlled.

validity
the extent to which a test measures what was intended

Reliability

An investigation must be repeated many times to ensure that the results are not due to chance. This is particularly important when using living organisms in investigations, because some individuals may respond to the experimental variable on the basis of their individual characteristics rather than those of the species. **Reliability** is the degree to which a measurement, test or investigation produces consistent results over multiple trials. It is based on the concepts of **repeatability** and **reproducibility**. Repeatability refers to the ability of the same scientist to obtain the same results with the same equipment. Reproducibility relates to whether a different scientist would be able to obtain the same results with different equipment.

reliability
the extent to which a measurement, test or investigation produces consistent results

repeatability
the extent to which the same results can be produced by a researcher when the experiment is performed again under the same conditions

reproducibility
the degree to which the same results can be generated by other researchers using different equipment and methods in different laboratory settings

FIGURE 3 Reliable investigations produce consistent results.

Factors that can influence validity and reliability

Many factors can influence how valid and/or reliable your investigation is. These factors include:

- number of replicates
- sample size
- number of data points
- quality of sources
- errors
- extraneous variables and confounding factors.

Number of replicates

A **replicate** is a repeated observation or measurement in an investigation used to improve the consistency and reliability of the results. There are two main types of replicates:

- biological replicates, which involve testing multiple biological samples (e.g. different individuals, bacterial cultures) under identical investigation conditions to make sure that the results generated are not specific to one individual, subject or sample
- technical replicates, which involve performing the same measurement or investigation on the same sample multiple times, to account for variance in measurements or procedures.

replicate
a result obtained by repeating a measurement using the same methodology, conditions and materials

Increasing the number of replicates helps to ensure that the results generated are not due to random chance. This increases the validity of the investigation, as there is more confidence that the results obtained can be attributed to the phenomenon being tested. If an investigation lacks replicates, its results may be skewed due to outliers or random events. Increasing the number of replicates can also increase the reliability of an investigation by providing consistent results across repeated trials.

Sample size

A **sample** is the number of subjects (e.g. individuals, specimens) tested in an investigation. It is a subset of the population you wish to draw conclusions about. Larger sample sizes tend to provide more accurate and generalisable results, because they reduce the influence of random variations between subjects, which would affect the results. This helps to ensure that the results obtained reflect the phenomenon tested and are therefore valid. Large sample sizes also increase the reliability of an investigation's results by reducing the margin of error and generating more consistent results. If a sample size is too small, the investigation may not be valid due to the results not accurately reflecting the population studied, and it may not be reliable due to the higher chance of variability between subjects affecting the results.

sample
a subset of the population of interest in a study

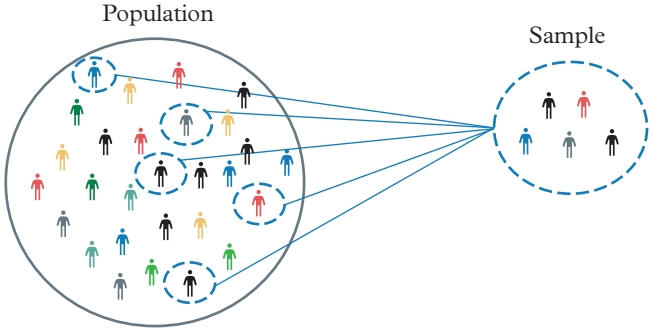

FIGURE 4 A sample is a subset of the population.

Number of data points

The number of data points used in an investigation can also affect the validity and reliability of the results. Using a larger number of data points can generate a clearer picture or representation of the phenomenon being investigated, increasing the validity of the results. For example, if you wanted to investigate the concentration of antibodies produced by an individual over 60 days but only took measurements on five of those 60 days, your graph would not provide as clear a picture as it would have if you had taken measurements each day for 60 days. Including a larger number of data points can also increase an investigation's reliability, because it improves the accuracy of the statistical analysis, reducing the effect of outliers on the results.

Quality of sources

Not all sources of information are equal. The quality of information or data used to inform or complete an investigation can affect the investigation's validity and reliability. High-quality sources will provide accurate, credible and relevant information or data about a phenomenon. Examples of high-quality sources are peer-reviewed scientific literature, textbooks, and information from

FIGURE 5 Scientific journals are a credible source of information.

trusted databases or organisations. Low-quality sources may introduce bias or unjustified claims.

Using high-quality sources to inform an investigation can improve the investigation's validity by ensuring that the methods used, the interpretations of the results and the conclusions drawn are representative of the phenomenon that has been investigated. Low-quality sources can lead to invalid conclusions being drawn about the phenomenon investigated. High-quality sources are also likely to provide more consistent and trustworthy data, increasing the reliability of the investigation. Low-quality sources may introduce inconsistencies and errors to the data, reducing its reliability.

Extraneous variables and confounding factors

extraneous variable
a variable other than the independent variable that may cause changes in the value of the dependent variable

An **extraneous variable** is any variable, other than the independent variable (IV), that may cause a change in the dependent variable. For example, when testing the effects of a fertiliser (IV) on plant growth, the researcher might not have grown all plants in the same temperature conditions. Because plants are sensitive to temperature, the results could be influenced by the varying temperatures in which the plants were grown. If the experimenter has not taken this into account, an incorrect conclusion could be drawn. Care must therefore be taken to work out all possible extraneous variables. An extraneous variable that is controlled for becomes a controlled variable.

If extraneous variables are not controlled, it is difficult to determine whether the changes in the dependent variable can be attributed to the independent variable. This can threaten the validity of the investigation. Extraneous variables can also cause variation in the results, making the results less consistent across repeated trials. This means the investigation's results are less reliable, because it might be impossible to reproduce them in similar experimental conditions.

confounding factor
an uncontrolled variable that has a systematic effect on the value of the dependent variable; if a confounding variable exists, no valid conclusions about the research can be drawn

A **confounding factor** is a variable, other than the independent variable, that has affected the dependent variable. This effect on the dependent variable confounds (confuses) the relationship between the independent variable and the dependent variable. A confounding factor might be an extraneous variable that has not been controlled for, or it could be a type of variable that cannot be controlled for. Additionally, some confounding factors may affect both the independent variable and the dependent variable, confusing the relationship between the two variables. Confounding factors reduce the reliability of an investigation by introducing invalid conclusions. The investigation's results are likely to vary due to the presence of the confounding factor, making it difficult to reproduce the results.

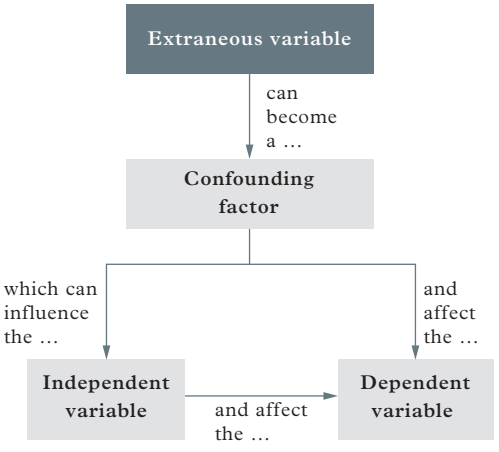

FIGURE 6 Summary of how extraneous variables and confounding factors can affect an investigation's results

Errors

An error is the difference between a measured value and the **true value** (the value of something if it was measured perfectly) of what is being measured. There are two main types of errors:

- **systematic error**
- **random error**.

true value
the value of a measurement if it were measured perfectly

systematic error
an error that causes readings to deviate from the true value by a consistent amount and in the same direction each time a measurement is made; it is affected by the accuracy of the measurement process

random error
an error due to the limitations (uncertainty) of the measurement equipment, and the uncontrollable effects of the method and the environment on the measurement

A systematic error is an error that is consistent and repeatable. It could be caused by faulty equipment or by using a measuring instrument that has not been calibrated. Systematic errors cause readings to differ from the true value in a consistent way. This means repeating the investigation will not reduce the systematic error. For example, if a weighing scale is not calibrated and measures 0.0 g as 0.02 g each time the scale is used, it will always cause the true value of what is being measured to vary by 0.02 g. Systematic error can be reduced by carefully considering and conducting the investigation method and by calibrating the equipment to be used. Systematic errors reduce the validity of the results, because the results deviate from the true value of what is being measured. Reliability is also reduced, because the deviance in results means the same results are less likely to be generated under similar conditions in another laboratory setting.

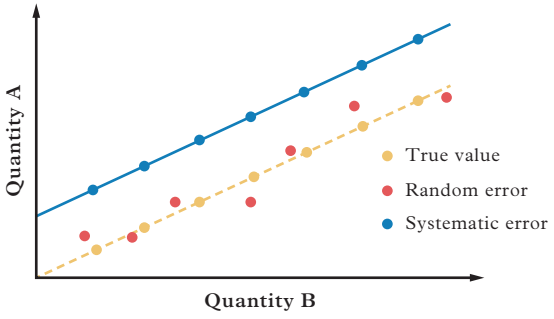

FIGURE 7 Representation of how random error and systematic error can affect results. Systematic error affects the accuracy of results; random error affects precision.

Random errors are errors that are unpredictable. They are caused by factors that vary from one measurement to another. For example, consider a researcher observing the number of times an animal exhibits a specific behaviour in a set time period. If the researcher drops their pencil and misses seeing a behaviour while picking up their pencil, this measurement has been affected by random error. Repeating measurements, trials and averaging results can reduce random error. Many students describe random errors as "human error". However, human error is a less scientific term and so "random error" should always be used.

Uncertainty

Uncertainty describes the degree to which you are unsure of the true value of a measurement. Uncertainty can arise from limitations in the equipment, lack of information or understanding about a phenomenon, or from the variability of different systems. For example, the thermometer shown in Figure 8 has a scale that increases in 1°C increments. The reading on this thermometer sits between 22°C and 21°C, and there are no smaller increments on the scale to discern exactly where the reading falls between these two numbers. Therefore, there is a degree of uncertainty in this measurement. The uncertainty of a measuring instrument is estimated to be plus or minus (±) half the smallest unit that the measuring instrument increases by. A thermometer with units that increase by 1°C would have an uncertainty of (±) 0.5°C. Therefore, the reading on the thermometer in Figure 8 can be recorded as 22°C (±) 0.5°C.

uncertainty
the degree to which the result of a measurement does not reflect the exact (true) value of what is being measured

FIGURE 8 Due to the limitations of the thermometer, there is a level of uncertainty with each reading.

Check your learning 1.4

Check your learning 1.4: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** the purpose of the following investigation types:
   - **a** comparative investigation (1 mark)
   - **b** case study (1 mark)
   - **c** descriptive investigation. (1 mark)

2 **Define** the following terms:
   - **a** reliability (1 mark)
   - **b** validity. (1 mark)

3 **Describe** what is meant by "extraneous variable". (1 mark)

4 **Explain** how small sample size can affect the reliability and validity of results. (1 mark)

5 The scale on a ruler increases in 1 mm increments. **Determine** the uncertainty of a reading of 13 mm. (1 mark)

Analytical processes

6 **Compare** correlational investigations and experimental investigations. (2 marks)

7 **Contrast** systematic error and random error. (1 mark)

Lesson 1.5
Considering safety and ethics

Key ideas

→ Before conducting research, scientists must consider whether the investigation is safe and ethical, and the potential impacts it might have on the environment.

Learning intentions and success criteria

Science inquiry skills

This lesson provides support for the following science inquiry skills:

- identify and implement strategies to manage risks, ethics and environmental impact, e.g.
  - ethical guidelines
  - material safety data sheets
  - workplace health and safety guidelines
  - appropriate disposal methods
  - standard operating procedures
  - acknowledgment of sources and referencing.

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Managing risks, ethics and environmental impact

Before conducting an investigation, scientists must consider whether the investigation is safe and ethical, and the potential impact it might have on the environment. If any safety, ethical

or environmental concerns are identified, it is the responsibility of the scientist to modify their investigation to reach a standard that would be accepted by an ethics committee. Strategies used to manage potential safety, ethical and environmental risks include:

- adhering to ethical guidelines
- using material safety data sheets
- following workplace health and safety guidelines
- using appropriate disposal methods
- following standard operating procedures
- correctly acknowledging sources and referencing.

Ethical guidelines

Investigations should not be conducted on vertebrate animals (including humans) without first submitting a full report on the experimental procedure to the bioethics committee in the area for approval. The guidelines for animal experimentation are extremely strict, to ensure the wellbeing of the animals. If humans are participants in an experiment, each participant needs to be given a form outlining the exact procedures to be undertaken, the established means of confidentiality (e.g. no names recorded) and the safety measures in place. Each participant (or their guardian if they are under 18 years old) needs to sign a consent form. No pressure (peer or personal relationship) should be placed on an individual to participate. School students should not undertake experimental investigations using human subjects.

FIGURE 1 Guidelines for experimentation using animals are extremely strict, to ensure the wellbeing of the animals.

Safety data sheets

A safety data sheet (SDS) is a document that provides detailed information on a specific chemical and its properties. It also includes potential hazards caused by use of the chemical, and safety precautions required when working with or handling the chemical. Safety data sheets are used to inform risk assessments for investigations. They can be accessed easily on the internet.

Workplace health and safety guidelines

Workplace health and safety guidelines are rules developed by governments to ensure that workers, including scientists, are working in conditions that protect them from injury, illness and accidents. They can include instructions for using equipment, handling various materials, personal protective equipment (PPE) that should be worn and how to manage emergencies to maintain safe working conditions.

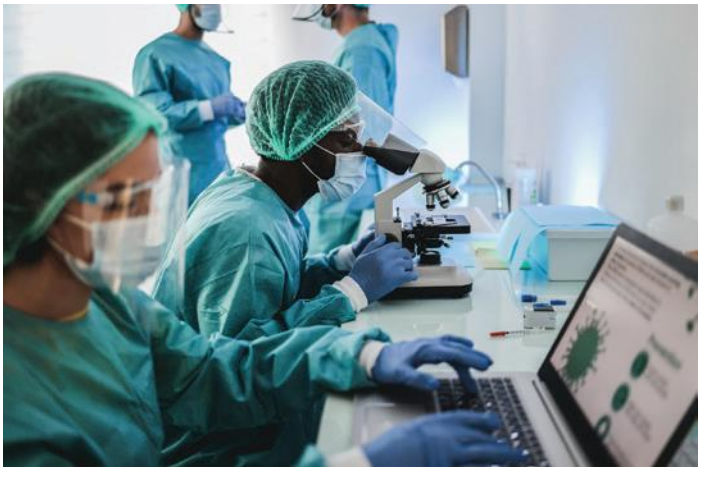

FIGURE 2 Workplace health and safety guidelines can include instructions and information on the type of PPE that must be worn when working.

Appropriate disposal methods

Some materials can be hazardous to different species, particularly if they are not disposed of correctly. Using the appropriate disposal method for a substance can reduce environmental

contamination and potential health risks. This includes disposing of hazardous materials, recycling, and following rules for waste management. Table 1 lists safe disposal methods for various materials.

TABLE 1 Safe disposal methods

Material	Examples	Disposal method
Biohazardous waste	Animal cells and tissue	Solids should be collected by your teacher for appropriate disposal. Liquids must be deactivated with bleach before they can be disposed of down the drain.
Grease and oils	Vegetable oil, lubricants	Collect in a bottle and dispose of in general waste. Machinery oils should be disposed of as hazardous chemical waste.
Corrosive liquids	Acids	Weak acids may be able to be poured down the drain. Strong acids must first be neutralised before they can be poured down the drain. Some schools have acid traps.
Solids	Paper towel	Dispose of in general rubbish.
Hydrogen peroxide	> 8%	Dilute before pouring down the drain.

Standard operating procedures

Standard operating procedures (SOP) are a set of instructions that detail all the tasks required to complete an activity or process in a routine way. They are often created by workplaces, schools, government agencies and equipment manufacturers to improve the safety of a process and minimise risks. In addition to information on how to carry out a task, SOPs often also include information on the equipment that should be worn during a procedure, how to handle or store equipment, how to dispose of materials and how to prevent injury.

Acknowledgment of sources and referencing

Acknowledging sources and correctly referencing materials are important in scientific research. They ensure that the work of researchers that has provided insights or findings that assist with an investigation is properly credited. You will learn more about referencing conventions in Lesson 1.10. Failing to credit or correctly reference the work of others is unethical, as it wrongfully uses the intellectual property of others. Plagiarising means presenting someone else's original ideas as your own. It is a serious offence that can arise from failing to acknowledge, or incorrectly referencing, the work of others.

Check your learning 1.5

Check your learning 1.5: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Identify** three things you must do if you want to ethically recruit human participants for a research experiment. (3 marks)

2 **Identify** two pieces of information you might find about a chemical in a material safety data sheet. (2 marks)

3 **Explain** how you would dispose of plasticine you used in a practical activity to model the respiratory system. (1 mark)

4 **Explain** why it is important to correctly acknowledge the work of others. (1 mark)

Lesson 1.6
Collecting data

Key ideas

- → There are many ways to collect primary and secondary data for an investigation.
- → Sampling is a way to select subjects for an investigation. Common sampling techniques are random sampling, systematic sampling and stratified sampling.
- → Microscopy techniques are important in biological science.
- → Tools such as information and communication technology, scientific texts, databases and online sources can be valuable in generating primary data and/or collating secondary data for an investigation.
- → Data collected for an investigation should be systematically recorded.

Science inquiry skills

Learning intentions and success criteria

This lesson provides support for the following science inquiry skills:

- use appropriate equipment, techniques, procedures and sources to systematically and safely collect primary and secondary data, e.g.
  - microscopy techniques: total magnification and field of view, scientific drawing
  - laboratory and field techniques: measurement, equipment calibration, species identification
  - sampling methods: random, systematic, stratified
  - sampling techniques: quadrats, line transect, belt-transect, capture-recapture
  - models and simulations
  - ICTs, scientific texts, databases, online sources
- use scientific language and representations to systematically record information, observations, data and measurement error, e.g.
  - symbols, units and prefixes
  - scale and magnification
  - indicators of measurement uncertainty
  - tables, graphs and diagrams
  - charts and maps
  - logbooks.

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Collecting primary and secondary data

There are many ways to collect primary and secondary data. The way you collect data will vary depending on the type of investigation you are undertaking. In this lesson you will learn about a variety of sampling methods and data collection techniques you can use to either generate your own primary data or collate secondary data.

Sampling

population
the group that scientists wish to draw conclusions about

In research, a **population** is the entire group of individuals or specimens of interest to the researcher. For example, if a researcher was conducting a study on the feeding habits

random sampling
a sampling procedure in which every member of the population has an equal chance of being selected for the sample

of Southern Cassowaries in the Daintree, the population would include every Southern Cassowary that lives in the Daintree. Because it is extremely difficult (often impossible) to study every individual that makes up a population, researchers select a subset or smaller group of individuals from the population to represent the population in the study. This subset is called a sample. There are three main methods of generating a sample to work with in an investigation: random sampling, systematic sampling and stratified sampling.

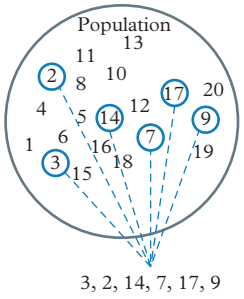

FIGURE 1 Random sampling is a selection process where everyone in the population has an equal chance of being selected for the sample.

Random sampling

Random sampling is a method of sample selection where every individual in the population has an equal chance of being selected for the sample. For example, if researchers wanted to study the average height of trees in the Daintree, the population would include every tree in the Daintree. To form a random sample of trees to measure, researchers could use a computer to randomly generate a set of coordinates in the Daintree and measure the heights of each tree closest to each coordinate. In this way, each tree has an equal chance of being selected into the sample. Random sampling helps remove selection bias.

systematic sampling
a sampling procedure in which samples are selected based on a systematic interval from a randomly chosen starting point

Systematic sampling

Systematic sampling is a method of sample selection that involves selecting members, or sections of a larger population, at consistent intervals. For example, if researchers wanted to study the health of NRL players, they could access an alphabetised list of all NRL players and systematically select every tenth player on the list, to form their sample.

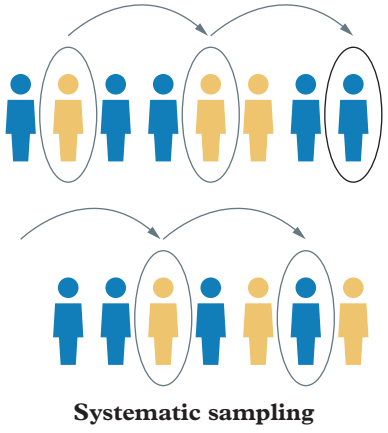

FIGURE 2 Systematic sampling selects members of the population at consistent intervals.

stratified sampling
a sampling procedure in which population is divided into strata and random samples are selected from each stratum

Stratified sampling

Stratified sampling involves breaking the population into subgroups (called strata) that share a similar trait and then randomly selecting from each stratum. For example, say researchers want to study a species of bird that can be found in three different environments in a region: grasslands, shrublands and coastal saltpans. They divide the bird population into three strata based on the three habitats and randomly sample from each stratum. In this way, the sample is representative of birds from each habitat.

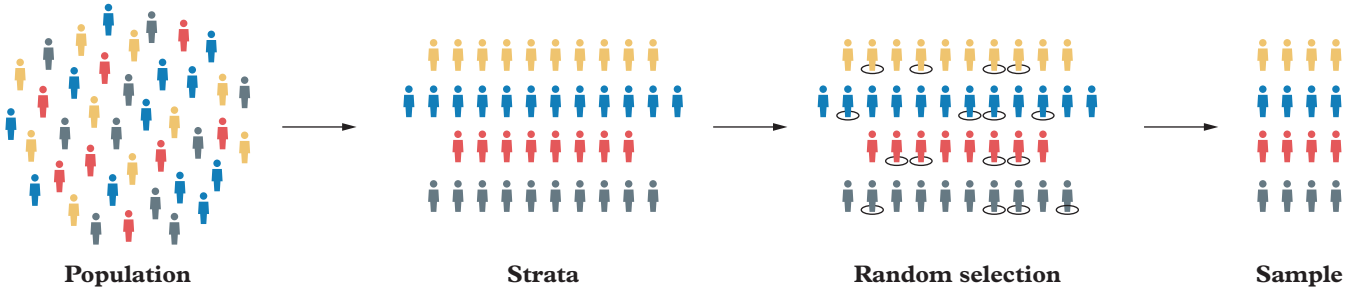

FIGURE 3 Stratified sampling involves breaking the population into strata and randomly sampling from each stratum.

In addition to sampling methods, there are also many sampling techniques you can use in Biology, particularly when conducting ecological fieldwork. You will learn more about sampling techniques, such as quadrats, line transect, belt transect and capture-recapture, in Units 3 and 4.

Laboratory and field techniques

When working in a laboratory or in the field, there are techniques you can apply to ensure that you collect data in a systematic and safe way. These techniques include considering measurement, equipment calibration and species identification tools.

Measurement

Research often involves taking measurements of different physical properties such as length, mass, temperature, time, capacity, area and volume. Data collected from measurements should be both accurate and precise. **Accuracy** describes how close a measurement is to its true value (what the measurement would be if it were measured perfectly). For example, if the true value of the length of a shell is 3.63 cm and the reading you get when measuring the shell is 3.62 cm, you can say that this measurement is accurate. If the length you get is 2.8 cm, it is less accurate. **Precision** refers to how close each of the measurements of the same thing are to each other. For example, if you take three readings of the length of the shell of 3.61 cm, 3.62 cm and 3.61 cm, your measurements are precise, because they are all very close to each other. If the readings you get are 2.8 cm, 3.61 cm and 3.2 cm, these are less precise. A visual representation of precision and accuracy is shown in Figure 4.

accuracy
how close a measurement is to its true value

precision
how close a set of data values are to each other

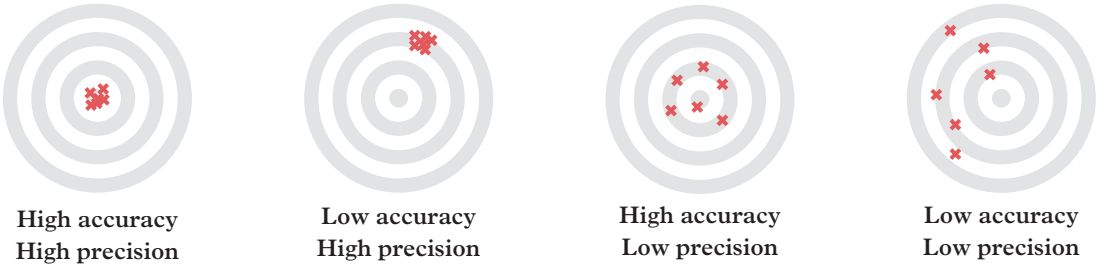

FIGURE 4 Accuracy and precision are different concepts.

It is important to make sure the instructions used to take measurements are reliable and calibrated (if necessary). Your process of measuring should also be consistent. For example, if you are using a ruler to take measurements of leaf length, you would want to ensure that the ruler you use is in good condition, to provide an accurate reading of length. An old wooden ruler with lots of scribbling and dents may lead to less accurate readings than a clean metal ruler. You would also need to ensure that the point you measure from remains consistent for each reading.

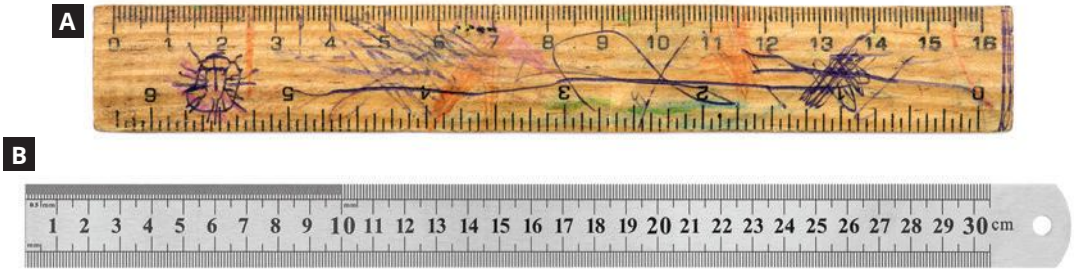

FIGURE 5 (A) An old wooden ruler could give less accurate readings than (B) a clean metal ruler.

Equipment calibration

Calibration is the process of configuring an instrument or measuring device to ensure it provides accurate readings. When using equipment to record data, it is important to make sure the equipment is calibrated. Common instruments used in research that should be regularly calibrated are listed in Table 1.

TABLE 1 Common laboratory equipment that requires regular calibration

Equipment	How to calibrate
Digital scales	Place a standard or known weight on the scale and adjust the reading until it matches the known weight.
Digital thermometer	Run a controlled temperature bath at a set temperature and place the thermometer in the bath. Let it sit for few minutes, then adjust the reading until it matches the reference temperature.
pH meter	Use standard buffer solutions with known pH values to test the reading given by the meter. Adjust the meter to match the reading of the known solution.
Micropipette	Fill the pipette with water and disperse onto a scale. Weigh the volume of water dispensed to make sure the pipette delivers the correct volume. If there is a difference, adjust the pipette.

Species identification

Being able to identify different species is an important skill in in biological research. Given the large number of species of organisms, biologists often rely on species identification tools to help identify what they are observing. Species identification tools include, but are not limited to, keys, field guides and mobile applications. A key is used to help determine species by first identifying a general characteristic of an organism, then breaking the characteristics into divisions, which a researcher can work through to reach the correct species. For example, Figure 6 shows a plant key. If you knew a particular plant forms seeds and has no true flowers, you could deduce that it is a type of gymnosperm. Other keys may ask a series of questions for the user to work through to eventually arrive at one species.

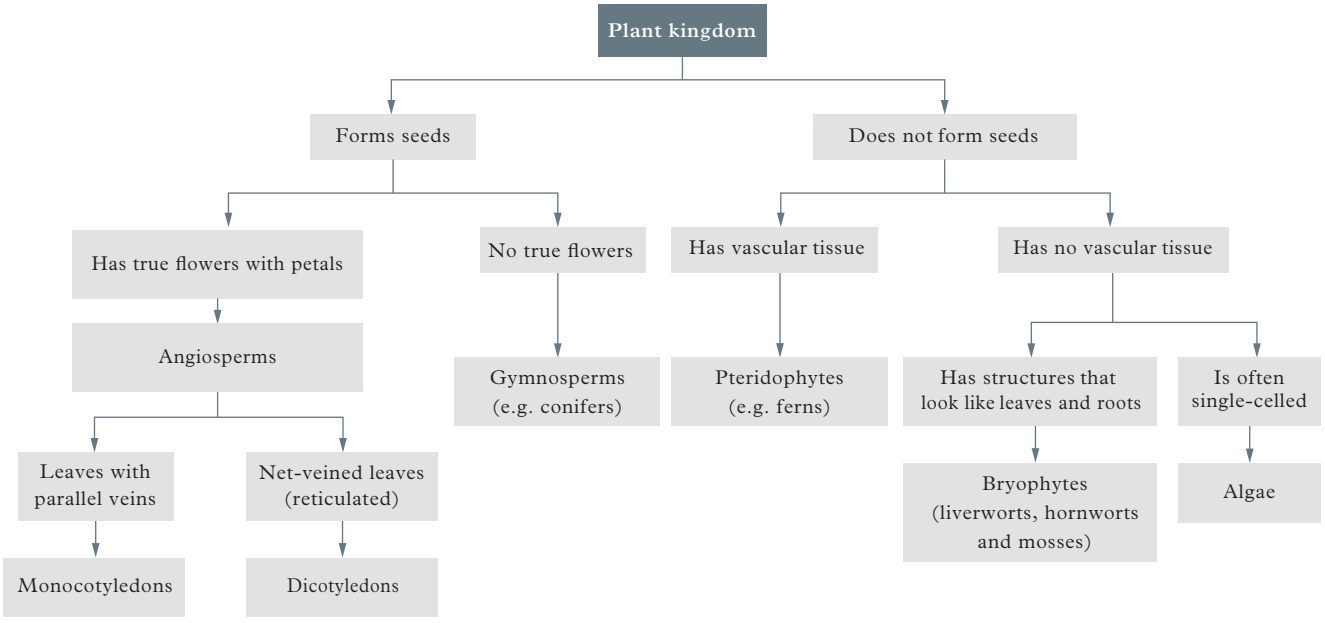

FIGURE 6 A sample plant key

A field guide presents specific information on a variety of species, as well as additional information such as diagrams, photos and distribution data. Depending on the field guide, it might include species for one type of animal in a region (e.g. *The Australian Bird Guide*) or multiple animals in a region (e.g. the *Queensland Museum Field Guide to Queensland Fauna*), or it might be very locally specific. In addition to field guides, online apps can also be useful in identifying species. Many apps have a database of species, which you identify by searching through images or by comparing species against photos you've taken.

Microscopy techniques

Microscopy is the use of microscopes to view and observe specimens and structures that cannot be seen or are difficult to see with the naked eye. Two of the main types of microscopes are **light microscopes** and **electron microscopes** (Table 2).

light microscope a microscope that uses visible light and lenses to magnify viewed specimens

electron microscope a microscope that uses a beam of electrons to form an image of the viewed specimen

TABLE 2 Summary of light and electron microscopes

	Light microscope	Electron microscope
How it works	Visible light is shone onto a specimen and the optical lenses magnify the image. Light reflects off the sample and the image can be observed through the eyepiece.	Electrons (which have much shorter wavelengths than visible light) are used instead of light to form an image on a screen.
Magnification	1,000× to 2,000×	Up to 1,000,000×
Applications	Viewing cells, large organelles, some larger bacteria and living specimens	Viewing smaller specimens and structures (e.g. viruses, macromolecules, small organelles); not for viewing living specimens

Scientific drawing

After viewing a specimen under a microscope, you might need to draw what you have seen. What is shown in your drawing should match what you see through the eyepiece of the microscope (Figure 7). A scientific drawing of a microscope image should include:

- a title or description of what has been observed
- labels that do not cross over each other
- the total magnification that the specimen was viewed at.

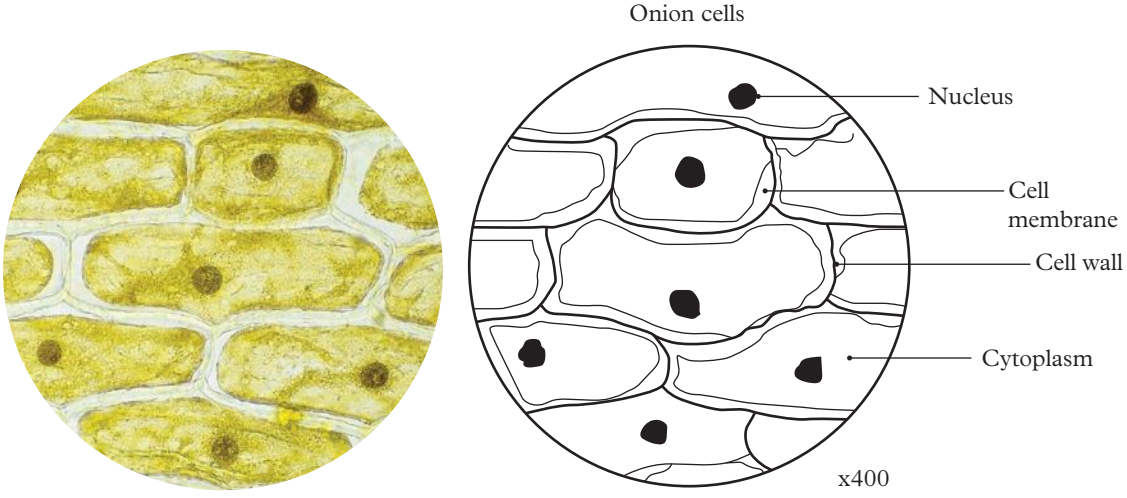

FIGURE 7 Scientific drawing of onion cells compared to the microscope view

Models and simulations

A model is a representation of a complex system or concept that has been simplified to make it more easily understood or to make predictions. There are many types of models including, but not limited to, physical models (e.g. a 3D model of a coastal ecosystem) and mathematical models. Models can be used to help break down complex ideas and predict how a real-life situation may unfold. Simulations are software programs that mimic or "simulate" the behaviour of a real-life phenomenon. Simulations can be used to test events or occurrences that may be too difficult, time consuming or expensive to test in real life.

Online tools and scientific texts

information and communication technologies (ICT)
computer and other technologies that process information to perform a range of tasks

Other tools, such as **information and communication technologies** (ICT), scientific texts, databases and online sources, can be valuable in generating primary data and/or collating secondary data for an investigation. Information and communication technologies are computer software and programs that perform a variety of operations. Different ICT can assist the collection of data in various ways. For example, an ICT may assist with processing the information received from a microscope, conduct statistical analysis of data, offer programs that help manage workflow and tasks, or enable quick communication with others you are working on a project with.

database
a large, organised collection of data

A **database** is an organised collection of data, often stored online in an electronic system. Databases can provide access to raw data that researchers can analyse to generate primary data. Data from databases can also be used to collate secondary data for an investigation. Some databases you may find useful for conducting your own biological research are:

- the Australian Bureau of Statistics (ABS), which provides statistics on a variety of economic, social, population and environmental factors
- the WildNet database, which contains information on more than 21,000 wildlife species
- the Australian Burden of Disease Database, which contains disease metrics for over 200 diseases and injuries.

Online sources

Online sources can also be valuable in providing information and data to assist in an investigation. Government websites often include credible information on medical, ecological, geographical and population data. In addition to these online sources, websites such as Google Scholar, JSTOR, ScienceDirect and PubMed contain a wide variety of peer-reviewed journal articles and scientific papers, which can be used to collate data or accessed to better understand a scientific concept being investigated.

Scientific texts

Many scientific texts, such as this textbook, can offer valuable information about conducting research. This includes information on research methods and experimental set-up, as well as background information and context that allows you to better understand the concept you are investigating.

Recording data

In addition to using the correct data collection techniques, you must also record and organise your data in a way that is consistent and clear. Things to consider when recording data:

- symbols, units and prefixes
- scale and magnification
- indicators of measurement uncertainty
- tables, graphs and diagrams
- charts and maps
- logbooks.

Symbols, units and prefixes

Biological data often includes symbols, units and prefixes. Examples of symbols you may come across in Biology are:

- μ, the symbol for the unit "micro", meaning 10^{-6}
- Σ, a symbol used in mathematical formulae that means "the sum of"
- Δ, which means "the change in a variable".

Other symbols to become familiar with are the symbols for some chemical elements frequently referred to in Biology (e.g. C for carbon, H for hydrogen, N for nitrogen, O for oxygen). You can revise these chemical symbols using the periodic table at the back of this textbook.

Measurements recorded should include appropriate units. The base units used in the International System of Units (SI) for a range of sciences are listed in Table 3. However, other units, such as grams (g) or milligrams (mg) for mass, or degrees Celsius (°C) for temperature, can be used if these are more appropriate for what you are measuring.

TABLE 3 SI base units

Base quantity		Base unit	
Name	Symbol	Name	Symbol
time	t	second	s
length	l	metre	m
mass	m	kilogram	kg
electric current	I	ampere	A
temperature	T	Kelvin	K
amount of substance	n	mole	mol
luminous intensity	I_v	candela	cd

scale
the relationship between the actual size of an object/specimen/area and how it is presented in a depiction

Prefixes are also commonly used in biological data. Common prefixes are:

- kilo-, meaning 10^3 or 1,000
- mega-, meaning 10^6 or 1,000,000
- milli-, meaning 10^{-3} or 0.001
- micro-, meaning 10^{-6} or 0.000001
- nano-, meaning 10^{-9} or 0.000000001

Scale and magnification

Where appropriate, **scale** and magnification should also be included. These details can help readers to understand and interpret the biological data. Scale describes the relationship between the actual size of an object/specimen/area and how it is displayed in a representation (e.g. a photo, diagram, drawing or model). For example, if you draw a map of a large ecosystem, you should include a scale to show how the length of your drawing corresponds to the actual length of the landscape being drawn. To do this, you could include a scale bar that shows that 2 cm (or another length) in your representation is equal to 50 metres in the landscape.

Magnification represents the size of a specimen as seen through an instrument's magnification settings compared to its actual size. Each time you produce a photomicrograph or draw what is seen in a microscope, you must include the magnification at which the specimen was viewed.

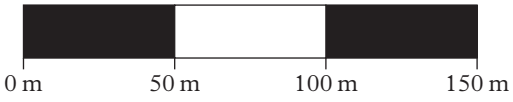

FIGURE 8 A scale bar showing that the length of one segment in the figure equals 50 metres

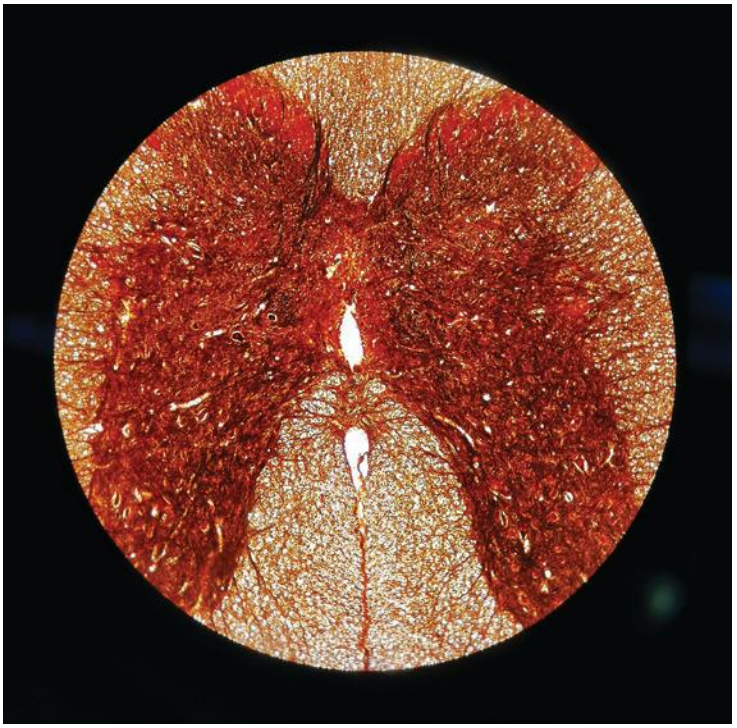

FIGURE 9 Cross-section of a spinal cord from a mammal, as seen under a light microscope at ×40 magnification

Indicators of measurement uncertainty

Indicators of measurement uncertainty are symbols or metrics used to highlight whether uncertainty exists in measurements. These indicators include error bars, standard deviation, standard error and uncertainty calculations. You will learn more about error bars, standard deviation and standard error in Lesson 1.7. Indicators of measurement uncertainty help scientists evaluate the reliability of data that has been collected.

Tables, graphs and diagrams

Raw data (measurements or observations of the dependent variable) can be difficult to interpret, and therefore should be presented in a way that is easy to analyse so conclusions can be drawn.

Tables

table
a format for presenting data in rows and columns

Tables can be used to present quantitative and qualitative data. The table has a heading, stating what the table is showing, and each column has a heading. Qualitative data may show trends, changes or variations in different conditions or over time, and so it is often useful to present such data in a table before comparing or contrasting the effects in a discussion.

A table of quantitative data consists of columns displaying the values of related variables. But these might not give an immediate or clear indication of the relationship between the variables. The table is usually the first step in recording the information and forms the basis for selecting the most appropriate graphical presentation. Various mathematical applications can be readily applied once the data is in tabular form. For example, Table 4 shows the times recorded for the heart rates of 10 participants in a medium-fitness group to return to resting rate after exercise.

TABLE 4 Time taken for heart rate to return to resting level after exercise, in participants of medium fitness

Participant	Recovery time (min)
1	6.4
2	5.2
3	1.5
4	2.1
5	4.2
6	7.5
7	2.4
8	2.6
9	2.4
10	3.0

Graphs

graph
a pictorial representation that displays values and data in an organised way

A **graph** is a two-dimensional plot of two or more measured variables. In its simplest form, a graph consists of two axes:

- the horizontal *x*-axis, which has values called abscissae, which show the magnitude of the independent variable. This is the known quantity and is the variable whose value is chosen by the experimenter.
- the vertical *y*-axis, which has values called ordinates, which show the magnitude of the dependent variable. This is the unknown quantity and is the variable whose values are not chosen by the experimenter.

Scientific graphs have the following features.

- The information on the graph is easily seen. This includes the heading, axis titles and numbers.
- The title is a descriptive statement that includes the independent variable and the dependent variable.
- The independent variable is on the horizontal axis (*x*-axis) and the dependent variable is on the vertical axis (*y*-axis).
- Each axis starts at zero, and the points on each axis are of equal unit size (scaled).
- Each axis is clearly labelled and includes the unit measurement.
- The data is not plotted beyond the axis.
- A pencilled point or circle is used for plotting each point.
- If there are two sets of data on a single graph, two different symbols or colours are used.

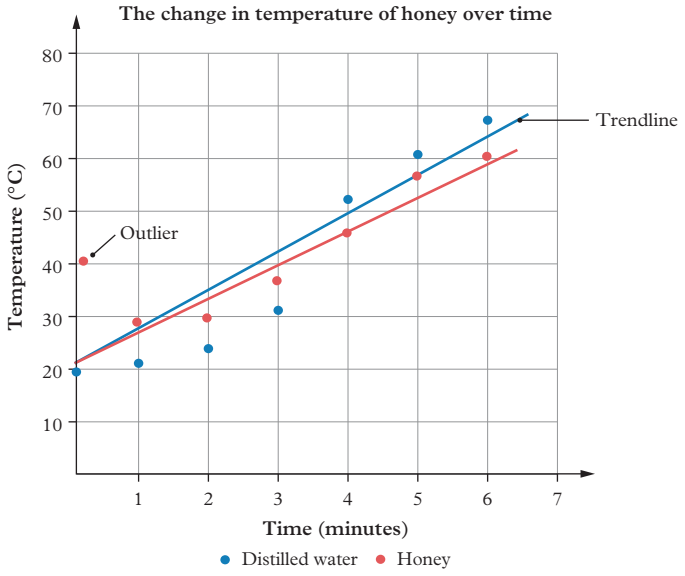

FIGURE 10 This graph shows the key features of a scientific graph.

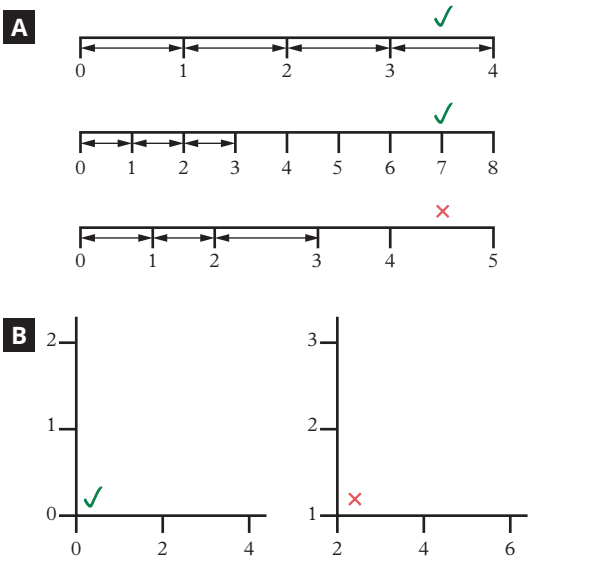

FIGURE 11 When drawing a graph, (A) use the correct scale for each axis, and (B) start each axis at zero.

You will learn more about specific types of graphs and the forms of data they help display in Lesson 1.7.

Diagrams

A diagram is a visual aid that shows the appearance, structure or set-up of something. Diagrams can be especially useful in Biology for presenting visual data or to show the set-up of an investigation. For example, diagrams of biological systems and cells show important features, their locations, sizes and composition, which allow the viewer to better understand how the system or specimen works. Diagrams should include labels with leader lines that do not overlap, and a title.

Scientific diagrams can be used to show how an experiment was set up. Equipment in these diagrams should be drawn in a simplified way, using two-dimensional figures (Figure 12). When drawing the set-up of an experiment, it is important to:

- keep drawings clear and neat
- use a sharp grey lead pencil
- draw equipment from a side-on view
- avoid shading
- use a ruler for straight lines
- label equipment with leader lines that do not cross over each other.

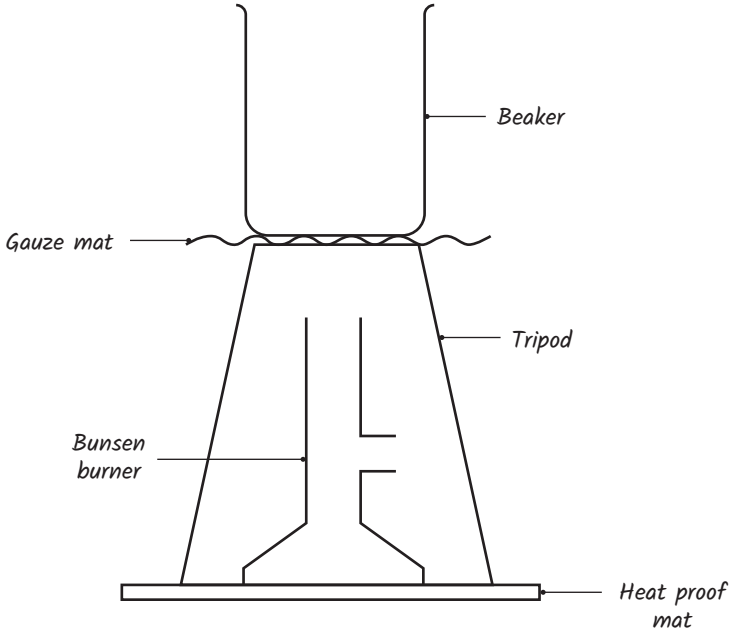

FIGURE 12 Example of a scientific diagram of equipment set-up

Charts and maps

Charts and maps can also be used to collect and present biological data. Some examples of charts are pie charts and bar charts, which help to show the frequency of a variable of interest. You will learn more about how to present data using charts and maps in Lesson 1.7. When reading charts to collect data, pay attention to labels and keys so you can understand what colours, shapes, plots or patterns represent in the chart. Maps can also be used to collect biological data. For example, the map in Figure 13 shows the distribution of sanderlings in Australia. While this map shows distribution data on sanderling species and their habitats, it can also be used to generate other types of data. For example, it could be used to help categorise sanderlings as a coastal species of bird.

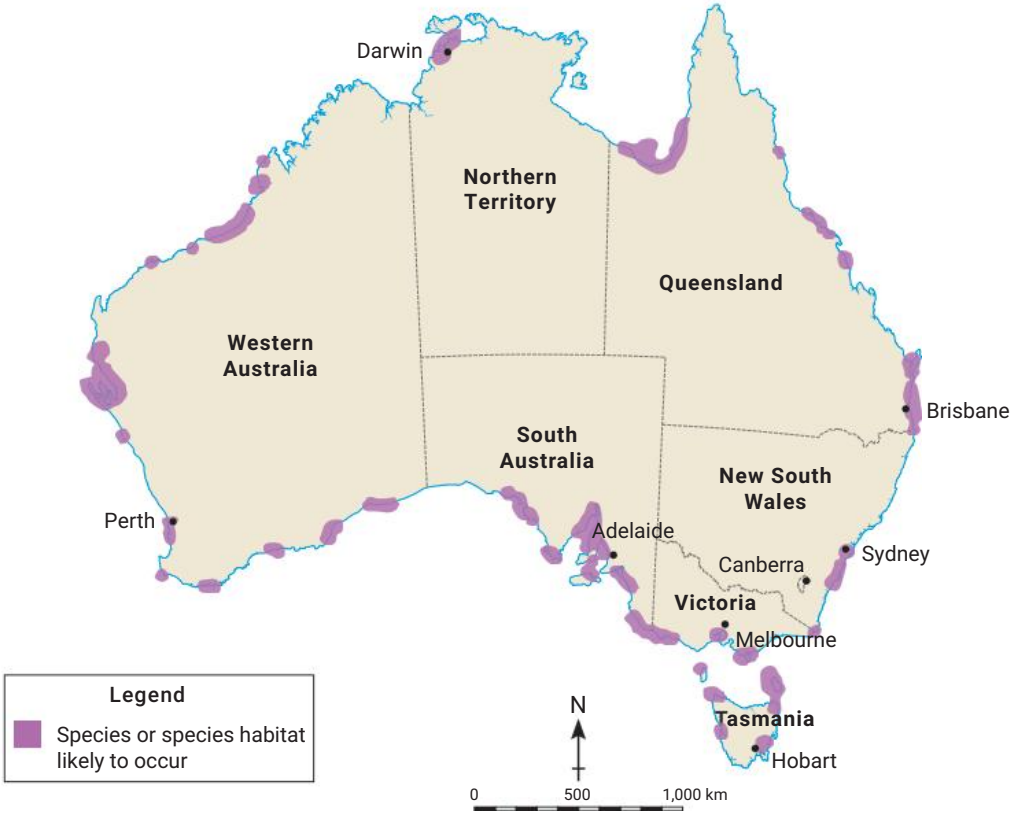

FIGURE 13 Map showing the distribution of sanderlings and sanderling habitat in Australia

Logbooks

logbook
an organised record of investigation ideas, events, results and interpretations

A **logbook** is a hard copy or digital record of how you completed an investigation or experiment. Each entry in a logbook must include:

- the date and entries, in chronological order
- acknowledgment of secondary resources, expert advice and teacher assistance when this information is referred to.

Your logbook could also include the following information as you complete your investigation:

- planning notes for experiments
- a description of the activities you have carried out
- the results or data from guided activities or investigations (including outliers and/or risk identification and management)
- personal reflections made during or at the conclusion of demonstrations, activities or investigations
- any links to spreadsheet calculations or other digital records and presentations you might use
- any notes and electronic (or other) images taken on excursions, or any database extracts
- notes of any additional work completed outside class time.

A well-organised logbook that contains all this information will make it easier to complete your student experiment and research investigation.

Check your learning 1.6

Check your learning 1.6: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the term "population". (1 mark)

2 **Describe** each of the following sampling techniques:
   - **a** random sampling (1 mark)
   - **b** stratified sampling (1 mark)
   - **c** systematic sampling. (1 mark)

3 **Identify** one advantage of using random sampling. (1 mark)

4 **Explain** why it is important for equipment to be calibrated regularly. (1 mark)

5 **Identify** three features you must include when drawing a specimen viewed under a microscope. (3 marks)

6 **Identify** the SI base units for:
   - **a** time (1 mark)
   - **b** mass. (1 mark)

7 **Identify** one advantage of presenting data in a table. (1 mark)

Analytical processes

8 **Distinguish** between accuracy and precision. (1 mark)

9 **Compare** light microscopes and electron microscopes. (2 marks)

Knowledge utilisation

10 **Construct** a graph using the data below, which shows the average growth of a plant species over a period of six weeks. (3 marks)

Week	Average height (cm)
1	3
2	4.5
3	6
4	7.5
5	9
6	10

Lesson 1.7
Processing and analysing data

Key ideas

→ Translating information between graphical, numerical and/or algebraic forms is an important skill in Biology.

→ Mathematical techniques can be used to summarise data and help identify relevant trends, patterns, relationships, limitations and uncertainty.

→ Data can be presented and communicated in many formats.

Learning intentions and success criteria

Science inquiry skills

This lesson provides support for the following science inquiry skills:

- translate information between graphical, numerical and/or algebraic forms, e.g.
  - units and measurement conversions
  - ratios and percentages
  - symbols and notation
  - charts and maps
- use mathematical techniques to summarise data in a way that allows for identification of relevant trends, patterns, relationships, limitations and uncertainty, e.g.
  - comparative investigations: mean, standard deviation, standard error, Student's t-test
  - correlational investigations: regression analysis, Pearson's correlation coefficient, Spearman's rank
- select and construct appropriate representations to present data and communicate findings, e.g.
  - summary tables
  - column graphs (with error bars)
  - scatterplots (with trendline and R2)
  - profile diagrams
  - scientific drawings
  - charts and maps
  - indexes and summary statistics
- analyse data to identify trends, patterns and relationships; recognising error, uncertainty and limitations of evidence

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Translating information

After data has been collected and organised in a systematic way, you can work with it to understand what it means. Processing your data the right way can help you discover trends, patterns or the significance of the data, to help answer your research question. In this section you will learn how to:

- translate information
- use mathematical techniques to summarise data

- select and construct appropriate representations to present data and communicate findings
- analyse data to identify trends, patterns and relationships.

Data can often be presented in different forms. In Units 1 & 2 Biology it is important to be able to translate information between graphical, numerical and/or algebraic forms. This may include unit and measurement conversions, ratios and percentages, symbols and notation, and charts and maps.

Units and measurement conversions

In Biology, the measurements used might need to be converted in order to calculate results, analyse data or make comparisons. Units commonly used in Biology are units of length, time, mass and capacity, and volume. Figures 1 to 5 summarise how different units can be converted.

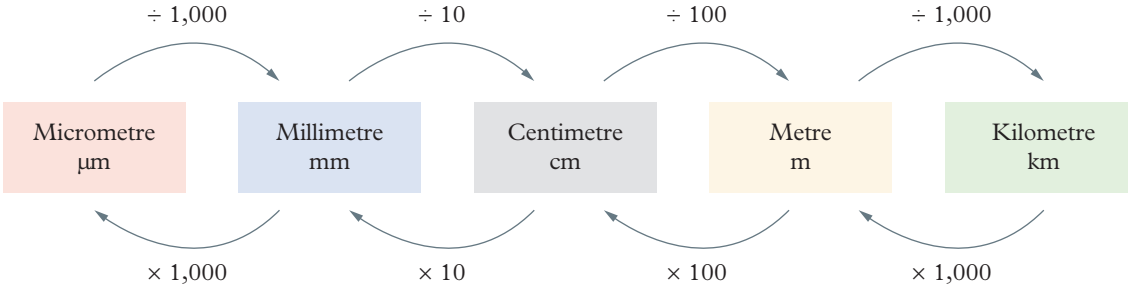

FIGURE 1 Unit conversions for length

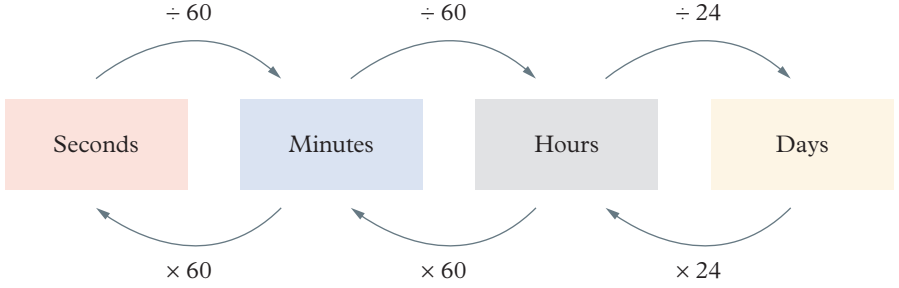

FIGURE 2 Unit conversions for time

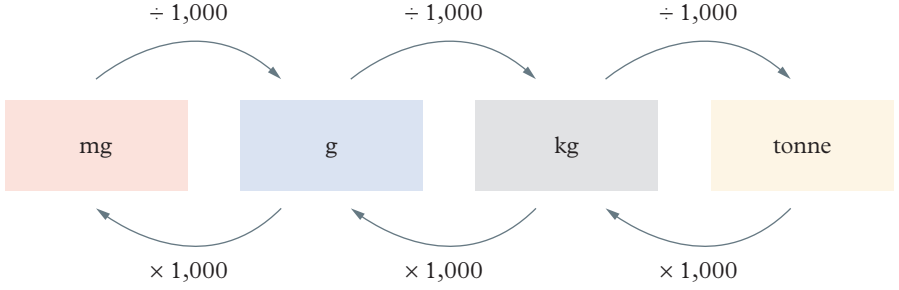

FIGURE 3 Unit conversions for mass

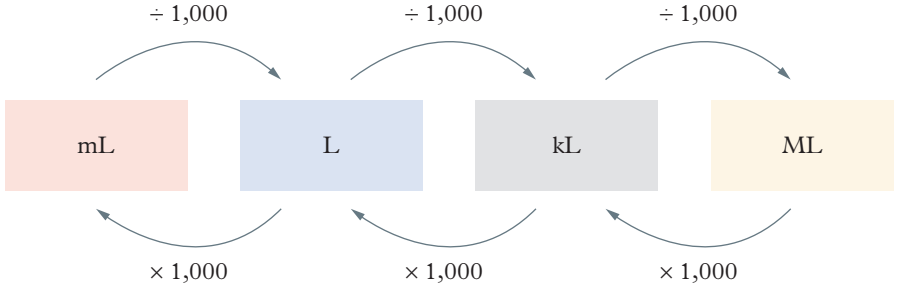

FIGURE 4 Unit conversions for capacity

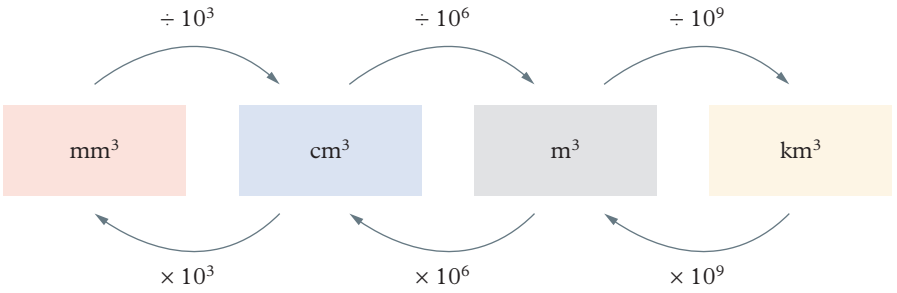

FIGURE 5 Unit conversions for volume

Ratios and percentages

ratio
a measure that compares the magnitude of two quantities in terms of how many times one value is contained within the other

A **ratio** is a mathematical representation that shows the relationship or a comparison between two numbers. For example, if there are 1,200 eucalyptus plants in a population and 200 of them show a particular trait, the ratio of eucalyptuses showing the trait to the total number of eucalyptuses in the population can be written as 200:1,200. Ratios can also be simplified as fractions. So, for the eucalyptus example, to convert the ratio to a fraction, divide the number of eucalyptuses with the trait by the total population $\frac{200}{1,200}$, which gives $\frac{1}{6}$. You can use this fraction to simplify the ratio to 1:6. This means that for every six eucalyptuses in the population, there is one that displays the trait.

percentage
a number expressed as a fraction of 100

A **percentage** is the amount of something expressed as a number out of 100. To convert a ratio into a percentage, write the ratio as a fraction and multiply it by 100. For example, to write how many eucalyptuses in the population are affected by the trait as a percentage, use the following calculation:

$$\frac{1}{6} \times 100 = 16.66\%$$

Symbols and notation

In Units 3&4 Biology you may come across symbols used to represent information. For example, chemical equations often use chemical symbols from the periodic table to show which elements are involved and the relative amounts in which they occur in a reaction. Consider the photosynthesis reaction:

$$6CO_2 + 6H_2O \rightarrow C_6H_{12}O_6 + 6O_2$$

In this equation, the element symbols C, O and H represent carbon, oxygen and hydrogen. The subscripts indicate how many times the element occurs in each molecule, and the whole numbers in front of molecules indicate how many molecules there are. From this representation you can deduce that photosynthesis begins with 18 oxygen, 6 carbon and 12 hydrogen atoms.

In addition to symbols, scientists often use scientific notation to write very large or very small numbers. In scientific notation, a number between 1 and 10 is written as multiplied by a power of 10. For example, to write the number 4,523,000 using scientific notation:

1. Change the number to a decimal between 1 and 10. So: 4.523000
2. Count the number of places you moved the decimal from the original number, and note the direction you moved it. This allows you to work out the superscript for the power of 10. In this case, the decimal was moved 6 places to the left. The count is a positive value. (If the decimal had moved to 6 places to the right, it would be negative value, −6.)
3. Write the number from Step 1 as a multiplication by 10, with 10 raised to the power of the number from Step 2. So: 4.523000×10^6
4. Remove any insignificant figures (zeros that are not positioned between whole numbers) to get your final notation. So: 4.523×10^6

Charts and maps

Biological information is sometimes communicated through charts (e.g. pie charts, bar charts) and maps. Different visual forms often express different types of data. Pie charts often show a ratio of values, while maps often show distribution data. Being able to translate visual data to numeric data is an important skill. The pie chart shown in Figure 6 shows the percentages of blood types in a population. Because this chart shows blood types as percentages, this information can be translated into a ratio to help people understand the data. The percentage of type B blood is 20% and is therefore a ratio of 20:100 or 1:5. This means one in five people in this population have type B blood.

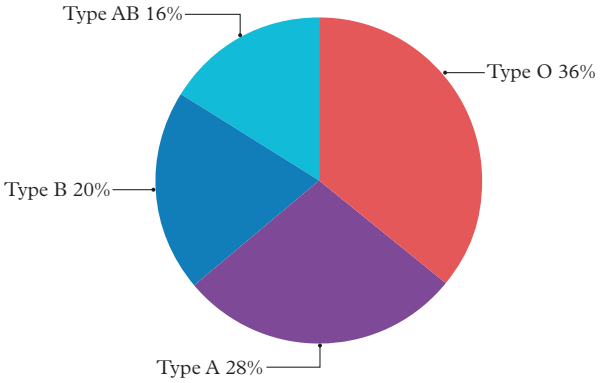

FIGURE 6 Pie chart showing percentages of blood types in a population

Maps are particularly useful in showing distribution data. For example, if you wanted to show the distribution of a species in an area, you could plot the coordinates of sightings to indicate where on a map it is likely to be found. The map in Figure 7 shows the distribution of Eastern Brown snakes in Australia. From the coordinates plotted, it is easy to see that Eastern Brown snakes are more prevalent in Victoria than they are in the Northern Territory.

FIGURE 7 Eastern Brown snake distribution in Australia

Summarising data

Once you have collected your data, you can do calculations and/or tests to process the data, to help you understand what it means. The types of calculations and tests you do will depend on the type of investigation you conducted, specifically whether you conducted a comparative investigation or a correlational investigation.

mean
the average of a set of numbers in a data set

measure of central tendency
summary statistic that represents a central point in a data set

Comparative investigations

If the data you collected has come from a comparative investigation, you may be able to use mathematical calculations such as mean, standard deviation, standard error and/or a student's *t*-test to better understand the data.

Mean

The **mean** is the average of all scores in a data set. It is a **measure of central tendency**, a summary statistic that focuses on a central point to represent your data set. To calculate the mean, add (sum) all the scores in the data set, then divide that number by the total number of scores.

$$\text{Mean} = \frac{\text{Sum of all scores}}{\text{Number of scores}}$$

TABLE 1 Heights of five tomato plants

Tomato plant	Height (m)
A	0.7
B	1.2
C	1.4
D	0.9
E	2.1

For example, Table 1 shows data on the heights of five tomato plants. To calculate the mean height, add all the heights of the plants together and then divide this by five (the number of plants).

$$\frac{0.7 + 1.2 + 1.4 + 0.9 + 2.1}{5} = 1.26$$

The mean height of the tomato plants is 1.26 metres.

Standard deviation

measure of variability
summary statistic that describes the spread of data in a data set

variance
a measure of how spread data is from the mean

In addition to measures of central tendency (e.g. mean), **measures of variability** are also useful in understanding data. Measures of variability are summary statistics that tell you how spread out the data in your data set is. **Variance** indicates how much, on average, each score differs from the mean. Because some scores are higher than the mean (have a positive difference) and some are lower than the mean (have a negative difference), they will cancel out when calculating a "mean difference". A mean variance can be determined by squaring the difference from the mean of each score. (A negative value squared results in a positive value: $-A \times -A = +A^2$). Continuing the tomato plant example, the mean height of the plants is 1.26 metres. To work out the variance of each plant, first calculate each value's difference from the mean, and then square this number.

TABLE 2 Tomato heights with difference from mean and variance

Tomato plant	Height (m)	Difference from the mean	Variance*
A	0.7	−0.56	0.31
B	1.2	−0.06	0.0036
C	1.4	+0.14	0.02
D	0.9	−0.36	0.13
E	2.1	+0.84	0.71

*Variance = the squared difference from the mean.

The mean variance can then be calculated. To do this, divide the sum of all the squared differences from the mean by the number of scores.

$$\text{Mean variance} = \frac{\text{sum of all squared differences}}{\text{number of scores}}$$

$$= \frac{31 + 0.0036 + 0.02 + 0.13 + 0.71}{5}$$

$$= 0.23$$

standard deviation
a measure that describes how far, on average, scores are different from the mean

The mean variance is therefore 0.23 metres. Mean variance gives an indication of the spread of the data, but because it is a squared value, it is difficult to compare with the mean score. **Standard deviation**, however, determines how different the scores are from the

mean. It is calculated from the square root of the mean variance. In our example of the tomato plants, the standard deviation is $\sqrt{0.23} = 0.48$. The closer the standard deviation is to zero, the less the data is spread (variability) and the more reliable it is (i.e. the data is clustered around the mean). As the value of the standard deviation increases away from zero, the data becomes more variable and therefore less reliable.

Standard error

Standard error (SE) is the standard deviation of a sample population. It measures how different the mean of the population is likely to be from the mean of a sample. Standard error can be calculated using the following formula, where SE is standard error, s is the standard deviation of the sample and n is the number of subjects in the sample:

standard error
the standard deviation of the sampling distribution of a statistic

$$\text{SE} = \frac{s}{\sqrt{n}}$$

Student's *t*-test

A **student's *t*-test** is a statistical test to determine whether the difference between the means of two groups is statistically significant (i.e., the difference is not due to chance). The student's *t*-test is an unpaired *t*-test, which means it compares the means of two independent or unrelated groups (often the control and the experimental group). Every significance test has two possible hypotheses:

student's *t*-test
a statistical test used to determine whether the difference between the means of two groups is statistically significant

- the null hypothesis – that there is no significant difference between the two groups (e.g. there is no significant difference between mean weight loss before and after treatment)
- the alternative hypothesis – that there is a significant difference between the two groups (e.g. there is a significant difference between mean weight loss before and after treatment)

In a *t*-test, *t* represents the extent to which the means of the two groups are apart. It is calculated using the formula shown below, where:

- x_1 is the mean of sample 1
- s_1 is the standard deviation of sample 1
- n_1 is the sample size of sample 1
- x_2 is the mean of sample 2
- s_2 is the standard deviation of sample 2
- n_2 is the sample size of sample 2

$$t = \frac{(x_1 - x_2)}{\sqrt{\frac{(s_1)^2}{n_1} + \frac{(s_2)^2}{n_2}}}$$

Once a *t*-value has been calculated, you must determine the degrees of freedom (df) for the test. This is the sum of the sample sizes of each group minus the number of samples compared. For example, if both sample sizes were 10, df would equal 10 + 10 – 2, which gives 18. You then use a *t*-distribution table (Figure 8) to work out the critical *t*-value against the level of statistical significance:

- If your calculated *t*-value is *greater* than the critical *t*-value shown in the table, then you reject the null hypothesis – this means the alternative hypothesis is correct, and there is a significant difference (that is, the difference is not due to chance). In the example in Figure 8, a *t*-value higher than 2.101 indicates that there is a significant difference between the two groups (at 0.05 significance, which is the most commonly used significance level).
- If your calculated *t*-value is *lower* than the critical *t*-value shown in the table, then you accept the null hypothesis – this means the alternative hypothesis is incorrect, and there is no significant difference (that is, any difference is due to chance). In the example in Figure 8, a *t*-value less than 2.101 indicates that there is no significant difference between the two groups.

Degrees of freedom (df)	.2	.15	.1	.05	.025	.01
11	1.363	1.548	1.796	2.201	2.593	3.106
12	1.356	1.538	1.782	2.179	2.560	3.055
13	1.350	1.530	1.771	2.160	2.533	3.012
14	1.345	1.523	1.761	2.145	2.510	2.977
15	1.341	1.517	1.753	2.131	2.490	2.947
16	1.337	1.512	1.746	2.120	2.473	2.921
17	1.333	1.508	1.740	2.110	2.458	2.898
18	1.330	1.504	1.734	2.101	2.445	2.878
19	1.328	1.500	1.729	2.093	2.433	2.861
20	1.325	1.497	1.725	2.086	2.423	2.845

FIGURE 8 Part of a *t*-distribution table. The numbers in the grey row at the top are levels of significance.

Correlational investigations

If data has been collected through a correlational investigation, there are calculations that can be applied or generated to determine the type of relationship that exists between variables. These calculations include regression analysis, Pearson's correlation coefficient and Spearman's rank.

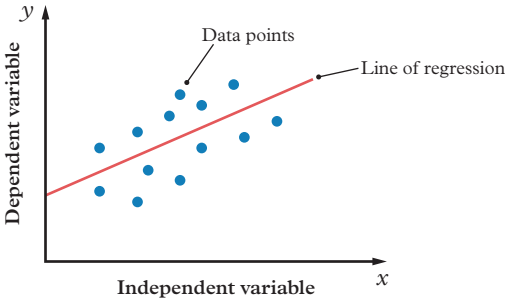

FIGURE 9 Regression analysis uses a mathematical formula to produce a regression line that shows the relationship between the IV and the DV.

Regression analysis

Regression analysis is a statistical technique used to model the relationship between a dependent variable (*y* on a graph) and the independent variable (*x* on a graph). A main function of regression analysis is to better understand how the dependent variable changes in response to the independent variable. It uses the mathematical formula $y = a + bx$ (where *y* is the dependent variable, *x* is the independent variable, *a* is the intercept and *b* is the slope) to generate a regression line to fit the data plotted on a graph. This regression line or **line of best fit** shows the relationship between the two variables and can be used to make predictions about the data.

Pearson's correlation coefficient

line of best fit
a trendline that gives an approximation of the linear relationship between two variables

Pearson's correlation coefficient (*r*)
a measure of the strength of the linear relationship between two continuous variables

Pearson's correlation coefficient (*r*) is a measure of the strength and direction of a linear relationship between two variables. It will generate a value that ranges from –1 to +1.

- An *r* value of +1 indicates a perfect positive correlation (when one variable increases by one unit, the other also increases by one unit).
- An *r* value of –1 indicates a perfect negative correlation (when one variable increases by one unit, the other variable decreases by one unit).
- An *r* value of 0 indicates that no relationship exists between the two variables.

It is important to remember that correlation does not equal causation. This means that if two variables happen to show a statistical relationship (correlation), it does not confirm that a change in one variable truly causes the change in the other variable.

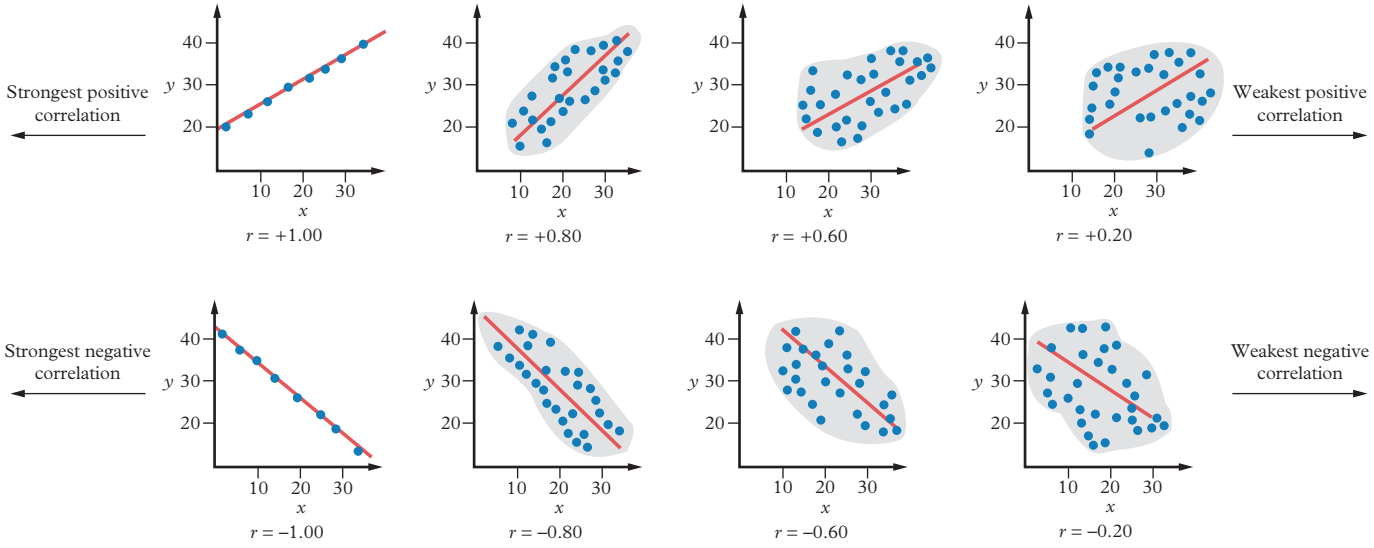

FIGURE 10 Scatterplots showing Pearson's correlation coefficient

Spearman's rank

Spearman's rank (*p*) is a measure of the strength of a relationship between two variables that often have a monotonic relationship (that is, when one variable increases, so does the other; when one variable decreases, so does the other). Like Pearson's correlation coefficient, Spearman's rank provides a value between +1 and –1. However, what is determined to be a strong relationship differs slightly between the two measures. Table 3 provides a summary of positive Spearman's rank values and the strength of the relationship they indicate.

Spearman's rank (*p*)
a measure of the strength and direction of a monotonic relationship between two variables

Spearman's rank is often used when:

- the data does not meet the assumptions of the Pearson's correlation coefficient
- the relationship is not linear, meaning it does not show a straight-line relationship but there is still a clear relationship between variables (e.g. Figure 11)
- ordinal data (categorical data that have a set order or scale) is included in the data set
- outliers are present in the data set.

TABLE 3 Spearman's rank values

Spearman's rank (*p*)	Strength of relationship
$p = 0$	No correlation
$0 < p \leq 0.19$	Very weak relationship
$0.20 \leq p \leq 0.39$	Weak relationship
$0.40 \leq p \leq 0.59$	Moderate relationship
$0.60 \leq p \leq 0.79$	Strong relationship
$0.60 \leq p \leq 1.00$	Very strong relationship

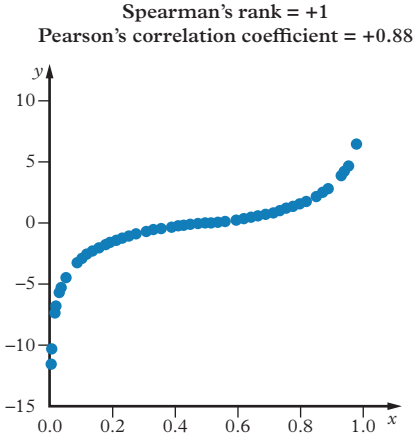

FIGURE 11 Spearman's rank is often used for data that is non-linear. In the graph, $p = +1$ while $r = +0.88$.

Presenting and communicating data

Once your data has been collected and analysed, you need to determine the best method of presenting or communicating that data to others. The best representation to use will depend on the nature of the data you have collected and the message you want to communicate.

Summary tables

Summary tables organise data into columns and rows. This can make it easy to compare and analyse values. Summary tables can also be used to present key findings or statistics you determined when analysing data. For example, if you measured 30 plants from two groups to compare their average leaf length, your raw data is likely to include all the lengths measured from both sets of plants. In your data analysis you would have worked out the average leaf length for the two sets of plants. A summary table can then present these two average values in a concise way (Table 4). The headings of your table should be clear and concise, and any units used in measurements should be included next to the appropriate heading.

TABLE 4 A summary table presenting the average leaf length of two plant species

Plant species	Average leaf length (cm)
Eucalyptus longifolia	16
Eucalyptus macrocarpa	10

Column graphs (with error bars)

Column graphs use vertical bars to present data, where each bar represents a group or category. They are particularly useful for comparing discrete (countable) data from different categories. The height or length of a rectangular column shows the value of one category of data. Column graphs can also include error bars. These are bars that show how variable or uncertain the data is for each column. Error bars may relate to different types of measures of uncertainty, including standard deviation and standard error, or they may relate to range (the difference between the maximum and minimum values in set of data). In Figure 12, from the error bars you can see that there is more uncertainty in the data related to percentage of female toads trapped with lights on than data related to the percentage of female toads trapped with lights off.

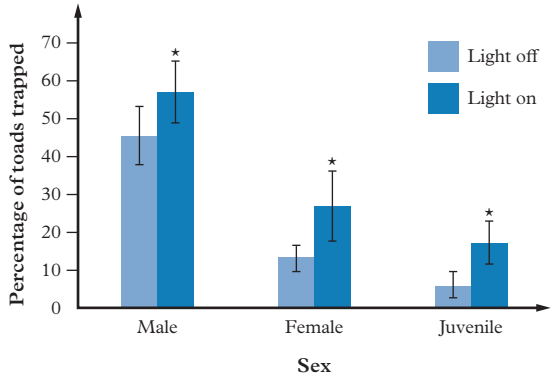

FIGURE 12 A column graph with error bars showing the percentage of male, female and juvenile toads trapped with and without lights

line graph
a graph of data linking two variables, where one variable is plotted on the *y*-axis and the other on the *x*-axis and the points are connected in a line

Line graphs

A **line graph** is a representation of data in which specific values of a function are plotted as dots on a coordinate plane. The adjacent pairs of dots are connected by straight lines. If the slope of the line is positive (Figure 13A), the conclusion is drawn that as the IV increases, so too does the DV – this is a positive correlation. If the slope of the line is negative (Figure 13B), then you can say that as the IV increases, the DV decreases – this is a negative correlation.

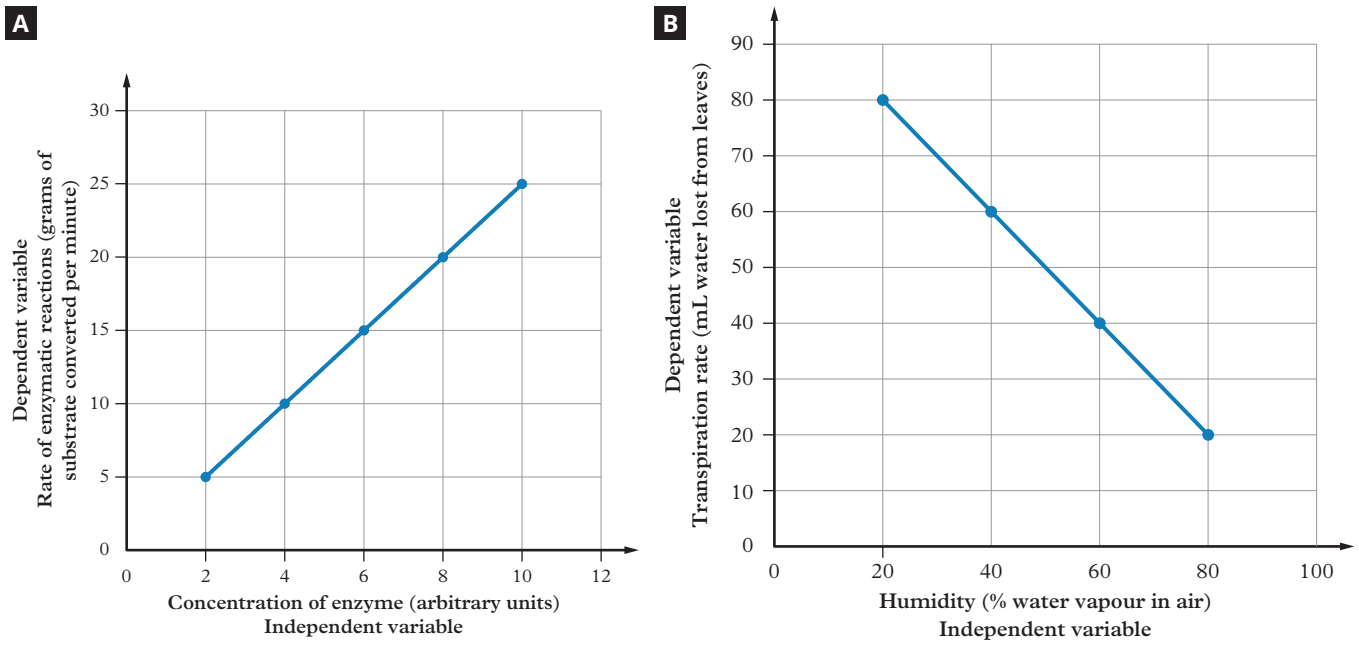

FIGURE 13 (A) The effect of enzyme concentration on the rate of conversion of a substrate: a positive correlation; (B) The effect of humidity on plant transpiration: a negative correlation

With a straight-line graph, the value of the dependent variable can be determined for a value of the independent variable that has not been measured. This can be done by extending the line *outside* the data set, at either end of the graph (**extrapolation**), or by reading between the measured points *within* the data set (**interpolation**). For example, in Figure 13A, at an enzyme concentration of 12 units, the expected reaction rate is 30 g/minute (extrapolation). At an enzyme concentration of 5 units, the reaction rate was 12.5 g/minute (interpolation).

extrapolation
an estimation of a value based on extending a known sequence of values beyond the values that are certainly known

interpolation
an estimation of a value within two known values in a sequence of values

The slope of the graph shows the mean change between the independent and dependent variables. The rate of change is calculated as the change in *y*-axis (dependent variable) values divided by the change in *x*-axis (independent variable) values.

$$\text{Rate of change} = \frac{\text{change in } y\text{-axis (dependent variable) values}}{\text{change in } x\text{-axis (independent variable) values}}$$

For example, from the graph in Figure 13A, for every 2 units of enzyme concentration increase there is an increase of 5 g substrate converted per minute.

Scatterplots

Often the points plotted on a graph do not form a straight line but are scattered – this is known as a **scatterplot**. In this situation, a line of best fit (or trendline) can be drawn so that the plotted points are evenly distributed above and below the line.

scatterplot
a graph in which the values of two variables are plotted along two axes, the pattern of the resulting points revealing whether a relationship (correlation) exists

The amount of scatter from the line of best fit indicates the closeness of the positive or negative relationship (correlation) between the two variables. The closer the points are to the line of best fit, the stronger the correlation between the variables.

When the points are so scattered that a line of best fit cannot be drawn, there is no correlation between the two variables.

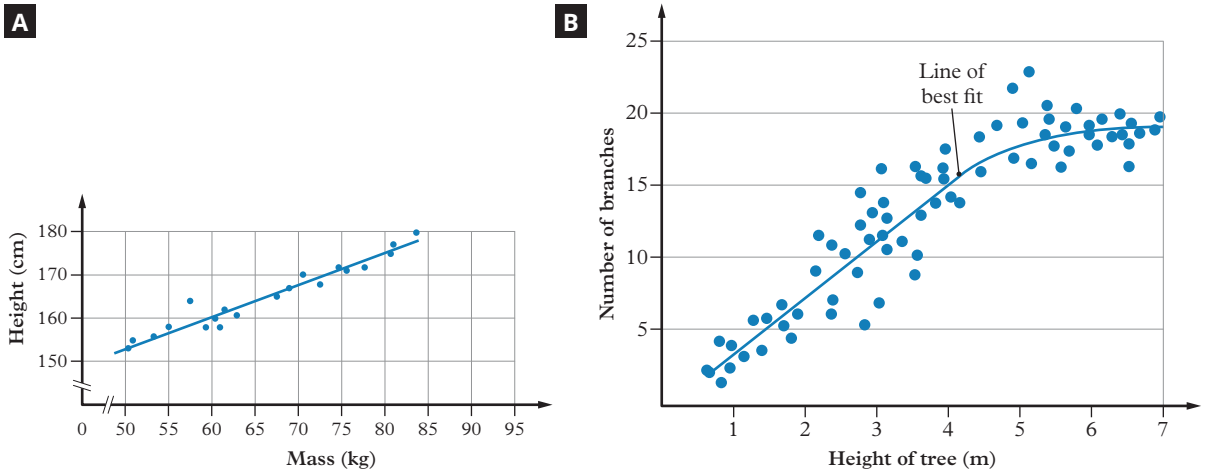

FIGURE 14 Lines of best fit on a scatterplot: (A) mass versus height of 20 sixteen-year-old males; (B) gum tree height versus number of branches over 3 cm in diameter

Indexes and summary statistics

index
a composite measure that summarises and compares multiple variables and presents these factors as a single number

summary statistic
a value that provides a summary of a data set

An **index** is a numeric, composite measure of multiple variables. It combines multiple variables from complex data sets into a single number that can summarise a general trend or state, based on different biological observations, conditions or processes. For example, a biodiversity index measures the variety and abundance of species in a locality. Biodiversity indices can be used to assess the health of ecosystems and compare changes in the overall health of ecosystems at different points in time. A **summary statistic** is a numeric value that summarises the main features of a data set. Examples of summary statistics are measures of central tendency (e.g. mean, median, mode) and measures of dispersion (e.g. range, variance, standard deviation). Presenting the summary statistics of key data can be effective in providing a snapshot of your findings to others.

Other methods of presenting data

Other methods of presenting data include:

- scientific drawings – for example, showing the structure of a cell you have observed under a microscope. Information on how to use scientific drawings can be found in Lesson 1.6.
- charts and maps – for example, using a pie chart to show the percentages of blood groups in a population, or plotting the distribution of disease on a map. For more information on charts and maps, refer to Lesson 1.6.
- profile diagrams – visual representations that show the vertical distribution of different ecological or environmental factors in an area.

Analysing data

Once you have collected, processed and presented your data in its most useful representation, you can analyse the data to identify trends, patterns and relationships, and recognise error and uncertainty. When analysing data, you may also become aware of limitations in the evidence collected.

Limitations

limitation
a factor or condition that can affect the validity and/or reliability of results

Limitations are factors that may affect the reliability or validity of findings from research. Limitations generally relate to the investigation methods used or the external environment in which the investigation was conducted (e.g. methods used, limited funding, time constraints,

sampling constraints, ethical considerations). Limitations are often outside the control of the researcher. They are not the same as extraneous variables or confounding factors. They may result in an extraneous or confounding factor existing within the study. For example, in a study examining the relationship between exercise and sleep duration, a limitation could be the inability to control for participants' dietary habits, which could introduce an extraneous variable that affects participants' sleep, independent of exercise. If any limitations in an investigation are identified, then recommendations should be suggested to negate the limitation in future. This might include suggesting improvements to the investigation methods or identifying whether further research needs to be conducted.

Check your learning 1.7

Check your learning 1.7: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Identify** the new measurements for:
   - **a** 360 millimetres converted to metres (1 mark)
   - **b** 3.6 minutes converted to seconds (1 mark)
   - **c** 760 millilitres converted to litres. (1 mark)

2 In a plot of 40 wattle trees, only 8 wattles are flowering.
   - **a** **Determine** the ratio of flowering wattles to non-flowering wattles. (1 mark)
   - **b** **Calculate** the percentage of wattle trees that are flowering. (1 mark)

3 **Identify** one example of data that may be beneficial when presented on a map. (1 mark)

4 The heights of students in a friendship group are: 170 cm, 148 cm, 150 cm, 180 cm and 136 cm.
   - **a** **Calculate** the mean height. (1 mark)
   - **b** **Calculate** the mean variance. (1 mark)
   - **c** **Calculate** the standard deviation. (1 mark)
   - **d** **Calculate** the standard error. (1 mark)

Analytical processes

5 **Contrast** the terms "positive correlation" and "negative correlation". (1 mark)

6 **Compare** Pearson's correlation coefficient with Spearman's rank. (2 marks)

7 **Distinguish** between interpolation and extrapolation. (1 mark)

Lesson 1.8
Evaluating evidence

Key ideas

- → Data and reasoning can be used to discuss and evaluate the validity and reliability of evidence.
- → Sources of information should be evaluated before being used to support scientific research.
- → If limitations or uncertainty in data have been identified, the researcher should suggest how these can be minimised in future research.
- → Peer review is a process that ensures the work of research scientists is evaluated and of high quality prior to publication.

Learning intentions and success criteria

Science inquiry skills

This lesson provides support for the following science inquiry skills:

- use data and reasoning to discuss and evaluate the validity and reliability of evidence, e.g.
  - discuss ways in which measurement error, instrumental uncertainty, the nature of the procedure, sample size or other factors influence uncertainty and limitations in the data
  - evaluate information sources and compare ideas, information and opinions presented within and between texts, considering aspects such as acceptance, bias, status, appropriateness and reasonableness
  - compare findings to theoretical models or expected values
- suggest improvements and extensions to minimise uncertainty, address limitations and improve the overall quality of evidence
- appreciate the role of peer review in scientific research.

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA 2024)

Evaluating the validity and reliability of evidence

evidence
data, observations or facts obtained from research

Evidence is information or data about a concept that has been systematically collected and can be used to form conclusions. Evaluating evidence is an important science inquiry skill in QCE Biology. Evaluating the evidence that has been used in an investigation should be done before conclusions are drawn about the data. In a scientific report, evaluation of the evidence and suggested improvements are typically included in the discussion section. To evaluate evidence, you should consider how measurement error, instrumental uncertainty, the nature of the procedure, the sample size and other factors may influence the level of uncertainty and limitations of the data. Table 1 provides some guidance to help you evaluate evidence based on these factors.

TABLE 1 Factors to consider and questions to ask when evaluating evidence

Factor to evaluate	Example of questions to ask to evaluate evidence	Impact
Measurement error	Were there random errors in the data?	Random errors reduce the precision of data.
	Were there systematic errors in the data?	Systematic errors reduce the accuracy of data.
Instrument uncertainty	Was the equipment calibrated before being used in the investigation?	Uncalibrated equipment may lead to incorrect readings or may introduce systematic errors into the data set.
Nature of the procedure	Were experimental procedures followed in a systematic way?	Variations in collection methods can result in variability in data.
Sample size	Was the sample size large enough?	A small sample size may not provide an accurate representation of the population of interest, and may also increase the effect of outliers skewing results.

Comparing findings to theoretical models or expected values

Another component of evaluating evidence is to compare the results obtained against biological models, or to compare the results against expected values. If the findings align with what is understood by biological models or with expected values, you can be more confident in the investigation methods and the conclusions drawn. If the findings contradict a theoretical model or deviate from expected values, it could indicate flaws in the investigation design or the hypothesis proposed.

FIGURE 1 To evaluate evidence, take a close look at the results and the investigation methods.

Evaluating information, ideas and opinions

Another important science inquiry skill is the ability to evaluate information sources and compare ideas, information and opinions presented within and between texts, considering aspects such as acceptance, bias, status, appropriateness and reasonableness. An important part of evaluating information from sources is the ability to distinguish between **scientific ideas** and **non-scientific ideas**. Scientific ideas are ideas that have been acquired, refined or supported by the scientific method (e.g. the theory of evolution, which is based on years of scientific research). Non-scientific ideas are ideas that have been established by techniques that do not follow the scientific method or are not supported by the scientific method (e.g. horoscopes are not supported by scientific evidence). Being able to distinguish between scientific ideas and non-scientific ideas will help you better evaluate information from different types of sources.

scientific idea
an idea or theory that is based on empirical evidence and has been tested or supported by the scientific method

non-scientific idea
an idea or theory that is not based on empirical evidence and has not been tested or supported by the scientific method

FIGURE 2 Predicting the future using tarot cards is a non-scientific idea.

Sources of information

Many sources of information can be used to help conduct research or understand the findings of research. Understanding the strengths and weaknesses of different sources of scientific information can help you evaluate the credibility of the information, assess claims, make informed decisions and communicate effectively. Table 2 outlines some common sources of information and their strengths and weaknesses.

TABLE 2 Sources of information and their strengths and weaknesses

Source	Description	Example	Strengths	Weaknesses
Journal articles	Scholarly papers published in academic journals that present original research findings, theories or reviews	A paper published in *The Journal of Infectious Diseases* that outlines a treatment for Ebola virus	• Provides detailed information about research methods, results and conclusions • Undergoes peer review by experts in the field	• Can be highly technical and difficult for non-experts to understand • Can take a long time to publish • May not be accessible to the public
Mass media communications	News articles or broadcasts that present information to a wide audience	A news segment on the ABC about a study on the impact of bushfires on wildlife populations	• Reaches a large audience • Can raise awareness of scientific issues	• May oversimplify complex scientific concepts or exaggerate findings for dramatic effect • May not provide sufficient context or detail
Opinions	Personal views or beliefs on topics	A TikTok video by a fitness influencer discussing a diet plan to improve muscle gain	• Can provide different perspectives on scientific issues • Can be accessible to the public	• May not be based on scientific evidence • Can be biased or influenced by personal beliefs or interests
Policy documents	Documents created by governments or organisations that outline plans or guidelines related to an issue	The *Environment Protection and Biodiversity Conservation Act*	• Can influence public policy and decision-making • Can provide a framework for addressing scientific issues	• May not be based on the most up-to-date scientific research • Can be influenced by political or economic interests
Reports in the public domain	Documents created by researchers or organisations that are publicly available and provide information about issues	Suicide Prevention Australia's annual report	• Can provide accessible information about scientific issues to the public • Can highlight areas for further research or action	• May not undergo the same level of scrutiny as peer-reviewed journal articles • May be biased or influenced by the interests of the organisation it was produced by

FIGURE 3 Mass media communications can reach a large audience.

Factors to consider when evaluating information

Not all information is reliable or written by experts. You need to be careful that you only refer to data and research that is credible. To evaluate the reliability of a source, consider the following factors:

- acceptance – the quality of the research as judged by major science journals. Research papers with high acceptance usually use high-quality methods, descriptive or qualitative analytical methods, and a large sample size, and they disclose any funding sources. Acceptance by a well-respected journal is evidence of reliability.
- bias – the tendency to present unbalanced consideration of a question that encourages one outcome or answer over others. As some degree of bias is nearly always present in a published study, also consider how bias might influence the study's conclusions. Internal bias could come from poor study design and implementation, or from data analysis that favours one side. External bias happens when the findings are generalised to other groups or populations without justification.
- status – how well a source is regarded by the community. This could range from generally reliable in its areas of expertise, to marginally reliable, generally unreliable, misleading or even blacklisted. Look for sources of high status.
- appropriateness – how well a source is suited to a particular purpose. In our case, appropriate sources would be scholarly, peer-reviewed articles and books. Less appropriate sources would be magazine articles and newspaper articles from well-established companies.
- reasonableness – whether the solutions proposed are based on results, assumptions and observations that make sense. Being able to judge whether an answer is reasonable requires a deeper understanding of biology than just being able to solve a problem mechanically.

Suggesting improvements

Once you have analysed and evaluated the evidence and the investigation methods, you should suggest improvements and extensions to minimise any uncertainty or limitations identified, and/or provide suggestions that can help improve the overall quality of evidence. Depending on what you have identified in your evaluation of evidence, you might suggest changes to sample size, equipment used, calibration procedures, sampling techniques used, data analysis methods applied, or to specific steps in the investigation.

The role of peer review in science

Peer review is a process in which the work of a researcher or author is evaluated by other experts in that field. Before a scientific article can be published, it must undergo peer review to ensure that the ideas presented in the research and the investigation methods used are valid and reliable. This process helps ensure that only high-quality findings are published and is why journal articles from science publications have high credibility.

peer review
the process in which experts evaluate the quality, relevance and validity of another researcher's work prior to its publication

Check your learning 1.8

Check your learning 1.8: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Identify** one strength and one weakness of each of the following sources of information.
   - **a** journal articles (2 marks)
   - **b** mass media communications (2 marks)
   - **c** opinions (2 marks)

2 **Identify** where evaluation of evidence and suggested improvements would be included in a scientific report. (1 mark)

3 **Describe** peer review and explain why it is important in scientific research. (2 marks)

Analytical processes

4 **Distinguish** between scientific and non-scientific ideas. (2 marks)

5 Libby is evaluating a research investigation and notices that the sample used seems much smaller than what is typically used in investigations of that kind. **Evaluate** how a small sample size may affect the reliability and validity of results. (2 marks)

Lesson 1.9
Communicating scientifically

Key ideas

- → Evidence can be used to construct scientific arguments.
- → Scientific arguments and evidence can be used to draw a conclusion, which is a short summary of the findings of an investigation in response to the investigation hypothesis.
- → There are many ways to communicate scientific information.
- → Correctly acknowledging sources using referencing conventions is an important part of scientific communication.

Learning intentions and success criteria

Science inquiry skills

This lesson provides support for the following science inquiry skills:

- select, synthesise and use evidence to construct scientific arguments and draw conclusions
- communicate to specific audiences and for specific purposes using appropriate language, nomenclature, genres and modes
- acknowledge sources of information and use standard scientific referencing conventions

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA 2024)

Constructing scientific arguments

When you have evaluated evidence and found it to be valid and reliable, you can use it to construct evidence-based, scientific arguments. In doing this, you may address the following broad questions:

- What is the origin of, or who was responsible for, the experimental results, findings, evidence or raw data collected?
- Are the experimental results, findings, evidence or raw data accurate, precise, reliable and/or valid?
- What kinds of errors, inconsistencies and outliers may have affected the experimental results, findings, evidence or raw data collected?
- What kinds of background information (such as biological concepts, scientific understanding or other researched information sources) were used to link or connect the experimental results, findings, evidence or raw data to the investigation question and to the aim?
- What series of steps or procedures could be used to improve the investigation design or methodology for future trials of this scientific investigation?

Argument structure

The structure of the overall argument usually follows a pattern. Its length is determined by the number of supporting arguments addressed. One supporting argument usually corresponds to one paragraph.

Introduction (what is your overall argument/point of view?)

- Position statement (what is your hypothesis or summary of the scientific investigation?)
- List the arguments that you will make.

Explain your supporting arguments

- Supporting argument 1:
  - Point – identify your argument in a topic sentence
  - Explanation – support the argument with evidence, scientific findings, results or data
- Supporting argument 2:
  - Point – identify your argument in a topic sentence
  - Explanation – support the argument with evidence, scientific findings, results or data
- Supporting argument 3:
  - Point – identify your argument in a topic sentence
  - Explanation – support the argument with evidence, scientific findings, results or data

Reinforce your main point – "To sum up …"

Language features

When writing a scientific argument, using the following language features will enhance your writing:

- connectives to show cause and effect – for example, "As an outcome of ...", "As a result of ...", "because ...", "consequently ..."
- scientific terminology and/or supporting figures
- supporting facts and/or quotes from experts or other researched external sources of information – for example, "A study conducted by XX found that …"

conclusion
a summary of the findings and results obtained from an investigation

support
agree with (in relation to the hypothesis)

refute
contradict or not support (in relation to the hypothesis)

generalisability
the extent to which findings can be applied to other situations or populations

externally valid
in relation to investigation results, applicable to other settings outside the investigation

- evaluative statements – for example, "The data shows a clear trend …", "Evidence contradicts the argument that …"
- formal language – avoid personal language (e.g. I, you, he, she, we, they, me, him, her, us, them); for example, use "The hypothesis was supported", not "I proved my hypothesis".

Drawing conclusions

Once you have evaluated your evidence and used this to construct your arguments, you can then develop an evidence-based **conclusion**. A conclusion is a statement or a few statements that summarise the findings of an investigation in response to the investigation hypothesis. Scientists never say that a hypothesis has been "proved" or "disproved". After all, there may be another hypothesis that explains the relationship even better than the one that was tested. Instead, the conclusion assesses whether findings either **support** or **refute** the hypothesis.

If the results or investigation methods had low validity or reliability, or did not address the research aim, then you should not draw a conclusion. **Generalisability** is the degree to which the findings of research can be applied to other situations. Most conclusions from an investigation only apply to the population of that specific study. Conclusions can only be drawn for wider populations if the investigation is **externally valid**.

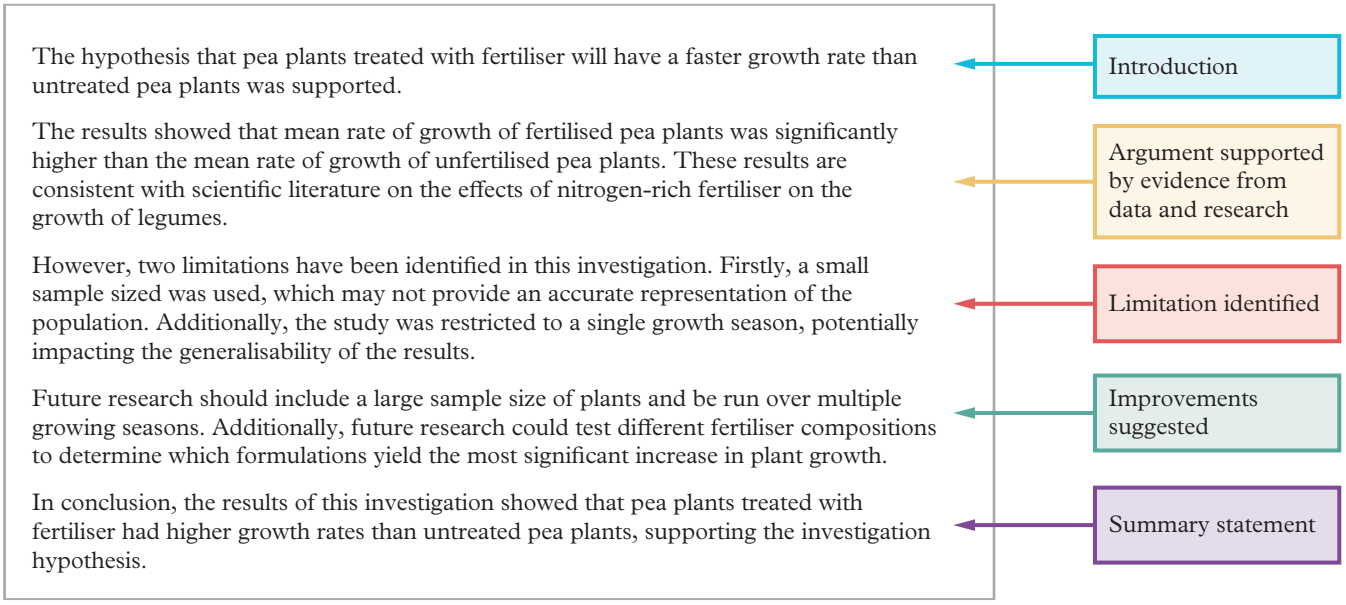

FIGURE 1 Example of using evidence to structure arguments and form a conclusion

Communicating findings scientifically

Scientific writing has its own requirements and expectations, just as any other type of writing does. It is important to pay attention to those writing conventions.

The findings of experiments can be presented in a number of formats: as a scientific report, a scientific poster, a conference presentation or a journal article.

When it is time to communicate your findings, you need to plan what is to be written. Time spent in planning will save time overall and result in a better report, which is also easier to write. Think about the different sections in a report in order, and plan each section (Table 1).

TABLE 1 Components of a scientific report

Section	Purpose
Title	Outlines the problem or research question under investigation
Introduction	Indicates what the report is about. It should include: • a rationale for the research question • findings from background research • identification and justification of modifications to the initial methodology • a hypothesis for the experiment that includes the IV and DV
Context	A background paragraph that helps to give the reader the knowledge required to understand the rest of the essay
Equipment list	Lists pieces of equipment or materials needed to carry out the experiment and information about concentration and amount of substances
Risk assessment	Outlines the possible hazards involved in the experiment, as well as the measures taken to control and/or remove these hazards
Method	Lists clearly and concisely all steps involved in conducting the experiment. There should be enough detail to allow another person to conduct the same experiment and collect sufficient data. It may be necessary to include a diagram or photo of the experiment set-up
Results	Displays the collected qualitative and/or quantitative data from the experiment in a format that can be interpreted easily (e.g. table, graph, photo, descriptions, or any equations necessary)
Discussion	Includes: • an analysis of the data in relation to the research question and an identification of trends, patterns and/or relationships • an evaluation of the validity of the experiment through the identification of uncertainty and limitations of the evidence collected • suggestions for improvements to the experimental design. Do *not* re-state the results in the discussion unless it is to analyse or interpret them in a meaningful way
Conclusion	States the findings in relation to the research question; acknowledges whether the hypothesis was supported or refuted
Bibliography	Lists all the references used in the research; may be presented in alphabetical order, using a consistent style for each entry

It is important to proofread what you have written. Look for spelling and grammatical errors. Be alert for unnecessary repetition and sentences that are too long. Strategies include proofreading from the bottom of the page and reading up one sentence at a time, or reading the report aloud. The first draft should never be the last draft.

Tips for writing scientifically

The following tips will help you write scientifically.

- Use shorter sentences and words where possible. This will make your meaning clearer and your argument easier to follow. When there are many subordinate clauses, each winding around a meaning lost somewhere in a muddle of obscurantism and verbosity, included to make the author seem more clever and important, this often instead results in the reader becoming lost, in a maze of impenetrable text, when the sentence really needs to be split up into shorter, more digestible sentences in order to facilitate comprehension of the written text. How hard was the preceding sentence to read? Instead, keep it short, keep it simple. For example, "The aim of the present study by the author was to provide insight into …" is too wordy. It could be better written as: "The aim of the experiment was to …".

- Scientific writing avoids the first person. So don't use "I" or "We", or if you must use it, do so sparingly.
- If you are reporting the results of an experiment, use the past tense because it is a report of work that you have already carried out. Often, instructions are given in the present tense, but a lab report reports what was done. For example, "The liquid was heated to 78°C, and the temperature was measured using a thermometer".
- When discussing analysis of data, use the present tense. For example, "The mean of the results in Table 2 is 6.4 cm, which overestimates the actual length of the stem by 15%".
- It is never possible to prove a fact definitively. For this reason, biologists talk about evidence being *consistent with* a hypothesis, rather than *proving* the hypothesis. It is possible that the results may show that a particular hypothesis should be rejected. If so, it is fine to say that.
- In referring to work done by others, some verbs that are commonly used are "claimed", "suggested" and "demonstrated" – these are in order of increasing confidence by the writer in what has been written.
- When using a key term or an unusual abbreviation for the first time, provide a definition. Some common abbreviations do not require an explanation – examples are e.g., i.e., et al., ca. and etc. Use these abbreviations correctly.
- Don't be vague. For example, do not use "structure" when you mean "organelle". If there is a specific biological or scientific term to describe what you are referring to, then you should use it.
- Always report numbers with their associated units. Consider using either scientific notation for very small or very large numbers, or a unit with an appropriate prefix. For example, 0.000045 grams is better written as 4.5×10^{-5} g or 45 µg.
- Pictures, graphs, equations, biological structures and reactions can all play an important part in communicating meaning in a scientific essay. These should be referred to in the main part of the text by a figure number. For example, "Reaction rate levelled off after 1 minute, as shown in Figure 1".
- In an essay or a report, where you are relying on the work of others, use references to indicate this. Your teacher will advise you on the precise format to use. One method is to put the surname of the author(s) and the year of the publication in brackets; for example (Smith and Jones, 2019). Another method is to insert a superscript number at the end of the relevant sentence or phrase. The full details of the source are provided in a references section (or bibliography) at the end of the essay or report. These details should include the authors' names and enough details for readers to find them for themselves. There are various free online and downloadable tools to help you keep track of references and to create a properly formatted bibliography (e.g. Zotero, Citation Machine). However, even though these tools will do much of the work, you still need to check the end result and proofread it, particularly when it comes to consistency in references.

Referencing

An important part of communicating in science is acknowledging the sources of information you have used to obtain and make sense of your findings. Correct acknowledgement of where you have sourced or collected data from is very important. When acknowledgement is not given, it can appear as if you are trying to pass off the work of other people as your own. This is called plagiarism.

There are many referencing styles that can be used to acknowledge sources. You should always check your assessment details to see whether a particular style of referencing is required. If not, two common referencing styles used in science are:

- Harvard-style referencing
- APA (American Psychological Association) referencing.

Whichever style you select, make sure you stick to it and only use one style consistently – do not mix and match different referencing styles.

in-text references references that appear in the flow of body text; also known as citations

bibliography a detailed list of all references used

In-text references are used each time you write about, refer to or quote the work of others in the body text of your response. These references are placed next to, or within, the flow of text or information in your response that has come from an external source. A final reference list or **bibliography** should be included at the end of every scientific report. This is the full list of sources you have used in your research. Each referencing style has specific conventions for how in-text references and references lists are presented. Different sources of information (e.g. a website versus a book) can have slightly different conventions. Many universities have online referencing guides that explain the conventions used in different reference styles. An example of APA style for an in-text reference and the corresponding entry in the references list is shown in Figures 2 and 3.

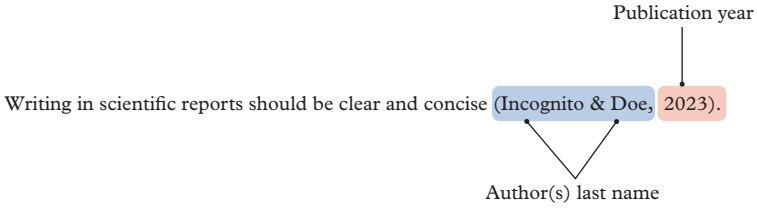

FIGURE 2 Example of an in-text reference (citation) from a journal article using APA 7 style

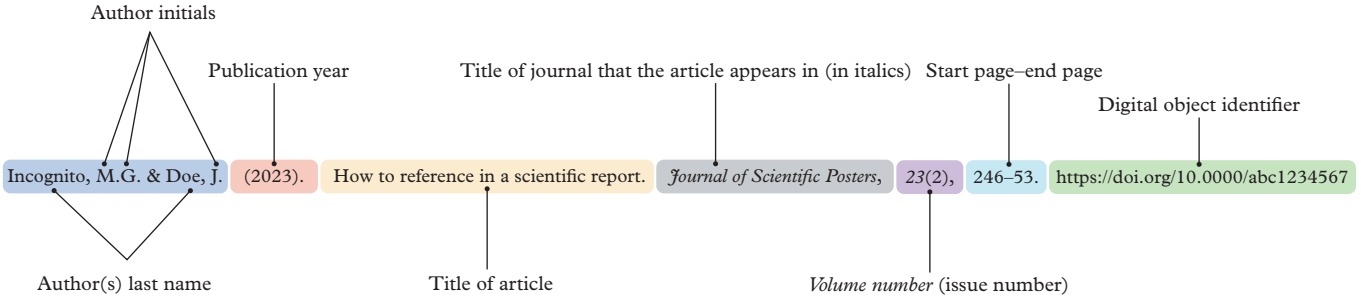

FIGURE 3 How to list the referenced (cited) journal article from Figure 2 in a references list using APA 7 style

Check your learning 1.9

Check your learning 1.9: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Identify** which section of a scientific report features the following:
   - **a** the hypothesis (1 mark)
   - **b** interpretation of results (1 mark)
   - **c** suggested improvements that could be made to the investigation (1 mark)
   - **d** a statement explaining whether the hypothesis was supported or refuted. (1 mark)

2 **Describe** how scientific writing differs in style from other kinds of writing. (1 mark)

3 **Explain** the purpose of a list of references at the end of a scientific report or essay. (1 mark)

Analytical processes

4 For each of the following statements, **identify** how the statement has not adhered to scientific writing conventions and **propose** how the statement could be rewritten to be scientific.

a "We hypothesised that tomato plants treated with fertiliser would have a faster rate of growth compared to untreated tomato plants." (2 marks)

b "The results of the experiment proved the hypothesis." (2 marks)

Lesson 1.10
Preparing for your data test

Key ideas

→ The data test is an assessment that gets you to apply understanding, analyse data and interpret evidence.

→ You can prepare for your data test by completing practical work, skill drills and data drills.

Learning intentions and success criteria

oxforddigital **The rest of this lesson is available on Oxford Digital.**

Lesson 1.11
Conducting your student experiment

Key ideas

→ Your student experiment requires you to modify an experiment and address your own related hypothesis or question.

→ You will research and plan your experiment, analyse, interpret and evaluate your evidence, and communicate your findings.

Learning intentions and success criteria

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Lesson 1.12
Conducting your research investigation

Key ideas

→ There are two parts to the research investigation: obtaining secondary evidence for your research question through scientifically credible sources and then, based on the research you have conducted, reaching a justified conclusion about whether your findings support the claim.

Learning intentions and success criteria

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Lesson 1.13
Preparing for your exams

Key ideas

→ There are a range of habits you can practise to maximise your success in exams.

→ Cognitive verbs tell you what information you need to provide in your answer to a question.

Learning intentions and success criteria

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MODULE 1

Lesson 1.14
Review: Biology toolkit

Summary

1.1
- Biology is the study of living organisms.
- Studying Biology can lead to a diverse range of career pathways.
- QCE Biology is divided into units and topics.
- The science inquiry skills and their application are important for success in QCE Biology.

1.2
- First Nations peoples are the traditional custodians of the land we know now as Australia.
- First Nations peoples have longstanding scientific knowledge.
- Correctly acknowledging cultural and/or language groups, rejecting deficit discourse, avoiding Eurocentrism and critically evaluating sources of information can help you to respectfully engage with First Nations perspectives in QCE Biology.

1.3
- A hypothesis is a statement that attempts to answer a question raised by observations and can be tested by experimentation.
- The scientific method is a way of testing a hypothesis through controlled experimentation.

1.4
- Primary data is data you collect firsthand; secondary data is data collected by someone else.
- There are many different types of investigations you can run to collect data.

1.5
- Before conducting research, scientists must consider whether the investigation is safe and ethical, and the potential impacts it might have on the environment.

1.6
- There are many ways to collect primary and secondary data for an investigation.
- Sampling is way to select subjects for an investigation. Common sampling techniques are random sampling, systematic sampling and stratified sampling.
- Microscopy techniques are important in biological science.
- Tools such as information and communication technology, scientific texts, databases and online sources can be valuable in generating primary data and/or collating secondary data for an investigation.
- Data collected for an investigation should be systematically recorded.

1.7
- Translating information between graphical, numerical and/or algebraic forms is important in Biology.
- Mathematical techniques can be used to summarise data and help identify relevant trends, patterns, relationships, limitations and uncertainty.
- Data can be presented and communicated in many formats.

1.8
- Data and reasoning can be used to discuss and evaluate the validity and reliability of evidence.
- Sources of information should be evaluated before being used to support scientific research.
- If limitations or uncertainty in data have been identified, the researcher should suggest how these can be minimised in future research.
- Peer review ensures the work of research scientists is evaluated and of high quality prior to publication.

1.9
- Evidence can be used to construct scientific arguments.
- Scientific arguments and evidence can be used to a draw conclusion, which is a short summary of the findings of an investigation in response to the investigation hypothesis.
- There are many ways to communicate scientific information.
- Correctly acknowledging sources using referencing conventions is important part of scientific communication.

1.10
- The data test is an assessment that gets you to apply understanding, analyse data and interpret evidence.
- You can prepare for your data test by completing practical work, skill drills and data drills.

1.11
- Your student experiment requires you to modify an experiment you have conducted and address your own related research question.
- You will research and plan your experiment, analyse, interpret and evaluate your evidence, and communicate your findings.

1.12
- There are two parts to the research investigation: obtaining secondary evidence for your research question through scientifically credible sources and then, based on the research you have conducted, reaching a justified conclusion about the whether your findings support the claim.

1.13
- There are a range of habits you can practise to maximise your success in exams.
- Cognitive verbs tell you what information you need to provide in your answer to a question.

Review questions 1.14A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

1 "Koalas are adapted to their environment." This statement communicates that

A due to features that they possess, koalas are able to survive in most environments.

B koalas developed special features that they needed in order to survive in their environment.

C koalas are able to develop features that make them better suited to the environment should the need arise.

D due to features that they possess, koalas are well suited to the environment in which they are naturally found.

2 Which of the following statements best describes the relationship between a hypothesis and an experiment?

A The results of an experiment may support a hypothesis.

B The results of an experiment are needed for a hypothesis to be formed.

C A hypothesis cannot be formed unless experimental evidence is available.

D An experiment is designed to show whether a hypothesis is supported or not.

Use the following information to answer questions 3 and 4.

A biologist is interested in a certain chemical compound (compound X) that might be used to promote the growth of plants.

To test the effect of compound X on plant growth, the biologist planted three groups of plants of the same species (50 plants in each group) and watered each plant with the same weighted quantity of rainwater or solution of rainwater and compound X. The results of the investigation are summarised in the table.

Group	Watered with	No. dead plants	No. surviving plants	Average weight of surviving plants (g)
I	Rainwater	3	47	310
II	1% compound X in rainwater	12	38	420
III	2% compound X in rainwater	26	24	410

3 Which of the following could explain the difference in average weight of the surviving plants in groups I and II?

A Compound X stimulated the growth of some plants.

B Compound X caused the death of some plants, which may have been the smaller ones.

C Compound X caused the death of some plants, which left more room for the rest to grow.

D All of the above could explain it.

4 In considering the causes of death of the plants in all groups, which of the following seems the most reasonable interpretation?

A The deaths could not have been due to compound X because some group I plants died.

B Compound X can kill plants but the lethal concentration (that required to kill) varies with individual plants.

C Twice as many plants died in group III as in group II because they were given twice as much compound X.

D Compound X caused the death of plants in groups II and III, but the amount applied to different plants must have varied.

5 A researcher is recording the length of gum leaves on a eucalyptus branch. The lengths of the leaves are as follows: 10.3 cm, 9.8 cm, 10.4 cm, 7.8 cm, 9.3 cm and 7.6 cm. What is the mean length of gum leaves on the branch?

A 9.2 cm
B 9.6 cm
C 9.2 mm
D 9.6 mm

6 Which of the following r values indicates the strongest correlation?

A +0.8
B +0.7
C −0.9
D −0.6

7 Which of the following investigation types involves a researcher manipulating variables to determine whether a cause-and-effect relationship exists?

A case study
B descriptive investigation
C correlational investigation
D experimental investigation

8 Which of the following statements is correct?

A Random errors reduce the precision of data, while systematic errors reduce the accuracy of data.
B Random errors increase the precision of data, while systematic errors reduce the accuracy of data.
C Random errors increase the accuracy of data, while systematic errors reduce the precision of data.
D Random errors reduce the precision of data, while systematic errors increase the accuracy of data.

9 In which section of a scientific report are limitations identified and suggested improvements recommended?

A Method
B Conclusion
C Discussion
D Introduction

10 Which of the following summary statistics relates to the spread of data around the mean?

A mean
B range
C variance
D standard deviation

Review questions 1.14B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

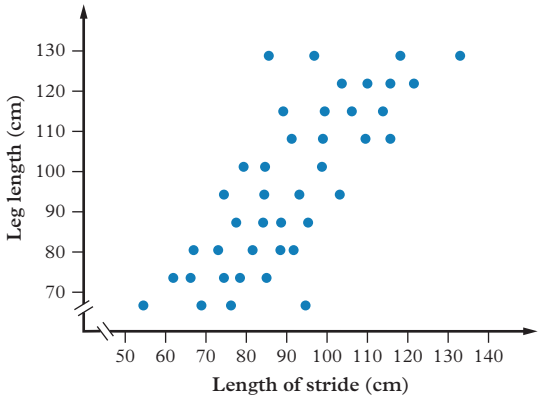
11 **Describe** the scientific method in three steps. (3 marks)

12 **Explain** the importance of a logbook during a student experiment. (1 mark)

13 **Define** validity. (1 mark)

Analytical processes

14 A student noticed that there seemed to be a direct relationship (correlation) between the length of a person's leg (measured in centimetres from the hip joint to the base of the ankle) and the length of their stride. To check the accuracy of this observation, the student measured the leg length and stride of several people. A sand area with a base board was set up. The subjects aligned the tips of their toes with this board and stepped into the sand. Length of stride was measured as the distance from the base board to the back of the heel marking in the sand. The results were plotted on the graph shown.



a **Deduce** what hypothesis the student was testing. (1 mark)

b **Identify** the IV and DV in the experiment. (2 marks)

c **Explain** whether this was a controlled experiment. (1 mark)

d **Determine** what scientists call the measurements shown on the graph. (1 mark)

e **Explain** why the results were presented graphically. (1 mark)

f **Determine** the range of lengths of stride recorded for people with legs 90 cm long. (1 mark)

g Divide the graph into four equal boxes to give four categories: short leg, short stride; short leg, long stride; long leg, short stride; and long leg, long stride. Count the number of people in each category. **Determine** which boxes most people fit into. (1 mark)

h **Reflect on** the hypothesis. Was it supported? (1 mark)

i **Identify** a possible extraneous variable in this experiment. (1 mark)

j **Describe** two ways this experiment could be improved to give a more accurate interpretation. (2 marks)

Knowledge utilisation

15 A student germinated 50 oat seeds. Once germinated, the height of each seedling was measured every 2 days for 26 days. The mean height of the seedlings was calculated for each set of measurements. The results are shown in the table.

Time (days)	Mean height (mm)
0	1
2	2
4	4
6	11
8	24
10	43
12	73
14	92
16	105
18	112
20	117
22	122
24	124
26	126

a **Deduce** how the student determined the mean height for each set of individual heights. (1 mark)

b **Construct** this data as a graph. (3 marks)

c **Determine** the rate of growth on:

i day 3 (1 mark)

ii day 15 (1 mark)

iii day 22. (1 mark)

d **Interpret** the data to draw a conclusion about the growth of oat seedlings over this period. (1 mark)

e **Judge** the reliability of the data. **Explain** your answer. (2 marks)

f **Predict** the mean height of the oat plants on day 28 from this data. **Explain** your answer. (2 marks)

16 School ovals are primarily well-maintained grass with heavy usage during school terms. The ovals are not used during school holidays, so weed and grass growth changes.

a **Design** an experiment to determine the percentage cover of grass on the school oval during term time and school holidays. (4 marks)

b Draw any equipment used and **explain** what and how outcomes will be measured to achieve consistent results. (4 marks)

c Write up a method and identify any uncontrolled variables. **Describe** how they might affect the validity and reliability of your results. (4 marks)

Module 1 checklist: Biology toolkit

UNIT 3

Biodiversity and the interconnectedness of life

Unit 3 overview

In Unit 3, students explore the ways biology is used to describe and explain: the biodiversity within ecosystems; a range of biotic and abiotic components; species interactions; adaptations of organisms to their environment; principles of population dynamics; and how classification systems are used to identify organisms and aid scientific communication. An understanding of the structure of ecosystems, the processes involved in the movement of energy and matter in ecosystems, and how environmental factors limit populations is essential to appreciate the dynamics, diversity and underlying unity of these systems. Students investigate the interactions within and between species, and the interactions between biotic and abiotic components of ecosystems. They also investigate how measurements of abiotic factors, population numbers, species diversity and descriptions of interactions between species can form the basis for spatial and temporal comparisons between ecosystems. They examine and analyse data collected from fieldwork to understand the interconnectedness of organisms, the physical environment and the impact of human activity.

Unit objectives

1. Describe ideas and findings about biodiversity and populations, and functioning ecosystems and succession.
2. Apply understanding of biodiversity and populations, and functioning ecosystems and succession.
3. Analyse data about biodiversity and populations, and functioning ecosystems and succession.
4. Interpret evidence about biodiversity and populations, and functioning ecosystems and succession.
5. Evaluate processes, claims and conclusions about biodiversity and populations, and functioning ecosystems and succession.
6. Investigate phenomena associated with biodiversity and populations, and functioning ecosystems and succession.

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Unit 3 Topics

Topic	Module	
Topic 1 Biodiversity and populations	**Module 2**	Biodiversity
	Module 3	Populations
Topic 2 Functioning ecosystems and succession	**Module 4**	Functioning ecosystems
	Module 5	Succession

MODULE 2

Biodiversity

Introduction

Ecosystems are classified based on both the biotic (living) and abiotic (non-living) factors that exist at the location. Factors within these ecosystems determine the distribution and abundance of the organisms that live there. Scientists have developed several methods of observing the distribution and abundance of species, in order to effectively manage ecosystems and protect biodiversity.

Prior knowledge

Prior knowledge quiz Check your understanding of concepts related to biodiversity before you start.

Subject matter

Science understanding

- → Describe genetic, species and ecosystem diversity.
- → Describe the biological species concept and identify its limitations.
- → Identify the major taxa in the Linnaean system of biological classification and explain how it is used to classify and name species.
- → Use dichotomous keys to identify and classify organisms.
- → Use the Lincoln index $\left(N = \frac{M \times n}{m}\right)$ to estimate the size of a population.
- → Determine the diversity of species using measures such as species richness, evenness (relative species abundance), percentage cover, percentage frequency and Simpson's diversity index, $SDI = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$
- → Describe how sampling can be used to investigate the species diversity of a given area, considering the most appropriate
  - sampling method: random, systematic, stratified
  - sampling technique: quadrats, line transect, belt-transect, capture-recapture
  - strategies to minimise bias: size and number of samples, random-number generators, counting criteria, calibrating equipment and noting associated precision
  - measure/s of diversity.

→ Describe how the distribution and abundance of species in an ecosystem are influenced by
  – biotic factors – food availability, competition for resources, predation, disease
  – abiotic factors – space, shelter, availability of water, nutrients, environmental conditions.
→ Explain that ecosystems are composed of varied habitats, including microhabitats, which may impact the distribution of species (e.g. uniform, random or clumped), and therefore the validity and reliability of different sampling methods/techniques.
→ Interpret data from an experiment investigating how abiotic factors affect the distribution, abundance and/or biodiversity of species in an ecosystem.
→ Interpret data to classify and name ecosystems using Specht's classification system and the Holdridge life zone classification scheme.

Science as a human endeavour

Appreciate that
→ there are multiple definitions for *species*, and each has limitations. Examples include the biological species concept, phylogenetic species concept, ecological species concept and morphological species concept.

Science inquiry

→ Use the process of stratified sampling to
  – identify different habitats within an ecosystem
  – investigate changes to abiotic factors in different strata
  – investigate changes to community composition in different strata, e.g. layers of a forest
  – infer species interactions within and between strata
  – classify an ecosystem.
→ Investigate
  – how abiotic factors affect the distribution and/or abundance of species in an ecosystem
  – changes in species composition along an environmental gradient
  – how environmental factors affect the global distribution of ecosystems
  – how the process of classifying ecosystems allows for effective ecosystem management.
→ Compare species diversity in two spatially variant ecosystems of the same classification.

Practicals

oxforddigital **These lessons are available on Oxford Digital.**

Lesson 2.11 Analysing vegetation patterns using a line transect
Lesson 2.12 Stratified sampling of vegetation patterns
Lesson 2.13 Quadrat sampling to estimate distribution and abundance
Lesson 2.14 Comparing species diversity in two spatially variant ecosystems

Lesson 2.1
Understanding biodiversity

Key ideas

- → The unique combination of biotic and abiotic factors within an ecosystem creates biodiversity.
- → Diversity exists between different species in an ecosystem.
- → Variation of the genes in individuals of the same species creates diversity within the species.

Learning intentions and success criteria

Biodiversity

Organisms (living things) exist in a variety of **environments**. They can be found in water, on land, in the air, in the soil or even inside or attached to other organisms. Some organisms have even been found in environments that we would consider uninhabitable. Each type of organism has special structures and behaviours (**adaptations**) that help it obtain food and water and avoid predation, to survive in its environment. Because **ecosystems** vary so much, organisms have developed a myriad of adaptations to best fit their environment. When studying or managing an ecosystem, it is important to know the types of organisms that make up the **community**, their needs for survival and how they interact with the world.

organism
an individual living thing, such as a plant, animal or bacterium

environment
the conditions (biotic and abiotic) in which an organism lives

adaptation
a physical or behavioural feature of an organism that enhances its ability to survive and reproduce in a particular environment

ecosystem
a biological community of interacting organisms and their physical environment

community
all the species that occupy a particular place at a given time

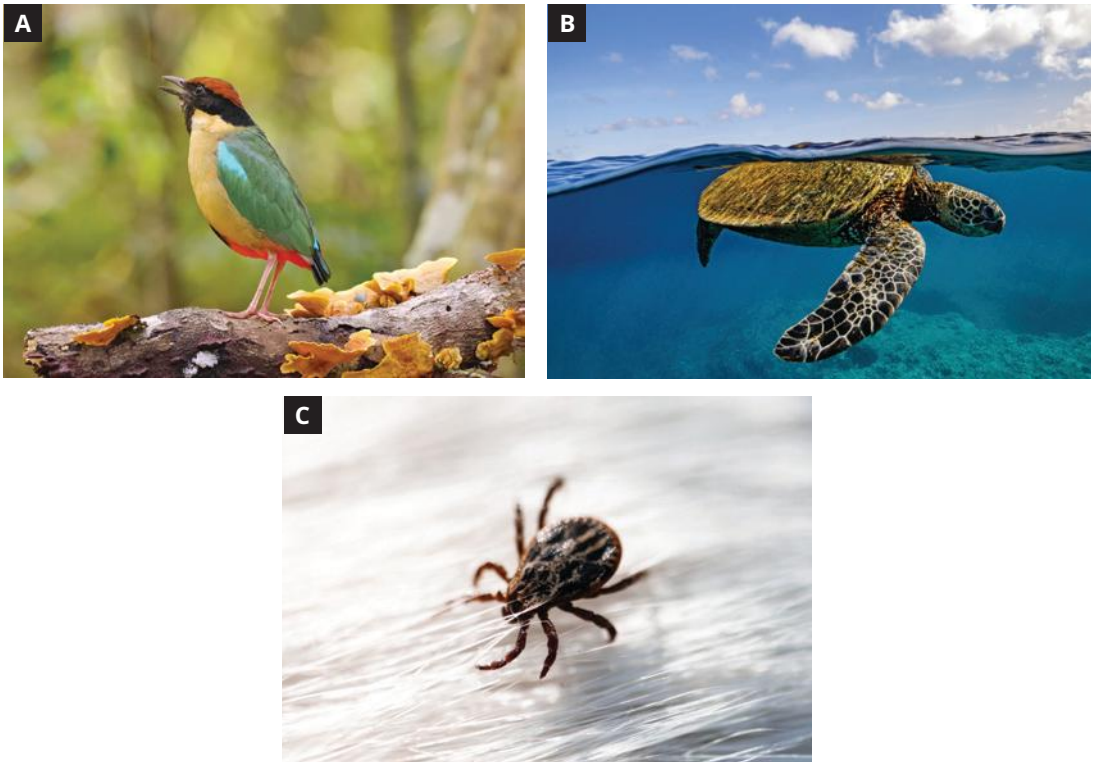


FIGURE 1 Different organisms can live in a variety of environments, including (A) land, (B) the sea and even (C) on another organism.

biodiversity
the range of living organisms and their environments

The term **biodiversity** refers to the variety of life, from the smallest microbe to the largest animals and plants, including the genetic material that gives them their specific characteristics, and the ecosystems in which they survive. In this lesson we will explore the three levels of biodiversity:

- species diversity
- genetic diversity
- ecosystem diversity.

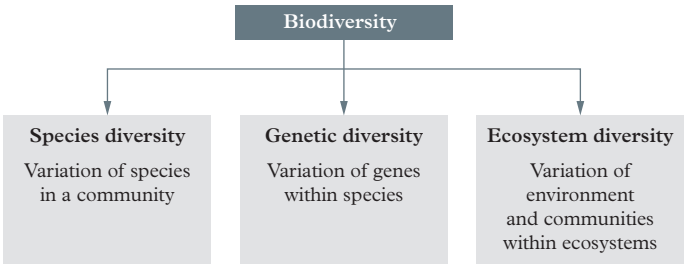


FIGURE 2 The three levels of biodiversity

Species diversity

species
the most specific taxonomic group containing very closely related organisms; allocated two (genus and specific) names; members of the same species can produce fertile offspring when mating under natural conditions

species diversity
the number of species, and the relative abundance of each species, in a community

A **species** is a group of organisms with similar characteristics that can mate and produce fertile offspring. **Species diversity** is the variety and abundance of different species within an ecosystem. In a natural ecosystem, there is usually a high level of diversity of species. The most diverse ecosystems on Earth are tropical rainforests and coral reefs. Factors such as high availability of resources, shelter and nutrition enable these locations to maintain a high diversity of species, from the trees and corals that epitomise these ecosystems to the many species of animals that live in, on and around them. For example, different species of fish, shrimp, starfish, coral and turtles can thrive in the reef and many species of birds, insects, mammals and plants can thrive in the rainforest. A rich variety of microbial species (e.g. bacteria) also inhabit every possible region of these environments. Species diversity relates to the wide array of organisms present in an area, as well as the diversity between closely related species, such as the Ulysses and birdwing butterflies in the Daintree rainforest in North Queensland.

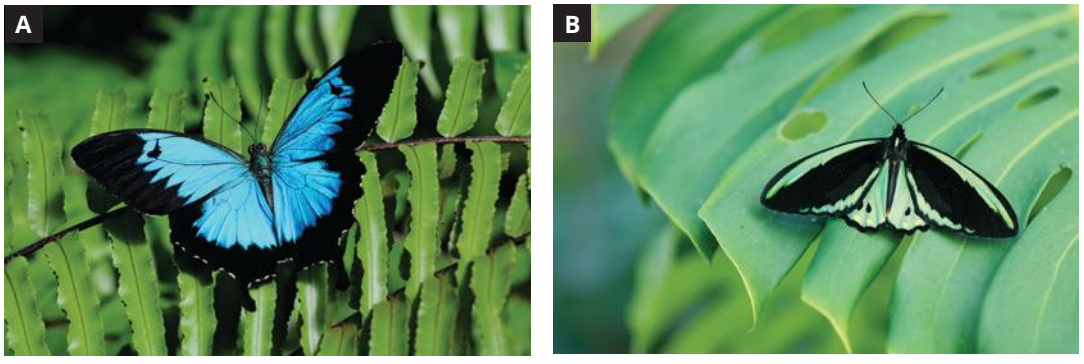


FIGURE 3 The closely related (A) Ulysses butterfly and (B) birdwing butterfly of the Daintree rainforest are evidence of species diversity.

genes
segments of DNA that are passed from parent to offspring and determine the attributes of an individual

genetic diversity
the variety of different genes and alleles in a species or population

Genetic diversity

Every individual has a unique set of **genes**, which create unique attributes for that individual. This unique combination of genes creates **genetic diversity**, the variation of genes within a species. This variation of genes within a species is the result of mutation (a change to the structure of a gene, which may lead to a change to the attribute that the gene expresses) as well as the exchange of different genes through sexual reproduction. You will learn more about the inheritance and mutation of genes in Unit 4.

FIGURE 4 All these dogs belong to the same species, *Canis lupus familiaris*, but they look different because of genetic diversity.

Ecosystem diversity

An ecosystem is a system made up of a community of organisms within a geographical area and their interactions with each other and the environment. **Ecosystem diversity** is the variety of habitats, communities and ecological processes that exist between different ecosystems. There are seven main types of ecosystems on Earth: terrestrial, forest, grassland, tundra, desert, freshwater and marine ecosystems. Every ecosystem varies, due to **abiotic** or "environmental" factors, such as temperature, rainfall, sunlight availability and soil type, as well as **biotic** or "living" factors, such as the types of organisms in a specific region. This means that each main type of ecosystem can be broken down even further, into more specific categories. Three examples of more specific forest categories are:

- tropical rainforests – defined by their proximity to the equator and large amounts of rainfall
- montane forests – defined by mountainous regions
- sclerophyll forests – defined by trees with hard, leathery, evergreen leaves (e.g. eucalypts) that are adapted to areas with lower, more erratic rainfall.

This diversity of ecosystems provides unique interactions for different species, which drives the species diversity that exists within a specific ecosystem.

ecosystem diversity
the variety of habitats, communities and ecological processes within and between ecosystems

abiotic
the non-living physical factors within an environment that affect an organism's ability to survive

biotic
the living components of an ecosystem

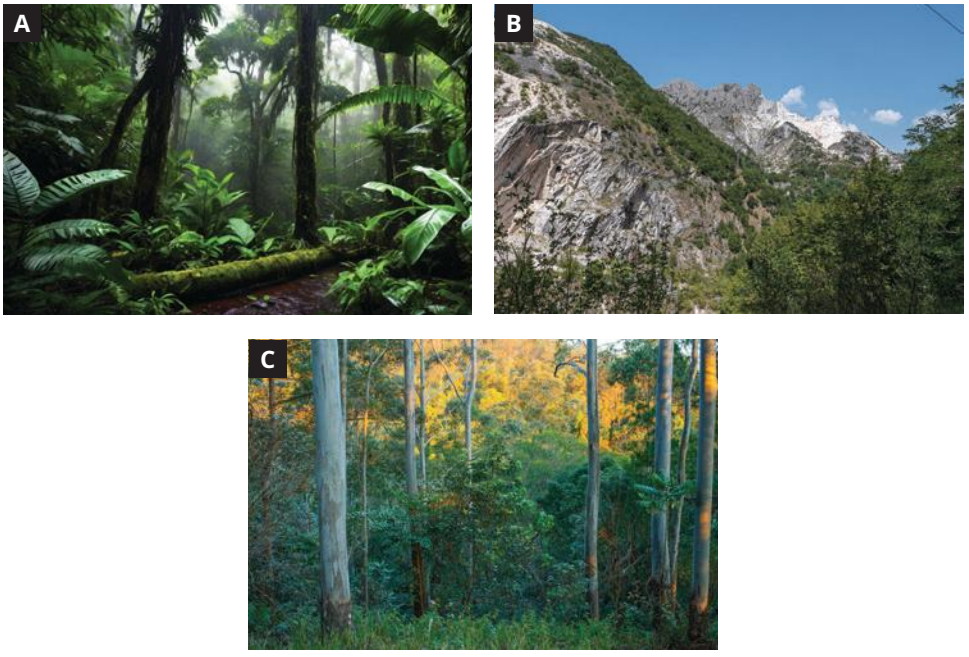


FIGURE 5 Three examples of forest categories: (A) tropical rainforest, (B) montane forest, (C) sclerophyll forest

Check your learning 2.1

Check your learning 2.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Summarise** the three levels of biodiversity. (3 marks)

2 **Identify** abiotic factors that may vary between two wetland ecosystems. (4 marks)

Knowledge utilisation

3 The table shown on the right lists some abiotic factors in two estuarine environments (where a river meets the sea).

- **a** **Deduce** which level of biodiversity this demonstrates. (1 mark)
- **b** Use the information in the table to **determine** which abiotic factor would most likely affect the species diversity of these ecosystems. **Justify** your choice. (2 marks)

Abiotic factor	Estuarine ecosystem 1	Estuarine ecosystem 2
Location	Moreton Bay, Qld	Botany Bay, NSW
Temperature (°C)	22–28	18–24
Salinity (ppt)	25–35	30–35
pH	7.5–8.1	7.6–8.0
Dissolved oxygen (mg/L)	6.5–8.5	6.0–7.5
Turbidity (NTU)	4–15	5–20
Water depth (m)	1–5	0.5–6

4 Large areas of native forest in Queensland have been logged and replaced by monoculture (growing one crop) pine plantations. **Discuss** the impact this process would have on the biodiversity of the area at each level of biodiversity. (3 marks)

Lesson 2.2
The biological species concept

Learning intentions and success criteria

Key ideas

- → The biological species concept is the most common method of classifying a species.
- → Alternative definitions of species are required for asexual organisms, fossils and hybrids.
- → All definitions of species have limitations.

biological species concept
a concept that defines a species as a group of similar organisms that are able to interbreed to produce viable, fertile offspring

reproductive isolation
the inability of different populations or species to interbreed due to behavioural, structural or physiological differences between the organisms

Understanding the biological species concept

The basic unit of biological classification is the species. The word "species" comes from the Latin word for *kind*. It is written in the same way in both singular and plural. The **biological species concept** is the most-used definition of a species. It defines a species as a group of similar organisms whose members can interbreed with each other in their *natural environments* to produce viable (living), fertile (can breed) offspring. This implies that two different species cannot interbreed to produce fertile offspring, meaning they experience **reproductive isolation**.

Reproductive isolation may result from:

- different types of behaviour, including different mating rituals (e.g. the visual and vocal displays of many bird species) or different mating times, including different times of day or different seasons
- different mating seasons (e.g. one species breeds during summer and another breeds during winter)
- different orientation or structure of the sex organs (e.g. different *Drosophila* fruit fly species have different penis structure)
- different arrangements of the genetic material (nucleic acid) within the cells.

FIGURE 1 A peacock spider performing a mating dance

While organisms that are closely related but not the same species have been known to interbreed, often in artificial situations (e.g. lions and tigers in zoos), their offspring, a **hybrid**, will typically be sterile.

hybrid
a plant or animal that is heterozygous for a particular trait; results from a cross between parents that are genetically unalike for that trait

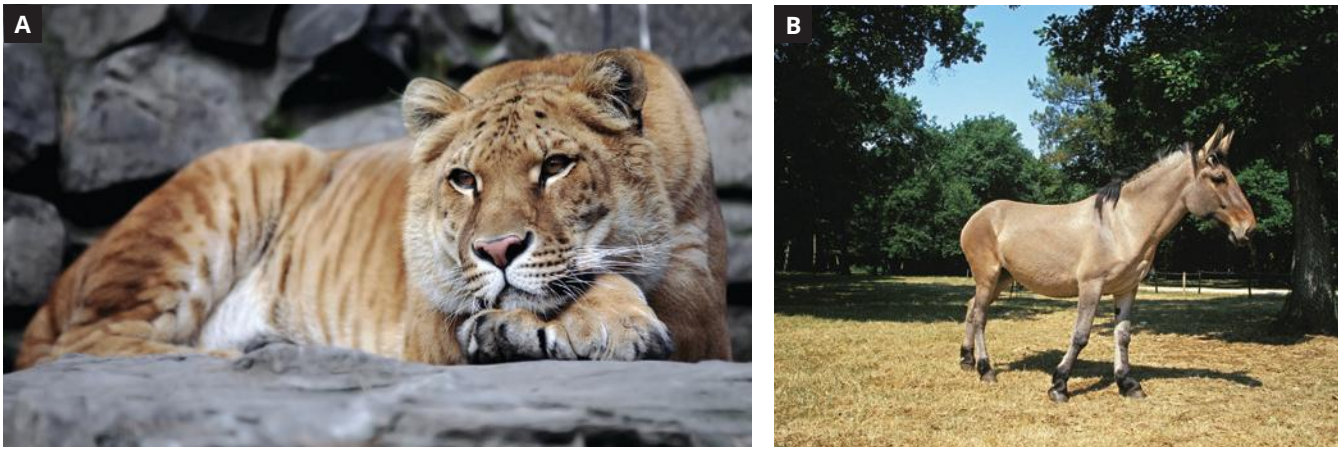


FIGURE 2 Examples of hybrids: (A) a liger (cross between a male lion and a female tiger) and (B) a mule (cross between a male donkey and a female horse)

Limitations of the biological species concept

Although the biological species concept works well with **extant** (currently living), sexually reproducing animals, it presents some problems in classifying many other organisms.

extant
currently living or existing

Fossils and extinct organisms

Fossils are the remains and/or impression of dead organisms embedded in the rock record. Because fossils are no longer alive, they cannot be classified on the basis of their ability to reproduce. Many partial fossils are discovered separately (such as leaves and flowers), so it is common for each to be given a different species name, then later found to be the same species. As more fossils are discovered, species identifications evolve.

Asexual reproduction

asexual reproduction
reproduction without fertilisation, leading to the formation of offspring that are genetically identical to the parent

Bacteria, archaea and several unicellular eukaryotes do not form gametes such as eggs or sperm and do not exchange genetic material through sexual reproduction. Instead, these cells produce genetically identical clones of themselves via **asexual reproduction**. Because of this, their ability to reproduce in natural conditions with other similar individuals to produce viable, fertile offspring cannot be tested. As a result, the biological species concept definition cannot be used for these organisms.

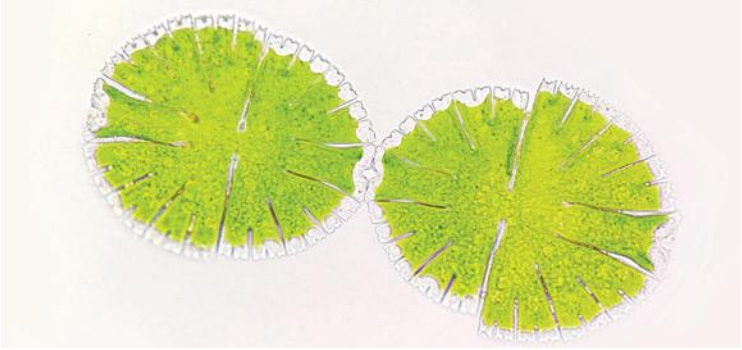


FIGURE 3 A green alga undergoing asexual reproduction

Apomixis

apomixis
in plants, asexual development of seeds or embryos

parthenogenesis
in animals, development of an embryo from an ovum without fertilisation

Many multicellular, sexually reproducing eukaryotes are also able to undergo asexual reproduction under certain circumstances. One form of asexual reproduction is **apomixis**, which is the ability of an embryo to develop without fertilisation. In animals, this process is called **parthenogenesis**. Parthenogenesis can also occur in plants, in another form of apomixis where the embryo develops from the cells of the ovule instead of the egg cell. This asexual process means that traits favourable for survival are passed on, but there is no variation provided through the process of fertilisation.

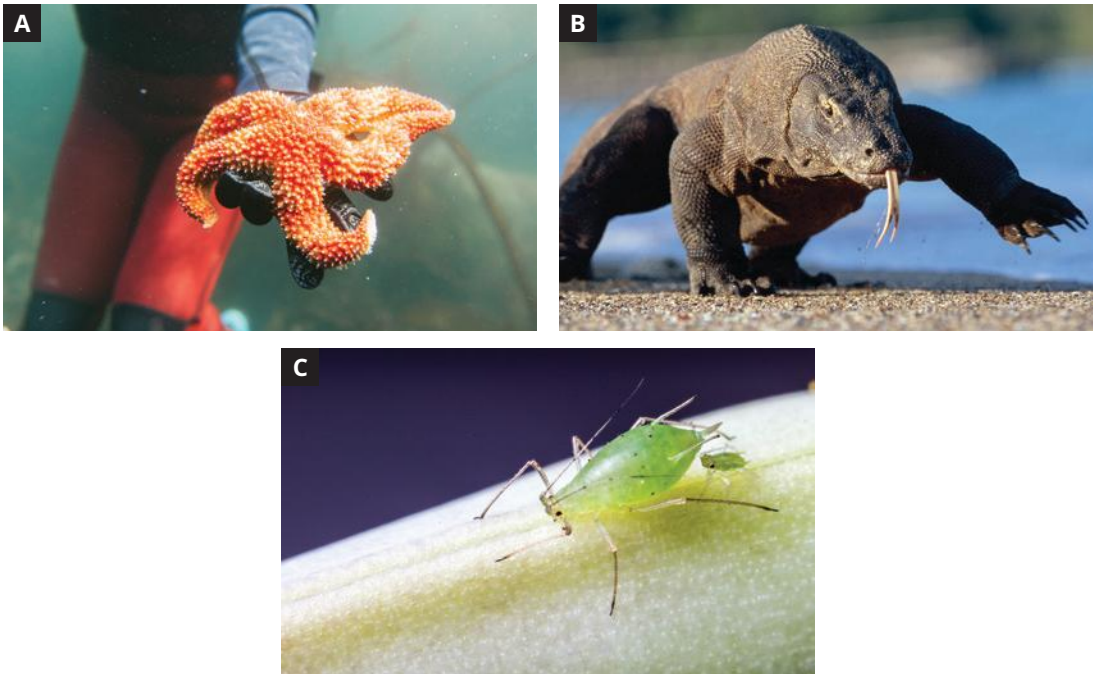


FIGURE 4 (A) Sea stars, (B) Komodo dragons and (C) aphids are examples of eukaryotic organisms that can reproduce via parthenogenesis.

Ring species

If a species evolves around a geographic barrier in a ring-like way, the adjacent populations that live within close proximity to each other around the barrier can interact regularly. Due to this regular interaction, these close neighbouring populations are capable of sexually reproducing even if the populations develop slight genetic variations due to their environment. However, the more isolated the populations are around the barrier or "ring", the more genetically different they can become. Eventually, when two populations of a species converge again at the end of a barrier, they may have evolved to be so genetically different that they are unable to produce viable fertile offspring. These are known as **ring species**.

ring species
a series of populations within a species where each population interbreeds with the neighbouring populations, but the end populations differ significantly and are unable to interbreed.

For example, seven linked populations of the salamander species *Ensatina eschscholtzii* interbreed around the Central Valley in California, which acts as a geographic barrier separating populations of the species (Figure 5). These seven populations of *Ensatina eschscholtzii* are thought to have evolved from a common ancestor and have developed unique characteristics as the species evolved around the Central Valley. At the two ends of the base of the Central Valley are *E. e. klauberi* and *E. e. eschscholtzii*, which cannot interbreed. This means that while there is only one species at most points of the ring, the two populations that meet at the end of the barrier may be considered separate species, making the differentiation of species ambiguous.

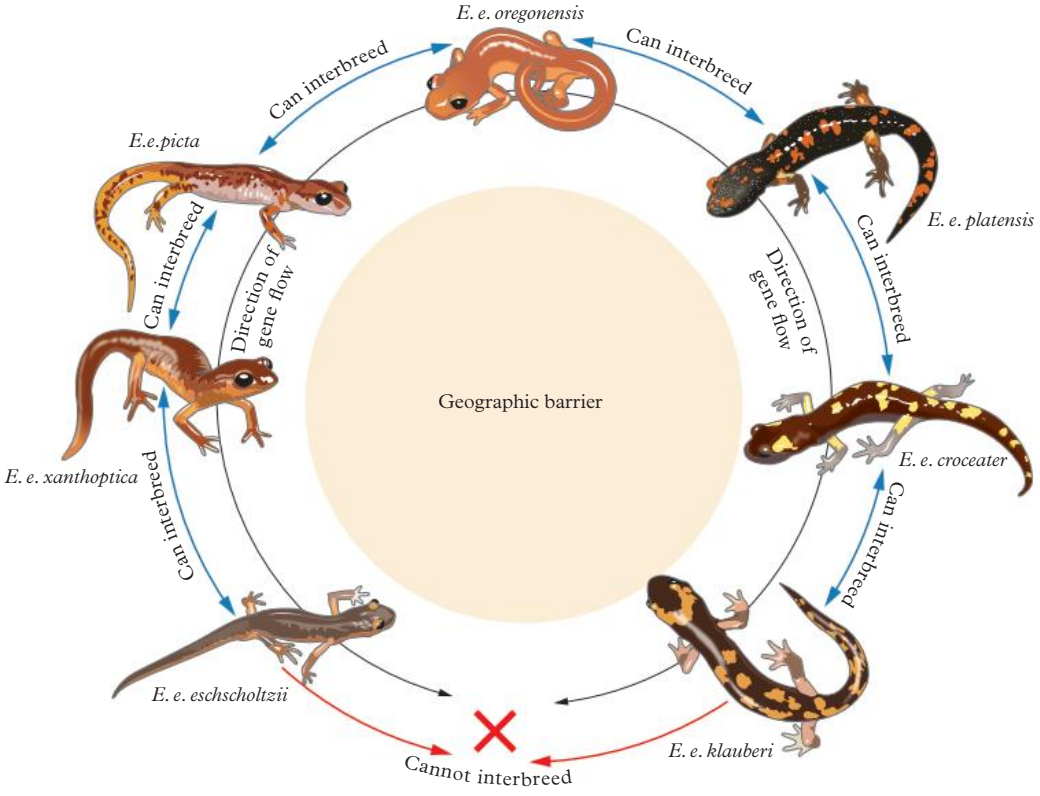


FIGURE 5 The neighbouring populations in this ring can reproduce with each other. However, two populations that converge at the base of the geographic barrier (*E. e. eschsholtzii* and *E. e. klauberi*) cannot interbreed.

Infertile organisms

Many social insects (e.g. bees, ants, termites) have different castes of males, fertile females and infertile females. For example, many of the ants in a colony are worker ants that are unable to reproduce. It is thought that the role of the ants is determined by the quantity and composition of food given to the larvae. Because some individuals of the species are unable to

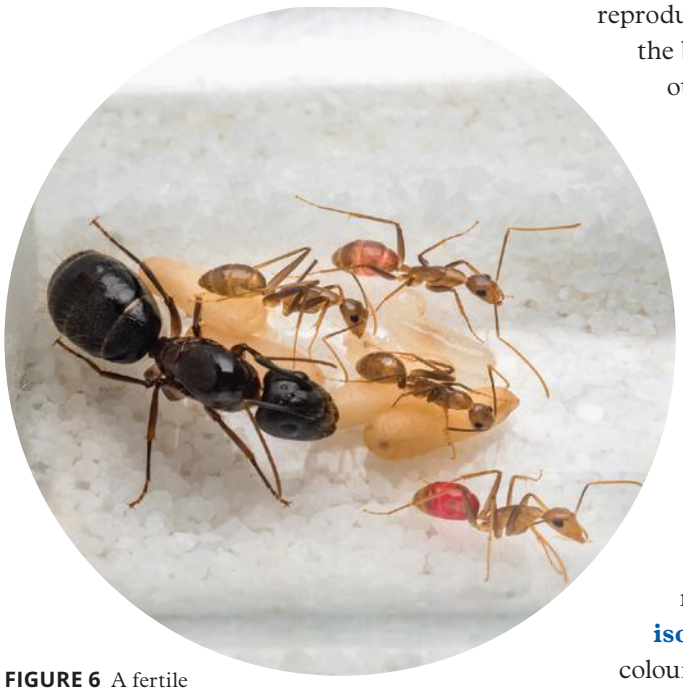


FIGURE 6 A fertile queen ant surrounded by infertile females (worker caste)

reproduce, they would not meet the description of a species in the biological species concept, as they cannot interbreed with other members of their species.

Varieties and subspecies

Members of a species may differ, but not enough to be considered separate species. They are placed into categories called **varieties**. For example, British shorthairs and Siamese are two varieties of the same species of cat (*Felis catus*). These different varieties may have differences in appearance, but they can interbreed freely. In other situations, members of a particular species may be reproductively isolated because they live in different places with limited overlap between their ranges. Those members at the far ends of the range are **geographically isolated**. These groups have adaptations (e.g. different colour patterns) that make them better suited to their particular habitats, but they still belong to the same species because they are most often capable of interbreeding. Biologists term these groups **subspecies**. They are distinguished from varieties beecause they are geographically isolated. This isolation increases the potential of subspecies to form new species, because genetic variation and adaptations are more likely occur in response to different environmental pressures.

variety
a group that has a set of characteristics distinct from other varieties within the same species, e.g. a poodle and a Great Dane

geographic isolation
when a physical barrier prevents interbreeding between members of different populations of a species

subspecies
a taxonomic rank immediately below a species; a population that is genetically isolated from other populations of the same species in a particular geographic region, often capable of interbreeding successfully where ranges overlap

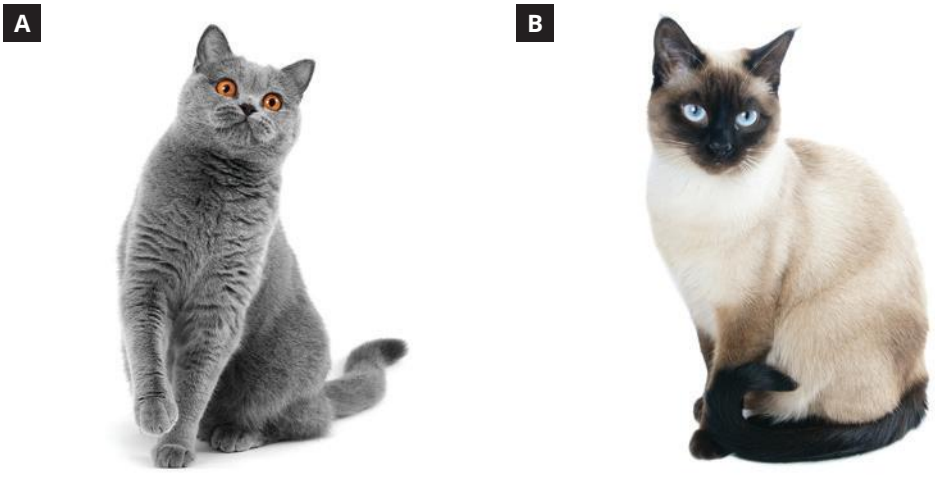


FIGURE 7 Two varieties of *Felis catus:* (A) a British shorthair and (B) a Siamese cat

Ring species (as discussed earlier) are now considered to be subspecies of a single species. Crimson, yellow and Adelaide rosellas, for example, were once considered separate species but are now classified as one species of rosella, *Platycercus elegans*. The crimson rosella in Queensland is *Platycercus elegans nigrescens*, but in eastern NSW and Victoria it is *Platycercus elegans elegans*. The yellow rosella is *Platycercus elegans flaveolus* and is found along the Murray River, while the Adelaide rosella, *Platycercus elegans fleurieuensis*, is found in the Adelaide region (Figure 8).

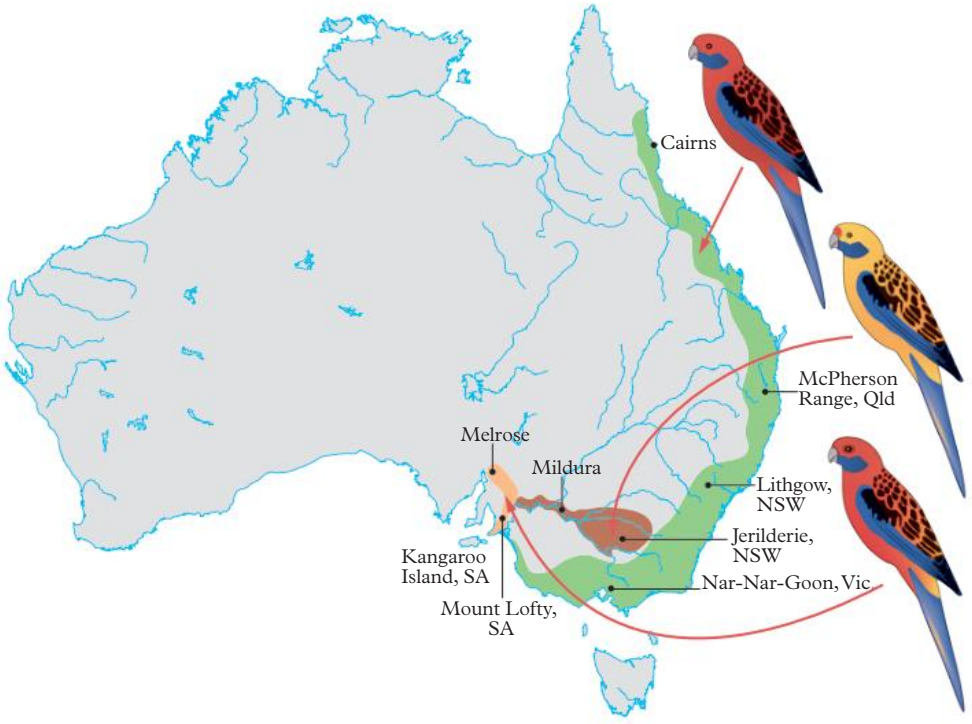


FIGURE 8 Subspecies of the crimson rosella include the crimson rosella (found along the eastern side of the Great Dividing Range), the yellow rosella (along the Murray River) and the Adelaide rosella (Adelaide region).

Real-world biology

Multiple definitions of species

There have been many attempts to establish an all-embracing definition of species. Some definitions refer only to fixed characteristics, mate recognition, genetic similarity or environmental requirements. In each case, some organisms do not fulfil all requirements of the definition.

Microraptor demonstrates the difficulties of classification. Fossils of this small, feathered dinosaur have been dated back to the Early Cretaceous period, approximately 120 million years ago. *Microraptor* is known for its unique combination of avian (bird-like) and reptilian traits, which makes its classification difficult.

Using the biological species concept is not possible for *Microraptor*, because there is no way to study its ability to interbreed and produce fertile offspring. For this reason, alternative concepts or definitions of species must be considered. Similarly, the ecological species concept, which considers an organism's role within an ecosystem, cannot be used for an extinct species.

The phylogenetic species concept defines a species as the smallest group of similar organisms that share a common ancestor. This can be used to help distinguish *Microraptors* from other organisms, as its unique characteristics suggest a close relationship with both birds and therapod dinosaurs. The lack of clear information for *Microraptors* and other, probably closely related species, such as genetic information, still makes this classification difficult and inaccurate.

The morphological species concept provides the method of classifying *Microraptors*. This concept defines a species based on shared physical traits. Given the unique combination of long feathers and reptilian features, scientists have classified *Microraptor* separately from birds and therapods. This method may still lead to confusion, however,

as more fossils with similar features are found. This is seen in specimens such as *Cryptovolans*, whose classification and distinction from *Microraptor* is still debated.

Each species concept provides a method of classifying organisms based on a variety of factors. However, each of these definitions is limited, especially when applied to extinct organisms, where direct reproductive and genetic data cannot be collected.

FIGURE 9 The fossils of dinosaurs, such as this *Microraptor*, show similarities in their skeletal structure and physical appearance, but cannot be used to determined species based on reproductive success.

Apply your understanding

1 **Summarise** each species concept in your own words. (3 marks)

2 **Evaluate** the use of the morphological species concept in fossils such as *Microraptor*. (2 marks).

3 "*Microraptor* is considered an evolutionary stepping stone between dinosaurs and birds." **Construct** a research question that could address an aspect of this claim. (1 mark)

Check your learning 2.2

Check your learning 2.2: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** "species" in terms of reproductive isolation. (1 mark)

2 **Identify** three limitations of the biological species concept. (3 marks)

3 **Explain** why lions and tigers are considered different species despite their ability to produce offspring. (1 mark)

4 **Describe** how a ring species presents difficulties in determining a species using the biological species concept. (2 marks)

5 A farmer bought two mules (a hybrid between a horse and a donkey) with the intention of breeding them. **Explain** why the farmer may not succeed. (1 mark)

Analytical processes

6 **Deduce** why it may be difficult to determine whether the following two groups of organisms are the same species. (3 marks)

- **a** The African plant genus *Acacia* and the Australian genus *Acacia*
- **b** The variety of bacteria in the human intestine
- **c** The fossilised remains of a pine tree, and the modern-day Woolamai pine found in Australia.

Knowledge application

7 "Biological classification is a dynamic and evolving process that keeps changing as our understanding of living organisms changes." **Justify** this statement, with two examples. (2 marks)

Lesson 2.3
Linnaean classification

Key ideas

- → Organisms are classified using hierarchical systems.
- → Modern-day classification is based on the Linnaean system and considers physical as well as genetic similarities.
- → Scientists use a consistent naming system to aid communication in biology.
- → The method of classifying organisms depends on the purpose of classification, and the classification changes as new information is discovered.

Hierarchical classification

Learning intentions and success criteria

hierarchical relating to grouping things from general to very specific subgroups

classification the grouping of organisms based on their similarities in morphology, anatomy and biochemistry

Humans characteristically name and group objects together to make sense of the world and communicate effectively with others. The more specific the object, the greater the detail in which it is described. For example, consider non-identical twins, a brother and sister, who go to Billabong High School. They are in Year 12 and study Biology. Specifically, they are Mirabelle Marconi (who has blue eyes) and Joshua Marconi (who has green eyes). This description or grouping started as general (they both go to Billabong High School, are in Year 12 and study Biology), before becoming specific (their eye colour). This method of grouping from larger general groups to specific detailed groups is termed **hierarchical**, with groups within groups. Arranging things into groups according to their observed similarities is known as **classification**.

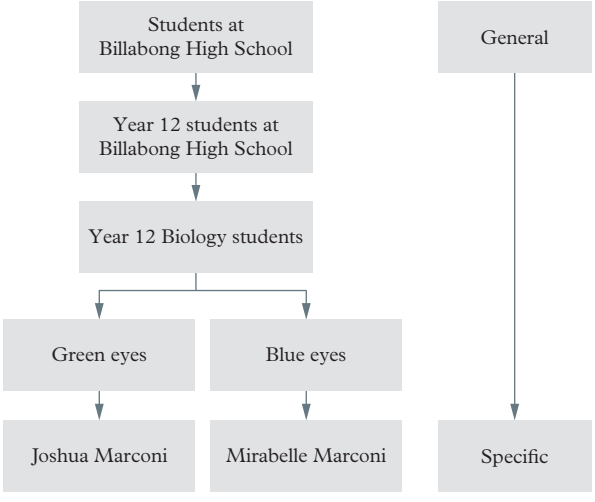


FIGURE 1 A hierarchical classification of students at Billabong High School

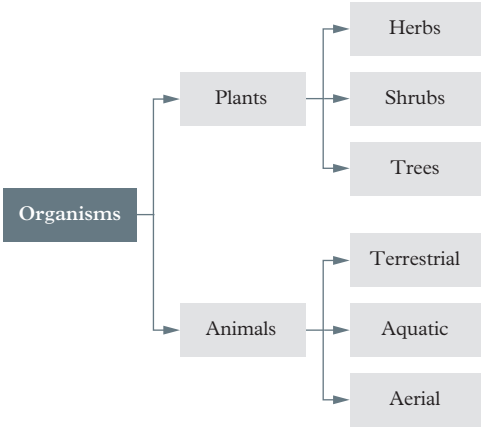


FIGURE 2 Aristotle's classification of organisms

In 300 BCE, the Greek philosopher Aristotle developed a biological system of classification. He distinguished two major groups: plants (herbs, shrubs and trees) and animals (according to where they lived, i.e. land, water or air). Since this time, there has been a massive expansion in knowledge of the different types of organisms and the means by which biologists can study them. This has led to the development of different classification systems.

Linnaean classification

taxonomy
the science of naming and classifying living things

taxon
any group in a biological classification into which related organisms are classified (e.g. phylum, class); plural *taxa*

genus
a classification category between family and species; the first part of the scientific name of an organism; plural *genera*

family
a subdivision within an order, in the classification of living things

order
a subdivision within a class, in the classification of living things

class
one of the groups used in the classification of organisms; consists of a number of orders (e.g. animals in class Mammalia all share specific characteristics)

phylum
a major classification group of the animal kingdom

division
a major classification group of the plants, fungi and plant-like protists

kingdom
a subdivision within a domain; a group of organisms with very general common features

domain
the broadest taxonomic group, based on cellular-level differences

The science of naming and classifying organisms based on physical and biochemical characteristics is called **taxonomy**. This system was devised in the eighteenth century by a Swedish naturalist, Carolus Linnaeus, and many of the methods he devised are still used today. He based the classification of plants on reproductive structures and those of animals on similar physical features – features he could readily see. Each category in the Linnaean system represents a level of grouping from a large general group (**taxon**) to a smaller group with more specific characteristics. With the development of microscopes, it was seen that many organisms could not be easily slotted into either of the two groups of living things (plants and animals) that Linnaeus used. Cellular and sub-cellular differences were found, which led to these general groups being divided up further.

Grouping organisms

In the modern hierarchical system of biological classification, related species are grouped together into a **genus** (plural *genera*), related genera are grouped into a **family**, related families are grouped into an **order**, related orders into a **class**, and related classes into a **phylum** (plural *phyla*) or **division**. The term "phylum" is used when describing animals and the single-celled *Protozoa*, whereas "division" is used in describing all other types of organisms (bacteria, plants, etc.).

Related phyla or divisions are grouped together into **kingdoms**, and kingdoms are placed into **domains**. Each of these groups is referred to as a taxon. Within each of these taxa there may be subdivisions. Thus, a phylum may include several subphyla.

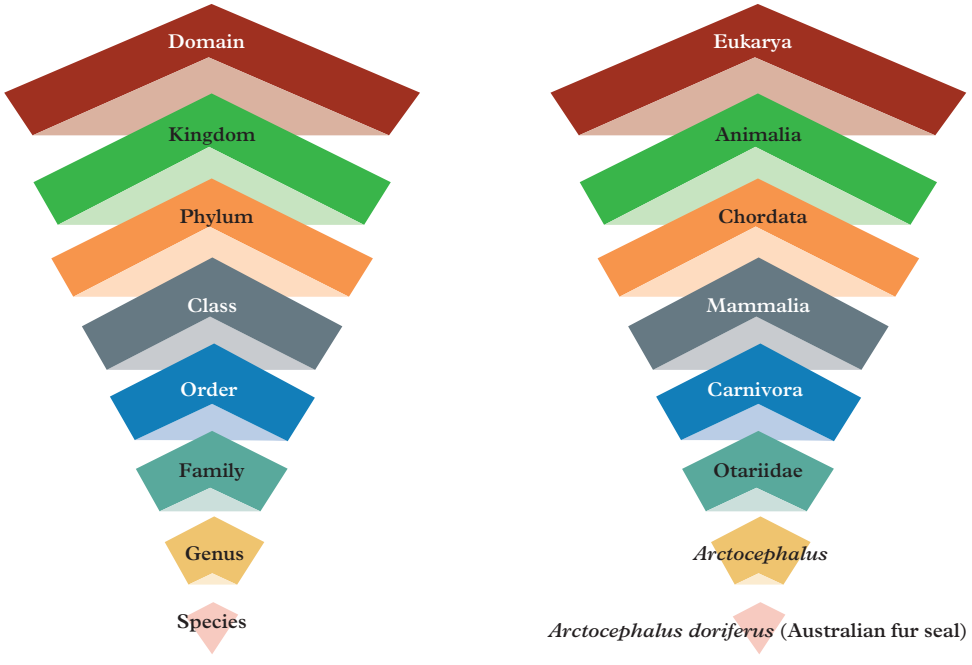


FIGURE 3 The hierarchical arrangement used in Linnaean taxonomy. An example of the hierarchical classification of an Australian fur seal is shown on the right. All members of the same species share characteristics at each taxon, from broad (domain) through to very specific (species).

With advances in technology, we have gained a greater understanding of the living world, with ongoing changes to classification, including the following:

- Until 1866, all organisms were classified into either the plant kingdom or the animal kingdom.

- In 1866, all single-celled organisms were grouped into the kingdom Protista. Many of these single-celled organisms cannot be classified as a plant or an animal.
- In 1938, prokaryotes were moved from the kingdom Protista to the kingdom Monera, based on their cell structure.
- In 1959, it was found that there were significant differences (e.g. cell wall composition) between plants and fungi, and so the kingdom Fungi was created.
- In 1977, the kingdom Monera was split into two new kingdoms – Archaebacteria (archaea) and Eubacteria (bacteria) – based on ribosomal RNA studies and cell wall structure.
- In 1990, the three-domain system (Archaea, Bacteria and Eukarya) was introduced.

TABLE 1 Classification showing separation of the Archaea, Bacteria and Eukarya domains

Domain	Archaea	Bacteria	Eukarya			
Kingdom	Archaebacteria	Eubacteria	Protista	Fungi	Plantae	Animalia
Characteristics	Distinguished on the basis of rRNA and cell wall composition					
Cell type	Prokaryote	Prokaryote	Eukaryote	Eukaryote	Eukaryote	Eukaryote
Chloroplasts	Absent	Absent	Present (in some forms)	Absent	Present	Absent
Mode of nutrition	Heterotrophic or chemo-autotrophic	Heterotrophic or autotrophic (photosynthesis)	Autrotrophic (photosynthesis), heterotrophic or both	Heterotrophic (absorption)	Autotrophic (photosynthesis)	Heterotrophic (ingestion)
Multi-cellularity	Absent	Absent	Absent	Present (except yeasts)	Present	Present
Locomotion	Absent	Absent (in most)	Present (in some)	Absent	Absent	Present
Nervous system	Absent	Absent	Absent	Absent	Absent	Present (except sponges)

The many levels, each with its own name, generated by this hierarchical Linnaean system of classification could result in very long scientific names for every organism. To simplify this, Linnaeus developed the two-word naming system, called **binomial nomenclature** (*bi* = two; *nomen* = name; *calator* = caller). This two-word naming system is used to designate the scientific name of each species.

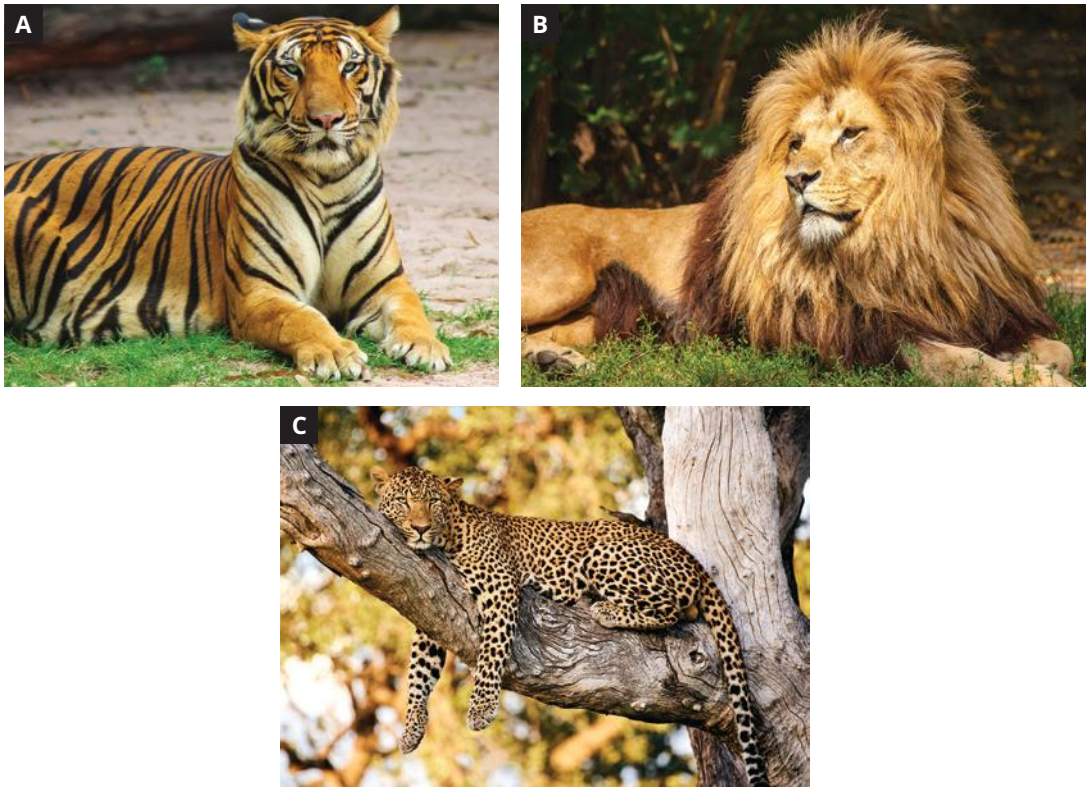
binomial nomenclature
a method of naming species of organisms with two parts: the generic and specific names, following particular formatting conventions (e.g. *Eucalyptus crebra*)

Scientific names

Each species is given a scientific name when it is formally described. The scientific name consists of the genus name and a **specific name**. A group of closely related species, most probably arising from a common ancestor, belong to the same genus. The specific name indicates the particular species within that genus. The genus name begins with a capital letter and the specific name is all in lower case. The genus is always placed first in the scientific name. For example, the lion, the tiger and the leopard have so many common characteristics that they are placed in the same genus, *Panthera*. The specific names distinguish between them:

- the tiger is *Panthera tigris*
- the lion is *Panthera leo*
- the leopard is *Panthera pardus*.

specific name
the descriptive name of a species



Study tip

The scientific name is in *italics* when typeset. When written by hand, it is underlined.

FIGURE 4 These three species all have strong features in common and are grouped together into the same genus, *Panthera*. Their specific names distinguish them from each other: (A) tiger (*Panthera tigris*), (B) lion (*Panthera leo*) and (C) leopard (*Panthera pardus*).

When referring to a particular group of organisms, it is common to use the genus name. The word *Panthera* refers to a particular group of large wild cats. A specific name, on the other hand, is meaningless when written alone, because it can be used as a descriptor for many unrelated genera. For example, two unrelated organisms have the specific name *alba*: *Ardea alba* and *Eucalyptus alba*. *Ardea alba* is a large white bird that feeds in shallow waters and swamps in tropical and temperate regions of the world. *Eucalyptus alba*, with its smooth white bark, is known as the poplar gum or white gum tree and is found in the tropical regions of northern Australia.

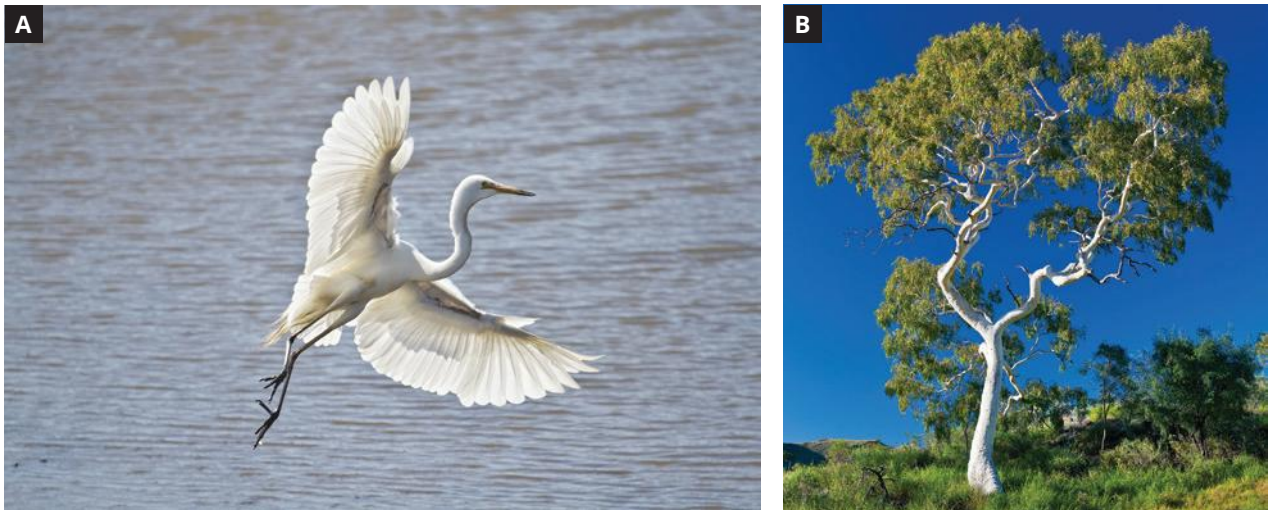


FIGURE 5 Both these organisms have the specific name *alba* (referring to their predominantly white colour) but they are not related: (A) *Ardea alba*, (B) *Eucalyptus alba*.

In a context where there is no possible confusion, the genus name may be abbreviated to its initial letter. An author discussing a particular species of fruit fly, for example, might write *Drosophila melanogaster* as *D. melanogaster* after the scientific name has already been mentioned in full.

Common names

Scientific names were originally written in Latin, because that was the common language of scientists in Linnaeus's time. Many organisms also have common names. While common names may be easier to learn, they can lead to confusion, because different common names can be used for the same species in different localities. For example, the fish *Coryphaena hippurus* (named by Linnaeus in 1758) is known by many common names, including dolphin fish, dolphin, dorado and mahi-mahi.

FIGURE 6 *Coryphaena hippurus* has a number of common names, including names shared with unrelated species.

Additionally, common names can be misleading. For example, the common name for the bird shown in Figure 7A is the Australian magpie. This name came from European settlers, who thought the bird was similar to the Eurasian magpie (Figure 7B). While their common names may imply that the two are closely related, these two species of bird belong to two different families: Artamidae and Corvidae. Because a scientific name always refers to one specific type of organism and is recognised globally, it avoids the confusion that can come from using common names.

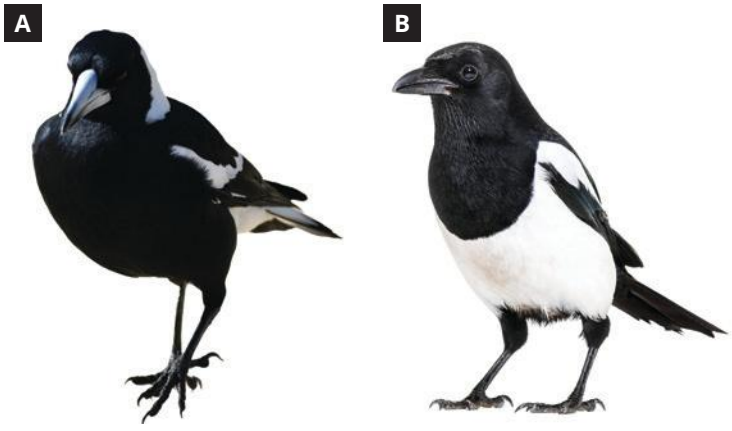


FIGURE 7 Two unrelated birds with the same common name: (A) the Australian magpie, *Gymnorhina tibicen* and (B) the Eurasian magpie, *Pica pica*

Naming organisms

The person who first discovers a species has the right to name it. There are various sources of scientific names. The scientist may name it after a person (but never themselves), or the locality in which it was first observed. Many Australian biologists have used words from Aboriginal and Torres Strait Islander languages. For example, the burramys, the mountain pygmy possum found in the high country on the NSW–Victorian border, belongs to the genus *Burramys* from the place name *Burra* (near Taralgo, NSW, where fossils of the animal were discovered) and the Greek *mys* (= mouse).

Some biologists have used their sense of humour in naming new species. For example, members of mosquito genera have been given the specific names of *tormentor* and *horrida*. The Asgard archaea have been given genera names after Norse gods, such as *Thoarchaeota*, *Lokiarchaeota* and *Odinarchaeota*. These archaea are newly discovered ancient **extremophiles** from hydrothermal vents on the ocean floor.

extremophiles
organisms that live in extreme environments

It is more common for a name to be descriptive. The scientific name for the red kangaroo is *Macropus rufus*, which gives a physical description: *Macropus* means "large-footed" (*macros* = large; *pus* = foot) and *rufus* means "red".

FIGURE 8 The scientific name of the red kangaroo, *Macropus rufus*, indicates that it has large feet and is red in colour.

Check your learning 2.3

Check your learning 2.3: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the term "classification". (1 mark)
2 Classification systems tend to be hierarchical. **Explain** the meaning of the term "hierarchical". (1 mark)
3 **Describe** how scientists name a species. (1 mark)
4 **Explain** why biologists use scientific names instead of common names. (1 mark)
5 *Bactrocera tryoni* is the Queensland fruit fly. It lays its eggs in soft-skinned fruit, and when the larvae hatch they use the ripening flesh for nourishment to complete their development. **Identify** which one of the following organisms it is most closely related to: *Rosana tryoni*, *Pinuta dacus*, *Bactrocera cucumis* or *Tryoni rosana*. **Explain** your choice. (2 marks)
6 **Identify** the taxon level where two species have the most features in common. (1 mark)

Analytical processes

7 Based on your own knowledge of their characteristics, **categorise** the animals listed below into groups and subgroups. Scientific terms are not required. (4 marks)

baboon, bear, lion, clam, fly, frog, earthworm, horse, jellyfish, lobster, mosquito, prawn, emu, panther, oyster, sparrow, turtle, tuna, whale, snake, snail

8 The smallest hummingbird is called *Mellisuga helenae* and the largest is called *Patagona gigas*. The hummingbird with the longest beak is called *Ensifera ensifera*, while the one with the smallest beak is called *Ramphomicron microrhynchum*.

For the hummingbirds described above, **deduce** which of the following they belong to. (1 mark)

A Same genus but different species

B Same family but different classes

C Same genus but different classes

D Same class but different genera

9 Listed below are some common Latin and Greek root words used in naming animals.

Root word	English meaning	Derived from Latin or Greek
a-	without	Greek
-cephalus	head	Latin
giga-, gigan-	giant	Greek
leuco-	white	Greek
macro-	large	Latin
natus	birth	Latin
ornitho-	bird	Greek
ptero-	wing, feather	Greek
-pus	foot	Latin
rhynchus	snout, beak	Greek

a **Identify** as many physical characteristics as possible, for the following species. (4 marks)

i *Macropus giganteus*

ii *Pteropus giganteus*

iii *Rattus leucopus*

iv *Ornithorhynchus anatinus*

b **Determine** a common name for each species based on the descriptions you gave in part **a**. (4 marks)

10 An organism has been found that has eukaryotic cells, and is multicellular and heterotrophic. **Determine** which domain and kingdom you would place it in. **Consider** what further information you would require to be sure of your answer. (2 marks)

Lesson 2.4
Dichotomous keys

Key ideas

- → Dichotomous keys use a series of questions to differentiate and classify things.
- → Biologists use keys distinguishing physical characteristics to differentiate species.

Dichotomous keys

Learning intentions and success criteria

dichotomous key
an identification key with two alternatives at each stage

Biologists often use keys to help them identify organisms. Observable features are used to separate organisms into smaller and smaller groups until the organism can be identified using its unique features. It is important that the observable features used in the keys are relatively constant, between individuals in the species and throughout the life of the individual. For example, it would not be appropriate to use the size of an organism, because this will change as the individual grows throughout its life. It also would not be appropriate to use colour to differentiate a species that changes colour throughout its life. Keys can be in the form of a series of questions or a flow diagram, with alternatives at each stage of the key. The alternatives in such keys should be comparative (e.g. legs or no legs). These keys may be very general.

To use a key, start at the top and work through the alternatives until the organism is identified. A decision is made about the characteristic at each branch point. A key with only two alternatives at each stage is known as a **dichotomous key**. "Dichotomous" refers to a division or contrast between two entirely different things. For example, using the key in Figure 1 to identify a vertebrate with scales but no fins would involve the following steps.

No feathers → No hair or fur → No fins → Scales present → Reptile

Rather than being diagrammatic, a key may be in tabular form. In the example shown in Table 1, the key is specific for a group of species known to exist in a particular locality and therefore would not be useful in other localities.

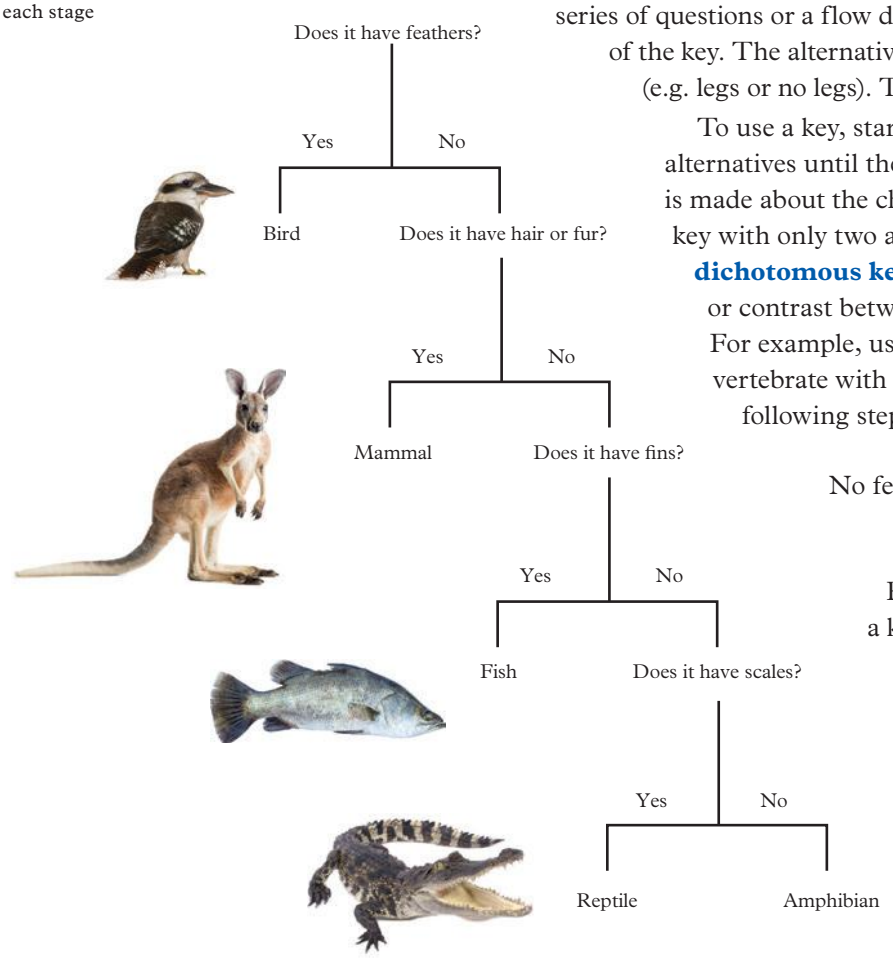


FIGURE 1 An example of a dichotomous key

FIGURE 2 *Eucalyptus sideroxylon* has mature buds greater than 2 cm long.

TABLE 1 Key to ironbark species of eucalypts in Brisbane, as identified by H.T. Clifford in 1972

1	Mature buds greater than 2 cm long	*E. sideroxylon*
	Mature buds less than 2 cm long	Go to 2
2	Leaves opposite	*E. melanophloia*
	Leaves alternate	Go to 3
3	Coppice leaves twice as long as broad	*E. siderophloia*
	Coppice leaves several times longer than broad	Go to 4
4	Mature buds about 1 cm long	*E. drepanophylla*
	Mature buds less than 1 cm long	*E. crebra*

Check your learning 2.4

Check your learning 2.4: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** dichotomous keys and how they are used. (2 marks)

Analytical processes

2 Use the tabular key provided here to **determine** which phylum each of the invertebrates in the images below belongs to.

1	Bilateral symmetry (left-right symmetry)	Go to 2
	Radial symmetry (body parts arranged around a central axis)	Go to 4
2	Elongated, worm-like body plan	Phylum Annelida
	No worm-like body plan	Go to 3
3	Segmented legs	Phylum Arthropoda
	No legs or non-segmented legs	Phylum Mollusca
4	Soft body, often with tentacles	Phylum Cnidaria
	Body has rough or spiny appearance	Phylum Echinodermata

a

(1 mark)

b

(1 mark)

c

(1 mark)

3 A dichotomous key identified each bird found in a particular environment. **Deduce** why it would be difficult to use the same key in another environment. (1 mark)

Knowledge utilisation

4 **Construct** a dichotomous key to distinguish between the koala, dingo, snake, lizard, turtle, emu and green tree frog:

a in the form of a table (7 marks)

b as a flow chart. (7 marks)

Lesson 2.5
Factors affecting ecosystems

Learning intentions and success criteria

Key ideas

- → Abiotic factors influence where an organism lives, how abundant it is and how individuals within the species are distributed throughout their habitat.
- → Intraspecific and interspecific interactions influence the distribution and abundance of species.

ecology
the study of relationships between organisms and their environment

environment
the conditions (biotic and abiotic) in which an organism lives

biosphere
the part of the Earth that supports life

habitat
a specific location, with a particular set of biotic and abiotic conditions; where an organism lives

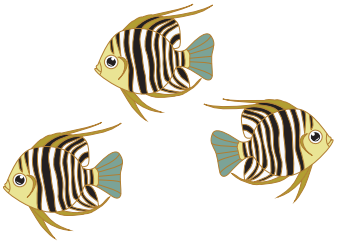
Defining an ecosystem

Ecology is the study of relationships between living things and their **environment**. The word "ecology" is derived from the Greek word *oikos* (home), and thus in its broadest sense, ecology is the study of the area of the world that provides homes for living things. This is known as the **biosphere**.

Each organism shares its living place or **habitat** with other organisms of the same species. When individuals of the same species live in the same habitat at the same time, they are called a **population**. Different species living in the same habitat form a **community**. When the members of a community interact with each other and their physical surroundings, they form an **ecosystem**.

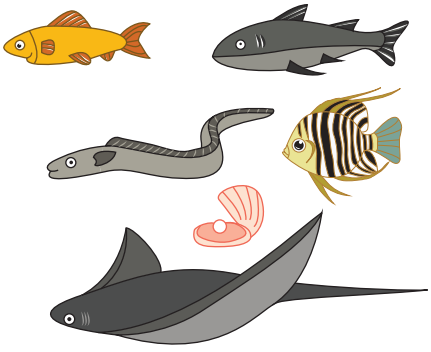
Population

A number of individuals of one species living in a particular place at a given time



Community

All the species that occupy a particular place at a given time



Ecosystem

A biological community of interacting organisms and their physical environment

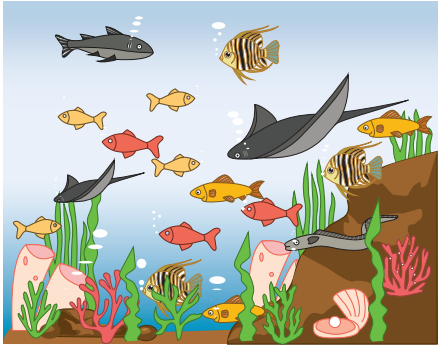


FIGURE 1 Summary of the terms population, community and ecosystem

population
a number of individuals of one species living in a particular place at a particular time

community
all the species that occupy a particular place at a given time

Ecosystems vary in size. They may be as small as a decaying log on the forest floor, or as large as the Great Barrier Reef. All ecosystems interact, and the output of one ecosystem may become the input of the next ecosystem. For example, the temperature of the water will affect the organisms on the shoreline, and the chemical composition of the shoreline will eventually affect the organisms in the water.

Two broad categories of factors affect the functioning of an ecosystem:

- **biotic** factors – the living factors that affect an organism's ability to survive
- **abiotic** factors – the non-living physical factors that affect an organism's ability to survive.

In this lesson we will look at how abiotic and biotic factors can affect the **abundance** and **distribution** of species in an ecosystem.

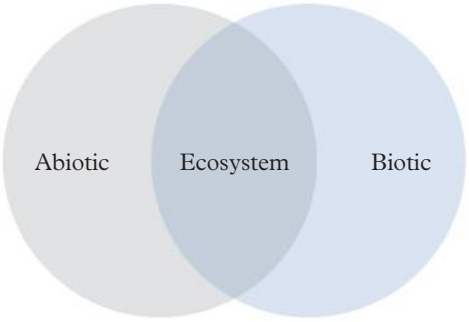


FIGURE 2 An ecosystem is the interaction between the abiotic and biotic components in an area.

Distribution refers to the region in which one or more members of a species may be found; abundance is the number of each species in that region at that time. In any locality, abundance can be referred to as **population density** – the number of individuals per unit area. Both distribution and abundance are affected by the biotic and abiotic factors in an ecosystem.

ecosystem
a biological community of interacting organisms and their physical environment

biotic
describes the living components of an ecosystem

abiotic
describes the non-living physical factors that affect an organism's ability to survive

abundance
the number of individuals in a population, within a given area

distribution
the density and pattern of spread of a population

population density
the number of individuals of a given species per unit area

Population density

Population density is one way of measuring the abundance of an organism. It is a measure of the number of organisms in a population in a predetermined area of an ecosystem. This can be determined by dividing the population by the size of the area.

$$\text{Population density} = \frac{\text{population size}}{\text{size of the area}}$$

For example, an ecosystem that is 100 m × 100 m in area was found to have 15 possums living within its boundaries. This means the population density is 15 possums for every 10,000 m^2.

The population density of these possums (or any other species) can be related to the features of the environment, including the accessibility of habitats, possible competition and predators, or the chemical elements present.

Biotic factors

Every organism in an ecosystem is impacted by the other organisms it encounters. The interactions between organisms affects the individual's ability to survive and thrive in an ecosystem. These relationships can be broken into two key types: **intraspecific** (between members of the same species) and **interspecific** (between members of different species). Four biotic factors that affect the distribution and abundance of species are:

- food availability
- competition for resources
- predation
- disease.

intraspecific
within a species; between individuals of the same species

interspecific
between different species

Food availability

The availability of food is an important factor for all heterotrophs (organisms that obtain their energy through ingestion). Put simply, a species can only live in an area where there is enough food for them to eat. If the food runs out in any given area, the species must move to find more food. This means that the abundance of a species in an ecosystem is dependent on the availability of food. If there is an abundance of food, the population can grow. However, if there is a lack of available food, members of the species may starve and die, and reproduction rates will be reduced due to lack of nutrition. Organisms will also tend to accumulate in an area where there is an abundance of food, affecting their distribution.

Competition for resources

niche
the particular role of an organism, including its interactions with the abiotic and biotic factors in the ecosystem

All resources in an ecosystem are limited to some degree, whether in quantity or access to the resource. Organisms will compete for the resources that are required for their survival, including water, shelter, light, space and mates. Every species has its own **niche** or role in the ecosystem. This includes the specific resources and conditions it requires to survive, as well as its interactions with other species, such as predators and prey. Because organisms of the same species share many of the same requirements, competition within a species (intraspecific competition) is usually fiercer than competition between individuals of different species (interspecific competition). Intraspecific competition also limits the available resources further for the species, which can decrease species abundance.

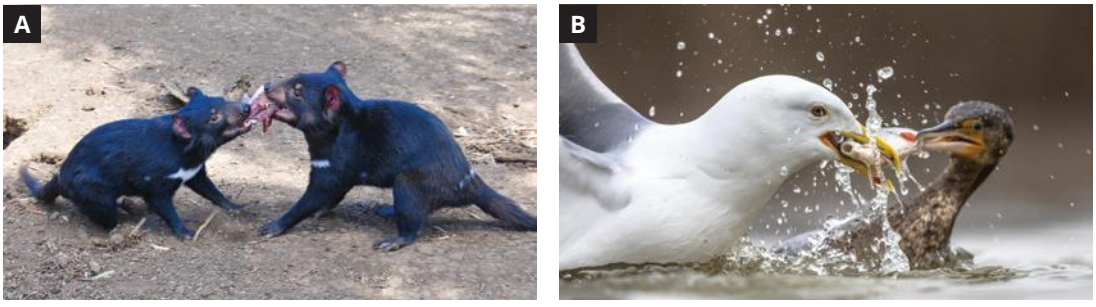


FIGURE 3 Examples of (A) intraspecific competition and B) interspecific competition

Because a large population of a species is harder to sustain in a small area with limited resources, individuals in a population often need to spread out so that each individual can obtain more resources. An example of this is seedlings. When plants first germinate, many grow right next to each other. However, over time the individual plants begin to compete for nutrients, water and light. Eventually the fastest-growing individuals shade out or take nutrients or water from their neighbouring plants, leading to a decrease in abundance and a relatively uniform distribution of the plants. This is why, when planting plants in your garden, there is a recommended distance between them. Competition for resources not only affects the distribution and abundance of an organism but also plays a key role in determining where an organism is able to survive at all. This will be explained further in Module 4.

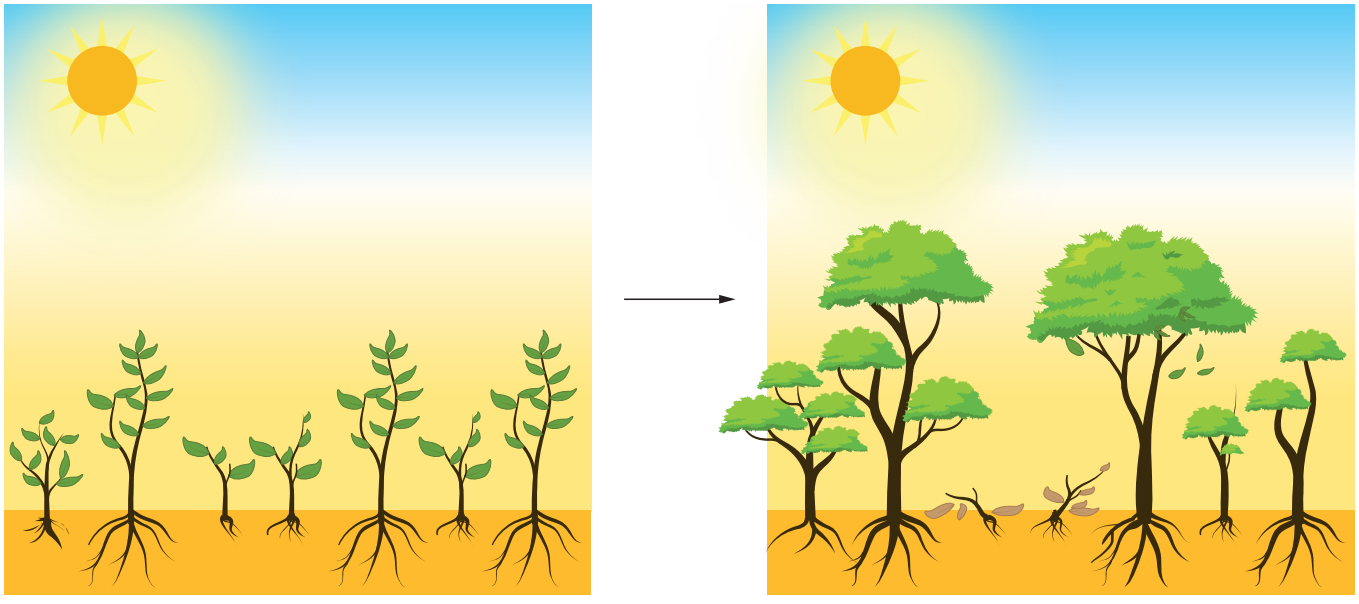


FIGURE 4 Competition between plants for light can lead to death or stunted growth of some individuals.

Predation

Predation is the act of killing an organism for food. **Predators** in an ecosystem reduce the abundance of their prey. A high population of predators in an area results in a decrease in the population of prey. Alternatively, a low population of predators in an area allows the prey population to increase. The ratio of predators to prey in an ecosystem tends to fluctuate. After an increase in predation has reduced the population of prey, this then limits the food available for the predators, and limits the number of predators that can be sustained in that area. This reduces the number of predators in the population, which in turn allows the prey population to increase again, and so the cycle continues.

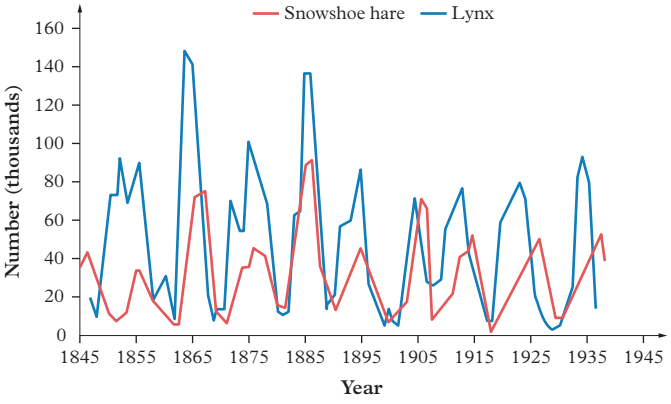


FIGURE 5 Populations of lynx (predator) and snowshoe hare (prey) in Canada

predator
an organism that catches, kills and feeds on another animal

Predation also affects the distribution of prey species in three key ways.

- If the prey species is mobile, they will often move around to avoid predation, affecting their distribution.
- Predators may prey on a competitor of a particular species, enabling that species to move into areas it was not previously able to inhabit, due to competition.
- Prey species may clump together tightly to avoid predation. When the threat of predation is high, the prey species may form a tight grouping (e.g. buffalo grouping together to protect their young), or they might remain close to shelter to escape predation (e.g. blue-green chromis keeping close to coral to hide from predators).

FIGURE 6 The grouping behaviour of buffalo protects their young from predators, such as lions.

FIGURE 7 Small fish like these blue-green chromis (*Chromis viridis*) often remain close to branching corals, where they can shelter from predators.

Disease

High-density populations are also vulnerable to the spread of infection. Crowded conditions can result in simple infections being easily spread through contact, food supply or water. Although not all infections cause death, an increase in sickness can cause a decrease in the birth rate of a population. The rapid spread of an infection with high mortality will reduce a species' population.

Abiotic factors

optimal range
the level of an abiotic factor at which an organism will best survive, grow and reproduce

physiological stress
the inability of an organism to function at maximum efficiency as a result of some factor, impacting the growth and reproduction of the organism

tolerance range
the range of a particular abiotic factor within which an organism can survive

The physical conditions that make up an environment (e.g. temperature range, humidity, wind and air currents, water currents, pH, availability of light, water and nutrients) vary dramatically. These factors are known as abiotic factors, from the Greek *a* (without) and *bios* (life). To survive, grow and reproduce, each organism in a particular habitat must be able to survive in the physical and chemical conditions that surround it.

Each species has an **optimal range** for each abiotic factor in the environment. This is the level at which it can best survive, grow and reproduce. If each of these abiotic factors falls within the optimal range, the numbers of individuals (abundance) will be high. The abundance may also increase if several of the factors are within the species' tolerance range, rather than its optimal range. For example, a certain plant will grow very well and be able to reproduce in a pH range of 6.5 (slightly acidic) to 8.0 (slightly basic). This is the preferred niche for that particular plant. Although it can grow in soils of pH 6.0 or pH 8.5, it does not function as efficiently and suffers **physiological stress**. This means the plant can tolerate these conditions but will struggle to grow or reproduce. The plant is said to have a **tolerance range** for soil with a pH of 6.0 to 8.5. An organism will only be found in an area where it encounters the tolerance range for all its abiotic requirements. Abiotic factors that affect the distribution and abundance of species include:

- space
- shelter
- availability of water
- nutrients.
- environmental conditions

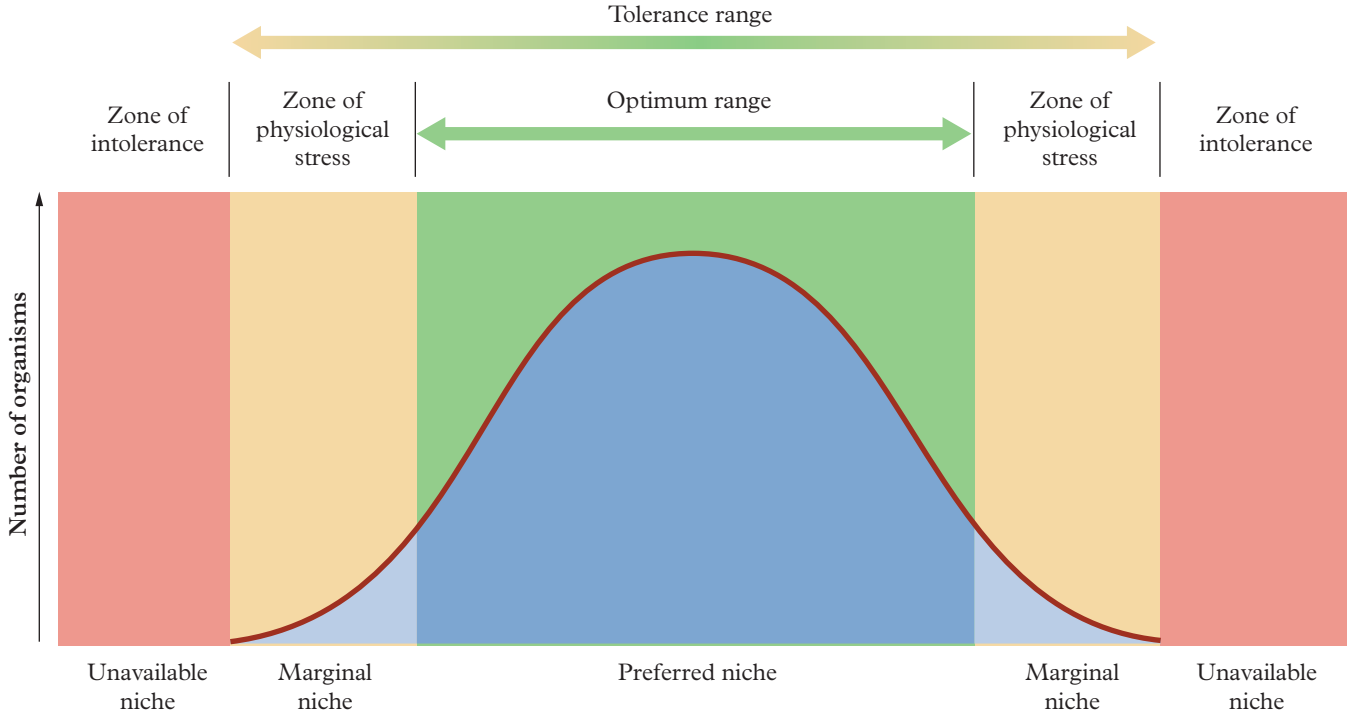


FIGURE 8 The relationship between tolerance range and optimal range of any abiotic requirement for an organism

Space

All organisms require space to live. The size and behaviour of the organism determines how much space it requires. Large organisms tend to require large amounts of space, particularly large herbivores as they require huge quantities of vegetation to survive. For example, an Asian elephant (*Elephas maximus*) in the wild could require between 200 and 1,000 square kilometres, depending on foliage density, to obtain enough food to survive. The abundance of a species in a geographic area will vary based on the amount of space available to sustain each individual. If there is not enough space available to sustain each member of the population, it will lead to intraspecific **competition**. Space also affects species distribution, as species may need to move around or relocate to other areas to ensure that their space requirements are met.

competition rivalry between individuals, of the same or different species, for a specific resource(s)

FIGURE 9 Asian elephants require large amounts of space.

Shelter

The availability of shelter is a critical factor for many organisms. Shelter provides protection from predation and harsh environmental conditions, so populations tend to be restricted to areas of protection. For instance, insectivorous bats need caves or hollows, and the spinifex hopping mouse must have an underground system of tunnels. Soil or rock strongly influences the presence or absence of such organisms, even if all other conditions are favourable. The abundance of species will be affected by how much shelter is available to members of the population. Limited amounts of shelter can lead to intraspecific competition, and individuals may need to move or relocate to ensure their requirement for shelter is met.

FIGURE 10 Bats often dwell in caves.

Availability of water

Water is essential for life. The extent to which an organism can tolerate dry environmental conditions is tied to its ability to conserve water. The distribution of an organism is therefore directly correlated to distance from a source of water. Many organisms depend on a constant supply of water and need to live relatively close to a water source. Some desert animals have adaptations to enable them to survive for long periods without access to water, meaning they can have a wider distribution and greater abundance in arid ecosystems. Camels are well known for their ability to go for weeks without needing to drink water. This is because they can store large amounts of water – not in their humps, which is a common myth, but in their blood due to their oval-shaped red blood cells – and have high water retention from their faeces and urine.

FIGURE 11 Camels store and retain water for weeks, enabling them to survive in arid areas such as outback Australia. Their humps contain fatty tissue, which is used as a food source.

Nutrients

The nutrients available in the soil play a pivotal role in determining the distribution and abundance of not only plant species but also the animals that depend on these plants for survival. Different plant species have different nutrient requirements, and so the availability of these nutrients and the relative quantities in which they are found determine how well plants succeed in living in each area. The distribution of herbivores that feed on specific plants species is therefore indirectly affected by the soil nutrients, via food availability.

Environmental conditions

A wide range of environmental conditions can affect the abundance and distribution of a species in an ecosystem. These include temperature, radiant energy, humidity, wind and air currents, pH, water currents, salinity and topography.

Temperature

Biochemical processes function over a narrow temperature range. Most multicellular life can only survive and reproduce between –2°C and 40°C. Organisms must therefore have physiological or behavioural adaptations to combat or avoid environmental temperature extremes. The highest temperature at which an organism is currently known to survive is 122°C. This organism is a bacterium that lives on hydrothermal vents.

Radiant energy

Light is essential for all green plants and photosynthetic prokaryotes, and for all animals that are directly or indirectly dependent on the plants. The amount of light required for a plant to

survive varies greatly between species. Many trees compete for direct sunlight for a large part of the day, while other plants, such as the semi-aquatic plant genus *Anubias*, are named after the Egyptian god of the underworld because they grow naturally in heavily shaded streams.

Humidity

Humidity affects the rate of water evaporation from the surface of an organism. High humidity can affect an organism's ability to cool itself by evaporative water loss. Low humidity can affect its ability to withstand drought.

Wind and air currents

Only plants with a strong root system and a tough stem can live in exposed areas with persistent strong winds. On the other hand, wind and air currents provide an important means of dispersing insects, spores and seeds, and are important factors in animal flight or gliding modes of locomotion.

FIGURE 12 Dandelions need wind currents to disperse their seeds.

pH

pH (a measure of acidity) influences the abundance and distribution of plants in soil and freshwater ponds. Some plants thrive in acidic conditions, while others thrive in neutral or alkaline conditions. Most plants are highly sensitive to changes in pH.

Water currents

Water currents and waves are particularly important in oceans, rivers and streams. Only organisms capable of swimming or avoiding strong currents can survive where this is a persistent feature of the environment. Waves have a substantial effect on organisms living in the intertidal zone. To survive periodic buffeting by waves and exposure to air, special adaptations are required. For example, on coral reefs, fragile branching corals are usually found where there is little wave action, whereas large boulder corals can survive the constant barrage of wave action on the reef crest.

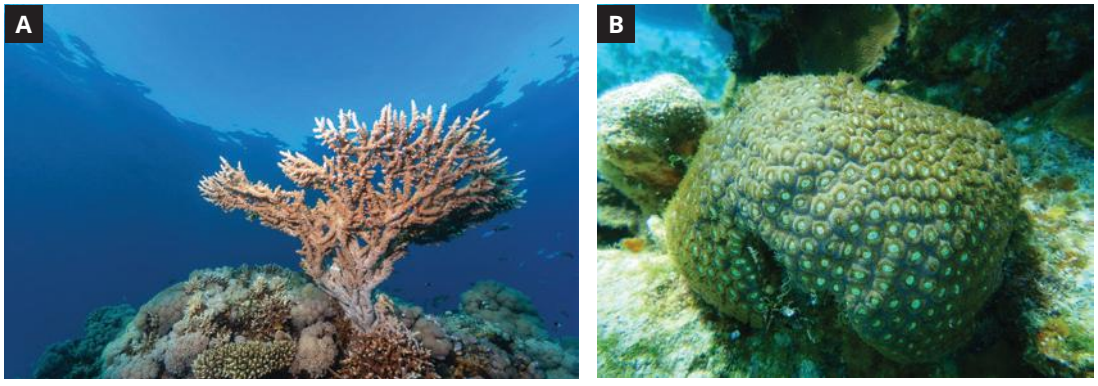


FIGURE 13 (A) Fragile branching corals are found where there is little wave action, while (B) boulder corals can survive rough wave action.

Salinity

There is a sharp distinction between marine and freshwater species. Estuarine organisms must have special physiological or behavioural adaptations for withstanding the daily fluctuations in salinity that accompany tidal rhythm and freshwater flow from the land.

Topography

Topographic features (geographical surface features) influence illumination, temperature, moisture and so on. Within a relatively small area (e.g. the slopes and base of a gully), the general texture and pattern of the habitat may affect survival.

Real-world biology

Intertidal zone

The intertidal zone is between the low tide and high tide levels on a beach or rocky shoreline. The organisms that live in this zone must be able to tolerate a wide range of abiotic conditions. When the tide is high, the organisms are covered in salt water. Although the temperature is relatively stable and there may be a supply of nutrients and food in the water, strong waves and currents exert force on the organism. There is also the difficulty of high salt levels in the surrounding water causing the organism's body to lose internal moisture.

When the tide is low, the organism faces new abiotic challenges. It is now exposed to bright sunlight and wide temperature variations. Water that was left by the tide is heated by the Sun and begins to evaporate, leaving behind traces of salt on the rocks or sand and puddles with higher salinity. There is also no access to nutrients or oxygen dissolved in water.

Animals such as the common limpet (*Cellana tramoserica*) have a wide tolerance range. The limpet excavates a small hollow in which to hide during low tide. When not covered by water, it clamps down tightly on the rock to limit water loss or desiccation. Its shell also provides a surface for sea lettuce to grow on, which aids with camouflage and maintains a moist microenvironment when the limpet is exposed, reducing its vulnerability to predation during the high tide and desiccation during the low tide.

Apply your understanding

1 **Identify** the abiotic factors that vary greatly in the intertidal zone. (1 mark)
2 **Describe** how the duration of exposure during low tides influences the distribution of the common limpet in an intertidal rocky shore. (1 mark)
3 Oysters live in the intertidal rocky shore. However, unlike limpets, oysters attach to the rock and do not move. **Deduce** how this may influence the abundance and distribution of oysters and common limpets in this environment. (1 mark)
4 "The common limpet (*Cellana tramoserica*) encourages sea lettuce to grow on its shell to aid with camouflage and maintain a moist microenvironment when exposed, reducing its vulnerability to predation during the high tide and desiccation during the low tide." **Construct** a research question that addresses an aspect of this claim. (1 mark)

FIGURE 14 A common limpet clamped down on a rocky surface in the intertidal zone

Check your learning 2.5

Check your learning 2.5: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** an ecosystem. (1 mark)

2 **Summarise** how predation and disease influence the distribution and abundance of species in an ecosystem. (4 marks)

3 Many Australian plants are sclerophylls – woody plants with evergreen leaves that are narrow and thick to reduce water loss. **Identify** what primary environmental factor these plants are adapted for. (1 mark)

4 The Australian owlet-nightjar is a small bird that nests and roosts in tree hollows, which can take hundreds of years to form.
   - **a** **Identify** one benefit that nesting in hollows provides the owlet-nightjar. (1 mark)
   - **b** **Explain** how the clearing of a section of old forest with many tree hollows could affect the distribution and abundance of the owlet-nightjar. (2 marks)

5 **Explain** why intraspecific competition tends to be stronger than interspecific competition for a limited resource. (1 mark)

Analytical processes

6 **Distinguish** between:
   - **a** abiotic and biotic factors (1 mark)
   - **b** community and population. (1 mark)

7 Due to a change in land use, including clearing of deep-rooted native vegetation for crop production, and the large-scale use of bore water, large areas of Western Australia are affected by dryland salinity (salinity at or near the soil surface). **Determine** how this issue might impact the distribution of plants and animals in these areas. Consider both abiotic and biotic factors in your answer. (3 marks)

8 **Compare** the abiotic differences between the habitat of an east-facing slope and that of a west-facing one, on the eastern Australian coast. **Consider** how these differences would influence the plants growing on them. (6 marks)

Lesson 2.6
Distribution and abundance

Key ideas

→ The distribution of organisms can be categorised into three patterns: random, uniform or clumped.

→ Individuals in a population are distributed as a result of interactions with their environment, other species and each other.

→ Distribution patterns impact the validity and reliability of sampling methods.

Learning intentions and success criteria

Distribution patterns

A population consists of members of the same species occupying a given area at the same time. As you learnt in Lesson 2.5, each species has specific environmental requirements and is only found in places that meet these requirements. Populations are distributed throughout an ecosystem depending on their relationships with each other, their interactions with other species and the variation of abiotic factors in the environment. Individuals in a population may be distributed at random, have uniform spacing or be clumped in some way.

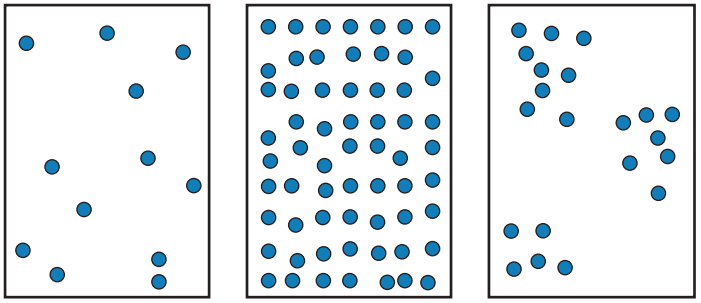


FIGURE 1 Population distribution patterns

Random distribution

random distribution
an unpredictable spacing of individuals of a species, where the position of each individual is independent of the other individuals of the species in a given environment

Random distribution occurs only in relatively uniform surroundings where the abiotic and biotic factors do not vary significantly across the ecosystem. Such distributions usually occur only for a short time while the availability of widely spread resources is greater than the demand. For example, weed seeds blown by wind over bare fertile soil will produce a random distribution of seedlings if the soil surface is even.

Uniform distribution

uniform distribution
a pattern of distribution in which individuals are more or less equally spaced throughout the entire area

Uniform distribution is also rare in nature and usually results from intense competition for space. Seeds from trees in a forest must compete for sunlight, water and soil nutrients. Any available space on the forest floor will be populated by saplings competing for resources. Over time, one sapling will dominate, clearing the surrounding area of any competing plants. In some mature forests, the large trees may have an almost uniform distribution (spaced at regular intervals) because of competition for sunlight and soil nutrients.

Some animals must compete for mates, resulting in territorial behaviour. This may play a significant role in creating an even distribution over the area. Penguins, for example, exhibit uniform distribution during the nesting season.

Clumped distribution

clumping
a pattern of distribution in which individuals are clustered in groups in particular parts of the habitat

Clumped distribution is the most common pattern of distribution of plants and animals in nature. This is because:

- environmental conditions are seldom uniform throughout, even in small areas
- reproductive patterns frequently favour clumping (e.g. young animals often stay with their parents)
- animals often exhibit behaviour patterns that lead to active congregation in loose groups, schools, flocks and herds.

A clumped distribution may increase competition for nutrients, food, space or light. Trees growing together may compete more for nutrients and light than they would if they were spread apart; however, clumping may make them better able to withstand strong winds. For some animals (e.g. the hyena), hunting in a pack makes it possible to bring down large prey, which a single individual could not do alone. If a solitary hyena kills its prey, it must then compete for the food with other scavengers. In contrast, prey species often clump together as a defence mechanism, to act like one larger organism, to confuse the predator, or simply to protect the weaker individuals with sheer numbers.

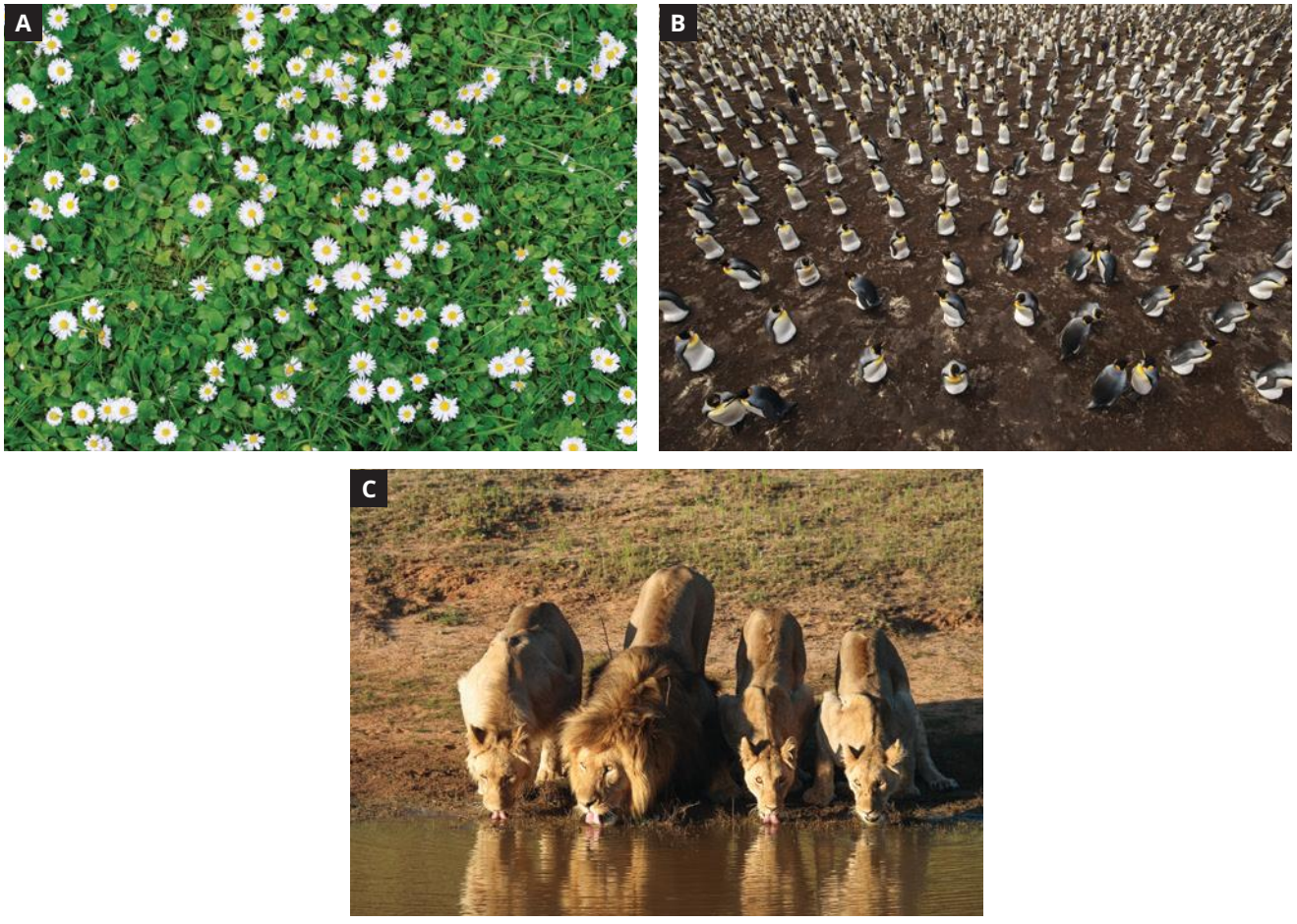


FIGURE 2 Examples of distribution patterns: (A) random distribution of daisies, (B) uniform distribution of penguins and (C) clumped distribution of lions

Distribution and sampling techniques

To investigate the distribution and abundance of different species within an ecosystem, scientists use a variety of **ecological sampling** techniques. The method used depends on the characteristics of the species being investigated, such as how much or how fast they move, as well as the purpose of the investigation (e.g. whether scientists are researching the population size or the species distribution in a given area). These sampling techniques (which will be explained in further detail in Lesson 2.10) include:

ecological sampling methods used to study the abundance and distribution of organisms in an ecosystem, particularly to look for correlations with biotic or abiotic factors and when developing effective ecosystem management

quadrat
a defined area (usually square) with a fixed size, used to count organisms within an area

sessile
fixed in one place; not mobile

transect
a line, often laid across an ecological gradient, along which the abundance of organisms is recorded, either within the whole area or at specified intervals

capture-recapture
a method of estimating population density of animals where animals are captured, marked and released; the proportion of tagged individuals in subsequent trapping is used to estimate population size

motile
able to move around freely

validity
the extent to which a test measures what was intended

reliability
the extent to which a measurement, test or investigation produces consistent results

- **quadrat** – a small square sample area, generally used to investigate the distribution or abundance of plants and **sessile** organisms in an area
- **transect** – a survey line generally used to investigate the distribution of plants and sessile organisms along an abiotic factor gradient (e.g. on a shoreline from dunes to waterline)
- **capture-recapture** – a technique used to observe the abundance and movement of **motile** species.

The distribution patterns of different organisms may have a significant impact on the **validity** and **reliability** of ecological surveys, due to the high number of variables at play in determining where organisms live within an ecosystem. With any ecological sampling technique, it is assumed that the distribution of organisms in areas that have the same abiotic parameters will be uniform. This means that, if the distribution of the species of interest is uniform, the results will be reliable and will accurately represent the population density, making the survey valid. If the distribution is random, both reliability and validity will be affected; however, a large enough sample can overcome this concern. If the population displays a clumped distribution, the reliability and validity of the results are greatly reduced, because samples taken in areas where there are no individuals or where there are dense patches of the population are likely to skew the results. For this reason, in any survey technique, it is important to ensure that enough data is collected to give accurate results.

Real-world biology

Possum and glider distribution in the Eden (NSW) forest

A study by CSIRO scientists revealed a patchy distribution of eight species of possums and gliders in forests near Eden in NSW. It found that 63 per cent of the possums and gliders were found in only 9 per cent of the forest area studied; none were found in 52 per cent of the area.

Further investigation showed a close correlation between the distribution of these animals and that of peppermint eucalypts. Analysis of the nutrient levels of various trees showed that the peppermint eucalypts were rich in nutrients, particularly potassium, nitrogen and phosphorus. These trees, as distinct from other species in the forest, had a wide trunk base, were found in areas that had not been subjected to recent fire, and grew only in fertile soils. This meant that the distribution of both the trees and the arboreal mammals was related to the underlying rock types, which produced high-nutrient soils.

FIGURE 3 Gliding possums in NSW are often referred to as gliders.

Apply your understanding

1 **Identify** the type of distribution observed in the glider and possum populations in the Eden forests. (1 mark)
2 **Identify** the abiotic and biotic factors that influenced the distribution of the glider and possum populations. (2 marks)
3 "There is a close correlation between the distribution of these animals and that of peppermint eucalypts." **Construct** a research question that could investigate an aspect of this claim. (1 mark)

Check your learning 2.6

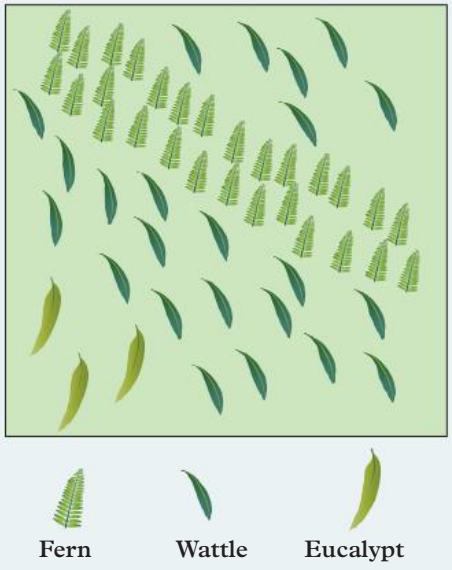
Check your learning 2.6: Complete these questions online or in your workbook.

Retrieval and comprehension

1 Distribution of a species may be random, uniform or clumped. **Describe** each of these conditions and provide a possible reason for the distribution. (6 marks)
2 **Describe** an example of how a clumped distribution could benefit a species and how it could disadvantage a species. (1 mark)

Analytical processes

3 The figure below shows the distribution of different Australian plants in a 10 m × 10 m plot.



a **Determine** the type of distribution pattern of each plant type, giving your reasons. (3 marks)
b **Calculate** the population density of each plant type. (3 marks)
c **Summarise** the abiotic differences that might account for the distribution patterns. (2 marks)

4 A capture-recapture study was conducted on wild rabbits to determine the population in south-eastern Queensland. Rabbits tend to form clumped distributions near areas with ample vegetation cover, proximity to water and suitable burrowing areas. **Determine** how these factors would impact the reliability and validity of the results of this survey. (2 marks)

Lesson 2.7
Aquatic and terrestrial ecosystems

Key ideas

- → Ecosystems are composed of habitats and microhabitats.
- → The habitat of an organism makes up a small part of the ecosystem.
- → The distribution of habitats and microhabitats affects how a species may be sampled.

Learning intentions and success criteria

Marine ecosystems

An aquatic ecosystem is one that exists in a body of water. There are two main types of aquatic ecosystems: marine and freshwater. Marine ecosystems are aquatic ecosystems that contain saline (salty) water. They include open and deep ocean environments, marshes and coral reefs. Approximately 71 per cent of Earth's surface is covered by sea.

Warm surface currents overlie a series of very deep "rivers" of cold, dense waters flowing from the poles towards the equator. This bottom water is rich in nutrients and low in dissolved oxygen. In equatorial regions, the warmer surface water is moved by the prevailing winds, causing the deep water to be "pulled" to the surface. These upwellings bring rich nutrients to the surface, providing food for phytoplankton (the primary producers of the ocean). The large population of phytoplankton that can survive in this environment is able to support a large, biodiverse community in the marine ecosystem. Some of the features of oceans that contribute to the great biodiversity of this environment are shown in Figure 1.

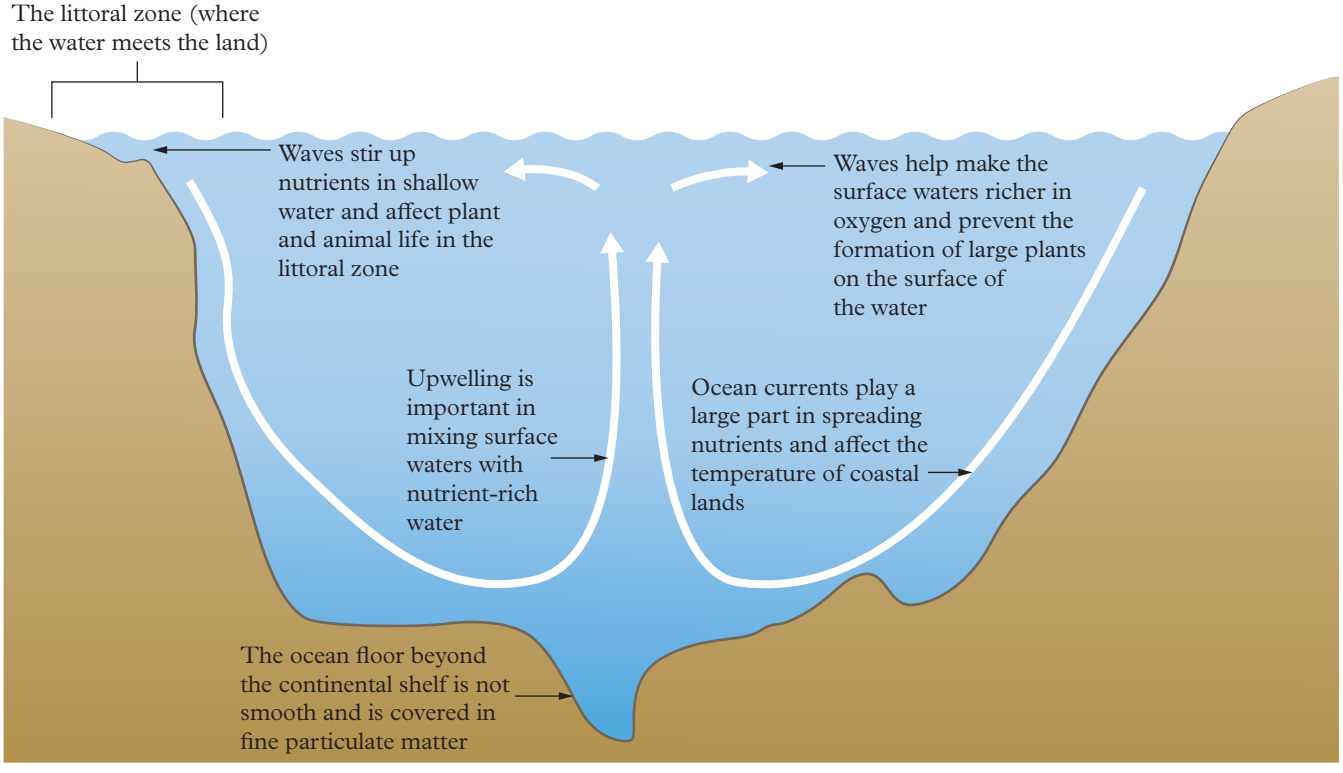


FIGURE 1 Cross-section through an ocean, showing some of its major features

Divisions of the ocean

The ocean can be divided broadly into two ecosystems: at the ocean surface and on the ocean floor. The **plankton–nekton ecosystem** is the ecosystem of the ocean surface. **Nekton** consists of free swimmers including fish, turtles and seals. Plankton consists of microscopic organisms. Phytoplankton refers to photosynthetic plankton, from zooplankton to planktonic animals.

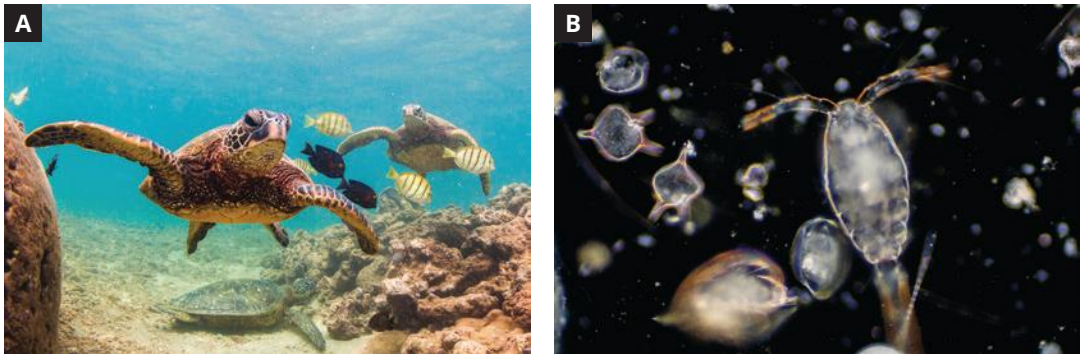


FIGURE 2 (A) Nekton consists of free swimmers like fish, turtles and seals. (B) Plankton consists of microscopic organisms.

The **benthic** (noun *benthos*) **ecosystem** is the ecosystem of the ocean floor. This ecosystem may be **littoral** (where the water meets land), **neritic** (shallow coastal water to 200 metres), bathyal (200 to 4,000 metres), **abyssal** (4,000 to 6,000 metres) or hadal (>6,000 metres). Sea water absorbs a large percentage of the visible spectrum in the upper layers. This means organisms that require light for photosynthesis can only live in the upper zones of the ocean. Organisms that live below this level tend to have poor vision and rely more on touch, chemical and sound stimuli.

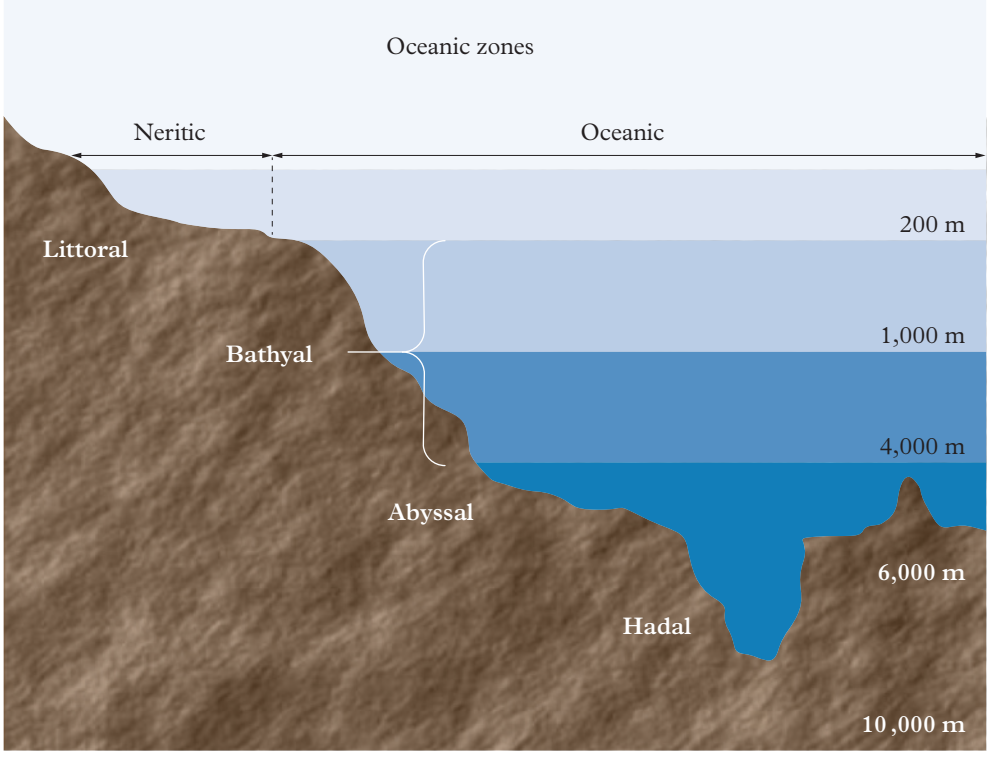


FIGURE 3 Oceanic zones according to depth of water

plankton–nekton ecosystem
the ecosystem of the ocean surface, consisting of nekton (free swimmers) and plankton (microscopic organisms)

nekton
free-swimming organisms of surface waters

benthic ecosystem
the ecosystem at the lowest level of a body of water; includes the sediment surface and some subsurface layers

littoral zone
the zone between water and land, which may be affected by tidal action

neritic zone
the shallow region of the ocean overlying the continental shelves

abyssal zone
the deep-water zone (depth 4,000 to 6,000 metres)

The littoral zone

The littoral zone is the area where the land meets the ocean. It is wide along shorelines and affected by tidal action. This zone is covered with water for only part of the daily tidal cycle. Therefore, organisms living in the littoral zone:

- are restricted to rock pools, where temperature variations may be great; or
- are able to exist both in water and on land, and therefore overcome the problems of desiccation (drying out), breathing in both water and air, locomotion and reproduction; or
- move in and out of the area with the tide.

FIGURE 4 Limpets are a type of aquatic snail that avoid desiccation by clamping down their shells to trap water.

There are many environments in the littoral zone, such as rocky shore, muddy flat, sandy beach or estuary. Each has its own distinctive community. Life in this area can be difficult because of the sun, wind, waves and variable water level. On the other hand, the littoral zone is a fertile area, because:

- nutrients are swept down from the land and in from the sea
- tides and waves circulate these nutrients
- tides and waves dissolve oxygen in the water
- light can penetrate all depths
- conditions are ideal for photosynthesis, which provides abundant algal and plant life for consumers
- high water temperatures cause rapid decomposition of dead organisms.

The neritic zone

The neritic zone consists of shallow coastal water (to a depth of approximately 200 metres), which is associated with the continental shelf. Phytoplankton and zooplankton are able to exist in large numbers due to a relatively consistent temperature range. This is due to the relatively shallow depth of the water and the action of waves and currents. The salt levels in this ecosystem can vary, due to evaporation in shallow waters and freshwater runoff (particularly floods) from land and rain. Tides and currents can have a significant effect on organisms. Life is plentiful in the first 50 to 100 metres of the ocean, because this region contains some light (this reduces rapidly with depth) and oxygen; it is also subject to wave action, which circulates oxygen and nutrients.

The abyssal zone

The abyssal zone is in the deep ocean water (4,000 to 6,000 metres). No light reaches this zone and therefore no photosynthetic organisms can survive, so the oxygen content of the water is low. Most animals tend to be small, sluggish organisms that rely on odour to detect food. Some of these are detritus feeders, obtaining their food from dead organisms and organic matter drifting down from the upper surfaces. Others are carnivores which, like the angler fish, have light-producing (bioluminescent) organs on their body surface to attract prey. The water pressure at these ocean depths is very great, so a hard outer surface is essential to protect the inner organs of most animals.

Deep trenches and rifts in the ocean floor support some communities at depths greater than 3,000 metres. In some of these regions, lava seeps through the surface of the ocean floor and produces geological structures such as hydrothermal vents. Geothermal energy from the radioactive material in the Earth's mantle raises the temperature of the water. This hot water reacts with minerals in rocks, producing hydrogen sulphide, which is metabolised by chemosynthetic prokaryotes. This allows the prokaryotic producers of this community to survive, providing energy for the variety of mussels and clams. These then become food for crabs, starfish, octopuses, fish and giant tube worms.

FIGURE 5 Angler fish can live in water over 2,000 metres deep.

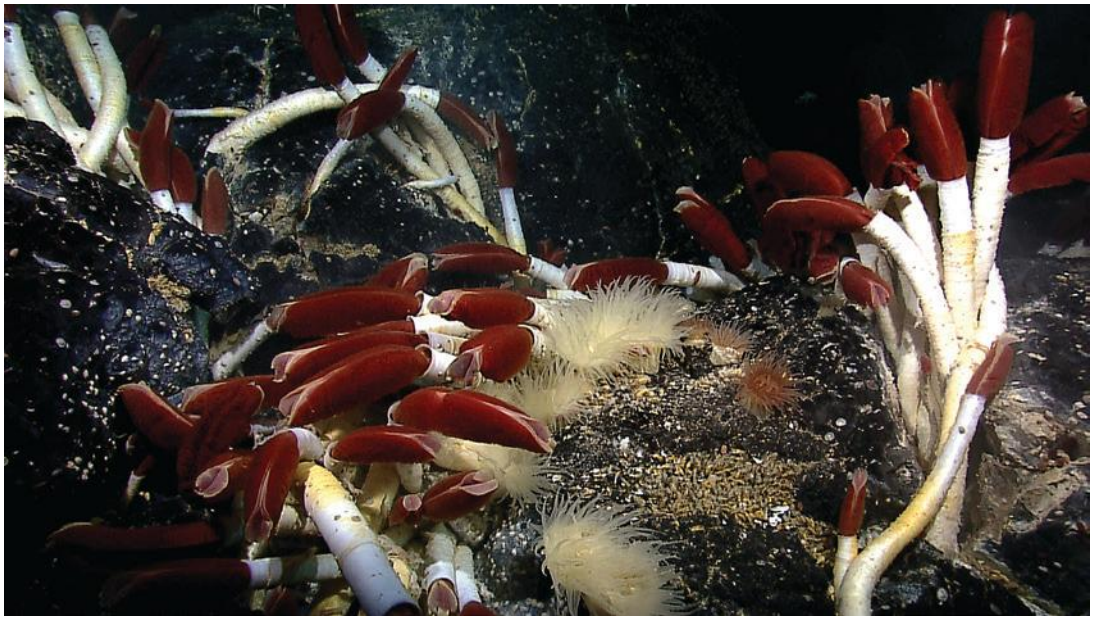


FIGURE 6 Giant tube worms living near hydrothermal vents are supported by chemosynthetic bacteria.

Freshwater ecosystems

Freshwater environments are classified as either standing water (lakes, ponds, dams and swamps) or running water (streams, creeks and rivers). The characteristics and organisms of some common freshwater environments are summarised in Table 1. Freshwater environments can also be isolated by large areas of land. Isolated permanent ponds approach a closed community, where inputs and outputs are balanced.

TABLE 1 Characteristics of freshwater ecosystems

Environment	Characteristics of environment	Typical organisms
Rapid stream	• Rapid flow of water producing a firm bottom • Rocks with crevices that protect organism • Often shallow with good light penetration and high oxygen concentration	• Larvae of insects with high oxygen requirement (e.g. mayflies, stoneflies, caddisflies, bloodworms, snails, bivalves, fish) • Minimal vegetation and plankton
Pool (quiet part of a stream)	• Slow movement of water • Bottom usually soft mud or sand, suitable for burrowing organisms	• Larvae of insects (e.g. dragonflies, damselflies, beetles, bugs, bloodworms), mussels, fish, water snakes, turtles, frogs • Vegetation more plentiful
Pond	• Slow movement of water due to wind or convection • Soft, muddy bottom	• Larvae of insects (e.g. dragonflies, caddis flies), mussels, snails, shrimp, amphipods, copepods, fish, water snakes, turtles, frogs • Vegetation and plankton plentiful
Lake	• Wave action depending on size, depth and wind strength • Bottom mud, sand and gravel, or rocks • Lakes larger and deeper than ponds	• Animals vary greatly according to the nature of the bottom • Vegetation limited to region of light penetration

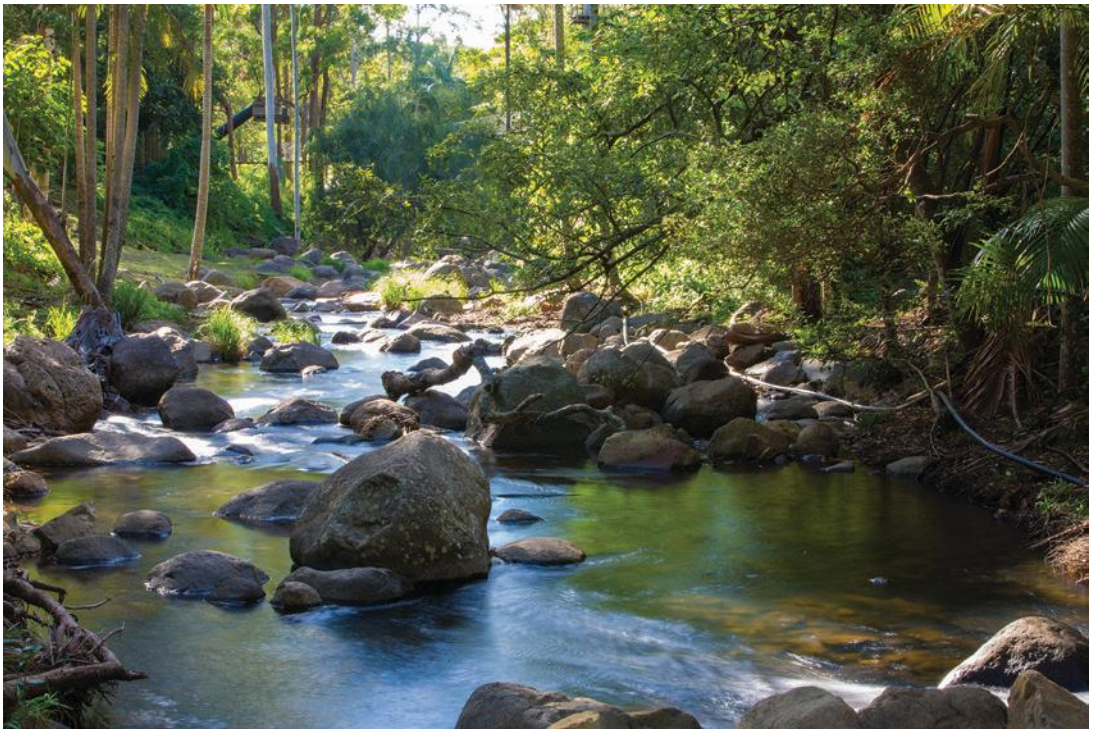


FIGURE 7 A freshwater creek in the Gold Coast hinterland, Queensland

Because of the impermanence of many freshwater ecosystems, the variety of organisms living in them tends to be less than in marine ecosystems. One of the major differences between the two environments is the depth and volume of water. The relative shallowness of freshwater ecosystems has both positive and negative effects, as summarised in Table 2.

TABLE 2 The effects of shallowness of water in freshwater environments

Positive effects	Negative effects
• Surface nutrients readily available • None of the problems of high water pressure as found in deep water • Buoyancy, although less than in marine environments	• Seasonal variations in depth, which may be dramatic • Salt and ion concentrations can vary with location • Temperature variations between day and night and between seasons can be great in shallow areas or in surface waters of deep lakes or dams • Oxygen levels decrease as water temperature increases • Water tends to be turbid, which reduces light penetration at the bottom • Deep water is low in oxygen due to inability to absorb it from the atmosphere

Terrestrial ecosystems

Terrestrial ecosystems are those on land. Land environments are controlled by a wide range of factors that make conditions more variable than aquatic environments. These factors can be grouped into four main categories:

- chemical (e.g. nature of the soil)
- geographical (e.g. topography and altitude)
- physical and climatic (e.g. transparency of air, lack of buoyancy)
- biological.

Some of these factors and their effects are listed in Table 3.

TABLE 3 Factors affecting terrestrial communities

Unfavourable factor	Effect	Favourable factor	Effect
Highly variable temperatures	Adaptation to specific temperature ranges	Plentiful oxygen supply	Animals can have high metabolic rate and thus be very active
Air not buoyant	Few floating forms; plants and animals need supporting structures; animals need structures for locomotion	Air transparent	Sunlight penetrates air easily, so high rate of photosynthesis; visual perception
Scarcity of water	Paucity of life in areas; concentrated excretory products; respiratory surfaces internal; internal fertilisation; seeds hard and dry; external surfaces prevent water loss	Low viscosity of air	Greater variation of animal shapes; sound production by a great variety of animals
		Greater variety of habitats	Diversity of form and requirements

All terrestrial communities ultimately depend on the vegetation that is the producer of the ecosystem. This may be trees, bushes or grasses, or a combination of all three forms. Because plants are immobile, they are completely controlled by their environment and therefore strongly reflect it. As environmental conditions (landforms, soils, animal life, human activities and climate) change from region to region, so does biodiversity.

Biomes

One way in which scientists classify terrestrial environments is by dividing them into areas, called **biomes**. Biomes are classified according to the community units, particularly the vegetation types, that exist in specific climate regions. The nature of the biome is based on abiotic factors, including the amount of light and water, and the temperature.

biome
the living organisms of a large area defined by its climate and dominant plant species (e.g. a desert community)

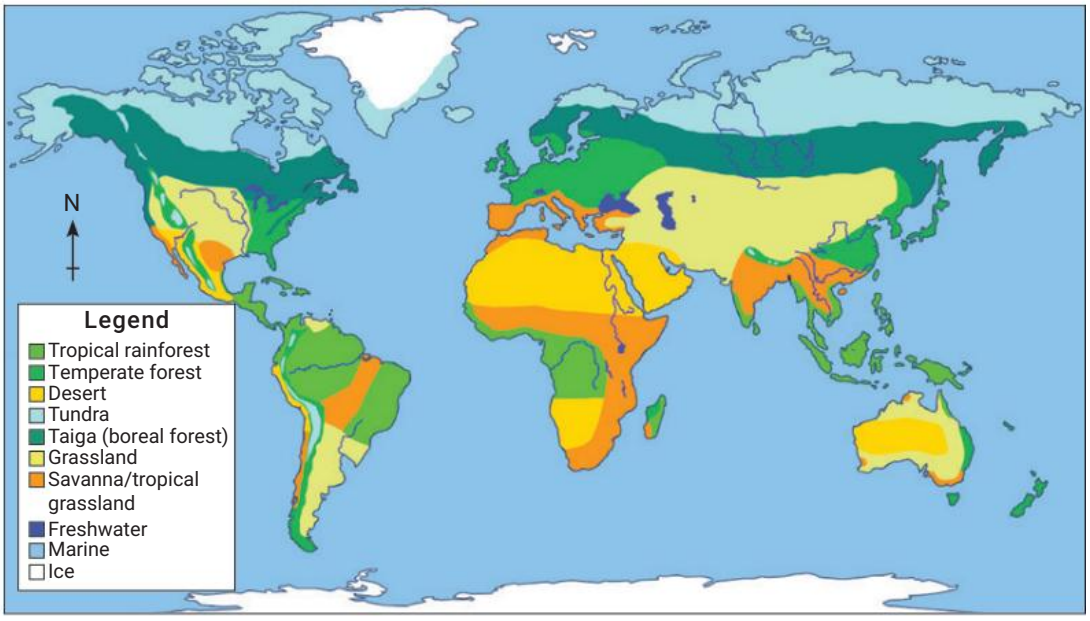


FIGURE 8 The major terrestrial biomes on Earth. Areas with similar climates belong to the same biome.

vertical stratification
the vertical arrangement of vegetation into layers (strata), providing a variety of niches

canopy
the upper layer or habitat zone, formed by mature tree crowns

microhabitat
a small habitat that may be different from the surrounding larger habitat

Some biomes consists of a series of vertical layers. This arrangement is called **vertical stratification**. The leafy branches, or **canopy**, of trees shade the ground below and provide food and shelter for a variety of animals. The small trees and shrubs growing beneath are limited by the amount of sunlight that can penetrate the canopy. If the trees are widely spaced, these are relatively abundant. The forest floor is even more limited by available sunlight. It has a layer of leaf litter, where arthropods, snakes, rodents and decomposers live.

Fallen logs provide **microhabitats** (small habitats that are different from the surrounding larger habitat) for other organisms. Sub-communities may form within these microhabitats. The canopy also influences the humidity and effect of wind at various strata. Humidity in a closed forest increases from the top of the canopy to ground level, while the effects of wind decrease. Each stratum, or layer, of the forest has its own set of environmental conditions and so will support different life forms.

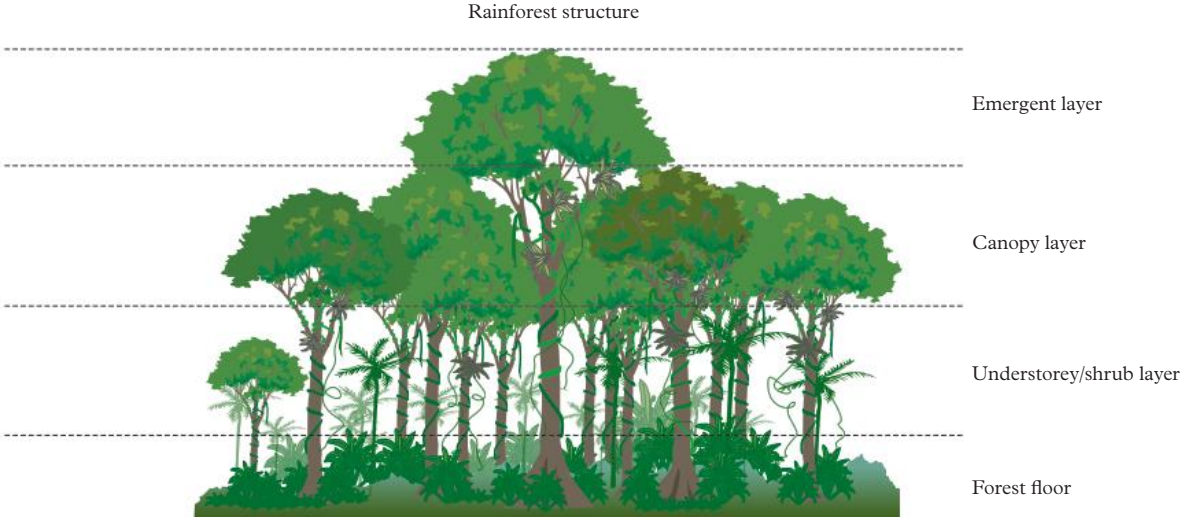


FIGURE 9 The vertical layers in a forest each have their own environmental conditions.

Types of terrestrial biomes

A summary of some of the major types of terrestrial biomes on Earth is provided in Table 4.

TABLE 4 Summary of the types of terrestrial biomes

Biome	Description
Tundra 	Low temperatures, little precipitation (only snow) and high soil moisture, which can stay frozen as permafrost Only low-lying vegetation, no trees
Taiga coniferous forest 	Found south of tundra. Rainfall is not high (35–40 cm/year), but the low temperatures inhibit evaporation, so soils are wet and acidic Tall trees provide shelter for organisms, so greater biodiversity
Temperate deciduous forest 	Vertical stratification; trees lose leaves in winter Found in warmer regions with distinct seasons; annual rainfall about 100 cm
Rainforest 	High annual rainfall; temperatures usually within a narrow range Dense forest communities with tall moisture-loving trees growing close together; canopy closed and layered, limiting sunlight on the forest floor, which is usually covered in leaf litter

Biome	Description
Grassland 	Occur in temperate and tropical regions with unevenly distributed rainfall of 25–75 cm/year; called steppe, prairie, plain, pampa or veldt, depending on the region Similar to grassland biome, but with scattered trees
Desert 	Rainfall less than 25 cm/year and irregular, with high evaporation rate Survival difficult for plants and animals, so adaptations are based on maximising water uptake and reducing water loss

Ecozones and ecoregions

ecozone
a large area in which organisms have been evolving in relative isolation over a long period of time

Another way to classify the terrestrial biosphere is **ecozones**. An ecozone is a large area where organisms have been evolving in relative isolation over a long period of time. Ecozones are characterised by the evolutionary history of the organisms they contain. As a result, an ecozone may contain more than one biome. Each ecozone is separated by a geographic barrier, such as an ocean, a broad desert or a high mountain range, and this barrier prevents migration between the ecozone and other ecozones. Australasia, therefore, is an ecozone.

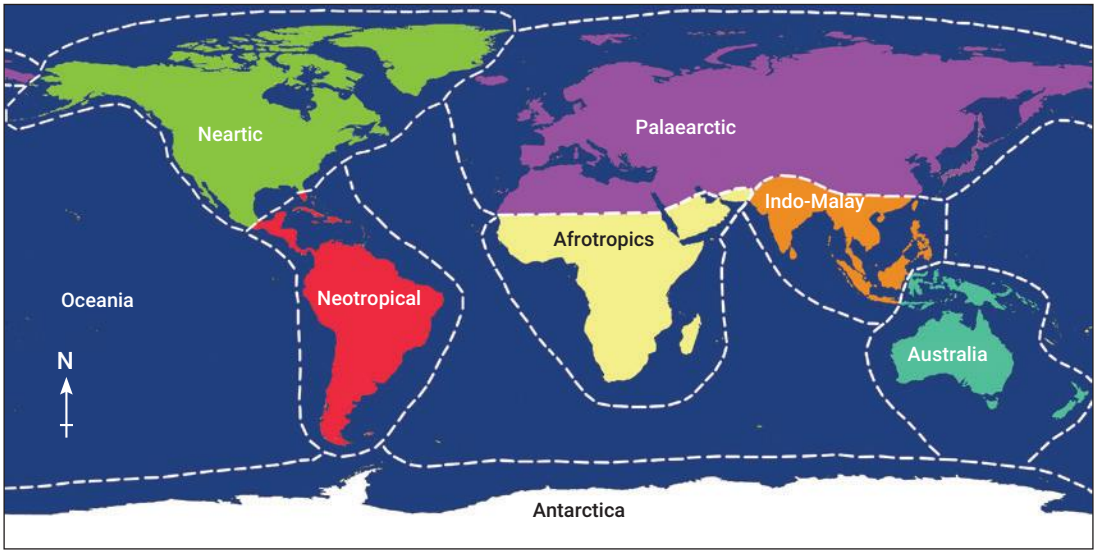


FIGURE 10 The ecozones of the world

Ecozones are further divided into **ecoregions**. These are geographically distinct communities based on geology, soils, climate and predominant vegetation.

ecoregion
a subdivision of an ecozone; a geographically distinct community based on geology, soils, climate and predominant vegetation

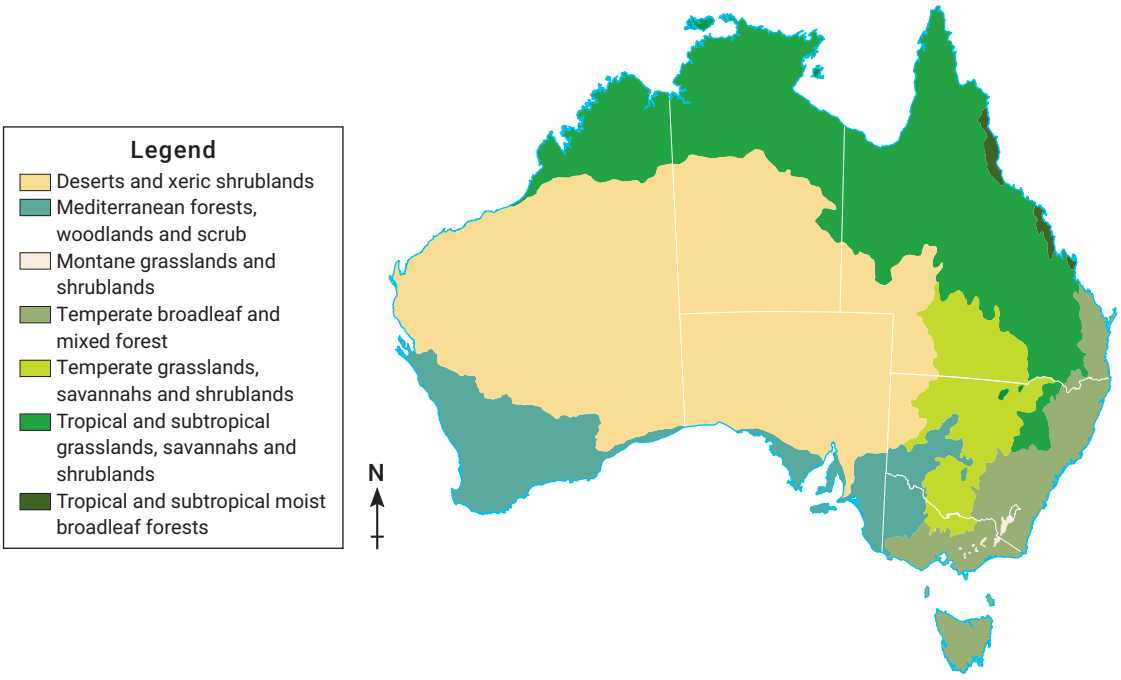


FIGURE 11 Ecoregions of Australia

Vegetation zones

Another method of categorising Australian vegetation zones is shown in Figure 12 and Table 5. This method is based on zones of decreasing moisture, from the coast to the dry interior.

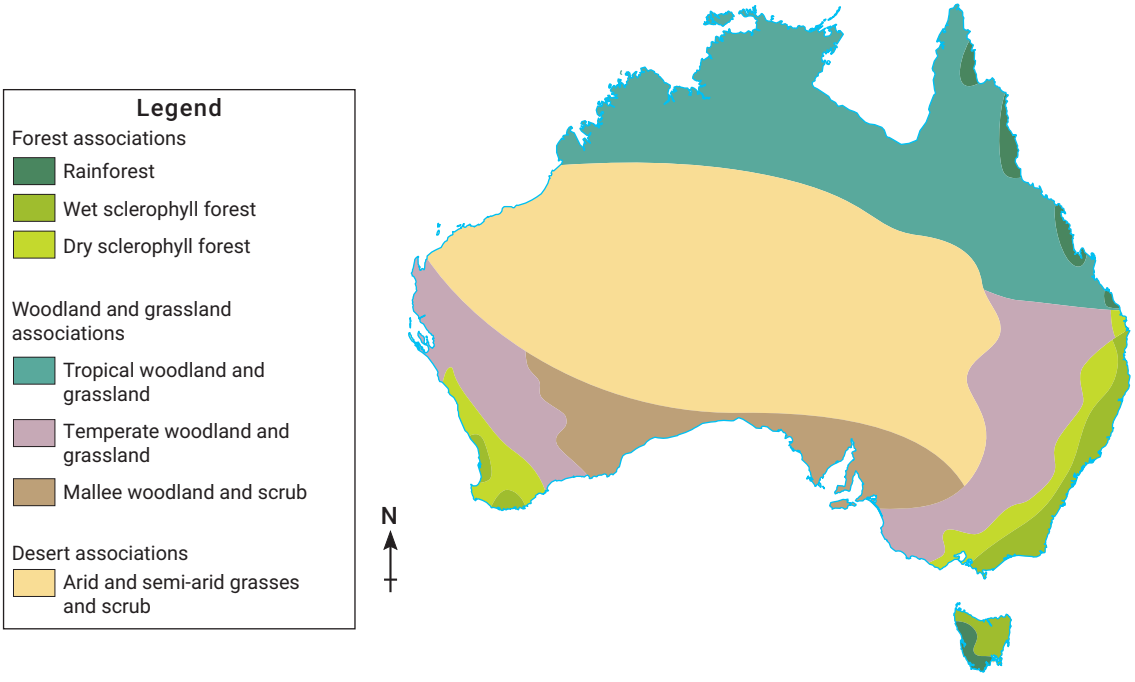


FIGURE 12 Australian vegetation zones. Although different terminology is used to describe them, the zones are very similar to ecoregions.

TABLE 5 Characterisation of Australian vegetation zones based on rainfall

Zone	Characteristics
Rainforest	• Found in high-rainfall regions near the coast • Require fertile soils, or soils with rapid decomposition and recycling of nutrients • Trees grow close together and display species diversity • The canopy forms a cover that excludes light from the forest floor • Grasses and herbs tend to be absent from the forest floor • Epiphytes (plants that use other plants for support) are present • Mosses and ferns survive well in the limited light and high humidity of the forest floor
Wet sclerophyll (hard-leaf) forest	• Found in high-rainfall coastal regions • Large number of eucalypts present • Shrubs and ferns on the forest floor due to the less dense canopy • Broad-leaved creepers present
Dry sclerophyll forest	• Found on drier soils than wet sclerophyll forests • Eucalypts are the main trees • Trees are not as tall as those of wet sclerophyll and canopy is more open • Trees are widely spaced • Fewer shrubs and ferns than in wet sclerophyll
Woodland	• Trees are more scattered than in forests; canopy is open • Grasses and shrubs cover the ground • In savannah woodland, grasses are more numerous than shrubs • In shrub woodland, shrubs are more numerous than grasses
Scrub	• No trees • Main plants are tall shrubs • Perennial grasses (grow for many years)
Saltbush	• Short, widely spaced shrubs only • Grasses between the shrubs • Shrubs have semi-succulent leaves
Desert	• Very little moisture available • Sparse covering of bunch grasses (e.g. spinifex) • Flowering ephemerals (fast/short life cycle) grow after rain

An ecosystem may be as large as the ecoregion, or a small portion of one, depending on the particular community's composition.

Real-world biology

Wallum heathland ecosystem

Wallum is the name given in Queensland to a type of country and a type of vegetation found close to the sea. These areas have poorly drained sandy flats interspersed with low sandy ridges, and sometimes slightly higher gravelly rises. The sandy flats may be rich in humus. Layers impervious to water often form and the area becomes swampy. Wallum grows in areas of high rainfall where the soil is naturally low in mineral nutrients, particularly nitrates and phosphates. The term "wallum" refers to the most obvious tree of the area, the wallum banksia (*Banksia aemula*).

The plants of the flats are typical of any heathland, including stunted trees (particularly banksias) that are rarely more than two metres high, boronias, heath, small-leafed tea trees, bush peas, Christmas bells and vanilla lily. The low sandy ridges carry banksias and other low trees, including

she-oaks, wedding bush and bush peas. The higher ridges can support eucalypts, particularly scribbly gum, bloodwoods and ironbarks. Where conditions are swampy, melaleucas (tea trees) dominate, and patches of rainforest may occur along moist gullies.

Several factors control the vegetation of the wallum.

Low-nutrient soils

The plants show various adaptations to lack of nutrients.

- Wattles have nitrogen-fixing bacteria in their root nodules.
- Mycorrhizal fungi grow in association with the roots of many species.
- Extensive, shallow root systems maximise absorption of minerals and moisture.
- Lignotubers (swollen roots) store excess nutrients and/or water.
- Some plants (e.g. sundew) are insectivorous.

Water stress

Plants experience water stress when there is too little or too much groundwater for their normal life functions. There can be water stress in wallum areas for the following reasons.

- The predominant rainfall is in the summer months and there can be prolonged periods of drought at other times.
- Soils tend to be sandy and thus do not retain moisture.
- Highly leached sandy soils tend to have an underlying hardpan of clay, which severely restricts water penetration and results in large surface run-off. In some flat areas, absorption of water by the hardpan can result in waterlogging.
- Seasonal flooding of flats reduces the oxygen content of the soil. Root cells need oxygen to survive and transport materials to the rest of the plant. Low levels of soil oxygen, therefore, reduce the uptake of water and mineral nutrients by root hairs.
- Summer is characterised by long hot days, with persistent prevailing winds that increase evaporation of water from both the soil and the plants themselves.

Apply your understanding

1 **Identify** two factors that influence the distribution of vegetation in wallum ecosystems. (2 marks)

2 **Describe** two adaptations that plants in wallum have developed to cope with nutrient-poor soils. (2 marks)

3 **Describe** the distribution of species in different elevations in wallum areas, and **explain** how this distribution is linked to habitat conditions. (2 marks)

4 "The plants (in a wallum heathland) show various adaptations to a lack of nutrients." **Construct** a research question that addresses an aspect of this claim. (1 mark)

FIGURE 13 Wallum scrub in Burrum Coast National Park, Queensland

Check your learning 2.7

Check your learning 2.7: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Identify** one advantage and one disadvantage for organisms living in a:
   a marine ecosystem (2 marks)
   b freshwater ecosystem. (2 marks)
2 **Identify** the abiotic factors that affect biodiversity in each of the following ecosystems.
   a Plankton–nekton ecosystem (1 mark)
   b Freshwater ecosystem (1 mark)
3 **Identify** the two major factors responsible for the distribution of the world's biomes. (2 marks)
4 **Explain** which terrestrial biome you would expect to show the greatest species diversity and species abundance. (1 mark)
5 **Explain** how vertical stratification influences species diversity in a community. (1 mark)
6 **Describe** the structural features of the plants in an open scrub ecosystem, and **explain** which ecoregion you would expect to find this community in. (2 marks)

Analytical processes

7 **Determine** the zone in a marine environment that would have the lowest biodiversity, and **describe** the biotic and abiotic factors that would contribute to the limited survival rate of organisms in this zone. (3 marks)
8 **Compare** the environments of the taiga and the temperate deciduous forest. (2 marks)
9 **Distinguish** between a biome and an ecozone. (1 mark)

Lesson 2.8
Classifying and naming ecosystems

Key ideas

- → Different classification systems are used to classify ecosystems.
- → The Holdridge life zone system is used to classify land areas globally.
- → Specht's classification system is used to classify Australian vegetation.
- → Classification is an important part of ecosystem management.

Learning intentions and success criteria

The importance of classifying ecosystems

As you have learnt throughout this module, distribution and abundance are directly influenced by the biotic and abiotic conditions of a species' environment. A community of coexisting organisms in a particular location is dependent upon the abiotic components of the environment.

One of the most important groups of organisms in any ecosystem are the producers. Any change in the abiotic factors (e.g. amount of light or water) can directly affect the size or growth of a photosynthesising producer population.

This in turn affects how much organic matter is formed. A lack of organic matter will result in a decrease in the types of animals (each of which has its own set of tolerance levels) that can be supported by these plants. This example not only emphasises the importance of producers in any ecosystem, but also illustrates the importance of abiotic factors in maintaining the biodiversity of an ecosystem.

As the human population continues to grow, there is pressure to increase areas available for agriculture, mining, industry and housing. This can result in further land clearing and so reduce the natural ecosystems. It is important, therefore, that ecosystems are identified, and fragile or unique areas are protected. Species diversity must be maintained while using natural resources in a sustainable manner. Identifying and classifying ecosystems is an important step towards effective ecosystem management.

FIGURE 1 (A) Mining, (B) property development and (C) clearing land for agriculture severely disrupt ecosystems.

Several systems are used to classify ecosystems – some are used globally and others work only for particular countries or regions. These various systems classify ecosystems based on either the abiotic factors in the region or the dominant producers in the ecosystem.

Holdridge life zone system

The **Holdridge life zone system** is a global system based predominantly on climate. This system considers:

- annual precipitation (as rain or snow)
- mean annual **biotemperature** (based on the growing season length and temperature, between 0°C and 30°C)
- potential evapotranspiration (the amount of water that would be evaporated or transpired if sufficient water were present)
- humidity levels in particular areas (provinces)
- latitudinal regions
- altitudinal belts.

This system assumes that the soil and vegetation communities can be mapped if climatic factors are known. One difficulty with this form of classification is the subpolar and polar regions, where temperatures are low and almost all available water is locked up in ice. This means the polar and subpolar regions have a very low potential evapotranspiration ratio and are equivalent to a desert for organisms living in that environment. Moisture availability is the determining factor for producers in any ecosystem. The Holdridge life zone system is, however, a useful tool in determining possible changes in natural vegetation patterns due to climate change.

Holdridge life zone system
a system of classifying areas of land, based on climate and ecological types

biotemperature
the average annual temperature in an area, adjusting all temperatures below 0°C or above 30°C due to plant dormancy at these temperatures

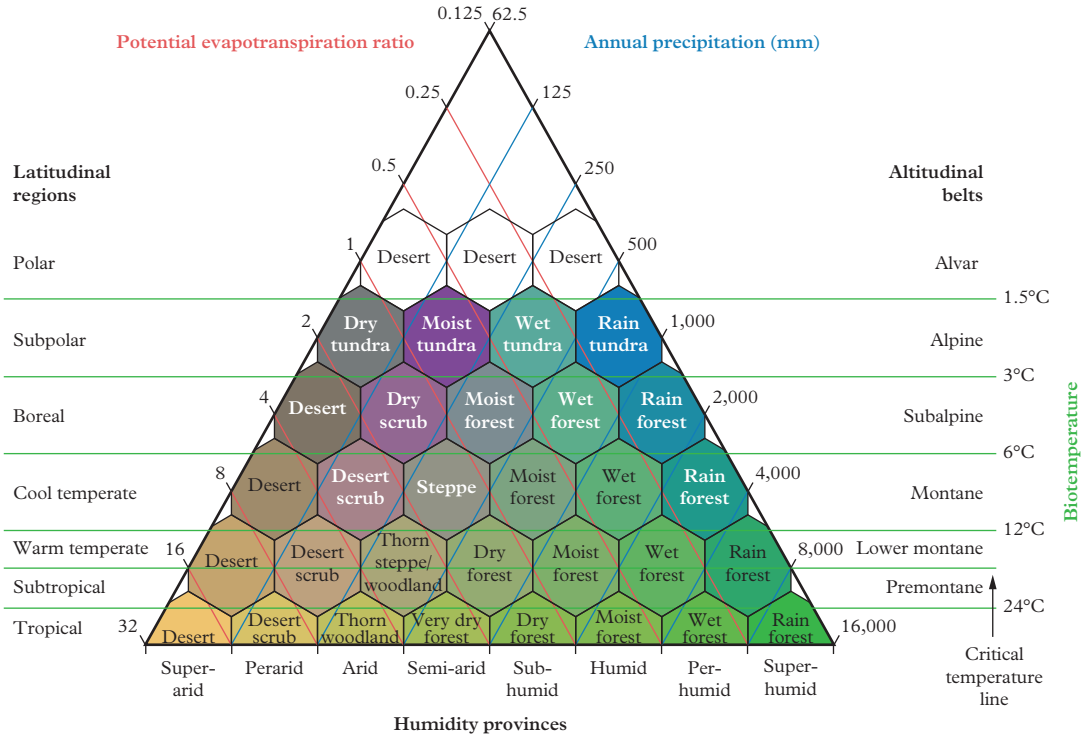


FIGURE 2 Holdridge life zones

To read the Holdridge scheme, the user needs to draw lines for each factor in the ecosystem being investigated. As an example, Figure 3 shows an ecosystem with an average biotemperature of 10°C (red line), an annual precipitation of 300 mm (orange line) and a potential evapotranspiration ratio of 1 (yellow line) in a montane altitude belt. In this example, this indicates that the ecosystem should be classified as a steppe.

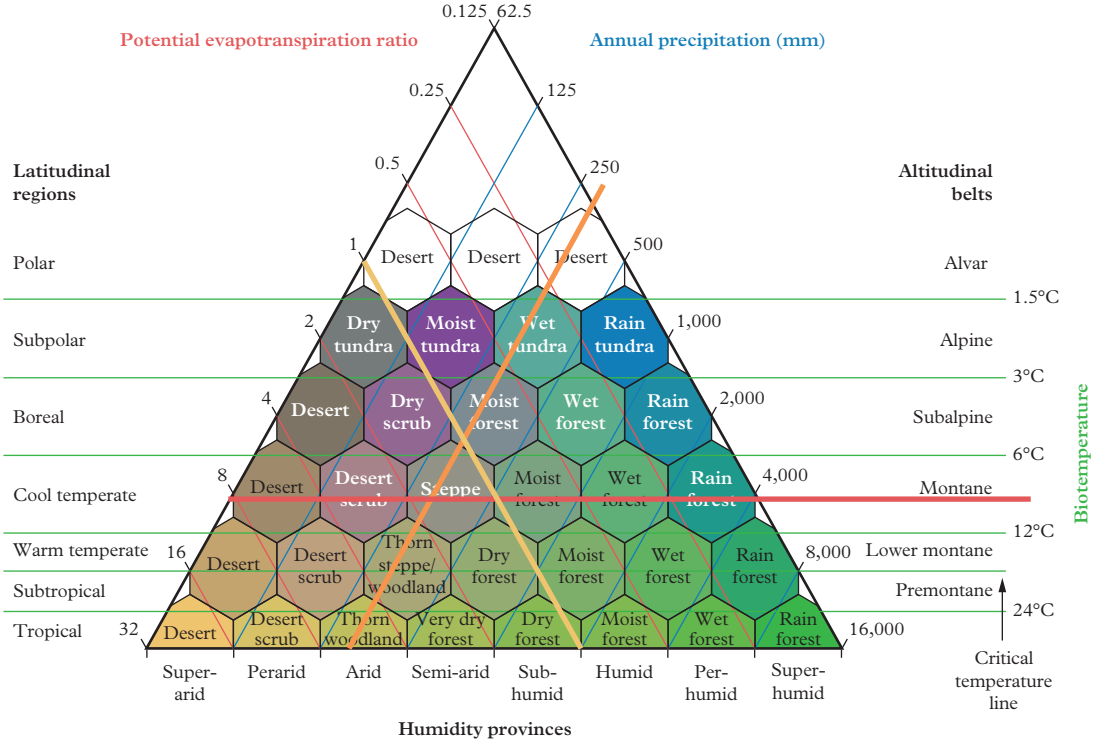


FIGURE 3 Example of classifying using the Holdridge classification scheme

Specht's classification system

Another method of classifying ecosystems is to use the structural features of the plants in an area. **Specht's classification** of Australian vegetation uses the foliage cover and height of the **ecologically dominant layer** of plants in an area. The dominant layer is the layer with the most above-ground biomass. Occasional trees that reach above this layer are considered "emergent" and are not used to determine the foliage height. The foliage cover is determined by the percentage of ground cover by foliage in the dominant layer. Therefore, if the area is investigated using a transect line, the foliage cover would be the cumulative distance covered by foliage, divided by the total length of the transect line, multiplied by 100. The ecosystem is classified using the parameters shown in Table 1. In the ecosystem shown in Figure 4, the ecologically dominant layer would lead to the area being classified as a closed forest.

Specht's classification system
an Australian system of classification of vegetation based on the height and coverage of the dominant layer

ecologically dominant layer
the layer of vegetation with the greatest biomass in a given area (the most common canopy height), ignoring emergent plants

TABLE 1 Specht's structural classification of Australian vegetation

Growth form of tallest stratum	Foliage cover by the tallest stratum			
	>70%	30–70%	10–30%	<10%
Tall trees (>30 m)	Tall closed forest	Tall open forest	Tall woodland	
Medium trees (10–30 m)	Closed forest	Open forest	Woodland	Open woodland
Low trees (<10 m)	Low closed forest	Low open forest	Low woodland	Low open woodland
Tall shrubs (>2 m)	Closed scrub	Open scrub	Tall scrubland	Tall open scrubland
Low shrubs (<2 m)	Closed heath	Open heath	Low shrubland	Low open shrubland
Hummock grasses			Hummock grassland	
Tufted/tussock grasses	Closed tussock grassland	Tussock grassland	Open tussock grassland	Dense open grassland
Graminoids	Closed sedgeland	Sedgeland	Open sedgeland	
Other herbaceous species	Dense sewn pasture	Sewn pasture	Open herb field	Sparse open herb field

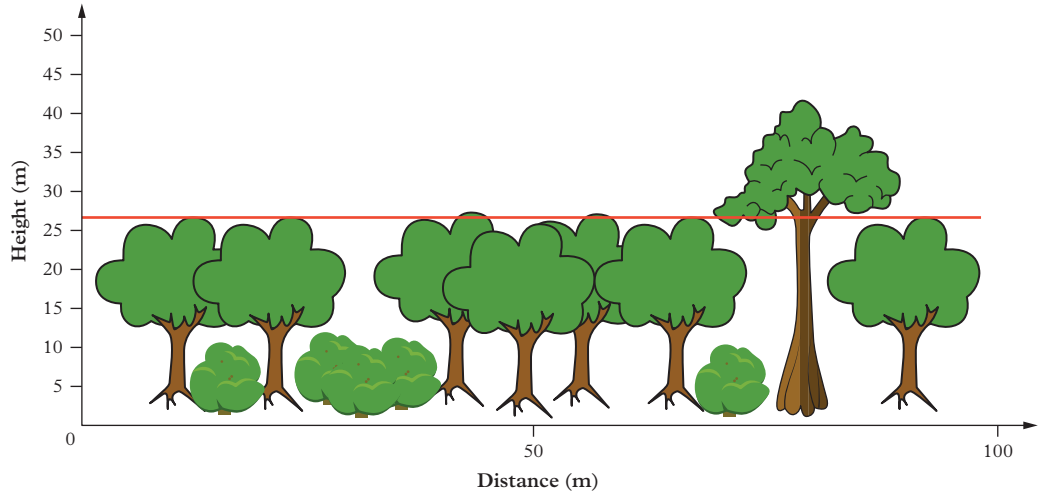


FIGURE 4 Example of a transect survey to classify a closed forest ecosystem using Specht's classification

Check your learning 2.8

Check your learning 2.8: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Identify** the similarities between the different classification systems described in this section. (2 marks)

2 **Identify** the major feature(s) that each of the described classification systems is based on. (8 marks)

3 A particular, humid locality has a potential evapotranspiration ratio of 1, an annual precipitation of 9,000 mm and a biotemperature of 20°C. Using Holdridge's classification:

a **identify** what type of plant community would be present (1 mark)

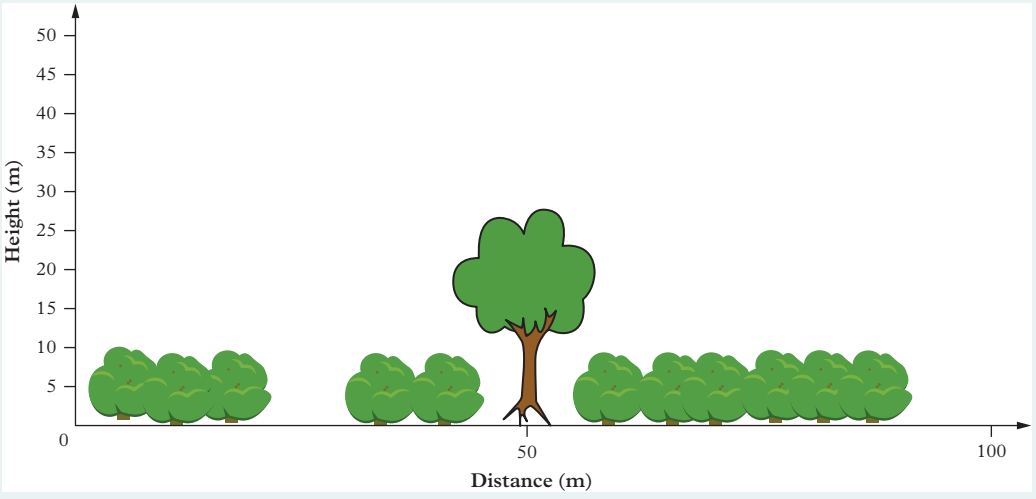
b **describe** what latitudinal region this community would be found in. (1 mark)

4 **Explain** how classifying ecosystems could lead better management and conservation measures. (1 mark)

Analytical processes

5 **Determine** the actual foliage height and foliage cover shown in Figure 3. (2 marks)

6 A student classified the ecosystem shown here as open woodland.



a **Determine** the error made by the student. (1 mark)

b Use the transect to **classify** this ecosystem using Specht's classification system. (1 mark)

Knowledge utilisation

7 The dominant trees in a large area of bushland are brush box (*Lophostemon confertus*) and smooth-barked apple (*Angophora leiocarpa*). Both trees grow to over 30 metres tall and have a combined foliage cover of 50 per cent. **Classify** this ecosystem using Specht's classification system and **justify** your classification. (2 marks)

Lesson 2.9
Determining species diversity

Key ideas

- → Different measures are used to determine the diversity of species for different sampling methods.
- → Species richness is a measure of the number of unique species in an ecosystem.
- → Species evenness is a measure of the relative abundance of species in an ecosystem.
- → Percentage cover is a measure of the amount of ground covered by a plant species.
- → Percentage frequency is a measure of the abundance of a species in an ecosystem.
- → Simpson's diversity index is a measure of biodiversity, accounting for the richness and evenness of species.

Measures of diversity

Learning intentions and success criteria

Ecosystems exist in a great range of abiotic conditions, and this is reflected in the types and abundance of organisms making up the community. The biodiversity of an ecosystem is a measure of the number of types and the abundance of populations in a community. Some ecosystems (e.g. desert ecosystems) have low biodiversity, and others (e.g. a coral reef ecosystem) have high biodiversity.

Some areas that once supported many species have been cleared for growing crops. These crops are usually of a single type (e.g. wheat), and so a **monoculture** is established. In these human-made ecosystems, other plants are actively eliminated. This then affects the types of fauna present in this agricultural ecosystem, which will be substantially different from the diversity that existed before.

A variety of measures can be used to assess the biodiversity of natural ecosystems. Two parameters are **species richness** and **species diversity**. Because most ecosystems are too large to measure all aspects of the entire area, random samples of the area are taken. These parameters are usually only applied to sub-communities (e.g. shrubs, trees or leaf litter organisms) rather than an entire community.

monoculture
a system that has very low species diversity; in agriculture, a crop that consists of a single species, with any other species eliminated as weeds

species richness
a measure of the number of species in an ecosystem

species diversity
a measure of the number of species, and the relative abundance of each species, in a community

FIGURE 1 (A) Cultivated land has a much lower level of diversity than the natural ecosystems it replaced, such as (B) the Clarence Valley, NSW.

Species richness

The number of species in a given area is known as species richness. The simplest way to determine species richness is to focus on the number of unique species. However, when the

sample size increases, the number of unique species also increases. Therefore, the Menhinick index can be used to determine species richness. The Menhinick index compares the number of species in a sample to the number of individuals. The number of species is divided by the square root of the total number of individuals in the sample:

$$S = \frac{s}{\sqrt{N}}$$

In this formula:

- S = species richness
- s = number of species in the sample
- N = number of individual organisms in the sample.

This means that if the number of species increases with the same number of individuals, the species richness is greater, whereas if the number of individuals increases with the same number of species, the species richness is lower, because there are fewer unique species in the ecosystem. An example of calculating species richness is shown in Worked example 2.9A.

Worked example 2.9A

Calculating species richness

1 **Calculate** the species richness for each community in Table 1. The same six species are represented in each community. (2 marks)

TABLE 1 Samples of organisms from two communities

Community A		Community B	
Species	Number of individuals	Species	Number of individuals
A	49	A	21
B	17	B	20
C	11	C	17
D	10	D	16
E	5	E	14
F	8	F	12
Total	**100**	**Total**	**100**

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking you to do.	To "calculate" means to determine or find a number using mathematical processes. The question asks for species richness, so use the Menhinick index formula: $S = \frac{s}{\sqrt{N}}$ The question is worth 2 marks, so two values should be provided: one for Community A and one for Community B.
Step 2: Gather any data that needs to be input into the formula.	s = number of species in the sample, so count the number of species = 6 N = total number of individuals in the sample = 100 So for Community A: s = 6 N = 100 For Community B: s = 6 N = 100

Think	Do
Step 3: Substitute the known values into the formula to solve for S.	Community A: $S = \frac{6}{\sqrt{100}}$ $= 0.6$ Community B has the same values, so $S = 0.6$ Therefore: Community A: $S = 0.6$ (1 mark) Community B: $S = 0.6$ (1 mark)

Your turn

Calculate the species richness for each community in Table 2. The communities have similar species due to their similar environments. (2 marks)

TABLE 2 Samples of organisms from two different communities

Community A		Community B	
Species	Number of individuals	Species	Number of individuals
A	31	A	82
B	18	B	14
C	26	C	21
D	1	D	3
E	17	E	0
F	6	F	0
Total	**99**	**Total**	**120**

Species evenness

species evenness a comparison of the relative abundance of different species in a community

A limitation of species richness is that it does not reflect how evenly the species are represented in each community. This is captured by **species evenness**, a measure of the relative abundance of species within a community. Relative species abundance can be calculated using the formula:

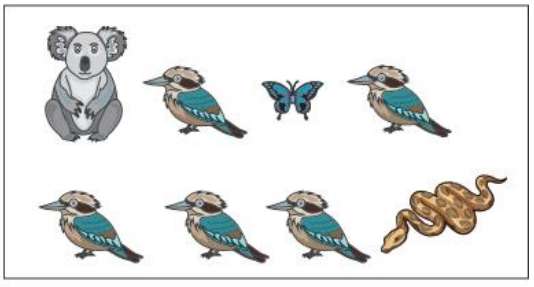
$$RA = \frac{TS}{TP} \times 100$$

In this formula:

- RA = relative abundance (%)
- TS = number of individuals of one species in the community
- TP = total number of individuals of all species in the community

The more even the relative abundances of the different species in a community, the higher the species evenness. For example, in Figure 2, Community A and Community B have the same species richness but different species evenness. In Community A, the RA for the kookaburra = 62.5%, carpet python = 12.5%, koala = 12.5% and Ulysses butterfly = 12.5%. In Community B, the RA for each species is = 25%. Community B has a higher species evenness than Community A.

Community A



Community B

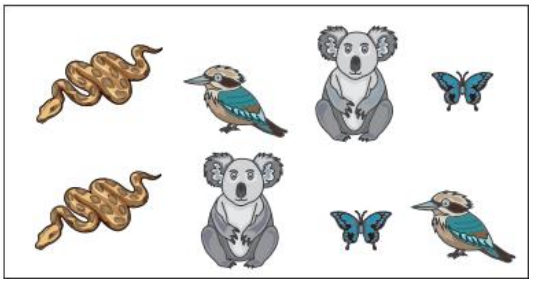


FIGURE 2 Community A and Community B have the same species richness but different species evenness.

An example of how to calculate the *RA* of a species to determine species evenness is shown in Worked example 2.9B.

Worked example 2.9B

Determining relative species abundance and species evenness

Use the data from Table 3 to:

a **calculate** the relative abundance of each species in Community A and Community B. (4 marks)

b **determine** which community has a higher species evenness. (1 mark)

TABLE 3 Samples of organisms from two communities

Community A		Community B	
Species	Number of individuals	Species	Number of individuals
X	45	X	40
Y	15	Y	50
Total	60	**Total**	90

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking you to do.	In part **a**, to "calculate" means to determine or find a number using mathematical processes. The question asks for relative abundance, so use the formula: $RA = \frac{TS}{TP} \times 100$ Part **a** is worth 4 marks, so four values should be provided: two for Community A and two for Community B. In part **b**, to "determine" means to conclude after calculation or investigation. Use your answer to part a to figure out part **b**. It is worth 1 mark, so only one statement is needed.
Step 2: Gather any data that needs to be input into the formula.	Community A, Species X: $TS = 45$ $TP = 60$ Community A, Species Y: $TS = 15$ $TP = 60$ Community B, Species X: $TS = 40$ $TP = 90$ Community B, Species Y: $TS = 50$ $TP = 90$
Step 3: Substitute the known values into the formula to solve for *RA* for each species in the two communities.	Community A, Species X: $RA = \frac{45}{60} \times 100$ $= 75\,\%$ (1 mark) Community A, Species Y: $RA = \frac{15}{60} \times 100$ $= 25\,\%$ (1 mark) Community B, Species X: $RA = \frac{40}{90} \times 100$ $= 44\,\%$ (1 mark) Community B, Species Y: $RA = \frac{50}{90} \times 100$ $= 56\,\%$ (1 mark)

Think	Do
Step 4: Use the values from part a to assess which community has a higher level of species evenness.	In Community A: RA (Species X) = 75% and RA (Species Y) = 25%. In Community B: RA (Species X) = 45% and RA (Species Y) = 56%. The relative abundance of species in Community B is more even than those in Community A. Therefore, Community B has a higher level of species evenness. (1 mark)

Your turn

Use the data from Table 4 to:

a **calculate** the relative abundance of each species in Community A and Community B. (4 marks)

b **determine** which community has higher species evenness. (1 mark)

TABLE 4 Samples of organisms from two communities

Community A		Community B	
Species	Number of individuals	Species	Number of individuals
X	68	X	53
Y	32	Y	47
Total	100	**Total**	100

Percentage cover

When sampling an ecosystem using quadrat sampling, a common method to determine the diversity and abundance of vegetation within an area is to estimate the **percentage cover**. Finding this value can be as simple as placing a quadrat over the sample area and estimating the area occupied by each species (living individuals). To make the estimate more accurate, the quadrat can be broken up into a 10 × 10 grid, and the cells counted where the species occupies at least half the area. This technique is only useful for plants, and there is a tendency to overestimate the more prominent, flowering plants and underestimate the undergrowth.

percentage cover the estimated percentage of a quadrat that is covered by one species

FIGURE 3 Percentage cover of vegetation can be estimated using a quadrat.

Percentage frequency

percentage frequency
the percentage of quadrats in which a species is found, divided by the total number of quadrats in a sample

Another measure of diversity used with quadrats is **percentage frequency**, which estimates the probability that a species will be observed within a quadrat. Percentage frequency is calculated using the formula:

$$\%\ \text{frequency} = \frac{\text{no. quadrats in which the species is found}}{\text{total no. quadrats}} \times 100$$

The number of quadrats used must be high enough to minimise the effect of anomalies on the reliability of the data and can only be used for plants or sessile organisms.

Species diversity

Simpson's diversity index (*SDI*)
the probability that two individuals randomly selected from a sample will belong to different species (or groups)

Species diversity differs from species richness in that it considers both the numbers of species present and the relative abundance of each species. As species richness and evenness increase, so does the diversity of the ecosystem.

Simpson's diversity index (SDI) represents the probability that two individuals randomly selected from a sample will belong to different species (or groups). If the two individuals are different, this indicates that there is diversity in the ecosystem. It can be calculated using the equation:

$$\text{SDI} = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$$

In this equation:

- SDI = Simpson's diversity index
- n = number of individuals of a particular species
- N = total number of individuals in the community
- $\sum$ means "the sum of", so $\sum n(n-1)$ is the sum of the calculations of $n(n-1)$ for each species in the community.

The value calculated for SDI will be between 0 and 1. The higher the value, the greater the diversity. An ecosystem with only one species would have a value of 0. An SDI value of 1 would indicate infinite diversity.

Study tip

When answering cognitive verbs such as **compare**, use the format: Answer, Evidence, Theory. This will help ensure you state your response (Answer), support it with data (Evidence) and link it back to scientific understanding (Theory) to concisely formulate your answer.

Worked example 2.9C

Calculating Simpson's diversity index

Use the information provided in the table to investigate the diversity of the two communities surveyed.

a **Calculate** the diversity of the two communities using Simpson's diversity index. (2 marks)

b **Determine** the probability that two individuals (in this survey) randomly selected from a sample belong to different species. (2 marks)

c **Compare** the diversity of the two communities. (2 marks)

Community A		Community B	
Species	Number of individuals	Species	Number of individuals
A	49	A	21
B	17	B	20
C	11	C	17
D	10	D	16
E	5	E	14
F	8	F	12

<table>
<tr><th>Think</th><th>Do</th></tr>
<tr><td>Step 1: Look at the cognitive verb and mark allocation to understand what the question is asking you to do.</td><td>In part a, to “calculate” means to determine or find a number using mathematical processes. Use the SDI formula:
$SDI = 1 - \left(\frac{\Sigma(n-1)}{N(N-1)}\right)$
Part a is worth 2 marks, so two calculations are needed.
In part b, to “determine” means to establish after investigation or calculation. So use your answers from part a to figure out the answers to part b. Part b is worth 2 marks, so two statements are needed.
In part c, to “compare” means to identify a similarity and a difference between the diversity of the communities. It is worth 2 marks, so 1 mark for a similarity and 1 mark for a difference.</td></tr>
<tr><td>Step 2: Create a table of data, or split the table already provided and add a column to calculate $n(n-1)$. The SDI equation can be tedious to calculate, so a table can be helpful.
At the bottom of the table, you can also calculate the N value, and the $\Sigma n(n-1)$ value, to reduce the inputs in the calculator. This also helps to identify any errors made in the calculations.</td><td>
<table>
<tr><th colspan="3">Community A</th><th colspan="3">Community B</th></tr>
<tr><th>Species</th><th>Number of individuals (n)</th><th>$n(n-1)$</th><th>Species</th><th>Number of individuals (n)</th><th>$n(n-1)$</th></tr>
<tr><td>A</td><td>49</td><td></td><td>A</td><td>21</td><td></td></tr>
<tr><td>B</td><td>17</td><td></td><td>B</td><td>20</td><td></td></tr>
<tr><td>C</td><td>11</td><td></td><td>C</td><td>17</td><td></td></tr>
<tr><td>D</td><td>10</td><td></td><td>D</td><td>16</td><td></td></tr>
<tr><td>E</td><td>5</td><td></td><td>E</td><td>14</td><td></td></tr>
<tr><td>F</td><td>8</td><td></td><td>F</td><td>12</td><td></td></tr>
<tr><td>Total
$N = \Sigma n$</td><td></td><td></td><td>Total
$N = \Sigma n$</td><td></td><td></td></tr>
<tr><td></td><td>Total
$\Sigma n(n-1)$</td><td></td><td></td><td>Total
$\Sigma n(n-1)$</td><td></td></tr>
</table>
</td></tr>
<tr><td>Step 3: Calculate the $n(n-1)$ value. It can be input into a calculator as $n \times (n-1)$.
For example, for Species A in Community A, this calculation would be:
$49 \times (49 - 1) = 2{,}352$
To calculate N, add the n value of each species.
To calculate $\Sigma n(n-1)$, add the $n(n-1)$ values of each species. Don’t worry if these numbers are large.</td><td>a
<table>
<tr><th colspan="3">Community A</th><th colspan="3">Community B</th></tr>
<tr><th>Species</th><th>Number of individuals (n)</th><th>$n(n-1)$</th><th>Species</th><th>Number of individuals (n)</th><th>$n(n-1)$</th></tr>
<tr><td>A</td><td>49</td><td>2,352</td><td>A</td><td>21</td><td>520</td></tr>
<tr><td>B</td><td>17</td><td>272</td><td>B</td><td>20</td><td>380</td></tr>
<tr><td>C</td><td>11</td><td>110</td><td>C</td><td>17</td><td>272</td></tr>
<tr><td>D</td><td>10</td><td>90</td><td>D</td><td>16</td><td>240</td></tr>
<tr><td>E</td><td>5</td><td>20</td><td>E</td><td>14</td><td>182</td></tr>
<tr><td>F</td><td>8</td><td>56</td><td>F</td><td>12</td><td>132</td></tr>
<tr><td>Total
$N = \Sigma n$</td><td>100</td><td></td><td>Total
$N = \Sigma n$</td><td>100</td><td></td></tr>
<tr><td></td><td>Total
$\Sigma n(n-1)$</td><td>2,900</td><td></td><td>Total
$\Sigma n(n-1)$</td><td>1,726</td></tr>
</table>
</td></tr>
</table>

Think	Do
Step 4: Input the values into the formula to solve for SDI in Community A and Community B. Ensure you use all the brackets in your calculator. The final answer must be between 0 and 1. If it is not, you have made an error in your calculation. The closer the value is to 1, the greater the diversity of the community.	Community A: $SDI = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$ $= 1 - \left(\frac{2{,}900}{100 \times 99}\right)$ = 0.71 (1 mark) Community B: $SDI = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$ $= 1 - \left(\frac{1726}{100 \times 99}\right)$ = 0.83 (1 mark)
Step 5: Convert the SDI values you calculated in part **a** into percentages by multiplying them by 100. This will give you the probability that two individuals randomly selected from each sample belong to different species.	**b** Community A: SDI = 0.71 0.71 × 100 = 71 Probability that two individuals randomly selected from Community A belong to different species = 71% (1 mark) Community B: SDI = 0.83 0.83 × 100 = 83 Probability that two individuals randomly selected from Community B belong to different species = 83% (1 mark)
Step 6: Compare the diversity of the communities by stating a similarity and a difference.	**c** The two communities each have relatively high diversity, based on their SDI values (Community B = 0.83 and Community A = 0.71) (1 mark). Community B's diversity (0.83) is higher than Community A's (0.71), making it more likely that two individuals selected at random from Community B would be from different species. This indicates that Community B is more diverse than Community A (1 mark).

Your turn

Use the information in the table below to investigate the diversity of the two communities surveyed.

a **Calculate** the diversity of the two communities in the table using Simpson's diversity index. (2 marks)

b **Determine** the probability that two individuals (in this survey) randomly selected from a sample belong to different species. (2 marks)

c **Compare** the diversity of the two communities. (2 marks)

Community A		Community B	
Species	Number of individuals	Species	Number of individuals
A	31	A	82
B	18	B	14
C	26	C	21
D	1	D	3
E	17	E	0
F	6	F	0
Total	99	**Total**	120

Check your learning 2.9

Check your learning 2.9: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the term "species richness". (1 mark)

2 **Explain** how higher species evenness indicates higher diversity. (1 mark)

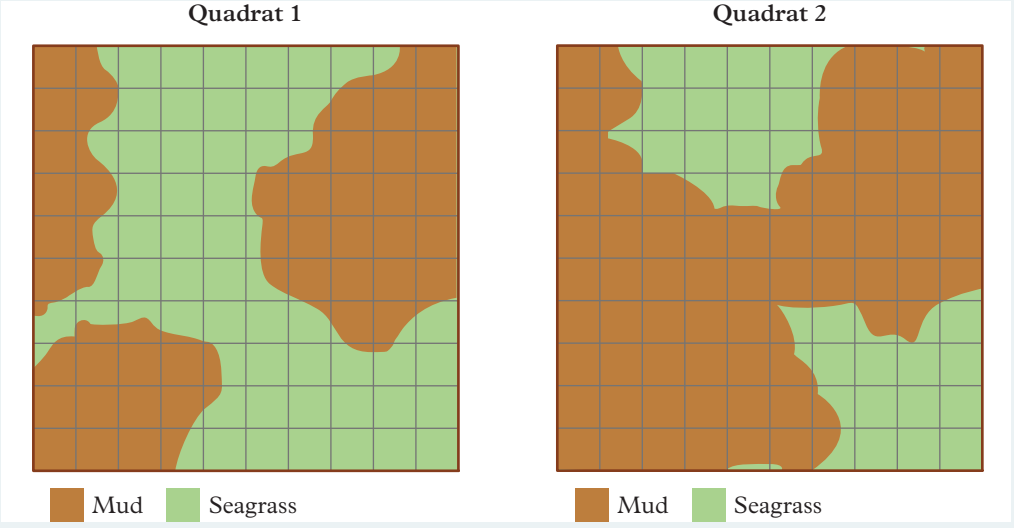
Analytical processes

3 **Contrast** species richness and species diversity. (1 mark)

4 A survey of a wallum heathland ecosystem (approximately 50 hectares in size) showed that there were 15 species of birds. A total of 100 birds were counted.

- **a** **Determine** how likely it is that these numbers were a sample of the community or represented the whole community. **Explain** your answer. (2 marks)
- **b** **Calculate** the species richness of this wallum heathland ecosystem. (1 mark)
- **c** **Identify** what further information would be needed to determine the diversity of birds in this ecosystem. (1 mark)

5 A survey of the distribution and abundance of seagrass on mudflats on the western side of Moreton Bay was carried out. Two of the quadrats surveyed are shown below.



- **a** **Determine** the percentage cover of seagrass in the two quadrats shown. (2 marks)
- **b** The seagrass species *Halophila spinulosa* was identified in 13 of the 150 quadrats. **Calculate** the percentage frequency of this species, and determine what this indicates about the diversity and abundance of *Halophila spinulosa* in Moreton Bay. (2 marks)

Lesson 2.10
Investigating species diversity

Key ideas

- → Various sampling techniques are used to study species diversity.
- → The purpose of a survey and the species being studied determine the appropriate sampling method.
- → When conducting ecological surveys, strategies to minimise bias must be put in place.
- → The Lincoln index is a measure of population size based on sample data.

Learning intentions and success criteria

Steps to investigate diversity

To better understand the diversity of the organisms in an ecosystem, ecologists need to determine the abundance of each species present. Because it is impractical, or impossible, to count all members of a population or community, ecologists rely on a variety of sampling techniques to estimate population sizes. Investigating species diversity is done using the following steps.

1. Define what is to be sampled. For example, if a researcher wishes to investigate the distribution of spotted gums on the western slope of Mt Coot-Tha, the intended measurement is distribution, the target species is the spotted gum and the sample area is the western slope of Mt Coot-Tha.
2. Determine the sampling technique to be used. Common techniques are quadrats, transects and capture–recapture studies, each of which will be explained in this lesson. The sample method chosen will depend on the purpose and species being investigated.
3. Determine how many samples will be taken, and the sampling locations. Normally, samples should be taken at random across the area being examined; however, sometimes other methods are more accurate.
4. Implement methods to minimise any bias in the sample, so an accurate population estimate can be obtained.

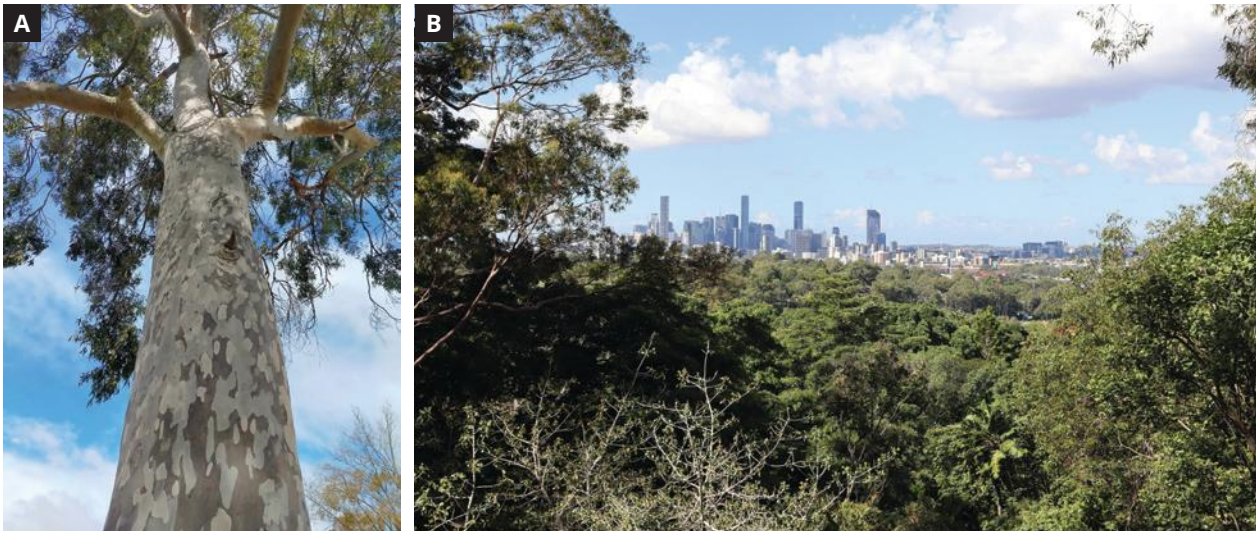


FIGURE 1 When investigating diversity of a species, it is important to define (A) the species to be sampled (e.g. spotted gum) and (B) the sample area (e.g. Mt Coot-Tha, Queensland).

Measuring abiotic factors

When studying an area, the type of environment and the variation of abiotic factors (and therefore habitats) in the ecosystem must also be considered. The distribution and abundance of any species is linked to the physical and chemical features of the habitat and to the other species present. Physical and chemical factors may be measured using a variety of techniques, as listed in Table 1. Measuring these factors alongside population data enables the identification of any correlations in species distribution with their environment.

TABLE 1 Common abiotic factors and the tools used for their measurement

Factor	Method of measurement
Light intensity	Light meter
Temperature	Thermometer
Topography and altitude	Measure slope; draw profile and transects to scale
Pressure	Barometer
Depth of soil	Soil profile cut down and measured; or soil corer
Soil moisture	Sample weighed, water evaporated and soil reweighed
Soil or water pH	pH meter or pH indicators
Organic matter (humus)	Sample weighed, burned then reweighed
Soil or water nutrients	Soil-testing kits
Dissolved oxygen	Oxygen meter
Rainfall	Collection and measurement
Humidity	Hygrometer; or measure evaporation rate over time
Wind	Rotating vane anemometer; or wind speed meter and compass

FIGURE 2 A researcher using a pH meter

Data loggers can be used to determine many chemical aspects of the abiotic environment, particularly in aquatic environments. Examples are pH, light intensity, oxygen and carbon dioxide levels, and salinity.

Sampling methods

Recall from Lesson 1.6 that there are three main methods of sampling: **random sampling**, **systematic sampling** and stratified sampling. The type of sampling you should select for an ecological investigation will depend on the nature of your target species and the measurement you wish to take.

random sampling
a sampling procedure in which every member of the population has an equal chance of being selected for the sample

systematic sampling
a sampling procedure in which samples are selected based on a systematic interval from a randomly chosen starting point

Random sampling

In random sampling, each member of the community in the study has an equal chance of being selected as part of the sample. In ecological research, this can be done by dividing an area into a grid pattern and assigning a number to each section of the grid. Sample sites can then be randomly selected using a number generator. Alternatively, a pair of numbers can be used as *x* and *y* coordinates from a fixed location, giving each location in the region the same probability of being selected.

bias
the occurrence of systematic errors or inclinations, which can lead to incorrect conclusions

precision
how close a set of data values are to each other

The benefit of random sampling is that it minimises selection **bias**. However, it can sometimes lead to small habitats within a study region being missed or to the over-representation of other habitats. When over- or under-representation occurs, it reduces the **precision** of the data collected. This is shown in Figure 3.

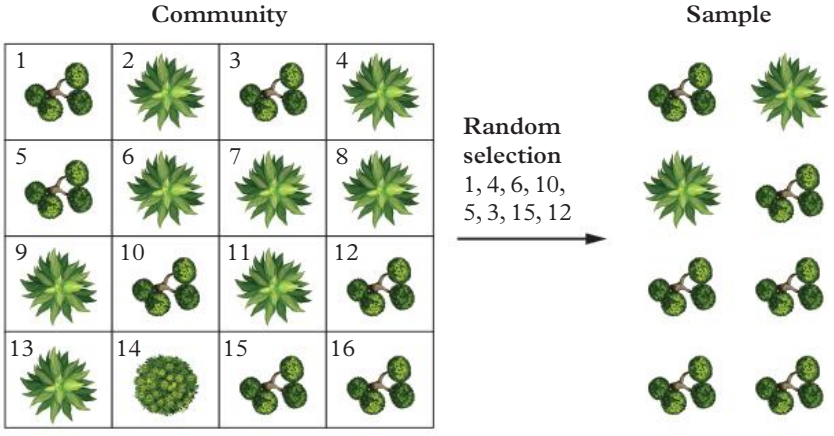


FIGURE 3 The random sample of this community does not represent the type of habitat found in Square 14 and has over-represented one of the habitats in the community.

Systematic sampling

An alternative to random sampling is systematic sampling, where each member of the sample is selected at predetermined intervals throughout the area or along the line being surveyed. Both random and systematic sampling methods help to minimise bias by ignoring features of the habitat, such as areas that are easy to get to, pleasant or clearly demonstrate the relationship being investigated.

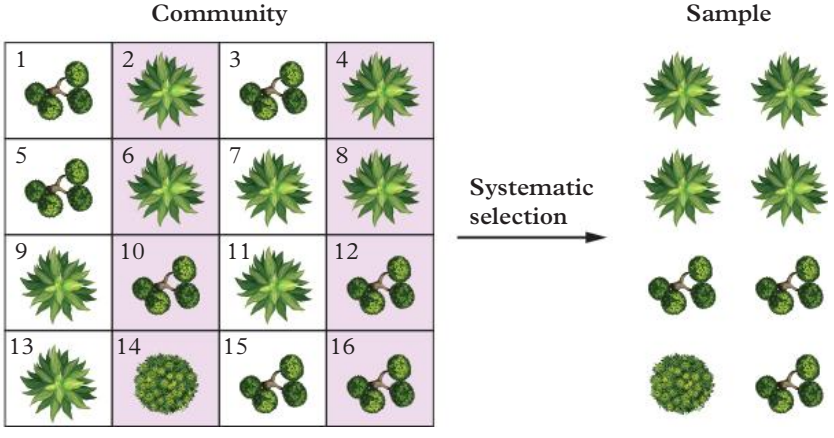


FIGURE 4 The sample of this community has been selected systematically by selecting every second plot in the grid.

Stratified sampling

Before decisions can be made about the management of an ecosystem, the type of environment and its biodiversity must be determined. Natural ecosystems are not homogenous, and this variation needs to be considered when analysing their biodiversity. Factors to be considered include: an estimation of the size, density and distribution of the population; the gradient or profile of the land; **zonation**; and any **stratification**. For the purpose of sampling, an ecosystem can be divided into smaller groups, known as **strata** (singular *stratum*). Once these strata have been determined, each stratum can be randomly sampled. The number of samples taken from each stratum must be proportional to how much of the ecosystem it represents. This method of stratified sampling incorporates the minimised bias of random sampling, and provides increased precision, because each region or stratum is represented equally.

zonation
the breaking of the biome into habitat zones

stratification
the division of the physical environment into smaller components for sampling

strata
distinct layers or zones within an ecosystem, based on vegetation type or abiotic factors

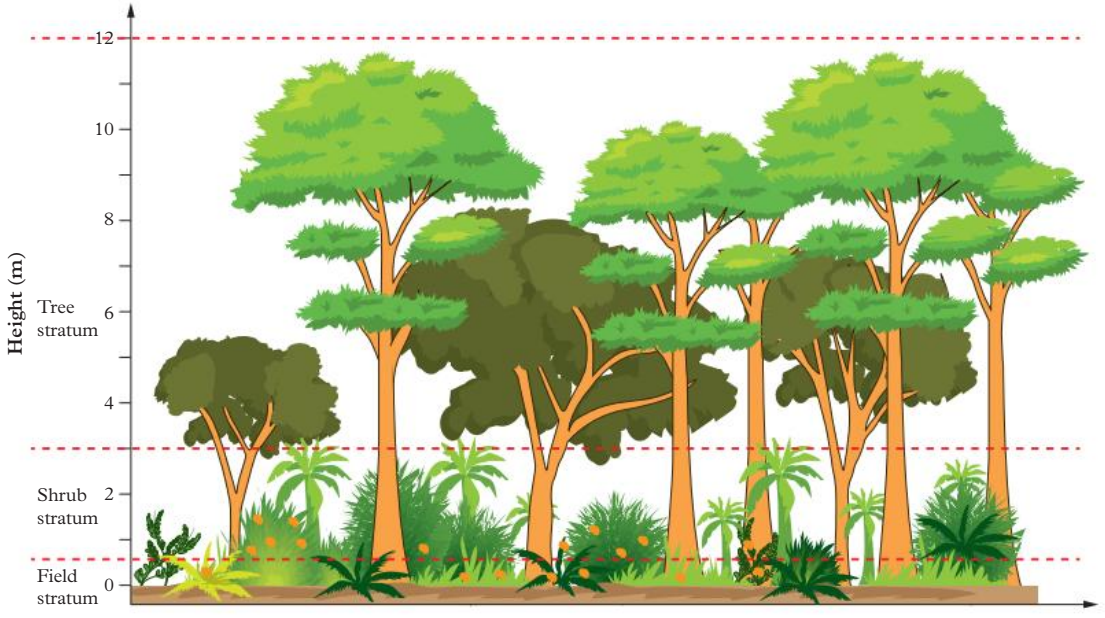


FIGURE 5 An example of three strata (field, shrub, tree) used to sample a forest ecosystem

Strategies to minimise bias

After selecting your sampling method, it is important evaluate whether it may be biased and take measures to reduce bias in the sample. Sampling is biased if:

- some members of any population are more likely to be recorded than others
- the recording of some samples affects the recording of others
- the investigator selects specific sample sites that are easy to reach, not unpleasant to work in or give the results they are expecting.

Four strategies can be used to minimise bias when planning and conducting an ecological survey.

- *Ensure sufficient size and number of samples*. A single measurement is generally insufficient for conclusions to be drawn about a characteristic, because repeated measurements can vary greatly. The exact number and size of samples required depends on the purpose of the study and the size and behaviour of the organisms being investigated. Generally, 10 per cent would be considered sufficient for a quadrat or transect study. The larger the

accuracy
the extent to which a result represents the true value being measured

sample size, the greater the **accuracy**, although this will be constrained by the resources and time available for the study.

- *Use random number generators*. When doing random sampling, random number generators and random number tables should be used rather than an individual making their own set of "random" numbers. This provides a truer representation of randomness.
- *Use counting criteria*. Before sampling, it is critical to establish protocols for how the sampling technique is to be carried out, as well as how the organisms are to be counted. For example, scientists would need to set criteria on how to count a plant species that undergoes asexual reproduction and might have a number of plantlets attached to the mother plant. Scientists also need to determine whether individuals that are partially captured within the sample area are to be included in the count or excluded.
- *Calibrate equipment*. It is important that any equipment used in testing abiotic factors has been calibrated for accuracy before use. Calibrating equipment ensures the accuracy of data, not only within the study but also between similar studies conducted in different areas or at different times, so that scientists can be confident that the measurements obtained are comparable and therefore reliable. The precision of the equipment being used also needs to be considered.

Types of assessment

The most common student field study is an environmental analysis that describes the geographical, physical, chemical and biotic characteristics of an area. Examples include assessment of environmental impacts; management of fish, wildlife and vegetation habitats for the benefit of desired species; and habitat reclamation. The principal objective is often one of the following:

- basic ecological research – proposing and testing hypotheses relating to ecological theories and principles
- ecological inventories – collection of data and samples to be used for reference
- environmental planning – use of ecological information for proposing potential sites for preservation, management or other environmentally sound uses
- environmental impact assessment – collection of information for assessing present or potential impacts of human activities
- ecological resource management – collection of information needed for management of populations and for reclamation of disturbed habitats.

The prime objective of the study determines what is to be measured and the sampling techniques to be used.

Sampling techniques

In most ecological surveys, one of three techniques is used to observe the distribution and abundance of species:

- quadrats
- transects
- capture-recapture.

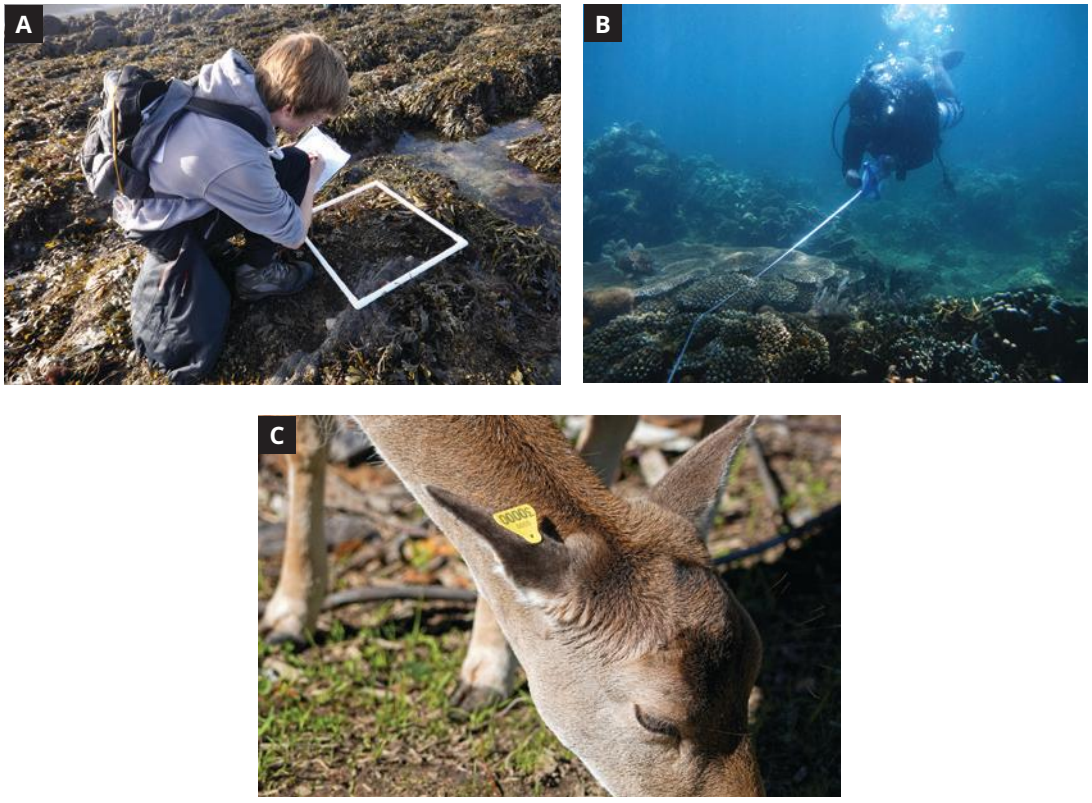


FIGURE 6 Examples of ecological sampling techniques: (A) quadrat, (B) transect and (C) capture-recapture

Quadrats

Recall from Lesson 2.6 that the quadrat method is a basic and commonly used procedure for sampling plants and sessile or slow-moving animals, such as snails. A sample **plot** is generally a rectangle or a square (quadrat), although circles or other shapes can be used. In sampling soil or aquatic organisms, a volume of the habitat is often analysed. Within this quadrat or volume, individual organisms can be identified, counted and measured. Random or systematic sampling can give indications of abundance and distribution over a much larger area. The abundance, percentage frequency or percentage cover can be determined using quadrats.

plot
an area under investigation, generally a subset of a larger area

Transects

In some types of vegetation, the use of quadrats may be impractical. Transects often give better information over large areas and show non-random distribution of some species. There are two main types of transect: line transect and belt transect.

A **line transect** involves walking a line through an established area and recording individuals observed along the length of the line. There are different types of line transects. For example, a continuous line transect involves running a line through a habitat and recording any individuals

FIGURE 7 Given the complexity of aquatic environments, a volume of water above or below a quadrat may be included in the sample.

line transect
an estimate of the numbers of organisms in an area by counting individuals observed along a predetermined line

that touch or fall under the line (Figure 8A). This type of line transect would be useful for surveying immobile species such as plants. Other types of line transect involve making observations of species that can be seen from the line. This method can be used in vertebrate population studies, such as roadkill censuses, bird counts and small mammal trapping. It can even be done on a large scale for highly mobile species. For example, drones or helicopters can be flown along a set transect line for a specified distance to assess the numbers of emus or kangaroos in large, remote areas of Australia.

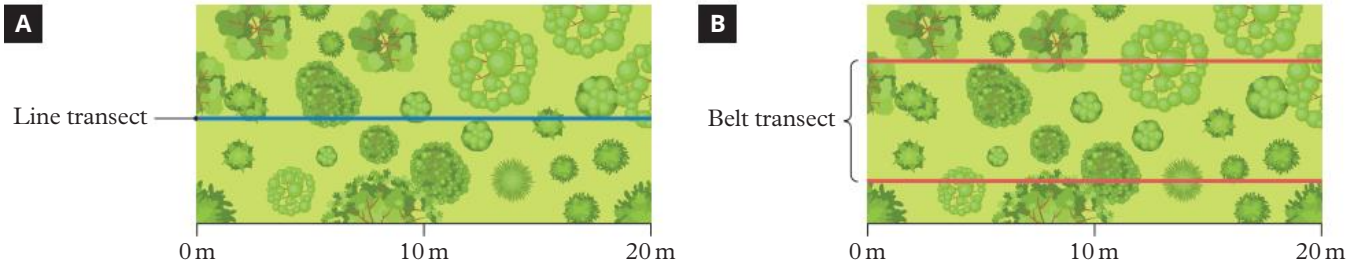
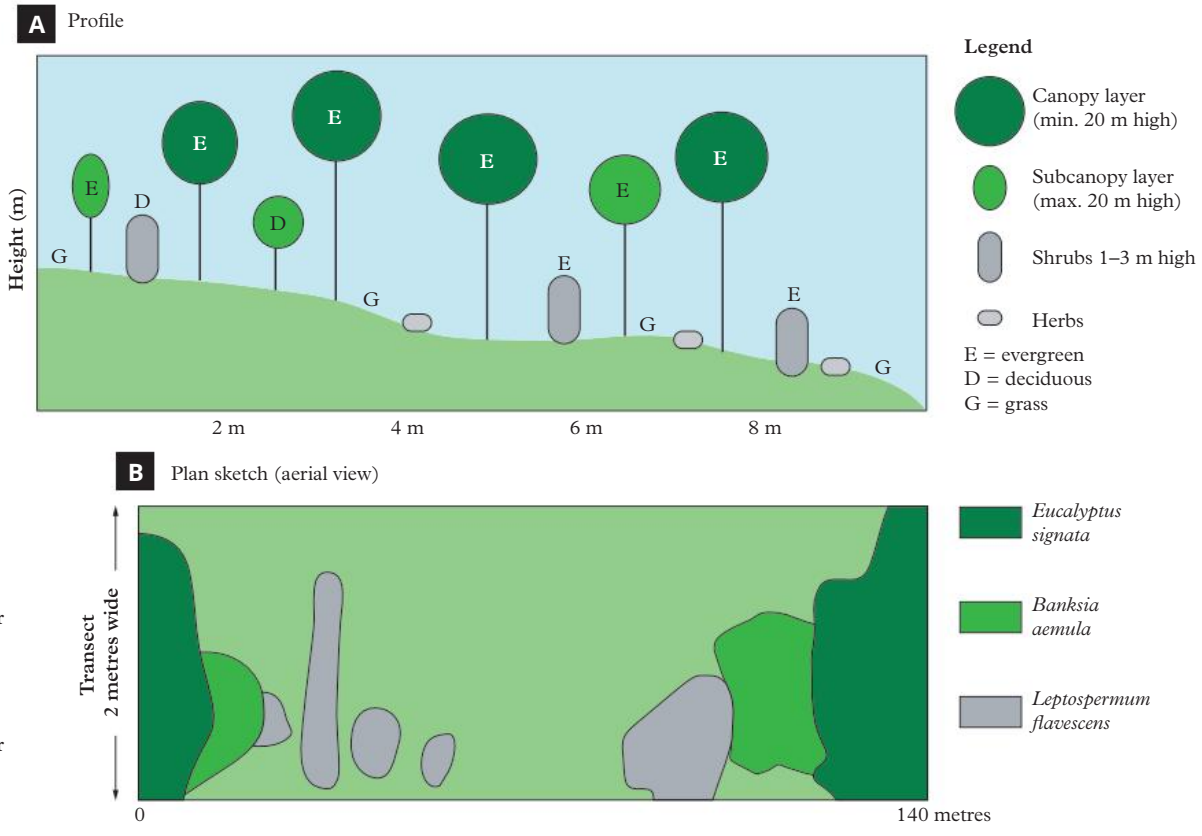


FIGURE 8 Examples of transects: (A) line transect and (B) belt transect

belt transect
an elongated area of known length and width through a particular environment in which specific community parameters are measured and recorded

A **belt transect** is a long rectangular strip (like a belt) of terrain in which all organisms are counted and/or measured (Figure 8B). Knowing the width and length of the transect makes it possible to estimate species diversity and abundance for the total area. Vegetation transects are often represented by a **profile** or a **plan sketch** (Figure 9). Profiles can also be constructed for many different types of habitats (e.g. rocky shores and freshwater ponds).



profile
slope of the terrain, position and height of vegetation types, and canopy cover

plan sketch
an aerial view showing position and canopy cover of species

FIGURE 9 Two ways of representing vegetation transects: (A) a profile diagram and (B) a plan sketch

Capture-recapture

Population density estimates of larger, more mobile or harder-to-observe animals can be made using the capture-recapture method. This method is especially common for birds and aquatic animals, but is also used for large, roaming mammals. A certain number of individuals from a population are captured, marked by some identifying means, and then released within a short period of time. At a later date, a second sample is taken from the population, using the same protocols. Some of the individuals in this second sample may already be marked from the first sample. If the population is large, the marked individuals will have become "diluted" within it and only a few would be expected to appear in the second sample. But if the population is relatively small, the proportion of marked animals in the second sample will be larger.

FIGURE 10 Biologists capture birds and tag them for tracking and recapturing.

Theoretically, the proportion of marked individuals in the second sample is the same as that in the entire population, and the total population can then be estimated using the **Lincoln index *(N)*** formula:

$$N = \frac{M \times n}{m}$$

Lincoln index *(N)* a method used to estimate the size of closed populations sampled using the capture-recapture method

In this equation:

- N = size of the population
- M = number originally marked
- n = total number captured in the second sample
- m = number of recaptured (marked) individuals in the second sample.

Skill drill

Lincoln index

Science inquiry skill: Processing and analysing data (Lesson 1.7)

A study was conducted to estimate the population size of Spanish mackerel (*Scomberomorus commerson*) offshore from the Gold Coast using the Lincoln index (also known as the capture-recapture method). During the survey, 200 Spanish mackerel were initially captured, marked and released.

After two weeks, another sample of 150 Spanish mackerel were captured, of which 30 were found to be previously marked.

Practise your skills

1 **Calculate** the population size using the Lincoln index. (2 marks)
2 **Identify** two factors that might reduce the reliability of this estimate. (2 marks)

Problems using the Lincoln index

Using the Lincoln index to estimate population size presents some problems.

- Weather conditions may vary at the times of sampling, and this may affect the activity of the particular organism under study. Wet or dry conditions, for example, would affect sampling of amphibians.
- Baiting a trap with food may continually attract the same members of a population. These animals are termed "trap happy" as they learn that there is food in the traps. This will make the population estimate lower than the actual population number because a higher proportion of the second sample will have been recaptured.
- The process of trapping and handling may make some members of the population "trap shy". This would result in proportionately fewer marked individuals in subsequent trapping, giving a population estimate higher than the actual population number.
- The method of marking may be unreliable. Tags may be torn off, and colour marking may be lost in feather moulting of birds. The process of tagging may also impact the individual, leading to poor health or a change of behaviour.
- The length of time between sampling is significant. If recapture occurs too quickly after the initial marking, then marked individuals may not have had enough time to mix back into their population, resulting in an inaccurate population estimate. Alternatively, if too much time passes between the initial marking and recapture, the population estimate may be affected by events including births, deaths, emigration and immigration.
- The method cannot account for deaths of tagged individuals after the first sample. If tagged individuals die at an increased rate compared to the rest of the population, the proportion of tagged individuals in the second sample will be lower, giving an estimate that is higher than the actual population size.

Challenge

Determining sampling methods and techniques

You are tasked with studying the distribution of Kurrajong (*Brachychiton populneus*), a shrub or small tree, in the woodlands of Carnarvon National Park. Some areas of the woodlands are characterised by dense, closed canopies, where tree crowns form a continuous layer that provides deep shade to the understorey. Other areas have more open woodlands with patchy canopy cover, allowing more sunlight to filter through to the forest floor, creating a range of habitats within the park. The Kurrajong thrives in the understorey of these woodlands with moderate canopy cover, where some light reaches the forest floor, promoting its growth; it cannot survive in areas where shade is sparse.

1 **Determine** which sampling method should be used to study the distribution and abundance of Kurrajong in Carnarvon National Park. **Justify** your choice. (2 marks)

2 **Determine** which sampling technique should be used. **Describe** how this could be done and **justify** your choice. (3 marks)

Check your learning 2.10

Check your learning 2.10: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** what random sampling means. (1 mark)

2 **Explain** why it is important that observations are replicated. (1 mark)

3 **Explain** how stratified sampling increases the precision of an ecological survey. (1 mark)

4 **Describe** the four ways to minimise bias in a random sample. (4 marks)

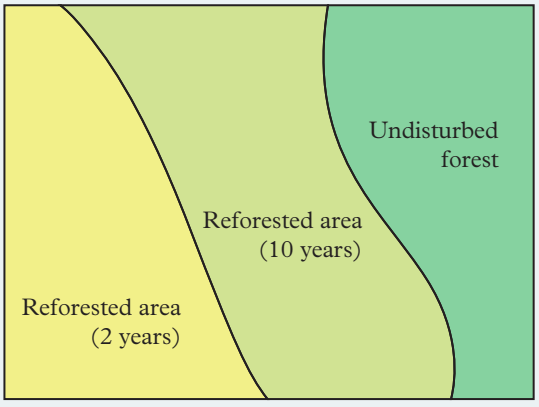
Analytical processes

5 **Distinguish** between a belt transect and a line transect. (1 mark)

6 One evening, 55 mice in an area were captured, marked and released. The following evening, 70 mice were captured in the same area, of which 35 were marked. **Infer** the mouse population of that area. (3 marks)

Knowledge utilisation

7 **Develop** a plan to investigate the success of reforestation after mining by studying the diversity of soil organisms in the area depicted below. This ecosystem includes an undisturbed forest and regions that were reforested 10 and 2 years ago, after mining. Your plan should include methods to minimise bias. (5 marks)



Practical

Lesson 2.11

Analysing vegetation patterns using a line transect

This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.

Learning intentions and success criteria

Practical

Lesson 2.12

Stratified sampling of vegetation patterns

Learning intentions and success criteria

oxforddigital

This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.

Practical

Lesson 2.13

Quadrat sampling to estimate distribution and abundance

Learning intentions and success criteria

oxforddigital

This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.

Practical

Lesson 2.14

Comparing species diversity in two spatially variant ecosystems

Learning intentions and success criteria

oxforddigital

This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.

MODULE 2

Lesson 2.15
Review: Biodiversity

Summary

2.1
- The unique combination of biotic and abiotic factors within an ecosystem creates biodiversity.
- Diversity exists between different species in an ecosystem.
- Variation of the genes in individuals of the same species creates diversity within the species.

2.2
- The biological species concept is the most common method of classifying a species.
- Alternative definitions of species are required for asexual organisms, fossils and hybrids.
- All species definitions have limitations.

2.3
- Organisms are classified using hierarchical systems.
- Modern-day classification is based on the Linnean system and considers physical as well as genetic similarities.
- Scientists use a consistent naming system to aid communication in biology.
- The method used to classify organisms depends on the purpose of classification and the classification changes as new information is discovered.

2.4
- Dichotomous keys use a series of questions to differentiate and classify things.
- Biologists use keys distinguishing physical characteristics to differentiate species.

2.5
- Abiotic factors influence where an organism lives, how abundant it is and how individuals within the species are distributed throughout their habitat.
- Intraspecific and interspecific interactions influence the distribution and abundance of species.

2.6
- The distribution of organisms can be categorised into three patterns: random, uniform or clumped.
- Individuals in a population are distributed as a result of interactions with their environment, other species and each other.
- Distribution patterns impact the validity and reliability of sampling methods.

2.7
- Ecosystems are composed of habitats and microhabitats.
- The habitat of an organism makes up a small part of the ecosystem.
- The distribution of habitats and microhabitats impacts how a species may be sampled.

2.8
- Different classification systems are used to classify ecosystems.
- The Holdridge life zone system is used to classify land areas globally.
- Specht's classification system is used to classify Australian vegetation.
- Classification plays an important part in ecosystem management.

2.9
- Different measures are used to determine the diversity of different species by different sampling methods.
- Species richness is a measure of the number of unique species in an ecosystem.
- Species evenness is a measure of the relative abundance of species in an ecosystem.
- Percentage cover is a measure of the amount of ground covered by a plant species.
- Percentage frequency is a measure of the abundance of a species within an ecosystem.
- Simpson's diversity index measures biodiversity, accounting for species richness and evenness.

2.10
- Various sampling techniques are used to study species diversity.
- The purpose of a survey and the species being studied determine the appropriate sampling method.
- When carrying out ecological surveys, strategies to minimise bias must be put in place.
- The Lincoln index is a measure of population size based on sample data.

2.11 • Practical: Analysing vegetation patterns using a line transect
2.12 • Practical: Stratified sampling of vegetation patterns
2.13 • Practical: Quadrat sampling to estimate distribution and abundance
2.14 • Practical: Comparing species diversity in two spatially variant ecosystems

Key formulas

Species richness	$S = \frac{s}{\sqrt{N}}$
Relative species abundance	$\text{RA} = \frac{\text{TS}}{\text{TP}} \times 100$
Percentage frequency	$\%\ \text{frequency} = \frac{\text{no. quadrats in which species is found}}{\text{total no. quadrats}} \times 100$
Simpson's diversity index	$\text{SDI} = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$
Lincoln index	$\text{Size of population}(N) = \frac{M \times n}{m}$

Review questions 2.15A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

1 Which factor did Carl Linnaeus base his system of classification on?
- **A** Size
- **B** Habitat
- **C** Genetics
- **D** Structures

2 Which of the following taxa includes the greatest number of different types of organisms?
- **A** Class
- **B** Genus
- **C** Family
- **D** Phylum

3 The biological species concept defines a species as
- **A** a group of organisms that look similar and have the same evolutionary history.
- **B** a group of organisms that are physically similar and share the same ecological niche.
- **C** a group of organisms that can interbreed in nature and produce viable, fertile offspring.
- **D** a group of organisms that share a common ancestor and can be distinguished by unique genetic or physical traits.

4 Which of the following is the correct form of the scientific name of a wombat?
- **A** Vombatus Ursinus
- **B** *Vombatus ursinus*
- **C** Vombatus ursinus
- **D** *vombatus ursinus*

5 An amateur birdwatcher sighted two robins that were both black, red and white in colour, but one had red head feathers and the other had black head feathers. One robin was male and the other was female. What would the birdwatcher need to do, to be certain that they belonged to the same species?
- **A** Refer to a catalogue of type specimens of robins
- **B** Determine whether the two robins would mate under natural conditions
- **C** Determine whether the offspring produced by mating these two robins were fertile
- **D** Refer to preserved specimens of robins that had been collected and labelled by experts

6 A savannah is a tropical ecosystem characterised by open grassland with scattered trees and sporadic water sources. Which type of distribution is most likely to be observed for elephants in this ecosystem?

A Uniform
B Random
C Clumped
D Systematic

7 Which of the following terms could be used to describe the collection of organisms living in and on a decaying log?

A Society
B Community
C Population
D Ecosystem

8 Which of the following statements is correct?

A A population refers to a collection of unrelated organisms living together in a specific area.
B An ecosystem refers to the physical features, such as water and rock, in a given area.
C The environment refers to the interaction of living and non-living components in a defined area.
D A microhabitat refers to the small, specialised region within a larger habitat where specific organisms live.

9 Shrubs seldom grow successfully on the floor of a dense forest. Which of the following factors mainly accounts for this phenomenon?

A They fail to compete with the extensive canopy of the trees to receive sufficient sunlight.
B They fail to compete with the extensive root system of the trees to obtain sufficient water and mineral salts.
C They fail to compete with the tall trees to obtain carbon dioxide from the atmosphere to support photosynthesis.
D They easily suffocate because most of the oxygen in the atmosphere has been absorbed by the leaves of the trees.

10 Many plants in Western Australia grow in nutrient-deficient sandy soil, and experience hot, dry summers and winter rainfall. Some of these will grow in south-eastern Queensland, although their growth and reproduction is reduced. The zone in south-eastern Queensland where these plants are growing is

A the optimal zone.
B the subliminal zone.
C an intolerance zone.
D a zone of physiological stress.

11 What are the three levels of biodiversity?

A Genetic, species and community
B Genetic, species and ecosystem
C Species, population and ecosystem
D Community, environment and ecosystem

12 The woolly mammoth, which became extinct approximately 4,000 years ago, was a large, herbivorous mammal adapted to cold environments. It was similar to modern-day elephants, had long, curved tusks, thick fur, and was primarily found in the grasslands of Europe, North America and Siberia. Why can't the biological species concept be used to classify the woolly mammoth?

A It is extinct.
B It is a ring species.
C It reproduces asexually.
D It is a hybrid of two distinct species.

13 The spinifex hopping mouse (*Notomys alexis*) is a nocturnal rodent that lives in sandy deserts and arid regions of central and western Australia, where food, water and shelter are sparse. Which distribution pattern is most likely exhibited by the spinifex hopping mouse?

A Uniform distribution
B Random distribution
C Isolated distribution
D Clumped distribution

14 The data in the table was collected from a forest ecosystem. Which metric best represents the species richness of the area?

Species	Individuals
W	15
X	10
Y	5
Z	20

A 5:1 ratio
B 4 species
C 20 individuals
D 50 individuals

Review questions 2.15B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

15 Most biologists use the Linnaean system when classifying organisms. **Identify** an advantage and a disadvantage of this system. (2 marks)

16 **Explain** why random sampling is important when conducting a field study. (1 mark)

17 Several indices can be used to determine the biodiversity of an ecosystem.

a **Explain** what "the biodiversity of an ecosystem" means. (1 mark)

b **Describe** two parameters that could be used to measure the biodiversity of an ecosystem. (2 marks)

18 **Describe** three limitations of the biological species concept. (3 marks)

19 In a study of a local bird population, researchers captured and marked 50 birds, then released them back into the wild. After a week, they captured a second sample of 60 birds, of which 10 were marked. **Calculate** the estimated total population size of the birds in this area, using the Lincoln index. (1 mark)

20 Use the information in the table to **calculate** the biodiversity of the ecosystem using Simpson's diversity index. (1 mark)

Species	Individuals
A	15
B	10
C	5
D	20

Analytical processes

21 Use the Holdridge life zones classification system (Figure 2 in Lesson 2.8) to:

a **determine** the range of each abiotic factor in a desert scrub (1 mark)

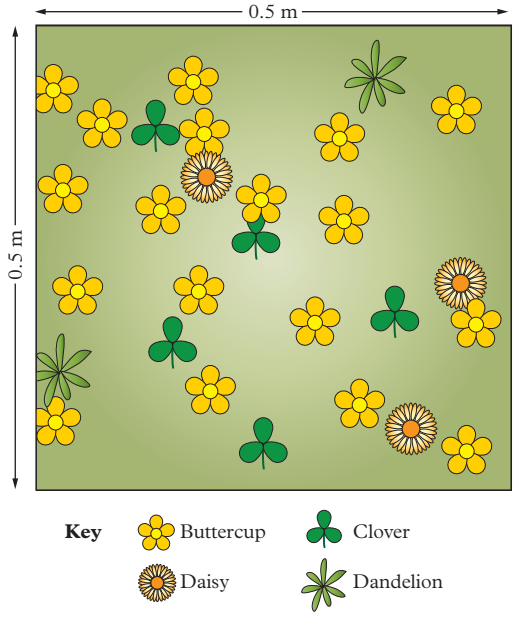
b **classify** an ecosystem that has a mean annual biotemperature of 24°C, annual precipitation of 2,500 mm and a potential evapotranspiration ratio of 0.25. (1 mark)

22 The fauna of the wallum area tend to be small and are either insectivorous or eat fruit, flowers and nectar. They include honey eaters, small insectivorous birds and a great variety of lizards and snakes. **Infer** two reasons for the types of fauna found in these areas. (2 marks)

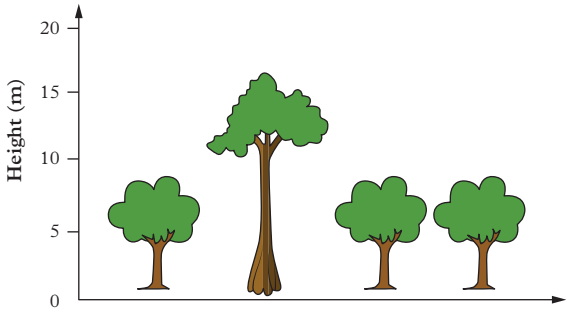
23 A student throws a 0.25 m^2 quadrat onto the school lawn. The figure below shows what was found.

a **Determine** the abundance of dandelions in 1 m^2. (1 mark)

b If the lawn area is 100 m × 50 m, **determine** the abundance of daisies in the entire lawn. (1 mark)



24 The figure below shows vegetation along a transect line. **Classify** the ecosystem shown, using Specht's classification system (Table 1 in Lesson 2.8). (1 mark)



Knowledge utilisation

25 Two groups of frogs resemble each other very closely. One group lives on the lower eastern slopes of the Eastern Highlands. The other group lives on the top of these mountains. A biologist discovers that the frogs on the lower slopes breed in September to November, whereas those on the higher slopes breed in January to March.

a **Propose** a possible reason for the different breeding times of these two groups. (1 mark)

b **Explain** whether you could classify the frogs as the same species, based on the information provided. (1 mark)

26 Residents of outer Brisbane suburbs sometimes find small mouse-sized mammals in their homes. Residents need to recognise whether these are a house/field mouse or a marsupial mouse, feathertail glider or water mouse, because many of these native species are rare and should be released back into the bush. Descriptions of mouse-like mammals found around Brisbane are given below.

- House mouse ("field mouse"), introduced pest species, *Mus musculus*
  Length: body 75 mm, tail 85 mm; weight 15 g. Typical mouse, olive-brown back and paler belly. Strong musky-mouldy scent. Small notch on inner side of upper incisors.
- Common planigale (marsupial mouse), *Planigale maculata*
  Length: body 80 mm, tail 77 mm; weight 11 g. Mouse-sized, mouse-coloured. Flat head; pointed snout; cat-like teeth; inner "big" toe on hind foot has no nail. Female has "kangaroo-like" pouch, male has pendulous scrotum; both these features are lacking in the house mouse.
- Common dunnart (marsupial mouse), *Sminthopsis murina*
  Length: body 90 mm, tail 80 mm; weight 22 g. Large mouse-size. Sharply pointed snout; large bulging black eyes; delicate white hind feet; grey-brown head and body; belly pure white; cat-like teeth; inner "big" toe on hind feet has no nail. Female has "kangaroo-like" pouch.
- Feathertail glider (marsupial), *Acrobates pygmaeus*
  Length: body 80 mm, tail 80 mm; weight 13 g. Mouse-sized; grey-brown back; white belly; tail like a small feather (not found in other Australian mammals).
- Water mouse (false water rat), *Xeromys myoides*
  Length: body 115 mm, tail 95 mm; weight 40 g. Large mouse-sized; silky, slate grey back sharply defined by pure white belly; tail short, sparsely haired, without white tip.

Construct a dichotomous key that could be used to help residents of Brisbane identify the different "mouse-like" mammals they may encounter in their homes. (5 marks)

27 Choose a non-domestic animal to research its characteristics and distribution.

a **State** the scientific name of the animal, using the correct notation. (1 mark)

b **Classify** the abiotic and biotic features of its environment. (2 marks)

c **Construct** a concept map to demonstrate the animal's ecological niche. (2 marks)

d **Deduce** one significant aspect of its environment and **predict** the outcomes for this species if that were to change. (2 marks)

28 Rainforest soils retain few nutrients, because they are used as soon as they become available from decomposer activity to support the large mass of plants in the community. **Evaluate** whether a section of cleared rainforest would be a viable site to set up a large vegetable farm. (2 marks)

29 You are preparing to conduct an ecological survey of the rocky shore shown in the image below. Rocky shores are a complex ecosystem, where organisms must tolerate wide fluctuations in many abiotic factors.

a **Appraise** how the differences in habitats along rocky shores would influence the distribution of the organisms found there. (2 marks)

b **Describe** an appropriate sampling method to survey the distribution and abundance of organisms in this rocky shore and **propose** strategies to improve the reliability and validity of the study. (4 marks)

Data drill

Interpreting ecological data from a grassland ecosystem

Ecologists surveyed a terrestrial grassland ecosystem. From initial surveys, the area appeared to be relatively homogeneous. The data in the table below was collected using random quadrat sampling of plant and animal species across 10 quadrats of equal size.

Species	Quadrat										Total count
	1	2	3	4	5	6	7	8	9	10	
Kangaroo grass	12	14	10	18	20	15	12	14	11	13	139
Wallaby grass	4	5	3	7	6	5	3	4	5	4	46
Native wildflower	7	6	8	5	4	4	7	6	5	6	58
Ant	0	12	15	13	0	14	10	12	13	11	88
Grasshopper	3	2	1	3	4	2	3	1	2	3	24

Apply understanding

1 **Determine** why a random sampling method might have been selected over a stratified or systematic sampling method. (1 mark)

2 **Calculate** the percentage frequency of ants in the survey. (1 mark)

3 **Calculate** the Simpson's diversity index for the ecosystem. (1 mark)

Analyse data

4 **Compare** the distribution and abundance of plant species in the ecosystem to identify any patterns in the data. (2 marks)

Interpret evidence

5 **Infer** the reason for the pattern shown in the distribution and abundance of plant species. (1 mark)

6 **Deduce** the dominant plant species in this ecosystem, using data to support your answer. (2 marks)

Module 2 checklist: Biodiversity

MODULE 3

Populations

Introduction

A population refers to members of the same species occupying a given area at the same time. Populations of all species have some common adaptations related to environmental factors. These factors determine where the populations are found, how they increase in number and the total number of individuals. Growth of a population can be either density-dependent or density-independent. Competition for resources and predator–prey relationships are significant in limiting population growth for some species. To cope with these and other factors, different species use different population growth strategies.

Prior knowledge

Prior knowledge quiz Check your understanding of concepts related to populations before you start.

Subject matter

Science understanding

→ Calculate population growth rate and change using birth, death, immigration and emigration data.
→ Compare the reproductive strategies and growth curves of K- and r-strategists.
→ Identify and explain different modes of population growth, including
  – exponential growth (J-curve)
  – logistic growth (S-curve).

Science inquiry

→ Investigate
  – how abiotic factors affect the distribution and/or abundance of species in an ecosystem

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Practicals

oxforddigital **These lessons are available on Oxford Digital.**

Lesson 3.4 Population study of yeast

Lesson 3.1
Calculating population growth rate and change

Key ideas

- → Population growth rate is the speed at which a population changes over a specific range of time.
- → Environmental factors influence the rates of births, deaths, immigration and emigration in a population.
- → Calculating population change informs conservation efforts.

Learning intentions and success criteria

Population growth rate

Population size can vary significantly over time, particularly in animal species. For example, there are periodic mouse plagues on the Darling Downs in Queensland. Not only do these plagues lead to devastation of crops, they also cause considerable damage as the mice infest homes. Numbers can also decline rapidly: the mouse population may be massive in April but insignificant in July.

The size of a population depends on the rates of birth, death, immigration (arriving into a new area) and emigration (leaving an area). If the number of deaths or emigration increases, the size of the population will decrease. In contrast, if the number of offspring born (births) increases, or if many individuals immigrate into an area, then population size will increase.

FIGURE 1 Population sizes of the house mouse, *Mus domesticus*, in the Darling Downs fluctuate throughout the year.

Population growth rate is the speed at which a population changes over a specific range of time. This is different from **population growth**, which is the change in the number of organisms in a population at identified times. An increase or decrease of the population growth rate provides a measure of how fast the change in population is occurring. It is calculated using the formula:

$$r = (b + i) - (d + e)$$

population growth rate
the rate of change of a population over a particular range of time

population growth
the change in the number of individuals in a population in a particular habitat

In this formula:

- r = population growth rate
- b = number of births
- i = number of immigrants
- d = number of deaths
- e = number of emigrants.

The graphs in Figure 2 show the relationship between population growth (change in numbers in the population) and population growth rate (change in numbers in the population over a certain period of time). Each population has specific limiting factors that influence its growth. The range of tolerance to light, temperature, available water, salinity, nesting space and required nutrients differs from species to species. Regardless of other factors, if any essential requirement is in short supply for a particular species, or if an environmental feature is too extreme, the population cannot increase. It will either remain the same size or decrease.

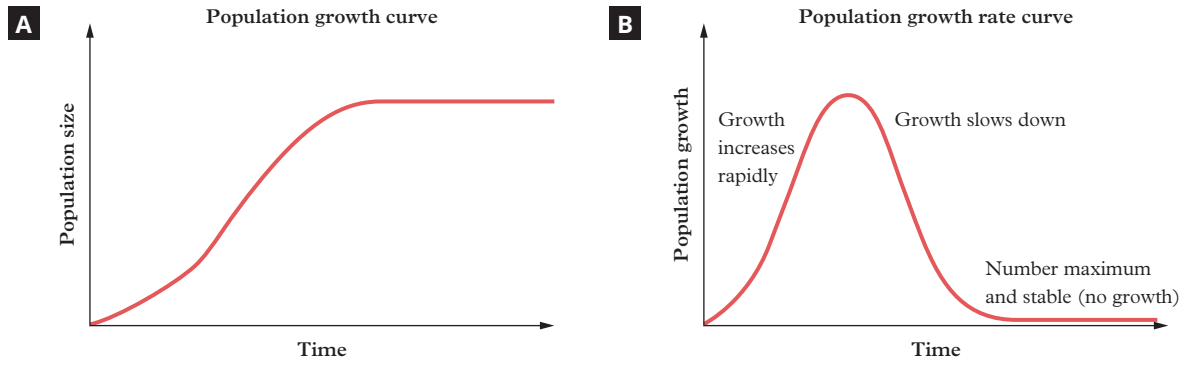


FIGURE 2 Comparison of (A) the growth curve and (B) the growth rate curve for the same population. Graph (B) reflects the gradient of graph (A).

Worked example 3.1A

Calculating population growth rate

A population of koalas in a wildlife sanctuary is being monitored. The initial population is 150 individuals. Over the course of a year:

- 19 koalas are born
- 0 koalas migrate into the sanctuary
- 13 koalas die
- 3 koalas migrate out of the sanctuary.

a **Calculate** the population growth rate for koalas in the wildlife sanctuary, using the formula:

$$r = (b + i) - (d + e) \quad (1 \text{ mark})$$

b **Calculate** the number of koalas in the sanctuary at the end of the year of monitoring. (1 mark)

Think	Do
Step 1: Look at the cognitive verbs and mark allocation to determine what the questions are asking you to do.	To "calculate" means to determine or find a number using mathematical processes. To determine part **a**, use the population growth rate formula, $r = (b + i) - (d + e)$. Then use this value to solve part **b**. Parts **a** and **b** are worth 1 mark each, so you need to provide one value for each.
Step 2: Gather any data required for the population growth formula.	**a** Number of births (b) = 19 Number of immigrants (i) = 0 Number of deaths (d) = 13 Number of emigrants (e) = 3
Step 3: Substitute the values into the population growth rate formula to solve for r. Remember: the question asks for the rate, so you should indicate the time period given in the question.	**b** $r = (b + i) - (d + e)$ $= (19 + 0) - (13 + 3)$ $= 3$ Therefore, population growth rate is 3 koalas per year. (1 mark)
Step 4: Use your answer from part **a** to solve for part **b**. This will be the initial population + population growth rate for one year.	Initial population = 150 Final population = 150 + 3 = 153 Therefore, there will be 153 koalas in the sanctuary at the end of the year. (1 mark)

Your turn

A lake is home to a silver perch population that initially consists of 500 fish. Over the course of a year:

- 100 fish are born
- 20 fish migrate into the lake
- 60 fish die
- 30 fish migrate out of the lake.

a **Calculate** the population growth rate for the silver perch population using the formula:

$$r = (b + i) - (d + e)$$ (1 mark)

b **Calculate** the number of silver perch in the lake after two years, assuming the population growth rate remains stable. (1 mark)

Density-dependent factors

As a population grows, the resources available to each individual within the population decrease. If the population becomes larger than the environment can sustain, competition for limited resources, such as food, shelter or water, will increase. This competition can lead to some individuals being relegated to resource-poor areas within the environment, and therefore can affect their ability to thrive and reproduce. Competition is therefore a **density-dependent factor**, where the influence of the factor on population growth increases as the population increases.

density-dependent factor
a factor that has a greater impact on the population as the population size increases

Disease and predation are also density-dependent. As a population increases, the likelihood of a disease spreading through the population also increases, because of the higher rate of contact between individuals of the population. In turn, this leads to an increased mortality rate within the population. Finally, as the population of a prey species increases, the food supply of their predator increases, so the population of predators will increase as the predators take advantage of the abundant food source. This then means that there is greater pressure from predation on the prey species, increasing the mortality rate.

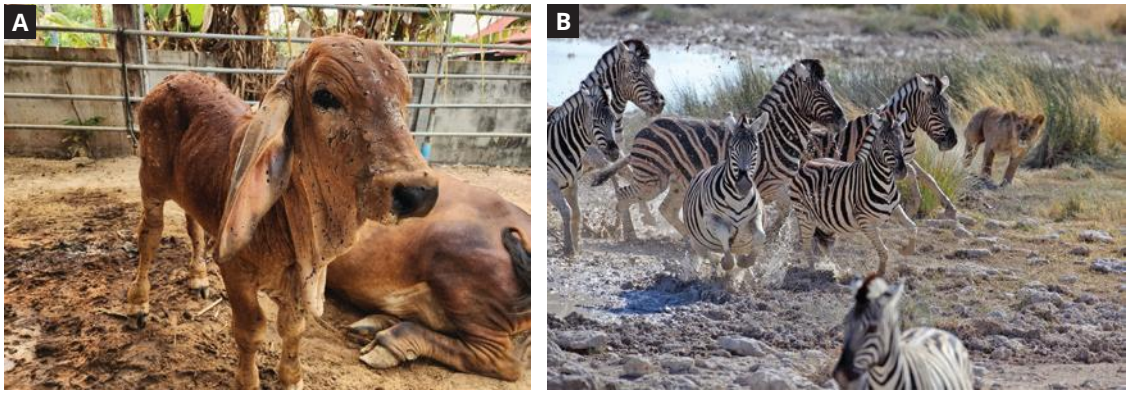


FIGURE 3 Two density-dependent factors: (A) disease and (B) predation

Density-independent factors

Birth rates and death rates may vary regardless of population density. The density of a population is, in this case, independent of the size of a population. A small population may be spread over a very large area and have a low density. Alternatively, it may be limited to a

very small area, causing the organisms to be crowded together in a high-density environment. Both environments (high density or low density) present their own challenges to the survival of an organism. Factors that affect a population regardless of its density are termed **density-independent factors**.

density-independent factor
an abiotic factor that is independent of the density of the population, that affects the size of a population

All organisms have a range of factors that can affect their survival. The availability of water or nutrients, or the temperature of the ecosystem, must be within a range that the organism can tolerate, for the organism to survive and reproduce. If abiotic conditions change in a way that becomes optimal for an organism, this can encourage population growth. For example, algal blooms can occur when the concentration of nutrients (e.g. nitrogen and phosphorus) increases in waterbodies due to run-off from fertilisers used on farms.

If an abiotic condition sits outside an organism's tolerance range, then the organism will die, increasing the mortality of a population. For example, if temperatures are higher than an organism's tolerance range, that organism will die regardless of whether it lives in a high-density environment or a low-density environment. The **limiting factor** of temperature will restrict the size of a population, independently of the density of the population. Other population-independent limiting factors relate to water, nutrients, sunlight, pH, salinity and humidity.

limiting factors
conditions that limit the growth, abundance or distribution of an organism or a population of organisms

FIGURE 4 Sunlight is a limiting factor influencing the density of grass at the edge of a forest.

Environmental disasters

Many density-independent factors are associated with environmental changes. In some cases, these changes are natural, such as the sudden flooding of an area, or destruction from volcanic eruptions. Although flooding may appear to have a negative effect on an ecosystem (as it does in many examples), it can also have positive effects. Floodwater can wash out excess salt or chemicals from the soil or from rivers, and may also clear debris. This enables fish and birds to breed, increasing the birth rate of the population. The floodwaters will also soak into the soil, increasing the amount of groundwater. This can provide a long-term water supply to plants in the ecosystem. Many ecosystems are dependent on regular floodwaters to maintain their communities.

Other environmental disasters are a result of extreme climatic events. Drought, cyclones, fires and enhanced climate change are all examples of events that will affect the size of a population, independently of the density of the population.

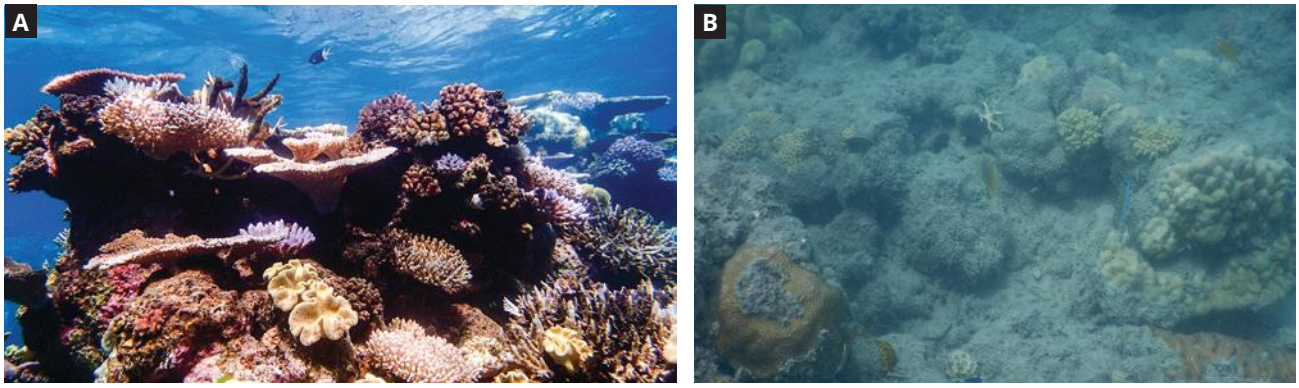


FIGURE 5 The Great Barrier Reef was heavily affected by cyclone Yasi in 2011. Here is the reef (A) before and (B) after the environmental disaster.

Pollution

High-density human populations can also affect the population of other organisms, independently of the organism's density. For example, clearing of the ecosystem or release of chemicals into the ecosystem can have a detrimental effect on the population of marine organisms, independently of the density of the marine population.

FIGURE 6 A protest against pollution in Sydney

Population change and conservation

Monitoring population change is an important step in the conservation of endangered organisms. The information collected from monitoring helps to determine the carrying capacity of an ecosystem and whether the population is growing or in decline. Tracking the increase and decrease of population sizes over time allows scientists to investigate the factors influencing a specific population, and make decisions about how best to manage and protect species. An example of this is the northern quoll *(Dasyurus hallucatus)* population in the Kakadu National Park, Northern Territory. It has been estimated that the population of quolls in this region was approximately 80,000 in the year 2000. However, since then, the population has undergone a dramatic decline as a result of poisoning from invasive cane toads and predation by feral cats, as well as habitat destruction by humans. This information has led to the northern quoll being classified as endangered, and conservation methods – including captive breeding programs and "toad-smart" northern quoll programs being–set in place to try to protect this species.

FIGURE 7 Northern quolls *(Dasyurus hallucatus)* are an endangered species of small marsupial carnivore, found only in northern Australia.

Check your learning 3.1

Check your learning 3.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** three density-independent factors that could contribute to an increase or a decrease in numbers. (3 marks)

2 **Identify** the four factors that determine population growth rate for a species. (4 marks)

Analytical processes

3 **Contrast** population growth and population growth rate. (1 mark)

4 At the beginning of a three-year survey, a population contained 2,000 individuals. During the survey, 1,700 individuals died, 240 migrated out of the area, 601 moved in and 870 were born.

- **a** **Calculate** the overall change in population size that occurred. (1 mark)
- **b** **Calculate** the average rate of change per year. (1 mark)
- **c** **Determine** the overall population size at the end of the survey period. (1 mark)

Knowledge utilisation

5 Research an example of an environmental disaster that has had an effect on land near you. **Propose** how this disaster might have changed the biodiversity of your selected area. (2 marks)

Lesson 3.2
Reproductive strategies

Key ideas

- → Organisms demonstrate a range of reproductive strategies.
- → *r*-selected species populations experience "boom" and "bust", due to rapid reproduction rates.
- → *K*-selected species populations grow slower than *r*-selected species and are more stable.

Learning intentions and success criteria

r-selected species

r-selected species a species that occupies an unstable environment and uses the evolutionary strategy of maintaining a high growth rate, occupying less crowded ecological niches and producing many offspring

Many species have evolved reproductive strategies to maximise their chances of dominating an ecosystem. This can be illustrated by the rate of their population growth. Some species, the ***r*-selected species**, can produce large numbers of offspring (often asexually) with little parental investment. This is important to those species that live in unstable environments where predation may be high. These organisms are generally small, mature rapidly and are short-lived. Examples of *r*-selected species are bacteria, grasses, corals, insects and small mammals such as rodents. By flooding the habitat with offspring, regardless of mortality or predation, at least some of the progeny are likely to survive to reproduce. Their population growth is typically "boom" and "bust". The bust phase is usually due to density-independent limitations. You will learn more about population growth curves for *r*-selected species in Lesson 3.3.

FIGURE 1 Examples of *r*-selected species: (A) bacteria, (B) rabbits and (C) wasp spiders

K-selected species

Other species, the ***K*-selected species**, tend to live in more stable environments and their population densities are as high as the ecosystem can maintain without collapsing, known as the **carrying capacity**. These organisms have a long life expectancy, produce few offspring, invest extensive parental care and can compete successfully for limited resources. Although *K*-selected species are generally large (e.g. elephants, whales), they include some long-lived, small species (e.g. Arctic terns). Their population size is often affected by the overall density of the species (density-dependent). You will learn more about population growth curves for *K*-selected species in Lesson 3.3.

K-selected species
a species whose population fluctuates at or near the carrying capacity (*K*) of the environment in which it resides

carrying capacity
the largest population that can be maintained within a given area without collapsing, determined by the limiting resources within the ecosystem

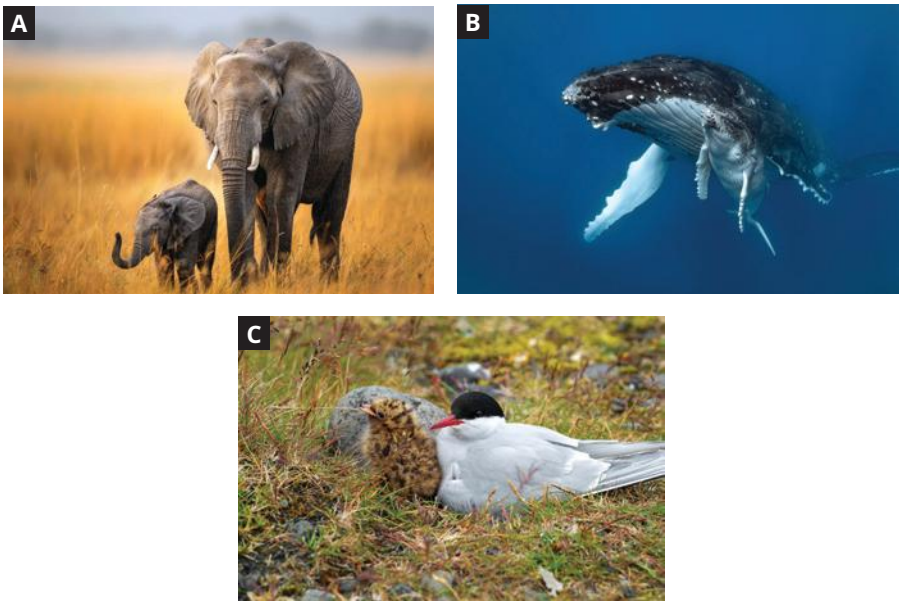


FIGURE 2 Examples of *K*-selected species: (A) elephants, (B) whales and (C) Arctic terns

Study tip

Think *r* for rabbits, *K* for koala.

TABLE 1 General characteristics of *r*- and *K*-selected species

r-selected species	*K*-selected species
Short-lived	Long-lived
Tend to be small in size	Tend to be large in size
Fast maturation	Slow maturation
Reproduce at an early age	Reproduce at a late age
Produce many offspring at a time	Produce few offspring at a time
Little care of offspring	Extensive parental care
Not strongly competitive for resources	Strongly competitive for resources

Modifications of *r*- and *K*-selected species

Many organisms adopt an intermediate strategy between these two extremes. Trees, for example, are large and long-lived, and are strongly competitive for resources – these are *K* attributes. They tend, however, to produce a large number of seeds that are dispersed away from the parent plant, which is an *r* trait.

biofilm
a layer on a solid matrix composed of microscopic bacteria, algae and protozoa in a complex polymer-linked assemblage

Some organisms can even alternate between the two strategies, depending on the local conditions, giving them the best chance of surviving a broad range of conditions. **Biofilms**, for example, are colonies of prokaryotes, algae or protozoa enclosed in a matrix that adheres to surfaces. Prokaryote biofilms are large and grow slowly compared with other prokaryote colonies (i.e. weeks rather than minutes). By producing a fluid matrix made of proteins and polysaccharides around the cells, the biofilm can resist predation and chemicals, including antibodies and antibiotics. New colonies are formed when fragments break off and attach to a new surface away from the main colony. Because many biofilms are composed of more than one type of prokaryote, the waste products of one species (which could accumulate and inhibit their growth) are often the substrate for another species. In all these features, the biofilm is a *K*-selected species.

When a biofilm receives an influx of specific nutrients, certain cells in the matrix become mobile. They modify their protein production to no longer produce the pili that hold the cells in position, and instead each prokaryote forms a whip-like flagellum. These mobile cells are released from the matrix and reproduce exponentially at the maximum rate possible in that environment. Although the chance of any one cell finding a suitable surface on which to establish a new biofilm is small, the number of cells increases rapidly. This motile form is a typical *r*-selected species.

When a large quantity of nutrients is available, the biofilm cells maximise the opportunity for dispersal and establish new biofilms as *r*-selected species. When more stable environmental conditions prevail, they become *K*-selected species. They also secrete a slimy extracellular matrix of proteins and polysaccharides that protects the biofilm from many chemicals, including antibodies and antibiotics.

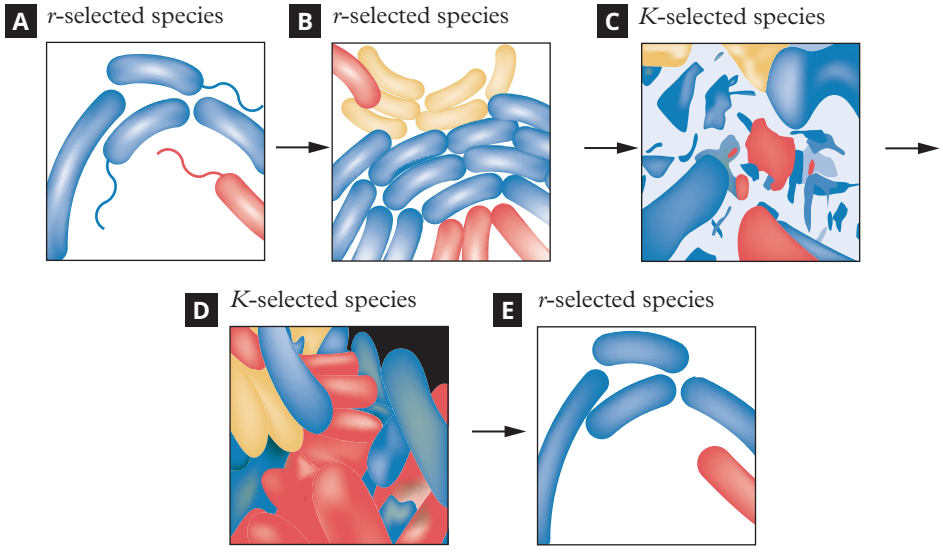


FIGURE 3 Biofilms are formed by (A) the attachment of motile prokaryotes to a surface. (B) They undergo exponential growth as an *r*-selected species, losing their flagellum in the process. (C) On maturation, growth slows down and the prokaryotes act as *K*-selected species. (D) When specific nutrients are available, some cells become motile and detach from the surface of the biofilm. (E) These cells attach to a new surface and again become *r*-selected species.

Real-world biology

Chinook salmon reproduction

FIGURE 4 Chinook salmon (*Oncorhynchus tshawytscha*) swim upstream from the ocean, while trying to avoid predators, to breed in freshwater gravel beds.

Chinook salmon (*Oncorhynchus tshawytscha*) are well known for their unique reproductive strategy. These salmon are relatively large and long-lived fish, living as long as 9 years and growing to 60 kg. Chinook salmon are born in freshwater rivers surrounding the north Pacific Ocean from Japan to California in North America, then migrate downstream into the ocean where they live until they reach maturity, and return up the same stream they were born in, to breed. This run upstream has become famous, with images of salmon leaping up small falls, risking being caught by bears waiting to catch them in mid-flight. Human structures, such as weirs and dams, may impede their ability to swim upstream, so scientists are developing designs such as fish ladders to enable the salmon to pass. These fish ladders allow salmon to swim and leap over a series of low steps to pass a barrier.

During spawning, the females form gravel nests in the riverbed, where they lay up to 10,000 eggs, which the males then fertilise. However, the salmon expend so much energy in producing the eggs and sperm cells, as well as swimming upstream, often for hundreds of kilometres, that once they reach the breeding grounds and spawn, they die. This means that, while the parents invest an extraordinary amount of energy in finding suitable spawning grounds, there is no parental care after the spawning, leading to a high mortality rate of the eggs. Once the eggs hatch, the offspring begin the migration downstream again, with many dying due to predation, lack of food or environmental factors.

Apply your understanding

1 **Argue** whether chinook salmon should be considered an *r*- or *K*-selected species. **Justify** your response. (3 marks)
2 **Critique** the use of fish ladders to enable salmon to pass human-made barriers. (2 marks)
3 "Human-made structures affecting the flow patterns of streams in North America are threatening the survival of chinook salmon." **Construct** a research question that addresses an aspect of this claim. (1 mark)

Check your learning 3.2

Check your learning 3.2: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** the conditions leading to the formation of a biofilm and the benefits of this reproductive strategy for prokaryotes. (2 marks)

2 **Identify** whether each of the following are *r*- or *K*-selected species. (1 mark each)
- **a** Rat
- **b** Cat
- **c** Whale
- **d** Penguin

3 **Explain** the advantage to an organism of being able to alternate between *r*- and *K*-selected modes of population growth. (2 marks)

Analytical processes

4 **Distinguish** between an *r*-selected species and a *K*-selected species. (1 mark)

5 Using the *r* and *K* categories, **determine** how you would classify a human. **Justify** your decision. (2 marks)

Lesson 3.3
Modes of population growth

Key ideas

- → Organisms demonstrate different modes of population growth.
- → *r*-selected species display exponential population growth.
- → *K*-selected species display logistic growth.
- → Logistic curves reach population equilibrium at around the carrying capacity of the ecosystem.

Learning intentions and success criteria

environmental limiting factor any factor that limits the growth of a population

exponential growth population growth where the reproductive rate of the individuals in a population remains constant, but the number of mature individuals increases due to no limiting factors, causing the population to grow faster and faster

Exponential growth

If a population is not pressured by any limiting factors, it will increase. This is commonly the case for small populations, such as a few individuals that have migrated to a new area. The **environmental limiting factors** that inhibit population growth, such as limited resource availability, predation and disease, will be non-existent or negligible. At first, the population will grow slowly, because few individuals are able to reproduce. However, if resources continue to abound and deaths due to predation and disease remain negligible, the growth rate of the population will increase due to an ever-increasing number of mature individuals in the population. This mode of population growth is known as **exponential growth**.

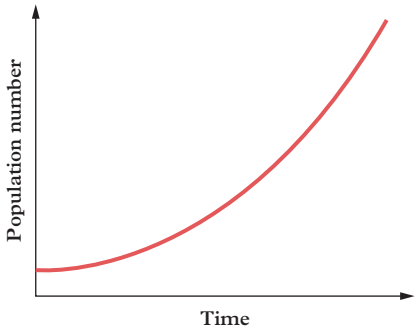


FIGURE 1 Exponential growth of a population. After an initial slow phase, the population grows at a constantly increasing rate, producing a J-shaped curve.

The species then realises its full reproductive **biotic potential** (the ability of a population to increase under optimum environmental conditions). If this were to continue indefinitely, the population would continue to rise without limit, producing a **J-shaped curve**, as shown in Figure 1.

biotic potential the number of offspring capable of being produced by individuals of a species

J-shaped population curve the graphical representation of the change in population density of an organism as it increases rapidly and then stops suddenly, due to environmental or other factors

Carrying capacity

Each environment has a particular carrying capacity for a population – the size of the population that can be supported indefinitely on the available resources of that ecosystem. For example, the house fly (*Musca domestica*) can produce seven generations in one year. Each female can lay 120 eggs. Assuming that each fly lives for only one generation, and that half the eggs hatch into females, a total of 5,598,720,000,000,000 flies (over 5 quadrillion) can be produced in one year from one original pair of flies. This is prevented by **environmental resistance** (the sum of all environmental limiting factors) such as lack of resources, increase in predators, parasites and disease, accumulation of toxic wastes or other factors such as overcrowding. As a result, the population of the house fly is restricted to the carrying capacity of the environment in which it lives.

environmental resistance the sum of all environmental limiting factors

There are two possible outcomes for the initial unrestricted growth of the house fly population, or any population demonstrating exponential growth. The species may experience rapid population growth until one of the following occurs: the population exceeds the environment's carrying capacity and over-exploits the local resources, a significant climatic event drastically reduces the population, or most of the population migrates. This results in a J-shaped curve on a population-versus-time graph, followed by a steep drop in population size – a "boom and bust" situation (Figure 2). In nature, short-term growth patterns of this type are characteristic of *r*-selected species and opportunistic species, such as weeds or insects, which invade an area, rapidly use up the local resources and then enter a phase of dormancy, die out or move on.

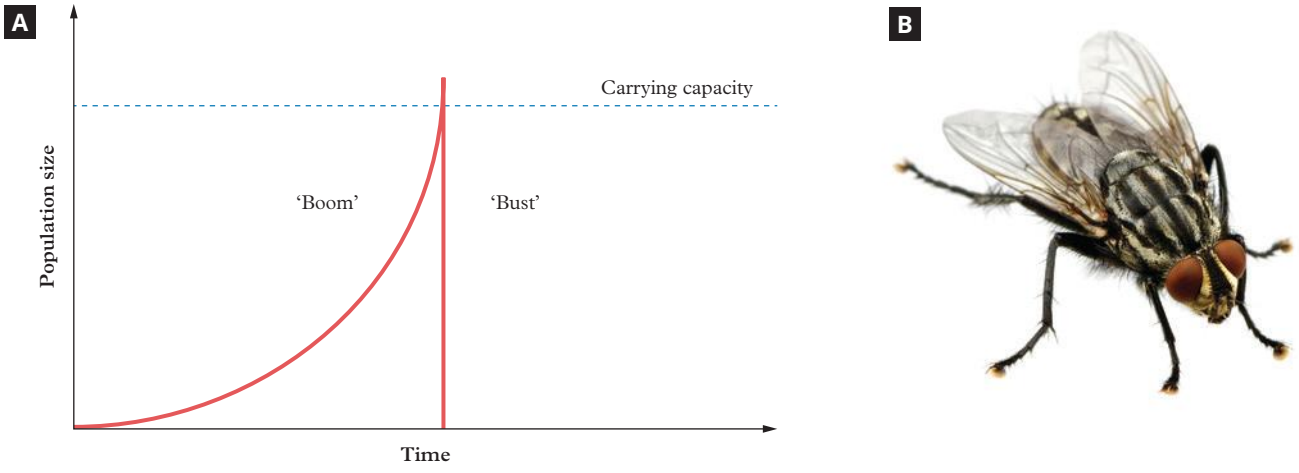


FIGURE 2 (A) A population growth curve of the house fly (density-independent) (B) A typical house fly

Logistic growth

Logistic growth occurs when a population gradually increases and then levels off when it reaches carrying capacity. In this mode of growth, as the population increases there is increased environmental resistance, which leads to an increased death rate and a decreased birth rate, slowing down the rate of growth as the carrying capacity is reached. The results are reflected in the formation of an **S-shaped population curve**.

For animals, the carrying capacity may be determined by factors such as available shelter or nest sites. For plants, access to sunlight might be the limiting factor. This type of growth pattern is typical of density-dependent *K*-selected species (Figure 3).

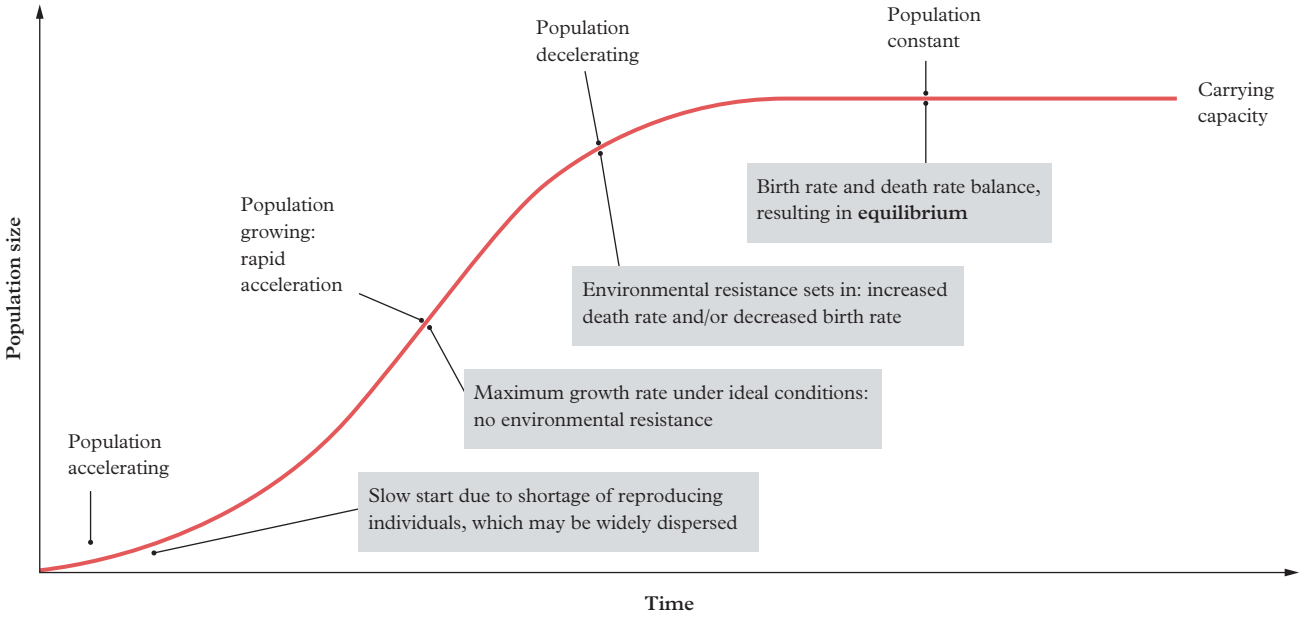


FIGURE 3 Generalised graph of density-dependent population growth resulting in an S-shaped curve

S-shaped population curve the graphical representation of the change in population density of an organism when it initially increases slowly and then rapidly as it approaches an exponential growth rate, but then decreases and levels off as the environmental carrying capacity is reached

There is usually a time lag before the organisms respond to environmental resistance. This may be due to individual growth rates, or the gap of a generation before the reproduction rate decreases. As a result, the population growth curve fluctuates around the carrying capacity. Figure 4 shows this pattern.

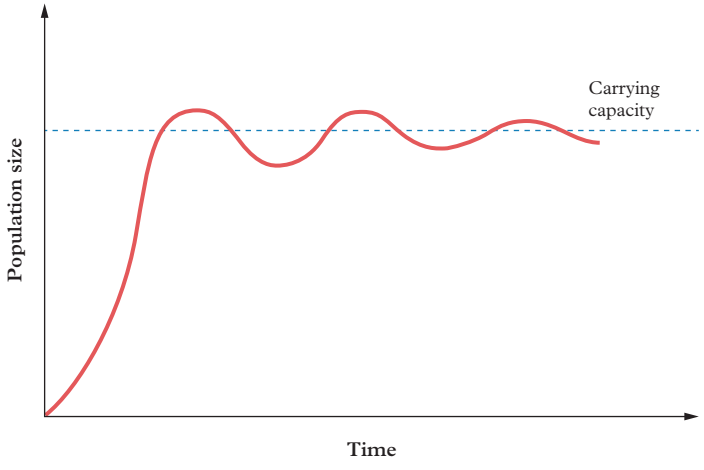


FIGURE 4 Typical response of a density-dependent population at carrying capacity

For a given species in a particular environmental situation, there will be a certain optimum population that the environment can support. This is the **equilibrium** or set point. If the population rises above the equilibrium, competition, predation or increased disease takes place to such an extent that the population falls. If it falls below the equilibrium, environmental resistance is relieved temporarily and the population again rises. This means the population tends to fluctuate around a set point, as shown in Figure 4.

equilibrium the point at which a system can be maintained, e.g. population size for a specific environment; also known as set point

Occasionally, environmental conditions can change. As a result, the carrying capacity changes to reflect the environmental conditions during any period. A long-term drought, for example, will bring about increasing numbers of deaths in a population, which will continue until the drought is broken.

Seasonal changes can alter, for example, the nutrients available for a period of time. This could either increase or decrease the population, depending on the circumstances. Because different populations in a community are interdependent, any change in one population has a flow-on effect on other populations. The sum of population-limiting factors of all populations in a community will therefore affect the carrying capacity of their ecosystem.

FIGURE 5 The world's human population grows by more than 1 per cent each year.

Skill drill

Graphing population growth curves

Science inquiry skill: Processing and analysing data (Lesson 1.7)

The United Nations has estimated that the human population on Earth reached 8 billion on 15 November 2022. It is predicted to reach 9 billion by 2037. The years for each billion-milestone reached are shown in Table 1.

TABLE 1 Billion milestones of the human population

Year	1804	1930	1960	1974	1987	1999	2011	2022
Population milestone	1 billion	2 billion	3 billion	4 billion	5 billion	6 billion	7 billion	8 billion

Practise your skills

1 **Graph** a population growth curve using the data from Table 1. (3 marks)
2 **Describe** the shape of the curve. (1 mark)
3 **Predict** the effect that each of the following events could have on the population growth rate of an area. (1 mark each)
   - **a** mass vaccination programs
   - **b** war
   - **c** famine and drought
   - **d** contraception.

Challenge

Influence of density-dependent and density-independent factors on population growth

Populations rarely fit perfectly into the theoretical growth models or categories of reproductive strategies. The complexity of the system is increased by variation over time of factors such as predation, disease, competition and environmental disturbances. In an undisturbed forest, a population of rhinoceros beetles will first grow exponentially, then become logistic as it reaches the carrying capacity of the ecosystem as a result of the density-dependent factors for the given area (competition, disease and predation).

This simple model is made more complex by the density-independent factors that occur in the surrounding environment. Climatic events, such as fluctuations between El Niño and La Niña in Australia and South America, change the availability of water and therefore the growth and decay of vegetation, affecting the availability of resources and the suitability of the area for the survival of the rhinoceros beetles. An area of forest where the population of beetles is relatively stable may be thrown out of balance by human activities, such as deforestation. This change in the environment will alter the carrying capacity for all organisms living there.

FIGURE 6 A rhinoceros beetle

1 **Deduce** whether density-dependent or density-independent factors would have a greater impact on the shape of a population growth curve. **Justify** your decision. (2 marks)
2 **Evaluate** how interactions between density-dependent and density-independent factors shape long-term population stability. (2 marks)

Check your learning 3.3

Check your learning 3.3: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the following terms.
   - **a** Biotic potential (1 mark)
   - **b** Environmental resistance (1 mark)

2 **Identify** resources (both biotic and abiotic) that would be considered environmental resistance. Which of these resources could be classified as density-independent? (4 marks)

3 **Explain** why the carrying capacity of an ecosystem is influenced by population-limiting factors. (1 mark)

4 **Describe** the shape of the curve of population growth for a *K*-selected species. (1 mark)

5 **Determine** whether each of the following statements is true or false. If false, rewrite it as a correct statement. (2 marks)
   - **a** A population with more offspring per generation will always have a faster growth rate (r) than a similar population with fewer offspring per generation.
   - **b** Predation usually acts as a density-independent limiting factor on populations.

Analytical processes

6 **Compare** a J-shaped and an S-shaped population growth curve. (2 marks)

Practical

Lesson 3.4
Population study of yeast

oxforddigital

This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.

MODULE 3

Lesson 3.5
Review: Populations

Summary

3.1
- Population growth rate is the speed at which a population changes over a specific range of time.
- Environmental factors influence the rates of births, deaths, immigration and emigration in a population.
- Calculating population change informs conservation efforts.

3.2
- Organisms demonstrate a range of reproductive strategies.
- *r*-selected species populations experience "boom and bust", due to rapid reproduction rates.
- *K*- selected species populations grow slower than *r*-selected species and are more stable.

3.3
- Organisms demonstrate different modes of population growth.
- *r*-selected species display exponential population growth.
- *K*-selected species display logistic growth.
- Logistic curves reach population equilibrium around the carrying capacity of the ecosystem.

3.4
- Practical: Population study of yeast

Key formulas

Population growth rate	$r = (b + i) - (d + e)$

Review questions 3.5A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

1 The two factors that lead to population growth are
- **A** births and deaths.
- **B** births and emigration.
- **C** births and immigration.
- **D** deaths and emigration.

2 The highest rate of reproduction of a population under ideal conditions is called the
- **A** birth rate.
- **B** biotic potential.
- **C** carrying capacity.
- **D** environmental resistance.

3 The population of red squirrels in the United Kingdom was estimated at 161,000 in 1995 and 287,000 in 2018. The population growth rate would be best described as
- **A** 5,500.
- **B** 126,000.
- **C** 23 years.
- **D** 5,500 per year.

4 A particular country has negligible immigration and emigration. In 2017 its population increased from 50 million to 51 million. If the birth rate was 30 individuals per thousand, then the death rate (per thousand) in 2017 was
- **A** 10.
- **B** 20.
- **C** 30.
- **D** 40.

5 If 2 male and 18 female wallabies are introduced onto a brush- and grass-covered island where there are no natural enemies or other large animals, what will happen in future years?
- **A** The wallabies will die from diseases.
- **B** The wallaby population will get smaller.
- **C** The wallaby population will remain at 20.
- **D** The population will continue to rise until there is little grass left.

6 There has been exponential growth in the world-wide human population over the past 1,000 years. The main reason for this rapid increase in numbers is
A the high reproductive potential of humans.
B the ability of humans to alter their environment.
C the dramatic reduction in the death rate during the past 1,000 years.
D none of the above.

7 An organism is small in size and has a short lifespan. It is fast maturing and produces many offspring at a young age. The young stay with the mother for only a short period of time. It is likely that this organism is
A a *K*-strategist.
B an *r*- strategist.
C intermediate between an *r*-strategist and a *K*-strategist.
D initially an *r*-strategist and becomes a *K*-strategist at maturity.

8 *r*-selected species are better adapted to survive in an unstable environment because
A they grow to maturity quickly.
B they are generally small in size.
C they have little to no parental care.
D they demonstrate logistic population growth.

9 Which type of growth curve is most associated with *K*-selected species?
A Linear growth curve
B Boom and bust curve
C Logistic growth curve (S-curve)
D Exponential growth curve (J-curve)

10 The carrying capacity of a species is *not* affected by
A the size of the population.
B the presence of predators.
C climactic changes, such as La Niña.
D seasonal changes in the environment.

Review questions 3.5B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

11 **Define** the term "carrying capacity" of an environment. (1 mark)

12 **Describe** how limiting factors determine the carrying capacity of an environment. (2 marks)

Analytical processes

13 Using the data from the Skill drill, **deduce** why the growth of the human population has stabilised and is predicted to slow. (2 marks)

Knowledge utilisation

14 The saltwater crocodile (*Crocodylus porosus*) is the largest species of crocodilian and is found in estuaries and rivers. It can live for up to 70 years and reaches maturity after 10 to 16 years. During a breeding cycle, females lay up to around 60 eggs, in nests made of soil and vegetation to incubate the eggs. Once the eggs are hatched, the female carries the hatchlings to the water, minimising deaths at this early stage. **Classify** the saltwater crocodile as an *r*- or *K*-selected species. **Justify** your answer. (2 marks)

15 A knowledge of population growth curves can help in controlling pests as well as in the conservation of endangered species.
a **Discuss** the most effective time to control a rat outbreak in a racing stables complex. **Justify** your answer. (2 marks)
b A minimum viable population is the size of a population below which numbers of a species must not fall if the species is to survive in the long term. How would you estimate the minimum viable population size necessary to save an endangered species such as the ghost bat (*Macroderma gigas*), the bilby (*Macrotis lagotis*) or the dusky hopping mouse (*Notomys fuscus*)? Conduct research and **evaluate** the requirements of the species you select.(2 marks)

16 The data in the table below was collected as a result of concerns about the numbers of kangaroos in particular areas and the possibility of overgrazing.

a On the basis of this data, which area is in most need of culling? **Justify** your answer using calculations from the data. (4 marks)

b **Evaluate** other factors that could influence your decision. (2 marks)

Location/number at beginning of year	Area (ha) and condition	Migrants		Births	Deaths		
		In	Out		Dingoes	Licensed shooters	Disease, starvation, roads
Simpson Desert / 7,318	23,000 ha – drought declared	1,274	4,392	346	84	746	329
Rervan area / 279	450 ha – pasture available	427	32	192	22	0	47

Data drill

Interpreting population data

The population dynamics within a population of snowshoe hares (*Lepus americanus*) were closely monitored from 2020 to 2024.

Year	Births	Deaths	Immigration	Emigration	Population change
2020	120	110	30	20	+20
2021	100	110	25	30	–15
2022	130	120	40	30	+20
2023	110	115	20	30	–15
2024	125	120	35	25	

Apply understanding

1 **Calculate** the population change in 2024 using the formula: $r = (b + i) - (d + e)$. (1 mark)

2 **Calculate** the population size at the end of 2024 if the population was estimated at 90 at the start of 2020. (1 mark)

Analyse data

3 **Determine** the greatest driver of population decline in this population. (1 mark)

Interpret evidence

4 **Predict** how the population would change if it became isolated, and no more migration occurred. (2 marks)

Module 3 checklist: Populations

UNIT 3

Topic 1 review

Multiple choice

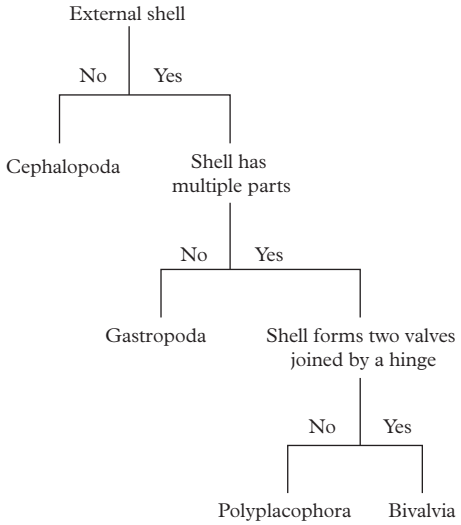
(1 mark each)

1 Species diversity can be defined as
- **A** the variety of extant species in the world.
- **B** the variety of species within an ecosystem.
- **C** the total number of species within an ecosystem.
- **D** variation between individuals of the same species.

2 The biological species concept states that a species is
- **A** a group of organisms with an identical set of DNA.
- **B** a group of organisms that share a common ancestor.
- **C** a group of organisms that share a similar physical appearance and traits.
- **D** a group of similar organisms that can interbreed to produce viable, fertile offspring.

3 The taxa in the Linnean system of biological classification, from least specific to most specific, are
- **A** Domain, Kingdom, Class, Family, Order, Genus, Phylum, Species.
- **B** Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species.
- **C** Domain, Phylum, Kingdom, Class, Order, Family, Genus, Species.
- **D** Kingdom, Phylum, Order, Family, Class, Genus, Species, Domain.

4 Use the dichotomous key below to determine the class of the mollusc pictured.



- **A** Bivalvia
- **B** Gastropoda
- **C** Cephalopoda
- **D** Polyplacophora

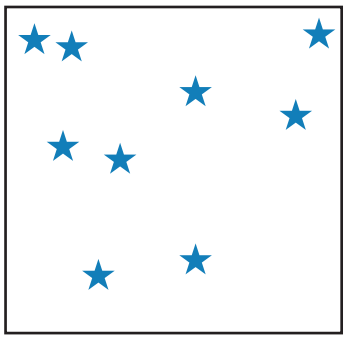
5 Species evenness is
- **A** the total number of species present in an area.
- **B** the uniform distribution of individuals in an ecosystem.
- **C** the similarity in ecological roles between species in an ecosystem.
- **D** the relative abundance of individuals of each species in a community.

6 Determine the percentage frequency of a particular weed species that was found in 3 quadrats in a lawn survey that used 15 quadrats.
- **A** 3%
- **B** 12%
- **C** 20%
- **D** 30%

7 Determine when a transect would be used, rather than random quadrats, to survey an area.
- **A** to measure species distribution along an environmental gradient
- **B** to investigate species abundance in an area with no obvious variation
- **C** to study changes in species diversity in a uniformly distributed habitat
- **D** to analyse species distribution along a linear feature, such as a river or a road

8 The benefit of stratified sampling is that
- **A** it reduces the number of samples required.
- **B** it ensures that all species in an area are sampled.
- **C** it minimises bias by sampling each habitat or stratum evenly.
- **D** it ensures that the most abundant area within an ecosystem is surveyed.

9 Identify the distribution pattern shown in the diagram.



- **A** uniform
- **B** random
- **C** clumped
- **D** bunched

10 Clumped distribution may be the result of
- **A** territorial behaviour.
- **B** availability of shelter.
- **C** no competition for space.
- **D** even distribution of resources.

11 The following data was collected to investigate how abiotic factors affect the distribution and abundance of the European brown hare.

Location	Temperature range (°C)	Annual rainfall (mm)	Soil type	Population density
A	10 to 20	600 to 800	Clay	High
B	5 to 15	1,000 to 1,200	Loamy	Low
C	15 to 25	400 to 600	Sandy	High
D	0 to 10	300 to 500	Peaty	Low
E	10 to 20	800 to 1,000	Clay	High
F	5 to 20	1,200 to 1,500	Loamy	Low

An appropriate conclusion to draw from this data is that
- **A** hares are more abundant in areas with low rainfall and peaty soil.
- **B** temperature has the greatest influence on hare population density.
- **C** hare population density is not affected by the abiotic factors measured.
- **D** rainfall and soil type have the greatest influence on hare population density.

12 In Specht's classification system, foliage height is determined by
- **A** the tallest individual plant.
- **B** the average height of all plants.
- **C** the height of the dominant plant species.
- **D** the height of the stratum with at least 50 per cent foliage cover.

13 Identify the population growth curve that would be expected for a species in an environment with an abundance of resources and negligible predation and disease.
- **A** J-curve
- **B** K-curve
- **C** R-curve
- **D** S-curve

14 Identify which of the following is a characteristic of an *r*-selected species.
- **A** short lifespan
- **B** high parental care
- **C** stable population size
- **D** multiple reproductive cycles with few offspring per cycle

15 Determine the growth rate of a population of 1,200 individuals that has 320 births, 245 deaths, 15 immigrants and 20 emigrants in a given year.
- **A** 6%
- **B** 9%
- **C** 28%
- **D** 50%

16 The capture-recapture method of measuring a population would most likely be used for measuring the population of
- **A** dairy cattle.
- **B** soil bacteria.
- **C** wedge-tailed eagles.
- **D** *Eucalyptus maculata*.

Short response

17 Scientists use multiple definitions of species to overcome any one definition's limitations.

a **Identify** two limitations of the biological species concept. (2 marks)

b For each limitation, **identify** a method of defining a species that overcomes this limitation. (2 marks)

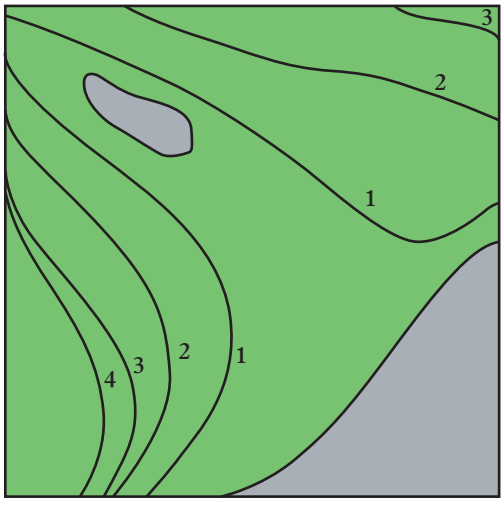
18 To assess the success of closed seasons in south-eastern Queensland, during which snapper (*Chrysophrys auratus)* cannot be targeted or kept by fishers, scientists have conducted biannual population surveys. The data collected is provided in the table.

Year	First capture	Second capture	Tagged in second capture
2020	354	291	15
2022	390	273	11
2024	297	408	7

a **Calculate** the population size in 2020 and 2024. (2 marks)

b **Draw a conclusion** about the success of the fisheries' closed seasons. (1 mark)

19 You are tasked with conducting a sample to investigate the distribution of the noxious weed lantana (*Lantana camara*) in local bushland. The study area is shown here.



Describe how sampling should be done in the area shown, to investigate lantana distribution. In your response, include:

- an appropriate sampling method
- an appropriate sampling technique
- strategies to minimise bias
- measure(s) of diversity. (5 marks)

20 Feathertail gliders (*Acrobates pygmaeus*) are adapted to live in tall, well-watered eucalypt forests. They are normally active at night throughout the year, moving swiftly along branches and leaping through the uppermost foliage. When temperatures become too cold, they go into torpor (i.e. lower their metabolic rate and become inactive) but can only sustain this condition for up to 48 hours. They are predominantly insectivorous and have a wide range of predators (e.g. owls, snakes, cats). They are communal animals living in groups of about 16 in nests of dried, overlapping eucalyptus leaves in hollow trees or old nests of other animals.

a **Identify** one density-dependent factor and one density-independent factor that affects the population size of the feathertail glider. (2 marks)

b Using the example, **distinguish** between the terms "distribution" and "abundance". (2 marks)

21 In a study of competition among frogs, a zoologist manipulated the numbers of frogs in several isolated farm dams. Fifteen almost identical dams without any frogs were stocked with tadpoles at five densities (three dams for each density) in the early spring. In this area, rainfall is predominantly over spring–summer. The number of adult frogs in each dam is determined by sampling on three successive years. The mean adult abundance for each treatment is given in the table below.

Initial stocking density	Mean adult abundance for each stocking density		
	2016	2017	2018
10	8	0	0
20	30	30	80
40	60	40	100
80	60	80	100
160	20	30	60

a **Discuss** these results in the context of intraspecific competition and a variable environment. (2 marks)

b **Propose** one possible factor that may have led to the results seen in the 2018 data. (1 mark)

22 **Contrast** the reproductive strategies of an *r*-selected species and a *K*-selected species, in terms of lifespan, size, age of maturity and number of offspring. (4 marks)

23 **Explain** the role of microhabitats in determining the abundance, distribution and diversity of species in an ecosystem. (4 marks)

24 **Explain** the effect of disease on the abundance and distribution of a species. (2 marks)

25 Below is a hypothetical data set from a survey of Eighteen Mile Swamp on North Stradbroke Island.

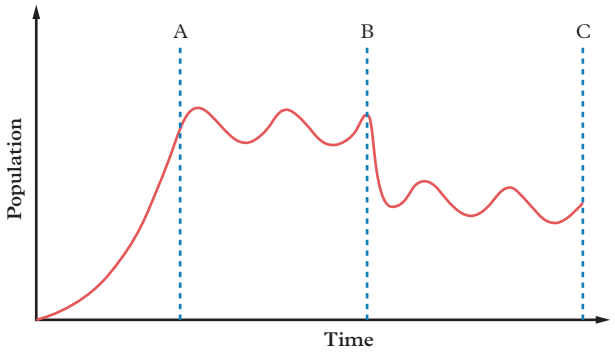
Species name	Abundance
Oxleyan pygmy perch (*Nannoperca oxleyana*)	50
Cooloola sedge frog (*Litoria cooloolensis*)	13
Wallum froglet (*Crinia tinnula*)	17
Glossy black cockatoo (*Calyptorhynchus lathami*)	9
Whiptail wallaby (*Macropus parryi*)	13
Macquarie turtle (*Emydura macquarii*)	5

a **Calculate** the Simpson's diversity index of the swamp. (1 mark)

b **Calculate** the species richness of the swamp, using the Menhinick index. (1 mark)

c **Discuss** the diversity of this swamp, using the calculated index values. (3 marks)

26 The graph shown here is a hypothetical population growth curve.



a **Identify** the mode of population growth shown in the graph. (1 mark)

b **Explain** the fluctuation in population between points A and B. (1 mark)

c **Hypothesise** what may have occurred at point B, then from B to C. (2 marks)

TOTAL MARKS

/54

MODULE 4

Functioning ecosystems

Introduction

Living organisms transform energy between many forms. Photosynthetic organisms convert energy from sunlight to chemical energy for use in their cells. Heterotrophs use some of the chemical energy available in the food they eat, but transfer a percentage as waste in their faeces to be used by decomposers. The metabolic functions of all organisms produce heat that is lost to the environment and must be replaced by producing or eating more food. Energy flow diagrams can be used to represent the transfer of matter through ecosystems from producer to apex predator. When organisms produce waste as faeces, or die, their organic molecules are broken into smaller parts by decomposers and returned to the environment for reuse. Chemical energy is transformed into heat energy during decomposition, and this is released into surrounding matter or the atmosphere. While matter is recycled in an ecosystem, energy flows through – from radiation in sunlight to stored organic molecules in living things, to heat energy released during decomposition. Some species play a more critical role in ecosystems than others in their community, influencing all other species.

Prior knowledge

Prior knowledge quiz Check your understanding of concepts related to functioning ecosystems before you start.

Subject matter

Science understanding

- → Explain the transfer and transformation of energy as it flows through the biotic components of an ecosystem, including the
  - conversion of light into chemical energy
  - production of biomass and its interactions with components of the carbon cycle
  - loss of energy as heat.
- → Analyse food chains, energy flow diagrams and ecological pyramids to determine
  - efficiencies of energy and biomass transfer
  - gross and net productivity
  - loss of energy through radiation, reflection and absorption.

- → Describe the transfer and transformation of matter (water, carbon, nitrogen) as it cycles through ecosystems.
- → Explain the following species interactions: predation, competition, mutualism, commensalism and parasitism.
- → Describe the concept of an ecological niche.
- → Explain the competitive exclusion principle.
- → Explain the critical role that keystone species play in maintaining the structure of a community.
- → Analyse ecological data (e.g. food webs, population data) to
  - identify keystone species
  - infer species interactions
  - predict the outcomes of removing species from an ecosystem.

Science inquiry

- → Investigate
  - species interactions, e.g. by looking for correlation in abundance data
- → Investigate
  - the competitive exclusion principle, e.g. by studying vertical zonation on a tree

Science as a human endeavour

- → Appreciate that
  - some biologists have advocated for keystone species to be special targets for conservation efforts and keystone species theory has informed many conservation strategies; however, there are differing views about the effectiveness of single-species conservation (such as keystone species, flagship species or umbrella species) in maintaining complex ecosystem dynamics.

Practicals

oxforddigital **These lessons are available on Oxford Digital.**

Lesson 4.2 A simplified food chain in leaf litter
Lesson 4.3 Measuring biomass
Lesson 4.7 The relationship between predator and prey
Lesson 4.8 Competitive exclusion in *Paramecium*

Lesson 4.1
Energy in ecosystems

Key ideas

- → Almost all living organisms on Earth rely on energy pathways that begin with the Sun's radiation.
- → Food chains are a visual representation of the simplified flow of energy from producers through multiple levels of consumers.
- → Producers convert energy from sunlight into stored chemical energy they can use as food, while consumers are heterotrophs and obtain energy by eating producers and other heterotrophs.
- → Trophic levels show the transfer of energy from one organism to another, with a loss of approximately 90 per cent of energy from each trophic level to the next.
- → Food webs show more complex feeding relationships between organisms in a community; they are built from several food chains.

Energy on Earth

Learning intentions and success criteria

Our Earth's Sun sustains most life on Earth. While approximately 30 per cent of the Sun's radiation is reflected back into space by our atmosphere, the remaining 70 per cent is absorbed by the atmosphere, oceans and land, and used by plants for photosynthesis.

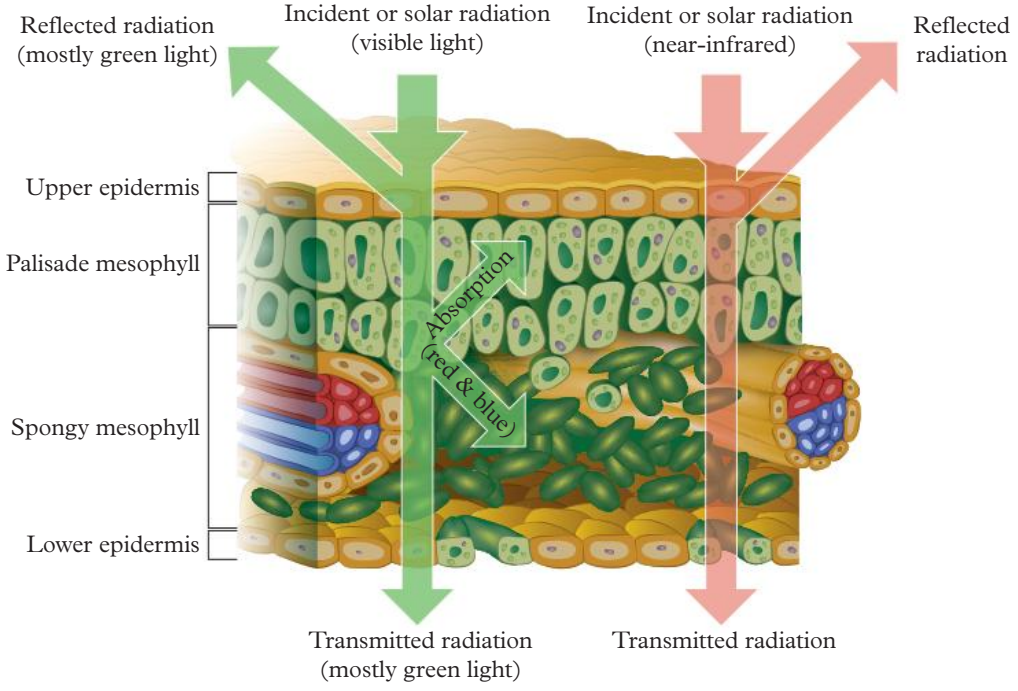


FIGURE 1 Radiation in the form of sunlight is absorbed by a leaf and transformed via photosynthesis into potential chemical energy. This energy is transferred to consumers when they eat the leaf, or it returns to the atmosphere as heat energy.

Energy is transformed from light energy into potential chemical energy by plants through photosynthesis. The chemical energy is transferred from molecule to molecule in the biosphere before it is radiated into space as heat energy. The amount of solar energy stored on Earth determines the amount of potential chemical energy, and therefore how much life can exist on Earth. Only a small proportion of the total solar energy reaching the Earth's surface is transformed by photosynthesis into organic matter. Most solar energy is reflected back into space, or absorbed by the Earth during the day and radiated back into the atmosphere at night. The patterns of flow of chemical energy can be tracked from molecule to molecule, and organism to organism in the biosphere.

Food chains

consumer
an organism that eats another living organism (or part of an organism) for nutrition

food chain
a simple linear arrangement of organisms showing the flow of matter and energy from one organism to another through feeding relationships

Autotrophs produce their own chemical energy and use this energy to produce their own matter. Autotrophic producers are eaten by other organisms (**consumers**), which are then eaten by other consumers (higher-order consumers). This flow of energy and matter can be followed through each organism from producer to highest-order consumer and then decomposers, through a **food chain**. Food chains use arrows to indicate the direction of movement of matter and energy through each organism (Figure 2).

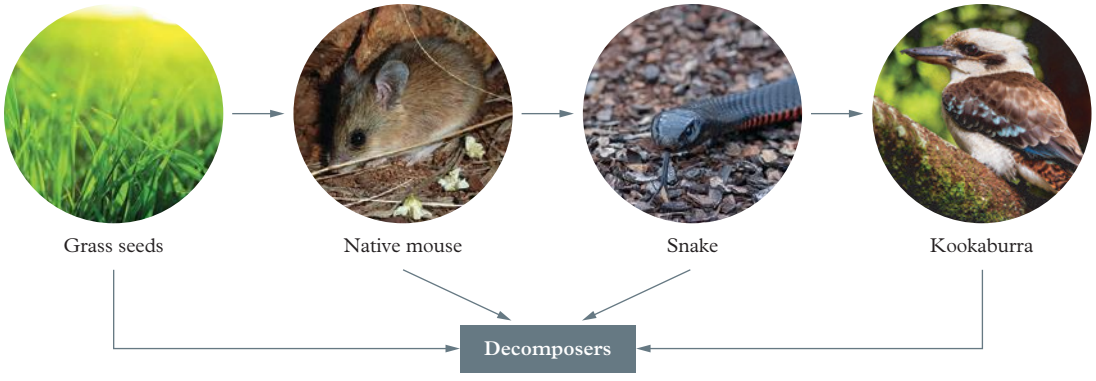


FIGURE 2 A food chain

On the basis of the way they obtain food, organisms can be categorised into three groups: producers, consumers and decomposers.

Producers

productivity
the amount of energy fixed in organic compounds; measured by the increase in biomass per unit of time

biomass
the amount of organic matter in a selected system

Producers convert simple inorganic chemicals to complex organic molecules (molecules containing carbon and hydrogen together with other atoms). Most producers use solar radiation as an energy source. **Productivity** is measured by the amount of energy fixed within chemical compounds at each level in the ecosystem. In producers it can also be an indication of how the amount of producer **biomass** (mass of all organic matter in an area) increases over a particular length of time.

Photosynthesis is a chemical reaction that produces glucose and oxygen from carbon dioxide and water in the presence of sunlight.

$$\text{carbon dioxide} + \text{water} \xrightarrow{\text{Sunlight}} \text{glucose} + \text{oxygen}$$

This means photosynthesis is affected by the temperature of the environment. Higher temperatures cause molecules to move faster, increasing the rate of photosynthesis and glucose production. Cold temperatures slow the rate at which glucose is produced.

The temperatures that determine the rate of photosynthesis change throughout the year, because the production of glucose by plants and its conversion into other organic compounds (biomass) are influenced by season, latitude and altitude.

Productivity in producers is also influenced by other factors, such as soil mineral availability and water. Although deserts may experience suitable temperatures for chemical reactions, there is little water present and therefore their productivity is low.

Plants and algae/phytoplankton also vary in their ability to convert light into chemical energy. This ability is the producer's **photosynthetic efficiency** – how effectively the producer in the ecosystem is able to produce glucose from sunlight. The total amount of organic matter in an ecosystem, which is produced as a result of photosynthesis or chemosynthesis, is called **gross primary production**. Not all of this energy can be used by the herbivore that eats the producer – some will be lost as heat and removed as waste product. The amount of energy the herbivore is able to gain when it eats the producer (after subtracting the energy it took to digest the plants) is called **net primary production**. The productivity can be measured for each level in an ecosystem. An example of this is secondary productivity, which is a measure of the amount of new tissue (biomass) generated by the growing herbivores in an ecosystem.

photosynthetic efficiency
the percentage of light energy that photosynthetic organisms convert into chemical energy during photosynthesis

gross primary production
the total amount of organic matter in an ecosystem produced as a result of photosynthesis

net primary production
the amount of energy available for herbivores in an ecosystem

Consumers

Consumers use food produced by other organisms as their energy source. First-order consumers are herbivores, which eat plant material. Second-order consumers are carnivores that eat herbivores. Third- and higher-order consumers are carnivores that eat other carnivores. These carnivores may be predators (killing other animals for food), parasites (feeding on living organisms) or scavengers (eating animals they have not themselves killed). Some consumers – omnivores – may be both a first-order consumer and a higher-order consumer simultaneously. Consumers that are **specialist feeders** eat a limited range of things. Koalas, for example, eat only the young leaves of specific eucalypt species. Other consumers, known as **generalist feeders**, eat a wide variety of food. A bandicoot is a generalist that eats insects, spiders, earthworms, berries, grass seeds, and young stems and roots.

FIGURE 3 The long-nosed bandicoot (*Perameles nasuta*) is a generalist heterotroph that eats animals and plants.

specialist feeder
a heterotroph that can thrive only on a limited diet

generalist feeder
a heterotroph with a varied diet

Decomposers and detritivores

All organisms in an ecosystem eventually die and fall to the ground – this could be the sea floor in the ocean, or the soil in a rainforest. This mixture of dead plant parts, skin, undigested food and dead organisms is called **detritus**. **Detritovores** ingest detritus to break it down, and **decomposers** digest detritus using an external process. Detritovores include

FIGURE 4 Dark honey fungus (*Armillaria ostoyae*) breaking down a tree stump on the forest floor

detritus
organic debris from decomposing plants and animals

detritivore
an organism that feeds on detritus

decomposer
an organism (e.g. bacteria and fungi) that uses dead organisms or waste matter for its nutrients, releasing simple inorganic molecules back to the soil to be reused.

organisms such as worms, that eat the decaying matter and digest it internally. Decomposers, such as bacteria and fungi, cover their food with enzyme-containing secretions to break down the matter into simple nutrients before absorbing these into their body. Because matter is limited on Earth, it is recycled through plants, animals, fungi, decomposers and other organisms.

Trophic levels

trophic level
one of the levels of a food chain, e.g. first-order consumer

Trophic levels (feeding levels) describe the relative positions of producers and consumers in a food chain. A food chain shows energy transferring through a group of organisms in an ecosystem. The organisms at each trophic level eat and obtain energy from organisms in the previous trophic level. In turn, they are consumed by the next organisms along the food chain, passing on the energy they had stored in their cells and tissues.

Energy transfer

Food chains usually have three to four trophic levels, but may have up to six. There are not more than this because, at each trophic level, energy is lost to the surrounding environment as heat and only around 10 per cent is transferred from one level and retained by the next (Figure 5). For example, if some grass contains 1,000 units of energy produced through photosynthesis and a grasshopper eats the grass, only 100 units of energy are assimilated into the body of the grasshopper. The remaining 900 units of energy are used up by the grass in its growth and flowering, which will release energy to the environment in the form of heat or waste.

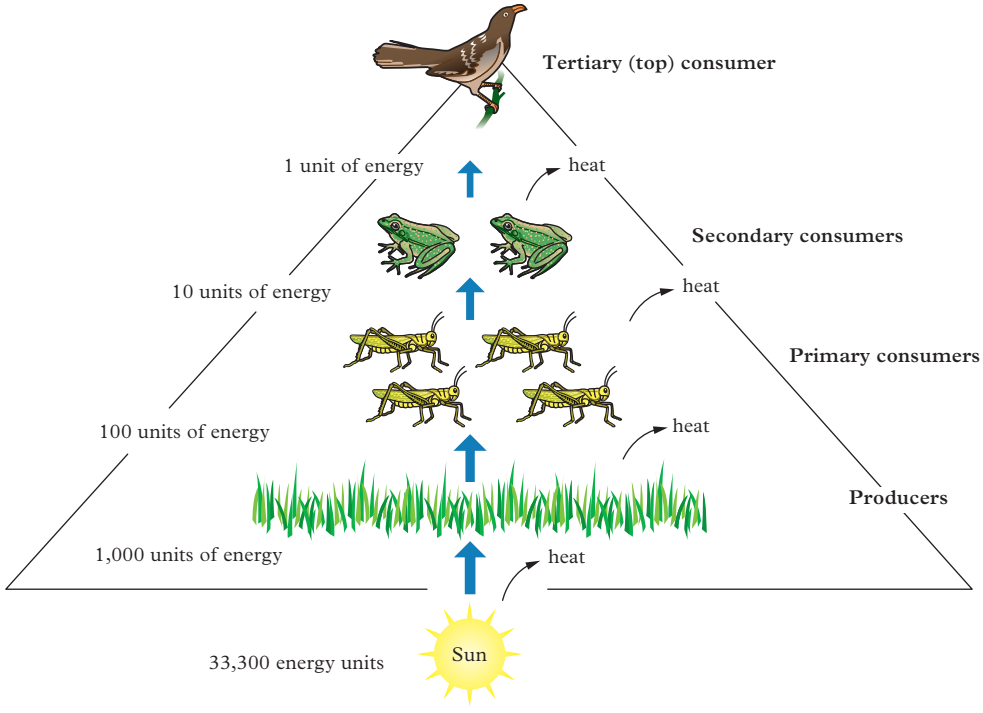


FIGURE 5 The transfer of energy through a food chain from producer to top-level consumer: only approximately 10 per cent of energy is retained at each trophic level.

There is more energy stored in the lowest (producer) level of a food chain than in the third trophic level (consumers). Therefore, the closer a consumer is to the producer, the more energy is available to be transferred.

In most cases, higher-order consumers tend to be larger than lower-order consumers (particularly when they are carnivores). Food chains, therefore, generally have fewer members in each successive energy level. Energy is released to the environment at each level, and this released energy is eventually re-radiated into the atmosphere as heat. Energy is not recycled in an ecosystem; it flows through the ecosystem.

Food webs

A food chain is a simple linear series in which each organism is completely dependent on a single food source. However, more often, the range of plant species is sufficient for herbivores to have several sources of food and carnivores to prey upon a variety of animals. This can be represented by a diagram that contains a variety of food chains linked together (Figure 6). This **food web** is a graphical representation of the many food chains that are interlinked to show the feeding relations between organisms in an ecosystem.

food web
all the possible feeding relations in an ecosystem

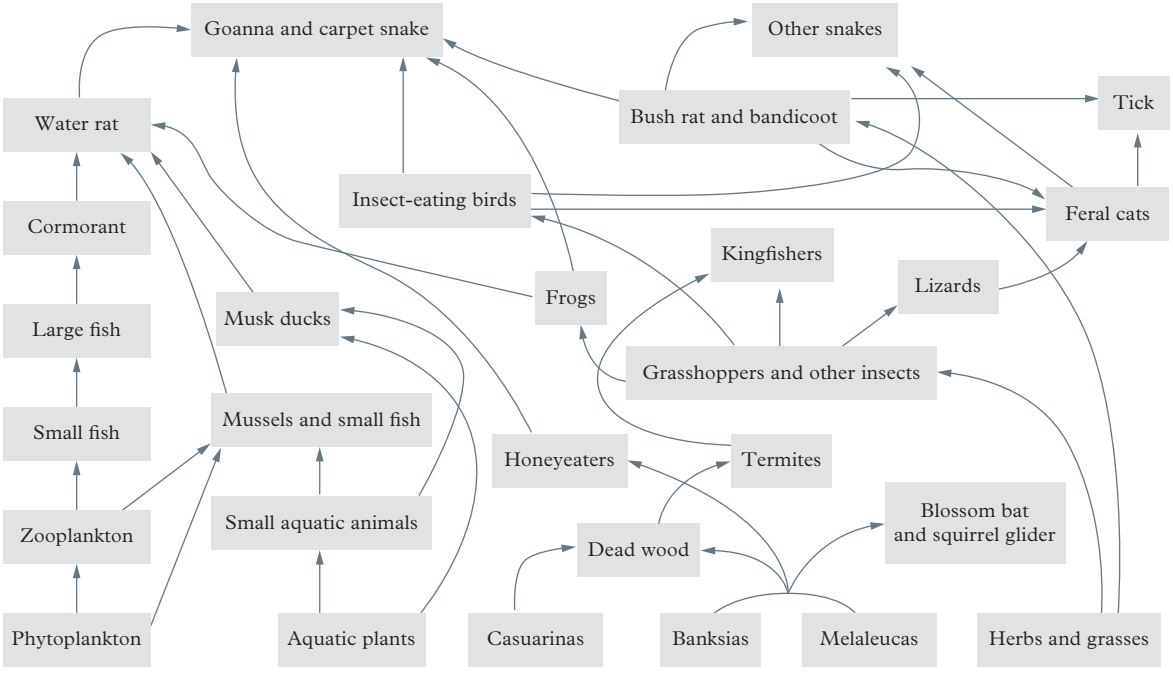


FIGURE 6 A simplified food web (decomposers not shown) of organisms on Moreton Island, Queensland

In a complex food web there is greater stability because most organisms have a variety of food sources to compensate for seasonal fluctuations.

All waste and dead materials are acted upon by decomposers. The organic debris may be totally consumed by bacteria, fungi and small animals, releasing carbon dioxide, water and heat. Alternatively, the organic molecules may enter other complex food webs when scavenging organisms (e.g. crabs) use the remains of dead animals and in turn are eaten by fish (e.g. mullet). Ultimately, however, decomposer organisms release nutrients back into the environment. This process is not always complete, and only partially broken-down products such as methane and alcohol may be released.

Ecosystems conform to the **law of conservation of matter and energy**, which states that matter and energy cannot be created or destroyed but can be changed to other forms.

law of conservation of matter and energy
a law stating that matter and energy cannot be created or destroyed but can be changed to other forms

Although complex ecosystems (indicated by the variety of organisms at each trophic level, and therefore the types of feeding interactions) may contain changing population sizes, the same pattern of energy distribution is maintained in the system over very long periods of time.

Study tip

Energy flows through an ecosystem; matter is recycled.

Check your learning 4.1

Check your learning 4.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** and give an example of a food chain. (2 marks)

2 **Explain** why simple food chains are rare in most ecosystems. (2 marks)

3 **Explain** why food chains usually do not have more than three or four trophic levels. (2 marks)

Analytical processes

4 Consider the way energy and matter move through an ecosystem. **Determine** how they differ. (2 marks)

5 Several large geckoes are found in Australian rainforests – for example, the banded gecko, the chameleon gecko and the leaf-tailed gecko. They feed on insects and other small animals, which they encounter as they forage in the forest. These lizards blend into the general pattern of bark and leaves around them and are extremely difficult to observe when they are motionless. All geckoes are insectivorous but will eat smaller lizards and sometimes frogs. They are nocturnal.

a **Identify** the position in the rainforest food web that a gecko would occupy. (1 mark)

b **Discuss** the abiotic requirements of these geckoes. (2 marks)

c **Infer** why being nocturnal may suit the feeding habits of geckoes. (2 marks)

Practical

Lesson 4.2

A simplified food chain in leaf litter

Learning intentions and success criteria

oxforddigital **This practical lesson is ava ilable on Oxford Digital. It is also provided as part of a printable resource that can be used in class.**

Practical

Lesson 4.3

Measuring biomass

Learning intentions and success criteria

oxforddigital **This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.**

Lesson 4.4
Ecological pyramids

Key ideas

→ An ecological pyramid is a model of relationships between trophic levels in an ecosystem.

→ An ecological pyramid can be used to represent the balance of populations, biomass or energy in an ecosystem.

Graphical representation of energy flow

Learning intentions and success criteria

ecological pyramid
a model of the relationships between different organisms in a food chain

population pyramid
a model of the numbers of organisms at each trophic level of a food chain

biomass pyramid
a model of the amount of living matter transferred through a food chain

energy pyramid
a model of the amount of energy transferred through a food chain

The flow of energy through a food chain is often depicted by a graph representing the quantity at each trophic level. At each level, energy is lost to the ecosystem through movement and heat. A similar loss in biomass (a measure of the amount of organic matter in a system) occurs when the organisms excrete matter through sweat and faeces. Each trophic level is smaller than the level before it. For this reason, diagrams showing these quantitative relationships nearly always take the form of a pyramid.

Types of ecological pyramids

There are three types of **ecological pyramids**:

- **population pyramid** – shows the number of individual organisms at each level
- **biomass pyramid** – based on the total dry mass of the organisms at each level
- **energy pyramid** – shows the productivity of the different trophic levels. Productivity is measured by the amount of energy that is fixed in chemical compounds or by the increase in biomass during a particular period of time.

The shape of any particular pyramid tells a great deal about the ecosystem it represents. In a population pyramid for a grassland ecosystem (Figure 1), the primary producers (usually grasses) are small, so it takes a large quantity of primary producers to support the primary consumers (herbivores).

In a food chain in which the primary producers are large (e.g. trees in a forest), one primary producer may support many herbivores (Figure 2).

FIGURE 1 A population pyramid of a grassland ecosystem

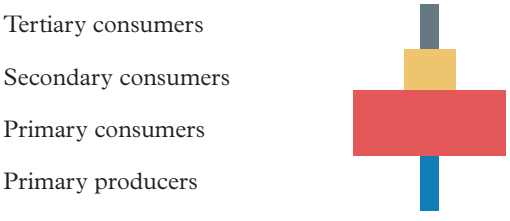


FIGURE 2 A population pyramid of a forest ecosystem

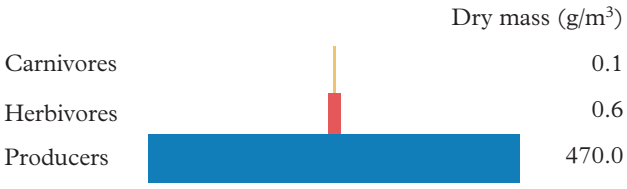


FIGURE 3 A biomass pyramid of a grassland ecosystem

FIGURE 4 A biomass pyramid of an ocean ecosystem

A biomass pyramid for a grassland ecosystem (Figure 3) takes the form of an upright pyramid.

Inverted pyramids of biomass occur only when the producers and primary consumers are small. For example, in the ocean, the biomass of phytoplankton is measured using the biomass at any particular moment. Because phytoplankton reproduce rapidly, their biomass in a short time period may be smaller than the biomass of the zooplankton feeding upon them (Figure 4).

Energy pyramids show the productivity relationships of the trophic levels. This means they are an indication of the amount of chemical energy stored in a set time period. Because energy cannot be created in the food chain, the amount of energy decreases at each trophic level, generating an upright pyramid shape only (similar to Figure 3).

Skill drill

Constructing ecological pyramids

Science inquiry skill: Processing and analysing data (Lesson 1.7)

A food chain of four organisms in Moreton Bay is represented in the table. Use the information in the table to answer the questions below.

Level number	Trophic level	Organism	Average no. organisms per m²	Biomass (g) per m²	Energy (kJ) per m²
1	Producer	Seagrass	10,000	500	20,000
2	Primary consumer	Isopods	300	125	4,000
3	Secondary consumer	Squid	45	80	1,500
4	Tertiary consumer	Shark	5	25	450

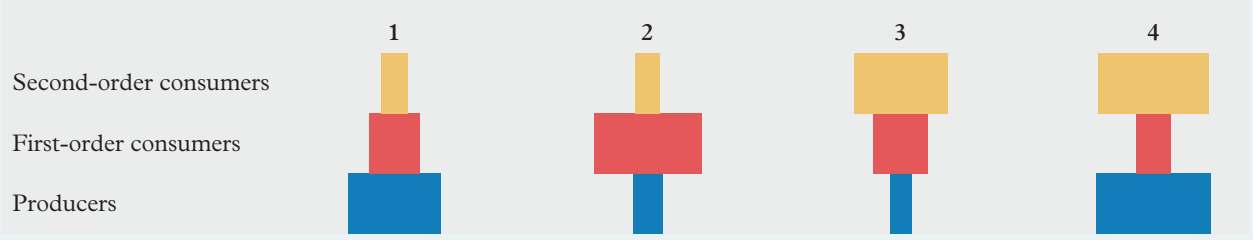
1 **Calculate** the percentage energy transferred from producers to primary consumers. (2 marks)
2 **Determine** which consumers are most efficient in transferring energy from the previous trophic level. Use the data to **justify** your response. (4 marks)
3 Using the data provided, **construct** a pyramid of biomass, a pyramid of numbers and a pyramid of energy. **Explain** why the shape of each of these pyramids is not exactly the same, even though they represent the same food chain. (4 marks)

Check your learning 4.4

Check your learning 4.4: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the term "biomass". (1 mark)
2 **Describe** an "ecological pyramid". (2 marks)
3 **Identify** which of the pyramids in the diagram would best show the relative numbers of individuals in a food chain containing:
   a sheep, sheep ticks and grass. (1 mark)
   b a tree, caterpillars and insectivorous birds. (1 mark)
   c trees, beetles and frogs. (1 mark)



Analytical processes

4 If an ecological pyramid is drawn for food chains in which a large tree is the producer, different-shaped pyramids can be obtained depending on the parameter used (e.g. number of organisms, biomass, energy flow). Giving specific examples, **interpret** why the pyramids for the same food chain may differ. (2 marks)

5 **Contrast** an energy pyramid and a biomass pyramid. (1 mark)

Lesson 4.5
Biogeochemical cycles

Key ideas

- → Key elements for life cycle through living things and their environment in nutrient cycles.
- → Water cycles through the atmosphere, waterways, oceans, living organisms and under the ground.
- → Carbon cycles through the atmosphere and geosphere, and is stored in the short term in living things, and in the long term in fossil fuels such as oil and coal.
- → Nitrogen is the most abundant gas in Earth's atmosphere and is essential for many processes in living organisms.

Learning intentions and success criteria

Nutrient cycles

Key elements required for life circulate through the biosphere, geosphere, hydrosphere and atmosphere in predictable patterns. These are known as **biogeochemical cycles** (*bio* = life; *geochemical* = the study of chemical exchanges between different parts of the Earth). Approximately 40 elements are essential to living organisms, and their pathway through these systems can be represented in a **nutrient cycle**.

biogeochemical cycles the circulation of chemical elements in the biosphere

nutrient cycle the cycling of a particular element between biotic and abiotic ecosystem components

Nutrient cycles are important because:

- they help retain necessary nutrients in usable forms for the living organisms of an ecosystem
- they help to maintain homeostasis in ecosystems where populations remain relatively unchanged.

TABLE 1 Cycling of some major macronutrients

Nutrient	Reservoir (unavailable in long-term storage)	Cycling (available in the cycle)
Water	Artesian, glacier, polar ice caps	Transpiration – evaporation – precipitation – uptake
Oxygen	Metal oxides	Photosynthesis – respiration
Carbon	Fossils, peat, coal, oil and gas, trees	Respiration – photosynthesis
Nitrogen	Deep-sea sediments	Nitrogen fixation – denitrification
Phosphorus	Phosphate rock, deep-sea sediments	Erosion – uptake – dephosphatising

Real-world biology

Galapagos Islands

The marine environment surrounding the Galapagos Islands is rich with life. This is largely due to the islands' location at an intersection between five major ocean currents. Together with the air temperature at the equator, the ocean currents dictate the islands' climate and extensive food webs above and below the water. When ice periodically melts into the Southern Ocean, the water is cold and dense. As a result, this water sinks to the base of the Southern Ocean, sweeping up the nutrients (from dead organisms) stored as sediment on the ocean floor. These sediments (containing many essential minerals and nutrients) follow the current along the coasts of Chile and Peru, to the Galapagos Islands, where the current turns west. As a result of the upwelling, the many producers in the waters surrounding the islands are provided with a constant source of nutrition. As the seasons change, so too does the strength of the current. During the "wet" season, warmer waters arrive from the north. This current of warm water is less dense and doesn't carry as many nutrients from the ocean floor, slowing the growth of phytoplankton producers. As a consequence, the rest of the islands' food webs are affected.

FIGURE 1 Brown pelicans (*Decapterus moruadsi*) and Galapagos sea lions (*Zalophus wollebaeki*) are among the diverse species of the Galapagos Islands.

Apply your understanding

1 **Identify** the biogeochemical cycles affecting life on the Galapagos Islands. (3 marks)

2 **Infer** the effect of an extended wet season on the food webs of the Galapagos Islands. (1 mark)

The water cycle

Water type and availability are closely linked to the distribution of animals and plants on Earth. All living organisms rely on water for their cellular processes, and some rely on water as their habitat.

Oceans, rivers, lakes and wetlands contain almost all the water on Earth. A small percentage is locked under the ground as groundwater or permafrost, or in the atmosphere, or incorporated into the bodies of living organisms. Solar radiation heats water in all these sources, causing its evaporation and return to the atmosphere, from where it once fell as rain

(Figure 2). Water vapour is carried by air currents into the atmosphere. When it meets cool air, the water vapour condenses and forms clouds of liquid water droplets or ice. When the volume of water in the clouds reaches a critical level, it falls to the ground as rain or snow, known as precipitation.

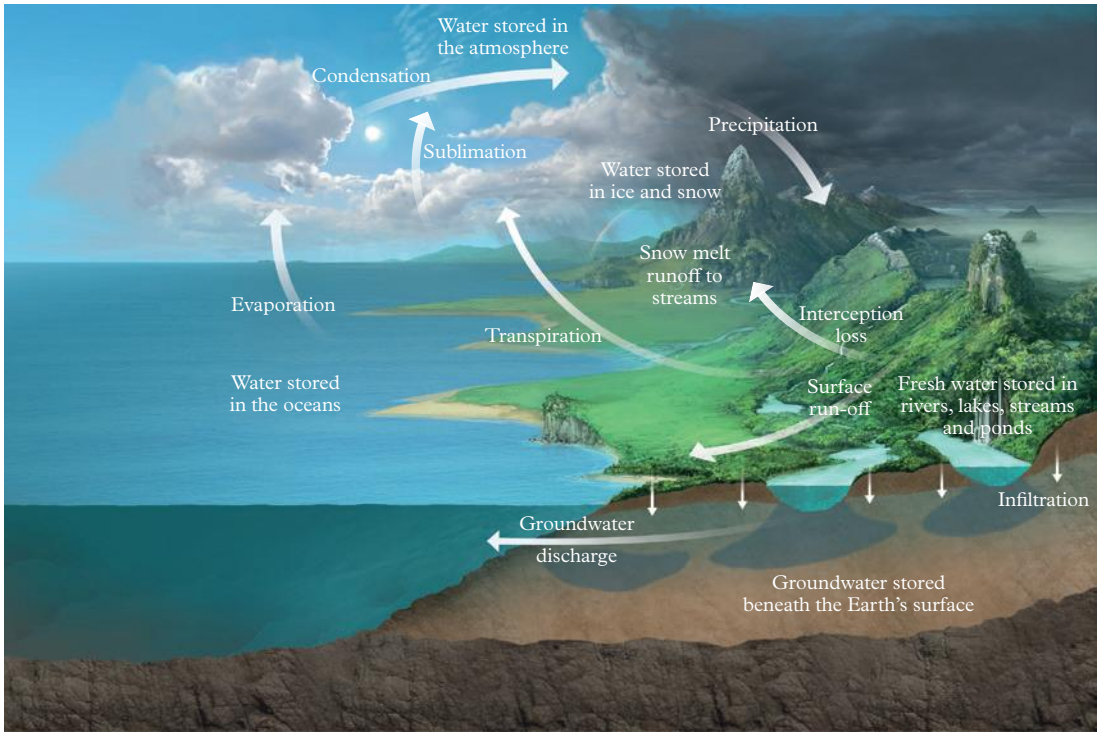


FIGURE 2 A simplified diagram of the water cycle

Because oceans cover most of the Earth, most rain falls on the oceans. The rain that falls over land moves (because of gravity) back towards the sea as run-off, and in streams, rivers and lakes. Some water soaks through the soil and percolates down to form the water table, which also moves slowly towards the oceans. Much of the water taken up by plants from the soil returns to the atmosphere during transpiration. Similarly, a very small amount of water returns to the atmosphere as it evaporates from the gas exchange surfaces of terrestrial animals.

Wind direction, temperature and topography all influence the amount of rainfall on land. Mountain ranges, for example, force water vapour in the atmosphere to rise to higher altitudes, creating a pattern where the ocean-facing side of mountains receives more rainfall than the inland side. As distance from the ocean increases, rainfall tends to decrease, which is evident in the drier regions of western Queensland compared to coastal areas that receive higher rainfall.

The carbon cycle

The carbon and oxygen cycles are interwoven. Photosynthesis incorporates carbon from atmospheric carbon dioxide into complex organic molecules and oxygen is released (Figure 3). These compounds are broken down during cellular respiration, to release carbon dioxide and water back into the atmosphere. A large amount of carbon is tied up in living matter in food chains, and organic carbon is also contained in the dead bodies of plants and animals and in excretory waste. Detritovores and decomposers break down the smallest particles of matter and release carbon back into the soil and atmosphere.

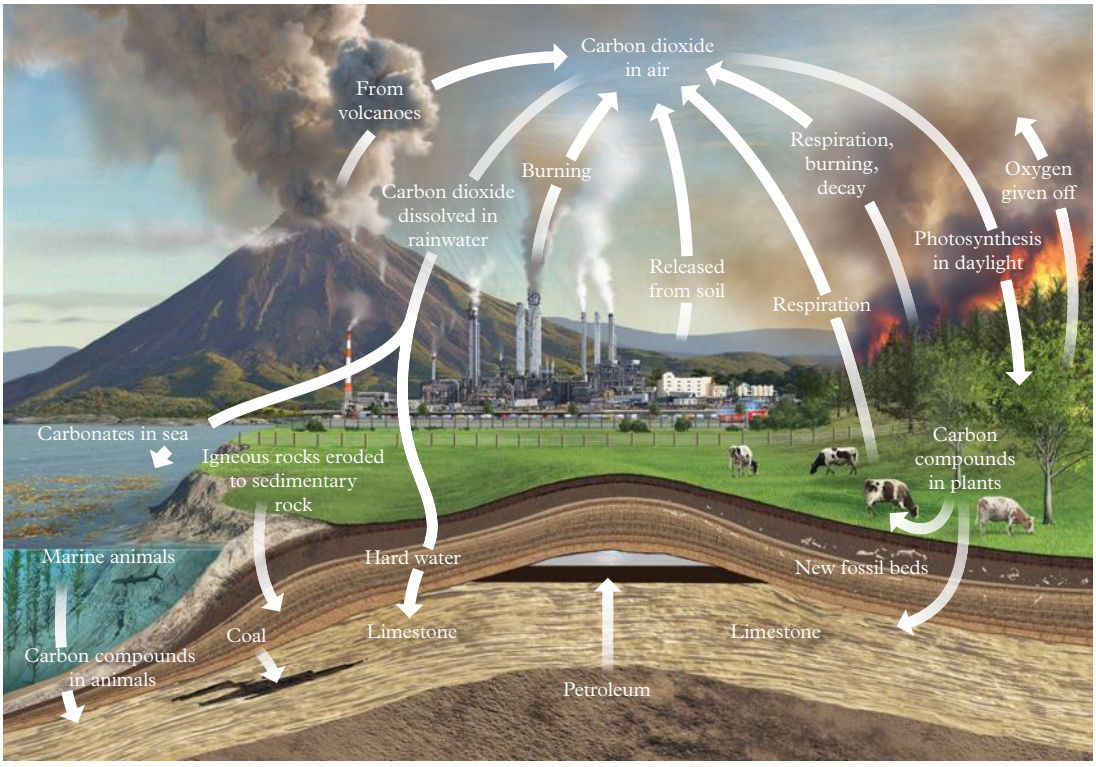


FIGURE 3 A simplified carbon cycle

Over geological time, carbon is locked in a reservoir of coal and oil, and in the wood of trees. As humans exploit this fossil fuel through burning, carbon is returned to the cycle, mostly in the atmosphere as carbon dioxide.

The nitrogen cycle

Nitrogen gas makes up approximately 70 per cent of the Earth's atmosphere. This nitrogen, however, cannot be used directly by plants. As an essential component of amino acids, nitrogen limits the supply of food available in a food chain more than any other plant nutrient.

nitrogen fixation
the conversion of atmospheric nitrogen to nitrate by bacteria and cyanobacteria

Nitrogen fixation (conversion of atmospheric nitrogen, N_2, to soluble nitrate, NO_3) is an essential process for life on Earth and is carried out by chemosynthetic microorganisms in the soil and the roots of certain plants.

The best-known nitrogen-fixing organisms are bacteria. They transform free nitrogen gas in the soil in metabolic reactions to release nitrates (NO_3), which are transferred to plants to form proteins. The plants obtain the proteins necessary for life, while the bacteria receive protection and a supply of carbohydrates (from the plants' photosynthesis) for the synthesis of protein.

nitrifying bacteria
bacteria that convert ammonia to nitrite, and nitrite to nitrate

Another important group of chemosynthetic organisms are **nitrifying bacteria**. These bacteria (e.g. *Nitrosomonas*) obtain energy by converting ammonia (NH_3) to nitrite (NO_2). Other nitrifying bacteria (*Nitrobacter*) convert nitrites to nitrates. Both forms of nitrogen can be absorbed and used by plants in the production of amino acids and proteins. These products are then available to animals as they pass from organism to organism in the food chain. The production of nitrites and nitrates releases energy, which is used by bacteria to synthesise the organic compounds they need.

Bacteria that remove nitrate from the soil are called **denitrifying bacteria** and tend to live in oxygen-depleted environments. By reducing nitrate to nitrite, ammonia or nitrogen, they liberate oxygen. The liberated oxygen is then used in aerobic respiration, and the released energy is used in the synthesis of organic compounds.

denitrifying bacteria
bacteria that convert nitrate to nitrite, or atmospheric nitrogen or nitrite to ammonia

The cyclic conversion of gaseous nitrogen into nitrites and nitrates constitutes the nitrogen cycle (Figure 4).

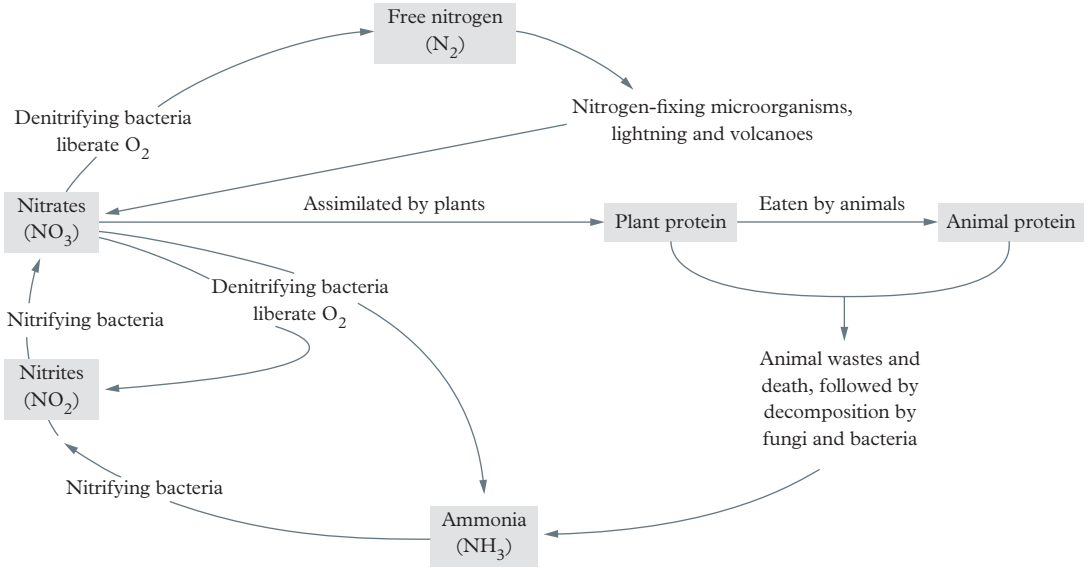


FIGURE 4 A simplified flowchart of the nitrogen cycle

Check your learning 4.5

Check your learning 4.5: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Explain** why matter needs to be recycled in an ecosystem. (3 marks)
2 Not all the carbon on Earth is being cycled continuously. **Describe** how carbon might be removed from the cycle for millions of years. (2 marks)
3 **Describe** the role of bacteria in the nitrogen cycle. (2 marks)
4 **Describe** the process of transpiration. (3 marks)
5 **Describe** the movement of carbon through living organisms. (3 marks)

Lesson 4.6
Species interactions

Key ideas

- → Intraspecific relationships exist between individuals or groups of the same species.
- → Interspecific relationships exist between individuals or groups of different species.
- → Predation occurs when an organism (the predator) hunts, kills and eats another organism (the prey).
- → Competition for a variety of resources drives the behaviour and success of organisms in their environment.

Learning intentions and success criteria

biotic
describes the living components of an ecosystem

intraspecific
within a species; between individuals of the same species

interspecific
between different species

predator
an organism that catches, kills and feeds on another animal

competition
rivalry between individuals, of the same or different species, for a specific resource(s)

Species interactions

Organisms are influenced by, and influence, all other species they share a community with. These **biotic** (living) factors can affect the success and survival of an organism in its habitat. These interactions can be described as one of two types: **intraspecific** (between individuals of the same species) or **interspecific** (between individuals of different species).

Intraspecific relationships

Many species take advantage of the benefits and protection of living together in a group. By cooperating, organisms such as ants and bees can share the workload of collecting food and caring for young. Individuals living in a group with others of their species are less vulnerable to attack by **predators**. If the group is attacked by a predator, not all individuals in the group need to outmanoeuvre the predator, just the individuals targeted.

While populations of a species often cooperate while living together, there is still **competition** between individuals of the same species. Individuals may compete for food, water and space, and males may compete against each other for mating rights with females.

FIGURE 1 An Australian magpie (*Gymnorhina tibicen*) protecting its young from predation by a hungry nankeen kestrel (*Falco cenchroides*)

When resources are scarce, competition sometimes leads to fighting or exclusion from the group, which can be deadly.

Interspecific relationships

Different species living in the same community interact with each other in a variety of ways, including:

- predation
- competition
- mutualism
- commensalism
- parasitism.

Predation

Predation is the capture, killing and eating of an individual by an individual of a different species. This short-term interspecific relationship is beneficial for the predator and deadly for the prey.

A population's mortality rate is increased by density-dependent factors. Predators are alerted to high-density populations of their prey for an 'easy' meal. For example, a sudden explosion in the population of rabbits on farmland will attract birds of prey, foxes and wild cats looking for food. This increase in food availability causes an increase in the birth rate of the predators, causing further stress on the prey population. This can start a cyclic pattern of an increasing predator population causing a decrease in the prey population. The decreasing number of prey causes intraspecific competition in the predator species, which results in a reduction in their population. When the predator population decreases, the prey population recovers and the cycle starts again.

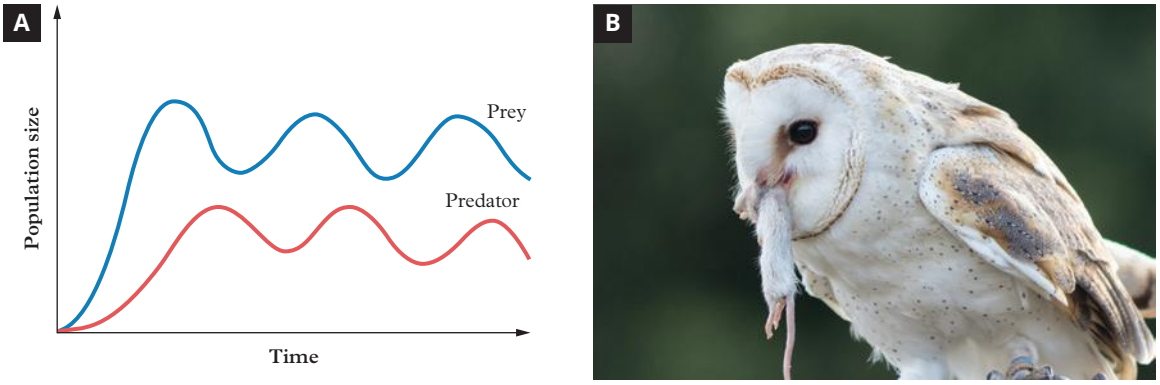


FIGURE 2 Predator–prey relationship. (A) The graph shows corresponding changes in predator and prey populations over time. The number of prey always exceeds the number of predators, and when the prey population increases, the predator population increases shortly after. (B) An owl with its kill

An example of this cycle is the relationship between populations of desert mice (*Pseudomys desertor*) and brown hawks (*Falco berigora*) (Figure 3). The population size of desert mice is normally limited by the scarce supply of food (e.g. grass seeds) and by the brown hawk, which preys upon it. At cyclic intervals, the desert is supported by monsoonal rain carried by channels. The increased water supply leads to rapid growth of plants, allowing the mouse population to increase dramatically. The sudden abundance of mice can result in the immigration of hawks or owls from surrounding areas and greater survival of their chicks.

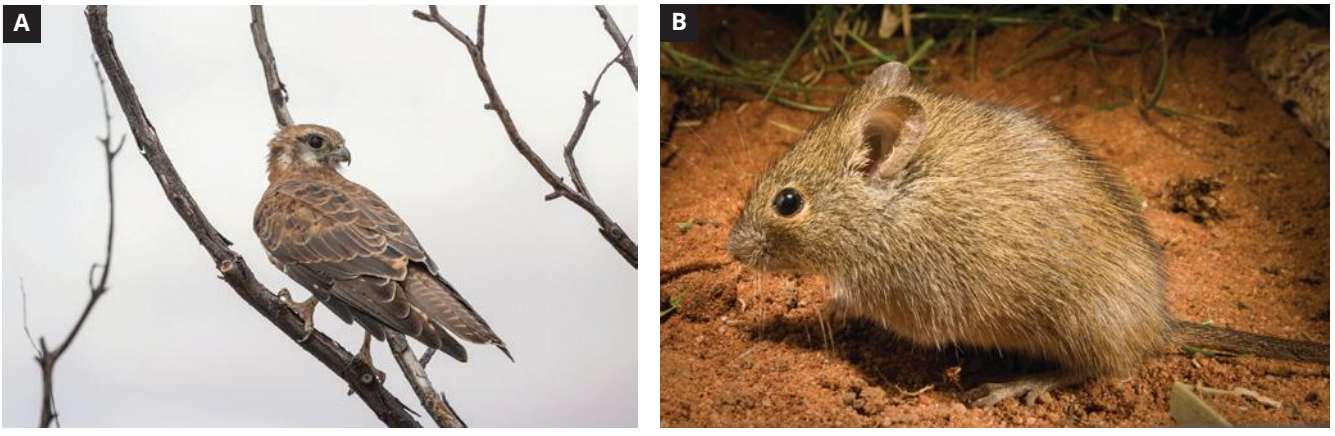


FIGURE 3 Predator and prey: (A) brown hawk (*Falco bengora*) and (B) desert mouse (*Pseudomys desertor*)

This increases the mortality of the mice, reducing the mouse population. The predator hawk and owl populations can no longer be sustained by the reduced food supply and so they must either emigrate from the area or starve. Removal of the predation pressure allows the mouse population to return to normal in that environment, until another influx of water to the area results in another large increase in population size and sets off the cycle again.

Predator – prey relationships are rarely this simple, because few organisms rely on a single source of food. A decrease in one source of food for the predator is often offset by an increase in another. Similarly, it has been shown that in natural situations, predation may alter the age structure of the population, because young, diseased or aged members are more easily captured. It has been argued that a sudden decline in numbers may be associated more with the stress of overcrowding (which may result in a lower reproductive rate), or with a time lag in response to density-dependent factors, than be solely the result of predation.

Competition

Different species living in communities often compete against each other for resources – this is called competition. For example, in eastern and southern Africa, lions and cheetahs compete for prey, such as impala and wildebeest. If prey populations shrink too far, this interspecific competition can harm both the cheetahs and the lions. Competition is one of the main density-dependent limiting factors of population size. The continued healthy existence of most organisms depends upon abiotic factors such as food, water, space and light. As the population density increases, competition for these resources becomes more intense and, as a result, can limit population growth and lead to increased mortality or decreased birth rates.

competitive exclusion principle
the principle that, when two species compete for the same ecological niche, both cannot occupy the niche simultaneously; one species will have an advantage (even if it is small) and outcompete the other

niche
the particular role of an organism, including its interactions with the abiotic and biotic factors in the ecosystem

character displacement
the evolutionary divergence of characteristics displayed by two or more species with the same niche in a particular habitat

resource partitioning
the division of environmental resources by coexisting species populations, to avoid competition for resources

The **competitive exclusion principle** states that two species cannot simultaneously and permanently occupy the same ecological **niche** in the same geographic location. A niche is sometimes likened to the job, or role, of an organism and is defined by the organism's:

- abiotic requirements
- needs for food, water and shelter
- behaviour within its environment.

If two species occupy the same niche in the same habitat, one of them is more likely to be better adapted to the environmental factors. The less-suited species may relocate to a similar nearby habitat or modify its behaviour to seek out its needs at different times of the day. For example, one species of bird may eat ground insects, while the other eats insects on the trunk of a tree. These variations would enable both bird species to survive, because they have different niches.

Often one or both species evolve to occupy different niches, minimising competition between the species. Divergence in those characteristics that overlap is known as **character displacement**. This may lead to the species dividing the resources in a niche, to avoid competition (**resource partitioning**). For example, the restless flycatcher (*Myiagra inquieta*) hovers a metre or so above the ground, emitting a grinding call that disturbs insects. It then suddenly becomes silent as it pounces on an insect, which it takes back to a perch to eat. The leaden flycatcher (*Myiagra rubecula*) takes insects from the leaves of trees, or chases and captures flying insects. Thus, the two species, whose requirements are otherwise similar, are able to live together in the same woodlands and open forests along the eastern coast of Australia.

FIGURE 4 (A) The restless flycatcher (*Myiagra inquieta*) and (B) the leaden flycatcher (*M. rubecula*) have overcome the problem of very similar niches by resource partitioning.

Symbiosis

Symbiotic relationships occur between individuals of different species that interact closely with each other over extended periods of time. For the relationship to be considered **symbiosis**, at least one organism must benefit directly from the interactions. The three main types of symbiosis are **mutualism**, **commensalism** and **parasitism**.

Mutualism is a mutually beneficial symbiotic relationship between two organisms – both organisms benefit from the close interaction. Flower-pollinating birds and the flowers they pollinate have a mutualistic relationship; the flowers benefit from pollination and the birds benefit by receiving nectar from the flower.

Commensalism is a symbiotic relationship that is beneficial for one organism, while the other remains unaffected. True commensalism is rare, because usually there are some small benefits or disadvantages experienced by the organism that appears unaffected. Epiphytes growing on trees in a rainforest are an example of commensalism. The epiphyte benefits from being closer to the sunlight above the canopy and by using the tree's trunk as an anchor point. There are very minimal effects on the tree because epiphytes do not take any nutrients from the tree; they only attach themselves to the strong bark of the trunk.

Parasitism is a symbiotic relationship that provides benefit to one organism while harming the other. Parasites are often partially or completely reliant on their hosts for food or habitat and resources for reproduction. The organism that is harmed by the parasite is called the host, and may be only mildly harmed by the parasite or killed by parasitic disease.

symbiosis
a relationship between two individuals of different species over a long time, where at least one benefits from the interactions.

mutualism
a symbiotic relationship between individuals of two species that is beneficial for both

commensalism
a symbiotic relationship in which one organism benefits and the other is either unaffected or only minimally affected

parasitism
a symbiotic relationship in which one organism (the parasite) obtains benefit and the other organism (the host) is harmed

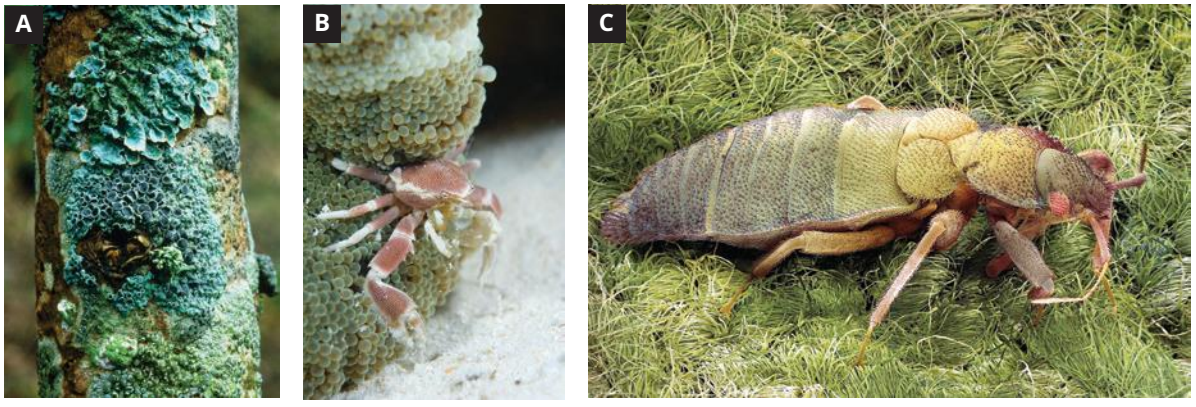


FIGURE 5 Examples of symbiosis: (A) lichen is a mixture of alga and fungus (mutualism); (B) a spotted porcelain crab living on an anemone (commensalism); (C) a bedbug, which feeds on the blood of other animals, viewed under a scanning electron microscope.

TABLE 1 Comparison of the types of interspecific relationships

Relationship	Species A	Species B
Mutualism	+	+
Commensalism	+	0
Parasitism	+	–
Predation	+	–
Competition	+ or –	–

+= advantaged; 0 = not affected; – = disadvantaged

Check your learning 4.6

Check your learning 4.6: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Suggest** an example of parasitism in mammals that can cause death. (1 mark)
2 **Define** the following terms.
   a Niche (1 mark)
   b Competitive exclusion (1 mark)
   c Resource partitioning (1 mark)
3 **Explain** why predators are not considered the main contributors to the maintenance of a stable population size of their prey. (2 marks)

Analytical processes

4 Resources are everything that a particular organism needs to survive. **Classify** general resources required by the human species under the headings "Biotic" and "Abiotic". (2 marks)
5 Many species living in the same area appear to have the same resource requirements. **Determine** how they can coexist in this community. (2 marks)

Practical

Lesson 4.7
The relationship between predator and prey

Learning intentions and success criteria

oxforddigital **This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.**

Practical

Lesson 4.8
Competitive exclusion in *Paramecium*

Learning intentions and success criteria

oxforddigital **This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.**

Lesson 4.9
Keystone species

Key ideas

- → Keystone species are vital in maintaining healthy ecosystems.
- → Keystone species can affect ecosystems in various ways, including changing populations, behaviour and the physical elements of their environment.
- → Keystone species have a disproportionately large impact on their ecosystem relative to their abundance.

Learning intentions and success criteria

The role of keystone species

Some species have a disproportionately large impact on their communities relative to their abundance, and these are termed **keystone species**. They are critical in maintaining ecological stability and diversity by controlling the behaviour and populations of other species, which has a flow-on effect on resource availability. Keystone species are often apex predators that have no natural predators themselves. Apex predators keep the populations of other species under control by preying on them for food and causing them to change their behaviour – for example, browsing in vegetation in a reduced geographic range to avoid predation. Some other keystone species have a disproportionate impact by changing the physical environment of their ecosystem, which in turn can change both abiotic and biotic factors.

keystone species a species that has a disproportionately large effect on its environment relative to its abundance, by maintaining local biodiversity within a community, either by controlling populations of other species that would otherwise dominate the community or by providing critical resources

Sometimes a keystone species is only identified once the effects of its removal from an ecosystem become evident. Characteristics of some keystone species include:

- preying on various species in an ecosystem, subsequently controlling several populations
- exerting a greater influence on the ecosystem and other species than would be expected, given its relatively small biomass or abundance
- negative effects resulting from its intentional or unintentional removal from an ecosystem.

In forests in Europe, the grey wolf (*Canis lupus*) acts as a keystone species by preying on grazing animals, such as deer and wild boar. If populations of these herbivores are allowed to grow unchecked, overgrazing of vegetation begins to negatively alter the habitat of other species. It is not only the grey wolf that acts as a keystone species in these forests. In the Swiss Alps, the Swiss stone pine (*Pinus cembra*) plays a crucial role in sustaining the ecosystem of these sub-alpine forests.

FIGURE 1 The ecosystems of the forests in the Swiss Alps are stabilised in many ways by the Swiss stone pine (*Pinus cembra*).

Some keystone species are called "engineers" because their behaviour modifies their physical environment in a way that enables the continuation of the ecosystem.

Oysters act as engineering keystone species by building physical structures with their shells that create habitats for a variety of marine life. They are also filter feeders that clean the water, improving the water quality for other organisms in their communities. In Queensland, oyster harvesting is controlled by limits on the size and numbers that may be collected, to protect this keystone species. Other examples of engineers are coral polyps, which build the structure of the Great Barrier Reef, and beavers, which change waterways by building dams.

While identifying keystone species is a useful tool in wildlife management, there are some dangers in singling out a particular keystone species in any ecosystem. The full significance of such species is not always known. The difficulty of determining a possible keystone species can lead to mistaking the exact influence of the species. The influence exerted by a species may be seasonal, depending on climatic conditions or the migratory behaviour of other species. The distribution and abundance of these species may change with cyclic weather events and migration of other species.

Real-world biology

Rewilding of sea otters to kelp forests

In recent years, there has been great interest in the concept of rewilding keystone species. "Rewilding" means re-establishing populations of keystone species in an area where populations have been lost. The reintroduction of these species can help bring balance to ecosystems and bring them closer to their original state.

FIGURE 2 A California sea otter (*Enhydra lutis*) floats amid its favourite food, sea kelp (*Macrocystis pyrifera* and *Nereocystis leutkeana*) off the coast of Monterey Bay, California.

An example of rewilding is the return of sea otters to the kelp forests of California. Sea otter populations once thrived along the California coastline, until they were hunted for the fur trade. Sea otters act as a keystone species by preying on sea urchins, a species that, if left to grow unchecked, quickly decimates the kelp forests. Kelp forests are important to these ecosystems because they provide habitats for a variety of marine life, they act as a buffer to prevent waves from eroding the coastline, and they are important carbon sinks, storing carbon dioxide and keeping it out of the atmosphere.

This rewilding project aims to return sea otter populations to their natural habitat range and improve the biodiversity of these coastal areas.

Apply your understanding

1 **Explain** why sea otters are considered a keystone species. (1 mark)

2 **Predict** how the rewilding of sea otters will affect sea urchin and kelp forest populations. (2 marks)

Challenge

Using food webs

Food webs can be used to study feeding relationships and competition between species in a community. They can also be used to predict the flow-on effects of removing an organism from an ecosystem.

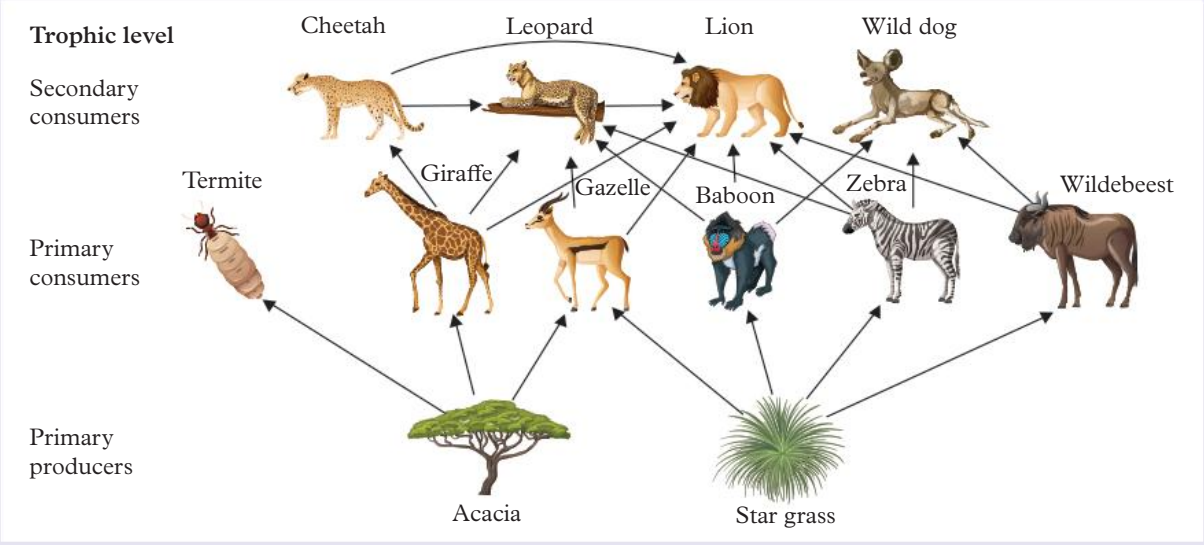


FIGURE 3 A simple food web of a community in the African savannah lands

1 **Identify** all the herbivores in the food web shown. (1 mark)

2 **Determine** which organisms are competitors with leopards. Justify your response using information from the food web. (1 mark)

3 **Predict** the effect on baboons, zebras and wildebeest if *Acacia* trees were no longer available. (3 marks)

Check your learning 4.9

Check your learning 4.9: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Identify** an example of a keystone species that is:
   - **a** a mutualist (1 mark)
   - **b** an engineer (1 mark)
   - **c** a carnivore. (1 mark)

2 **Explain** why most keystone carnivores are apex predators. (2 marks)

3 **Explain** why it may be difficult to identify a keystone species while it has a stable population and is performing its function well in an ecosystem. (2 marks)

4 **Explain** why not all species are keystone species. (2 marks)

5 **Explain** the potential disadvantages of focusing on a single keystone species in conservation management. (2 marks)

MODULE 4

Lesson 4.10
Review: Functioning ecosystems

Summary

4.1
- Almost all living organisms on Earth rely on energy pathways that begin with the Sun's radiation.
- Food chains are a visual representation of the simplified flow of energy from producers through multiple levels of consumers.
- Producers convert energy from sunlight into stored chemical energy they can use as food, while consumers are heterotrophs and obtain energy by eating producers and other heterotrophs.
- Trophic levels show the transfer of energy from one organism to another, with a loss of approximately 90 per cent of energy from each trophic level to the next.
- Food webs show more complex feeding relationships between organisms in a community; they are built up from several food chains.

4.2
- Practical: A simplified food chain in leaf litter

4.3
- Practical: Measuring biomass

4.4
- Ecological pyramids are models of relationships between trophic levels in ecosystems.
- Pyramids can be used to represent the balance of populations, biomass or energy in an ecosystem.

4.5
- Key elements for life cycle through living things and their environment in nutrient cycles.
- Water cycles through the atmosphere, waterways, oceans, living organisms, and under the ground.
- Carbon cycles through the atmosphere and geosphere, and is stored in the short term in living things, and in the long term in fossil fuels such as oil and coal.
- Nitrogen is the most abundant gas in Earth's atmosphere and is essential for many processes in living organisms.

4.6
- Intraspecific relationships exist between individuals or groups of the same species.
- Interspecific relationships exist between individuals or groups of different species.
- Predation occurs when an organism (the predator) hunts, kills, and eats another organism (the prey).
- Competition for a variety of resources drives the behaviour and success of organisms in their environment.

4.7
- Practical: The relationship between predator and prey

4.8
- Practical: Competitive exclusion in *Paramecium*

4.9
- Keystone species are vital in maintaining healthy ecosystems.
- Keystone species can affect ecosystems in a variety of ways, including changing populations, behaviour and physical elements of their environment.
- Keystone species have a disproportionate impact on their ecosystem relative to their abundance.

Review questions 4.10A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

1 Decomposers are important in an ecosystem because
- **A** the food web of the community is a dynamic, continuously changing system.
- **B** large quantities of dead plant and animal matter would not otherwise be consumed.
- **C** they release nutrients, otherwise locked up in the dead matter, for the use of producers.
- **D** the dead plant and animal matter would otherwise harbour dangerous decay organisms.

2 Gross primary production refers to
- **A** the amount of energy available to an organism for growth.
- **B** the amount of food available for carnivores in a food chain.
- **C** the amount of energy passed on to herbivores by producers.
- **D** the rate at which solar energy is converted into chemical energy by autotrophs.

3 A study of an estuary showed that, after a storm, large quantities of eelgrass were washed up along the shoreline. With the aid of microorganisms, the eelgrass became broken down into small pieces and was consumed by beach worms. These worms were eaten by small fish, such as whiting, which in turn were eaten by large fish. Which of the following organisms has the greatest biomass?
- **A** Eelgrass
- **B** Large fish
- **C** Small fish
- **D** Beach worms

4 The biomass of oceanic phytoplankton can be smaller than the biomass of zooplankton, because
- **A** phytoplankton are larger than zooplankton.
- **B** there are few zooplankton compared with phytoplankton.
- **C** the growth rate of phytoplankton is greater than that of zooplankton.
- **D** zooplankton feed on a variety of organisms, including phytoplankton.

5 A nutrient cycle describes
- **A** how an organism uses a particular element.
- **B** the pathway of a particular element in a food chain.
- **C** the study of chemical exchange between different parts of the substrate.
- **D** the pathway of a particular element between living and non-living parts of the ecosystem.

6 Which of the following is a significant feature of a nutrient cycle?
- **A** Evaporation and transpiration
- **B** Underwater currents and geological settling
- **C** The formation of coal and oil from fossil organisms
- **D** Nitrifying bacteria reducing nitrates to nitrites, to release oxygen

7 An ecological pyramid is used to
- **A** show the composition all species in an ecosystem.
- **B** represent all possible feeding relationships in an ecosystem.
- **C** represent the balance of populations, biomass or energy in an ecosystem.
- **D** represent a simple linear arrangement of organisms showing the flow of matter and energy from one organism to another through feeding relationships.

8 The amount of energy available for herbivores in an ecosystem is termed
- **A** gross biomass.
- **B** net primary production.
- **C** photosynthetic efficiency.
- **D** gross primary production.

9 The relative position of producers and consumers in a food chain is called
- **A** a trophic level.
- **B** a trophic cascade.
- **C** an intraspecific relationship.
- **D** an interspecific relationship.

10 Competitive exclusion occurs between
- **A** predator and prey.
- **B** producers and consumers.
- **C** individuals of the same species.
- **D** different species occupying the same niche.

Review questions 4.10B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

11 **Explain** why simple food chains are rare, and how food webs provide greater stability in ecosystems. (3 marks)

12 **Describe** how nitrogen moves from the atmosphere to plants. (3 marks)

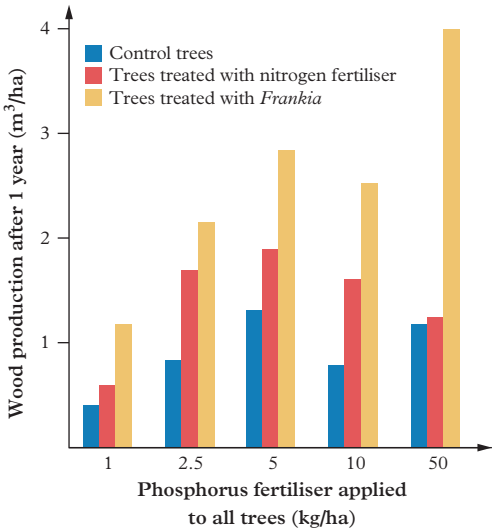
13 **Explain** the meaning of "engineer" in relation to keystone species. (2 marks)

14 **Explain** why apex predators often act as keystone species in an ecosystem. (2 marks)

15 Many species of bats are nocturnal, clinging to the rocky walls of caves during daylight hours and emerging after dark to find food. On these cave walls are generally found small blood-sucking flies and bat bugs, which suck the blood of bats. The droppings of bats build up on the cave floor and form a habitat for some fungi, particularly moulds. These moulds provide food for cave crickets, which are eaten by other insects, spiders and scorpions. These other insects may also be eaten by predators, including spiders.
Construct a food web to show the relationships that exist in the cave community described. (3 marks)

Analytical processes

16 *Frankia* are bacteria that can provide nitrogen to a plant. Trees in a forest plantation were treated in three ways. The results are shown in the graph.



a **Identify** the experimental conditions of the control trees. (1 mark)

b **Explain** the reason for the treatment of the control trees. (1 mark)

c **Analyse** the graph and draw a conclusion about the effectiveness of *Frankia* and nitrogen fertiliser in increasing wood production. Use data to support your conclusion. (2 marks)

17 In an experiment investigating the rate of disappearance of leaf litter, uniform discs were cut from leaves, placed in mesh bags made of 7 mm or 0.5 mm mesh and buried in newly cultivated pasture. The table shows the disappearance of the leaf discs from the bags between June of one year and April of the next.

Month	Percentage (%) of leaf area remaining	
	7 mm mesh	0.5 mm mesh
June	100	100
August	81	94
October	30	91
December	13	66
February	9	62
April	6	60

a **Construct** a graph of the data. (3 marks)

b **Describe** the effect of mesh size on the rate of disappearance of leaf litter between June and October. Infer the causes of this. (4 marks)

c **Explain** the variation in the rate of disappearance of litter from the 0.5 mm mesh bags during the period of the experiment. (2 marks)

Knowledge utilisation

18 Herbivores have generally been considered to have a negative impact on their plant prey. However, a controlled study of a natural community provides evidence to the contrary. The crustacean herbivore *Daphnia pulex* was fed on planktonic algae, and it was shown that the *Daphnia* had a stimulatory effect on the algal populations that approximately balanced its impact on algal mortality. **Predict**, with justification, mechanisms for the *Daphnia*-induced stimulation of algal growth. (3 marks)

19 Phytoplankton are the autotrophs of ocean surfaces. In addition to being the major oxygen supply for Earth, many small animal plankton (zooplankton) feed on them. These two groups of organisms are the basis for most oceanic food webs. The biggest of all animals, the blue whale, depends entirely on plankton in Antarctic seas. Seals, penguins and other birds feed on small fish that eat the zooplankton. In recent years, krill (zooplankton) oil has become a popular remedy for arthritis and the krill themselves have become an important food for commercially reared prawns. Japanese and Russian ships are harvesting millions of tonnes of krill from these cold southern waters. **Predict** the possible effects of this unnatural predation on stocks of krill on Antarctic ecosystems. (2 marks)

20 For several decades after the Second World War, giant tritons (*Charonia tritonis*) were removed in great numbers from the Great Barrier Reef by shell collectors. This large, carnivorous mollusc (see the image below) is one of the few animals known to feed on the crown-of-thorns starfish (*Acanthaster planci*), which in turn feeds on coral polyps. By the 1960s the numbers of crown-of-thorns starfish had increased to such an extent that large sections of the reef were becoming bleached due to the death of the polyps. At that time, it was considered that the giant triton was a keystone species for the reef, maintaining the crown-of-thorns starfish populations at low, non-destructive levels. Further research indicated that the giant triton had never been common and so had little impact on the crown-of thorns starfish. In 2017, however, a breeding program for the giant triton was established for the purpose of releasing these molluscs onto the reef to control the crown-of-thorns starfish.

Draw a conclusion about whether the crown-of-thorns starfish or the giant triton can be considered keystone species for the Great Barrier Reef. **Justify** your response using the information provided and your knowledge of keystone species. (4 marks)

Data drill

Recognising species relationships by comparing abundance data

The abundance of five species was recorded over the course of a year in an equatorial ecosystem, where seasonal fluctuations in temperature and rainfall are minimal. The results are shown in the table.

Month	Abundance				
	Species A	Species B	Species C	Species D	Species E
January	90	90	1,020	340	25
February	110	115	1,030	350	40
March	105	110	1,100	350	55
April	115	105	1,000	380	70
May	140	115	870	430	95
June	150	95	770	480	110
July	170	100	710	520	135
August	180	100	650	560	140
September	190	110	480	610	145
October	150	105	440	500	155
November	125	90	410	400	160
December	105	95	375	370	170

Apply understanding

1 **Calculate** the mean yearly abundance for each species. (5 marks)

Analyse data

2 **Identify** which species had the least amount of variation in abundance throughout the course of the year. (1 mark)

Interpret evidence

3 **Determine** which two species demonstrate the abundance pattern of a predator–prey relationship. **Justify** your choice by using data to identify the species most likely to be the predator and the prey. (3 marks)

4 **Determine** which two species demonstrate the abundance pattern of a mutualistic relationship. Use data from the table to **justify** your response. (3 marks)

Module 4 checklist: Functioning ecosystems

MODULE 5

Succession

Introduction

An ecosystem is a dynamic entity that undergoes both short-term and long-term changes. Long-term changes usually result from succession, with a pioneer community altering the environment in a way that makes it progressively unsuitable for them but suitable for other species, until a relatively stable climax community is achieved. This succession can be primary, from bare ground, or secondary when an existing community is destroyed. Fossil records can be used to determine past ecosystems and changes in biotic and abiotic conditions over time. Human activity has a profound impact on communities and is a key driver of change in an ecosystem.

Prior knowledge

Prior knowledge quiz Check your understanding of concepts related to changing ecosystems before you start.

Subject matter

Science understanding

- → Explain how overexploitation, habitat destruction, monocultures and pollution affect community structure and ecosystem functioning.
- → Explain how the carrying capacity of an ecosystem can be impacted by changes to biotic and abiotic factors, including climatic events.
- → Describe the process of ecological succession.
- → Distinguish between primary and secondary succession.
- → Identify the features of pioneer species that make them effective colonisers.
- → Explain successional changes, with reference to species interactions, abiotic factors, K- and r-selected species, biodiversity and biomass.
- → Interpret ecological data to compare ecosystems across spatial and temporal scales.

Science as a human endeavour

→ Appreciate that
- First Nations peoples' knowledges of environmental change and interactions between abiotic and biotic elements of ecosystems has developed over thousands of years and provides valuable data for understanding ecosystem dynamics. This includes knowledge of land management practices that can maintain ecosystems at specific successional points
- the fossil record and sedimentary rock characteristics provide evidence of past ecosystems.

Science inquiry

→ Investigate
- factors affecting carrying capacity
- how the fossil record and sedimentary rock characteristics provide evidence of past ecosystems.

→ Explore how First Nations peoples' knowledges of environmental change and interactions between abiotic and biotic elements of ecosystems inform land management practices.

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Lesson 5.1
Human impacts on biodiversity

Key ideas

- → Overexploitation and habitat destruction have a direct impact on community structure and ecosystem function.
- → Human-made monocultures reduce biodiversity by reducing the complexity of a region.
- → Human pollution has the potential to affect both local and distant ecosystems.

Humans as consumers

Learning intentions and success criteria

The first humans, recorded from fossils believed to be approximately 150,000 years old, were nomadic hunter-gatherers. Because their numbers were small and they moved constantly, they had little impact on the environment. In time, in many parts of the world, hunting was succeeded by domestication of some animals (e.g. sheep, goats, cattle, llamas). Eventually, forests were cleared to increase the pastures for flocks, which led to the cultivation of land, with deliberate sowing of seed, to produce more pastures and make collecting edible plant products easier. Cultivation of land was associated with more permanent settlements, and trees were felled for timber to construct solid buildings. The development of towns and cities, and a society with division of labour and industrialisation, further added to destruction of the highly diverse, natural environment, replaced by flattened fields dominated by single plant species.

FIGURE 1 An "island" of natural vegetation surrounded by agricultural land

Habitat destruction

Human activity (agriculture, mining or urban development) begins with clearing the natural vegetation from the land. With modern machinery, huge areas of land can be cleared in a relatively short time. This has immediate catastrophic effects on the biodiversity of the area. As land is cleared, the complex structures within the ecosystem are lost. This loss of complexity means that the small, unique habitats and microhabitats that existed in the natural ecosystem are destroyed. With the loss of variety of tree species, the things they provide – including food and nesting sites for insects, birds and arboreal mammals – are also lost. Those that cannot relocate, perish. Species that are endemic to a region may be lost completely, leading to a reduction in diversity, while others may be affected indirectly by the loss of key relationships, such as the loss of prey from the area. Pasture grasses, crops or a "concrete jungle" replace the natural understorey and grasses, further diminishing biodiversity. With this change of environment and loss of structure, few organisms are able to adapt and survive in the new environment. The **community structure** in the ecosystem is changed, as some species die out while others are able to repopulate an area more effectively and new species migrate into the region.

community structure
the composition and relative abundance of organisms in a community

FIGURE 2 The Asian house gecko (*Hemidactylus frenatus*) is an introduced species that is well adapted to the urban ecosystem, benefitting from the moth-attracting lights in modern houses.

Clearing land in an area can bring about changes to local **ecosystem functions** as well as affecting other ecosystems far from human development. Reduced vegetation results in less photosynthesis, decreasing the energy input to the ecosystem, as well as reducing the amount of organic matter returned to the soil, leading to nutrient depletion. The rain causes soil compaction, reducing its ability to absorb water. This increases surface run-off, which results in erosion, with less root mass to hold the sediment in place. This loss of nutrient-rich sediment inhibits plant growth, and the eroded topsoil can end up contaminating freshwater and marine ecosystems.

The lack of vegetation can also result in less water being absorbed by plant roots. This causes an increase in the height of the water table, leaching minerals and bringing salt water to the surface. The high concentration of salt can further degrade the soil and reduce vegetation in the area.

ecosystem function
the interactions between the biological, geological, meteorological and physical factors that sustain an ecosystem

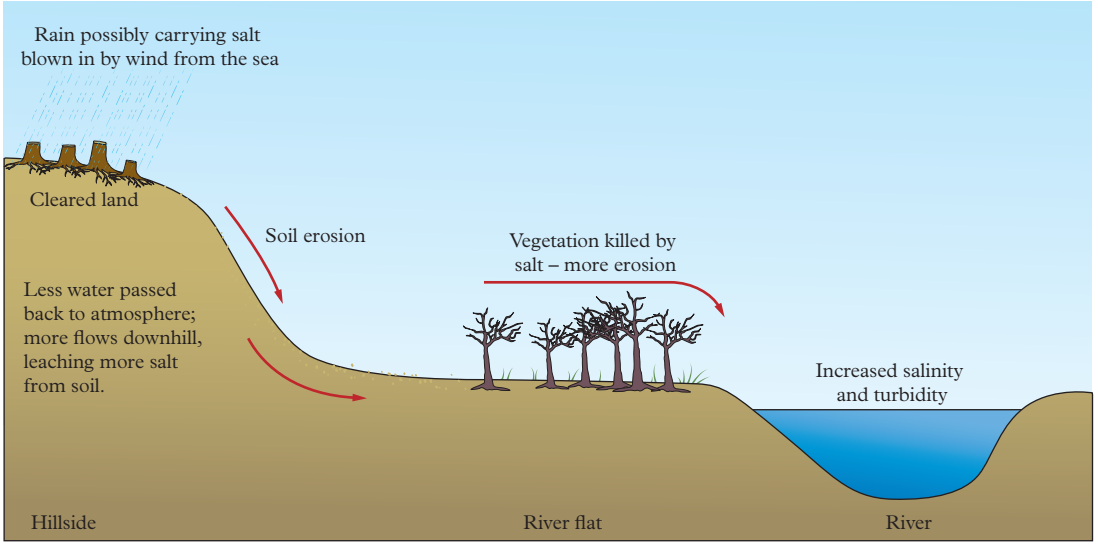


FIGURE 3 Possible effects of erosion on a slope as a result of vegetation clearing

Because of the natural contours of the land, some areas are more suitable for human development than others. Patches of clearing occur in some places, leaving fragments of natural vegetation in less accessible or less fertile areas. This process is called **habitat fragmentation**. These areas are often too small to support viable populations of once-abundant species. In this way, the distribution and abundance of many species (e.g. the koala) have been greatly altered by vegetation clearing. The shape and size of the remaining fragmented islands of vegetation are important factors in determining which species can survive and/or remain in the area. The outer edges of each vegetation island receive more sunlight and are more prone to wind disturbance. Some species are therefore abundant at the edges of these "islands", whereas others are found only in their interior. Other factors within these fragments may be lost completely. For example, an area may be too small to trap the humidity under the leaf canopy to the extent possible in an untouched forest. The largest rainforests in the world, such as the Amazon, influence their own weather through evapotranspiration. The water vapour released through transpiration, as well as the water that evaporates from rivers, condenses into cloud, leading to local rainfall. As the rainforest is destroyed, this function will decrease and potentially cease, completely changing the ecosystem.

habitat fragmentation
the division of a habitat into smaller, isolated portions as a result of human activities in the intervening spaces

While the vegetation islands can be important for isolated species, it is important that appropriate "corridors" be left, joining tracts of natural vegetation between cleared land to allow movement of native fauna and maintain biodiversity.

Monocultures

As mentioned, one of the main reasons areas are deforested and flattened is for the development of agricultural land. To optimise crop production, farmers create areas with minimal obstacles, removing trees, rocks, undulations and gullies, and often planting just a single crop species, known as a monoculture. Monocultures are not just found in agriculture. The efficiency of growing a single plant species on a large scale is ideal for other products, including timber (leading to vast pine plantations throughout Queensland) and oil (with palm oil plantations in Malaysia and Indonesia). These monocultures have an inherently low biodiversity because there is only one type of producer within the region. This reduces the variety of herbivores that can survive in the region – not only affecting the herbivores, but also decreasing biodiversity as a whole by affecting species that live in and around native vegetation or in the soil. This decline in biodiversity has a cascading effect up the food chain. Because all the plants in the area are the same type and all require the same nutrients, this may lead to an imbalance of nutrients in the soil, as some nutrients are required more than others, leading to poor soil health and potentially further affecting soil-dwelling organisms. These human-made ecosystems also lack the stability of a natural ecosystem – a pest or disease can cause the whole ecosystem to collapse, rather than only affecting a portion of the producers present.

FIGURE 4 Monocultures such as palm plantations, timber pine forests, crops or lawns have low biodiversity due to the lack of variety of producers.

Overexploitation

Most of the food that humans eat today is from a domesticated or agricultural source. However, a number of organisms used by humans for food, particularly marine life, are collected from their natural environment. In 1883, English biologist Thomas Huxley proclaimed that nothing humans do seriously affects the number of fish and that the seas are inexhaustible. This attitude led to unregulated exploitation of fish and other marine products, such as crustaceans and pearls from oysters. Examples such as the Atlantic northwest cod fishery, which collapsed to 1 per cent of historical levels after the advent of radar and sonar technology, indicate how much humans have overexploited these resources. As well as fish, overexploitation affects game animals (e.g. passenger pigeons and bison), ornamental animals (e.g. parrots and ornate rainbowfish), and plants (e.g. the Huon pine in Tasmania, or ginseng for medicinal purposes). The overexploitation of these species disrupts the food web in an ecosystem, because when a species is massively reduced, this can lead to a cascade effect, potentially changing the entire ecosystem, particularly if a producer or keystone species is removed.

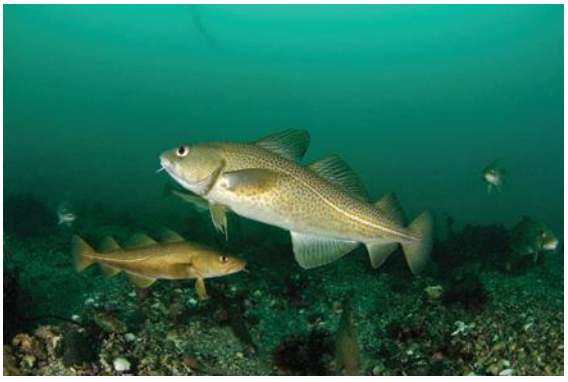


FIGURE 5 The Atlantic cod (*Gadus morhua*) was fished almost to extinction in 1972.

Pollution

Land pollution occurs through land clearing, from the extraction of raw materials for industry and from the disposal of wastes, as well as from agriculture. The solid waste is placed on unused land at the edges of cities. Apart from aesthetic undesirability, two side effects can result: air pollution from burning refuse, and water pollution as organic matter reacts to form acid that leaches into the soil. As the landfill begins to compact and decompose, large amounts of methane gas are generated. If this gas escapes to the atmosphere, it contributes to enhanced global warming. These landfills can have a number of undesirable effects on local ecosystems. First, as organic matter within the landfill decomposes, large amounts of methane and carbon dioxide – two key greenhouse gases – are produced. This methane may also cause fires and explosions in the landfill. Landfills are often the cause of soil or groundwater contamination, through the leaching of toxic chemicals and heavy metals. Plastics are another concern, because they may escape from bins and landfills or be carelessly left where they can move into waterways. These plastics may then have an immediate impact on organisms through physical harm by ingestion or entrapment. They may also have long-term effects as they break down slowly, causing blockages in waterways, providing a new surface for small organisms to grow on or forming microplastics. Microplastics can accumulate within an organism's body and block its digestive system, or release toxic chemicals such as bisphenol A (BPA) within the body. Finally, landfills can change the local community, as some organisms, including migratory birds, feed from landfill, altering their natural habits and leading to them ingesting harmful materials.

FIGURE 6 Landfill can have a significant impact on local and distant ecosystems.

The effect of fertilisers

The use of fertilisers to overcome soil nutrient deficiencies in agricultural settings, as well as private and public gardens, has become standard practice.

After heavy or repeated applications, fertilisers can be washed by rain into dams, lakes and streams, increasing the concentration of nutrient ions in the water. **Eutrophication** is a natural process in which mineral nutrients (particularly nitrates and phosphates) build up in a body of water. As long as the increase is not excessive, these nutrients are taken up by plants at an increased rate and passed through the community, maintaining a balance between inputs and outputs.

eutrophication
a build-up of nutrients in water; may result in oxygen depletion

biological oxygen demand (BOD)
a measure of the quantity of oxygen used by microorganisms (e.g. aerobic bacteria) in the oxidation of organic matter in aquatic environments; the higher the BOD, the less oxygen available for other organisms

Excessive use of fertilisers can cause rapid population growth of water-based producers. Photosynthesis during the day produces enough oxygen for the producer's cellular respiration. At night, there is no photosynthesis or oxygen production. As a result, the water can become oxygen deficient overnight and many water-borne organisms die. This contributes to an increased population of decomposer bacteria, which further creates a **biological oxygen demand (BOD)**. The natural balance of the freshwater ecosystem is thereby destroyed and may even result in the "death" of that body of water.

Pesticides

The need to control weeds and other pests has led to the large-scale use of pesticides. Unfortunately, pesticides cause widespread pollution of the environment, seeping into rivers, killing fish, and contaminating groundwater, drinking water and food. Many pesticides, such as the herbicides DDT and atrazine, mimic the female hormone oestrogen, causing feminisation in a number of species of amphibians, birds and mammals. This results in low reproductive rates and possible extinction of species.

For example, in Clear Lake, California, in the 1940s to 1950s, in an attempt to clear the lake of midges, enough DDT to give a concentration of 0.02 ppm (parts of DDT per million parts of water) was dumped into the lake. Over time, the DDT levels were found to have accumulated in organisms further along the food chain (**biological magnification**) because these substances cannot be excreted and are stored in fat tissues. This action can lead to an imbalance of the community as the top predators die off, while organisms in lower trophic levels survive, and are likely to increase due to a decreased rate of predation.

FIGURE 7 Eutrophication results in an extreme build-up of algae and cyanobacteria, which may produce toxins. Oxygen deficiency in the water creates a biological oxygen demand that results in the death of the aquatic plants and animals.

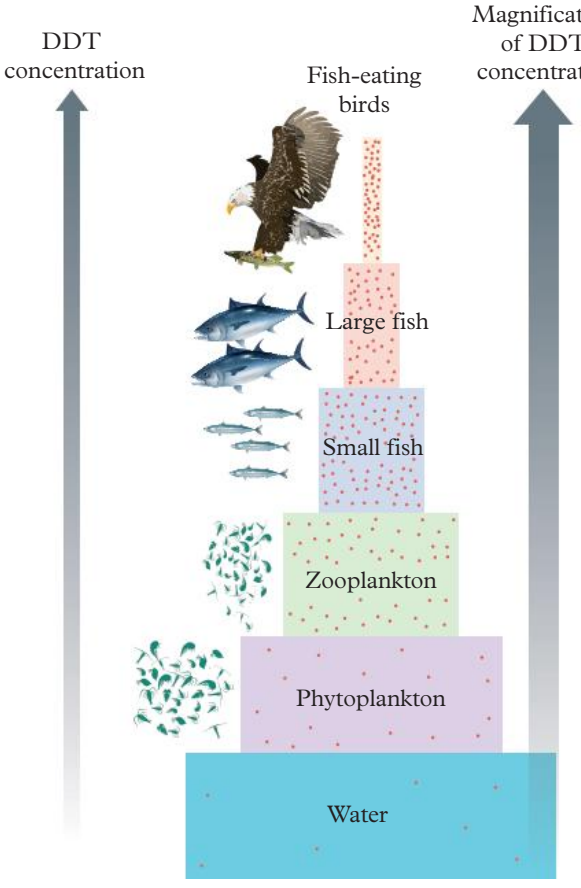


FIGURE 8 Increasing concentrations of DDT in a food chain and biological magnification of the DDT concentration

biological magnification the concentration of substances within the tissues of organisms as they pass along a food chain

Air pollution

There are various types of air pollution, from a number of sources. The main forms of air pollution that affect natural ecosystems are nitrogen compounds and sulphur dioxide. Harmful nitrogen compounds, including ammonia and nitrogen oxides, are often produced by agricultural practices, including fertilisers, as well as by petrol and diesel engines. Sulphur dioxide is produced by burning fossil fuels, primarily coal. These compounds may be toxic to sensitive plants and can affect an ecosystem through the deposition of excess nutrients or the formation of acid rain. This then leads to the soil being too acidic, causing plants and soil microbes to perish.

Check your learning 5.1

Check your learning 5.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** the possible consequences, in relation to the soil, associated with removal of vegetation. (2 marks)

2 **Define** the following terms. (1 mark each)
- **a** Habitat fragmentation
- **b** Overexploitation
- **c** Monoculture
- **d** Eutrophication
- **e** Biological magnification

3 **Explain** the importance of corridors for biodiversity in land clearing. (1 mark)

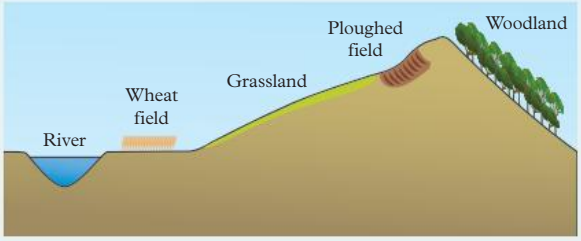
4 **Explain** how the application of fertilisers to farmland can result in the death of organisms in nearby freshwater ecosystems. (2 marks)

5 **Explain** how habitat fragmentation can influence species diversity. (1 mark)

6 **Explain** why monocultures sustain a lower biodiversity than a natural ecosystem. (2 marks)

Knowledge utilisation

7 **Determine** which region in the hillside shown in the cross-section below is most susceptible to erosion. **Justify** your answer. (2 marks)



8 Atlantic cod feed mainly on herring and mackerel, while their main predator is grey seals. **Predict** the effect of overexploitation of Atlantic cod on these species. (2 marks)

Lesson 5.2
Factors affecting carrying capacity

Key ideas

→ Climatic changes alter the abiotic factors in an ecosystem and influence the carrying capacity.

→ Food availability, predation and disease affect the carrying capacity of an ecosystem.

Learning intentions and success criteria

Carrying capacity

carrying capacity the largest population that can be maintained within a given area without collapsing, determined by the limiting resources within the ecosystem

In any ecosystem, the community is constantly changing, with variations in the environment as well as the behaviours of the organisms present. Many plants, and some animals, reproduce at specific times of year in response to certain weather patterns, such as rainfall or temperature changes. Some animals constantly roam throughout their habitat or follow migration patterns throughout the year to breed or have the best access to food throughout the year. The number of individuals of any given species that can persist in an ecosystem, known as the **carrying capacity**, is therefore always changing.

The factors that affect carrying capacity are called limiting factors. These factors may be abiotic or biotic, and the key factors vary depending on the requirements of the species. For an ecosystem to be habitable for an organism, the parameters of the area, such as temperature and pH, must be within the organism's tolerance range. If these minimum requirements are met, a range of density-independent and density-dependent factors determine the carrying capacity of the ecosystem.

Water availability

For land-dwelling organisms, availability of water is a primary concern. Water is essential as the main component of fluids within cells (cytosol) and between cells (interstitial fluid), and is important for a number of metabolic processes within organisms. Therefore, all organisms must maintain a specific balance of water within their body. Plants and fungi absorb water from their environment, particularly soil moisture, and therefore rely on precipitation to bring water to the ecosystem, as well as a suitable substrate to trap and hold water during dry periods. Sandy soils allow water to drain from an environment, loamy soil is able to absorb moisture, and clay has the greatest water retention. The combination of precipitation rates and substrate type determines which plants can survive in a region, as some require high soil moisture, while the roots of others may rot in higher soil moisture levels.

Most animals require access to surface water, such as rivers and waterholes to drink from. While rivers and creeks may provide water from a distant source, many areas rely on water from local precipitation. The organisms' ability to retain water, their osmoregulation and the amount of water available determine the number of individuals that can survive in the area.

Nutrient availability

Nutrient availability refers to the presence of nutrients required for plant growth in an ecosystem, particularly compounds of nitrogen and phosphorous. Nutrients are introduced into soil or water through the decomposition of organic matter. The availability of these nutrients for uptake by plants is strongly influenced by pH and soil moisture levels. Even if the soil in an area has a high nutrient load, if the pH is outside the ideal range, or if there is not enough water in the soil, plants may not be able to absorb these nutrients. As nutrient levels increase, the carrying capacity of the ecosystem increases. However, if nutrient levels increase too dramatically, eutrophication events may occur, destabilising the community.

FIGURE 1 Humus, the product of decaying organic matter produced by bacteria, fungi and other microorganisms, provides nutrients and helps retain moisture in the soil.

Oxygen availability

Almost everywhere on land, oxygen is readily available and therefore not a limiting factor in most environments. However, at high elevations the oxygen molecules are more spread out, reducing the amount of oxygen available for exchange on leaf surfaces of plants or in an animal's lungs. This reduces the number of species that can survive in these conditions, and therefore high-altitude environments are sparsely populated. The movement of oxygen throughout the atmosphere means that the level of oxygen availability in these areas is consistent and closely correlates with altitude.

FIGURE 2 Billabongs may have low levels of dissolved oxygen, especially at the start of summer before the monsoon season begins.

In aquatic environments, oxygen availability can be less consistent. Oxygen enters an aquatic environment through the air–water boundary. The concentration of oxygen that can dissolve into the water depends on the temperature, because cooler water can hold more dissolved oxygen than warmer water. Oxygen levels also fluctuate due to the abundance of plants and phytoplankton present, because photosynthesis increases the oxygen in the water during the day, whereas cellular respiration at night uses up this oxygen. The more organisms living in a body of water, the more cellular respiration occurs, which can lead to intolerably low levels of dissolved oxygen. Therefore, the carrying capacity of an aquatic environment is influenced by the amount of dissolved oxygen, which is affected by temperature, water movement and the presence of other organisms, especially producers.

Light availability

Sunlight is the ultimate source of energy in most ecosystems on Earth. Plants and other producers need light to photosynthesise. The amount of light available therefore impacts the carrying capacity of producers, as well as organisms up the food chain. Polar regions receive lower levels of sunlight due to the low angle of the Sun. These regions also experience extended periods (weeks or months) of continuous sunlight in summer and continuous darkness in winter. Aquatic plants are also affected by water depth and clarity, because light is quickly absorbed by water and particulates in the water, reducing the light available for photosynthesis. Finally, dense foliage coverage reduces the available light for lower-lying and emerging plants, reducing carrying capacity.

Space

The space available for an individual determines its access to resources, including food, water, shelter and breeding spots. Different species use space differently, with some being highly territorial and always living in a very small area, while others – often in areas with sparse resources – travel large distances throughout their lives. Limited space increases competition for resources, limiting the carrying capacity of a given area.

Food availability

The availability of food is a key factor for the carrying capacity of all heterotrophs. When food is abundant, the population can increase rapidly. However, as a population grows, the amount of food for each individual decreases, limiting population growth. The availability of food for an organism low in the food chain has a flow-on effect on those higher up, potentially affecting all species in an ecosystem.

Predation

Predation regulates the population of prey species, creating a density-dependent control of carrying capacity. As the prey species population increases, there is an abundance of food for the predator. This leads to an increase in the predator population, leading to a decrease in the prey population, in turn causing a decrease in the predator population. This cycle continues unless another factor impacts this equilibrium.

Disease

Disease spreads more easily and quickly in a dense population, and affects the health, survival and reproductive success of a population. When individuals are stressed by suboptimal conditions or by intense competition as a result of other limiting factors, this further increases the likelihood of disease, which reduces the carrying capacity of the population.

Seasonal and climatic changes

All the factors discussed so far vary with both seasonal and climatic changes. In Queensland, for example, the average rainfall in summer is much higher than in winter. This impacts the water availability directly, but also has flow-on effects, as nutrients are moved between systems through surface run-off and are more readily absorbed by plants. Oxygen availability in aquatic environments is also increased as oxygen-rich rain and surface run-off flow into stagnant pools. At the same time, daytime periods are longer in summer, leading to longer periods of light as well as increased temperatures. This can lead to a decrease in dissolved oxygen in these pools when no fresh water is introduced. Because of the increased availability of resources, populations grow, leading to an increase in competition for space, light and food. When the weather cools again and it moves into winter, the reduced temperatures, precipitation and daylight hours limit the availability of resources, decreasing population sizes.

Climate events can also have a significant impact on the carrying capacity of an ecosystem. Bushfires cause an immediate decrease in carrying capacity because they cause habitat loss through the destruction of vegetation and shelter, and removal of resources such as water sources. The Australian bush is well adapted to this phenomenon and, over time, the regeneration of this ecosystem will cause an increase in carrying capacity as some species of vegetation thrive in this environment due to the increase in light and nutrient availability.

Cyclones affect ecosystems, such as the Great Barrier Reef, in a similar way. The devastation of the event causes a decrease in carrying capacity as structures, food sources and light availability are decreased. Once the damaged area begins to recover, however, faster-growing coral can inhabit areas they were previously unable to because of competition. This growth restores or potentially increases the carrying capacity of species in the area.

FIGURE 3 Floods damage the environment, but also distribute nutrient-rich sediments to the affected regions.

Similarly, floods can damage large areas of land and aquatic environments, forcing organisms to survive in much smaller areas, increasing competition in these areas. However, floods also distribute nutrient-rich soil to the affected areas, enhancing these areas and increasing their carrying capacity for a time.

Real-world biology

First Nations peoples' land management practices

First Nations peoples use knowledge of the environment to maintain land management practices through the process of fire-stick farming (traditional burn off). This practice, historically used by many First Nations cultures throughout Australia, has had a recent resurgence through the traditional teaching of tribal elders. It involves the controlled use of fire to manage the landscape, which enhances biodiversity. Traditional knowledge of a fire's role and importance in an ecosystem has been passed down for generations, and it reflects a sophisticated understanding of how fire interacts with both abiotic and biotic elements of the environment.

Bushfires are a relatively common natural occurrence in the Australian bush, due to the combination of long periods of dry weather and drought, the composition of fuel sources due to fallen bark and leaves, particularly those from eucalypt varieties, combined with the severe seasonal dry lightning storms that create natural fire-starting environments. First Nations peoples learned the value of these frequent bushfires, which cleared the landscape for new growth, promoting hunting and gathering. Awareness of the power of these fires and how seasonal controlled burning can reduce the severity of fires has allowed First Nations peoples to increase biodiversity in seasonal living environments.

Fire-stick farming was used to create a patchwork of different-aged vegetation, providing a range of habitats for animals and promoting the growth of fire-tolerant plant species. For example, certain plants, such as the grass tree (*Xanthorrhoea*), require fire to stimulate regeneration, while others, such as yam daisies (*Microseris lanceolata*), were encouraged by fire to sprout. The timing and intensity of the fires were carefully managed to ensure they were beneficial, avoiding damage to valuable resources and preventing the risk of uncontrollable bushfires. The intervals between burnings also promoted biodiversity, meaning areas would not be dominated by a single eucalypt species.

Additionally, cultural burning was used to manage soil health by promoting nutrient cycling and reducing the build-up of dead plant matter, which could otherwise increase the risk of large-scale fires. This practice demonstrates an intimate understanding of how fire interacts with soil, vegetation and wildlife. Today, cultural burning is being revisited and integrated into modern land management practices, highlighting the importance of First Nations knowledges in fostering resilient ecosystems and mitigating climate change impacts.

FIGURE 4 First Nations elders pass down knowledge of fire-stick farming to maintain biodiversity in the Australian bush.

Apply your understanding

1 **Summarise** the role of fire-stick farming in maintaining biodiversity in Australian bushland. (1 mark)
2 **Deduce** the impact of fire-stick farming on the population of native herbivores such as kangaroos. (1 mark)
3 **Generate** a research question to address an aspect of the claim that fire-stick farming enhances biodiversity. (1 mark)

Check your learning 5.2

Check your learning 5.2: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Summarise** how each of the following factors affects carrying capacity.
   - **a** Nutrient availability (1 mark)
   - **b** Light availability (1 mark)
   - **c** Predation (1 mark)
   - **d** Water availability (1 mark)

2 **Identify** the relationship between temperature and oxygen availability in an aquatic environment. (1 mark)

3 **Explain** why climatic events initially decrease the carrying capacity of an ecosystem. (2 marks)

Analytical processes

4 North Queensland and the Northern Territory experience a monsoon season each summer, with extended periods of heavy rain. **Deduce** the effect of this phenomenon on the limiting factors and therefore the carrying capacity of:
   - **a** tropical savannah (grassland) (2 marks)
   - **b** flood plains and billabongs. (2 marks)

Knowledge utilisation

5 Using a specific example, **discuss** how species composition in any particular ecosystem can change seasonally. (3 marks)

6 Cyclone Yasi was the largest cyclone to be recorded in Queensland history, crossing the coast near Mission Beach in 2011. **Investigate** the immediate and long-term effects on the biodiversity and carrying capacity of the area of the Great Barrier Reef that was damaged by cyclone Yasi. (4 marks)

Lesson 5.3
Ecological succession

Key ideas

- → Ecosystems are constantly changing, due to disturbance and succession.
- → Ecosystems may begin on bare rock or in the location of a destroyed ecosystem.
- → Ecosystems have distinct stages of succession, called seres, which are determined by the most abundant species present.
- → Pioneer species are resilient in harsh environments and can colonise barren environments.
- → Successional changes vary in different ecosystems, due to the specific biotic and abiotic factors present.

Learning intentions and success criteria

ecological succession
the gradual change in the species composition of an ecosystem over time

sere
an intermediate community in ecological succession in an ecosystem advancing towards its climax community

Primary succession

Ecological succession is the process of gradual evolution of an ecosystem. Many environments start with bare soil before being colonised by grasses. Over time, the grasses are replaced by a succession of larger plants and trees until the final, relatively stable, climax community is reached. Each of these community stages has recognisable characteristics and is termed a **sere**.

primary succession
the process of development and change in plant communities over time, leading eventually from bare ground to a climax community

pioneer species
species of plants that colonise bare ground

Primary succession is the process by which an ecosystem develops from bare surfaces, such as exposed rock. This occurs due to natural events, such as volcanic eruptions (e.g. the island of Rakata) or glacial retreat uncovering barren landscapes. It can also result from human activities, such as mining, which strip the land of vegetation and soil. Colonisation is initiated by the dispersal, usually by wind, of spores or seeds of hardy autotrophs (**pioneer species**). These autotrophs can survive in areas where limiting factors often include very high light intensity, and low water-holding capacity of the soil due to a lack of organic matter. These plants therefore have one or more of the following features:

- can tolerate extreme conditions
- photosynthesise
- have rapid spore or seed germination
- use wind pollination and/or dispersal of spores or seeds
- can fix nitrogen from the air
- in the case of opportunists or *r*-strategists that disperse rapidly, have a large number of offspring and a short life cycle.

FIGURE 1 Lichens are the first species to start breaking down rocks.

FIGURE 2 Worms are major contributors to the formation of soil.

Lichens (Figure 1) consist of fungi and photosynthetic algae in a mutualistic relationship, and are often the pioneer species of bare rock. A product of their metabolism is an acid that may cause the rock to become eroded. Temperature differences (day and night, or seasonal) cause expansion and contraction of rocks, creating cracks and fragmentation. As the lichens age and die, decomposing bacteria break down small amounts of organic matter that collect in rock cracks, which begins the formation of soil.

The gradual build-up of soil makes these places unsuitable for rock-dwelling lichens, but suitable for colonisation by mosses. Further soil enrichment is provided by the decomposition of the mosses as they in turn die. Over time, more complex plants that require deeper soil beds are able to grow, progressing from ferns to grasses, to shrubs, to small trees and finally a forest. At each successive change in vegetation type, the replacement plants are better able to compete for resources than their predecessors. The larger shrubs and trees that begin to dominate the area are *K*-strategists that may release chemicals to prevent the germination of their seeds in close proximity. This decreases competition for light, nutrients and water and increases life expectancy.

As the vegetation in an area changes, so too does the animal life. Bacteria, decomposer fungi and worms become

more abundant in the ever-deepening soil. Insects and birds aid dispersal and pollination of flowering species of plants. Denser vegetation also provides habitats for reptiles and mammals. Over time, the bare rock becomes covered in increasingly deep soil that supports a growing biodiversity of organisms and increases the overall amount of biomass in the ecosystem.

Succession also occurs on sand and coral islands. The area near the sea, just above high tide level, is not an easy place for plants to live. Salt spray is blown onto them by the wind, and fresh water is in short supply. The sand is unstable, unable to retain water and tends to move with wind action. A few plants can cope with these conditions and begin to colonise the area. These pioneer plants include the grass *Spinifex hirsutus*, which sends out runners, and the prostrate creeper *Ipomoea pes-caprae*. The seed heads of the spinifex grass form large round bundles that are rolled by the wind, and so disperse the seed. Once established, the pioneer plants trap wind-blown sand around them and the dune begins to build up and stabilise.

FIGURE 3 *Ipomoea pes-caprae*, more commonly known as bayhops or goat's foot, is often one of the first to colonise sandy dunes.

Stabilised areas out of direct contact with sea water can support other plant species, such as *Pandanus*, *Casuarina*, stunted wattles and banksias. These plants increase the humus layer of the sand, and the soil is better able to retain moisture. Wattles, through their symbiotic nitrogen-fixing bacteria, also add nitrogen to the soil. Blade grass (*Imperata cylindrica*), couch and vines such as *Hibbertia scandens* form ground cover in these areas.

Animals living in and on these plants add to the nutrient value of the soil, through their excretions and decomposition when they die. With further increases in humus, and therefore water retention, other plants such as heath and forest species can grow. The community inland will depend upon general climatic conditions, the humus build-up in the soil and the seeds dispersed by birds, ocean currents and wind.

Climax community

During succession, each stage changes the abiotic and biotic conditions of the environment. This paves the way for another species to colonise the area through dispersal from an adjoining area. For example, larger plants cast shadows that cause subtle changes in temperature, moisture and light in some parts of the community. These slight differences result in the formation of **microenvironments**, which support some species but not others. Eventually, a relatively stable, complex community is reached. This community of organisms has reached an equilibrium, where the populations and overall biomass do not vary a great deal. Usually a particular plant, the **dominant species**, is prevalent. This stage is termed the **climax community**, because it tends to remain much the same over long periods of time. Forests that have developed in this way are termed **primary forests**.

microenvironment
an area within a general habitat with specialised environmental conditions, e.g. a hollow log

dominant species
the most common species in a community

climax community
a relatively stable plant community

primary forest
a climax forest formed through primary succession

Secondary succession

secondary succession
successive, natural changes in plant communities in an area where a previous community has been removed

secondary forest
a climax forest formed through secondary succession

Primary succession starts with bare rock and is the first to colonise an area. **Secondary succession** is the "second time" the area has been colonised as a result of disturbance. When the dominant species of a plant community is removed (e.g. by natural disasters such as fire, disease or violent storm activity, or by interference from humans) and the area is left to natural interactions, secondary succession will occur.

Abandoned grazing land will become overgrown with weeds and small shrubs, and trees such as wattles. Eventually the wattles will be replaced by the climax open forest community. Secondary succession is invariably faster than primary succession because there are already soil, plants and animals in the area being colonised. Forests formed as a result of secondary succession are called **secondary forests**.

Real-world biology

Colonisation of Rakata

In a series of violent volcanic eruptions in 1883, much of the island of Krakatoa (between Sumatra and Java, Indonesia) was destroyed. All life on the remainder (now called Rakata) and nearby islands was buried under a deep layer of hot ash and pumice stone. In 1930 a new volcanic island arose from the sea nearby. Because it originated from the sunken crater of Krakatoa, it was named Anak Krakatoa (Krakatoa's child).

FIGURE 4 An artist's impression of Krakatoa erupting in 1883

These two islands have been the subject of considerable investigation because they provide natural "laboratories" for observing colonisation of bare land, relatively free of human interference.

On Rakata, the first plants to become established in the volcanic ash were grasses. The seeds could have been blown by wind from Sumatra or Java, or accidentally carried by birds (attached to their legs or feathers). By 1930, much of the grassland had been replaced by she-oak woodland and trees of the open forest. In parts of the forest, the canopy (upper leafy layer) was beginning to close over as a result of colonisation by new tree species. A closed canopy is typical of rainforest. Light penetration to the forest floor is obscured by the heavy foliage of these trees, limiting the growth of plants (grasses, herbs and shrubs) in these areas.

By 1980, however, the extent of the closed forest was still limited. The animal life on the island, too, is restricted to those that can cross the water. Therefore, insects, birds, bats and a few reptiles (presumably crossing to the island on organic debris) form the nucleus of the island fauna. Their survival on the island is dependent on the availability of suitable resources.

Apply your understanding

1 **Determine** whether the colonisation of Rakata is an example of primary or secondary succession. (1 mark)
2 **Describe** the role of birds throughout the stages of succession. (2 marks)
3 **Explain** the successional changes of plant species on Rakata in terms of abiotic factors, reproductive strategies and biomass. (3 marks)

Disclimax communities

A **disclimax community** results from degradation of a community due to activities of organisms. Typical of this process are the changes resulting from overgrazing of natural grassland. As grasses are depleted, the water cycle (evaporation from plants, condensation and rain) is disrupted, and the area becomes even more arid than normal. The grasses have soil-binding roots, which aid in preventing wind and water erosion. As the grasses decrease, erosion increases, and this accelerates the change. Ultimately, only desert plants can survive in the artificially stable area. Grazing practices in Australia have resulted in this country having the highest rate of **desertification** in the world.

disclimax community
the final community formed after succession as a result of degrading environmental factors

FIGURE 5 Overgrazing causes significant land degradation and ultimately desertification.

desertification
the formation of desert conditions, usually resulting from overgrazing of susceptible areas

Challenge

Coastal dunes – succession or zones of environmental difference?

The diagram in Figure 6 is a profile of the shoreline from a beach to the vegetation behind the dunes, showing zonation. These zones are often described as illustrating the stages of succession through which the vegetation behind the dunes would have passed during its development. Other scientists claim that these zones merely reflect different environmental conditions that exist due to gradients in salinity, wind, availability of fresh water, and erosion from storms, as distance from the surf increases.

Appraise each viewpoint of the formation of sand dunes and **decide** what further evidence would be required to determine which viewpoint is correct. (3 marks)

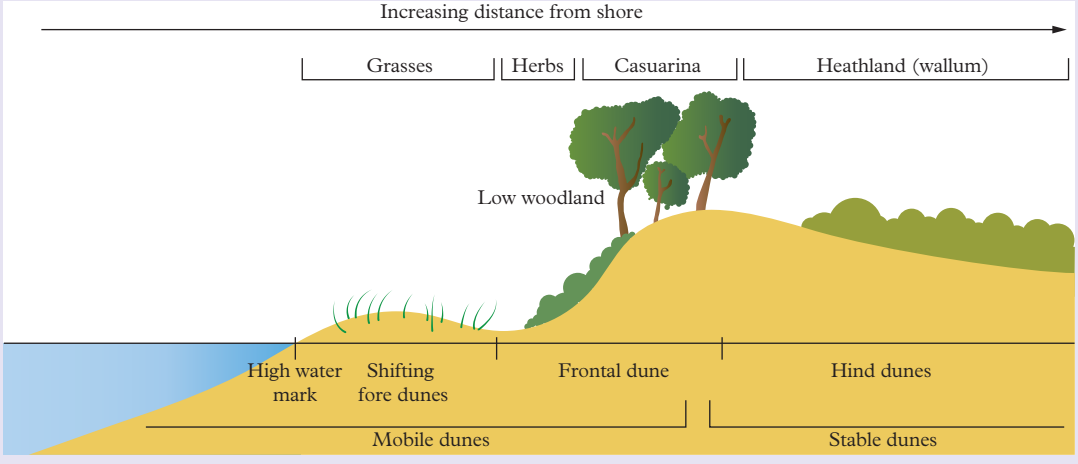


FIGURE 6 Profile of the shoreline from a beach to the vegetation behind the dunes, showing zonation

Check your learning 5.3

Check your learning 5.3: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the following terms: (1 mark each)
   - **a** pioneer species
   - **b** sere
   - **c** climax community
   - **d** disclimax community
   - **e** primary succession
   - **f** secondary succession.

2 **Identify** the adaptations that are an advantage to pioneer species, including lichen. (7 marks)

3 **Explain** why succession will continue at a sere unless there is distubance. (1 mark)

Analytical processes

4 **Determine** why being an *r*-strategist would be an advantage for a pioneer species but not for a plant in a climax community. (2 marks)

5 **Compare** primary and secondary succession. (2 marks)

Knowledge utilisation

6 The highest biodiversity in an ecosystem has been found to occur in areas with an intermediate level of disturbance. **Discuss** why these areas are more diverse than areas that sustain constant disturbance and areas that remain undisturbed for long periods of time. (3 marks)

Lesson 5.4
Comparing ecosystems across spatial and temporal scales

Key ideas

- → Ecosystems vary across spatial scales as a result of the variation of abiotic factors.
- → Ecosystems vary throughout temporal scales due to successional changes.
- → Fossils and ice cores provide evidence used to compare ecosystems over long periods of time.

Learning intentions and success criteria

temporal scale the time period in which an event or process occurs

Temporal scales

Because ecosystems are dynamic entities, we can assume that they have changed dramatically over Earth's long history. Scientists study change in ecosystems over different **temporal scales** (time periods). Short-term changes occur due to disturbances over days or years (described in Module 5.3) and can be observed through changes in the environment. Long-term changes occur over thousands of years, and are observed through fossils and ice cores. Earth has experienced periods of climate change with dramatic alternations between global cooling (periods of glaciation) and warming (interglacial periods). It has been subjected to large meteor damage, resulting in mass extinctions over a large scale, and volcanic activity in which everything in the vicinity of the eruption and lava flow is killed. Scientists have devised ways to measure some abiotic and biotic changes that have occurred in the past.

The length and severity of glaciation events can be determined, for example, from carbon dioxide levels in the ice of the polar ice caps. As snow falls, it traps atmospheric carbon dioxide. The snow compacts as ice and, like the growth rings of a tree, forms a layer corresponding to each season of snowfall. By taking core samples of polar ice, scientists can determine:

- the age of each layer
- the depth of each layer and thus the duration of the extreme cold period
- the level of carbon dioxide in each layer – the higher the global temperature, the more carbon dioxide in the atmosphere.

Similar techniques are used when examining deep-sea sediments. Two slightly different forms of oxygen (isotopes) exist: ^{16}O and ^{18}O. ^{18}O has two more neutrons than ^{16}O and so it is a little heavier. Because ^{16}O is lighter, it evaporates more easily from the oceans, particularly during cold phases. Analysis of the ratio of ^{18}O to ^{16}O in deep-sea sediments therefore gives a strong indication of climate variations. If ^{18}O is higher, it indicates that a cold period occurred when ^{16}O was able to evaporate. In contrast, a higher ^{16}O (compared to ^{18}O) indicates that warmer temperatures occurred during that period.

FIGURE 1 Analysing sediments: (A) a scientist taking ice core samples and (B) International Ocean Discovery Program (IODP) drilling for sub-seafloor sediments

These changes in climate also affected the different species of plants and animals growing and reproducing during that time. The fossilised remains or traces of organisms that existed during that period can also provide an indication of how the ecosystem has changed. The presence or absence of particular species can provide more evidence of the components of an ecosystem. Because all organisms depend upon other organisms, either directly or indirectly, the presence of particular fossils at a site provides good evidence of other organisms that were able to survive in the environment. Unfortunately, fossil records are inherently incomplete, because the conditions for fossil formation are not uniform in any environment. Fossils are found in areas where, on death, the organisms' remains are protected from predatory consumption or bacterial decomposition. Boggy marshes, floodplains or estuaries, where the remains are rapidly covered by silt and where oxygen is limited, are significant areas of preservation. As silt accumulates over the fossils, the remains become deeper and deeper. Generally, the further the fossil is from the surface, the older it is. Places that have rapid burial events, such as landslides, are also good fossil preservation locations.

Pollen grains and spores are produced in large quantities and are extremely resistant to decay. Pollen can accumulate on any undisturbed surface and has been found in sediments from peat bogs, lake beds, alluvial deposits and ocean bottoms, and in ice cores. The actual amount of pollen or spores found in an area may not be indicative of the relative abundance

of the plant, because different species produce different amounts of pollen, or the pollen has different dispersion rates.

The pollen grain of each species has a unique size and shape (Figure 2). Scientists can therefore analyse core samples of sediments to determine the exact species that existed in that area at any particular time. Using pollen grain analysis, vegetation maps of an area can be produced that show changes over hundreds of thousands of years. Comparison with recent trends in vegetation can also assist in determining the impact of human activities on ecosystems.

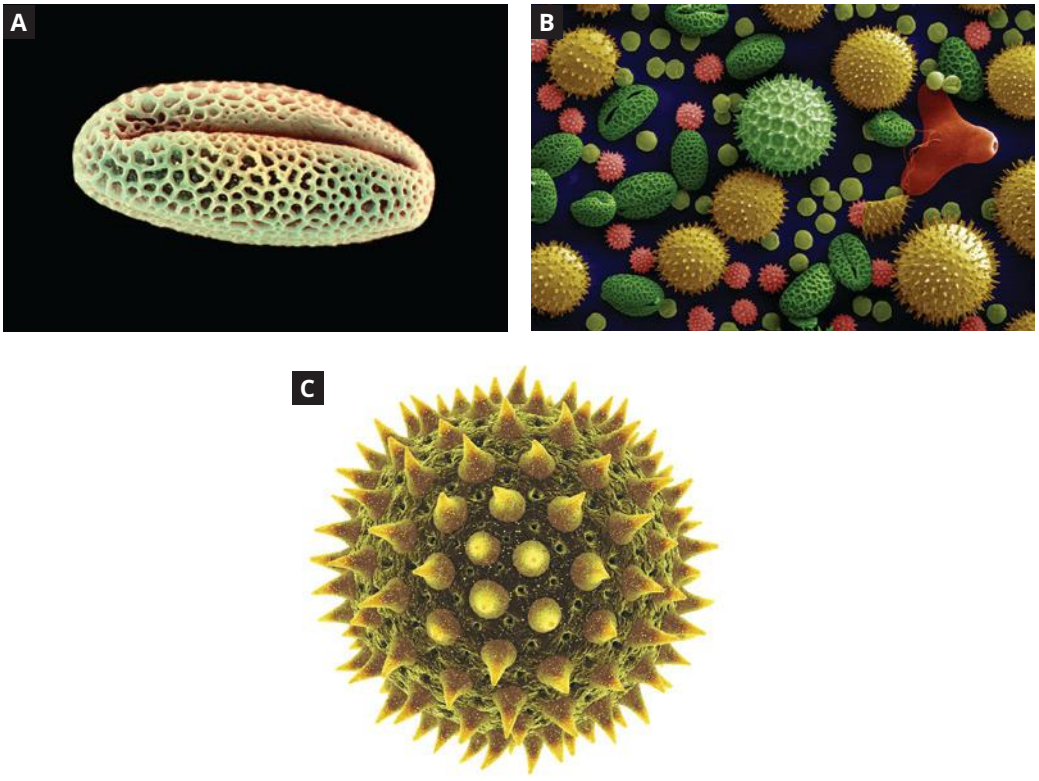


FIGURE 2 Pollen grains for individual species of plants have unique features that enable plant identification.

A deep core soil/rock sample taken from a mature dry forest may reveal that the area was once a deep lake that gradually became filled with silt. The fossilised plant remains would have progressively changed from floating forms to submerged species as the water level decreased. With further loss of water, the fossils would indicate a prevalence of plants at the edges of waterways – spores of mosses and ferns, and seeds of sedges. Higher strata would show progression from herbs and grasses to shrubs and then a series of trees until the most recent community is achieved.

Fossil samples (pollen, cupules that hold the fruit, and leaves) of the southern beech (*Nothofagus* sp.) have been found in South America, southern and eastern Australia, New Guinea, New Zealand, New Caledonia and Antarctica. The pattern of distribution suggests that the spread of the genus occurred before Gondwana separated into Antarctica, South America and Australasia and that the trees were more widely dispersed than they are currently.

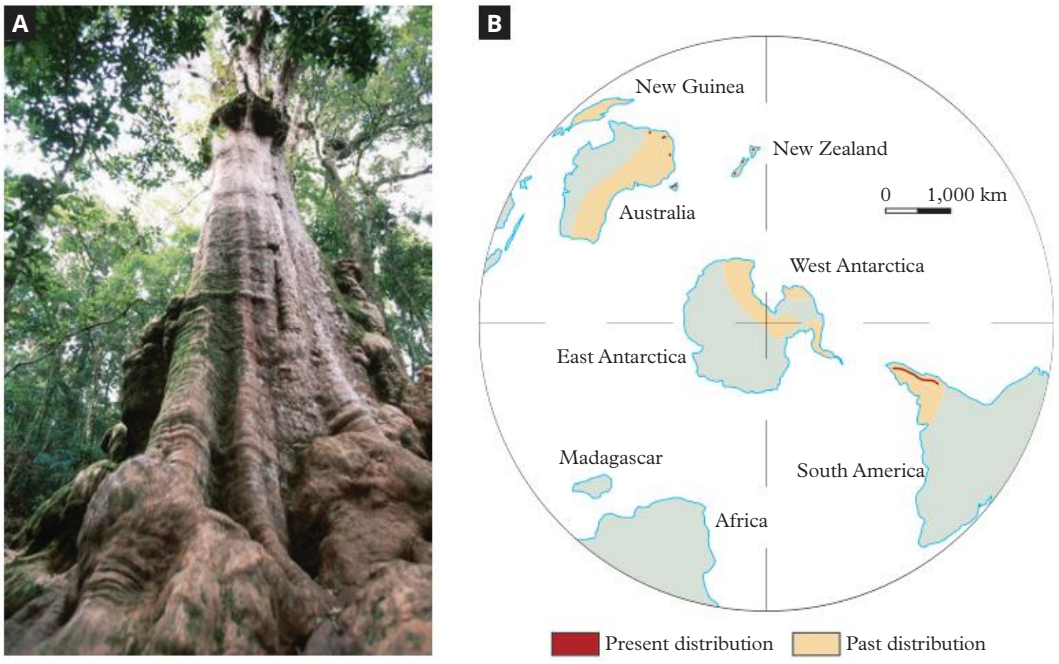


FIGURE 3 *Nothofagus* distribution: (A) *N. moorei* on the southern edge of the Lamington Plateau, south-eastern Queensland; (B) past and present distribution of *Nothofagus*

Although the southern beech is now only found in isolated pockets in cool, high-altitude environments in tropical and subtropical regions (e.g. *N. moorei* at the southern edge of the Lamington Plateau in south-eastern Queensland, *N. gunnii* in Tasmania and *N. nitida* in the southern regions of South America), the fossil record shows that in the past it survived in warmer climates than those it now occupies.

Spatial scales

As well as temporal scales, ecosystems can be compared over **spatial scales**. Ecosystems may be considered at different scales:

spatial scale
the size of an area at which an event or process occurs

- local (e.g. a lake or a mountain)
- regional (e.g. a forest)
- continental
- global.

This allows scientists to better understand the cause and effect of changes in ecosystems at each level. Ecosystems at the local and regional levels are small enough to be studied directly, through experimentation to investigate the underlying factors that lead to change. At the continental and global levels, patterns are observed, because experimentation is not feasible. A number of drivers determine the ecosystems and biodiversity that play a role at these different levels. At larger spatial scales, the main drivers of ecosystem types are climate and geodiversity (the variation of abiotic features and processes on Earth). At smaller scales, previous land use, variation between different populations of the same species, and frequency of disturbance, have a more significant impact on the biodiversity of an ecosystem.

At the local and regional levels, metrics of biodiversity and ecosystem classification (discussed in Module 2) can be used to compare ecosystems. At the continental and global levels, models demonstrating patterns of change in abiotic factors, such as temperature, elevation, soil types and geological age, are considered.

Skill drill

Investigating temporal ecosystem change

Science inquiry skill: Lesson 1.7 Processing and analysing data

The data in the graph (Figure 4) comes from the ice core pollen record from Ellesmere Island in Canada. Pollen counts in ice cores provide information about the vegetation in the surrounding ecosystems as the pollen is trapped in the layers of ice.

Practise your skills

1 **Identify** the trends shown in the data set. (3 marks)
2 **Deduce** changes in the surrounding ecosystems over the past 11,500 years. (2 marks)

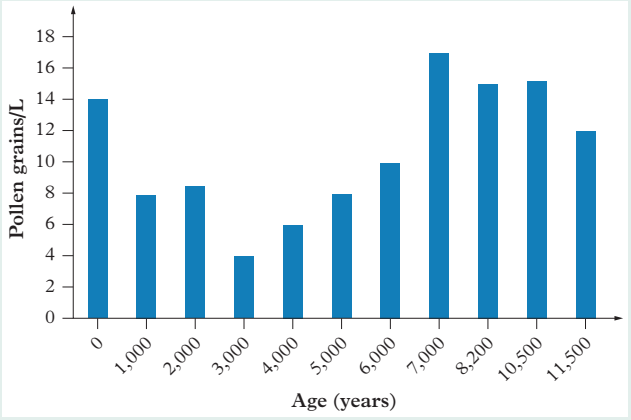


FIGURE 4 Pollen counts per litre in ice core samples collected from Ellesmere Island, Canada

Check your learning 5.4

Check your learning 5.4: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Explain** why global temperature changes bring about changes in ecosystems. (2 marks)
2 **Recall** two ways that scientists can determine past global temperatures. (2 marks)
3 **Describe** the features of pollen and spores that make them good indicators of past ecosystems. (2 marks)
4 **Explain** why disturbance frequency is not considered when comparing ecosystems at the continental or global level. (2 marks)
5 **Identify** two measures of biodiversity and two ecosystem classification systems that could be used at the local level. (4 marks)

Analytical processes

6 Fossils collected from Riversleigh in western Queensland indicate that the area has changed from humid, lowland rainforests during the Oligocene period (33.9 million to 23 million years ago), to dry eucalypt forests and woodlands of the Miocene (23 million to 5.3 million years ago), and dry grasslands of the Pleistocene (2.58 million to 11,700 years ago). **Determine** the environmental changes that are likely to have led to this shift in the organisms in the Riversleigh area. (2 marks)

MODULE 5

Lesson 5.5
Review: Succession

Summary

5.1
- Overexploitation and habitat destruction have a direct impact on community structure and ecosystem function.
- Human-made monocultures reduce biodiversity by decreasing the complexity of a region.
- Human pollution has the potential to affect both local and distant ecosystems.

5.2
- Climatic changes alter the abiotic factors within an ecosystem and influence the carrying capacity.
- Food availability, predation and disease affect the carrying capacity of an ecosystem.

5.3
- Ecosystems are constantly changing due to disturbance and succession.
- Ecosystems may begin on bare rock or in the location of a destroyed ecosystem.
- Ecosystems have distinct stages of succession, called seres, which are determined by the most abundant species present.
- Pioneer species are resilient in harsh environments and are able to colonise barren environments.
- Successional changes vary in different ecosystems due to the specific biotic and abiotic factors present.

5.4
- Ecosystems vary across spatial scales as a result of the variation of abiotic factors.
- Ecosystems vary throughout temporal scales due to successional changes.
- Fossils and ice cores provide evidence that can be used to compare ecosystems over long periods of time.

Review questions 5.5A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

Use the following information to answer questions 1 to 3.

In 1883, a volcanic explosion removed all life from the island of Krakatoa, near Java in East Indonesia. After only three months, 11 species of ferns and 15 species of flowering plants had returned. Ten years later, there were 263 species of animals on the island, mainly insects. Less than 50 years after the explosion, the whole island was covered in dense forest.

1 The above paragraph is a description of
- **A** evolution.
- **B** succession.
- **C** a community.
- **D** an ecosystem.

2 Which of the following factors would not influence the rate at which organisms reappeared on the island?
- **A** ocean tides
- **B** temperature
- **C** spontaneous generation
- **D** the distance from another island

3 The first organisms to reappear on the island were plants. Identify which of the statements below helps to explain this.
- **A** Plants are able to make their own food.
- **B** Seeds and spores are easier to disperse than animals.
- **C** If animals reached the island first, they would die from lack of food.
- **D** All of the above.

4 The climax stage of a biotic succession
- **A** is the stage in which trees are always dominant.
- **B** is the first stage in the reclamation of land from a lake bottom.
- **C** persists until the environment undergoes a significant disturbance.
- **D** changes rapidly from time to time, seldom remaining at any stage for more than a decade or so.

5 Which of the following is not a characteristic of a pioneer species?
- **A** able to absorb nutrients
- **B** rapid growth and reproductive rate
- **C** able to disperse over long distances
- **D** able to outcompete established species for resources

6 The effects of an algal bloom in waterways are collectively called
- **A** eutrophication.
- **B** decomposition.
- **C** nutrient recycling.
- **D** biological magnification.

7 The most serious threat to native animals from human activity is
- **A** bushfires.
- **B** off-road vehicles.
- **C** clearing of their native habitat.
- **D** hunting of animals for pelts and pet food.

8 The relationship between nutrient availability and carrying capacity is that
- **A** as nutrient availability increases, carrying capacity increases.
- **B** as nutrient availability increases, carrying capacity decreases.
- **C** carrying capacity remains the same, regardless of nutrient availability.
- **D** carrying capacity increases with nutrient availability, until certain nutrients reach toxic levels.

9 Primary succession can be described as
- **A** the re-establishment of vegetation after a forest fire in an area with existing soil.
- **B** the process by which an ecosystem recovers after a disturbance in an established community.
- **C** the rapid growth of plant life in an area following a volcanic eruption, facilitated by human intervention.
- **D** the gradual process of change in an ecosystem that occurs in an area where no soil or living organisms previously existed.

10 The usual effect of disease on the carrying capacity of an ecosystem is that
- **A** disease has no impact on carrying capacity.
- **B** disease decreases the carrying capacity by increasing the death rate of the species.
- **C** disease temporarily increases the carrying capacity by reducing competition among species.
- **D** disease increases the carrying capacity by eliminating weaker individuals and strengthening the population.

Review questions 5.5B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

11 **Explain** this statement: "Ecological succession cannot occur without dispersal." (1 mark)

12 **Explain** how altitude can affect an ecosystem. (1 mark)

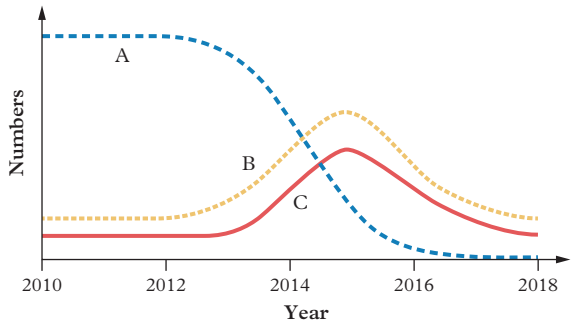
13 **Define** secondary succession. (1 mark)

14 **Describe** the changes that occur in an ecosystem during different seasons. (2 marks)

15 **Describe** how ice cores can be used to determine past ecosystems. (2 marks)

16 In the early settlement of Brisbane in the nineteenth century, most of the Big Scrub along the Brisbane River was heavily logged. The blackbean, silky oak, red cedar and most eucalypt trees were used for construction as the settlement grew. Mangroves were burnt for their ash, to produce soap. Similarly, most of the lowland areas were cleared for farming. Over time, much of this land was deemed unproductive and farming ventures were abandoned. Just over 100 years later, most of these areas that are not part of urban development are covered in well-established secondary dry sclerophyll forests. **Explain** why they are called secondary forests, the process of their formation and why forests returned after such a short time period. (3 marks)

17 The following graph displays population numbers for three organisms: an alga, a fish and a herbivore that eats algae. In 2012, hot water was emptied into the river, and in 2014 there was pollution from a chemical factory. **Identify** the organism that each line (A, B and C) represents, giving reasons for your choice. (6 marks)



Analytical processes

18 **Critique** whether any natural ecosystem can be isolated from other ecosystems. Provide examples in your response. (3 marks)

Knowledge utilisation

19 The CSIRO has observed bushfire and flood events in Australia over the past 30–50 years. Given the effect of these climatic events on carrying capacity, **discuss** how these phenomena may affect Australian ecosystems. (2 marks)

20 Many amateur conservationists believe that a climax community is the final, best adapted community in an area. Any changes to the area are opposed for fear that the species composition will not be preserved.

a **Evaluate** whether these fears are justified. (2 marks)

b **Determine** whether the amateur conservationists' premise of a climax community is correct. (1 mark)

21 One of the biggest problems facing the Wildlife Conservation Society of Tanzania is the naturalisation of a black wattle (*Acacia mearnsii*).

As a means of boosting a poor economy, farmers were encouraged to develop plantations of these low trees on the many plateaux (about 2,000 m altitude) in the area. The trees are an important source of tannins (chemicals in the bark, used in tanning leather), construction timber and charcoal. Experience in South Africa, however, showed that this species rapidly escaped the plantations. Because they were more competitive in obtaining water than indigenous tree species, they readily took over large areas; they have now been declared a noxious weed, and the cost of eradication is very high.

Wildlife officers have noticed a similar trend in southern parts of Tanzania. Faced with an ailing economy, and because the plantations are financially lucrative, the government is reluctant to ban the cultivation of the black wattle.

Generate a scientific report to the government to convince it that short-term gains could lead to long-term crippling of the economy if it does not reverse its current policy. As part of your argument, **generate** a list of the broad environmental effects of replacement of native vegetation on the plateaux by an invading monoculture. (6 marks)

22 **Investigate** the effects of agricultural run-off on the corals of the Great Barrier Reef. Tabulate your findings under these headings:

- Types of run-off
- Effects on coral organisms
- Effects on other reef organisms.

Generate a short report using this data to predict the long-term effects on this significant ecosystem if changes to current agricultural practices are not implemented. Taking natural climatic factors into account, **predict** some changes that could reduce this problem. (5 marks)

Data drill

In 2015, the gates of the Leslie Harrison Dam were removed, after being in use since 1984. A study was conducted to observe the successional stages of vegetation in an area of the dam that was exposed by the lowered water level. The data is shown in Table 1.

Apply understanding

1 **Identify** this successional process as primary or secondary. (1 mark)

2 **Determine** whether this ecosystem has reached carrying capacity. (1 mark)

Analyse data

3 **Identify** the trend observed in tree foliage coverage from 2020 to 2024. (2 marks)

Interpret evidence

4 **Infer** a reason for the decrease in foliage height and coverage in the July 2017 data. (1 mark)

TABLE 1 Survey results of vegetation within a region of the exposed land after the removal of the Leslie Harrison Dam gates in 2015

Date	Dominant plant type	Foliage height (m)	Foliage coverage (%)
Jul 2015	Grass	0.15	60
Dec 2015	Grass	0.3	70
Mar 2017	Grass	0.3	85
Jul 2017	Grass	0.2	65
Jun 2019	Shrub	3.0	30
Mar 2020	Trees	5.0	40
Feb 2021	Trees	6.0	45
Aug 2022	Trees	6.5	50
Oct 2023	Trees	7.0	50
Jun 2024	Trees	7.0	50

Module 5 checklist: Succession

UNIT 3

Topic 2 review

Multiple choice

(1 mark each)

1 Overexploitation affects
- **A** the entire ecosystem.
- **B** only the overexploited species.
- **C** the overexploited species and their predators.
- **D** the overexploited species, their predators and their prey.

2 During rain events, fertilisers may run off agricultural land and be transported into aquatic environments, causing eutrophication. This phenomenon impacts aquatic environments by
- **A** improving water quality, which promotes plant growth.
- **B** enhancing biodiversity, due to the increased nutrient availability.
- **C** causing an unsustainable algal bloom, which dies off and depletes oxygen as it decays.
- **D** increasing photosynthesis, leading to increased oxygen levels, which promotes fish growth.

3 How does oxygen availability influence the carrying capacity of an aquatic environment?
- **A** Higher oxygen levels reduce the carrying capacity by supporting fewer species.
- **B** Oxygen availability has no impact on the carrying capacity of aquatic environments.
- **C** Lower oxygen levels increase the carrying capacity by limiting predator populations.
- **D** Higher oxygen levels increase the carrying capacity by supporting more diverse and abundant life.

4 A sere can be defined as
- **A** a distinct intermediate stage of ecological succession.
- **B** a temporary ecosystem that forms after a natural disaster.
- **C** a community of species that exists in a human-made environment.
- **D** a type of habitat that remains unchanged over a long period of time.

5 Primary succession occurs when
- **A** an ecosystem forms in a previously barren area.
- **B** an ecosystem remains undisturbed for a long period of time.
- **C** a pioneer species is outcompeted by the second sere species.
- **D** an existing ecosystem is disturbed by a climatic event or human impact.

6 Identify the characteristic that makes lichen the most common pioneer species in primary succession.
- **A** its ability to photosynthesise
- **B** its ability to live on bare rock
- **C** its ability to reproduce quickly
- **D** its tolerance of harsh conditions

7 With reference to species interactions, successional change occurs in an ecosystem
- **A** independently of species interactions and is driven solely by abiotic factors.
- **B** because late-successional species eliminate early colonisers through predation.
- **C** because pioneer species outcompete all other species, preventing further successional changes.
- **D** because early colonising species modify the environment, making it more suitable for other species that outcompete them.

8 Which of the following organisms are primarily responsible for recycling nutrients back into the ecosystem?
- **A** producers
- **B** herbivores
- **C** decomposers
- **D** keystone species

9 The maximum population that can be sustained by an ecosystem is called its
- **A** logistic growth.
- **B** biotic potential.
- **C** carrying capacity.
- **D** exponential growth.

10 Which of the following processes converts energy in the form of radiation to stored chemical energy in ecosystems?
- **A** decomposition
- **B** photosynthesis
- **C** nitrogen fixation
- **D** aerobic respiration

11 Plants produce ATP energy for cellular processes through which set of reactions?
- **A** denitrification
- **B** decomposition
- **C** photosynthesis
- **D** aerobic respiration

12 In the nitrogen cycle, denitrification is the process responsible for
- **A** converting nitrogen gas to nitrates.
- **B** returning nitrogen gas to the atmosphere.
- **C** converting ammonia to nitrite and then nitrate.
- **D** making nitrogen bioavailable for uptake by plants.

13 Which of the following statements about the carbon cycle is correct?
- **A** Carbon dioxide is used by plants for respiration.
- **B** Decomposition is not a part of the carbon cycle.
- **C** Mangroves use carbon dioxide for anaerobic respiration.
- **D** The largest carbon storage reservoir on Earth is the ocean.

14 Exponential growth of the population of a species is best represented by which shape on a graph?
- **A** straight line
- **B** J-shaped curve
- **C** S-shaped curve
- **D** normal distribution

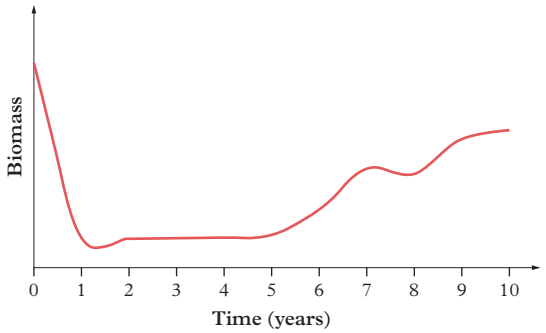
15 Fossil fuels are stores of which important resource for humans?
- **A** water
- **B** carbon
- **C** nitrogen
- **D** fossil evidence

Short response

16 According to the CSIRO, the frequency of cyclones in Australia has decreased since 1900.
- **a** **Identify** the three main abiotic factors affecting carrying capacity on the Great Barrier Reef that would be impacted by a cyclone. (3 marks)
- **b** **Determine** whether this trend would increase the abundance of *K*-strategists or *r*-strategists. (1 mark)
- **c** **Explain** how a decrease in cyclones will affect the biodiversity and carrying capacity of coral species on the Great Barrier Reef. (2 marks)

17 An area of pine plantation was harvested and the land was cleared by controlled fire. However, the land has been deemed unsuitable and will no longer be used as a plantation.
- **a** **Describe** the steps of succession that would take place if the land is left fallow. (3 marks)
- **b** **Identify** the type of ecological succession. (1 mark)

18 The graph shows the biomass of an ecosystem over time.



- **a** **Describe** the relationship between biomass and successional changes. (1 mark)
- **b** With relation to successional change, **infer** what caused the decrease in biomass between years 7 and 8. (1 mark)

19 **Contrast** the transfer and transformation of energy as it moves through an ecosystem. Provide an example of each. (3 marks)

20 **Contrast** logistic population growth and exponential population growth of species. (1 mark)

21 **Explain** why pioneer species are important in primary succession. (4 marks)

22 The image shows a bridge in Spain covered in a swarm of *Epheron virgo,* a species of mayfly. These mayflies spend most of their life cycle in their aquatic nymph and terrestrial larval stage, feeding on detritus and algae, and are therefore an important indicator of water quality in rivers and streams. Adults of the *Epheron virgo* species emerge simultaneously from their pupal stage and swarm in populations of millions, focused on breeding over a very short period of hours or days.

a **Identify** the reproductive strategy of the *Epheron virgo* mayfly. (1 mark)

b **Explain** the key characteristics of this reproductive strategy. (3 marks)

23 **Contrast** the reactants and products of photosynthesis. (1 mark)

24 **Explain** how carbon moves into and out of the atmosphere in the carbon cycle. (2 marks)

25 **Explain** how the abiotic factors of a rainforest ecosystem influence plant growth. (4 marks)

26 **Explain** why lions would become extinct if they employed an *r*-selected reproductive strategy rather than a *K*-selected reproductive strategy. (3 marks)

27 **Explain** the role of nitrogen fixation in plant growth. (2 marks)

28 **Describe** the process of photosynthesis in plants. (4 marks)

29 **Explain** how fossil fuels are formed on Earth. (3 marks)

30 Data was collected to compare temperate forests in south-eastern and south-western Australia, as shown in the table below.

a **Identify** which location is more diverse. (1 mark)

b **Compare** the two ecosystems in terms of dominant vegetation and abiotic factors. (4 marks)

c **Discuss** how the abiotic factors recorded may contribute to the differences between these two ecosystems. (4 marks)

Location	Average temperature (°C)	Average annual rainfall (mm)	Soil type	Elevation (m)	Dominant vegetation	Foliage height (m)	Number of species recorded
South-eastern Australia	15–20	800	Clay, loamy	250	Eucalyptus, acacia, ferns	10–15	120
South-western Australia	12–18	950	Sandy, gravel	150	Eucalyptus, banksia, grass	8–12	110

TOTAL MARKS

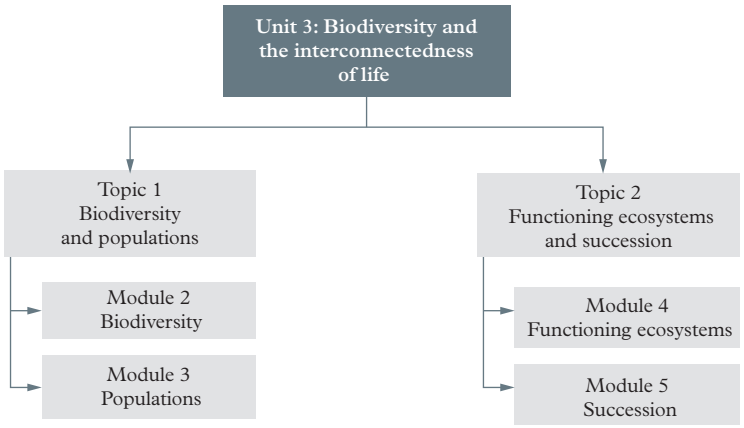
/67

UNIT 3

Review

Part A – Revisit and revise

Part A of the Unit review asks you to reflect on your learning and identify areas in which you need more work.



Part B – Exam essentials

Now that you've completed your revision for Unit 3, it's time to learn and practise some of the skills you'll need to answer exam questions like a pro! Our expert authors have created the following tips and advice to help you maximise your results on the end-of-year examination.

Exam tip 1: Don't just show your working – check your working

Students are always reminded to show their working in mathematical questions, but checking your working is equally important. If you have time after you have finished all the questions in the exam, go back through and check your working. A missed step or an error in your working could cost you a mark.

See it in action

Read the exam question below and the two responses on the following page. See how the tip has made a difference between a response that has scored full marks and a response where marks have been lost.

QUESTION 12 (5 marks)

An investigation compared mangrove species diversity for two areas of different size in the same catchment.

The table shows species population counts for each area.

	Species	Area 1	Area 2
Total species count	Grey mangrove	37	7
	Red mangrove	32	3
	Yellow mangrove	25	88
	SDI	0.67	?

a) Calculate Simpson's diversity index for Area 2. Show your working. *[2 marks]*

$SDI = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$

SDI = _____ (correct to two decimal places)

Source: *QCAA Biology 2021, Paper 2* © State of Queensland (QCAA)

Complete response

$$SDI = 1 - \left(\frac{7(7-1) + 3(3-1) + 88(88-1)}{98(98-1)}\right)$$

$$= 1 - \left(\frac{7 \times 6 + 3 \times 2 + 88 \times 87}{98 \times 97}\right)$$

$$= 1 - \left(\frac{42 + 6 + 7656}{9506}\right)$$

$$= 1 - \left(\frac{7704}{9506}\right)$$

$$= 1 - 0.81$$

$$= 0.19$$

Shows substitution correctly performed [1 mark]

Determines SDI = 0.19 [1 mark]

Incomplete response

$$SDI = 1 - \left(\frac{7(7-1) + 3(3-1) + 88(88-1)}{98(98-1)}\right)$$

$$= 1 - \left(\frac{7 \times 6 + 3 \times 2 + 88 \times 87}{98 \times 97}\right)$$

$$= 1 - \left(\frac{42 + 6 + 7656}{9506}\right)$$

$$= \left(\frac{7704}{9506}\right)$$

$$= 0.81$$

Shows substitution correctly performed [1 mark]

Student has forgotten to subtract this value from 1 in this line of the equation, so final value for SDI is incorrect [0 marks]

Think like an assessor

To maximise your marks on an exam, it can help to think like a QCAA assessor. Consider how many marks each question is worth and what information the assessor is looking for.

Read the question below, and a student's response on the following page. Imagine you are a QCAA assessor and use the marking guide provided to mark the response.

QUESTION 4 (6 marks)

An ecologist investigated the species composition of mangrove trees in a natural mangrove forest and an adjacent 30-year-old planted mangrove forest.

Three 10 m-wide belt transects were sampled from inland to the sea for each of the forests, each covering 100 m on average and placed to cover various strata.

The species diversity of Forest A was determined using the Simpson's diversity index (SDI):

$$\text{SDI} = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$$

Species	Population count	
	Forest A (natural)	Forest B (planted)
Grey mangrove	91	77
Red mangrove	23	14
River mangrove	11	8
Orange mangrove	3	0
Diversity	0.46	?

a) Use the SDI formula to calculate the diversity index for Forest B. Round your answer to two decimal places. *[2 marks]*

SDI = 0.37

Source: *QCAA Biology 2020, Paper 2* © State of Queensland (QCAA)

Marking guide

Question 4a	Demonstrates correct substitution [1 mark] States that SDI = 0.37 [1 mark]

Fix the response

Consider where you did and did not award marks in the above response. How could the response be improved? Write your own response to the same question to receive full marks from a QCAA assessor.

Exam tip 2: Know your terminology

Biology introduces many new terms, and at times can feel like learning another language. Some of these terms are very similar – for example, "transcription" and "translation", or "meiosis" and "mitosis". When responding to external examination questions, it is essential that you understand the terminology of the questions. In the example below, students are asked to describe the "transformation" and "transfer" of carbon. Two marks are available for "transformation" and one mark is available for "transfer". If these two terms are mixed up, marks will be lost.

See it in action

Read the exam question below and see how the tip has made a difference between a response that has scored full marks and a response where marks have been lost.

QUESTION 22 (3 marks)

Describe two ways carbon is transformed and one way it is transferred as it cycles through the biotic components of an ecosystem.

Source: *QCAA Biology 2021, Paper 1* © State of Queensland (QCAA)

Complete response

States 1 transformation [1 mark]

Atmospheric carbon exists mainly as carbon dioxide, which is transformed from carbon dioxide gas to produce glucose (and other complex organic molecules) via photosynthesis. This also covers the transfer from atmosphere to plants by diffusion. Respiration transforms glucose into carbon dioxide.

States another transformation [1 mark]

States 1 transfer [1 mark]

Incomplete response

This is incorrect as it is a transformation of carbon, not a transfer of carbon. [0 marks]

Carbon is transferred from the atmosphere into plants through photosynthesis, and transformed from glucose into carbon dioxide by respiration. Carbon is transformed when decomposers eat decaying plant matter.

This is a correct transformation. [1 mark]

This is incorrect, as it is a transfer of carbon, not a transformation of carbon. [0 marks]

Think like an assessor

To maximise your marks on an exam, it can help to think like a QCAA assessor. Consider how many marks each question is worth and what information the assessor is looking for.

A student has given the following response in a practice exam. Imagine you are a QCAA assessor and use the marking guide below to mark the response.

QUESTION 1 (4 marks)

Explain how one abiotic and one biotic factor will affect the population of mosquito larvae in a freshwater pond.

A biotic factor that would affect population would be temperature.

An abiotic factor that would affect population would be the presence of a predator species.

Source: *QCAA Biology 2021, Paper 2* © State of Queensland (QCAA)

Marking guide

Question 1	• States a relevant abiotic factor [1 mark] • States a relevant biotic factor [1 mark] • Explains the effect of the identified relevant abiotic factor [1 mark] • Explains the effect of the identified relevant biotic factor [1 mark]

Fix the response

Consider where you did and did not award marks in the above response. How could the response be improved? Write your own response to the same question to receive full marks from a QCAA assessor.

Exam tip 3: Understand the data before attempting the question

It can be tempting to skim over data sets or diagrams and go straight into attempting a question. Sometimes this may work out, but often it leads to mistakes that could have been avoided and will cost you marks. A good strategy is to take the time to understand the data properly before reading the question or any of the options available. In the example on the next page, a graph is provided. Follow the steps below to ensure you understand it completely, before moving ahead.

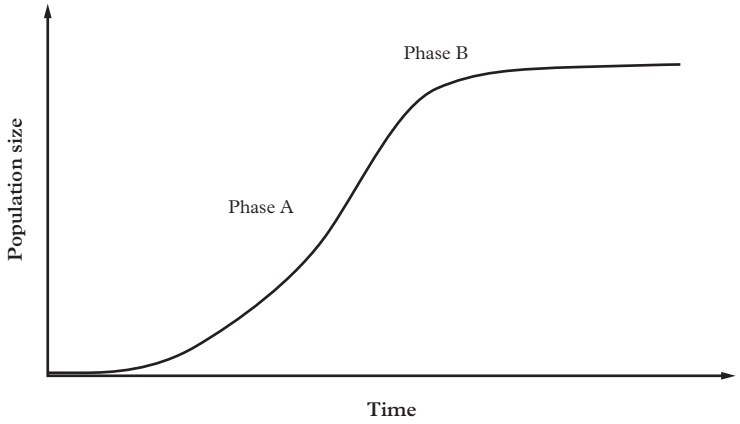
1. Read the axis labels – do you understand what the graph is depicting or measuring?
2. Read the question. It is asking you to refer to Phase A and Phase B and determine the population growth model. Consider the different types of growth models and their characteristic shapes. What do Phase A and Phase B represent in the graph in relation to population growth?
3. Now that you understand the graph and Phase A and Phase B, construct your answer.

See it in action

Read the exam question below and the two responses that follow. See how the tip has made a difference between a response that has scored full marks and a response where marks have been lost.

QUESTION 28 (3 marks)

The graph depicts the population change of a species after it is introduced into a previously disturbed environment.



Referring to Phase A and Phase B, determine the population growth model for the species.

Source: *QCAA Biology 2021, Paper 1* © State of Queensland (QCAA)

Complete response

Refers to the features of Phase A [1 mark]

In Phase A, the population is low and resources are plentiful, maximum growth rate is observed and births consistently outnumber deaths. In Phase B, birth and death rates become balanced as the population reaches carrying capacity. The curve of the graph and phases depict an s-curve characteristic of logistic growth.

Refers to the features of Phase B [1 mark]

Determines population growth model as logistic [1 mark]

Incomplete response

The student has mentioned that Phase A occurs before Phase B but does not provide enough information on what the phases represent in relation to population growth. [0 marks]

Phase A occurs before Phase B and the population growth model is logistic.

Determines population growth model as logistic [1 mark]

Think like an assessor

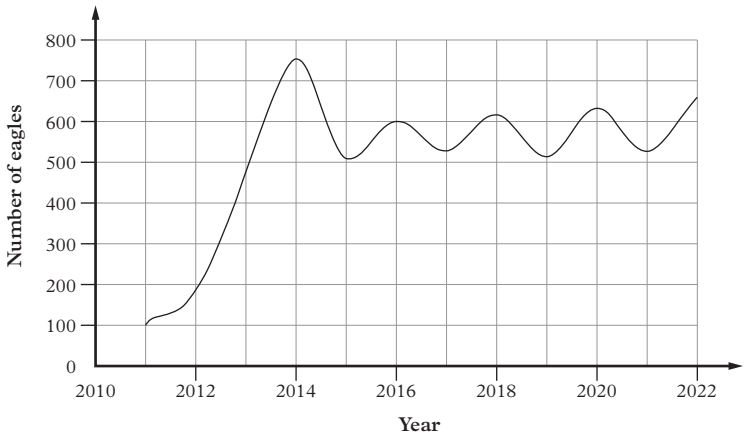
To maximise your marks on an exam, it can help to think like a QCAA assessor. Consider how many marks each question is worth and what information the assessor is looking for.

Read the exam question below and the student's response. Imagine you are a QCAA assessor and use the marking guide provided to mark the response.

QUESTION 26 (3 marks)

Wedge-tailed eagles are large birds that reside in tall trees, where they build nests for their young. They often feed on ground-dwelling herbivores such as kangaroos and rabbits.

The graph shows the number of wedge-tailed eagles observed in an ecosystem over time.



a) Determine the carrying capacity of wedge-tailed eagles in this ecosystem. *[1 mark]*

Carrying capacity = 750

Source: *QCAA Biology 2023, Paper 1* © State of Queensland (QCAA)

Marking guide

Question 26a

- Identifies carrying capacity [1 mark]

Fix the response

Consider whether you did or did not award marks in the above response. How could the response be improved? Write your own response to the same question to receive full marks from a QCAA assessor.

Part C – Practice exam questions

Now it's time to put the tips and advice you've learned into practice while you complete these exam-style questions!

Multiple choice

(1 mark each)

1 An ecosystem's carrying capacity is best defined as the
- **A** number of ecological niches available in an environment at a given point in time.
- **B** total number of individuals of the species living in a geographical area at the same time.
- **C** total number of individuals of all species that can be supported by an environment at the same time.
- **D** maximum number of individuals of a species that can be supported by an environment at the same time.

2 The role of a keystone species in its environment is
- **A** to control populations as predators.
- **B** as a producer that provides energy for heterotrophs in the food web.
- **C** disproportionately important relative to its population size or biomass.
- **D** to dominate the ecosystem by having the highest population of all species.

3 In an ecosystem, approximately what percentage of energy is transferred from one trophic level to the next?
- **A** 10%
- **B** 15%
- **C** 25%
- **D** 50%

4 A newly formed volcanic island with few established plant species is likely to be undergoing
- **A** genetic drift.
- **B** primary succession.
- **C** ecological disturbance.
- **D** secondary succession.

5 High-diversity ecosystems are characterised by
- **A** low species richness and low species evenness.
- **B** low species richness and high species evenness.
- **C** high species richness and low species evenness.
- **D** high species richness and high species evenness.

6 Lightning strikes a large tree in a forest, causing it to fall and knock down several other trees in its path. This produces a clearing in the forest where other smaller species of plants begin to grow. This is an example of
- **A** genetic drift.
- **B** primary succession.
- **C** competitive exclusion.
- **D** secondary succession.

7 Which of the following statements is true?
- **A** All producers are plants.
- **B** All producers are autotrophs.
- **C** All consumers are carnivores.
- **D** All producers are heterotrophs.

8 Which of the following best describes a symbiotic relationship classified as commensalism?
- **A** Both species benefit from the relationship.
- **B** One species benefits, while the other is killed by the relationship.
- **C** One species benefits, while the other is harmed by the relationship.
- **D** One species benefits, while the other is unharmed by the relationship but does not benefit in any way.

9 In Linnaean classification, organisms are grouped primarily based on
- **A** homologous structures.
- **B** observable physical characteristics.
- **C** the presence of a recent shared common ancestor.
- **D** molecular sequencing that compares similarities in DNA.

10 The biological species concept classifies a species as organisms that
- **A** occupy the same ecological niche.
- **B** can interbreed to produce fertile offspring.
- **C** have the same observable physical characteristics.
- **D** share a high percentage of similarities in their genetic material.

11 Which of the following is a characteristic of an *r*-selected species?

A Large body size

B High reproductive rate

C High level of paternal care

D Slow development to reproductive maturity

12 A species of fruit bat lives in a rainforest ecosystem, where it feeds on tropical fruit and disperses the seeds through its droppings. Scientists observe that in an area where the fruit bats no longer roost, tree diversity is declining. This suggests that the fruit bats

A are a keystone species in the rainforest.

B are parasitic and the trees act as their host.

C have a symbiotic relationship with the trees, called mutualism.

D have a symbiotic relationship with the trees, called commensalism.

13 In a marine ecosystem, seagrasses are the dominant producer, storing 500,000 kJ of energy. If there is 10 per cent energy transfer efficiency between trophic levels, how much energy is available to tertiary consumers in this ecosystem?

A 50 kJ **B** 500 kJ

C 5,000 kJ **D** 50,000 kJ

14 Population growth rate refers to

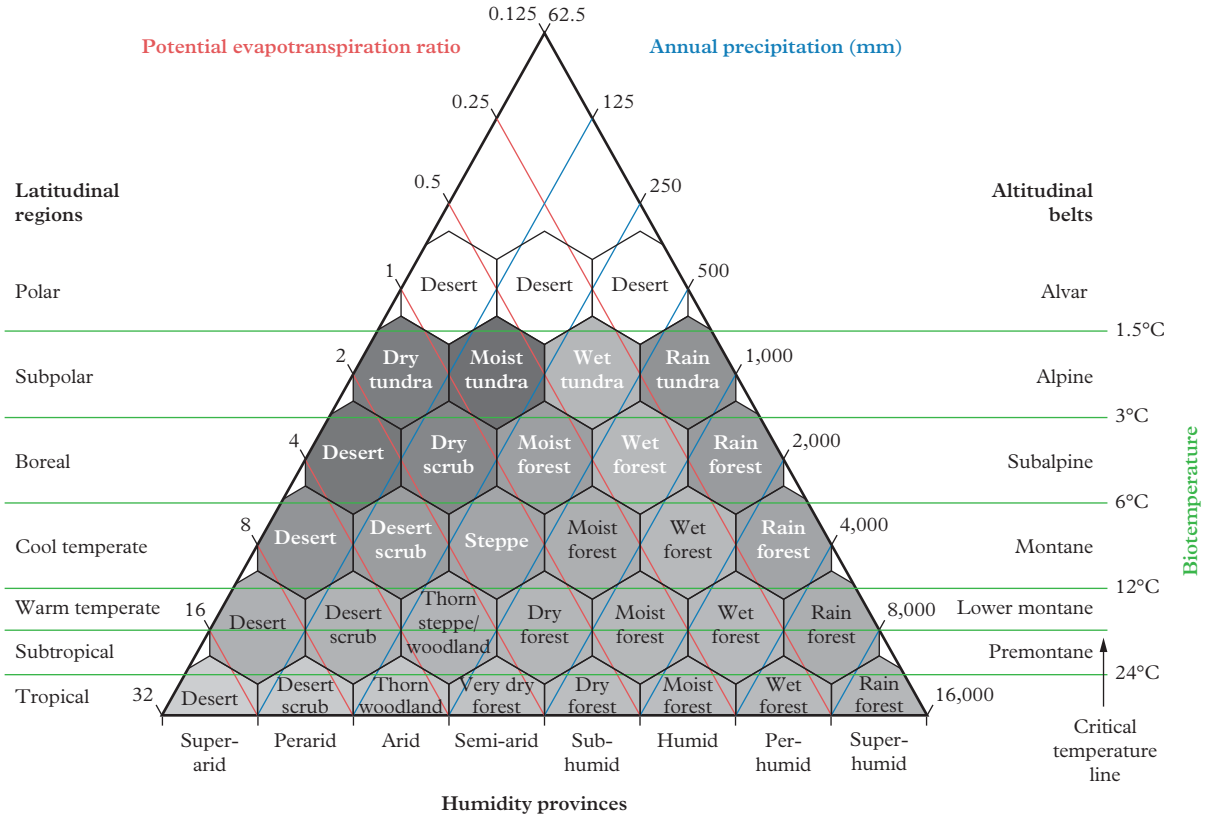
A the change in population size.

B the speed at which the population changes.

D an increase in population size due to births and immigration.

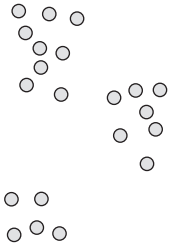
D the number of deaths and emigration that occur in the population.

15 Jardine River National Park, on Cape York Peninsula, receives 1417 mm of rain each year, with an evapotranspiration rate of 2033 mm. The potential evapotranspiration ratio is found by dividing the annual precipitation by the evapotranspiration rate. What type of ecosystem is Jardine River National Park according to the Holdridge life zone system?



A rainforest **B** moist forest **C** desert scrub **D** moist tundra

16 A species has the following distribution pattern.



What type of distribution pattern is shown?

A solitary
B uniform
C random
D clumped

17 How does environmental resistance affect carrying capacity?

A Environmental resistance and carrying capacity are not linked.
B Environmental resistance limits the carrying capacity for a population.
C Environmental resistance increases the carrying capacity for a population.
D Environmental resistance and carrying capacity are the same, and the terms are used interchangeably.

18 In a food chain and a food web, arrows are used to represent relationships between organisms. Which of the following is true?

A All arrows originate at the decomposers.
B Arrows are used to show which organisms are decomposers.
C Arrows are used to show which organism consumes which, e.g. frog → fly.
D Arrows are used to show the movement of energy through a food web, e.g. fly → frog.

19 The channel-billed cuckoo is a species of bird that lays its eggs in the nests of other birds. Those birds raise the cuckoo chick, which can result in the other chicks being pushed out of the nest by the much larger cuckoo chick. Which of the following best describes the type of relationship between the cuckoo and the adoptive parent birds?

A predation
B parasitism
C competition
D commensalism

20 Butterflies and moths occupy the same niche in an ecosystem. They are both nectar feeders and prefer the same conditions. Butterflies feed during the day, and moths feed at night. In a particular ecosystem, both populations have a healthy number of organisms. Which population concept is being demonstrated?

A biotic potential
B carrying capacity
C resource partitioning
D competitive exclusion principle

Short response

21 **Contrast** primary succession and secondary succession. Support your response with one example of each succession type. (3 marks)

22 **Calculate** the population growth rate, per day, for an invertebrate species when there are 220 births, 0 immigrants, 126 deaths and 7 emigrants in one day. (1 mark)

23 **Explain** the principle of competitive exclusion, and provide an example to support your response. (4 marks)

24 **Describe** one advantage and one disadvantage of Linnaean classification. (2 marks)

25 **Explain** the role of a keystone species in its ecosystem. (3 marks)

26 **Explain** the biological species concept. (2 marks)

27 The image shows the aftermath of a wildfire in a climax community.

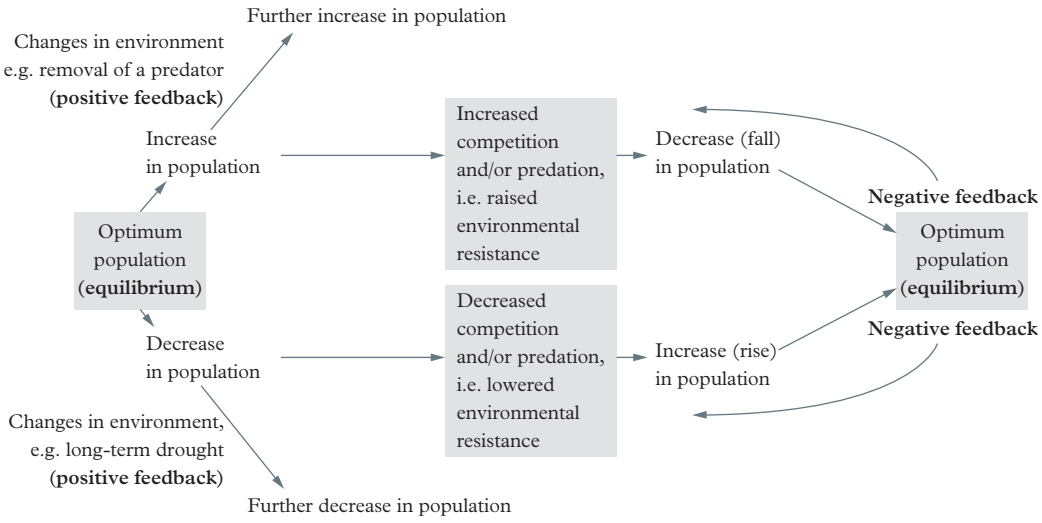
a **Determine** the type of succession that will occur in the years following the fire. (1 mark)
b **Describe** two abiotic factors that will change as a result of the fire. (2 marks)
c **Predict** how this section of forest will appear compared to unharmed sections 50 years after the fire. **Justify** your response. (3 marks)

28 The African elephant (*Loxodonta africana*) is a keystone species of the grasslands of sub-Saharan Africa. By grazing on and uprooting saplings of larger trees, these elephants prevent large forests from growing, and thereby maintain the grassland ecosystem.

a **Describe** how the feeding behaviour of the African elephant makes it a keystone species in its environment. (2 marks)

b **Predict** what would happen to other large, grazing herbivores, such as zebra and antelopes, if elephants were removed from the ecosystem. (2 marks)

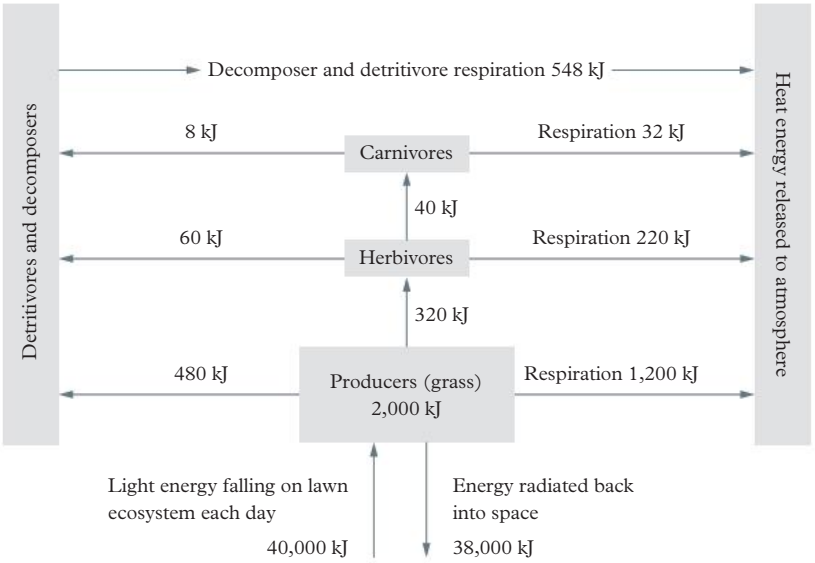
29 The flowchart below shows homeostatic control of population growth.



a **Describe** two changes in the environment (other than removal of a predator) that would lead to an increase in a population. (2 marks)

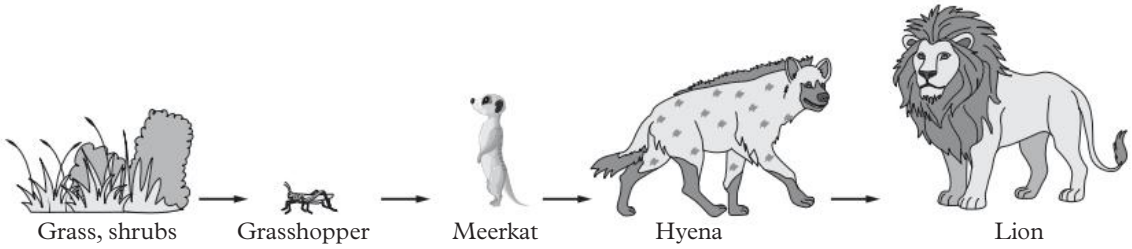
b **Describe** two changes in the environment (other than long-term drought) that would lead to a decrease in a population. (2 marks)

30 An energy-flow model of a food web in a lawn ecosystem is shown below.



Contrast the percentage heat loss by producers and carnivores and **explain** reasons for this difference. (3 marks)

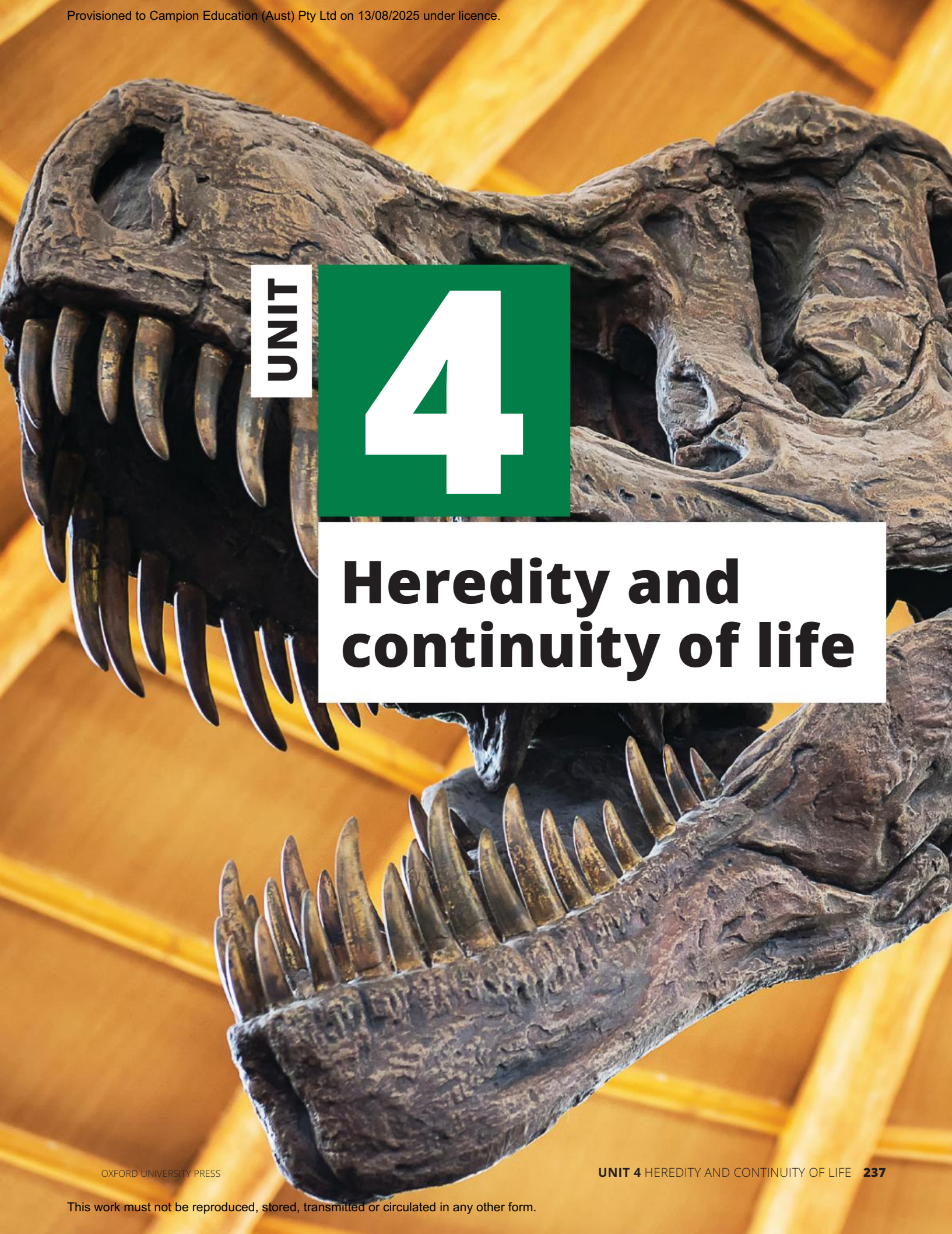
31 The simple food chain shown below represents feeding relationships in the savannah lands of Central Africa.



a **Identify** the second-order consumer (1 mark)

b **Infer** which organism is most likely to be the keystone species in this ecosystem. (1 mark)

c **Predict** the effects on the populations of other organisms if this keystone species were to be removed from the food chain. (3 marks)



UNIT

4

Heredity and continuity of life

Unit 4 overview

In Unit 4, students explore the ways biology is used to describe and explain the cellular processes and mechanisms that ensure the continuity of life. An understanding of the processes and mechanisms of how life on Earth has persisted, changed and diversified over the past 3.5 billion years is essential to appreciate the unity and diversity of life. Students investigate different factors that affect cellular processes and gene pools. They examine different patterns of inheritance and the genetic basis of the theory of evolution through natural selection to analyse the use of predictive models in decision-making.

Unit objectives

1. Describe ideas and findings about genetics and heredity, and the continuity of life on Earth.
2. Apply understanding of genetics and heredity, and the continuity of life on Earth.
3. Analyse data about genetics and heredity, and the continuity of life on Earth.
4. Interpret evidence about genetics and heredity, and the continuity of life on Earth.
5. Evaluate processes, claims and conclusions about genetics and heredity, and the continuity of life on Earth.
6. Investigate phenomena associated with genetics and heredity, and the continuity of life on Earth.

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Unit 4 Topics

Topic	Module	
Topic 1 Genetics and heredity	**Module 6**	DNA structure and replication
	Module 7	Gene expression
	Module 8	Meiosis
	Module 9	Mutations
	Module 10	Inheritance
	Module 11	Biotechnology
Topic 2 Continuity of life on Earth	**Module 12**	Evolution
	Module 13	Evidence of evolution

MODULE 6

DNA structure and replication

Introduction

The model of the structure of the DNA double-helix molecule proposed by Watson and Crick was based on chemical analyses undertaken by Franklin and Wilkins. This model has stood the test of time and explains how DNA can be replicated and transmitted from one cell or generation to the next.

Prior knowledge

Prior knowledge quiz Check your understanding of concepts related to DNA structure and replication before you start.

Subject matter

Science understanding

→ Describe the structure and function of DNA, genes and chromosomes in prokaryotes and eukaryotes, including
- helical structure, nucleotide composition (nitrogenous base + sugar + phosphate), complementary base pairing, hydrogen bonds
- introns and exons, promotor region
- homologous chromosomes (i.e. sister chromatids, centromeres, telomeres, gene loci, alleles), role of histones
- circular chromosomes (i.e. prokaryotes, mitochondria, chloroplasts) and plasmids.

→ Describe the process of DNA replication with reference to helicase, DNA polymerase and the joining of Okazaki fragments.

Science inquiry

→ Extract DNA from strawberries, kiwifruit or wheat germ.

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Practicals

These lessons are available on Oxford Digital.

Lesson 6.2 Extraction of DNA from strawberries

Lesson 6.1
DNA, genes and chromosomes

Key ideas

- → Deoxyribonucleic acid (DNA) has a double-helix structure that consists of two complementary strands of nucleotides held together by hydrogen bonds.
- → Each nucleotide in a DNA molecule consists of a deoxyribose sugar, phosphate and a nitrogenous base (adenine, thymine, cytosine or guanine).
- → Ribonucleic acid (RNA) is single stranded and is composed of nucleotides that consist of a ribose sugar, a phosphate group and a nitrogenous base (adenine, uracil, cytosine or guanine).
- → DNA in eukaryotic organisms is in the form of linear chromosomes contained within the nucleus of the cell, and circular chromosomes within mitochondria and chloroplasts.
- → Sequences of nucleotides in DNA code to produce functional RNA and can be categorised as either protein-coding or non-coding genes.

Learning intentions and success criteria

Nucleic acids

Nucleic acids are the macromolecules (large molecules) that make up the genetic material of all living organisms. There are two types of nucleic acid: **deoxyribonucleic acid (DNA)** and **ribonucleic acid (RNA)**. DNA is often called the "blueprint of life". It contains the set of instructions needed for the development of all structural features and cell activities in an organism. DNA also passes on genetic information during reproduction and during cell replication. RNA synthesises proteins. The three major types of RNA – messenger (m), transfer (t) and ribosomal (r) RNA – are each involved in translating the DNA code into the proteins needed by the cell.

deoxyribonucleic acid (DNA)
a thread-like chain of nucleotides carrying genetic instructions in a double helix of antiparallel strands

ribonucleic acid (RNA)
a thread-like chain of nucleotides carrying genetic instructions for forming a protein in a cell

Study tip

The different types of RNA are written as mRNA, tRNA and rRNA, with a lowercase letter defining each type.

The structure of nucleic acids

Each nucleic acid strand is a chain of nucleotides. Each nucleotide consists of a five-carbon sugar ring, a phosphate and a nitrogenous base (Figure 1).

The phosphate of one nucleotide forms a strong covalent bond with the sugar ring of the next nucleotide, to form a continuous polymer chain. This chain is called the **sugar–phosphate backbone** of the nucleic acid. The chemical reaction that joins the nucleotides together is called **condensation polymerisation** because water is produced (condensed) when the nucleic polymer is formed (polymerised).

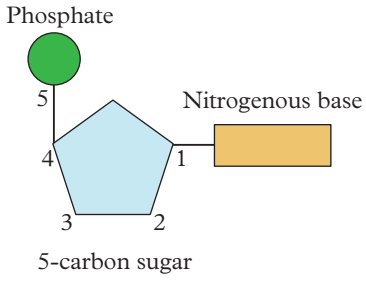


FIGURE 1 A nucleotide consists of a five-carbon sugar ring, a phosphate and a nitrogenous base

sugar–phosphate backbone
the structural framework of nucleic acids, composed of alternating sugar and phosphate groups

condensation polymerisation
the formation of a polymer by the reaction between two monomers, with the loss of a small molecule (e.g. water)

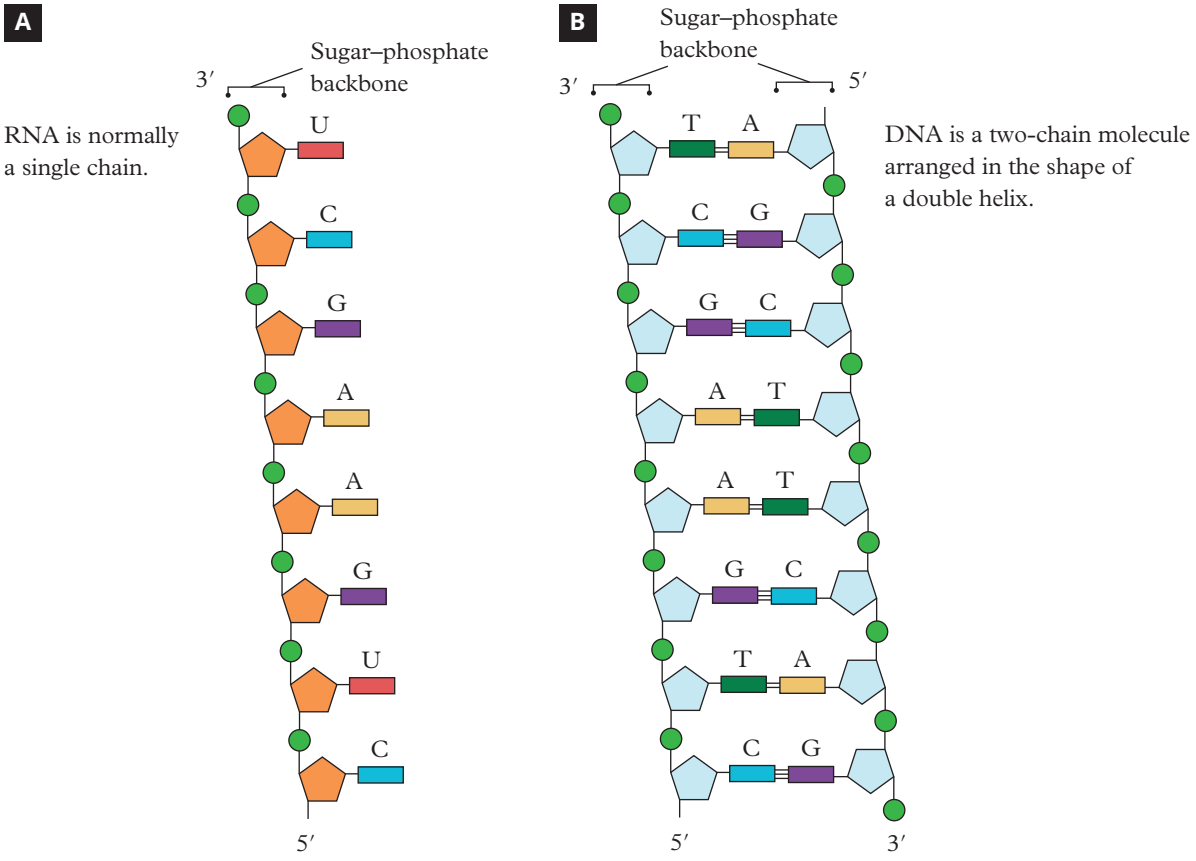


FIGURE 2 Individual nucleotides bond together in a condensation polymerisation reaction to form sugar–phosphate backbones, in (A) RNA and (B) DNA

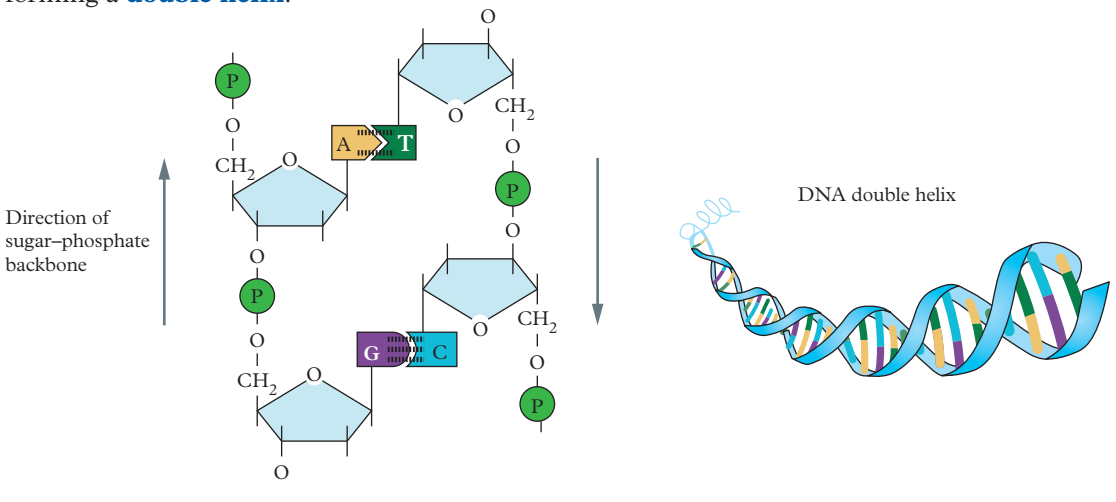
Study tip

A polymer is a long chain of repeating chemical units called monomers. It can be visualised as a necklace of repeating monomer beads linked together

DNA and RNA differ in many ways. The sugar in DNA is deoxyribose, whereas the sugar in RNA is ribose. RNA is typically composed of a single strand of nucleotides, whereas DNA consists of two strands held together by the pairing of the nitrogen bases between adjacent strands. The two strands in DNA are **antiparallel**, meaning that that one strand starts with a (5′) sugar, while the other strand is facing the opposite direction and has a (3′) phosphate at the end. This gives a ladder-like structure to the DNA molecule, which twists on its axis, forming a **double helix**.

antiparallel
the arrangement of DNA strands where one strand runs in the 5′ to 3′ direction while the complementary strand runs in the opposite (3′ to 5′) direction

double helix
the structure of DNA; two linked strands that are twisted on their axis, forming the shape of a helical (spiralled) ladder



Purines: A = adenine; G = guanine
Pyrimidines: T = thymine; C = cytosine

FIGURE 3 DNA consists of antiparallel strands of nucleotides with a sugar–phosphate backbone and complementary nitrogen base pairs

Complementary base pairing

There are five types of bases in nucleic acids. In DNA these bases are adenine, guanine, thymine and cytosine. In RNA, the thymine is replaced by uracil. Each base has a particular type of structure and linking of atoms. Adenine and guanine (purines) are similar in structure, and thymine, cytosine and uracil (pyrimidines) are similar. The structure of guanine is complementary to that of cytosine, forming three (relatively weak) hydrogen bonds between the two molecules. Similarly, the nitrogen base adenine is complementary to either thymine (DNA) or uracil (RNA). In DNA, the adenine on one strand forms two hydrogen bonds with the thymine on the complementary strand. Because only these combinations of bases (adenine–thymine, cytosine–guanine) can form hydrogen bonds, the two strands of the DNA molecule are always complementary strands.

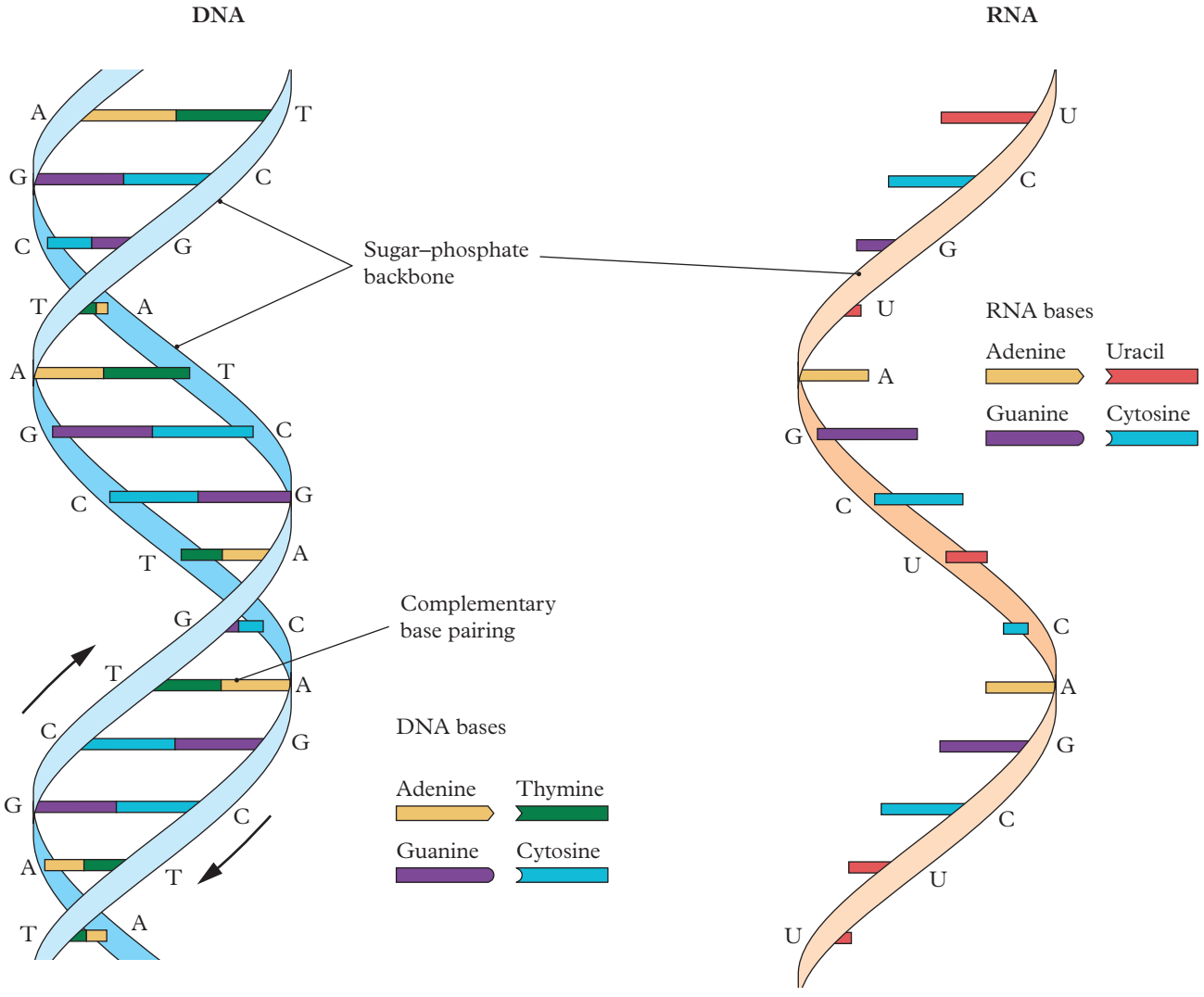


FIGURE 4 DNA consists of two nucleic acid chains strung together by complementary base pairing, while RNA usually consists of a single nucleic acid chain

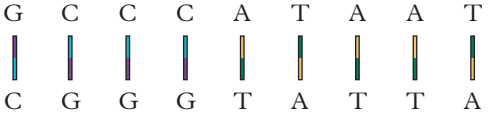


FIGURE 5 In DNA, the base guanine pairs with cytosine and thymine pairs with adenine

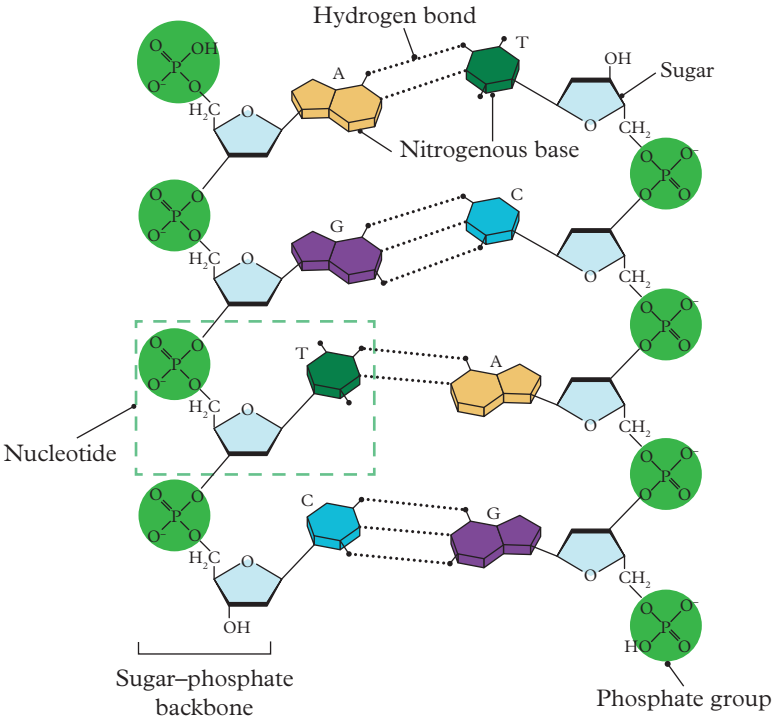


FIGURE 6 In DNA, guanine forms three hydrogen bonds with cytosine, while adenine forms two hydrogen bonds with thymine

TABLE 1 Comparison of DNA and RNA

Feature	DNA	RNA
Sugar	deoxyribose	ribose
Bases	adenine, thymine, guanine, cytosine	adenine, uracil, guanine, cytosine
Chains	double	usually single

chromosome
tightly wound strands of DNA and protein

histone
a protein that DNA is wound around, to package and organise DNA and regulate gene activity

nucleosome
the basic unit of chromatin, consisting of a length of DNA coiled around a core of eight histone protein molecules

chromatin
a DNA–protein complex in the nucleus, where DNA wraps around histones to form nucleosomes, helping package and regulate genes

epigenetic factors
a chemical tag that determines the degree of coiling of the DNA around the nucleosome and thus gene expression

Chromosomes

A molecule of DNA may contain millions of nucleotides. The two chains of each strand are base-paired and fully complementary throughout the entire DNA molecule. The average human cell contains almost two metres of DNA. To organise the DNA and prevent it from tangling, each DNA is highly condensed into **chromosomes**. DNA condenses into chromosomes in a series of steps.

1 The DNA is wound, at intervals, one and three-quarter times around eight proteins, known as **histones**, forming a DNA–histone complex called a **nucleosome** (Figure 7).
2 Nucleosomes further condense to form **chromatin**. The eight histone proteins have chemical tails that are exposed, and these tails can be chemically modified by binding with **epigenetic factors** so that the tails are tied to each other. This locks away the DNA (chromatin) so that it cannot be copied to make protein. If the DNA needs to be copied (DNA synthesis) or make a protein (gene expression), the histone tails are freed and drawn into the histone protein (and so are not in contact with the tails of other nucleosomes).

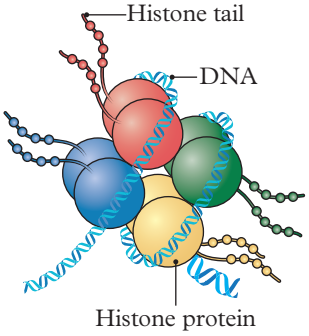


FIGURE 7 Model of the DNA–histone complex (nucleosome)

3 To prevent tangling or breaking of the DNA, the DNA–histone components begin to coil even more closely together (super coiling). As the coiling becomes tighter and tighter, the chromatin becomes shorter, and this tightly coiled DNA–histone complex forms a chromosome.

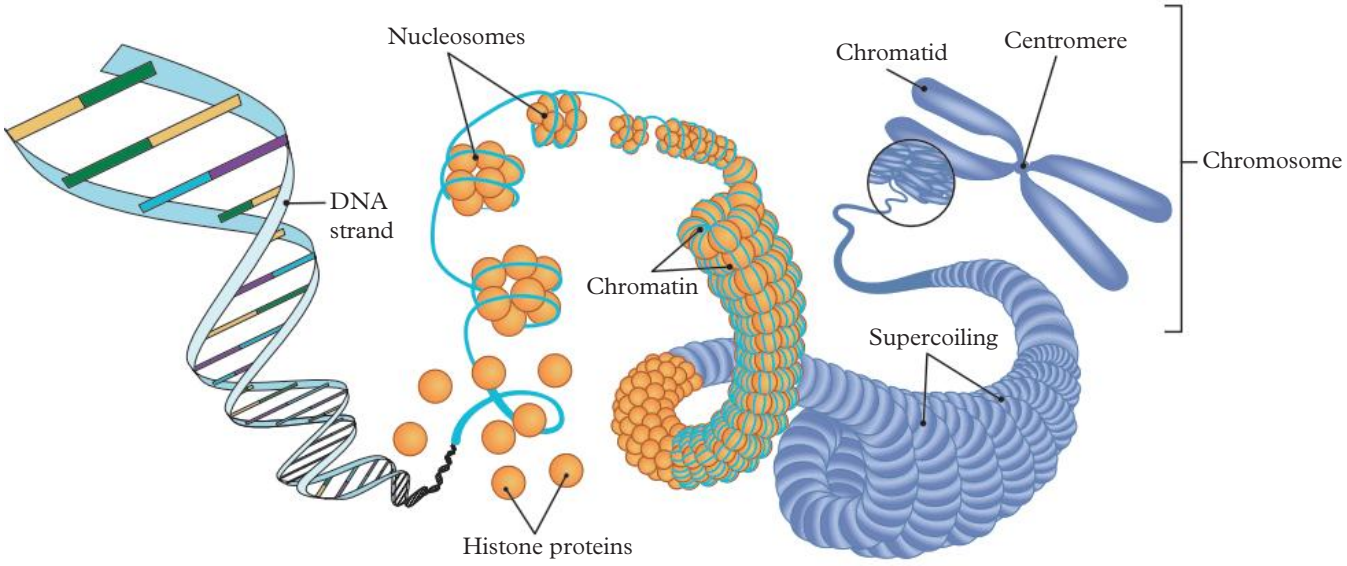


FIGURE 8 How DNA condenses into a chromosome

After DNA replication, the chromosome forms a characteristic "X" shape, where the two identical copies of the chromosome, called sister chromatids, are held together at a central region called the **centromere**. Sister chromatids remain attached until they are separated during cell division (either mitosis or meiosis), which ensures that each new cell receives an identical set of chromosomes. At the ends of each chromosome are repetitive DNA sequences, called **telomeres**, that protect the chromosome from deterioration and prevent fusion with other chromosomes. Telomeres shorten with each cell division, playing a crucial role in ageing and cellular lifespan.

centromere
the region of a chromosome where two sister chromatids are joined together and where spindle fibres attach during cell division

telomeres
repetitive DNA sequences at the ends of chromosomes that protect the chromosome from degradation and maintain genomic stability

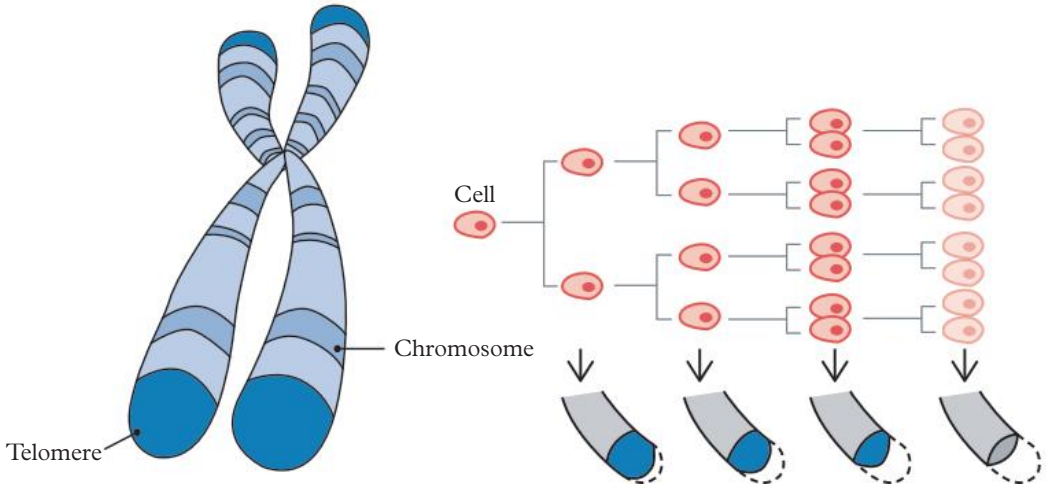


FIGURE 9 After each round of cell division, the telomeres shorten

Real-world biology

Discovering telomeres

The joint efforts of Elizabeth H. Blackburn, Carol W. Greider and Jack W. Szostak have significantly advanced our understanding of telomeres and their role in genetics and heredity. Building on previous discoveries by scientists about the existence of special structures at the ends of chromosomes, Blackburn, Greider and Szostak collaboratively discovered that telomeres, the protective caps at the ends of chromosomes, play a crucial role in maintaining genomic stability and preventing the loss of important genetic information during cell division. Greider and Blackburn's research discovered the enzyme responsible for the creation of telomeres, telomerase. Blackburn and Szostak discovered how the telomeres protect the chromosome from degradation. With each round of DNA replication, the telomeres at the ends of each chromosome are shortened slightly, which helps to safeguard the coding regions of DNA from being lost during replication. The trio's groundbreaking work, which earned them the Nobel Prize in Physiology or Medicine in 2009, demonstrates how interdisciplinary collaboration can lead to profound discoveries in genetics. This ongoing exploration of telomeres continues to shape our understanding of ageing, cancer and various genetic disorders.

FIGURE 10 From left to right: Carol W. Greider, Elizabeth H. Blackburn and Jack W. Szostak

Apply your understanding

1 **Identify** the role of telomerase. (1 mark)
2 **Describe** how telomeres help maintain genomic stability during cell division. (1 mark)

Homologous chromosomes

In eukaryotes, DNA is contained in chromosomes that are in linear pairs (diploid) and arise through sexual reproduction. One chromosome of each pair comes from the male parent via the sperm, and the other comes from the female parent via the ovum. When the two sets of chromosomes are combined (fertilisation), a zygote is formed. The zygote develops into an individual by repeated cell division and differentiation. Pairs of chromosomes, termed **homologous chromosomes**, have the same genes at the same positions (**gene loci**), but may carry different versions, or **alleles**, of those genes. The number of chromosome pairs present in the cells of an individual depends on the species.

homologous chromosomes
pairs of chromosomes, one inherited from each parent, that are similar in size, shape and gene content, although they may carry different versions of those genes

gene locus
a specific, fixed position on a chromosome where a particular gene is located; plural *gene loci*

allele
a different version of a gene that occupies a particular position (gene locus) on a chromosome

Circular chromosomes

Prokaryotes do not have a nucleus. Their genetic material is a single chromosome (made of DNA) that floats freely in the liquid cytosol of the cell. The DNA is:

- circular and double stranded
- not bound to histone proteins.

Some prokaryotic cells also contain additional smaller pieces of circular DNA, called plasmids. Plasmids often carry genes that provide additional functions for the cell, including allowing for genetic exchange between different prokaryotic cells, contributing to genetic diversity.

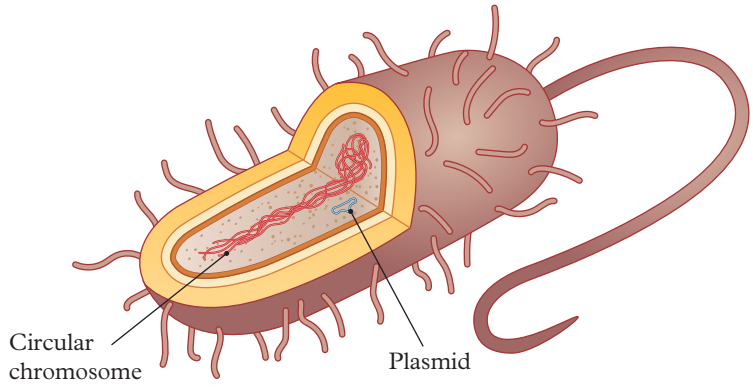


FIGURE 11 A circular chromosome and a plasmid in a prokaryotic cell

Some eukaryotic organelles, including mitochondria and chloroplasts, have their own genetic material. Like prokaryotic DNA, the DNA in these organelles is circular, double stranded and not bound to histones. The similarities in DNA structure between prokaryotes, mitochondria and chloroplasts contribute to the evidence that supports the endosymbiotic theory of the formation of eukaryotic cells.

Genes

Each DNA molecule is made up two strands of paired nucleotides (nitrogen base pairs). Short segments of these paired nucleotides (from 200 to 2,000,000 base pairs) contain the set of information for a specific function or trait and are called **genes** (the units of heredity). All DNA is made up of the same four key nucleotides (adenine, thymine, cytosine and guanine), but the order of these nucleotides along the length of each DNA molecule differs from chromosome to chromosome and from species to species. The nucleotide sequence of a protein-coding, or structural, gene is used to create an mRNA copy, which is then used to produce a protein by following a set of rules known as the **genetic code**, determining the sequence of amino acids in that protein. Each chromosome contains several different genes

gene
a segment of DNA that is passed from parent to offspring and determines an attribute of an individual

genetic code
a code used by the body to convert instructions contained in DNA into the proteins essential for life

that can carry the code for different proteins. These differences account for variations within and between species. The DNA molecule is therefore responsible for transmission of the genetic information from one generation to the next and for controlling the actions of the cell through protein synthesis.

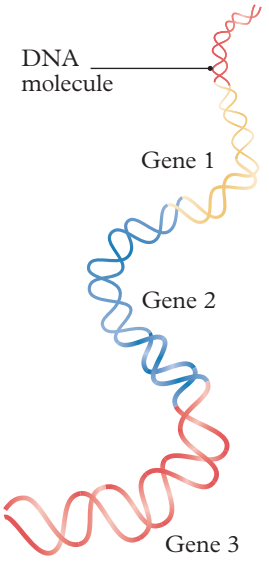


FIGURE 12 A gene is a section of DNA that contains the information for a specific function or trait

Introns, exons and promoter regions

intron
a segment of DNA or RNA within a gene that does not code for proteins and is removed during RNA processing

exon
a segment of DNA or RNA within a gene that contains the code for producing a protein

promotor region
a DNA sequence located before a gene that helps initiate the process of transcribing the gene into RNA

Introns and **exons** are segments of a gene that serve different purposes in the process of protein production. Exons are coding regions that contain information for making proteins and are retained in the final messenger RNA (mRNA), while introns are non-coding regions that are removed during mRNA processing. The **promoter region** is a specific section of DNA located before a gene that helps control when the gene is turned on or off. By interacting with various proteins, the promoter region ensures that the right genes are expressed at the right times in response to different signals. This will be discussed in more detail in Module 7.

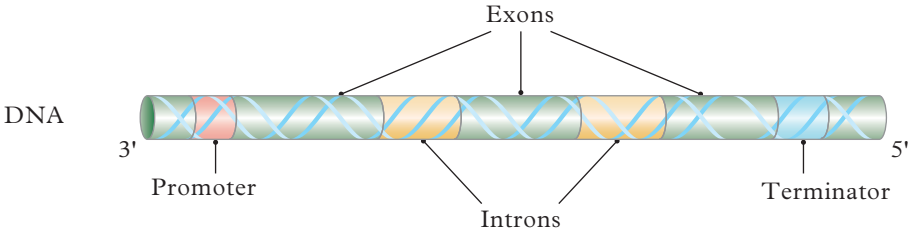


FIGURE 13 Structure of a gene

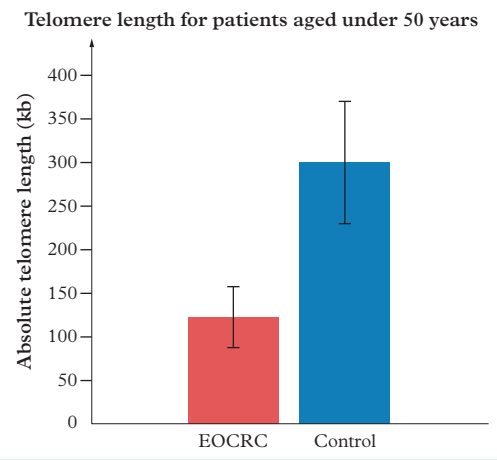
Skill drill

Interpreting standard error

Science inquiry skill: Processing and analysing data (Lesson 1.8)

Standard error (SE) is a measure of how reliable the mean of a data set is. The smaller the standard error, the more accurate the calculated mean, and the closer it is to the "true" mean of the population. A larger SE suggests more variation. Considering SE is useful for evaluating the accuracy of results, determining whether differences in the data are significant, and understanding whether the results are due to random chance or an observed effect. When comparing groups of data on a graph, if the SE bars do not overlap between two collected samples, it can be inferred that the means calculated for the two samples are statistically different from each other. This means that differences between means are not likely to be due to random variation. If the SE bars overlap, it suggests that the difference between the group means may not be statistically significant, meaning the variation could be due to chance. However, it is important to note that even with overlapping SE bars, it is still possible for the difference to be statistically significant, so further statistical testing is often needed to confirm the result.

The graph below shows data collected about the telomere length (kb/kilobases) of a group of patients aged less than 50 years, who are either healthy (control) or affected by early-onset colorectal cancer (EOCRC).



Practise your skills

1 **Describe** the difference in mean telomere length between the colorectal cancer group and the control/healthy group for individuals under 50 years old, using data from the graph to justify your response. (2 marks)

2 The standard error bar for the colorectal cancer group is smaller than the bar for the control group. **Describe** the reliability of the results for both groups, using evidence from the graph to justify your response. (4 marks)

3 The standard error bars for the colorectal cancer and control groups do not overlap. **Draw a conclusion** about the statistical significance of the difference in telomere lengths between these groups. (1 mark)

Check your learning 6.1

Check your learning 6.1: Complete these questions online or in your workbook.

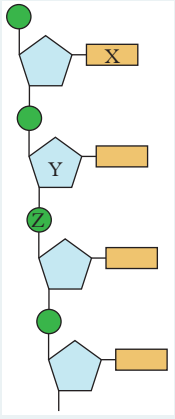
Retrieval and comprehension

1 **Identify** the three components of a nucleotide. (1 mark)

2 **Identify** three differences in structure between DNA and RNA. (3 marks)

3 **Describe** the function of the centromere. (1 mark)

4 The figure shows part of a DNA complementary strand. **Identify** the chemical groups labelled X, Y and Z. (1 mark)



5 **Describe** the structure of a nucleosome. (1 mark)

6 **Explain** how DNA condenses into chromosomes. (3 marks)

7 **Explain** how the differences observed between species are related to nucleotide sequences. (3 marks)

8 **Identify** which nitrogenous base pairs with thymine in DNA. (1 mark)

9 **Describe** how the bases of the two adjacent strands of DNA are held together. (1 mark)

Analytical processes

10 **Distinguish** between chromatin and chromosomes. (1 mark)

11 A section of DNA is made up of two strands, strand I and strand II. If 31 per cent of the nucleotides on strand I contain thymine, **determine** the percentage of:

a adenine on strand I (1 mark)

b cytosine on strand II. (1 mark)

Knowledge utilisation

12 When revising for his biology exam, Luca writes the following note: "Circular chromosomes are only found in prokaryotes". **Evaluate** whether Luca's note is accurate. (2 marks)

Practical

Lesson 6.2
Extraction of DNA from strawberries

Learning intentions and success criteria

oxforddigital **This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.**

Lesson 6.3
DNA replication

Key ideas

- → DNA replication is semiconservative.
- → DNA helicase unwinds DNA and separates hydrogen bonds to expose the nitrogenous bases of DNA.
- → DNA polymerases are enzymes that create new complementary strands of DNA by bonding new nucleotides to the 3′ end.
- → The leading strand of DNA forms a continuous strand of new DNA.
- → The lagging strand of DNA forms in a series of Okazaki fragments joined together by DNA ligase.

Learning intentions and success criteria

Stages of DNA replication

Before a cell can divide, a second copy of the DNA of the cell must be made, to ensure that each daughter cell receives a complete and accurate complement of DNA. This is achieved through DNA replication, the process in which a DNA molecule is copied to produce two identical strands of DNA. DNA replication occurs in four main steps:

1. separation of DNA strands
2. initiation
3. elongation
4. termination.

Each these steps involves complex enzyme-controlled and coordinated processes.

Separation of DNA strands

DNA helicase
an enzyme that breaks down the hydrogen bonds holding two DNA strands together

Before replication can take place, the DNA must first be unwound and unzipped by an enzyme called **DNA helicase**. This enzyme separates the two strands of parent DNA by breaking the hydrogen bonds between the nitrogenous bases. Other enzymes (DNA polymerases) start moving along the separated strands, generating new DNA strands that are complementary to the original template strands.

This DNA replication is termed **semiconservative replication** because each replicated DNA contains one strand of the original DNA and one newly synthesised strand (Figure 1). Free nucleotides, which are formed in the cytoplasm, pass through the pores of the nuclear membrane to be available for DNA replication (or the formation of messenger RNA for protein synthesis). Various cellular processes occur to prevent mutations or mistakes in replication. These involve DNA polymerases "proofreading" and "error checking" to ensure that the replicated DNA is an exact copy of the parent DNA.

DNA strands have directionality. Each strand has a **5′ (five-prime) end**, named after the C_5 carbon atom of the sugar molecule that is linked to the phosphate. The opposite end of each strand ends in a **3′ (three-prime) end**, named after the C_3 carbon atom of the sugar molecule that has a "free" OH (hydroxyl) group that is not linked. Each nucleotide on the complementary strand is reversed. The strands of the double helix therefore run from 5′ to 3′ on one strand and from 3′ to 5′ on the opposite strand – the strands are antiparallel. This directionality is important in DNA replication, because the enzyme **DNA polymerase** can only synthesise DNA in one direction, by adding nucleotides to the 3′ end of the template DNA.

semiconservative replication
replication of DNA resulting in two copies that each contain one of the original strands and one new strand

5′ (five-prime) end
one end of a DNA strand in which the C_5 carbon atom of the sugar molecule in the DNA's sugar backbone has a "free" phosphate group that is not linked to another chemical group

3′ (three-prime) end
one end of a DNA strand in which the C_3 carbon atom of the sugar molecule in the DNA's sugar backbone has a "free" OH (hydroxyl) group that is not linked to another chemical group

DNA polymerase
a type of enzyme that assembles nucleotides to form new copies of DNA

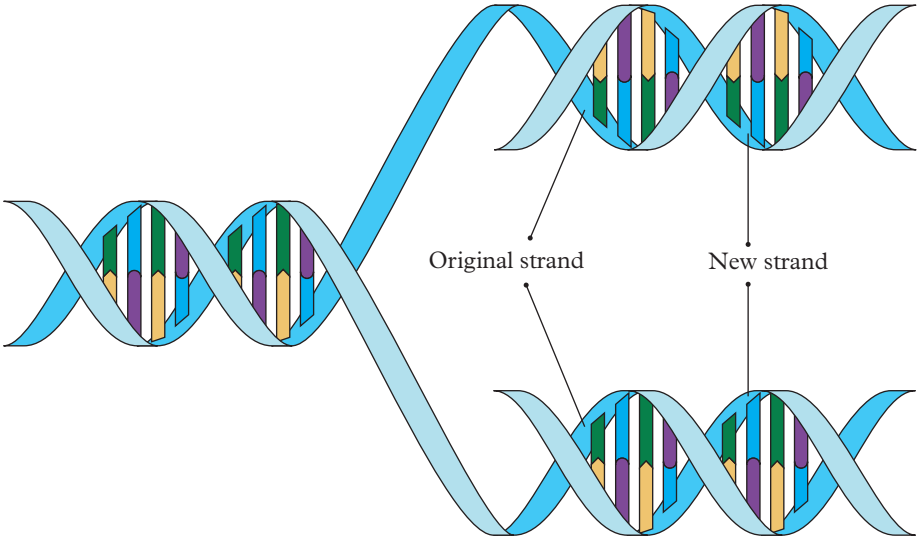


FIGURE 1 Semiconservative replication of DNA

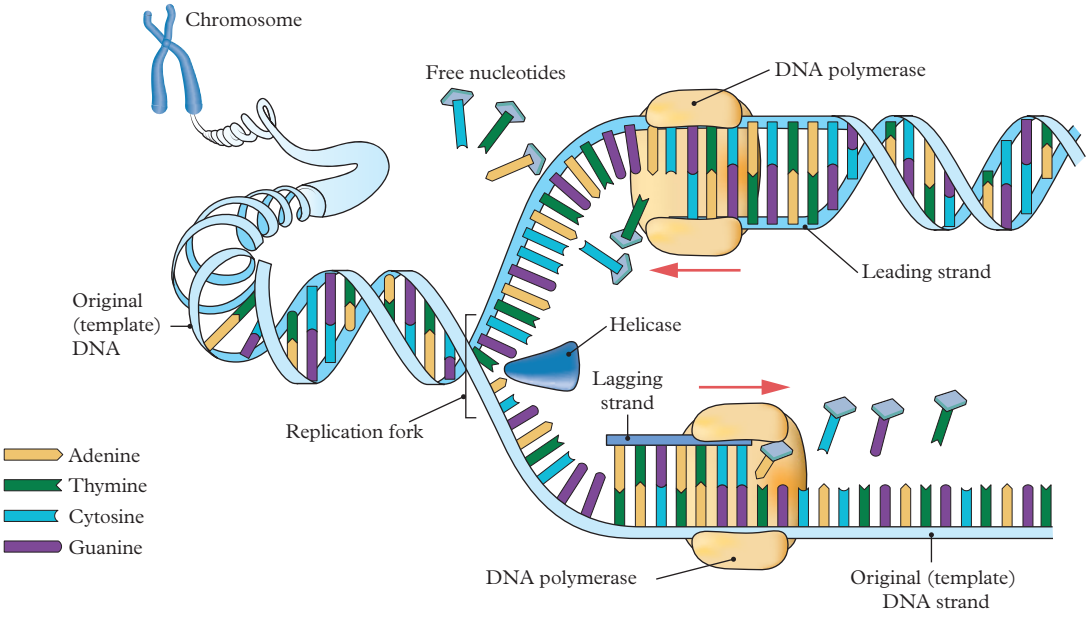


FIGURE 2 Helicase unzips DNA, and DNA polymerase adds nucleotides to the template DNA

Study tip

Everything always happens at the 3′ end. The primer and then the DNA polymerase binds to the 3′ end of the original strand and attaches a complementary nucleotide. Any new nucleotides are then added to the 3′ end of the previous nucleotide, synthesising the new strand of DNA from 5′ to 3′.

origin of replication
a particular sequence in the DNA molecule at which replication is initiated

replication fork
a structure with two branching sections that is created when DNA helicases break the hydrogen bonds holding two DNA strands together at a certain point

Initiation

Initiation does not start at one end of the double-helix strand and finish at the other end. There are particular initiation points, known as **origins of replication**, all along the strands. These are the origin points for "unzipping" DNA to start replication. The DNA helicase enzymes attach at these origin points, unzipping and unwinding the DNA by breaking the hydrogen bonds holding the two DNA strands together. The two released DNA strands provide original templates of DNA from which the new complementary strands can be formed. The unzipped DNA forms a **replication fork**, which moves apart (in two directions), forming a **replication bubble**. This means many sections of the DNA replicate at once, thus speeding up the process.

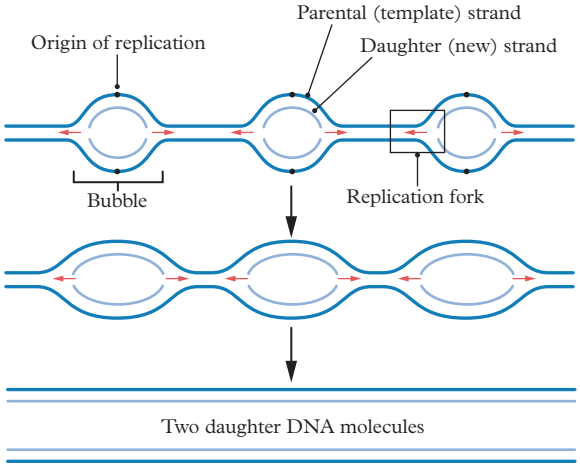


FIGURE 3 Points of origin in DNA replication showing replication bubbles and the resultant semiconservative replication

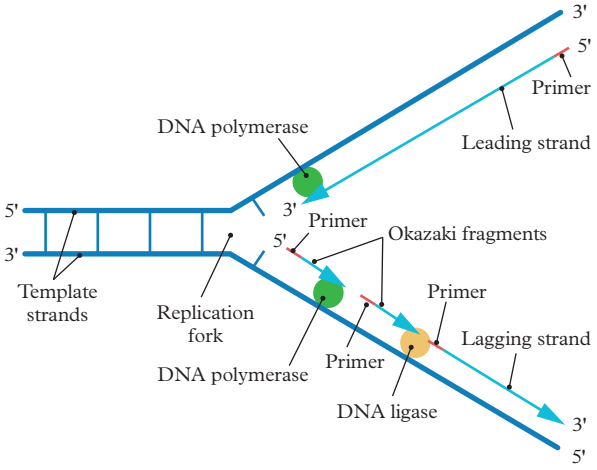


FIGURE 4 Schematic diagram of a replication fork

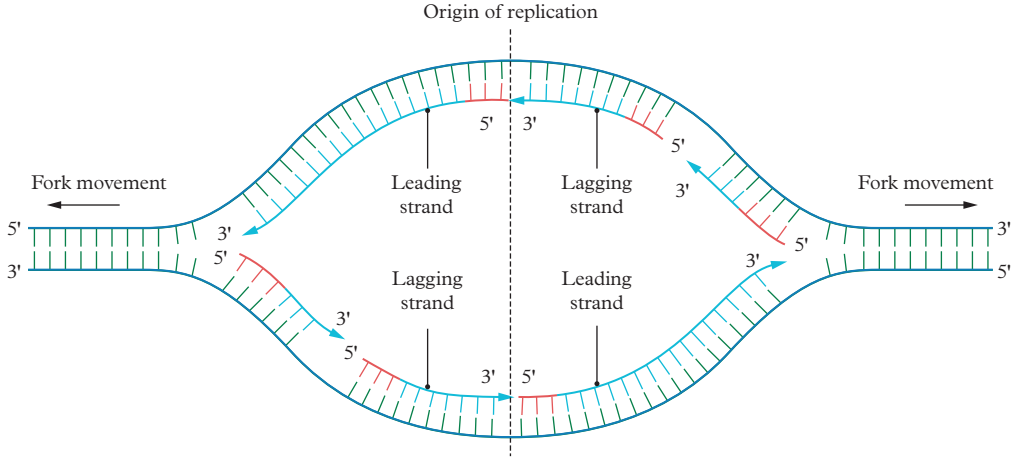


FIGURE 5 A replication bubble

replication bubble
an unwound and open region of DNA in which DNA replication occurs, created when the enzyme DNA helicase separates the two strands of DNA

Elongation

RNA primer
a short strand of RNA that acts as an initiation point for DNA synthesis

Before DNA replication can occur, an **RNA primer** (a short strand of RNA) must bind to the starting point of replication. This occurs at set recognition points along the DNA template strands. DNA polymerase can only add new nucleotides to the 3′ end of the previous nucleotide. This means the formation of the new complementary DNA strand will start from the 3′ end of the RNA primer.

The **leading strand** of DNA is formed from the middle of the bubble, towards the fork. The DNA polymerase starts adding new nucleotides to the 3′ end of the RNA primer. This allows it to continuously extend the new complementary DNA molecule from the primer (it leads the way).

The **lagging strand** is formed from the fork towards the centre of the bubble. It receives several RNA primers, starting at the replication fork on the 3′ side. Because DNA polymerase starts adding the complementary nucleotides to the 3′ end of the primer, the new strand of DNA is replicated in the opposite direction to the leading strand. The DNA polymerase extends short sections of DNA from each primer, generating fragments of DNA called **Okazaki fragments**. These fragments appear to "lag behind" the leading strand, as the strand is synthesised more slowly and in a discontinuous manner. When the Okazaki fragments cover the whole length of the lagging strand template, the RNA primers are then removed from both the leading and lagging strands and replaced with DNA by DNA polymerase. The gaps that remain after the primers are replaced, and the gaps between the Okazaki fragments, are joined by an enzyme called **DNA ligase**.

leading strand
a DNA template from the middle of the replication bubble (point of origin) to the fork

lagging strand
a DNA template from the fork to the middle of the replication bubble (point of origin)

Okazaki fragments
fragments of DNA that are formed on the lagging strand of replicating DNA

DNA ligase
an enzyme that facilitates the joining together of DNA strands

Termination

Termination of DNA replication occurs when two replication forks meet, typically when the entire template has been replicated. The result of replication is two DNA strands that are exactly like the original.

In many cases, the two identical double-stranded DNA molecules remain joined by the centromere. This is a special kinetochore protein that produces the X-shaped bivalent chromosome (with two chromatids) seen during mitosis and meiosis (Module 8).

Challenge

Semiconservative replication

Each new DNA strand is created using a template strand of DNA. So after cell division, each cell will contain DNA composed of both an original and a newly synthesised strand of DNA. This means half the original DNA is preserved in each of the daughter molecules.

If DNA replication were not semiconservative but instead fully conservative (each new cell contained an entirely newly synthesised DNA molecule), how might this affect genetic stability across generations? (1 mark)

Check your learning 6.3

Check your learning 6.3: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Identify** the complementary strand for a template strand of DNA with the following sequence. (1 mark)
5′ – A T G C C G G A T C G C – 3′

2 **Describe** the purpose of DNA replication. (2 marks)

3 **Explain** why the different strands of replicating DNA are called "lagging" or "leading" in a replication bubble. (2 marks)

4 **Explain** how replication bubbles speed up the process of DNA replication. (2 marks)

5 **Describe** the role of the following enzymes in DNA replication. (1 mark each)
a DNA helicase
b DNA polymerase
c DNA ligase

MODULE 6

Lesson 6.4
Review: DNA structure and replication

Summary

6.1
- Deoxyribonucleic acid (DNA) has a double-helix structure that consists of two complementary strands of nucleotides held together by hydrogen bonds.
- Each nucleotide in a DNA molecule consists of a deoxyribose sugar, phosphate and a nitrogenous base (adenine, thymine, cytosine, guanine).
- Ribonucleic acid (RNA) is single stranded and composed of nucleotides that consist of a ribose sugar, a phosphate group and a nitrogenous base (adenine, uracil, cytosine, guanine).
- DNA in eukaryotic organisms is in the form of linear chromosomes contained within the nucleus of the cell, and circular chromosomes within mitochondria and chloroplasts.
- Sequences of nucleotides in DNA code to produce functional RNA and can be categorised as either protein-coding or non-coding genes.

6.2
- Practical: Extraction of DNA from strawberries

6.3
- DNA replication is semiconservative.
- DNA helicase unwinds DNA and separates hydrogen bonds to expose the nitrogenous bases of DNA.
- DNA polymerases are enzymes that create new complementary strands of DNA by bonding new nucleotides to the 3′ end.
- The leading strand of DNA forms a continuous strand of new DNA.
- The lagging strand of DNA forms in a series of Okazaki fragments joined together by DNA ligase.

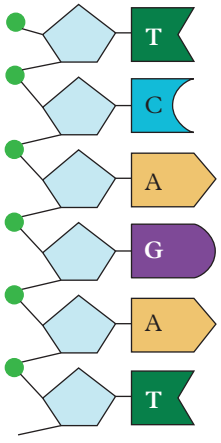
Review questions 6.4A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

Use the following information to answer questions 1 and 2.

The figure below represents a portion of a nucleic acid molecule.



1 What type of nucleic acid molecule is represented?
- **A** a protein
- **B** double-stranded RNA
- **C** a single strand of RNA
- **D** a single strand of DNA

2 What structure is represented by the small green circles?
- **A** A sugar
- **B** A phosphate
- **C** A nucleotide
- **D** A nitrogenous base

3 A nucleotide always consists of
- **A** a triose sugar, phosphate and a nitrogen base.
- **B** a pentose sugar and the nitrogen base guanine.
- **C** a pentose sugar, phosphate and a nitrogen base.
- **D** a pentose sugar, phosphate and the nitrogen base thymine.

4 In the nucleus of eukaryote cells,

A nucleosomes are composed of proteins.

B DNA occurs bound to histones in chromosomes.

C the DNA is in the form of chromosomes in non-dividing cells.

D chromosomes revert to chromatin by coiling around a group of eight histone molecules.

5 DNA in prokaryotes, chloroplasts and mitochondria is a

A single-stranded, straight molecule.

B double-stranded molecule bound by histone proteins.

C circular, double-stranded molecule bound by histone proteins.

D circular, double-stranded molecule not bound by histone proteins.

6 Semiconservative replication of DNA means that

A "proofreading" ensures no errors are ever made.

B DNA ligase matches free nucleotides to the templates.

C each of the two DNA molecules formed is composed of an original strand and a new strand.

D all new strands of the DNA molecule start at the 3′ end of one template and the 5′ end of the complementary template.

7 During DNA replication, the following events occur.

i Winding brings about the formation of two double helices.

ii Nitrogenous bases of free nucleotides bond with complementary bases on the DNA chains.

iii Hydrogen bonds are broken by helicase, allowing the DNA strands to unzip.

iv New nucleotides bond with the 3′ end of the new DNA strand.

The correct order in which these processes occur is

A i, iii, ii, iv.

B i, ii, iii, iv.

C iii, ii, iv, i.

D iii, iv, ii, i.

8 Analysis of the DNA bases in the cells of a cow's pancreas gave the results shown below.

% base composition			
X	Guanine	Y	Z
28.5	21.5	21.5	28.5

Which of the following is a possible correct identification of bases X, Y and Z?

	X	Y	Z
A	cytosine	adenine	thymine
B	thymine	adenine	cytosine
C	adenine	cytosine	thymine
D	cytosine	thymine	adenine

9 A "replication bubble" refers to

A one segment of unzipped DNA.

B another term for an Okazaki fragment.

C a missed section of DNA that is not replicated.

D the point of origin at which replication is initiated.

10 A structural gene is

A a segment of DNA that codes for an RNA or protein product.

B an essential part of the chromosome that maintains its structure.

C a segment of DNA that regulates production of a specific protein.

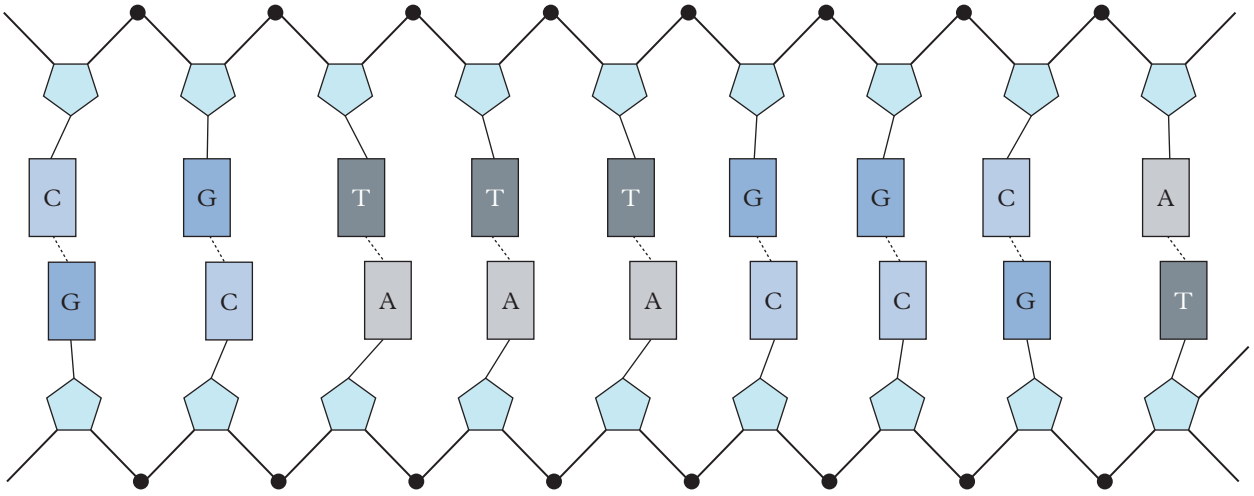
D the part of the genome that codes for the physical structure of an organism.

Review questions 6.4B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

11 The figure shows a model of an untwisted segment of DNA.



Based on this figure:

- **a** **Identify** and **sketch** a single nucleotide. (1 mark)
- **b** **Identify** three structures or features that support the conclusion that this is a representation of DNA. (3 marks)

12 **Identify** the three steps of DNA replication. (1 mark)

13 **Describe** the role of DNA polymerase in DNA replication. (2 marks)

14 **Explain** what is meant by "antiparallel strands of DNA". (2 marks)

15 **Describe** how Okazaki fragments are formed. (2 marks)

16 **Describe** the role of histones. (2 marks)

17 **Identify** the direction in which DNA is synthesised by DNA polymerase. (1 mark)

18 **Identify** the complementary strand for the nucleotide sequence below. (1 mark)
5′ G C A C C T T A C G T A A G C G 3′

19 If the rate of replication in a particular prokaryote is 800 nucleotides per second, **calculate** how long it would take to make two copies of a 1.4 million base pair genome. (3 marks)

20 **Explain** how the amount of each nitrogenous base (adenine, thymine, cytosine, guanine) can be used to identify different species. (3 marks)

21 **Explain** why half (one strand) of DNA is replicated in a discontinuous manner. (3 marks)

Analytical processes

22 Analysis of a sample of DNA extracted from a tissue showed that 38 per cent of the bases were adenine. **Determine** what percentage of the bases in the DNA would be guanine. Show how you arrived at your answer. (2 marks)

23 **Contrast** the structure of DNA and RNA. (1 mark)

24 **Contrast** the structure of DNA in prokaryotic and eukaryotic cells. (1 mark)

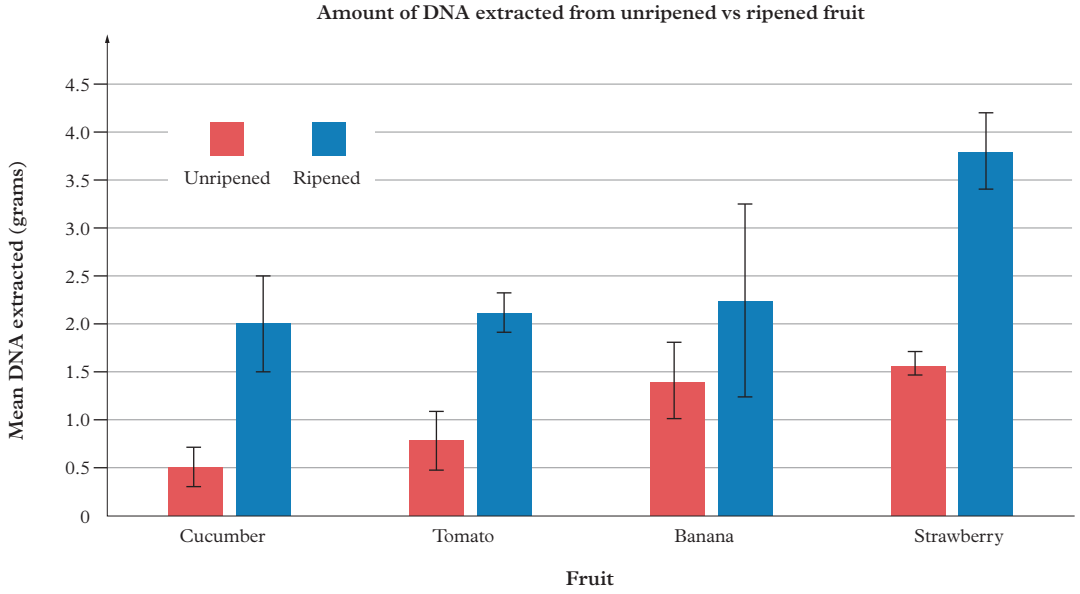
Knowledge utilisation

25 Bacterial cells were supplied with nutrients that contained radioactively labelled nitrogen. After division, the DNA strands of the daughter cells were found to contain labelled nitrogen. These daughter cells were then fed normal (not radioactive) food and, when they in turn divided, it was found that only half the "granddaughter" cells contained DNA with radioactive nitrogen atoms. **Justify** this finding. (4 marks)

Data drill

Interpreting data from a DNA extraction experiment

An experiment was conducted to extract DNA from 20 grams of unripened and ripened cucumber, tomato, banana and strawberry. The results are shown here.



Apply your understanding

1 **Identify** the amount of DNA extracted from unripened tomato. (1 mark)

2 **Calculate** the difference in mean amount of DNA extracted from unripened and ripened cucumber. (1 mark)

Analyse data

3 **Contrast** the amount of DNA extracted between unripened and ripened banana, using data from the graph (2 marks)

4 **Contrast** the reliability of the calculated mean amounts of DNA extracted from strawberry. (2 marks)

Interpret evidence

5 **Draw a conclusion** about the amount of DNA extracted from unripened and ripened fruit varieties, giving reasons for your conclusion. (2 marks)

Module 6 checklist: DNA structure and replication

MODULE 7

Gene expression

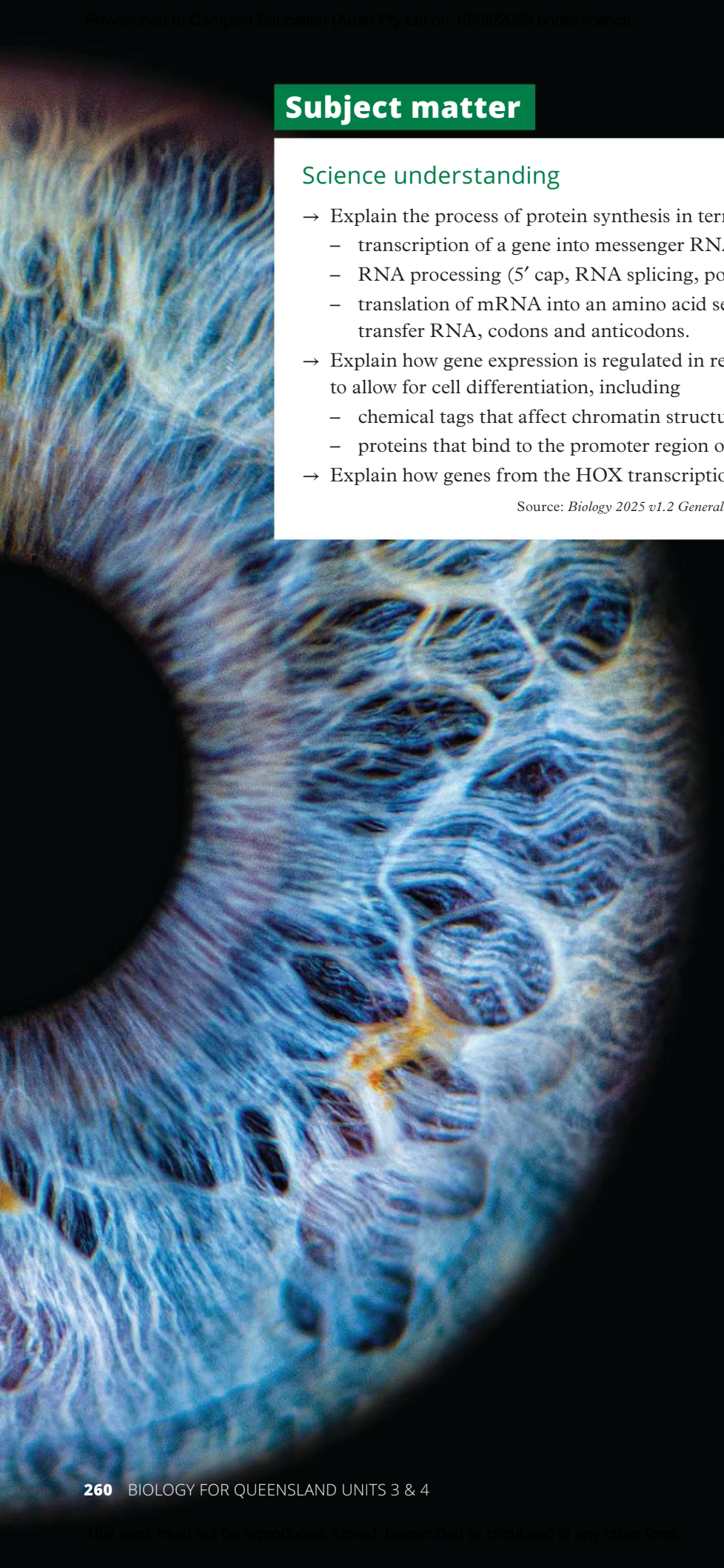
Introduction

The genome is all the genetic material in an organism. It is composed of coding and non-coding DNA. Gene expression is the process by which an organism's genotype gives rise to its physical traits, or phenotype. In this process, the information in the organism's DNA is converted into proteins in two stages: transcription and translation. In transcription, DNA in the nucleus is copied into mRNA and leaves the nucleus. In translation, the mRNA is converted into an amino acid sequence in the ribosomes. The amino acids are then assembled into proteins. A structural gene is a segment of DNA that produces a specific protein. Each amino acid in the polypeptide chain has a DNA code of three nitrogen bases. Sequences of codes are transcribed as complementary triplet codons of mRNA and translated at the ribosomes of the rough endoplasmic reticulum to form a polypeptide chain.

Gene expression is controlled by several factors, including non-coding regulatory genes involved in transcription and post-transcriptional processes. Epigenomic factors and specific developmental genes (e.g. homeotic genes and sex-determining genes) are also involved in gene expression.

Prior knowledge

Prior knowledge quiz Check your understanding of concepts related to gene expression before you start.



Subject matter

Science understanding

→ Explain the process of protein synthesis in terms of
  – transcription of a gene into messenger RNA in the nucleus
  – RNA processing (5′ cap, RNA splicing, poly-A tail)
  – translation of mRNA into an amino acid sequence at the ribosome, referring to transfer RNA, codons and anticodons.
→ Explain how gene expression is regulated in response to environmental signals and to allow for cell differentiation, including
  – chemical tags that affect chromatin structure (heterochromatin vs. euchromatin)
  – proteins that bind to the promoter region of a gene (transcription factors).
→ Explain how genes from the HOX transcription factor family regulate morphology.

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Lesson 7.1
Protein synthesis

Key ideas

- → DNA contains the information for protein synthesis.
- → In the process of transcription, DNA in the nucleus is copied into messenger RNA (mRNA), which exits the nucleus.
- → Translation of mRNA into an amino acid sequence occurs in the ribosomes.
- → Ribosomes assemble proteins by matching the amino acids delivered by tRNA to the mRNA sequence.

Learning intentions and success criteria

The genome

The **genome** is all the genetic material (genes and DNA sequences) in the chromosomes of an organism. Every cell (except mature red blood cells and gametes) in an organism's body contains a full "blueprint" – genome – and therefore contains all the genetic instructions required to build and maintain the entire body. In theory, this means that any cell, from a skin cell to a nerve cell, contains the genetic instructions to develop into any other type of cell in the organism. For example, the skin cells in your fingertips have the genetic material to develop into eye cells, and the nerve cells your brain have the genetic material to develop into a tooth. Luckily, your cells don't turn into these different types of cells, due to **cellular differentiation** – only some genes in the DNA of a cell are active, meaning different types of cells express different genes, determining the cell's structure and function.

genome
the complete set of nucleotide sequences encoded in the total DNA of an organism

cellular differentiation
the process of different cell types developing due to different sets of genes being turned on or off

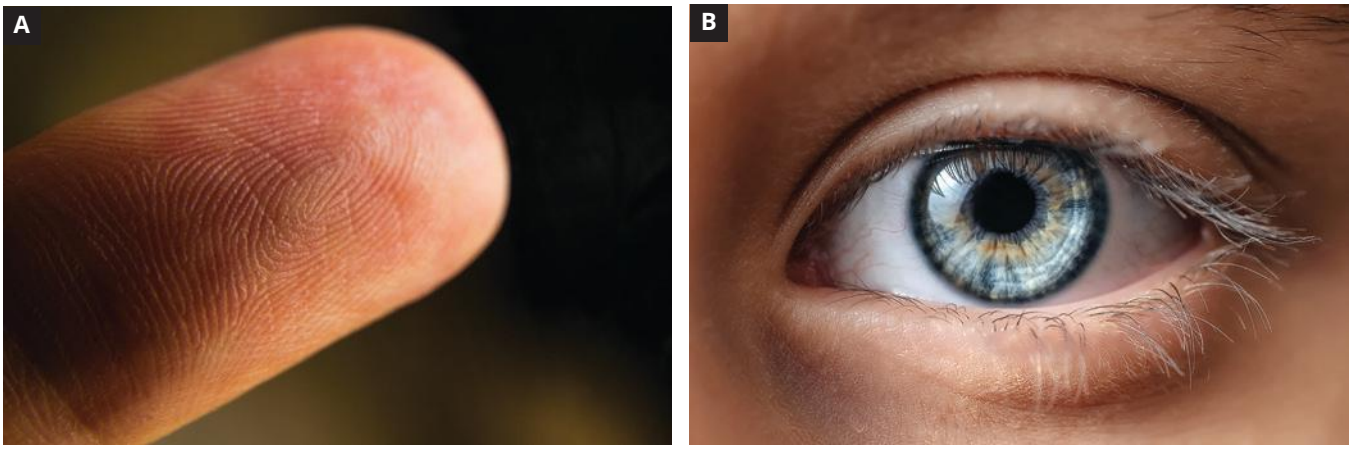


FIGURE 1 Different types of cells, such as (A) skin cells and (B) eye cells, express different genes, determining their structure and function

Gene expression

A **structural gene** is a segment of DNA that controls a specific characteristic. It is the molecular unit of heredity, with genes passed from parent to offspring. For example, the *TYR* gene in mammals is responsible for producing the enzyme tyrosinase. This enzyme causes the production of melanin, the brown pigment responsible for eye, skin and hair colour.

structural gene
a section of DNA that carries the instructions for production of a protein

FIGURE 2 The *TYR* gene causes the production of melanin, the pigment responsible for eye, skin and hair colour

Some people have an allele for this gene that produces a malformed enzyme. If a person has two copies of this recessive allele (homozygous recessive), they cannot produce melanin, and have an albino appearance. If a person is heterozygous (has one copy of each of the dominant and recessive alleles) then only the dominant allele that produces the tyrosinase enzyme is expressed. **Gene expression** is the most fundamental level at which the genotype, the allelic combination for a gene, gives rise to the phenotype (observable traits or characteristics) of an organism.

gene expression
the process of information encoded in a gene being used to produce a functional product, such as a protein

If a gene is expressed, the **genetic code** stored in DNA is "interpreted" and translated into the organism's phenotype. Phenotypes are often expressed by the synthesis of proteins that control the organism's shape or act as enzymes catalysing specific metabolic pathways that characterise the organism.

genetic code
a code used by the body to convert instructions contained in DNA into the proteins essential for life

Non-coding DNA

DNA that is responsible for producing proteins is known as "coding DNA". But not all DNA produces proteins. Recent studies have shown that a large proportion of DNA in each gene is **non-coding DNA**, which has various biochemical and structural functions, including:

- producing RNA (mRNA, rRNA, tRNA and non-coding RNAs that influence gene expression)
- regulating gene expression
- adding the end caps (telomeres) to each chromosome
- forming the centromere (point of attachment of chromatids during replication)
- developing the origin and terminus sequences involved in chromosome replication.

non-coding DNA
the part of the DNA molecule that does not contain structural genes; most DNA is non-coding

If segments of non-coding DNA control the expression of structural genes, they are termed **regulatory genes**.

regulatory gene
a non-coding segment of DNA that controls the expression of other genes, by producing transcription factors for gene expression

The role of DNA in protein synthesis

DNA contains information for protein synthesis. Proteins include structural components of the cell, hormones, antibodies and enzymes. Like DNA, protein is a polymer – a long chain of repeating monomer units. In the case of protein, the units are amino acids. DNA has only four types of nucleotides, and the order of these nucleotides determines the order of amino acids in a protein polymer. Similarly, there are only 20 types of amino acids, but these can be arranged in a wide variety of combinations to form many different proteins.

messenger RNA (mRNA)
a type of RNA molecule formed during transcription

There are 20 amino acids but only four kinds of bases in DNA. So a single base does not determine which amino acid will be used in a protein sequence. Instead, the nucleotides in DNA are grouped into threes (a triplet). Each triplet contains the code for a single amino acid. This series of nucleotide triplets forms the basis of the genetic code.

transcription
the first step of gene expression, in which a particular segment of DNA is copied into mRNA

codon
a triplet of nucleotides on mRNA that codes for a particular amino acid

Transcription

During protein synthesis, the DNA does not leave the cell's nucleus. Instead, the code is transcribed (copied) into another nucleic acid, known as **messenger RNA (mRNA)**. The process of transferring the code from DNA to mRNA is called **transcription**.

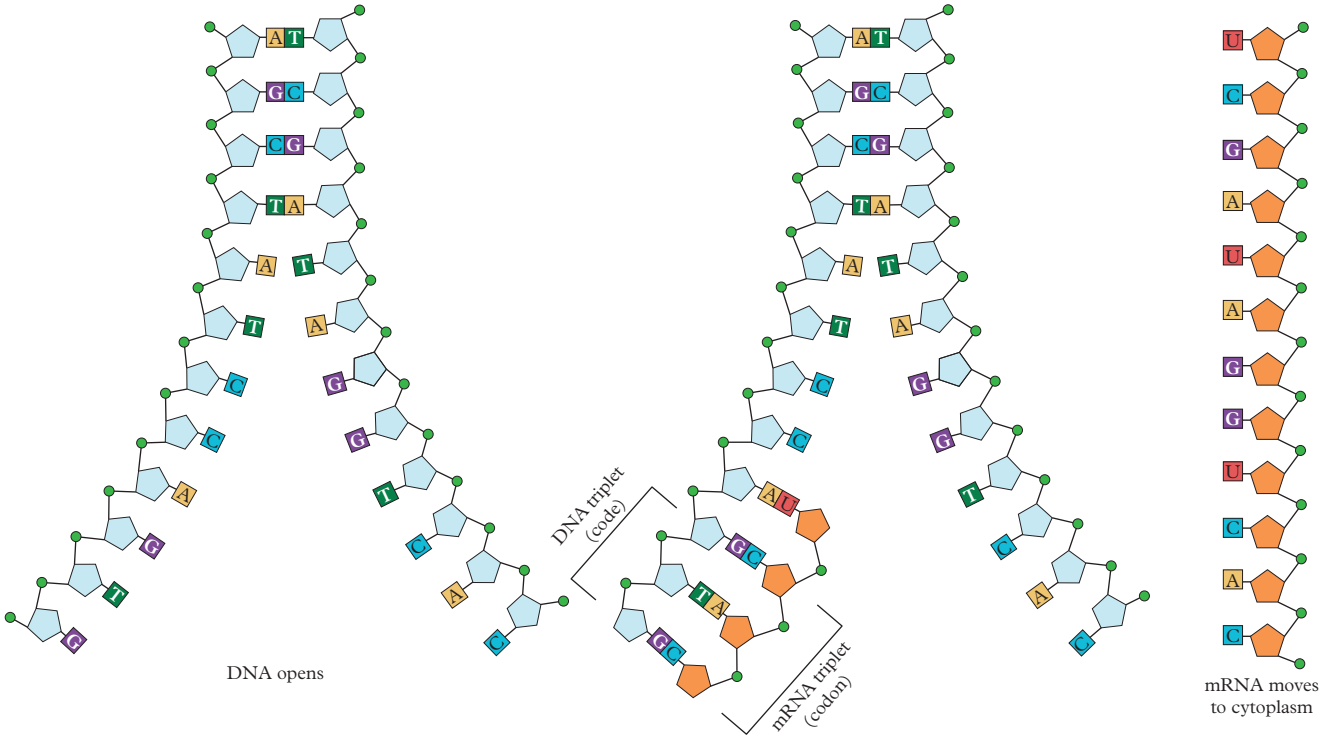


FIGURE 3 Transcription: the formation of messenger RNA

Transcription begins with part of the DNA molecule "unzipping" to expose the nitrogen bases that will form the template for the mRNA. Each gene has a specific recognition sequence of nucleotides that is able to bind to an enzyme called RNA polymerase. As the RNA polymerase moves along the template DNA strand, it adds an RNA nucleotide that is complementary to the DNA. RNA molecules do not contain thymine; instead, uracil is used as a complement to adenine. When the messenger RNA is complete, it detaches and the two DNA chains then re-join. The triplets on DNA have now been transcribed into **codons** on the mRNA:

DNA base sequence (triplet codes): GTG ACC TAT CGA
mRNA base sequence (triplet codons): CAC UGG AUA GCU

split gene
a gene that contains coding regions, called exons (expressed as RNA and protein), interrupted by non-coding regions, called introns

splicing
a post-transcriptional process in which introns are removed and exons are connected, to produce mature mRNA

intron
a segment of DNA or RNA within a gene that does not code for proteins and is removed during RNA processing

exon
a segment of DNA or RNA within a gene that contains the code for producing a protein

Post-transcriptional modification

In bacteria, the mRNA is now ready to be translated into a protein. In eukaryotes, the mRNA can contain non-coding sections that are not needed to produce a functioning protein (**split gene**). In a process termed **splicing**, these non-coding **introns** are removed by enzymes in the nucleus, and the remaining coding **exons** are re-joined to form mature mRNA.

trimming
the removal of non-coding sections at the beginning and end of mRNA

Study tip

To remember which sections are removed during splicing, think "**in**trons are **in** the way, **ex**ons are **ex**cellent".

capping
the addition of methyl-guanine at the start of the trimmed mRNA

tailing
the addition of a long tail of adenines at the end of mRNA

After transcription, before the mature mRNA can leave the nucleus there are extra nucleotides at the beginning and end that need to be removed (**trimming**). The start of the mRNA is then **capped** with methyl-guanine, and a long "tail" of adenines (poly-A tail) is added to the other end (**tailing**). These caps and tails are thought to aid the binding of the mRNA to the ribosomes and make it more stable.

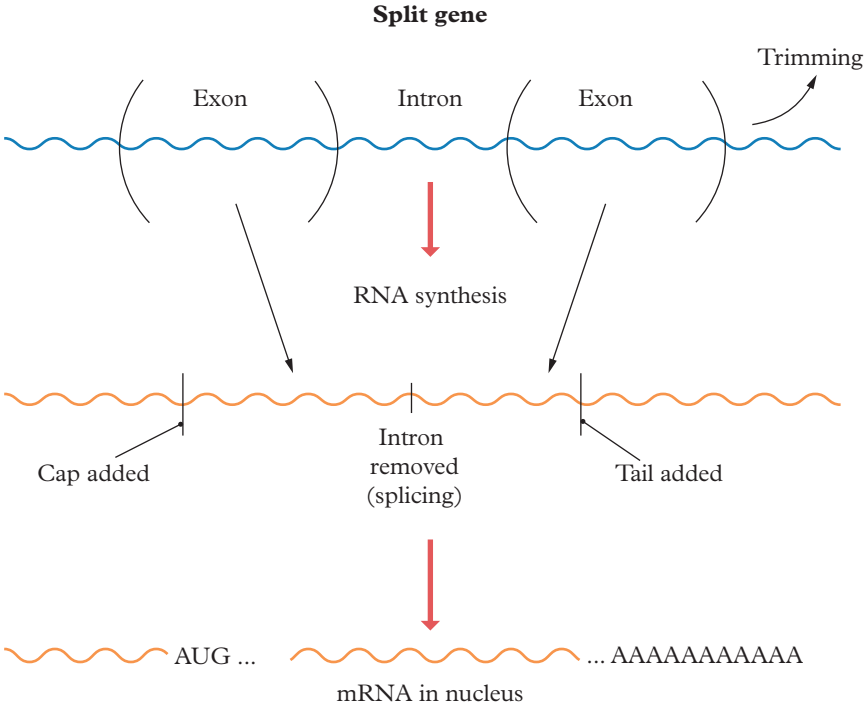


FIGURE 4 Splicing, capping and tailing of mRNA in eukaryotic cells

Transfer RNA

transfer RNA (tRNA)
small segments of RNA that transport specific amino acids to the mRNA attached to a ribosome during translation

anticodon
a triplet of nitrogen bases on tRNA

Certain genes produce another type of RNA, called **transfer RNA (tRNA)**. The chain of nucleotides in tRNA is folded into a clover-leaf arrangement (Figure 5). The open end of the chain is the site for attachment of a specific amino acid (determined by the base sequence). Each tRNA links with only one type of amino acid, in a reaction that requires a specific enzyme and ATP. As a result, there are many types of tRNA. At the central loop of the clover leaf is a triplet of unpaired bases. These three bases serve as an **anticodon** to match a specific mRNA codon. This means the tRNAs must line up to match the codons on the mRNA. As a result, the amino acid sequence will exactly match the correct codon sequence of the mRNA (which matches the triplet code on the DNA).

Translation

translation
the production of a polypeptide sequence from a sequence of mRNA codons

ribosomal RNA (rRNA)
the RNA component of a ribosome

Translation is the process of using the information encoded on the mRNA to synthesise a protein. Protein synthesis begins when RNA becomes associated with a ribosome – (composed of **ribosomal RNA (rRNA)** – either on the rough endoplasmic reticulum or free-floating, in the cytoplasm. The ribosome serves as the site for protein synthesis. Translation of the mRNA into a protein chain is initiated by the ribosome identifying the "start" codon, AUG, on the mRNA. This is also the codon for the amino acid methionine. A tRNA with a matching anticodon to AUG, and correspondingly carrying the amino acid methionine, binds to the mRNA codon within the ribosome.

The ribosome moves along the mRNA strand, one codon at a time. As the ribosome moves to each new codon position, a tRNA carrying its specific amino acid approaches. If the tRNA's anticodon is complementary to the codon, it binds to the codon on the mRNA. The ribosome then catalyses the formation of a peptide bond between the amino acid of the incoming tRNA and the amino acid of the previous tRNA, growing the chain. The formation of the bond releases the first tRNA, which can now join with another amino acid in the cytoplasm.

Study tip

Non-coding DNA used to be called "junk" DNA, but it is now known that many of these small sections of DNA are important in controlling how genes are expressed, or the length of time that mRNA can survive in the cell.

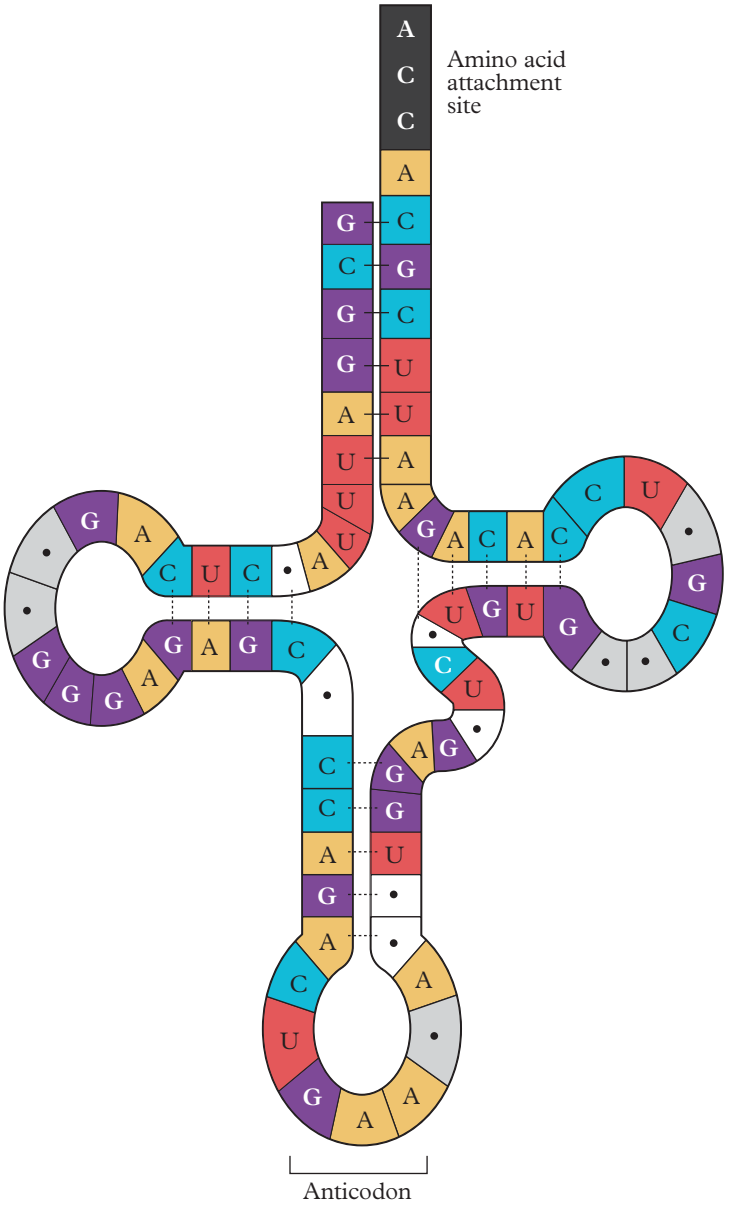


FIGURE 5 Structure of a tRNA molecule

As the ribosome moves along the mRNA, more and more amino acids are added to the growing polypeptide chain. This process is repeated until the ribosome reaches a "stop" codon on the mRNA, where it drops off and liberates its polypeptide chain. A "stop" codon is one of three codons – UAG, UAA or UGA – that stops the ribosome reading the "message".

Once released from the ribosome, the polypeptide chain will either undergo changes to form a functional protein in the cytoplasm or be released into the endoplasmic reticulum canals for further reactions. Some proteins may also be transferred to the Golgi apparatus, where they are processed further.

polysome
a chain of ribosomes that "read" mRNA

Because many ribosomes (**polysomes**) can move along the mRNA simultaneously, each synthesising a polypeptide chain, many polypeptides can be assembled on a single mRNA strand in a comparatively short time. Eventually, the mRNA is broken down and production of that specific polypeptide ceases.

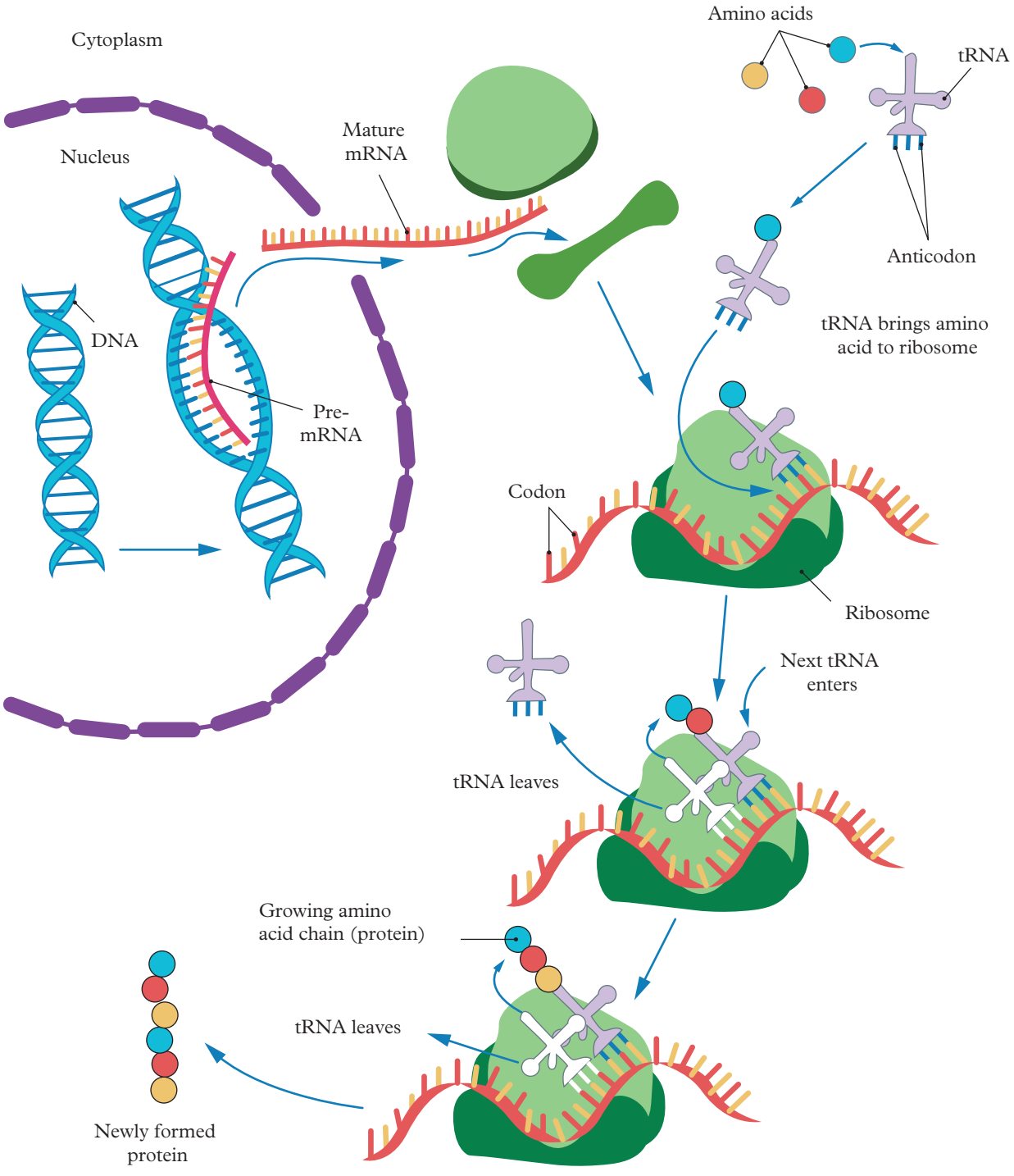


FIGURE 6 Summary of protein synthesis

Skill drill

Codon combinations

Science inquiry skill: Processing and analysing data (Lesson 1.7)

There are 64 possible codon combinations. All but three of these combinations have been found to correspond with an amino acid. Those that do not are the "punctuation marks" (e.g. stop or start signals) of the code. These 61 triplets code for only 20 amino acids, so some amino acids have more than one codon. For example, the mRNA codons AAA and AAG both code for the amino acid lysine.

A codon chart can be used to identify which codon sequence in the mRNA corresponds with which amino acid. For example, if the first nucleotide of the codon in cytosine, the second is adenine, and the third is uracil, then a tRNA with a histidine (His) amino acid will bind to the mRNA and add its amino acid to the growing peptide chain.

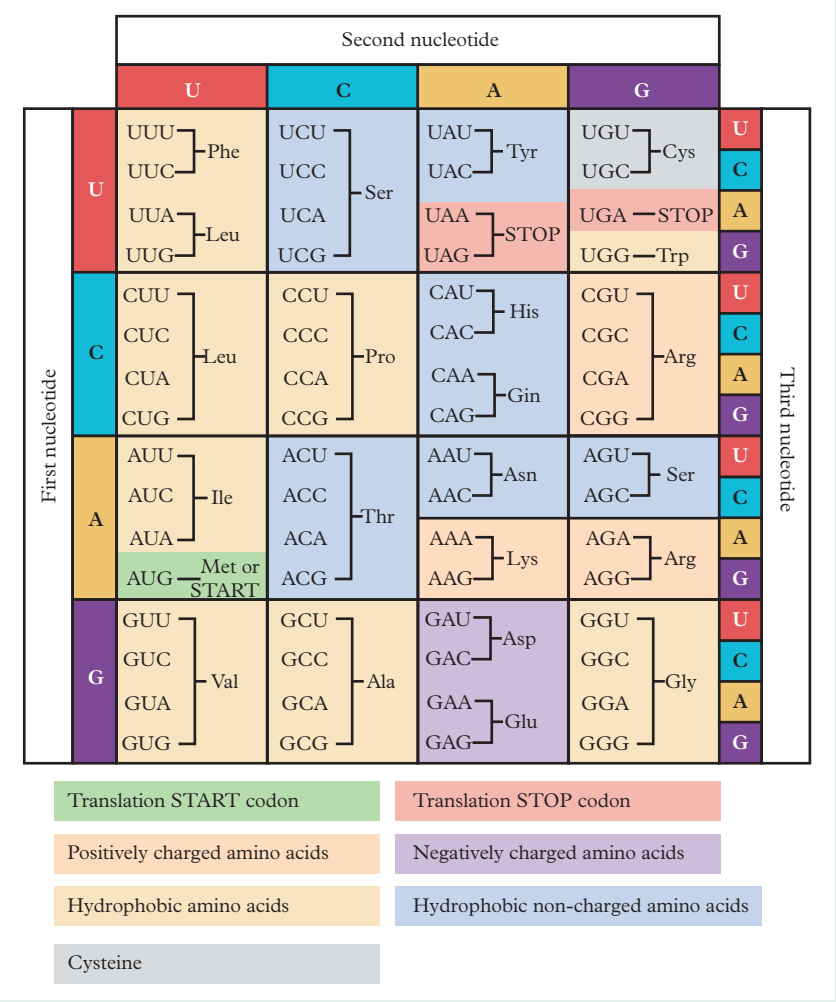


FIGURE 7 Codon chart

Practise your skills

1 **Identify** the mRNA sequence that would be translated from the following DNA sequence: 5′ TAC CAA CDA TGG CTA CCA ACU 3′. (1 mark)

2 **Determine** the corresponding amino acids by using the codon chart to transcribe the mRNA sequence from question **1**. (1 mark)

3 **Determine** the effect on the peptide chain produced if the first base in the DNA sequence was changed from a thymine to a cytosine. (1 mark)

Check your learning 7.1

Check your learning 7.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Identify** the molecular unit of heredity. (1 mark)
2 **Identify** the part of a cell in which the following processes occur.
   a Transcription (1 mark)
   b Translation (1 mark)
3 **Describe** the role of RNA polymerase in protein synthesis. (2 marks)
4 **Explain** the process of
   a transcription of a gene (3 marks)
   b translation of mRNA. (5 marks)
5 **Explain** why the mRNA used for translation is shorter than when it was originally copied during transcription. (3 marks)

Analytical processes

6 **Differentiate** between structural genes and regulatory genes. (1 mark)
7 If a DNA codon is represented by AAT, **determine** the anticodon on the appropriate tRNA. (1 mark)
8 **Contrast** the roles of mRNA and tRNA in protein synthesis. (1 mark)

Lesson 7.2
Regulation of gene expression

Key ideas

→ Transcription of genes is tightly regulated by transcription factors, and allows for cell differentiation.
→ Chemical tags on DNA can affect the expression of genes without changing the DNA sequence.
→ The epigenome is influenced by environmental factors.

Learning intentions and success criteria

gene regulation the process that controls when, where and how much a gene is expressed in a cell

Gene regulation

Cells require different proteins at different times and in different amounts. Some genes constantly transcribe the proteins involved in basic metabolic functions. Other genes are only active in specific circumstances. **Gene regulation** is the process of controlling which genes in a cell's DNA are expressed. The expression or "switching on" of certain genes and repression or "switching off" of other genes results in cell differentiation. For example, the active genes of muscle cells only transcribe the polypeptides that are essential for muscle cell operation. In a muscle cell, the genes that are important in nerve cells are switched off.

If all the genes were continuously activated (expressed), the muscle cell would use a lot of energy and resources to produce unnecessary proteins. Regulation of gene expression is therefore important in cell differentiation. Genes can be regulated at different stages:

- pre-transcription
- post-transcription
- translation.

FIGURE 1 Gene regulation determines which genes in a cell will be expressed (switched on) and which will be repressed (switched off)

Pre-transcriptional control

Transcription occurs only when the chromosomes are in the form of chromatin threads. This is initiated when the DNA coding for a specific polypeptide "unzips" to expose the nucleotide bases and its starting point, to which the RNA polymerase attaches. Regulatory genes associated with the structural gene can produce functional RNA or proteins that act as **transcription factors**. These factors can attach to the promotor region of a structural gene to either:

- block the attachment of RNA polymerase, and so block the expression of that gene, or
- alter (accelerate or decrease) the rate at which the gene is expressed.

In some situations, gene expression is altered by the environment influencing the regulatory gene. The presence of a large amount of glucose, for example, would result in increased expression of the gene coding for insulin, and block the gene for glucagon. In contrast, minimal amounts of glucose would block insulin production and enhance glucagon production in pancreas cells.

transcription factor
a protein produced by regulatory genes that regulates the phenotypic expression of structural genes

FIGURE 2 The presence of a large amount of glucose can result in increased expression of the gene coding for insulin

Post-transcriptional control

Once mRNA has been produced, cells can control the amount of protein produced. This is achieved by modifying the post-transcriptional process, or the longevity of the mRNA. Non-coding DNA can block or alter the rate of trimming, capping and tailing of the mRNA. For example, if the non-coding introns are not removed correctly, the resulting mRNA may be broken down by enzymes.

Some small non-coding RNA molecules may bind to the mRNA to form a double-stranded RNA (either by true pairing with the nucleotides or by imperfectly pairing), which then cannot be translated.

Once the mRNA is completed, it must pass through the nuclear pores to the cytoplasm. This is an active process that requires recognition of the transcript by receptors lining the interior of the nuclear pores. This allows further control, and gene expression is achieved by alteration of the pore receptors.

Translational control

Ultimately, any particular mRNA will be enzymatically degraded. Gene expression can be regulated by controlling the length of time the mRNA survives before it is degraded. For example, microRNA (small single-stranded non-coding RNA molecules) can bind to mRNA to either mark it for destruction by enzymes or preserve it to be translated later.

Many proteins and amino acids are involved in the translation process. Controlling the amounts of these molecules can increase or decrease the rate of gene expression.

Even after a polypeptide chain has been formed, chemical modification is required before the final protein is produced. Again, the availability of additional chemical groups, or enzymes, will affect the complete expression of the gene.

Epigenetic control of gene expression

Studies of identical twins (who have exactly the same genome) have determined that environmental factors play a large part in controlling the transcription of a gene. Over the past 20 years, a great deal of research has been undertaken to determine the extent to which the environment affects gene expression, how this is achieved and whether these factors are inheritable.

The **epigenome** ("above the genome") is a set of factors that affect which part of the DNA is activated. These factors may occur due to intracellular or extracellular stimuli, by neighbouring cells, by physiology, or entirely by the environment the organism is exposed to.

epigenome
a system of gene control that extends beyond DNA ("above the genome")

Each cell type in an individual's body has its own epigenome. Muscle cells (which express only the genes they need) can only replicate to form muscle cells. Throughout the individual's life, the DNA in all cells remains constant (excluding chance mutations), but the epigenetic factors in each cell may change. This may be due to puberty, the stage of the menstrual cycle, environmental stress or lifestyle changes.

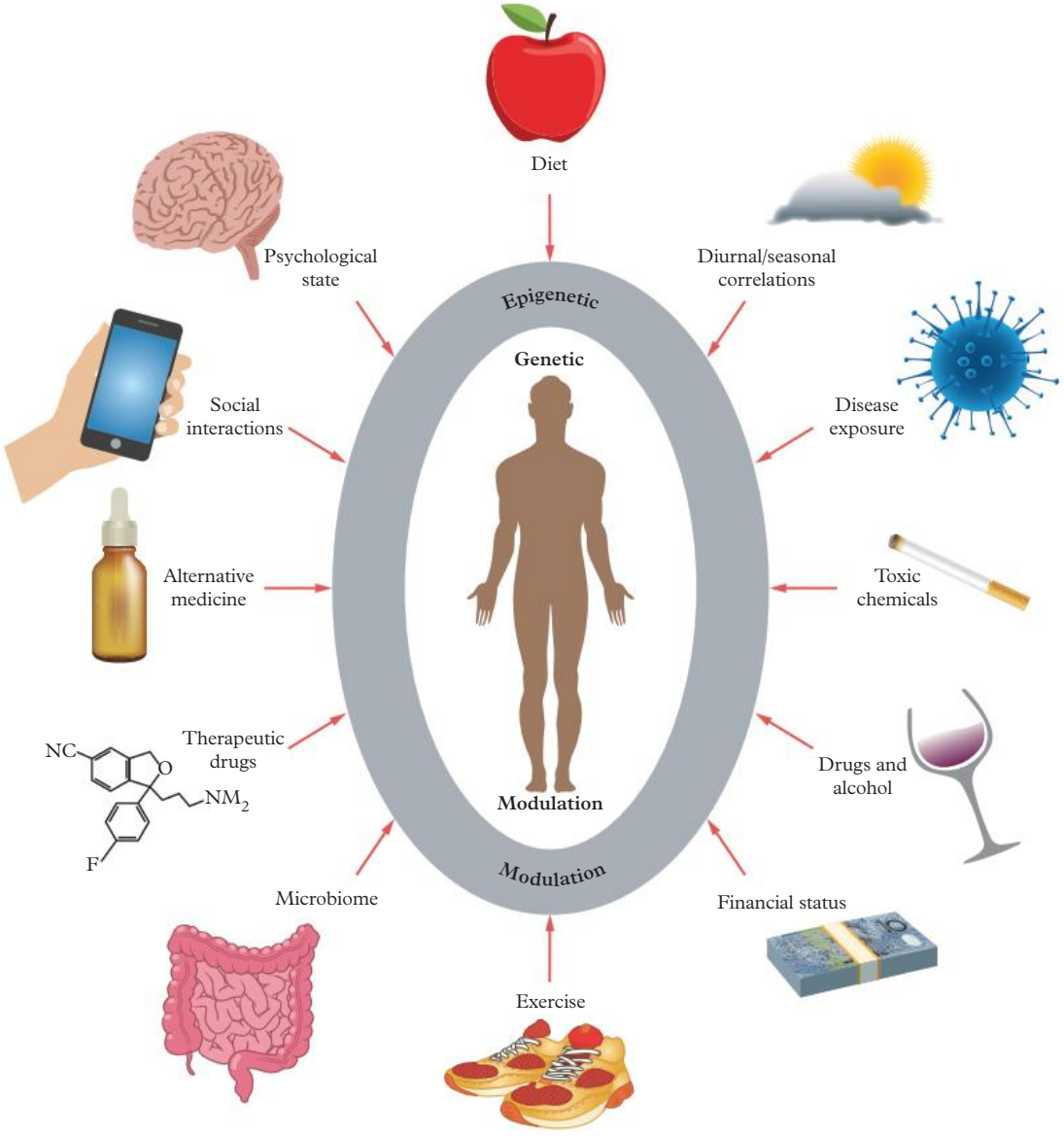


FIGURE 3 Environmental factors affecting epigenetic control in humans

The epigenome acts by producing chemical tags or factors (methyl or acetyl groups) that do not change the DNA "blueprint", but determine which genes are switched on (expressed) and which are switched off (repressed). This can occur at several levels.

FIGURE 4 During puberty, epigenetic factors in your cells change

Histone modification

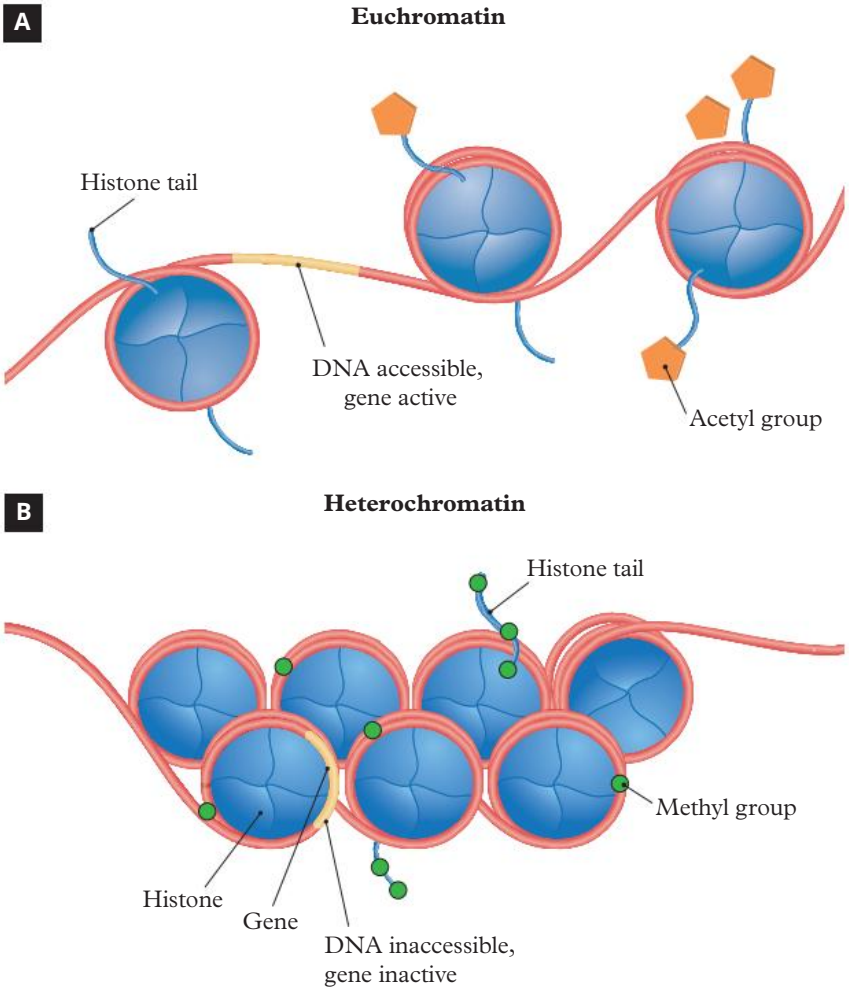
Each DNA molecule in the non-dividing cell nucleus is in the form of fine threads of chromatin that at intervals are wrapped around four pairs of histone protein molecules to form nucleosomes. There are two forms of chromatin:

- **heterochromatin**
- **euchromatin**.

heterochromatin chromatin that is tightly coiled around histone proteins in the nucleosome, making the genes inaccessible, so they cannot be transcribed

euchromatin "relaxed" chromatin that is loosely coiled around histone proteins in the nucleosome; contains genes that can be accessed for transcription

Heterochromatin is tightly coiled around the histone proteins, whereas euchromatin is not so condensed, allowing the DNA to be loosely packed (Figure 5). Euchromatin contains most of the active genes of an organism and so is actively involved in the transcription of DNA to mRNA.



histone modification the addition of chemical tags that vary the width between nucleosomes and thereby determine whether a gene can be transcribed

FIGURE 5 The two forms of chromatin, euchromatin and heterochromatin, exist naturally in cells, regardless of epigenetic tags. However, chemical modifications such as DNA methylation and histone modifications (acetylation or methylation) shift chromatin between the two states. (A) In euchromatin, an acetyl group attaches to histone tails, the nucleosome coiling is loosened and the gene can be expressed. (B) In heterochromatin, a methyl group attaches to the histone tails and the nucleosomes pack tightly together, resulting in gene inactivation

The nucleosomes can be spaced tightly together or far apart. The spacing is controlled by the presence or absence of chemical tags attached to the tails of the histone proteins that either pull the nucleosomes closer together or allow the structure to be more open.

When an acetyl group tag attaches to specific amino acids on the tails of the histone molecules in a nucleosome, the histone structure relaxes, and the nucleosomes move further apart. This section of the DNA is more easily accessed for transcription – the gene is switched on. Methyl group tags on other sites of the tails of histone molecules of the nucleosome make the coiling of the chromatin tighter and the nucleosomes closer together. The DNA between the nucleosomes cannot be accessed and any genes contained in those sections cannot be read. The genes are switched off in those sections of DNA.

Histone modifications are often transitory and can be reversed according to the chemical environment of the cell at any particular time. Studies have suggested that tags associated with histone modification are not inherited.

DNA tags

A chemical tag (methyl group) can also be attached to the start of the functional gene (**DNA methylation**). If the attachment of RNA polymerase is blocked, the gene cannot be transcribed.

Some tags are environmentally induced, but generally the pattern of DNA tags is a stable epigenetic marker set in early development. During fertilisation and the first few rounds of cell division, most DNA tags are removed, so cells in the early embryo are able to express any of their genes. These are totipotent stem cells. Some of the remaining tags on certain genes of either the mother or the father may be retained. Sometimes other DNA tags are not completely removed and are passed down from parent to offspring. The inheritance pattern may therefore be unpredictable.

DNA methylation
the addition of a chemical tag (a methyl group) to the start of a structural gene, to block transcription

dizygotic twins
twins that develop from two separate eggs, each egg having been fertilised by a different sperm cell

monozygotic twins
twins that develop from one zygote, when it splits and forms two embryos; because both twins have the same genotype, they are considered identical

concordance
the extent to which both twins exhibit the same trait or condition, indicating the influence of genetic and environmental factors

Real-world biology

Identical twins

Twins result when two embryos develop simultaneously, They can be either monozygotic or dizygotic.

Dizygotic (two zygotes) **twins** result when two ova are fertilised in one cycle. They are also known as fraternal twins. Because two eggs are released, two different sperm are involved in fertilisation. The twins will therefore have different combinations of their parental genes. Not only will they look and behave differently, but they can also be different sexes.

Monozygotic (one zygote) **twins** result from changes in a single zygote during early cell division. These twins have the same genetic information, so they are the same gender and can be termed "clones". Twinning occurs during the early development of the embryo, but different timing of separation gives rise to several forms of monozygotic twins.

- If separation occurs 4–8 days after fertilisation, these twins are completely identical.
- If separation occurs after the 8th day, these twins are mirror-images of each other (e.g. one is right-handed, the other is left-handed). It is as though they are facing a mirror.
- If the twinning process occurs after the 13th day, the separation is not complete. These twins remain co-joined physically at any part of the body, often sharing one or more organs. These twins are commonly called "conjoined" twins.

Concordance refers to the presence of the same trait or characteristic in both members of a pair, such as twins. In genetic studies, concordance is often used to measure how frequently both individuals in a twin pair (especially identical twins) exhibit the same trait or disease. Identical (monozygotic) twins share nearly 100 per cent of their genes.

If both twins have the same trait, such as eye colour, height or a genetic disorder (e.g. cystic fibrosis), they are said to be concordant for that trait. If only one twin has the trait, they are discordant. Fraternal (dizygotic) twins, on the other hand, share about 50 per cent of their genes, like regular siblings. The rate of concordance for traits in fraternal twins can give insights into the relative influence of genetics versus environment on the development of that trait. Therefore, a high concordance rate for a trait among identical twins compared to fraternal twins suggests a stronger genetic component for that trait.

Although monozygotic twins are genetically identical (i.e. clones), there are often considerable differences between the individuals, in things such as height, head shape and size. This is because the prenatal and post-natal environments in which two individuals develop may be different. If twins share a common placenta, there may be competition between them for nutrient supply and waste removal, resulting in serious imbalances in the weight and size of each individual that may persist for life. Also, contrary to popular belief, identical twins do not have identical fingerprints.

Studies of identical twins reared apart have shown how significant genes are in development. In one study, a set of twins who were separated at birth and reared in different countries both wore rubber bands around their wrists, sneezed loudly to get attention and clipped their moustaches in a particular way. Similar studies suggest that other traits, such as leadership ability, imagination and vulnerability to stress, are strongly influenced by heredity. This genetic phenomenon has been seen in most separated twins.

Apply your understanding

1 **Contrast** monozygotic and dizygotic twins. (1 mark)

2 **Explain** how the effect of the environment on gene expression can be investigated using twin studies. (3 marks)

FIGURE 6 Types of twins: (A) dizygotic (fraternal) twins, (B) monozygotic (identical) twins and (C) mirror-image twins

Inheritance of epigenetic factors

During World War II, Nazi troops occupied the Netherlands, and from 1944 to 1945 a German blockade cut off food supplies to the country. It has been found that people who were conceived during this time had increased rates of coronary heart disease and obesity compared with people whose mothers were not exposed to famine during pregnancy. These problems were found to be associated with less DNA tagging of insulin-like growth factor II. This epigenetic control has been shown to be inherited over at least three generations.

Similarly, a study of children born after World War II to Holocaust survivors with post-traumatic stress syndrome (PTSS) found that these children were more likely to develop this condition or depression compared with children born to adults who had not experienced PTSS. They shared epigenetic tags with their parents that made them more reactive to stress.

It is not exactly clear how these epigenetic tags are inherited across generations, but because the basic DNA tags are laid down during development, the environment or diet of the pregnant mother can potentially have subtle effects upon the DNA tagging patterns of the epigenomes during prenatal and early post-natal development. In a female, a lifetime supply

of eggs is created in the foetus, as are the sperm stem cells of a male, meaning it is also likely that the mother's epigenomes can affect the egg or sperm cells of the developing foetus. The activity of a pregnant woman could, therefore, affect the lives of her grandchildren.

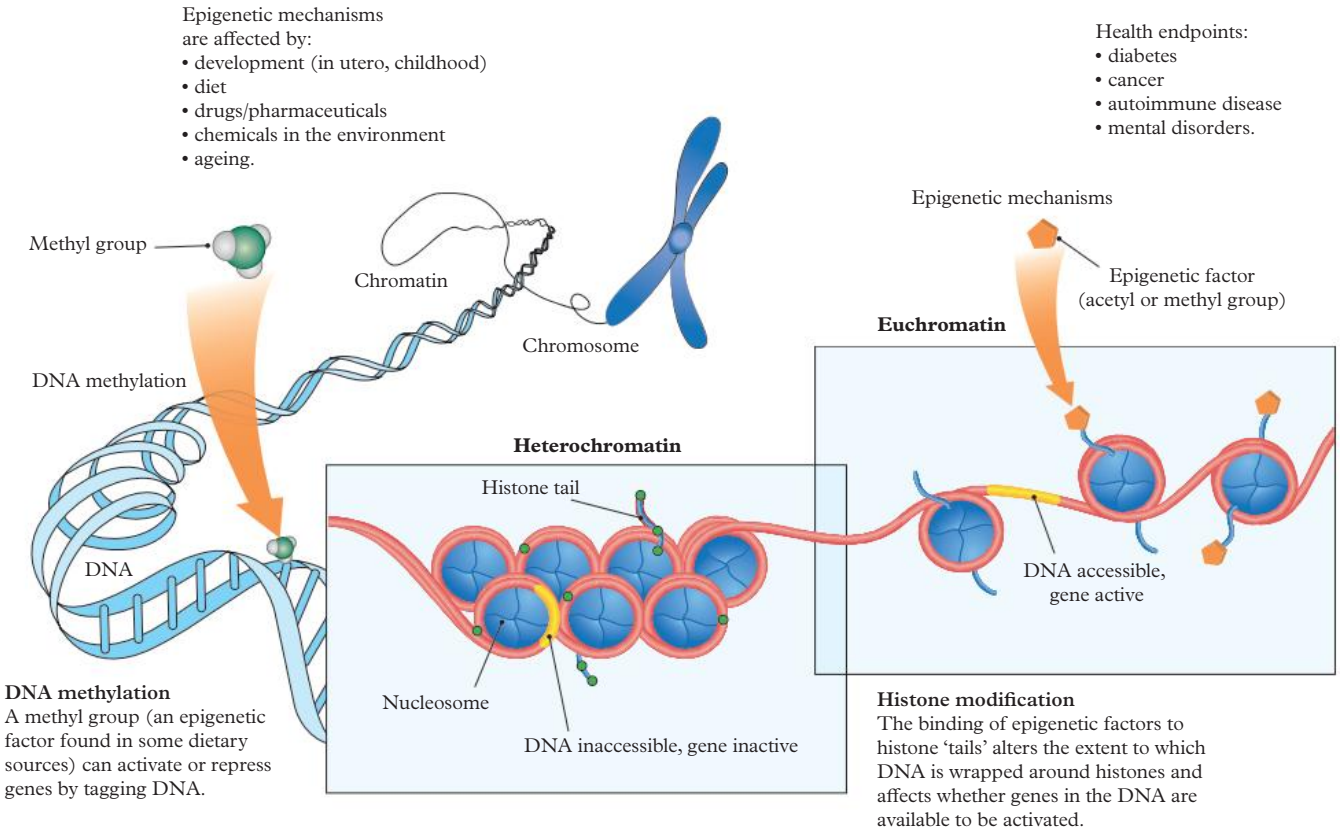


FIGURE 7 Chromatin structure, which incorporates histones and DNA, can become accessible to epigenetic mechanisms. This diagram is a summary of epigenetic control of gene expression. Note that not all epigenetic effects are negative

Challenge

How to make a queen bee

In honeybees, the development of a queen versus a worker bee is a remarkable example of how epigenetics, rather than genetic differences, shapes an organism's destiny. All bee larvae are genetically identical, but their developmental pathways diverge based on their diet. Larvae fed royal jelly, a nutrient-rich secretion produced by worker bees, undergo significant epigenetic changes. These changes occur primarily through DNA methylation, a process that silences certain genes. In the case of a future queen bee, royal jelly suppresses the genes responsible for the development of a worker bee, allowing the activation of genes that promote queen characteristics, such as larger size, reproductive capabilities and longevity. Studies have also found that DNA methylation varies between bees with different roles in the hive, such as those that nurse the growing offspring versus those responsible for foraging.

FIGURE 8 A queen bee surrounded by worker bees

1 **Explain** the role of DNA methylation in the differentiation between queen and worker bees, and how this process is influenced by environmental factors. (3 marks)
2 **Suggest** how epigenetic changes in honeybees, like those triggered by royal jelly, might provide insights into the potential effects of environmental factors on gene expression in other species, including humans. (2 marks)

Check your learning 7.2

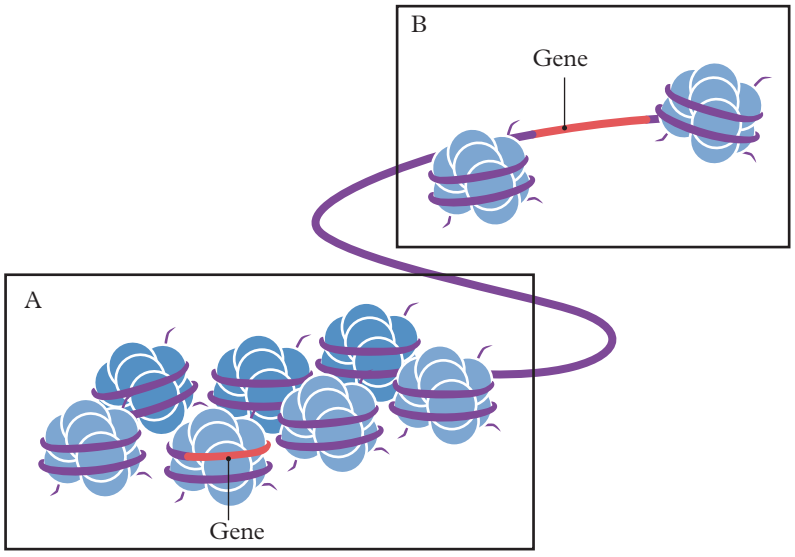
Check your learning 7.2: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** two post-transcriptional processes that influence gene expression. (2 marks)
2 **Define** the "epigenome". (1 mark)
3 **Explain** how transcription factors regulate gene expression. (3 marks)

Analytical processes

4 **Contrast** histone modification and DNA methylation. (1 mark)
5 The figure below depicts the process of histone modification. **Determine** which diagram, A or B, is euchromatin and which is heterochromatin, giving reasons for your response (4 marks)



Lesson 7.3
HOX genes

Key ideas

→ Transcription factors enable differential gene expression and cell differentiation.
→ The HOX transcription factor family regulates the homeotic genes that determine which anatomical structures of the body the cells will differentiate into.

Learning intentions and success criteria

homeotic gene any of a group of related genes that control the body plan of an embryo along the head–tail axis during early embryonic development

HOX transcription factor family

Many transcription factors regulate gene activity. Some are produced by non-coding DNA, while others are produced by structural genes. Every sexually produced organism starts life as a single cell. Over the first few hours and days of life, this cell first multiplies, then the cells start specialising into heads, limbs and tails. **Homeotic genes** are genes in the cells that

determine which anatomical structures of the body the cells will differentiate into. The term *HOX* is a contraction of **homeobox**, which is a DNA sequence of approximately 180 base pairs within the genes. These are involved in the regulation of anatomical development in animals, plants and fungi.

homeobox
DNA sequence (of about 180 base pairs) contained in a gene (e.g. the *HOX* gene) that is highly conserved and can bind to DNA to control gene expression

homeobox (*HOX*) genes
a subgroup of homeotic genes that control the body plan of an embryo along the head–tail axis

HOX protein
a transcription factor produced by a *HOX* gene

HOX genes

Homeobox (*HOX*) genes (a subset of homeotic genes) are a group of related genes that control the body plan of an embryo along the head–tail axis. In animals they control the formation of the segmentation of the embryonic body plan. After these segments have formed, **HOX proteins** (the products of *HOX* genes) act as transcription factors that determine the type of appendages that will form on a segment. HOX proteins control the identity of the body segments through gene regulation, but do not form the actual segments themselves.

HOX genes were first discovered in fruit flies, where developmental errors were seen (e.g. legs appearing on the head instead of antenna, due to an error in the antenna gene) (Figure 1). Mutations in any one of the *HOX* genes may cause the growth of an extra and sometimes non-functioning body part (e.g. a set of wings on each of two thoraxes, known as a homeotic mutation). The normal body plan has one thorax.

Although a very large number of genes are involved in morphological animal development, *HOX* genes exert the most powerful influence. These are master controllers that can turn genes on or off using transcription factors, and so control gene expression. The sequencing and positioning of the *HOX* genes on chromosomes indicate a common ancestor of the fruit fly, the mouse and human beings.

The body segmentation of the fruit fly is easy to see, but in humans it is only evident in the vertebrae and spinal nerves of the vertebral column (Figure 2). In a well-developed muscular person, segmentation can be seen in the "six pack" of their abdominal muscles (Figure 3).

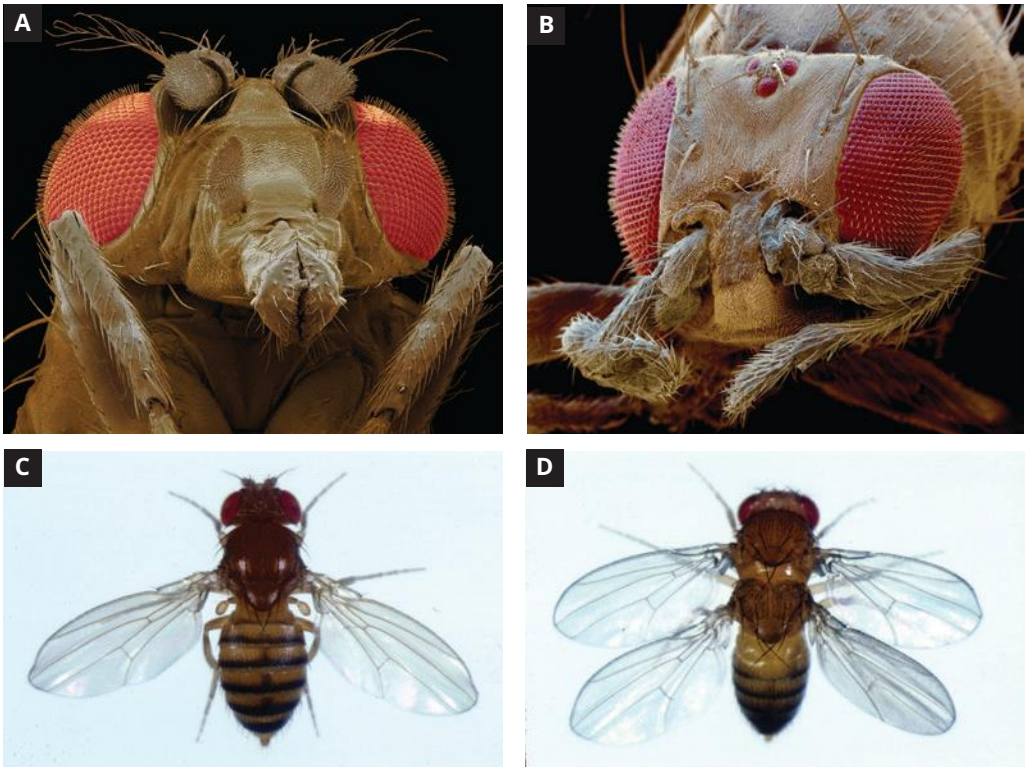


FIGURE 1 Fruit fly mutations: (A) normal fruit fly antenna, (B) fruit fly with mutation in antenna gene, (C) normal fruit fly thorax, (D) fruit fly with a homeotic mutation that gives it two thoraxes

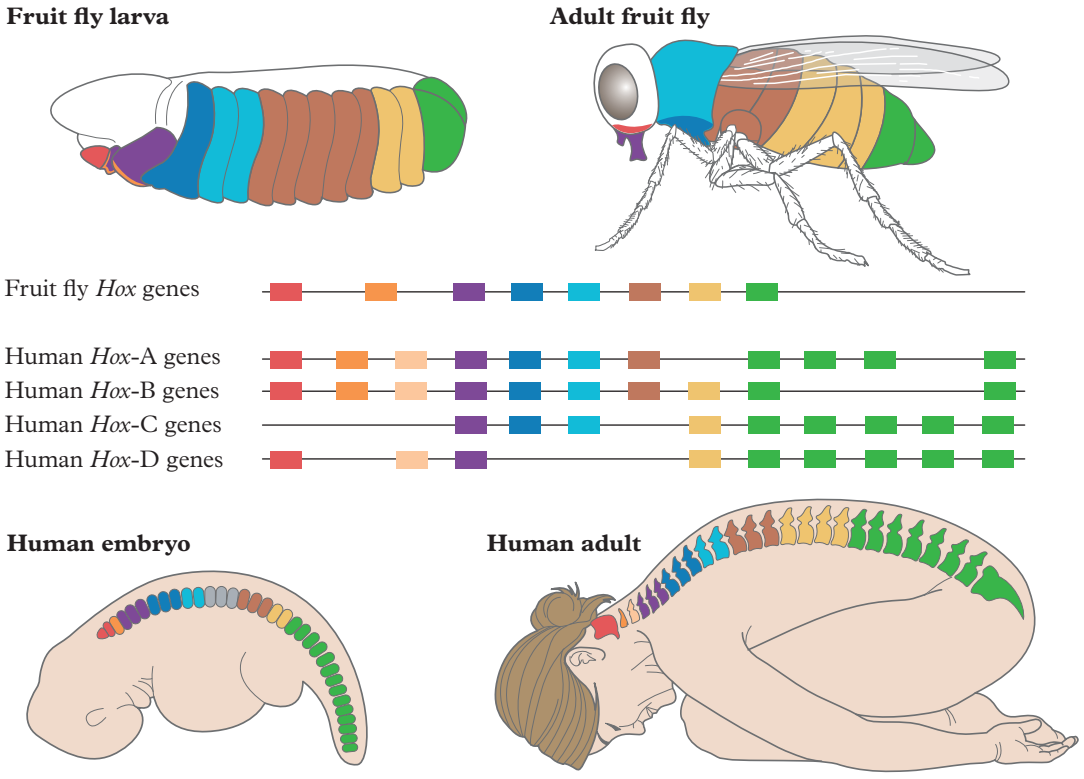


FIGURE 2 *HOX* genes in fruit flies and humans. Fruit flies have one set of eight *HOX* genes, whereas humans have 38 *HOX* genes arranged in four sets. Each box in the diagram shows the *HOX* genes. These control the organisation of embryonic body development, from head to tail. The head *HOX* genes are to the left, through the middle section, and tail *HOX* genes are to the right

FIGURE 3 Well-developed abdominal muscles show body segmentation

Real-world biology

Cell differentiation by the sex-determining region Y

Regardless of their genetic sex (XX versus XY), all embryos initially have the potential to develop phenotypically as male or female. Primordial components of both male and female reproductive tracts are present in all early embryos. The pattern for female development is expressed initially, as this is the default mode. If a male is to develop, this female default mode must be actively overridden by secretions of the foetal testes.

The *SRY* gene is the male sex-determining region on the Y chromosome. This gene produces a transcription factor that attaches (binds) to specific regions of DNA and helps control the activity of other genes. It is responsible for the production of the SRY protein, which starts processes that cause a foetus to develop male gonads (testes).

As SRY protein production increases, the male testes start to develop (weeks 6–8 in embryo development). Specialised cells within the testes begin to make testosterone, which inhibits other hormones and begins to override the production of female reproductive organs.

In weeks 9 to 12 of embryonic development, there is a peak in the production of these hormones. This coincides with the differentiation of the male internal genitalia. Differentiation of external genitalia occurs between weeks 8 and 12. This differentiation is determined by the presence of male sex hormones, which are present due to the *SRY* gene.

During this time, if there is no overriding testosterone present, or if the testosterone receptors are blocked, the embryo will continue to develop female internal reproductive structures and external genitalia.

Apply your understanding

1 **Identify** the chromosome location of the *SRY* gene. (1 mark)
2 **Describe** the action of the *SRY* gene. (1 mark)
3 **Determine** the stage at which male testes are formed in the womb. (1 mark)

Check your learning 7.3

Check your learning 7.3: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** "HOX protein". (1 mark)
2 **Describe** the role of homeotic genes. (1 mark)
3 **Explain** how the order of *HOX* genes on a chromosome relates to the spatial patterning of body structures during embryonic development. (3 marks)

Analytical processes

4 **Predict** the outcome of a mutation in the *HOX* gene, for the morphology of an organism. (1 mark)

MODULE 7

Lesson 7.4
Review: Gene expression

Summary

7.1
- DNA in the nucleus is copied into messenger RNA that can exit the nucleus in the process of transcription.
- Translation of mRNA into an amino acid sequence occurs in ribosomes.
- The ribosome assembles a protein by matching tRNA-delivered amino acids to the mRNA sequence.

7.2
- Transcription of genes is tightly regulated by transcription factors, and allows for cell differentiation.
- Chemical tags on DNA can affect the expression of genes without changing the DNA sequence.
- The epigenome is influenced by environmental factors.

7.3
- Transcription factors enable differential gene expression and cell differentiation.
- The HOX transcription factor family regulates the homeotic genes that determine which anatomical structures of the body the cells will differentiate into.

Review questions 7.4A Multiple choice

Review questions: Complete these questions online or in your workbook.

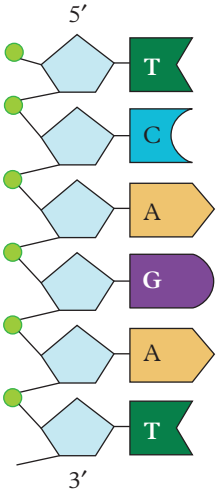
(1 mark each)

1 The genetic code is generally accepted as being provided by the linear arrangement of
- **A** sugar units in DNA.
- **B** nucleotide bases in RNA.
- **C** nucleotide bases in DNA.
- **D** amino acids in chromosome proteins.

2 The synthesis of specific proteins by an organism is determined by the
- **A** organism's genes.
- **B** fatty acids in the cell.
- **C** RNA present in the cell.
- **D** number of ribosomes present in a cell.

3 Transcription is the process in which
- **A** the DNA for a gene unzips.
- **B** the Golgi apparatus converts the polypeptide chain into a specific protein.
- **C** a piece of messenger RNA is produced that is complementary to the DNA code for a gene.
- **D** amino acids in the cytoplasm are placed, by transfer RNA, into the correct sequence for protein synthesis.

Use the following figure to answer questions 4 to 6.



4 The correct complementary sequence for this DNA molecule is
- **A** TAGACT.
- **B** AGTCTA.
- **C** TCAGAT.
- **D** GACTGC.

5 If the molecule portion were being transcribed, the correct sequence of complementary mRNA for this molecule would be
A AGUCUA.
B UGTCTU.
C UAGUGA.
D AUCUGA.

6 The highest number of amino acids coded for by the molecule shown is
A 1.
B 2.
C 3.
D 6.

7 Genes exert their control over cellular activity mainly by
A controlling cellular metabolism.
B contributing to epigenetic histone modification.
C producing transcription factors that block production of mRNA.
D preventing the passage of materials into the cell through its membrane.

8 A particular tRNA molecule attaches to a specific
A protein.
B genome.
C ribosome.
D amino acid.

9 In relation to gene expression, translation is the process in which
A the energy from ATP is used by RNA polymerase.
B certain environmental stimuli are required before a set of genes is expressed.
C the template strand of DNA is used by RNA polymerase to synthesise an mRNA molecule.
D a protein is synthesised as an amino acid sequence determined by the mRNA nucleotide sequence.

10 DNA methylation is a process that
A tightens the coiling of a nucleosome.
B epigenetically blocks expression of a gene.
C works in the same way as a histone modification.
D is instigated by regulatory genes to increase the rate of transcription.

Review questions 7.4B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

11 **Explain** the process of protein synthesis in terms of transcription and translation. (4 marks)

12 The epigenome is defined as "above the genome". **Explain** what this means. (3 marks)

13 **Describe** two ways in which epigenetic control is achieved. (2 marks)

14 **Identify** five environmental factors that may affect gene expression. (1 mark)

15 In multicellular organisms there are several post-transcriptional controls on gene activity. **Describe** how these controls regulate gene expression. (3 marks)

16 Certain genes produce transcriptional factors that control the development of a foetus. **Explain** how these transcription factors regulate the morphology of a developing foetus. (4 marks)

17 **Describe** how the *HOX* gene can be used to explain that insects and humans have a common ancestor. (3 marks)

Analytical processes

18 A certain protein is composed of 1500 amino acids. **Determine** how many base pairs the gene responsible for synthesis of this protein would have. (1 mark)

19 **Compare** structural genes and regulatory genes. (2 marks)

20 The following sequence of bases in DNA codes for the formation of a section of polypeptide containing ten amino acids.

GTTAACCGAACGGTTAGATGTACATTTAAG

a **Determine** the base sequence of the mRNA responsible for transcribing this code. (1 mark)

b Using the codon table provided, **determine** the sequence of amino acids in the resulting polypeptide. For example, GCA codes for the amino acid alanine. (1 mark)

First base	Second base: U	Second base: C	Second base: A	Second base: G	Third base
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
	UUA Leu	UCA Ser	UAA STOP	UGA STOP	A
	UUG Leu	UCG Ser	UAG STOP	UGG Trp	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC Leu	CCC Pro	CAC His	CGC Arg	C
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
	AUC Ile	ACC Thr	AAC Asn	AGC Ser	C
	AUA Ile	ACA Thr	AAA Lys	AGA Arg	A
	AUG Met or start	ACG Thr	AAG Lys	AGG Arg	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC Val	GCC Ala	GAC Asp	GGC Gly	C
	GUA Val	GCA Ala	GAA Glu	GGA Gly	A
	GUG Val	GCG Ala	GAG Glu	GGG Gly	G

Ala	Alanine
Arg	Arginine
Asn	Asparagine
Asp	Aspartic acid
Cys	Cysteine
Gln	Glutamine
Glu	Glutamic acid
Gly	Glycine
His	Histidine
Ile	Isoleucine
Leu	Leucine
Lys	Lysine
Met	Methionine
Phe	Phenyl-alanine
Pro	Proline
Ser	Serine
Thr	Threonine
Trp	Tryptophan
Tyr	Tyrosine
Val	Valine

Knowledge utilisation

21 In certain situations (e.g. disturbed soil at mine sites), some individuals of a species can grow prolifically, while others with different phenotypic expressions can only grow in the surrounding undisturbed soil. **Propose** the probable process(es) involved in this resulting difference in two closely situated populations. (1 mark)

22 **Hypothesise**, with reasons, the possible outcome if an organism had no homeotic genes. (1 mark)

23 Epigenetic DNA tagging (methylation) plays a crucial role in maintaining cell differentiation in multicellular organisms. Embryonic stem cells are totipotent at the early stages of development, meaning they have the potential to differentiate into any type of cell in the organism. **Discuss** the factors that lead to DNA methylation, and explain how methylation influences the formation of totipotent embryonic cells and their subsequent differentiation. (3 marks)

24 It has been demonstrated that some epigenetic tags can be inherited. **Discuss** the type(s) of tag that can be inherited and propose mechanisms for the inheritance. (3 marks)

Data drill

Interpreting correlation data

The genetic information stored in mRNA is represented by codons, which are sequences of three nucleotides. These codons are translated into amino acids, which then join together to form proteins. Some amino acids have multiple possible codons (e.g. leucine has 6 codons – CUU, CUA, CUC, CUG, UUA, UUG), while others only have a single codon (e.g. tryptophan – UGG). It could therefore be assumed that amino acids with multiple codons would have a higher frequency, but this is not always the case. Figure 1 shows the expected frequency of amino acids based on number of possible codons versus their observed frequency in nature.

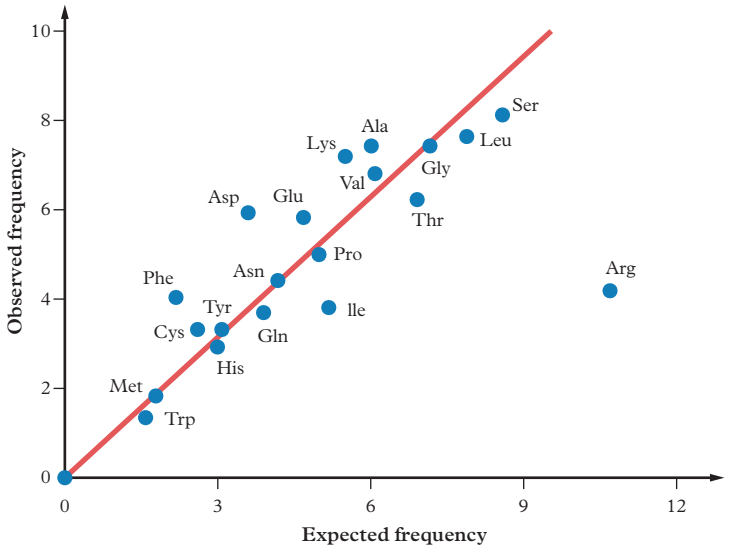


FIGURE 1 Expected frequency of amino acids versus their observed frequency in nature

Apply understanding

1 **Determine** the outlier for the data set. (1 mark)

Analyse data

2 **Identify** the amino acid with the highest observed frequency. (1 mark)

3 **Identify** how many amino acids have equal observed and expected frequencies. (1 mark)

Interpret evidence

4 The correlation between the expected frequency and the observed frequency of amino acids is 0.89. **Draw a conclusion** about the relationship between expected and observed frequency of amino acids in nature. (2 marks)

Module 7 checklist: Gene expression

MODULE 8

Meiosis

Introduction

In sexually reproducing animals, sperm are produced in the testes by the process of spermatogenesis, and ova (eggs) in the ovaries by oogenesis. Both processes involve mitotic and meiotic cell divisions and are under hormonal control.

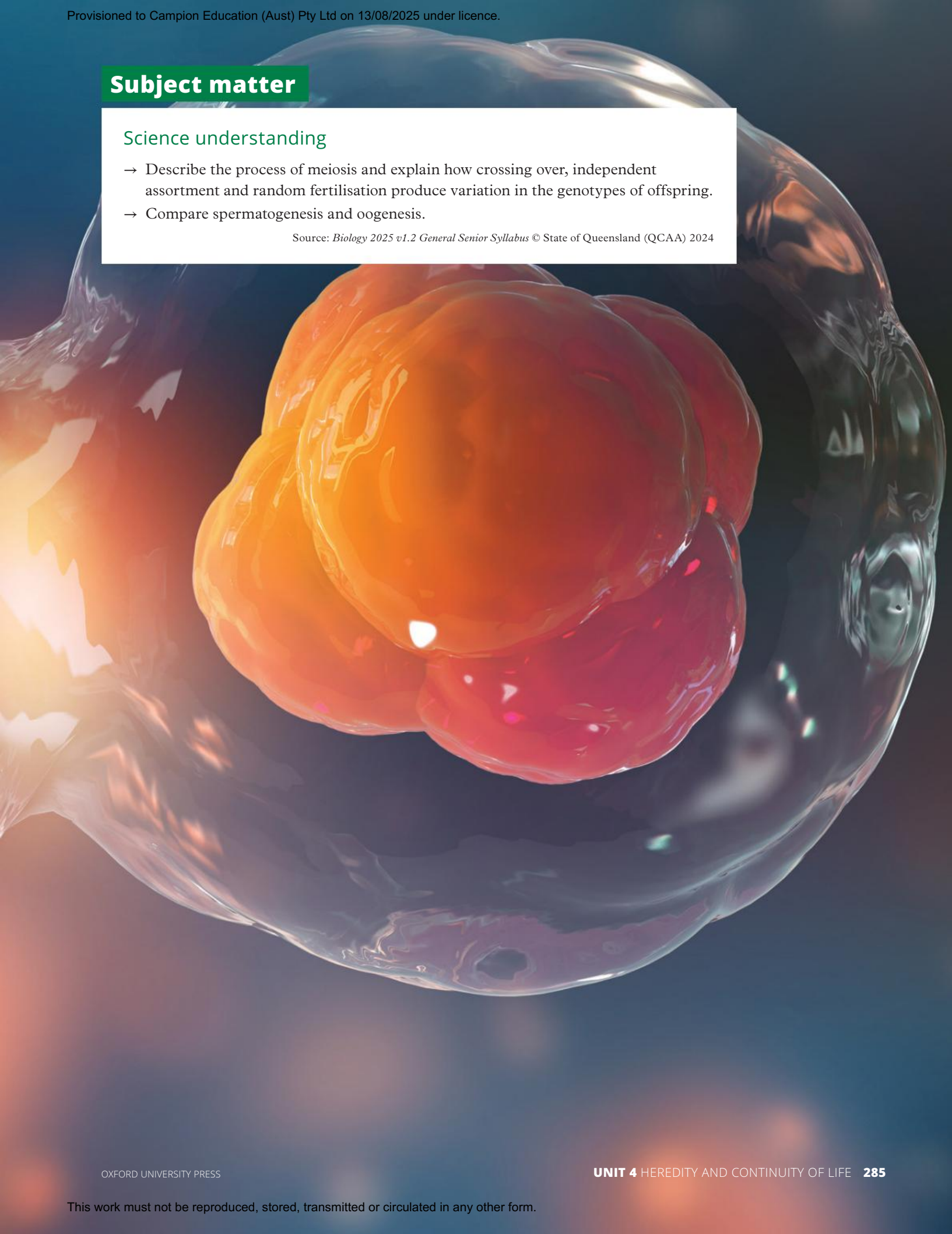
To maintain the correct number and types of chromosomes in each individual cell of a sexually reproducing species, the egg and sperm cells must contain a single copy of each chromosome. This is achieved by the process of meiosis in the gonads.

The genes carried on a specific chromosome are inherited together (linked). Alternative forms of a gene are termed alleles. The allele for a gene on one chromosome may be different from the allele on the homologous chromosome. The combination of the two alleles present is termed the genotype for that characteristic.

During meiosis I, adjacent chromatids of a pair of homologous chromosomes may intertwine and swap segments at one or more places. In this way, recombination of genetic material can occur, increasing genetic variation. Additionally, the fertilisation of the ovum by a sperm is random, further increasing variation in the genotypes of the offspring.

Prior knowledge

Prior knowledge quiz Check your understanding of concepts related to meiosis before you start.



Subject matter

Science understanding

→ Describe the process of meiosis and explain how crossing over, independent assortment and random fertilisation produce variation in the genotypes of offspring.

→ Compare spermatogenesis and oogenesis.

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Lesson 8.1
Meiosis

Learning intentions and success criteria

Key ideas

- → Mitosis creates diploid cells for the purpose of growth, repair and asexual reproduction.
- → Meiosis creates haploid gametes for the purpose of sexual reproduction.
- → In meiosis, there are two successive divisions: meiosis I, the separation of pairs of homologous chromosomes into separate cells; and meiosis II, the separation of sister chromatids.
- → A karyotype visually depicts all the chromosomes of a cell, organised numerically.

homologous chromosomes
pairs of chromosomes, one inherited from each parent, that are similar in size, shape and gene content, although they may carry different versions of those genes

diploid
the cellular condition in which there are two of each type of chromosome in the nucleus

haploid
the cellular condition in which there is one of each type of chromosome in the nucleus

Study tip

The prefix *diplo-* means "double" or "in pairs", whereas *haplo-* means "single". These prefixes help communicate the chromosome combinations in diploid and haploid cells.

mitosis
nuclear division resulting in daughter cells that have the same number and types of chromosomes as the parent cell

meiosis
nuclear division resulting in daughter cells that have half as many chromosomes, but the same types, as the parent cell; a reduction division, from the diploid to the haploid condition

Cell division

Each species has a specific number of chromosomes, each carrying different kinds of genetic information. A dividing parent cell must ensure that the new cells have the same number and the same types of chromosomes as the original.

Usually the cells of the adult organism contain pairs of chromosomes. There are two of each type of chromosome (e.g. 2 × chromosome 1), which carry the same kinds of genetic information. Pairs of matching chromosomes (that carry the same genes) are called **homologous chromosomes**. Cells that have homologous chromosomes are said to be **diploid** (having two complete sets of each chromosome) and are represented as $2n$, where n is the number of types of chromosomes. Each diploid cell has one set of paternal chromosomes from the male parent (father) and one maternal set from the female parent (mother). The sex cells from each parent (the egg and sperm cells) contain only one of each type of chromosome. These cells are described as **haploid** cells and are represented as n.

Cell division in eukaryotic cells is initiated by the division of the nucleus. There are two types of nuclear division:

- mitosis
- meiosis.

Mitosis takes place during the growth of an organism and is the basis of growth, repair, budding and vegetative propagation in multicellular organisms. It yields daughter cells that have the same number and types of chromosomes as the parent cell. Each cell produced via mitosis should be an exact diploid copy of the original cell. Some organisms use mitosis to reproduce asexually (reproduction resulting in offspring genetically identical to the parent).

Meiosis takes place during the formation of gametes (sex cells – ova and sperm), although in plants it occurs during the formation of spores. During sexual reproduction, two gametes from the parents (one from each parent) fuse to form the zygote, the start of a new individual. To maintain species continuity, the zygote must have the same number and types of chromosomes as the adults. This means the gametes must have half the number but the same types of chromosomes as an adult cell. During meiosis, therefore, diploid cells, each containing two sets of chromosomes, divide to form haploid cells, each with one set of each chromosome. When haploid cells fuse during fertilisation, the diploid condition is restored and species continuity is assured.

Interphase

Most cells spend most (90%) of their time doing their regular functions: producing proteins, repairing damage, and so on. This phase is called interphase G1. Before a cell can divide by meiosis or mitosis, it must replicate its DNA (discussed in Module 6). This is the synthesis (S) phase of interphase. As a result of this process, the cell now has twice the amount of DNA (because each DNA molecule has been replicated). However, the number of chromosomes (or chromatin) remains the same. This is because the DNA is described as a single chromosome whether it is a single or bivalent (**chromatid**) molecule (Figure 1).

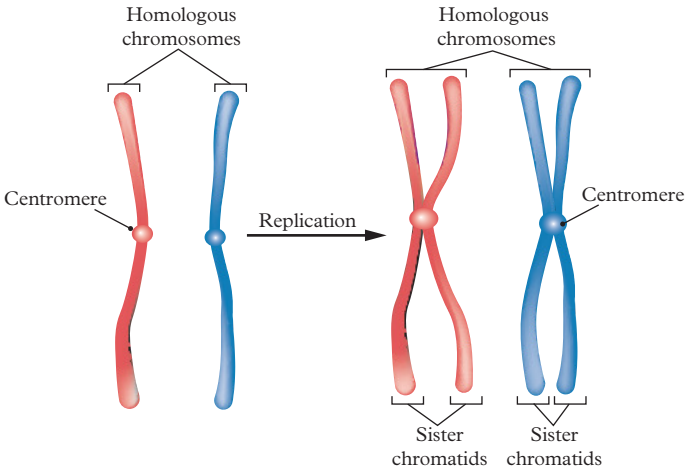


FIGURE 1 A chromosome may be single or bivalent (containing two sister chromatids)

DNA synthesis (S phase) is followed by the G2 phase of interphase, when there is further growth of the cell and replication of organelles. The cell is then ready to undergo the cell division of mitosis or meiosis.

chromatid
a replicated chromosome, still attached to the original at the centromere

Meiosis

In meiosis, there are two successive divisions. The first (meiosis I) involves the separation of the pairs of homologous chromosomes into separate cells. The second (meiosis II) involves separation of the sister chromatids at the joining point, called the centromere (Figure 2).

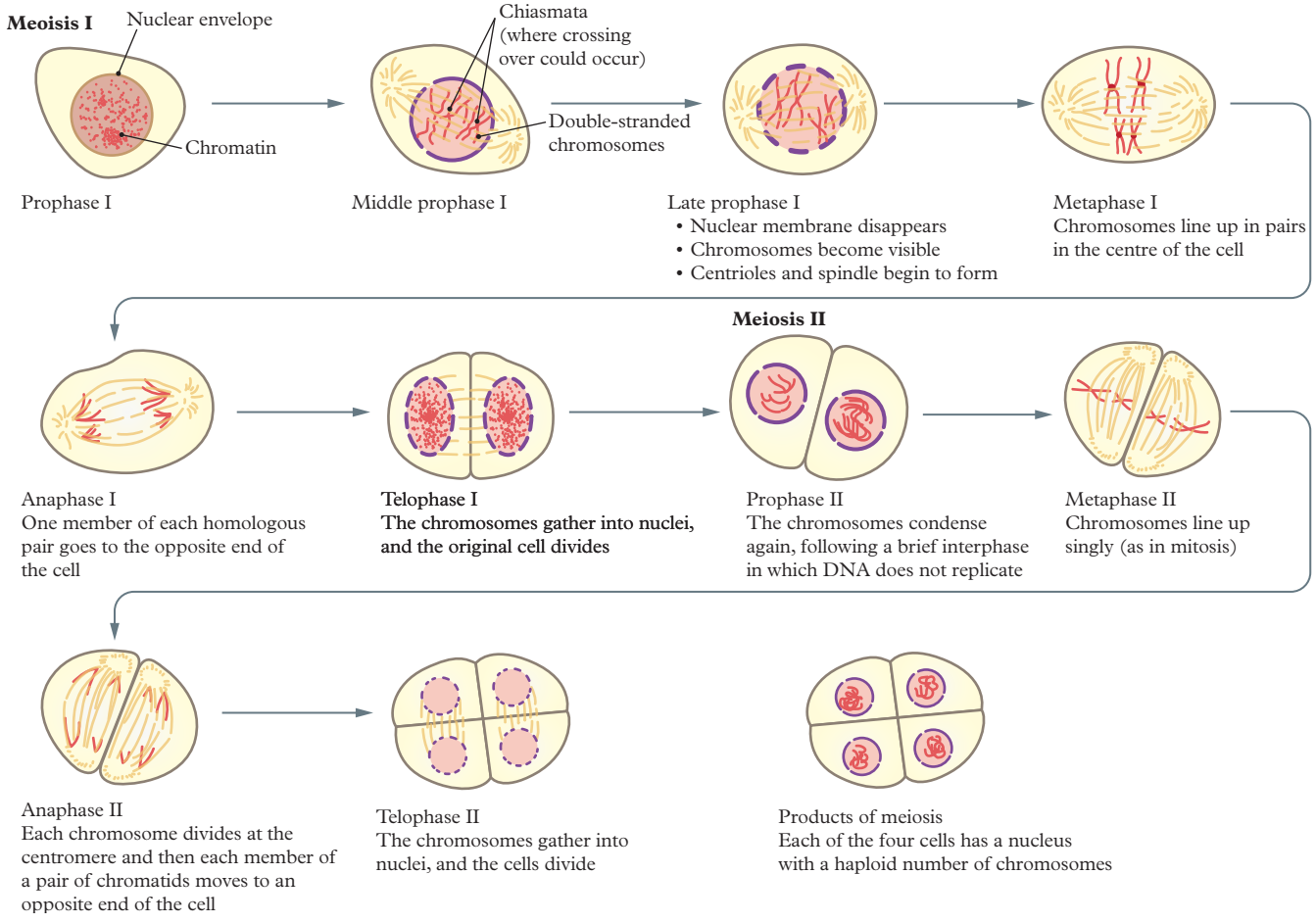


FIGURE 2 The stages of meiosis

Meiosis I

Prophase I

During prophase I, the nucleolus (place of ribosome production) disappears and the nuclear membrane breaks down, as in mitosis. In animal cells, the centrioles migrate to opposite poles (ends) of the cell and spindle fibres form. The bivalent chromosomes, each consisting of two chromatids joined at the centromere, become visible (condense). As they do so, they align in pairs of homologous chromosomes. This can be seen by the paired chromosomes having identical lengths, positions of centromeres and location of genes (banding). Homologous chromosomes consist of four sister chromatids (Figure 1), termed a **tetrad**.

tetrad
two homologous chromosomes, each consisting of two chromatids, lying side by side

chiasma
the connection between non-sister chromatids of homologous chromosomes during meiosis, where interchange occurs during crossing over; plural *chiasmata*

These chromatids may become very entwined and occasionally join together at points called **chiasmata**. At this point, genetic material can be exchanged (crossing over) between the chromatids (see Figure 3, Lesson 8.3). This means the chromosome that originally came from the organism's father can exchange genes with the chromosome from the organism's mother. The significance of this will be discussed later in this module.

Metaphase I

During metaphase I, the homologous chromosomes arrange themselves along the equator (middle) of the cell. The kinetochore proteins, which link the two chromatids together at the centromere, attach to the spindle fibres. Each homologous bivalent chromosome (containing two chromatids) aligns itself towards an opposite pole.

Anaphase I

Contraction of the spindle fibres separates the homologous chromosomes and pulls them towards opposite poles of the cell. So at each end of the cell there is one of each type of bivalent chromosome, each consisting of two chromatids.

Telophase I and cytokinesis I

The cell divides across the equator of the spindle. The spindle fibres break down and the cell divides to form two complete cells. Some cells may then go into a short interphase or they may proceed directly to the second meiotic division. A nuclear membrane is not formed around the chromosomes at this stage.

Each of these cells proceeds to meiosis II.

Meiosis II

Prophase II

A new spindle is formed perpendicular to that of the original cell.

Metaphase II

Individual chromosomes, each consisting of two chromatids, migrate to the equator of the spindle and attach at the kinetochore proteins that surround the centromeres.

Anaphase II

Contraction of the spindle fibres separates the kinetochore protein, and the chromatids separate at the centromere. The sister chromatids are pulled to opposite poles of the cell.

Telophase II and cytokinesis II

The spindle fibres disappear, the cell divides across its equator and a new nuclear membrane is formed around the chromosomes.

Significant features of meiosis are as follows:

- There are two successive divisions.
- The first division separates homologous chromosomes into separate cells.
- The second division, like mitosis, separates the chromatids into separate cells.
- Four haploid daughter cells are produced, each containing one complete set of chromosomes.

Karyotype

A karyotype is a pictorial display of the total complement of a species' chromosomes. A photograph is taken of the specially prepared chromosomes. This is then enlarged and can be colour enhanced. In the karyotype of a normal non-dividing diploid cell, the chromosomes are cut out digitally and arranged with the autosomal chromosomes in pairs, from the largest to the smallest; the sex chromosomes are placed at the end (Figure 3). If done during prophase I, the position of the centromere, and therefore the length of the "arms" of the chromatids, are used to identify homologous pairs. This means a karyotype can be used to identify species, determine gender and detect certain anomalies, such as an extra chromosome or piece of chromosome. A karyotype can also be prepared of the haploid sperm (Figure 4) and ovum (Figure 5).

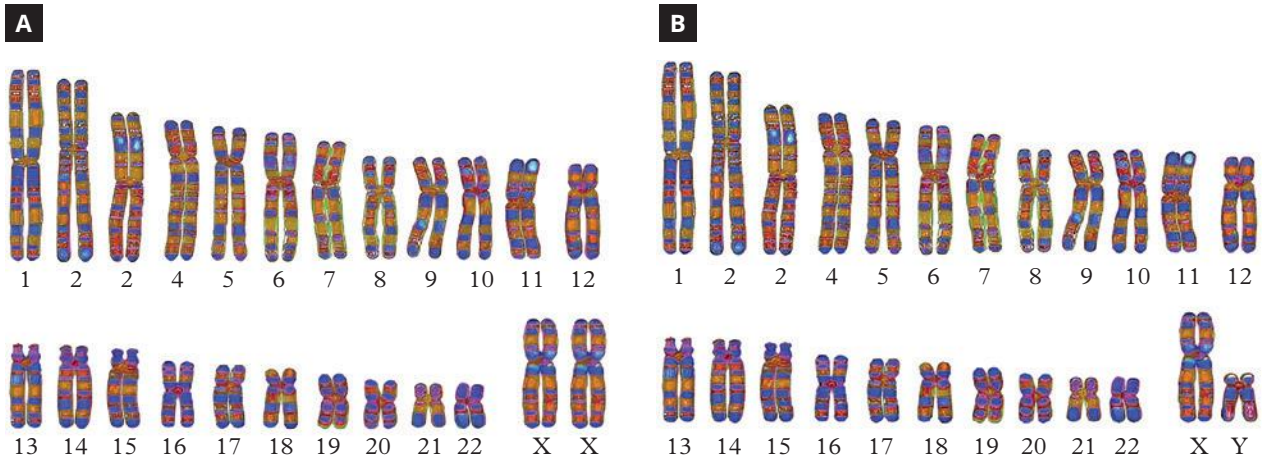


FIGURE 3 Karyotypes of (A) a human female and (B) a human male. The karyotypes show replicated bivalent chromosomes. In the 46 replicated chromosomes, there are 92 chromatids joined at their centromeres

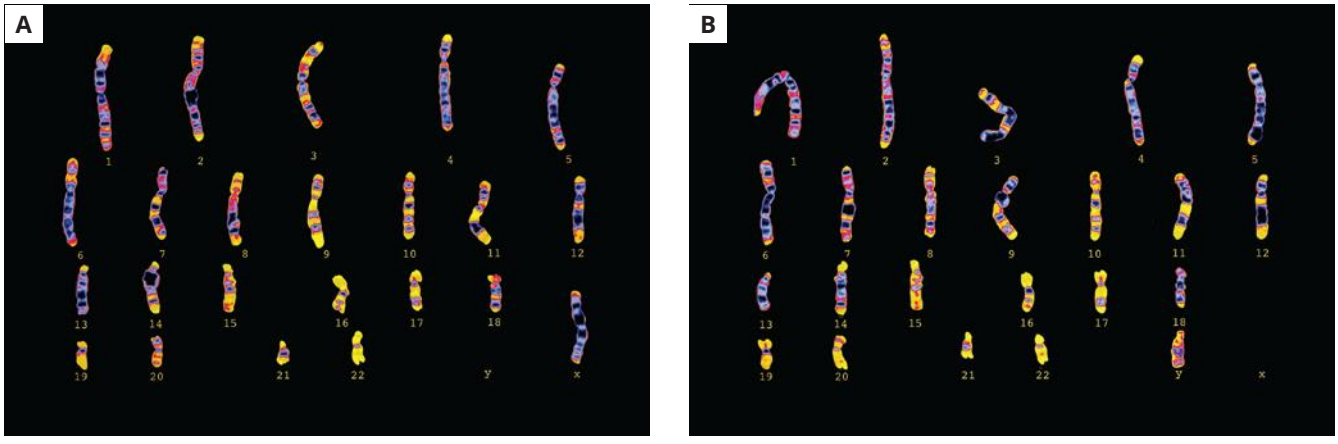


FIGURE 4 Colour-enhanced karyotypes of human sperm, which are haploid and carrying either (A) the X sex chromosome or (B) the Y sex chromosome

autosome
a non-sex chromosome

sex chromosomes
chromosomes carrying information that determines the sex of the individual

X chromosome
one of the two sex chromosomes in vertebrates and some other animals; females typically have two X chromosomes, while males have one X and one Y chromosome

Y chromosome
one of the two sex chromosomes in vertebrates and some other animals; males have one copy

Humans have 46 chromosomes. These include 22 pairs of homologous chromosomes, called **autosomes**. The structure of the remaining two chromosomes differs between males and females – these are termed the **sex chromosomes**. In females the two sex chromosomes, both **X chromosomes**, are similar, whereas males have one X chromosome and a smaller **Y chromosome**.

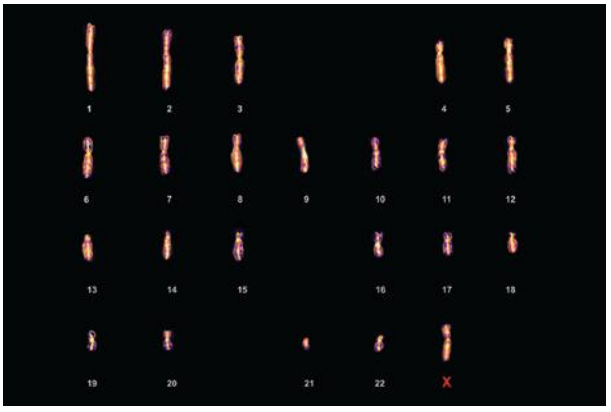


FIGURE 5 Colour-enhanced karyotype of a human ovum, which is haploid and carries only the X sex chromosome

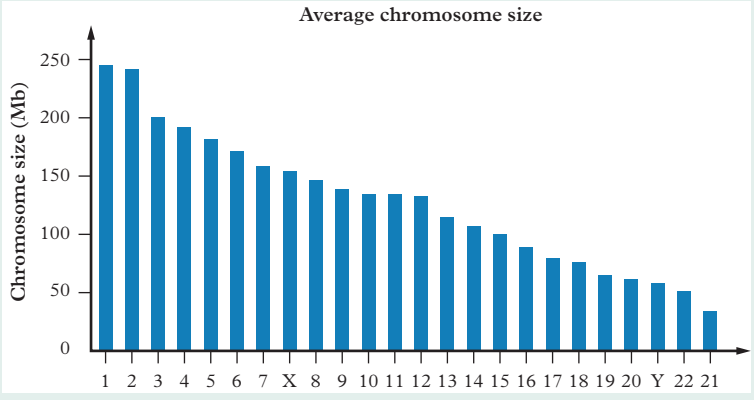
Skill drill

Chromosome length and genes

Science inquiry skill: Lesson 1.7 Processing and analysing data

Humans have 23 pairs of chromosomes, each varying in size and gene content. Chromosomes are measured in megabases (Mb), which represent millions of DNA base pairs. Genes, the functional units of heredity, are segments of DNA that code for proteins. In Figure 6, Graph A shows the average size (in Mb) of the 24 possible human chromosomes (autosomes 1–22, X and Y). Graph B shows the number of genes per chromosome.

A



B

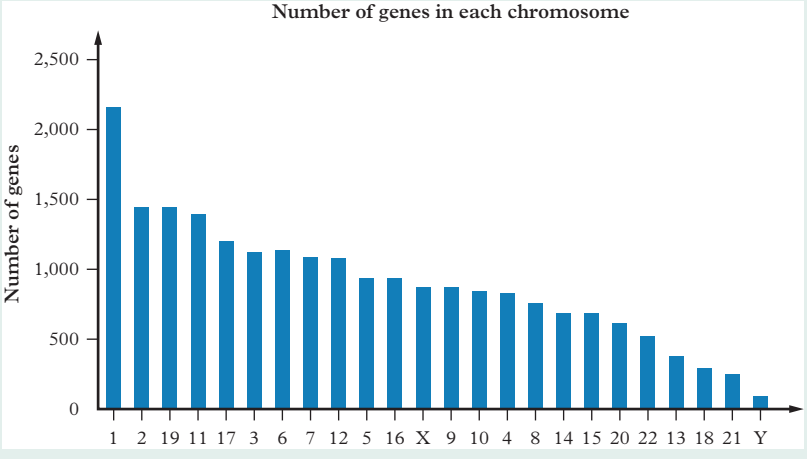


FIGURE 6 (A) Average chromosome size of the 24 possible human chromosomes, and (B) number of genes in each human chromosome

Practise your skills

1 **Identify** the number of genes of chromosome 8. (1 mark)
2 **Compare** the chromosome size of the X and Y chromosomes. (2 marks)
3 **Draw a conclusion** about the relationship between chromosome length and number of genes on the chromosome. (3 marks)

Challenge

Polyploid organisms

Most eukaryotic organisms are diploid, meaning they have two copies of each chromosome ($2n$). Some organisms, however, are polyploid, meaning they have more than two paired sets of chromosomes. For example, durum wheat, commonly used to make pasta, has four copies of its chromosomes ($4n$), and is termed tetraploid, whereas bread wheat is hexaploid, with six copies ($6n$). Some plants are triploid ($3n$), having three sets of chromosomes – one from the male parent and two from the female parent – but these are often sterile (cannot reproduce sexually).

1 Using your understanding of meiosis, **explain** why triploid organisms cannot reproduce sexually. (3 marks)
2 **Construct** a diagram of meiosis in a triploid organism to support your response to question **1**. (2 marks)

Check your learning 8.1

Check your learning 8.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define**:
  a diploid (1 mark)
  b haploid. (1 mark)
2 **Describe** what would occur during sexual reproduction if gametes were diploid rather than haploid. (2 marks)
3 **Describe** what happens to homologous pairs of chromosomes during meiosis I. (2 marks)
4 **Identify** whether each of the following is the result of mitosis or meiosis. (1 mark each)
  a Two diploid cells
  b Four haploid cells
  c Repair of damaged skin cells
  d Gamete formation in dogs
5 **Explain** the difference between a female karyotype and a male karyotype. (2 marks)
6 **Describe** the information that can be obtained from a karyotype. (2 marks)

Analytical processes

7 **Compare** mitosis and meiosis. (3 marks)
8 **Distinguish** between an autosome and a sex chromosome. (1 mark)
9 In Figure 3 there are 92 chromatids.
  a **Determine** whether this occurs in both types of cell division. **Explain** your answer. (3 marks)
  b **Identify** the phase of cell division in which this karyotype would be seen. (1 mark)

Lesson 8.2
Gametogenesis

Key ideas

- → Gametogenesis includes spermatogenesis and oogenesis, and creates gametes.
- → Spermatogenesis creates sperm cells, the male gametes, within the male reproductive organs, the testes.
- → Oogenesis creates ova, the female gametes, within the female reproductive organs, the ovaries.

Learning intentions and success criteria

The formation of gametes

Gametogenesis is the series of mitotic and meiotic divisions that occur in the gonads, resulting in the formation of gametes. Although mitosis and meiosis are both part of this process, gamete formation begins with meiosis. Spermatogenesis and oogenesis are both forms of gametogenesis. **Spermatogenesis** is the formation of sperm cells in the testes, while **oogenesis** is the formation of eggs (ova) in the ovaries. While these two processes both result in gamete production, they vary in many aspects.

gametogenesis the formation of gametes

spermatogenesis the formation of spermatozoa in animals

oogenesis the formation of ova in animals

Spermatogenesis

At puberty (the onset of sexual maturity) in males, the spermatogenesis process starts in the diploid germ (stem) cells in the testes, called **spermatogonia**. These stem cells are formed during gestation and are present in an inactive state from birth through to the beginning of adolescence.

During adolescence, hormones from the anterior pituitary gland cause the activation of these cells and the production of viable sperm. The spermatogonia go through mitosis; each mitotic division produces one **primary spermatocyte** (diploid), which will proceed to gamete formation, while the other diploid cell is retained as a diploid stem cell. In this way the stem cells are maintained, and so males can produce sperm from puberty to death.

At the first meiotic division (meiosis I), the primary spermatocyte produces two haploid cells, called **secondary spermatocytes** (Figure 1). These cells then proceed through the second meiotic division (meiosis II), each cell producing two haploid **spermatids**.

spermatogonium a germ (stem) cell in a layer of cells lining the tubules in the testes; plural *spermatogonia*

primary spermatocyte a diploid cell formed by mitosis of a spermatogonium; undergoes meiosis I to produce two haploid secondary spermatocytes

secondary spermatocyte a haploid cell that undergoes meiosis II to form spermatids

spermatid an immature spermatozoon

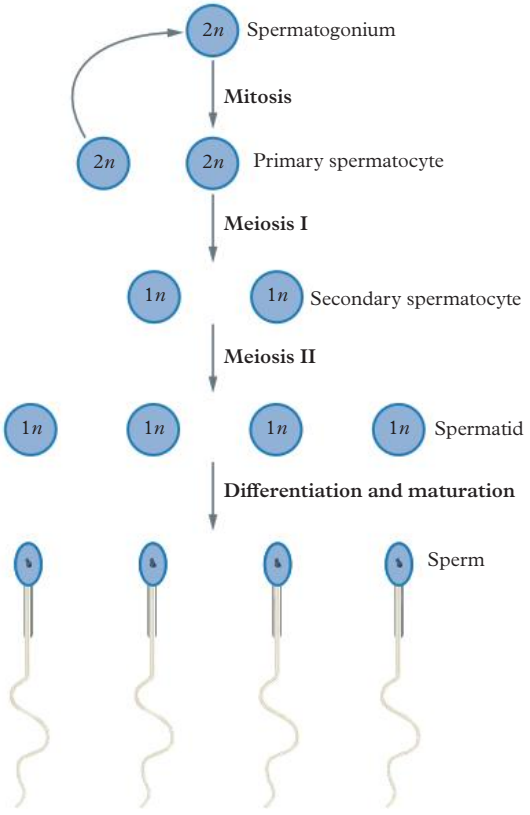


FIGURE 1 Spermatogenesis, showing the cell types and divisions involved

Four spermatids are produced from one primary spermatocyte. Specialised protective "nurse" cells in the male tubules in the testes, called **Sertoli cells**, protect and provide nourishment for the spermatids, which mature into **spermatozoa**. These cells are needed to protect the haploid cells from the body's defence mechanisms. It takes approximately six weeks for the spermatids to differentiate into mature spermatozoa.

When fully developed, the mature spermatozoa (sperm) are released into the tubules of the testes, ready for delivery to a female. The head of each spermatozoon contains the haploid nucleus and enzymes to dissolve the protection coating the ovum. The tail (flagellum) provides propulsion to enable the sperm to reach the ovum.

In males, spermatogenesis begins at puberty and continues into old age.

Sertoli cell
a type of cell in the epithelium of tubules of the mammalian tests that protects and nourishes the developing spermatozoa

spermatozoon
a small, motile male gamete; plural *spermatozoa*

Oogenesis

The production of a female gamete or **ovum** is termed oogenesis. It occurs in the ovaries of the female. The process begins during early embryonic development and is completed only after the ovum is fertilised. During development of a female foetus, germ or stem cells called **oogonia** (singular *oogonium*) undergo repeated mitotic division to form diploid **primary oocytes** (Figure 2). These primary oocytes begin to undergo meiosis I but this cell division is halted at prophase 1. Each of the primary oocytes is enclosed in a single layer of follicle cells, forming a **primary follicle**. At birth, a female has a finite number of these follicles, which are inactive and suspended from continuing meiosis I. Although approximately 200,000 primary follicles are present in the ovaries at birth, only about 450 ever develop.

ovum
a haploid female gamete; plural *ova*

oogonium
a small diploid cell in the ovary that forms a primary oocyte in a female foetus; plural *oogonia*

primary oocyte
a diploid cell developed by an ovarian germ cell in mammals, which may later develop into an ovum

primary follicle
a single-layered structure in the mammalian ovary that contains the primary oocyte

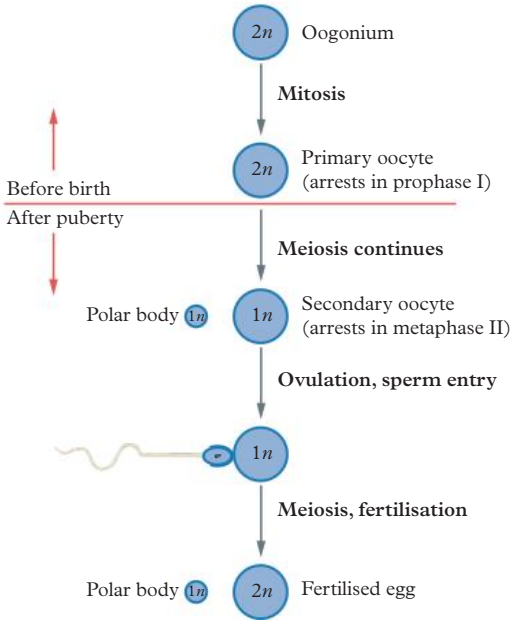


FIGURE 2 Oogenesis, showing the cell types and divisions involved

From puberty, hormones are cyclically released from the anterior pituitary gland. These stimulate one primary oocyte within a primary follicle to complete the meiosis I cycle. The division of the cytoplasm at the end of meiosis I is uneven, producing a large haploid **secondary oocyte** and a small haploid **polar body**. The polar body often degenerates, although it may proceed through meiosis II to produce two haploid polar bodies. The large secondary oocyte progresses through meiosis II as far as metaphase II before its development is halted again. The secondary oocyte is released from the ovary in the process of **ovulation**.

secondary oocyte
a large haploid cell produced during meiosis I of the primary oocyte

polar body
a small haploid cell produced during both meiosis I and II during oogenesis as a result of uneven cell division

ovulation
the release of the secondary oocyte that has started meiosis II from the ovary

After ovulation, this released secondary oocyte travels toward the uterus through the oviduct. If the secondary oocyte is fertilised, the cell completes meiosis II, producing a second smaller polar body and a fertilised egg containing the haploid set of chromosomes from the ovum and the haploid set from the sperm. Fertilisation of the ovum by the sperm results in a diploid zygote. At the completion of meiosis II, all the polar bodies disintegrate.

The production and release of a secondary oocyte is cyclic – it usually occurs once each month (approximately every 28 days).

TABLE 1 The properties of gametogenesis

Spermatogenesis	Oogenesis
Production of sperm cells (gametes) in males	Production of an ovum (gamete) in females
Occurs in male testes	Occurs in female ovaries
Starts from a primary spermatocyte	Starts from a primary oocyte
Results in four functional spermatozoa from a primary spermatocyte	Results in a single ovum and three polar bodies from a primary oocyte
All four sperm are the same size and very small	Ovum is large, whereas the three polar bodies are small and disintegrate
Sperm cell is motile	Ovum is immotile
Sperm cell does not contain any nutrients	Ovum contains nutrients
Completed inside the testis	If the ovum is fertilised, the final stages of meiosis II occur outside the ovary (in the oviduct)
Begins at puberty	Begins before birth, during the embryonic developmental stage
Results in billions of sperm cells	Results in one ovum per month (occurs in a cyclic pattern)
Involves a short growth phase	Involves a long growth phase
Diploid cell produces four haploid sperm	Diploid gamete mother cell produces one haploid egg cell
Meiosis is completed in days or weeks	Completion of meiosis is delayed for months or years
A continuous process, completed in 74 days	A discontinuous process, completed in a few days or years

Check your learning 8.2

Check your learning 8.2: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** "gametogenesis". (1 mark)
2 **Determine** the difference in the number of gametes produced between spermatogenesis and oogenesis after one full cycle. (1 mark)
3 **Describe** three major differences between spermatogenesis and oogenesis. (3 marks)
4 **Describe** how spermatogenesis and oogenesis are similar. (2 marks)
5 **Explain** the types of cell division involved in gametogenesis. (3 marks)

Analytical processes

6 **Compare** the process of spermatogenesis and oogenesis (with reference to haploid and diploid cells). (4 marks)

Knowledge utilisation

7 **Draw a conclusion** about the evolutionary advantage of producing only one viable ovum per cycle during oogenesis, compared to four sperm cells in spermatogenesis. (4 marks)

Lesson 8.3
Genetic variation

Key ideas

- → The processes of crossing over and recombination, independent assortment and random fertilisation increase the genetic variation in a species.
- → Independent assortment results in homologous chromosomes being randomly distributed to daughter cells, with the different chromosomes segregating independently of each other.
- → Crossing over and recombination between homologous chromosomes during prophase I produce unique allele combinations.
- → The fertilisation of an ovum by a sperm is random, further increasing genetic variation.

Gene structure and linkage

Learning intentions and success criteria

A gene is a region of DNA that has a particular function. A gene may be directly or indirectly involved in the production of protein. This protein may then be responsible for a particular physical or chemical characteristic of an organism, or it may work in conjunction with other proteins in the formation of the characteristic.

The order of nucleotides in each type of chromosome is different. Each type of chromosome, therefore, carries genes that are unique to that chromosome. The total number of genes in a cell is far greater than the number of chromosomes, because each chromosome carries many different genes. Genes that are located on the same chromosome are said to be linked. This phenomenon is known as **gene linkage**. Because sexually reproducing organisms have homologous pairs of chromosomes, one from each parent, they have two of each type of gene.

gene linkage
the location of genes on the same chromosome

Alleles

The protein produced from a gene is not always identical, due to slight variations in the sequence of nucleotides in the gene. An allele is an alternative form of a gene at the same location on the same chromosome. Although there may be a number of different alleles for a gene, a single individual can only carry two, one on each homologous chromosome. For example, a person may have two genes for hair colour, one version (allele) from their mother, and another from their father.

If the two alleles for a gene are the same, the individual is said to be **homozygous** for that gene. If the two alleles are different, the individual is described as **heterozygous** for that gene. How the two alleles combine to form a particular characteristic depends on the type and amount of protein produced by each. For example, there is a gene that carries the code to produce an ion channel in membranes. Although most people have the allele to produce a fully functioning ion channel protein, approximately 1 in 25 people have one copy of an allele that produces a malformed version of this protein.

homozygous
describes a condition in which both alleles for a gene are the same

heterozygous
describes a condition in which the two alleles for a gene each exhibit a different expression

If the person is heterozygous (carries one normal allele and one allele that produces the malformed protein), then their cells will still have enough of the functioning ion channel to be

recessive allele
an allele on a chromosome that can be masked by its dominant form in the heterozygous condition; can be autosomal or sex-linked

healthy. If the person inherits two copies of the allele that produces the malformed protein (one from their mother and one from their father), then they are unable to produce a fully functioning ion channel protein. As a result, their membranes are unable to control the movement of ions (and hence water) across their membrane. This is the mechanism of cystic fibrosis, in which individuals can have difficulty with thick mucus in their lungs or digestive system.

In this situation, an individual must have two copies of the allele (homozygous) for the trait (cystic fibrosis) to be evident. The trait is said to be recessive, and the alleles are described as "alleles for the recessive trait" or **recessive alleles**.

Study tip
It is the physical expression of the alleles that is described as a recessive trait, rather than the alleles.

Sometimes only a single gene is responsible for a characteristic. In this case, one allele exerts full control over another allele in a heterozygous condition – this is the **dominant allele**. For example, the allele for freckles results in a high level of the brown protein melanin being produced in the skin. This coloured protein dominates any other proteins that may be produced. Only one copy of the allele is needed for the **dominant trait** to be evident. This means a person with a dominant trait may be either homozygous or heterozygous for that trait.

FIGURE 1 The presence of freckles is determined by genetics

dominant allele
an allele for a gene that overrides the effects of the recessive allele in the heterozygous condition; can be autosomal or sex-linked

dominant trait
the particular trait of a characteristic that is expressed in the phenotype of a heterozygous individual

The **genotype** names each allele that is present in an individual. Each gene is represented by a letter (or group of letters). The different alleles are indicated by a capital letter (dominant traits) or a lowercase letter (recessive traits). For example, if the gene for freckles is given as either F or f, then the allele for freckles will be F (dominant trait) and the allele for no freckles will be f (recessive trait).

genotype
the genetic make-up of an organism, including the specific set of genes and their alleles (different versions of a gene) that it carries

The **phenotype** indicates the way in which the gene is chemically or physically expressed. This is determined by the types of alleles that are present (the genotype), as well as the environmental conditions of the individual. For example, a person may have the genotype of a tall person, but if they experience low nutrition levels they may never achieve their full height.

phenotype
the observable traits or characteristics of an organism, resulting from the interaction of its genotype with the environment

The law of segregation and the law of independent assortment

The process of meiosis and the structure of DNA and the gene were not known when Mendel undertook his ground-breaking studies of the inheritance of characteristics in the pea plant in the mid-nineteenth century. By chance, the features he studied were each controlled by a single gene and were on different chromosomes (or behaved as though they were on different chromosomes). From his intensive work, Mendel proposed two laws.

law of segregation
a Mendelian law that states that genes for a characteristic occur in pairs in an individual, one inherited from each parent, and these pairs are separated when the reproductive cells are formed

The **law of segregation** states that, during the production of gametes, the two copies of each hereditary factor segregate so that each offspring acquires one copy of the factor from each parent. Each parent has two copies of each gene in their cells (one from their mother and one from their father). When the gametes were formed in the mother (or father), one copy of each chromosome went into each gamete (they segregated).

The **law of independent assortment** states that individual genes assort independently during gamete production, giving different traits an equal chance of occurring together. In independent assortment, which happens during metaphase I of meiosis, homologous chromosome pairs are randomly distributed into gametes (Figure 2). Each pair aligns independently, so maternal or paternal chromosomes can assort in various combinations. This means the chromosomes in the ova inherited from the mother are a mix of her parents (the maternal grandparents' chromosomes), and similarly for the sperm cells inherited from the father. This means that each daughter cell has a 50/50 chance of receiving the maternal or the paternal homologous chromosomes. For a human, with 23 different chromosome types, this results in 2^{23} possible chromosome combinations for each gamete.

law of independent assortment
a Mendelian law that states that each allele pair segregates independently during gamete formation; applies when genes for two traits are located on different pairs of homologous chromosomes

This law only holds when the genes are located on different chromosomes and when there is no swapping of information between homologous chromatids.

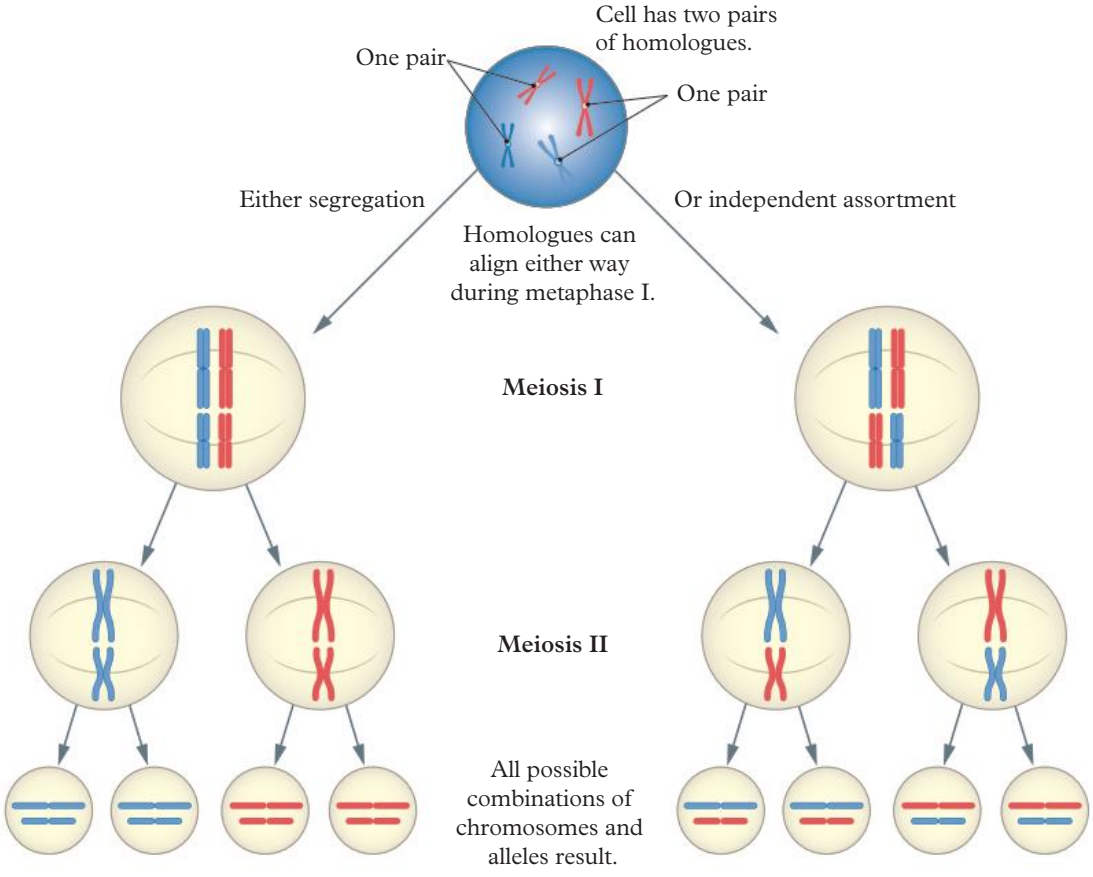


FIGURE 2 Segregation and independent assortment in a cell with two pairs of homologues. The blue homologues (homologous genes) are paternal in origin, the red homologues maternal. The way the homologues are distributed provides variation in the next generation of gametes and thus in the genotype of the offspring

Crossing over and recombination

Crossing over occurs when there is an exchange of segments of DNA between homologous chromatids during prophase I. It may occur at one or more places along the chromosome.

crossing over
the breaking and rejoining, with exchange of DNA, of non-sister adjacent chromatids of homologous chromosomes during meiosis I

During prophase I, the homologous chromosomes pair and the four chromatids lie side by side. They are positioned so that the alleles of one chromosome are beside the alleles for the same trait on the other chromosome. Adjacent segments of chromatids from the homologous chromosomes can break off and rejoin with the partner chromatid. By the end of metaphase I, this process is completed, so that segments of one chromatid from each of the homologous chromosomes may have interchanged (Figure 3).

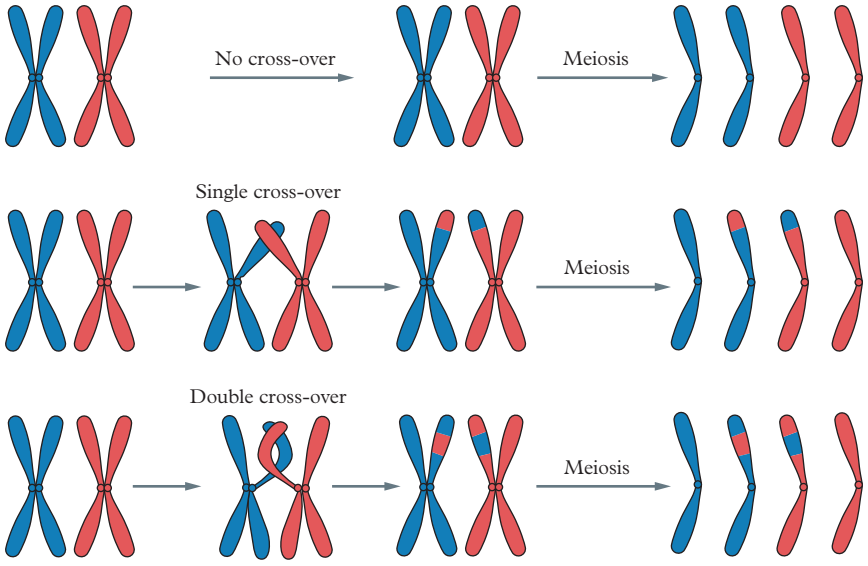


FIGURE 3 The differences in genetic make-up of gametes produced with no cross-over, a single cross-over and two cross-overs

Separation of the homologous chromosomes in meiosis I and subsequent separation of the chromatids in meiosis II may result in four possible allele arrangements in the gametes – two similar to each of the original chromosomes, and two that have different combinations.

Crossing over has survival value for the individual, because some of the gametes have combinations of linked genes that are different from the parental combination. These gametes are called **recombinant gametes**. This helps explain why offspring can have different genotypes (and phenotypes) to those of their parents, and also those of their siblings.

recombinant gametes
gametes produced as a result of crossing over of the chromatids of homologous chromosomes during meiosis

The processes of segregation, independent assortment and crossing over can potentially give rise to a vast array of allele combinations in the gametes produced. These factors are extremely important in their contributions to genetic variation and the random nature of fertilisation. Oogenesis results in only one ovum being available for fertilisation, because other possible combinations are lost in the polar bodies.

In spermatogenesis, vast quantities of sperm are produced, with millions of possible gene combinations, but only one will actually achieve fertilisation to produce a zygote. The more chromosome pairs there are in a cell, the more variation is possible. This means the process of fertilisation is completely random in natural conditions. Which sperm gets to fertilise the ovum is a matter of chance, referred to as **random fertilisation**, and this increases the number of possible chromosome combinations for the offspring. Because of independent assortment, crossing over and random fertilisation, it is impossible for sexually reproducing organisms to produce an identical clone to either parent. The offspring of sexual reproduction are genetically similar to their parents but not identical to either parent. The main advantage of sexual reproduction is that it gives rise to many variations in the genotype of the offspring upon which natural selection may act.

random fertilisation
the process in sexual reproduction where any of the genetically unique sperm may fuse with a genetically unique ovum, and the combination is entirely up to chance

Real-world biology

Genetic variation and coat colours

Coat patterns in animals are a striking and visible example of genetic variation resulting from meiosis. The processes of crossing over, independent assortment and random fertilisation ensure that each individual inherits a unique combination of

genetic information, influencing the development of coat colour, pattern and texture. Genes that control coat colour and patterning are often located near each other on the same chromosome. Crossing over can shuffle these genes, producing novel combinations. For example, in cats the tabby pattern is influenced by multiple genes, with crossing over and recombination altering the expression of dominant or recessive alleles, leading to variations in the striping pattern or its intensity. In dogs, coat length, texture and colour are controlled by multiple genes on different chromosomes. Independent assortment creates genetic diversity, leading to a variety of phenotypes within a litter. When gametes fuse during fertilisation, the combination of alleles from the two parents is entirely random, resulting in each zygote having a unique genetic make-up, further diversifying coat traits. In zebras, the distinct stripe patterns are determined by genetic factors. The random union of sperm and egg ensures that each zebra has a unique stripe pattern, much like human fingerprints.

FIGURE 4 Meiosis creates genetic diversity in coat patterns through crossing over, independent assortment and random fertilisation

Apply your understanding

1 **Describe** the process of independent assortment and its role in generating unique gametes and, therefore, unique coat patterns. (3 marks)
2 **Describe** how random fertilisation contributes to coat variation in the genotypes of offspring. (3 marks)

Check your learning 8.3

Check your learning 8.3: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** the processes of crossing over and recombination. (2 marks)
2 **Identify** at what phase of meiosis crossing over is likely to occur. (1 mark)
3 **Explain** the difference between the law of segregation and the law of independent assortment. (2 marks)
4 For the genotypes below, **identify** whether they are homozygous dominant, homozygous recessive or heterozygous.
   a Pp (1 mark)
   b TT (1 mark)
   c ff (1 mark)
5 **Explain** how random fertilisation may result in a variety of phenotypes in offspring. (3 marks)

MODULE 8

Lesson 8.4
Review: Meiosis

Summary

8.1
- Mitosis creates diploid cells for the purpose of growth, repair and asexual reproduction.
- Meiosis creates haploid gametes for the purpose of sexual reproduction.
- In meiosis, there are two successive divisions: meiosis I, the separation of the pairs of homologous chromosomes into separate cells; and meiosis II, the separation of the sister chromatids.
- Karyotypes visually depict all the chromosomes of a cell, organised numerically.

8.2
- Gametogenesis includes spermatogenesis and oogenesis, and involves the creation of gametes.
- Spermatogenesis creates sperm cells, the male gametes, within the male reproductive organs, the testes.
- Oogenesis creates ova, the female gametes, within the female reproductive organs, the ovaries.

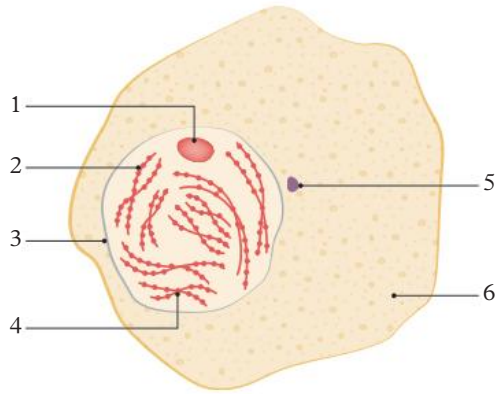
8.3
- The processes of crossing over and recombination, independent assortment and random fertilisation increase genetic variation in a species.
- Independent assortment results in homologous chromosomes being randomly distributed to daughter cells, with the different chromosomes segregating independently of each other.
- Crossing over and recombination between homologous chromosomes during prophase I produce unique allele combinations.
- The fertilisation of the ovum by a sperm is random, further increasing genetic variation.

Review questions 8.4A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

Use the following diagram to answer questions 1 to 3.



1 The structure labelled 4 that holds the two bead-like strings together is called a
- **A** centriole.
- **B** centromere.
- **C** centrosome.
- **D** chromosome.

2 The chromosome number of the cell nucleus is
- **A** 2.
- **B** 4.
- **C** 8.
- **D** 16.

3 The number of chromatids visible in the cell is
- **A** 4.
- **B** 8.
- **C** 12.
- **D** 16.

4 When a normal diploid cell undergoes complete meiosis, it produces
- **A** two diploid cells.
- **B** four diploid cells.
- **C** two haploid cells.
- **D** four haploid cells.

5 The chromosomes of a human cell were analysed. The scientist found 22 chromosomes plus a Y chromosome. From this information, the scientist could conclude that the cell was a
- **A** male cell.
- **B** female cell.
- **C** male gamete.
- **D** female gamete.

6 In normal meiosis in human males and females,
- **A** all sperm contain the same kind and amount of DNA.
- **B** each egg and each sperm contains a single sex chromosome.
- **C** each egg produced contains one more autosome than a sperm cell.
- **D** equal numbers of functional gametes are formed from each participating cell.

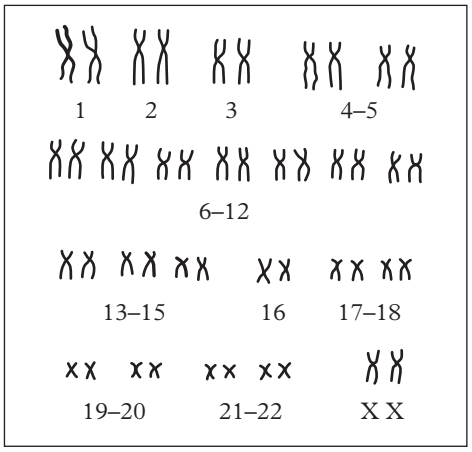
7 Oogenesis
- **A** occurs from adolescence through to old age.
- **B** results in the monthly release of an ovum from the ovary.
- **C** is the equivalent of spermatogenesis, except that it occurs in the ovary.
- **D** produces one ovum and three polar bodies from a single primary oocyte.

8 During oogenesis, the secondary oocyte arrests during
- **A** prophase I.
- **B** prophase II.
- **C** anaphase II.
- **D** metaphase II.

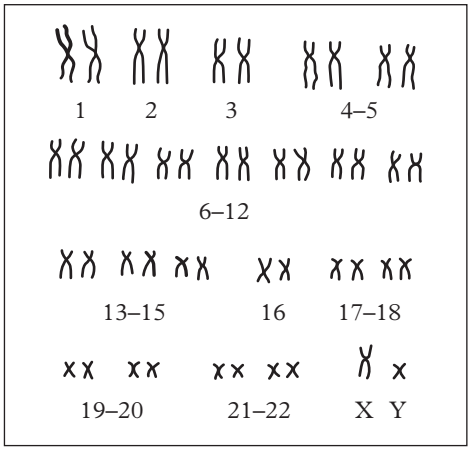
Use the following information to answer questions 9 and 10.

Consider the two diagrams of arranged and numbered chromosomes. These chromosomes came from individuals who are twins.

Twin A



Twin B



9 Using the karyotypes, it can be determined that
- **A** both twins are male.
- **B** both twins are female.
- **C** twin A is male and twin B is female.
- **D** twin A is female, and twin B is male.

10 From the karyotype, it is reasonable to assume that
- **A** twin A is chromosomally abnormal.
- **B** the twins are chromosomally abnormal.
- **C** the twins have arisen from two separate zygotes.
- **D** the twins have arisen from a normal zygote that split into two cells.

Review questions 8.4B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

11 **Define** "gametogenesis". (1 mark)

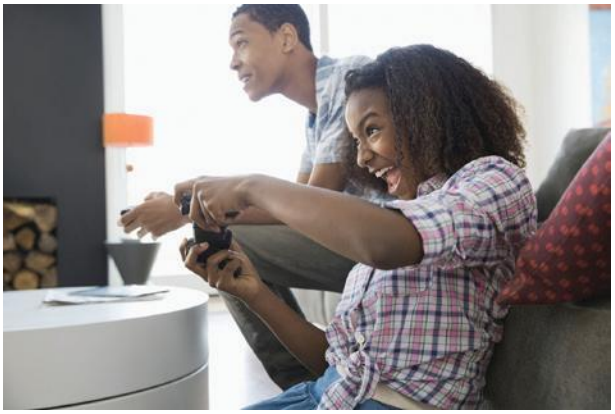
12 **Describe** the role of crossing over and recombination. (2 marks)

13 **Describe** the production of gametes in the mammalian ovary. (4 marks)

14 **Describe** how a karyotype of an individual is produced, and **identify** one purpose of karyotyping. (3 marks)

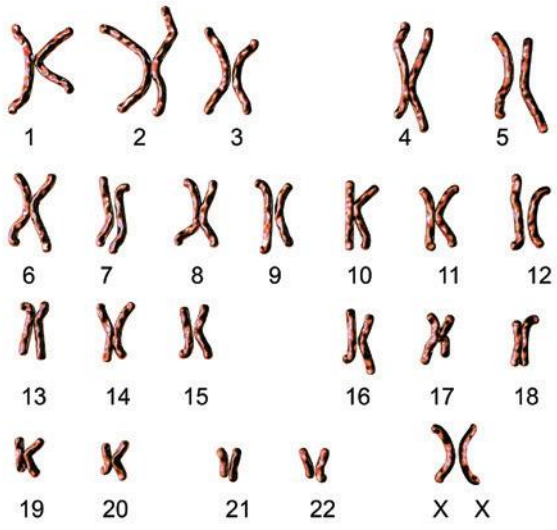
15 **Explain** why siblings with the same parents can have different phenotypes. (5 marks)

16 **Explain** how independent assortment contributes to genetic diversity in offspring. (3 marks)



Analytical processes

17 The diagram shows a karyotype from an individual with a normal chromosome count.



Determine:

a the sex of the individual (1 mark)

b the number of autosomes of the individual (1 mark)

c the likely stage of the cell cycle when the karyotype was taken. (1 mark)

18 **Distinguish** between diploid and haploid cells. (2 marks)

19 **Compare** the phases of meiosis of spermatogenesis and oogenesis with regard to the gametes produced. (4 marks)

20 **Discuss** the genetic advantages that a diploid organism has over a haploid organism. (3 marks)

Knowledge utilisation

21 **Discuss** the genetic advantages that a diploid organism has over a haploid organism. (3 marks)

22 **Propose** reasons why gametogenesis involves unequal division in oogenesis but not in spermatogenesis. (2 marks)

23 **Predict** the result of errors in crossing over during prophase I on the genetic composition of gametes. (3 marks)

24 **Discuss** why some types of organisms rely on mitosis exclusively, while others use meiosis and sexual reproduction. (2 marks)

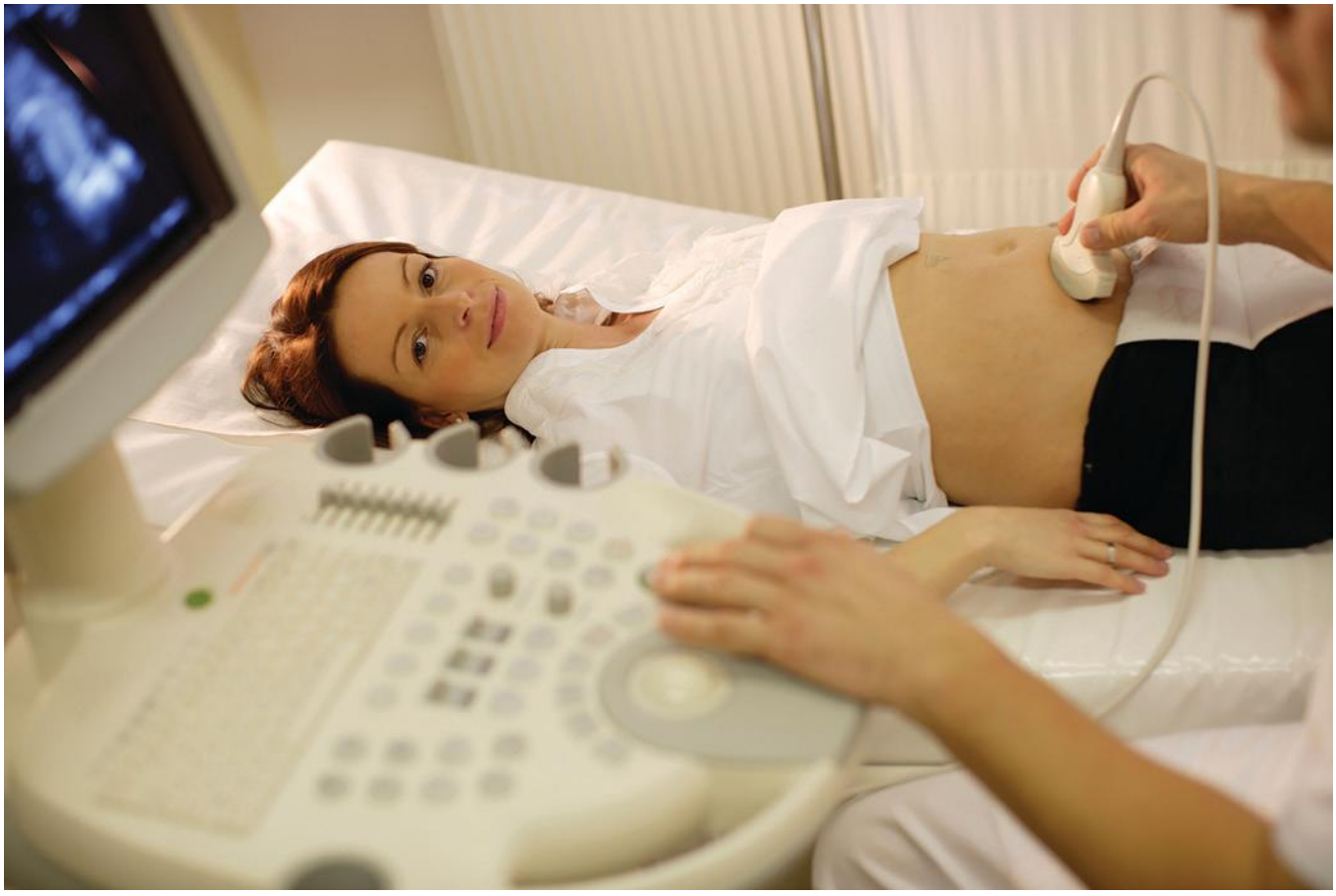
25 Two allelic versions of different genes were found to always be inherited together. **Propose** a conclusion about their relative positions on the chromosome. (2 marks)

26 Pacific salmon exhibit remarkable reproductive behaviour: adult salmon return from the ocean to the freshwater streams where they were born. During this migration, they overcome significant obstacles, such as predators and strong currents, to reach their spawning grounds. Once there, females dig nests in the gravel beds of the stream and lay up to 17,000 eggs, which are then fertilised externally by males. **Discuss** how the reproductive strategy of Pacific salmon contributes to genetic variation in the offspring. (4 marks)

27 In a study of the menstrual cycle, a Canadian researcher did daily ultrasound scans of 63 women who had normal menstrual cycles, over a period of six weeks. The researcher measured the diameter of every follicle in the ovary and its waves of growth. They discovered that up to 20 follicles develop prior to ovulation, but generally one is larger, and as it ruptures to release the ovum, the others degenerate. The researcher also found that all the women had at least two growth waves in a cycle and half of them had three. Regardless of the number of growth waves, the actual ovulation differed between the women. Fifty of the women ovulated once, seven did not ovulate and six ovulated twice over a month and on separate days. This would explain why 10 per cent of conceptions are non-identical twins. It has been suggested that those women who have three follicular growth waves in a cycle would run out of primary follicles at a faster rate than women who have two waves. This would explain why the onset of menopause is earlier in some women than in others.

a **Evaluate** the experimental protocol in this study. (2 marks)

b **Design** an experimental procedure to determine whether the number of follicular waves per cycle is related to time of menopause, and whether this is an inherited characteristic, ensuring that bias is minimised where possible. (3 marks)



Data drill

Meiosis and quantity of DNA

An experiment was conducted to quantify the amount of DNA in a cell during meiosis. Because DNA is so small, the mass is given in femtograms (fg), with one femtogram being equal to one quadrillionth of a gram (10^{-15} g). Figure 1 shows the average amount of DNA per cycle after induction of meiosis (in hours), and the raw data is provided in Table 1.

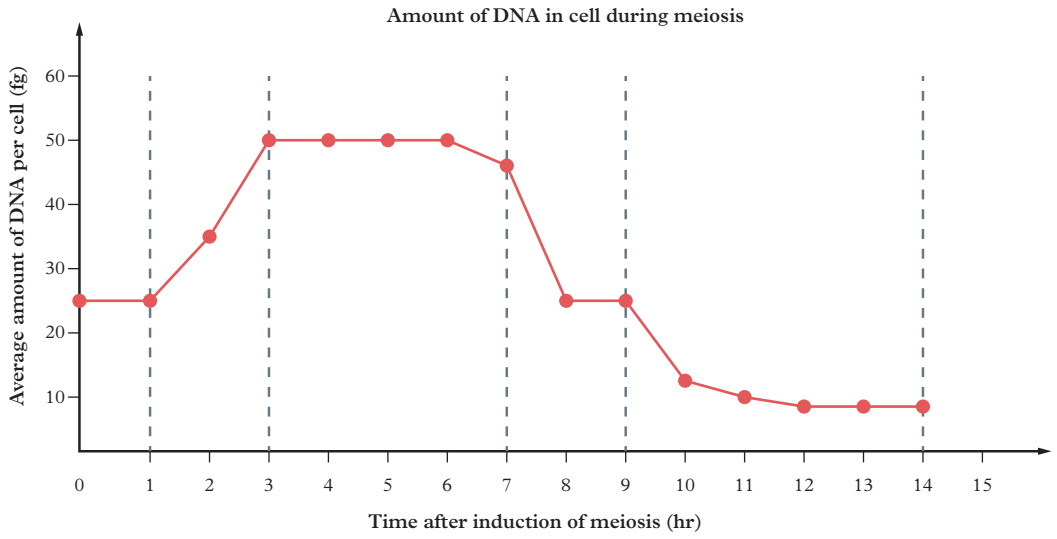


FIGURE 1 Amount of DNA per cell (fg) after induction of meiosis

TABLE 1 Raw data on amount of DNA per cell (fg) after induction of meiosis

	Amount of DNA per cell (fg)				
Time (hours)	Trial 1	Trial 2	Trial 3	Average	Standard error
0	25.1	20.5	26.4	24	1.79
1	25.6	22.7	21.9	23.4	1.12
2	42.2	40.3	38.7	40.4	1.01
3	48.8	49.2	48.1	48.7	0.32
4	49.1	50.2	48.9	49.4	0.40
5	50.3	49.7	49.1	Question **1**	0.35
6	50.7	48.9	49.5	49.7	0.53
7	46.5	48.2	47.2	47.3	0.49
8	25.2	22.7	23.2	23.7	0.76
9	24.3	25.3	23.3	24.3	0.58
10	19.2	9.2	10.9	13.1	3.09
11	11.8	9.8	11.1	10.9	0.59
12	12.5	9.9	12.1	11.5	0.81
13	11.8	11.7	9.8	11.1	0.65
14	11.6	10.9	9.9	10.8	0.49

Apply understanding

1 **Calculate** the average amount of DNA (fg) per cell 5 hours after induction of meiosis. (1 mark)

2 If 1 fg of DNA = 9.78×10^5 base pairs, **calculate** the number of base pairs present 13 hours after induction of meiosis. (2 marks)

Analyse data

3 **Compare** the uncertainty of the experiment results at times 10 hours and 11 hours. (2 marks)

Interpret evidence

4 **Infer** what stage of meiosis is occurring from 9 hours, giving reasons for your response. (2 marks)

Module 8 checklist: Meiosis

MODULE 9

Mutations

Introduction

Mutations are caused by changes or errors in DNA replication or chromosomes, which can result in changes in the phenotype of an individual. Chromosomal genetic disorders arise from non-disjunction of chromosomes during the nuclear division of meiosis for gamete production. Karyotypes show the numbers of chromosomes present in an individual and are used to predict whether there is a chromosomal genetic disorder. Errors in DNA replication tend to result from damaging mutagens, such as chemicals that are carcinogenic, radiation, heat and physical influences such as the environment. The consequences of these DNA errors depend on the type of change caused in the DNA and therefore on the phenotype of the individual.

Prior knowledge

Prior knowledge quiz Check your understanding of concepts related to mutations before you start.

Subject matter

Science understanding

→ Explain how errors in DNA replication and damage by physical/chemical factors in the environment can lead to point and frameshift mutations.

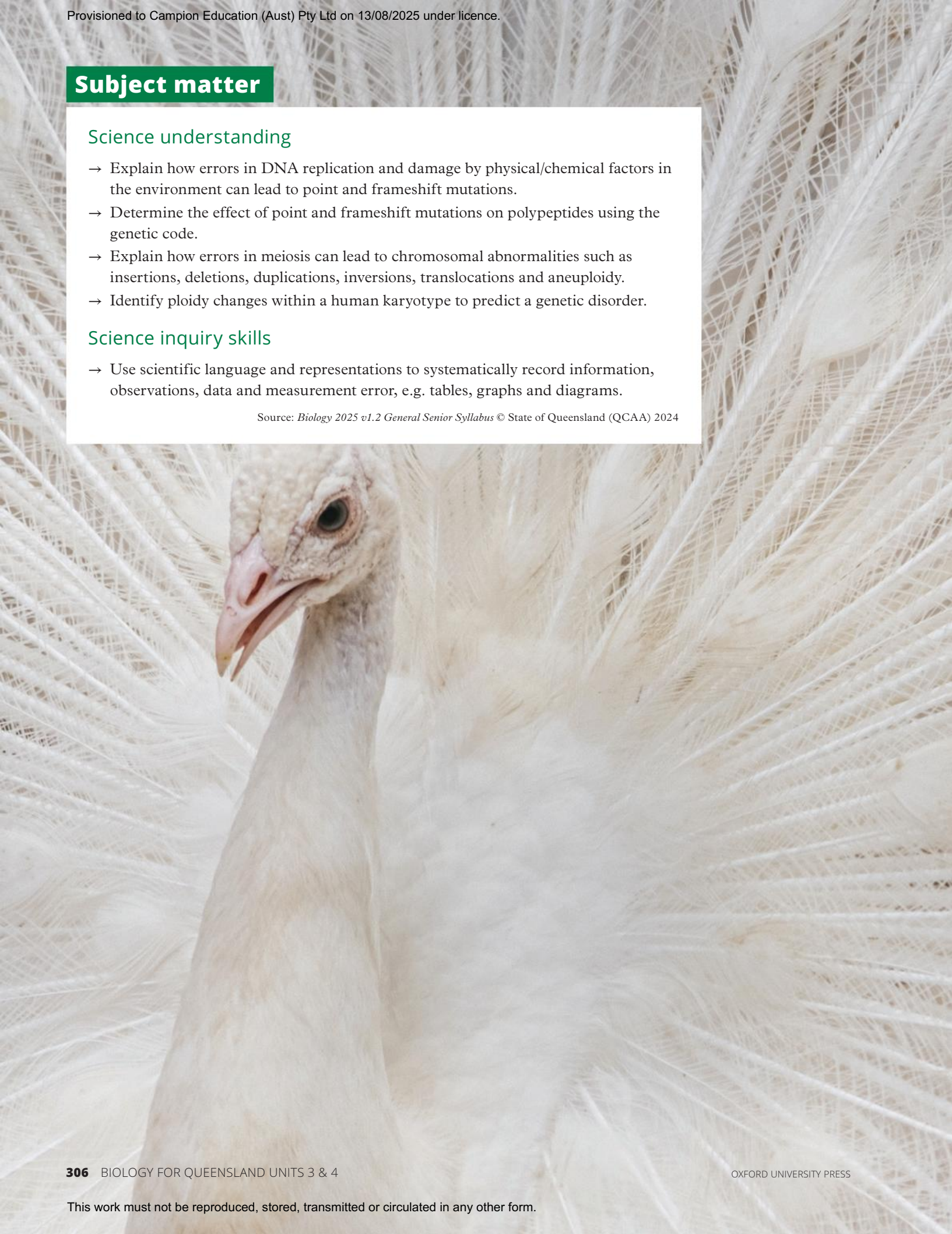
→ Determine the effect of point and frameshift mutations on polypeptides using the genetic code.

→ Explain how errors in meiosis can lead to chromosomal abnormalities such as insertions, deletions, duplications, inversions, translocations and aneuploidy.

→ Identify ploidy changes within a human karyotype to predict a genetic disorder.

Science inquiry skills

→ Use scientific language and representations to systematically record information, observations, data and measurement error, e.g. tables, graphs and diagrams.



Lesson 9.1
Genetic mutations

Key ideas

- → A mutation is a permanent change to DNA.
- → Mutations in somatic cells affect only the individual, whereas mutations in germline cells are inheritable.
- → Point mutations result from the changing of a single nucleotide in a DNA triplet, and may result in a silent, missense or nonsense mutation.
- → Frameshift mutations result from insertion or deletion of a nucleotide in a DNA triplet and alter the reading frame of all DNA triplets following the mutation.

Mutations

Learning intentions and success criteria

Each time a cell replicates its DNA, there is the potential for a mistake to occur. Many of these mistakes are repaired by specialised proteins such as BRCA1 and BRCA2 proteins, which act as a built-in auto-correcting system. Occasionally, an error in the DNA sequence is missed and is passed on during transcription to mRNA. The error is translated into an incorrect amino acid in the protein produced. Such an error is called a gene **mutation** (a permanent change in the nucleotide sequence of the genetic material). Mutations that result in a change in the final transcribed protein can cause a different phenotype to be expressed.

mutation
a small, permanent change in the DNA of an organism

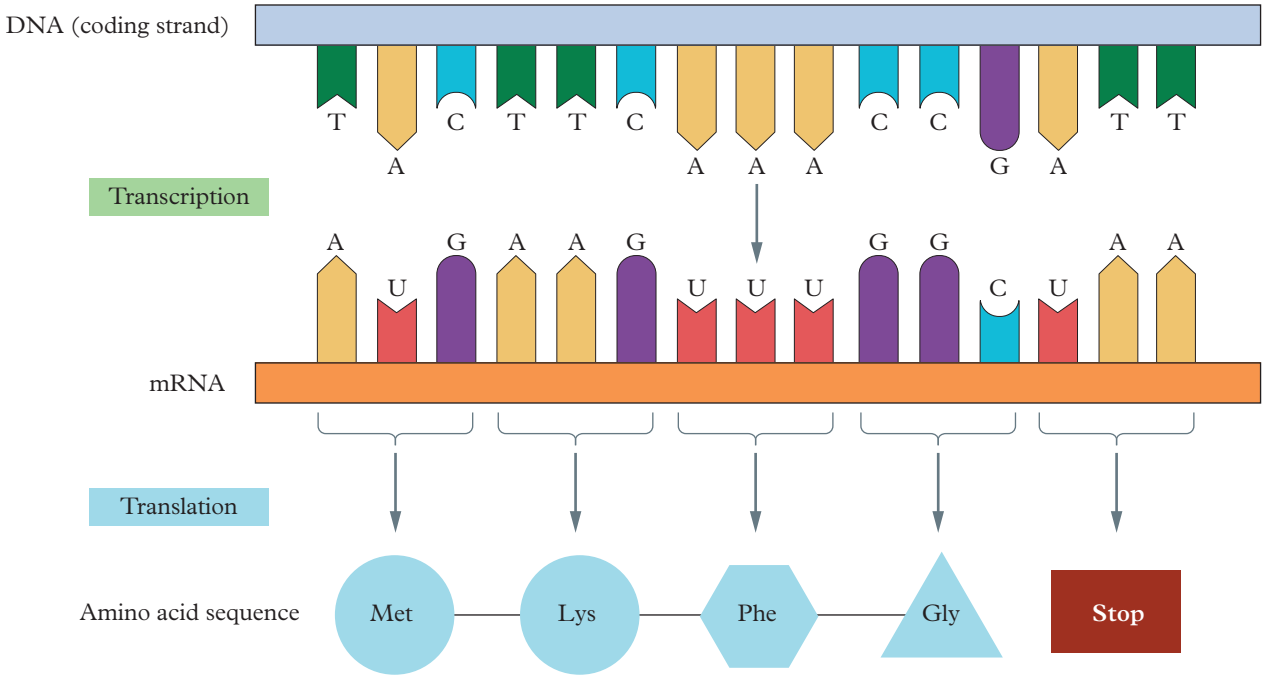


FIGURE 1 Transcription and translation of a normal DNA molecule

Point mutations

point mutation
a change in a single nucleotide in the DNA code that may result in translation of one different amino acid in a polypeptide sequence

somatic mutation
a mutation in a non-reproductive cell and therefore non-inheritable, affecting only the individual

germline mutation
a heritable change in DNA that occurs in a germ cell (a cell destined to become an egg or a sperm) or in a zygote at the single-cell stage and so is incorporated into every cell of the body

Many mutations are the result of a change in a single nucleotide in the sequence. Such changes are called **point mutations**. For example, a change in a single nucleotide of the *BRCA1* gene will result in a non-functioning protein that cannot repair other DNA mutations.

Point mutations seem to occur more regularly in older individuals and are believed to be a function of the natural ageing process, or senescence. Because this type of mutation generally affects body cells, not germ cells, it is referred to as **somatic mutation**. Only those DNA mutations that occur in **germline** (reproductive) cells can be passed on to future generations.

A point mutation occurs inside one DNA nucleotide triplet, where there is a substitution of one nucleotide for another, or the order within the triplet may be changed. While this may cause changes in the amino acid sequence, the actual frame of the DNA strand is not altered.

There are three main types of point mutation:

- silent
- missense
- nonsense.

Silent point mutations

In a silent point mutation, one nucleotide is substituted for another, or the order may be changed within the triplet. Because many DNA triplets can code for the same amino acid, the replacement of a single nucleotide may not result in a change in the amino acid sequence, and so there may be no effect on the protein produced. As a result, the mutation usually remains undetected, because the resulting protein remains functional.

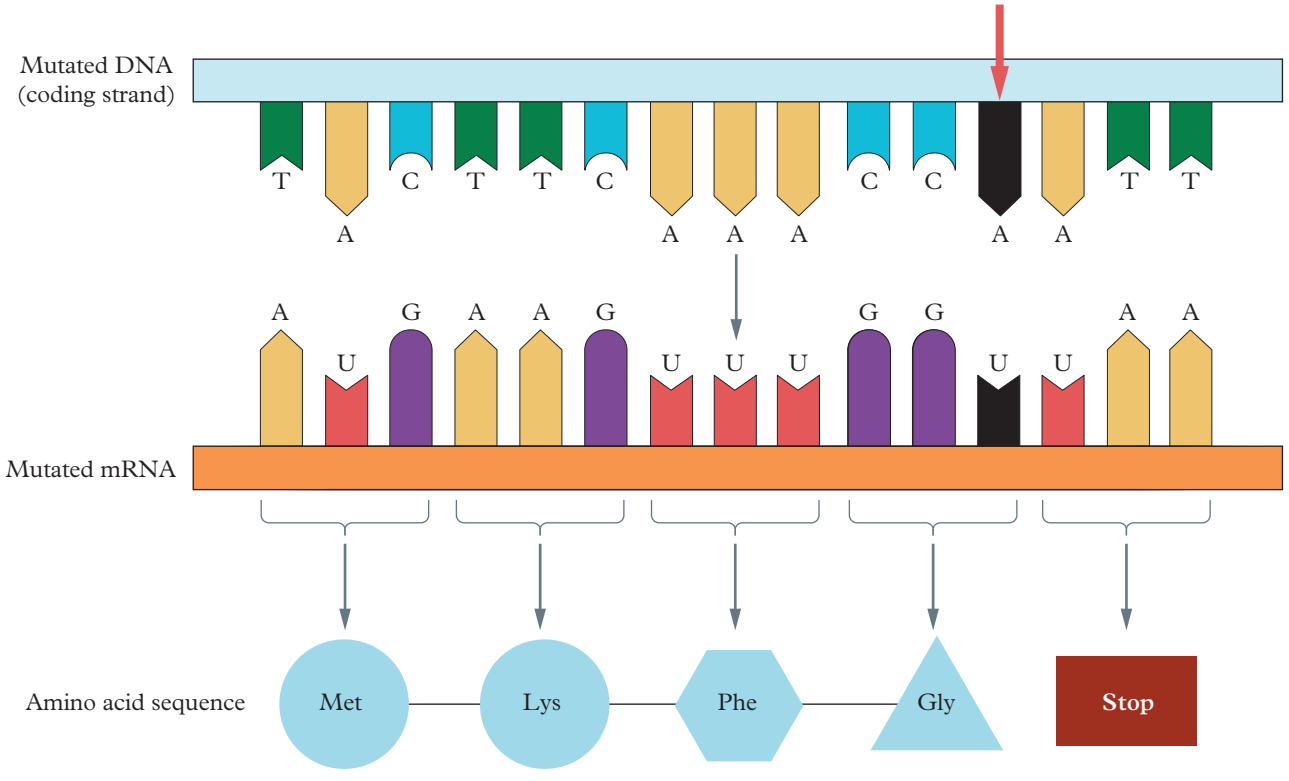


FIGURE 2 Silent mutation: in the DNA strand from Figure 1, a mutation in the DNA has an adenine base instead of a guanine base in the fourth triplet. (The error is in black and is indicated with a red arrow.) The new triplet still codes for the amino acid glycine; there is no change in the amino acid sequence.

Missense point mutations

Some point mutations result in production of a protein in which one amino acid is substituted for another. In the substitution error shown in Figure 3, the cytosine nucleotide has been replaced by thymine. This results in coding for an incorrect amino acid, which means the resulting protein may be non-functional or possibly harmful to the organism.

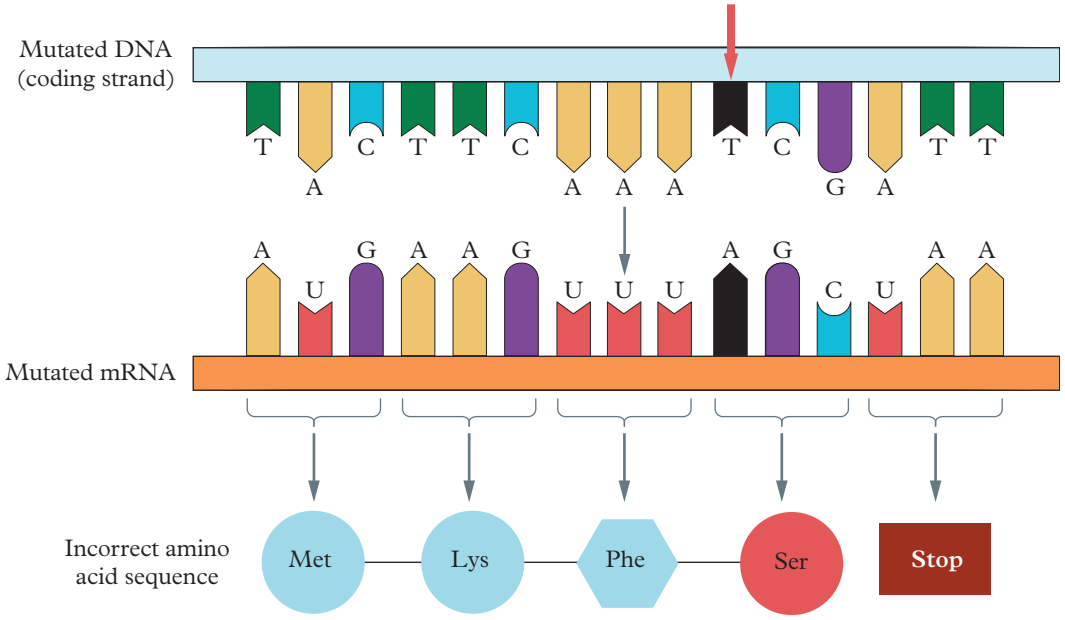


FIGURE 3 Missense mutation: the mutated DNA has a thymine base instead of a cytosine base in the fourth triplet. The new triplet codes for the amino acid serine instead of glycine, resulting in a change in the amino acid sequence.

Nonsense point mutations

Occasionally a point substitution will result in an amino acid codon being changed to a stop codon, leading to premature termination of protein translation. This is illustrated in Figure 4, where there is a substitution error in the second triplet (the thymine nucleotide has been replaced by adenine). This results in the stop codon UAG, and so the amino acid sequence is halted, causing a shortened polypeptide chain that may be non-functioning.

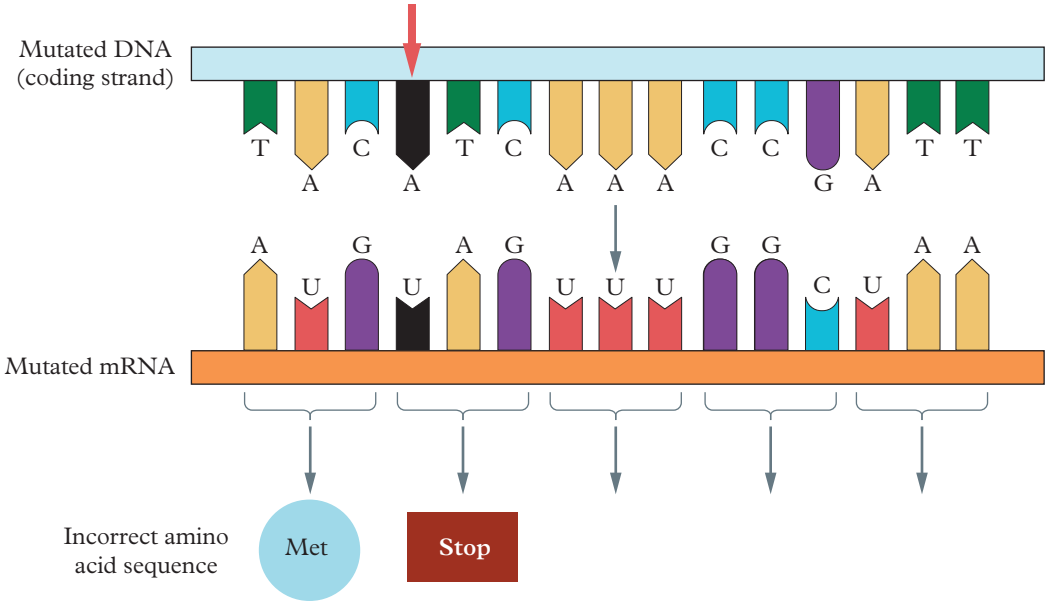


FIGURE 4 Nonsense mutation: the mutated DNA has an adenine base instead of a thymine base in the second triplet. The new triplet UAG codes for "stop", and so the amino acid sequence is ended.

Frameshift mutations

A mutation may involve nucleotides being added or removed from the DNA sequence. This may or may not be a problem if three nucleotides are added or removed, because it results in the addition or removal of a whole amino acid in the protein.

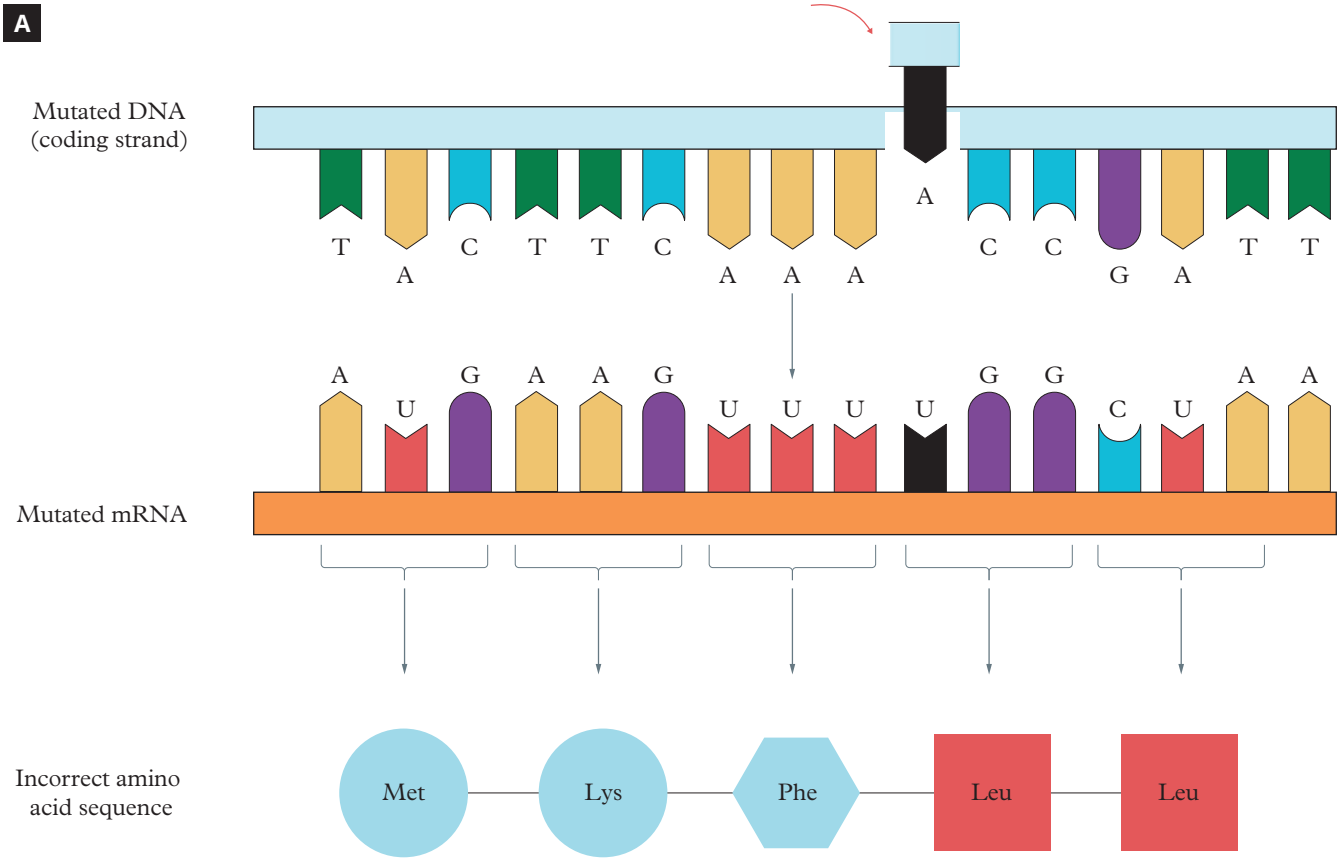
If a single base is added to (or deleted from) a triplet, this will alter the reading frame for all triplets following this mutation. From that point on, the reading frame of three nucleotides (triplets and then the mRNA codons) will have shifted, resulting in completely different proteins being produced. This is called a **frameshift mutation**.

frameshift mutation
the deletion or insertion of a single nucleotide, or a non-multiple of three nucleotides, into DNA

(normal sequence)	THE CAT ATE THE RAT AND RAN FAR
(point mutation)	THE CA**R** ATE THE RAT AND RAN FAR
(frameshift deletion)	THE C<u>AA</u> TET HER ATA NDR ANF AR
(frameshift insertion)	THE CAT **T**AT ETH ERA TAN DRA NFA R

An insertion results in shifting of the DNA frame to the right, while a deletion moves the frame to the left. In framing errors, there is an increase or decrease in the number of nucleotides in the DNA strand. All triplet codes (and therefore the codons) following the frameshift will be altered. This results in the production of a very different protein that may not be functional.

A



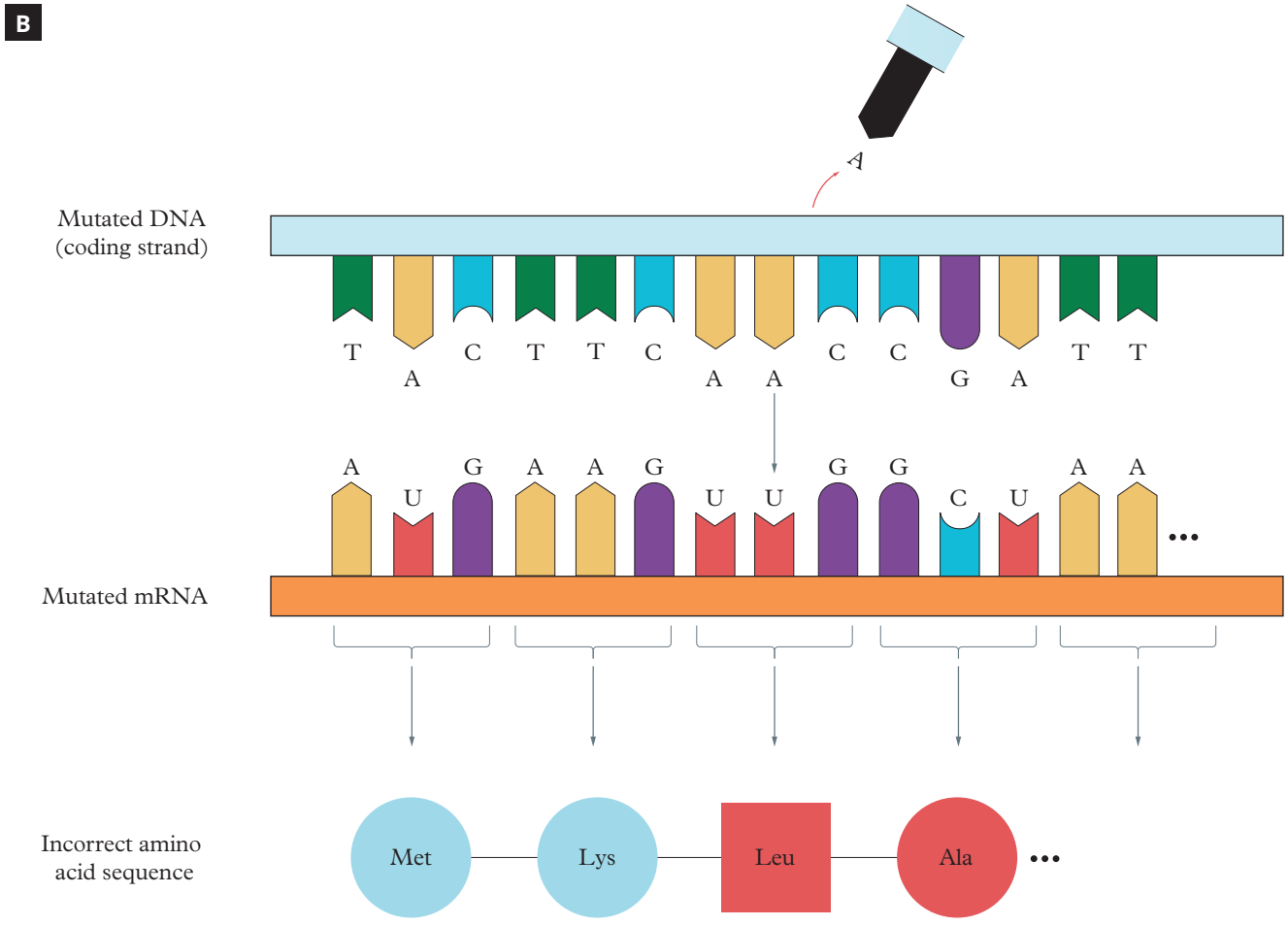


FIGURE 5 Frameshift mutations. (A) The mutated DNA has an adenine base added after the third triplet (error is shown in black). (B) The mutated DNA has an adenine base deleted from the third triplet. In both cases, the DNA reading frame has been "shifted" – to the right in (A) and to the left in (B).

Deletions, insertions or substitutions can also occur during transcription of mRNA, in translation between mRNA and tRNA, or when tRNA transfers an amino acid to an amino acid sequence. These changes, however, are not permanent and only affect the protein being produced at that time.

The differences between point mutations and frameshift mutations are as follows.

- A point mutation does not change the reading frame of the DNA strand. In a frameshift mutation, the frame of the DNA strand is shifted in one direction or the opposite direction.
- A point mutation causes only the structure of one code of the gene to change. A frameshift mutation changes the gene structure, by changing the number of nucleotides.
- A point mutation is the result of a nucleotide base substitution or a change of order in one triplet code during DNA replication. A frameshift mutation results from a nucleotide deletion or insertion.

Skill drill

Interpreting codon charts to determine the effect of mutations

Science inquiry skill: Processing and analysing data (Lesson 1.7)

A section of DNA that codes for a structural protein was sequenced, with the order of nucleotides given below.

5′ … A T G T G G G C C T G C C G C T G A … 3′

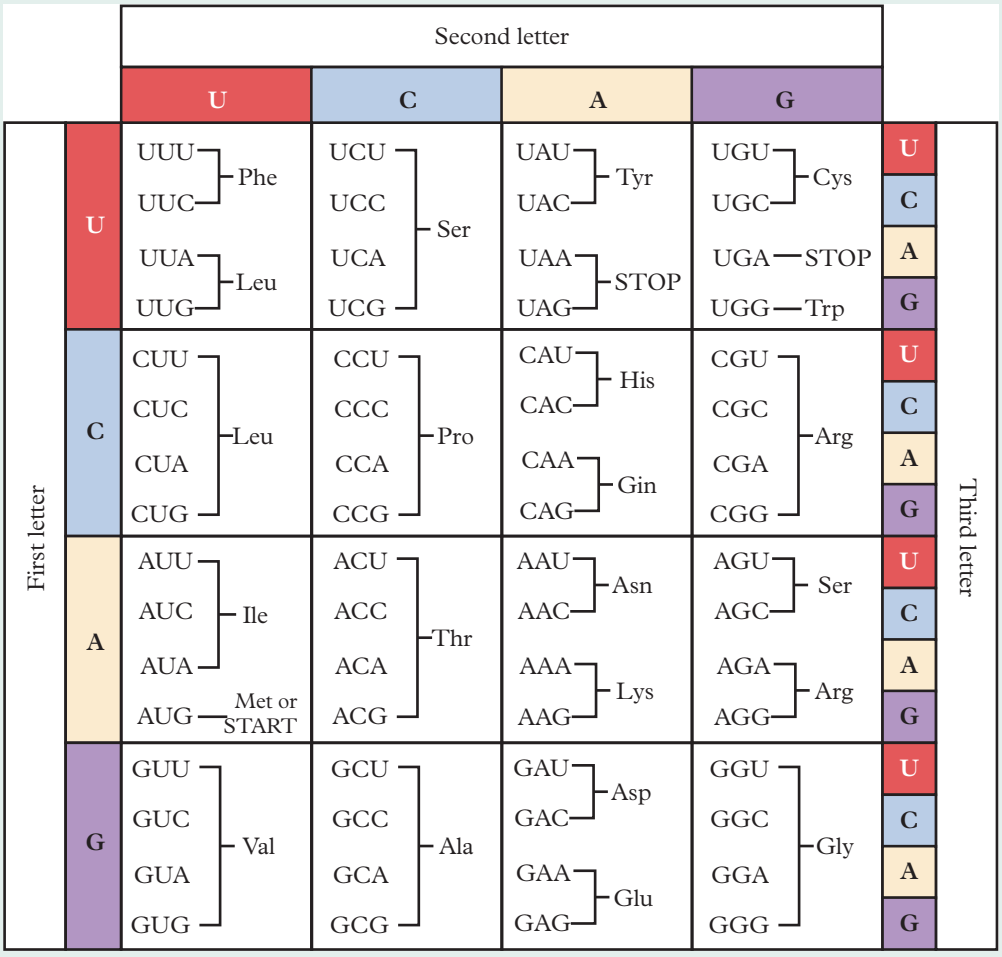


FIGURE 6 Amino acid codon chart

Practise your skills

1 **Determine** the mRNA and amino acid sequence for the DNA strand. (1 mark)
2 If a missense point mutation occurred, changing the 12th nucleotide to guanine (G), **infer** the change to the amino acid sequence. (1 mark)
3 **Infer** the change to the amino acid sequence if the 12th base were changed to adenine. (1 mark)
4 **Determine** the amino acid sequence if the 9th base were deleted. (1 mark)

Real-world biology

Sickle cell anaemia – a point mutation

The most common form of sickle cell anaemia is caused by a point mutation in the gene that makes haemoglobin. This iron-rich compound allows red blood cells to carry oxygen from the lungs to all parts of the body. In sickle cell anaemia, an abnormal form of haemoglobin causes the red blood cells to "sickle" into a rigid shape and so clump together, blocking capillaries.

Healthy humans have adult haemoglobin (haemoglobin A), which consists of two alpha (α) chain proteins and two beta (β) chain proteins. These four protein chains are held tightly together by many weak hydrogen bonds or by covalent bonds between sulphur atoms in certain R groups.

The gene responsible for sickle cell anaemia is located on chromosome 11, where a point mutation

in the DNA has occurred. In this case, adenine has been replaced by thymine. This change results in the amino acid in normal haemoglobin A, known as glutamic acid, being replaced by valine. This point substitution mutation in the DNA causes the β-chain subunits of haemoglobin A to become sticky (haemoglobin S), causing the red blood cells to change shape.

The types of haemoglobin a person produces in their red blood cells depends on what haemoglobin alleles they have inherited from their parents. For a person to have the disease, both their parents must have passed a defective allele to them. If only one parent passed the sickle cell allele to the child, that child will carry the trait and will have both normal and sickle haemoglobin. Although their blood may contain some sickle cells, they will tend to be symptom free. Often, the effects of the disease only show if the person engages in very vigorous activities, and this can lead to death.

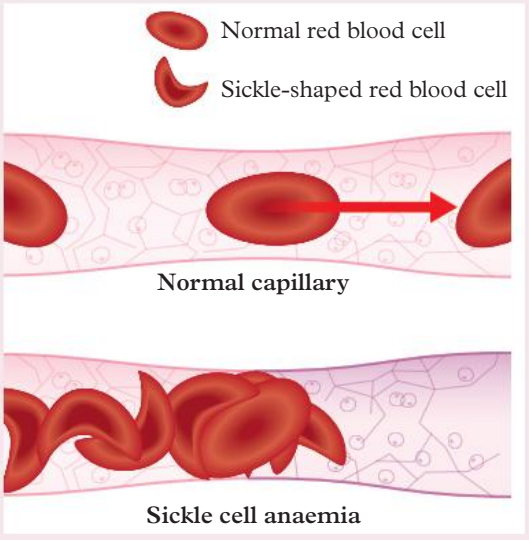


FIGURE 7 Comparison of the shapes of normal and sickle-shaped blood cells

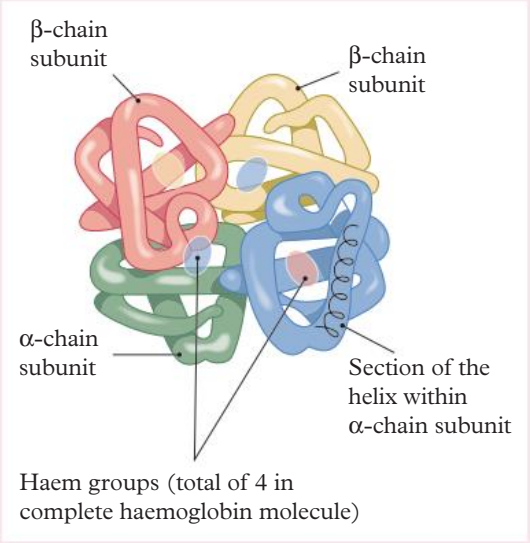


FIGURE 8 Haemoglobin A, showing the two alpha chains and two beta chains

Apply your understanding

1 **Identify** the type of point mutation responsible for sickle cell anaemia. (1 mark)

2 **Describe** the changes in haemoglobin and red blood cells caused by the mutation. (2 marks)

3 **Explain** why individuals with one sickle cell allele experience different symptoms than those with two defective alleles. (2 marks)

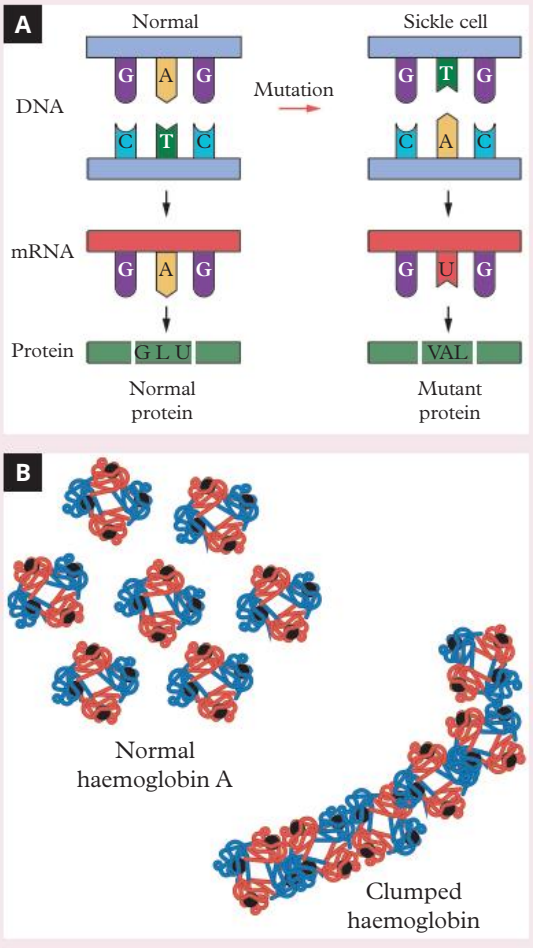


FIGURE 9 Sickle-cell anaemia. (A) The point mutation at the DNA level. (B) Effects at the protein level: normal haemoglobin A (left) and haemoglobin S in sickled red blood cells (right). The mutation in the DNA results in changes in the shape of the haemoglobin S molecule, which causes clumping in conditions of slightly higher oxygen demand.

Causes and effects of mutations

Mutations can have various effects on an individual. Some mutations may result in a new characteristic that has a selective advantage – that is, it benefits the organism and may improve the organism's chance of survival. For example, blue eyes are the result of a mutation 10,000 years ago. Humans with this mutation who migrated from Africa to northern Europe benefited from increased vision in poor light conditions. Another example is the mutation that led to humans having trichromatic vision, which is the ability to discriminate between three colours, compared to only two, as in most of the mammal kingdom.

FIGURE 10 Blue eyes are the result of a mutation.

Over time, some mutations accumulate and can ultimately be harmful for the individual. Lethal mutations may have an immediate effect on the cell (or the individual). This type of lethal mutation is therefore not transmitted to offspring. Other types of mutation may not exert an effect until some specific stage of development. Examples of such mutations are sickle cell anaemia and cystic fibrosis. Many mutations can become important in the future, by providing variations in a population that may benefit the population during changing environmental conditions. All alleles for any particular gene have arisen from mutation; therefore, mutations are key to increased genetic variation in populations.

If a mutation occurs in a body cell, it will not be important to the species as a whole, although it could bring about significant changes to a particular organ or tissue of the individual (e.g. tumour formation). However, if a mutation occurs in the gametes of an individual, it becomes part of the genetic framework of the cell and, with subsequent cell divisions, will be perpetuated through DNA replication. Therefore, mutation in the sex cells may affect the entire population, because the mutation may be passed on to subsequent generations through the gametes.

Gene mutations can be classified into two major types:

hereditary mutation
a gene change in a body's reproductive cell that can be passed from parent to offspring

- **hereditary** – inherited from a parent, present throughout life and found in virtually every cell
- somatic – acquired; may occur at some time in a person's life in non-reproductive cells and are not passed on to the next generation. These changes or mutations can be the result of environmental factors or human-made agents.

Some mutations occur naturally, while others arise as a reaction to external forces.

mutagen
a physical or chemical agent that changes the genetic material of an organism

A **mutagen** is a physical or chemical agent that changes genetic material by directly interacting with DNA. For example, high-energy radiation can cause breaks in the DNA strand, which may lead to the loss or gain of nucleotides during repair, in turn causing a frameshift mutation.

carcinogen
a substance or agent that can cause cells to become cancerous, by altering their genetic structure so that they multiply continuously and become malignant

Mutagens affect the replication or transcription of DNA, increasing the frequency or likelihood of mutations in the DNA of an organism. Some mutagens are also **carcinogens**, meaning they lead to the development of cancerous cells. Not all mutagens are carcinogens because not every mutation causes cancer. Similarly, not all carcinogens are mutagens – some promote cancer through mechanisms such as enhancing cell division or suppressing the immune response, rather than inducing mutations. However, there is an overlap: many carcinogens are mutagens, because DNA mutations often contribute to cancer development. For example, UV radiation is both a mutagen and a carcinogen.

Types of mutagens

Some examples of mutagens in everyday life (including those that are carcinogenic or cancer causing) are given in Table 1. While the mutagens in this list can affect many aspects of everyday life, it is only a very small sample of mutagens that can cause mutation of DNA.

TABLE 1 Some common mutagens

Type of mutagen	Example	Exposure source/effects
Physical (ionising radiation)	X-rays	Used in medical imaging
	Radioactive decay	Used in medicine and laboratories. Gamma rays, α particles, β particles emitted by radioactive substances
	Solar radiation	Sun (infrared, ultraviolet). Causes sunburn, melanomas and other skin cancers
Chemical	Asbestos	In buildings, brake pads, insulation products. Can cause asbestosis or malignant mesothelioma (cancer of the lung and heart lining)
	Benzopyrene	In fireplaces, car exhaust fumes, chargrilled meat and tobacco smoke. Formed during combustion of many organic materials
	Boric acid	Used in insecticides, fungicides and for many industrial purposes
	Nicotine	In tobacco. Highly addictive, and so increases the risk of lung cancer in humans
	Nitrous acid	Preservative in meat products
	Sodium bisulphite	Preservative in fruit juices, wine and dried fruits
	Most organic solvents, insecticides and fungicides	
Heavy metal	Arsenic, chromium, cadmium, lead, nickel and their compounds	In nickel–cadmium batteries, lead paint
Biological	Viral infection	Viral DNA can be inserted into the host's genome, disrupting host DNA. Viruses cause many diseases

FIGURE 11 X-rays can cause DNA mutations.

FIGURE 12 Viruses attack host DNA and can cause mutations.

Challenge

Tobacco smoke

Tobacco smoke contains chemicals such as benzopyrene, which directly damages DNA, causing mutations (making it a mutagen). These mutations can disrupt genes involved in cell cycle control, such as tumour suppressor genes or oncogenes, leading to the development of cancer (making it a carcinogen). Long-term exposure to tobacco smoke significantly increases the risk of cancers, particularly lung cancer, due to its combined mutagenic and carcinogenic properties.

FIGURE 13 Tobacco smoke contains mutagens and carcinogens

1 **Explain** how exposure to compounds in tobacco smoke can lead to mutations, and **describe** how such mutations might contribute to the development of lung cancer. (2 marks)

2 UV radiation and tobacco smoke are both classified as mutagens and carcinogens. **Compare** the mechanisms by which these agents cause DNA damage and **discuss** why they both increase cancer risk. (3 marks)

3 Scientists have developed therapies to target mutations caused by carcinogens, such as those in tobacco smoke. **Propose** how understanding the specific mutations caused by carcinogens might influence the development of personalised cancer treatments. (3 marks)

Check your learning 9.1

Check your learning 9.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** where a genetic mutation can occur. (1 mark)

2 **Explain** how a genetic mutation can occur without the amino acid being changed. (2 marks)

3 **Describe** the meaning of the term "frameshift". (1 mark)

4 **Explain** the difference between an inherited mutation and an acquired mutation. (2 marks)

5 **Explain** why nickel–cadmium batteries must be disposed of correctly. (1 mark)

6 Melanoma (skin cancer) can be lethal. **Describe** the mutagen that causes this cancer. (1 mark)

7 **Explain** why many chemical mutagens are still available on supermarket shelves. (2 marks)

Analytical processes

8 A student claimed that a point mutation could be described as a frameshift mutation. **Evaluate** whether their claim is accurate, using examples in your response. (2 marks)

9 **Distinguish** between a mutagen and a carcinogen. Use examples to support your response. (3 marks)

Lesson 9.2
Chromosome mutations

Key ideas

- → Errors during meiosis can lead to chromosomal mutations where "blocks" of genes are altered (insertions, deletions, duplications, inversions, translocations).
- → Non-disjunction, resulting in aneuploidy, occurs when a pair of homologous chromosomes fail to separate correctly during meiosis.
- → Recognising aneuploidy in a karyotype can be used to predict genetic disorders in an individual (e.g. Down syndrome).

Learning intentions and success criteria

homologues
two chromosomes that are homologous; during meiosis, the set of pairing maternal and paternal chromosomes; both have the same genes at the same loci but they may have different alleles

block mutation
a type of genetic mutation involving a segment of a chromosome, rather than a single nucleotide

chromosome mutation
a change in the chromosome structure or number, often due to an error in pairing during the crossing over stage of meiosis

deletion
loss of a part of a chromosome during DNA replication

duplication
a repetition of a region of DNA that contains one or more genes

insertion
the addition of a segment of one chromosome into another chromosome

Errors in meiosis

During meiosis I, there is often exchange of pieces of chromatids between **homologues** (homologous chromosomes). When the homologous chromosomes pair up during prophase I, crossing over can occur. Occasionally the crossing over is incomplete. A **block mutation** occurs when there is a change in a "block" of genes located together on a single chromosome. This is due to a mistake that can occur during meiosis. A **chromosome mutation** is a change in the arrangement of blocks of genes, or the number of chromosomes, in a cell.

Types of chromosomal abnormalities

A **deletion** can occur when a segment that has broken off one homologue is not replaced by the corresponding segment of the other homologue. The resulting chromosome will therefore not have all the genetic information it should (Figure 1).

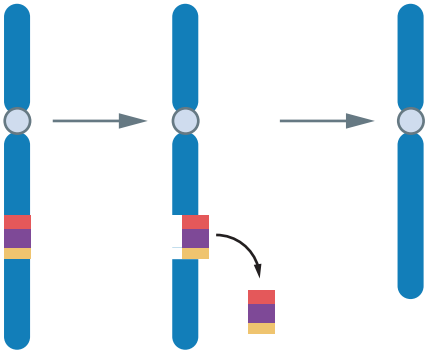


FIGURE 1 A chromosomal deletion

Sometimes the broken-off segment becomes incorporated into the homologue, which then has two sections of that piece of information – a **duplication** has then occurred (Figure 2).

In other instances, the broken-off segment becomes inserted into a completely different (non-homologous) chromosome. This is known as **insertion** (Figure 3).

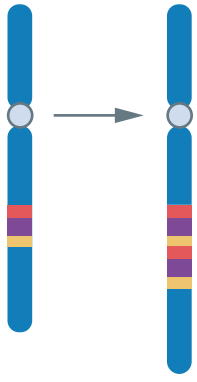


FIGURE 2 A chromosomal duplication

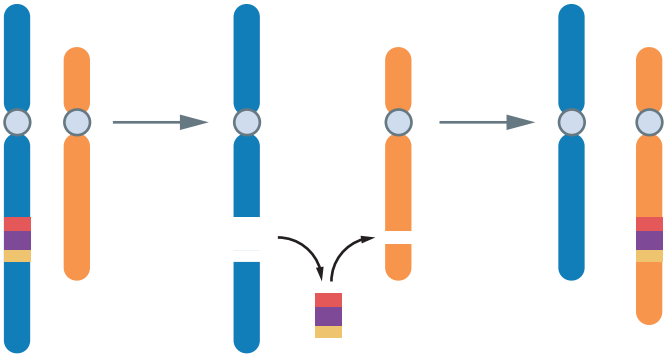


FIGURE 3 A chromosomal insertion

translocation
the exchange of chromosomal segments from one position to another, either within the same chromosome or to another chromosome

inversion
a chromosome rearrangement in which a segment of a chromosome is reversed end-to-end

Once removed, segments from two different chromosomes may also exchange positions. This is known as **translocation** (Figure 4).

An **inversion** occurs when the broken-off segment reattaches "back-to-front" (Figure 5). Depending on the size of the segment and the genetic information it carries, this form of misinformation can result in death of the developing embryo.

An example of a disorder caused by a chromosomal block mutation is cri-du-chat (French for "cry of the cat"). Cri-du-chat syndrome is caused by deletion of the top section of the small arm of chromosome 5 (Figure 6).

The name arises from the infant having a very high-pitched cry that sounds like the cry of a cat. About one-third of these children lose this cry by age two. Most cases of this syndrome are not inherited and there is no history of the disorder in the family. It appears to arise from an error during gamete (ova or sperm) formation or during early foetal development.

Children with this condition may experience:

- severe intellectual disabilities, including delayed speech and motor ability
- delayed physical development
- a small head and jaw
- low birthweight and poor growth associated with swallowing and sucking difficulties
- weak muscle tone
- distinctive facial features (e.g. low-set ears, wide nasal bridge, skin tags in front of the eyes)
- general health and behavioural difficulties.

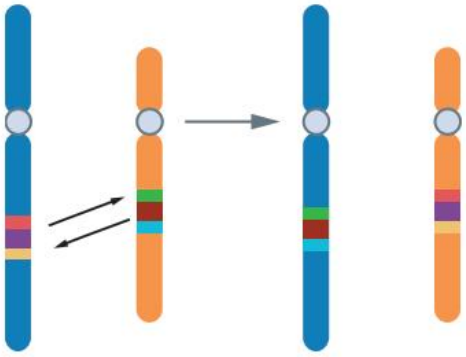


FIGURE 4 A chromosomal translocation

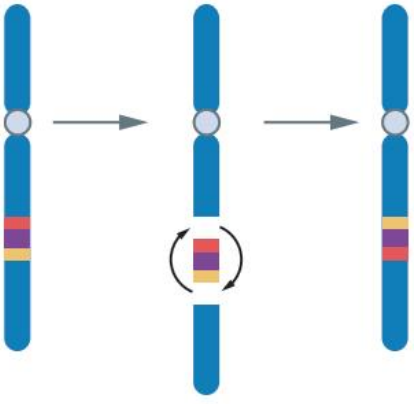


FIGURE 5 A chromosomal inversion

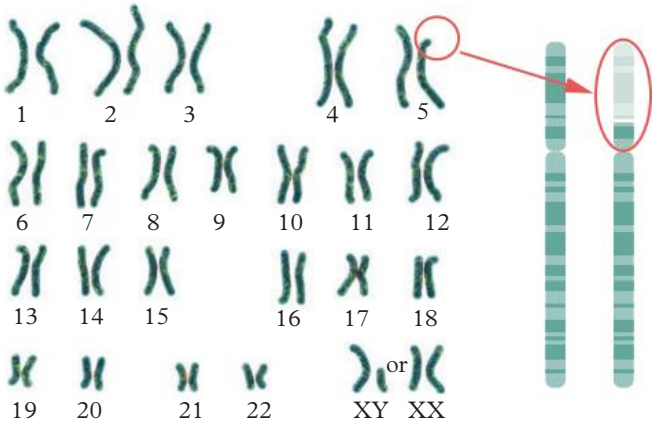


FIGURE 6 Karyotype of cri-du-chat syndrome

Chromosomal non-disjunction mutations

non-disjunction
the failure of homologous chromosomes or sister chromatids to separate during meiosis

aneuploidy
the presence of an abnormal number of chromosomes in a cell

Occasionally, during meiosis, a pair of homologous chromosomes fail to separate. This process is termed **non-disjunction**. It results in some of the gametes receiving two copies of a particular chromosome, while other gametes lack that chromosome entirely. After fertilisation, the diploid zygote will have an incorrect number of chromosomes. The presence of an abnormal number of chromosomes in a cell (**aneuploidy**) will occur in every cell in the resultant individual. For example, in a human, non-disjunction resulting in a gamete lacking a chromosome will lead to each cell in the offspring having 45 chromosomes instead of the usual 46.

There are two main categories of chromosomal aneuploidy errors: **autosomal aneuploidy**, which involves the 44 autosomal (body) chromosomes, and **sexual aneuploidy**, which involves the X and Y sex chromosomes.

autosomal aneuploidy
the presence of an abnormal number of autosomal chromosomes in a cell

sexual aneuploidy
the presence of an abnormal number of sex chromosomes in a cell

Non-disjunction may occur during meiosis I or meiosis II. It is caused when:

- homologous chromosomes fail to separate during meiosis I
- sister chromatids fail to separate during meiosis II, resulting in an abnormal number of chromosomes in the gametes.

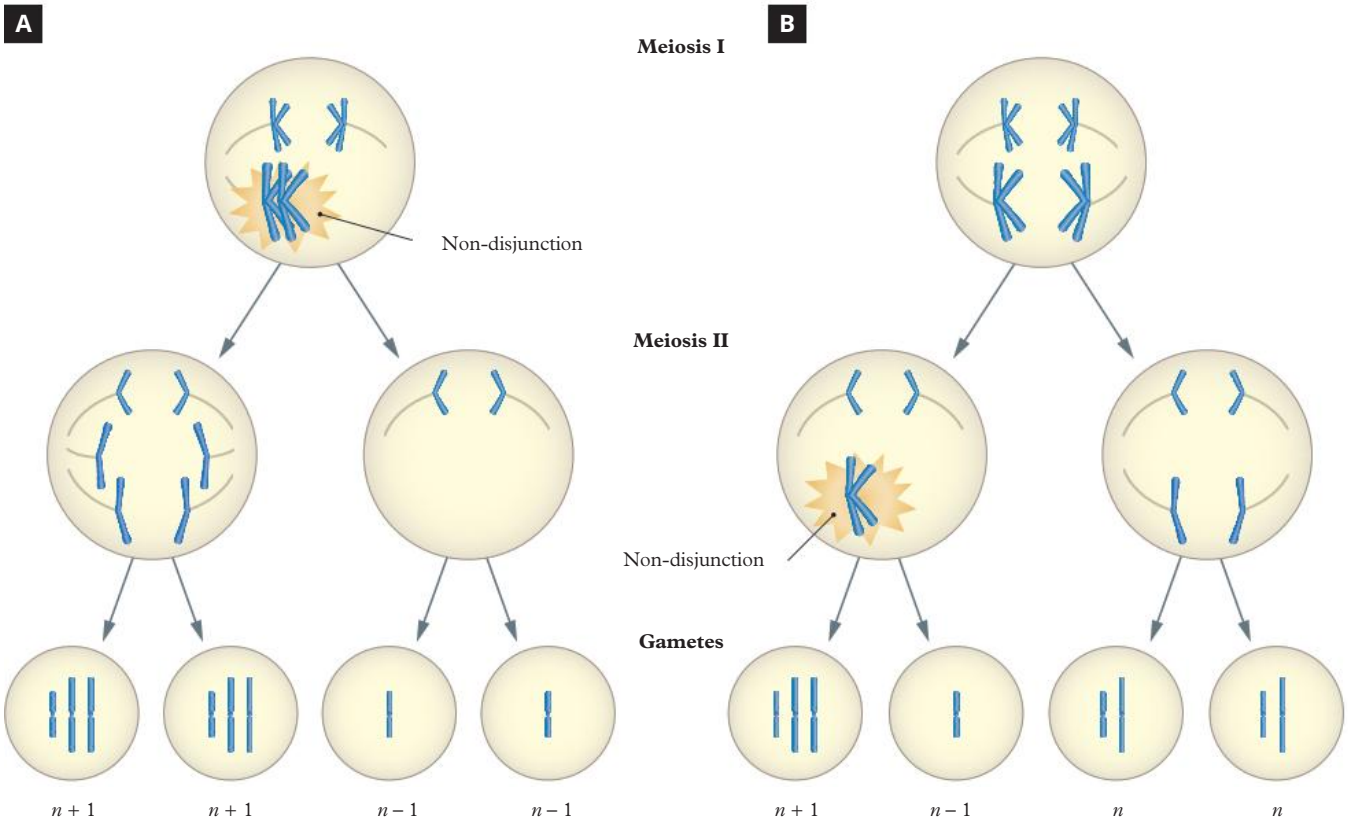


FIGURE 7 Non-disjunction of (A) homologous chromosomes in meiosis I, and (B) sister chromatids in meiosis II

If a male gamete with one missing autosome fertilises an ovum, the embryo will not develop. If there is an extra autosome present, the embryo may develop.

In 1959, it was discovered that the presence of an extra chromosome 21 was associated with Down syndrome in humans. The **trisomy** (three chromosomes) condition is not limited to chromosome 21. Trisomy 18 (Edwards syndrome) and 13 (Patau syndrome) are two other syndromes that have been identified as resulting from non-disjunction.

trisomy
a condition in which a diploid organism has three copies of one of its chromosomes instead of two

Non-disjunction can produce individuals with unusual combinations of sex chromosomes. In humans, the male sex results from the presence of the Y chromosome. A normal male's sex chromosome complement is XY. Non-disjunction may result in a person having additional copies of the X or Y chromosomes.

Klinefelter syndrome is a genetic condition that affects males who, through non-disjunction, receive additional copies of the X chromosome (Figure 8). Males with Klinefelter syndrome may have sex chromosome complements of XXY, XXXY or XXXXY, with the severity and range of symptoms varying among individuals. Common symptoms experienced can include tall stature, reduced muscle mass, sparse facial and body hair, lowered testosterone levels, and lower sperm production, leading to fertility issues.

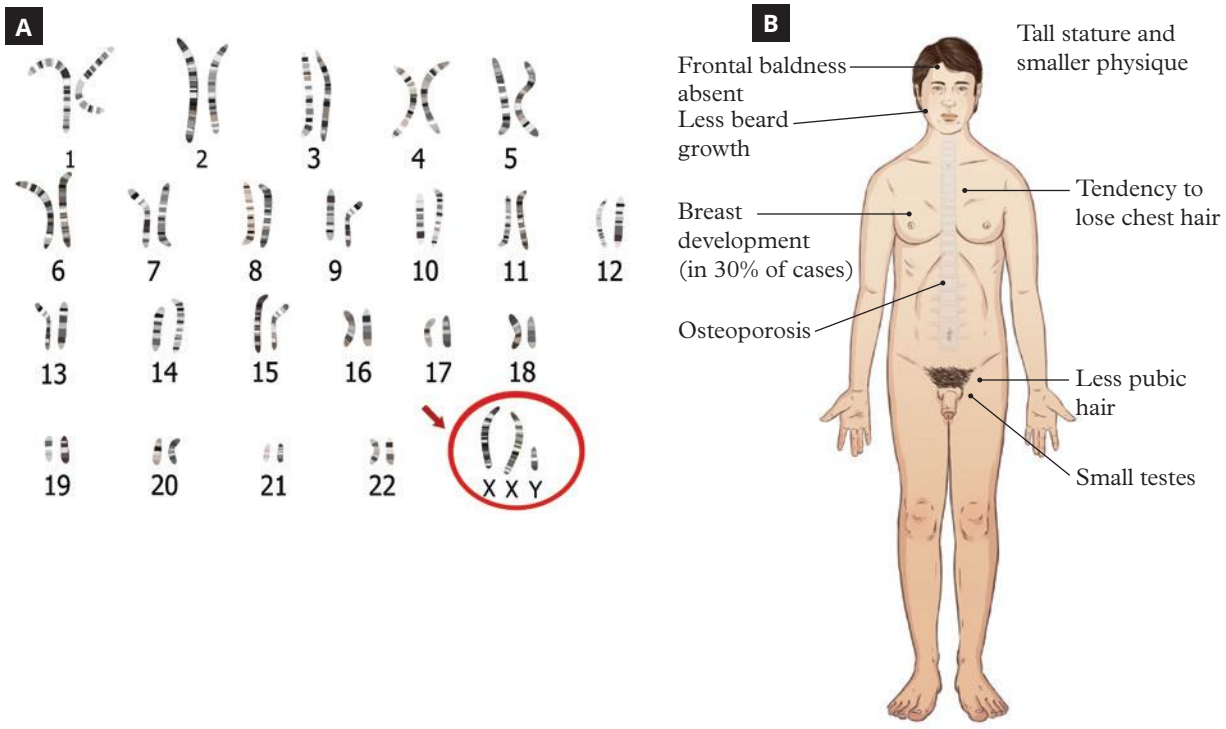


FIGURE 8 Klinefelter syndrome: (A) karyotype and (B) characteristics

Turner syndrome is a genetic condition that affects females and occurs when non-disjunction results in one of the two X chromosomes being partially or completely missing (Figure 9). This means that, rather than having the typical female sex chromosomes of XX, a person with Turner syndrome has a karyotype with only one X chromosome. The severity of symptoms varies but may include shorter stature, underdeveloped ovaries, menstrual irregularities and increased risk of some medical conditions (e.g. congenital heart defects) and autoimmune disorders.

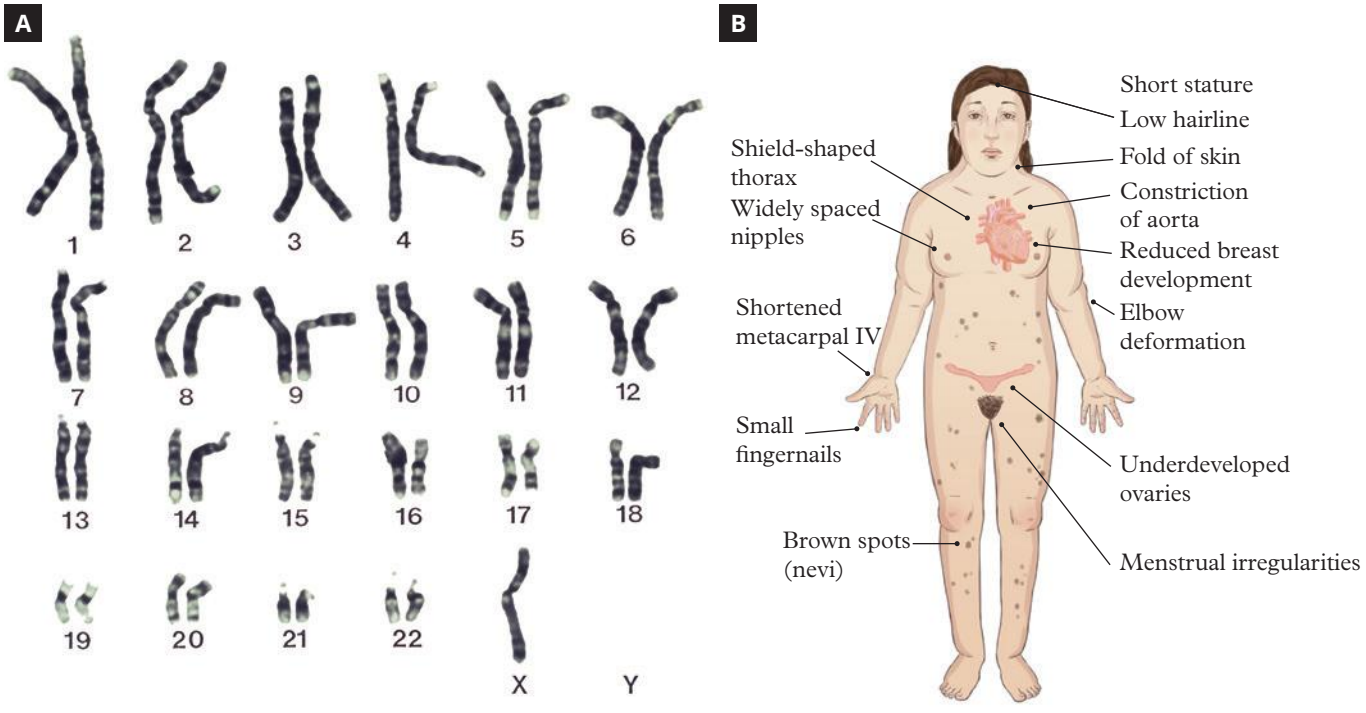


FIGURE 9 Turner syndrome: (A) karyotype and (B) characteristics

Studying chromosomes – the karyotype

A **karyotype** is a display of the total complement of an individual's chromosomes. It is prepared using mitotic metaphase chromosomes. In humans, a blood sample is usually taken, and the white blood cells are separated from the other constituents. Cells in the process of dividing are interrupted by the addition of a drug (colchicine). This drug prevents anaphase from occurring by interfering with the spindle microtubules. The addition of water causes the cells to rupture. Photographs of the ruptured cells are taken. These are enlarged, and the chromosomes are cut out and arranged in pairs. The position of the centromere, and thus the length of the "arms" of the chromatids, is used as a determinant for the pairs. Certain anomalies, such as an extra chromosome or piece of chromosome, can then be detected.

karyotype
the number and visual appearance of the chromosomes in the cell nuclei of an organism or species

Real-world biology

Fragile X syndrome

Fragile X syndrome results from repeated duplication of three nucleotides of one gene (called *FMR1*) on the X chromosome. This repeated replication of three nucleotides lengthens the gene, causing it to stop the production of a protein that is essential for development and other functions. Because the gene is located on an X chromosome, most females (who have two X chromosomes) have at least one "normal" X chromosome. Males (who have only one X chromosome) are more likely than females to have the disease phenotype. During cell division, this section of the chromosome appears as though it is hanging from a thread, giving it the name "fragile".

The extent of the symptoms depends on the number of times the trinucleotide duplicates. Up to 40 repeats does not appear to have any effect, but if a person has more than 200 duplications of this segment, the gene completely "switches off" and does not attempt to make the coded protein. The exact function of the protein coded for by the *FMR1* gene is not known at present, but it is thought to be associated with communication between nerve cells in the brain.

The symptoms of this disease involve varying degrees of learning, behavioural and emotional difficulties, and physical features. In children they may include:

- delayed development (e.g. sitting, walking, speaking)
- difficulty paying attention
- hand flapping and biting associated with high levels of anxiety
- physical signs, such as a long narrow face, large ears, a high arched palate, flat feet and extremely flexible joints
- seizures.

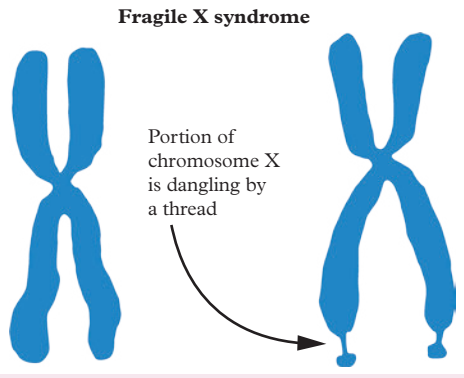


FIGURE 10 The "fragile" X chromosome in fragile X syndrome

Apply your understanding

1 **Identify** the gene responsible for fragile X syndrome. (1 mark)
2 **Describe** the impact of the number of trinucleotide repeats on the severity of fragile X syndrome symptoms. (2 marks)
3 **Explain** why males are more likely to express fragile X syndrome compared to females. (2 marks)

Check your learning 9.2

Check your learning 9.2: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** the purpose of a karyotype test. (1 mark)
2 **Describe** what occurs in chromosomes during meiosis when a block of genes is:
   a deleted (1 mark)
   b duplicated (1 mark)
   c translocated (1 mark)
   d inserted (1 mark)
   e inverted. (1 mark)
3 **Explain** the events during meiosis that result in the non-disjunction of chromosomes. (3 marks)
4 **Define** aneuploidy, and give an example of one autosomal non-disjunction and one sex chromosome non-disjunction in which the offspring survives. (3 marks)

Analytical processes

5 **Distinguish** between autosomal aneuploidy and sexual aneuploidy. (1 mark)

MODULE 9

Lesson 9.3
Review: Mutations

Summary

9.1
- A mutation is a permanent change to DNA.
- Mutations in somatic cells affect only the individual, whereas mutations in germline cells are inheritable.
- A point mutation results from the changing of a single nucleotide in a DNA triplet, and may result in a silent, missense or nonsense mutation.
- A frameshift mutation results from insertion or deletion of a nucleotide in a DNA triplet, and alters the reading frame of all DNA triplets following the mutation.

9.2
- Errors during meiosis can lead to chromosomal mutations where "blocks" of genes are altered (insertions, deletions, duplications, inversions, translocations).
- Non-disjunction, resulting in aneuploidy, occurs when a pair of homologous chromosomes fail to separate correctly during meiosis.
- Recognising aneuploidy in a karyotype can be used to predict genetic disorders in an individual (e.g. Down syndrome).

Review questions 9.3A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

1 In a point mutation
- **A** the mutation only occurs in somatic cells.
- **B** one nucleotide is substituted for another in a triplet code.
- **C** there is a deletion of a group of genes from the chromosome.
- **D** the effects are always silent, because each amino acid has several codes.

2 A point mutation that results in a change from coding for an amino acid to a stop codon is known as
- **A** silent.
- **B** missense.
- **C** nonsense.
- **D** aneuploidy.

3 Aneuploidy in an individual always results in
- **A** a different chromosome number than that of the species.
- **B** one extra chromosome, compared to the species number.
- **C** one fewer chromosome, compared to the species number.
- **D** several extra chromosomes, compared to the species number.

4 The least severe form of mutation is likely to be
- **A** the substitution of a nucleotide.
- **B** the loss or gain of a chromosome.
- **C** the loss or gain of part of a chromosome.
- **D** the insertion of a single DNA nucleotide in the middle of a sequence.

5 Factors in the environment that have been shown to increase the chance of mutation in an organism include all the following except
- **A** an increase in temperature.
- **B** extremely large populations of other similar organisms.
- **C** certain compounds, such as some industrial and horticultural chemicals.
- **D** high-energy radiation, such as ultraviolet light, X-rays, and beta and gamma rays.

6 An error during replication produced the following change to mRNA transcripts.

mRNA before: AUGUUGUACUGGCCGCAU
mRNA after: AUGUUGUACAUGGCCGCAU

The most likely DNA replication error involved is

A deletion of uracil.
B insertion of arginine.
C substitution of arginine with uracil.
D substitution of uracil with cytosine.

Use the following information to answer questions 7 and 8.

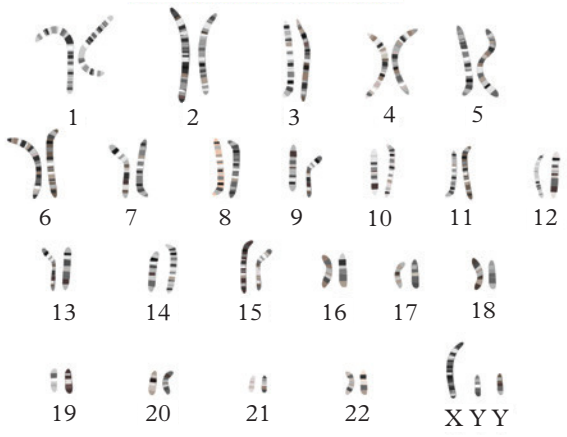
The table lists syndromes associated with aneuploidies of the sex chromosomes.

Syndrome	Affects	Karyotype
Klinefelter	Males	XXY
Turner	Females	X
Jacob	Males	XYY
Triple X	Females	XXX

7 For a person with 45 chromosomes ($2n - 1$) due to sexual aneuploidy, the likely condition they have is

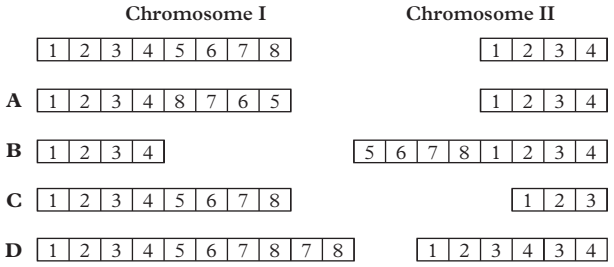
A Turner syndrome.
B Jacobs syndrome.
C triple X syndrome.
D Klinefelter syndrome.

8 Identify the syndrome affecting a person with the following karyotype.



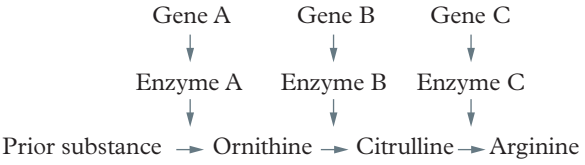
A Turner syndrome
B triple X syndrome
C Jacobs syndrome
D Klinefelter syndrome

9 If an insertion occurred between chromosomes I and II (see figure), which of the following would result?



Use the following information to answer questions 10 to 13.

The bread mould *Neurospora* normally produces its own amino acids from raw materials through a system of enzymes.



To answer each question, use the table to assign a response (A, B, C or D).

A	The statement is a logical hypothesis based on the diagram.
B	The statement is an illogical hypothesis.
C	The statement is a hypothesis unrelated to the diagram.
D	The hypothesis is a restatement of the information given in the diagram.

10 Enzyme A catalyses the reaction in which ornithine is formed from the prior substance.

11 If gene B underwent a frameshift mutation, arginine would be formed directly from ornithine.

12 If gene A underwent a frameshift mutation, the mould would survive if ornithine were added to the medium.

13 If a nutritional mutant of *Neurospora* can only survive when provided with the amino acid citrulline, the mutation probably affected
- **A** gene A only.
- **B** gene B only.
- **C** gene C only.
- **D** either gene A or gene B.

14 Which of the following statements is correct?
- **A** A neutral mutation will ultimately be beneficial to the species.
- **B** Mutations provide variations in a species that can be acted upon by natural selection.
- **C** Natural selection weeds out all but beneficial mutations in a species.
- **D** Some alleles for particular genes have arisen by mutation.

15 A mutation that occurs in the body tissues of an organism but is not passed to its offspring is referred to as a
- **A** homologue mutation.
- **B** translocation.
- **C** somatic mutation.
- **D** germline mutation.

Review questions 9.3B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

16 **Explain** the biological risks associated with any process involving regular screening with X-rays. (2 marks)

17 A child has a karyotype of XYY for the sex chromosomes. In which parent did this non-disjunction occur? **Explain** your answer. (3 marks)

18 Gene mutations can occur in various ways and may have different effects, depending on the type of mutation and the cells involved.
- **a** **Define** a gene mutation. (1 mark)
- **b** **Explain** why mutations may appear:
  - **i** immediately in somatic cells (1 mark)
  - **ii** in the first generation (1 mark)
  - **iii** not until several generations of offspring have appeared. (2 marks)

19 Suppose a gene contains the code for the synthesis of an enzyme. During replication of the gene, a mutation occurs so that one of the nucleotides is left out. Is it more likely that the enzyme produced will be close to "normal" if the deleted base occurs near the beginning or near the end of the gene? **Explain** your reasoning. (2 marks)

20 Read the following summary, based on information from "Telomeres, telomerase and cancer" by Carol Greider and Elizabeth Blackburn (*Scientific American*, February 1996) and answer the question that follows.

The tips of chromosomes are called telomeres. They are made of many short, repeated sequences of DNA nucleotides, e.g. in humans each telomere has about 70 repeats of the sequence TTAGGG.
During each cell division a number of these repeats are lost – they are not copied while the rest of the chromosome is. When the telomeres are too short (i.e. too many repeats have been lost and only 1–2 are present) then all cells (except those in testes and ovaries) die. The enzyme telomerase is present in the cells of testes and ovaries and can rebuild the telomeres. Thus, telomerase can make a cell able to live forever. It is usually present in cancer cells after uncontrolled mitosis has started.

Cancer is "uncontrolled mitosis" of a cell. Using the information from the extract and your knowledge of how errors can occur during cell division, **explain** how cancer is caused and **identify** why many cancer cells do not die. (4 marks)

Analytical processes

21 **Contrast** a point mutation and a frameshift mutation. (1 mark)

22 **Distinguish** between a somatic mutation and a germline mutation, and state how they differ in their effect on the next generation. (2 marks)

23 A strain of bacteria (strain A) produced a protein that contained the following sequence of amino acids:

serine – proline – serine – leucine – asparagine

A second strain of bacteria (strain B) produced a slightly altered protein, caused by a deletion at the start of the sequence and an insertion at the end of the sequence, resulting in the following sequence of amino acids:

valine – histidine – histidine – leucine – methionine

mRNA codons are translated into amino acids during protein synthesis according to the genetic code shown below. Therefore, the codon for the amino acid methionine is AUG.

First position	Second position				Third position
	U	C	A	G	
U	phe	ser	tyr	cys	U
	phe	ser	tyr	cys	C
	leu	ser	STOP	STOP	A
	leu	ser	STOP	trp	G
C	leu	pro	his	arg	U
	leu	pro	his	arg	C
	leu	pro	gin	arg	A
	leu	pro	gin	arg	G
A	ile	thr	asn	ser	U
	ile	thr	asn	ser	C
	ile	thr	lys	arg	A
	met	thr	lys	arg	G
G	val	ala	asp	gly	U
	val	ala	asp	gly	C
	val	ala	glu	gly	A
	val	ala	glu	gly	G

Note that several codons may translate into the same amino acid, while others may be punctuation messages.

a **Apply** the genetic code to complete the grid below for strain B, showing all the possible codons for the respective amino acids. For example, the grid for strain A would be:

Grid for Strain A

ser	pro	ser	leu	asn
UCU	CCU	UCU	UUA	AAU
UCC	CCC	UCC	UUG	AAC
UCA	CCA	UCA	CUU	
UCG	CCG	UCG	CUC	
AGU		AGU	CUA	
AGC		AGC	CUG	

Grid for Strain B

val	his	his	leu	met

Using the grids for both strains A and B:

b **Determine** the sequence of strain A codons from which the mutant strain B was derived. (1 mark)

c **Determine** the relevant strain B codons. **Identify** the nucleotide that was deleted and **identify** the one that was inserted in the process. (3 marks)

Knowledge utilisation

24 In a family where one parent has Klinefelter syndrome (47,XXY) and the other has a normal karyotype (46,XX), **predict** the possible chromosomal combinations in their offspring and explain the likelihood of Klinefelter syndrome occurring. (2 marks)

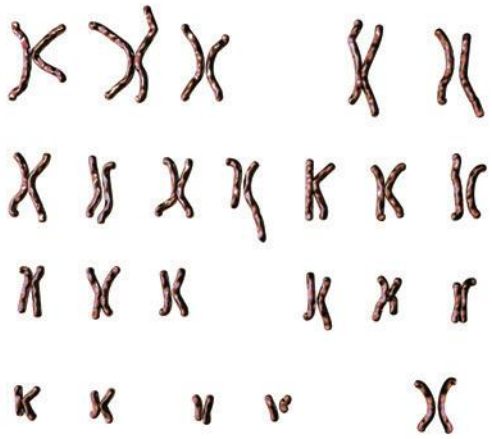
25 An individual with Turner syndrome (45,X) undergoes hormone replacement therapy. Based on your knowledge of chromosomal mutations, **predict** how this therapy might help manage some of the symptoms of the syndrome and improve the person's quality of life. (2 marks)

Data drill

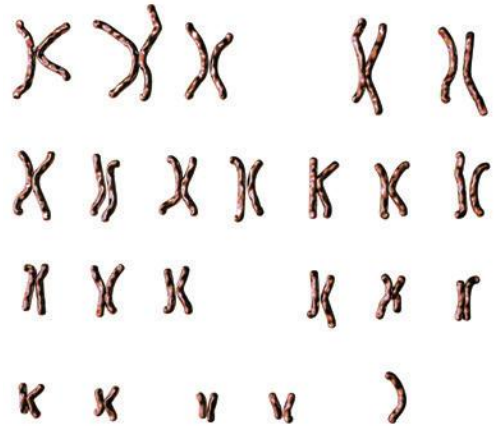
Interpreting karyotypes

The karyotypes below are those of two patients: patient A, who was diagnosed with a chromosomal block mutation; and patient B, who exhibits aneuploidy. The table provides a summary of aneuploidies and their corresponding syndromes.

Patient A



Patient B



Syndrome	Affects	Karyotype
Klinefelter	Males	47, XXY
Turner	Females	45, X0
Creutzfeld-Jakob	Males	47, XYY
Triple X	Females	47, XXX
Down	Males, females	47, Trisomy 21
Edwards	Males, females	47, Trisomy 18

Apply understanding

1 **Identify** the chromosomes affected in patient A. (1 mark)

Analyse data

2 **Determine** the syndrome associated with the karyotype of patient B, giving reasons for your response. (2 marks)

3 **Describe** the karyotype of an individual with Edwards syndrome. (1 mark)

Interpret evidence

4 **Propose** the type of chromosomal block mutation shown in the karyotype of patient A, providing reasons for your response. (2 marks)

Module 9 checklist: Mutations

MODULE 10

Inheritance

Introduction

Traits are inherited through the combination of maternal and paternal alleles. Each gene can be expressed differently as a result of its allele combination and mode of inheritance. The frequencies of phenotypes and genotypes can be predicted from probability models and patterns of inheritance.

Prior knowledge

Prior knowledge quiz Check your understanding of concepts related to inheritance before you start

Subject matter

Science understanding

- → Describe dominant, recessive, autosomal, sex-linked, polygenic and multiple-allele inheritance.
- → Infer patterns of inheritance and predict frequencies of genotypes and phenotypes from genetic data, including
  - histograms (polygenic inheritance)
  - pedigrees (dominant/recessive, autosomal/sex-linked)
  - Punnett squares (dominant/recessive, autosomal/sex-linked and multiple-allele inheritance).

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Lesson 10.1
Dominant, recessive and autosomal inheritance

Key ideas

- → Alternative forms of a gene, called alleles, determine an individual's genotype and traits.
- → Dominant alleles mask recessive alleles, which only show when an individual is homozygous recessive.
- → Punnett squares are used to predict inheritance patterns and offspring traits in monohybrid or dihybrid genetic crosses.
- → Inheritance patterns follow Mendel's laws of segregation and independent assortment, governed by probability.
- → Pedigrees are used to analyse inheritance, to identify dominant, recessive, autosomal or sex-linked traits in families.

Learning intentions and success criteria

pure-bred
describes an organism that is homozygous for a trait and thus has the same phenotype as the parents

wild type
the most common phenotype for a feature in a population

autosomal dominant trait
a trait due to an allele on an autosome that overrides the effects of the recessive allele, in the heterozygous condition

recessive trait
a trait due to an allele that is masked by the dominant allele in the heterozygous condition but expressed in the homozygous condition

autosomal recessive trait
a trait due to an allele on an autosome that is masked by the dominant allele, in the heterozygous condition

Alleles, genotypes and phenotypes

The way in which a gene is expressed is not always the same, due to slight variations in the DNA composing the gene. An allele is an alternative expression of a gene. Although there may be several alleles for a gene, a single individual can only carry two alleles, one on each homologous chromosome. If the two alleles for a gene in an individual are the same, the individual is said to be homozygous for that gene. If two homozygous individuals breed together, the offspring are said to be **pure-bred** for that trait. Alternatively, if the two alleles in an individual are different, that individual is heterozygous and is called a hybrid. The most common phenotype in any environment is called the **wild type**.

In some situations, where a single gene is responsible for a characteristic, one allele may be fully expressed while the other allele is not evident in the phenotype. In this situation, the first, fully expressed, allele codes for the dominant trait. If this allele code is located on an autosome (i.e. not on an X or Y chromosome), it codes for an **autosomal dominant trait**, which is represented by a capital letter (e.g. "A"). The allele for a **recessive trait** located on an autosome (**autosomal recessive trait**) is only expressed if the individual is homozygous for the recessive allele. Alleles for this recessive trait are represented by a lowercase letter (e.g. "a"). The genotype describes the alleles that are present in an individual. The phenotype of an individual indicates the way in which the combination of alleles is expressed. For a dominant trait, an individual that is heterozygous for that trait (Aa) will have the same phenotype as an individual that is homozygous (AA). Occasionally, both alleles are expressed (codominant trait) or moderated by regulatory genes blending the expression of the two alleles (intermediate dominance).

TABLE 1 The effect of genotype on phenotype for pea flowers, where the purple allele (A) is dominant over the white allele (a)

Genotype		
AA (homozygous dominant)	Aa (heterozygous)	aa (homozygous recessive)
Phenotype		
		
Dominant trait – purple	Dominant trait – purple	Recessive trait – white

Punnett squares

Punnett square
a mathematical device used to calculate probable genotype and phenotype outcomes of genetic crosses

A **Punnett square** is a square diagram or tabular summary of the possible combinations of maternal alleles with paternal alleles of a cross. It was devised by Reginald Punnett and is used to predict the probability of the offspring's possible genotypes, and therefore phenotypes, for a particular cross. The steps involved in this process are as follows.

1 Determine the possible genotypes of each parental gamete.
2 Draw a Punnett square showing the parental gametes.
3 Determine the possible genotypes of the offspring.
4 Determine the possible phenotypes of the offspring.
5 Determine the probability of each phenotype.

The first generation of offspring is called the F_1 generation. If two individuals of this F_1 generation are bred with each other, the offspring are called the F_2 generation.

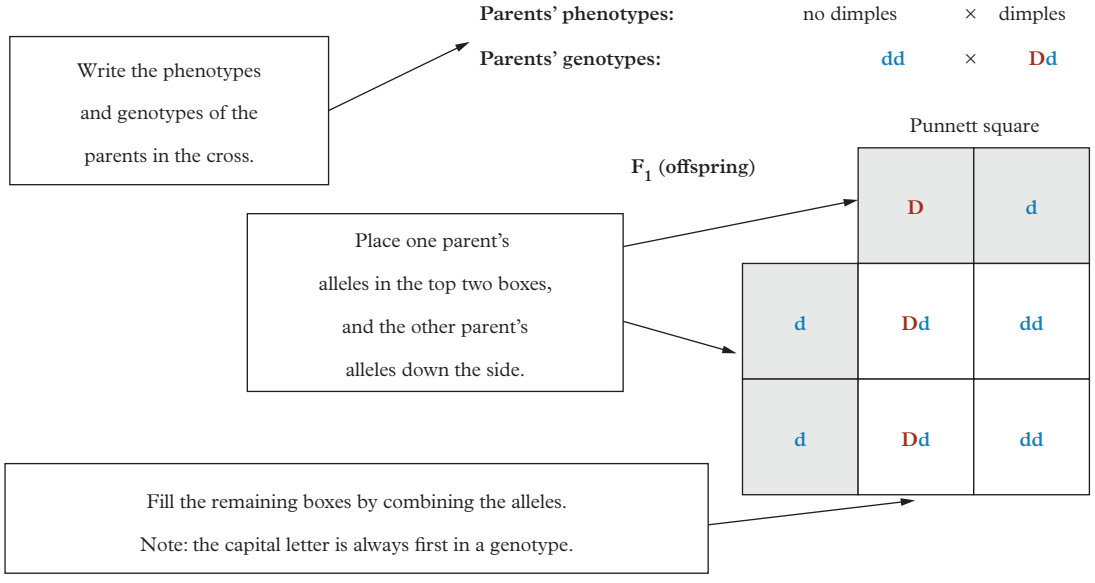


FIGURE 1 The layout of a Punnett square

monohybrid cross
a genetic cross between two individuals, both heterozygous for a specific trait

dihybrid cross
a genetic cross between two individuals, both heterozygous for two specific traits

The Punnett squares described so far are for inheritance of alleles for a single gene (**monohybrid cross**). They can also be used to predict the inheritance of more than one gene (e.g. **dihybrid crosses**). These genes may be on the same chromosome (linked) or on different chromosomes (unlinked). Unlinked chromosomes will sort independently, resulting in random combinations of the alleles for the two (or more) genes.

Predicting phenotypes

If the parent genotypes are known, the genotypes, and therefore phenotypes, of the offspring may be predicted. For example, a couple expecting a child may try to predict whether the child will be male or female. All eggs contain a single X chromosome. Sperm cells contain either an X or a Y chromosome. Representing this in a Punnett square (Figure 2) shows that the probability that the child will be male (XY) is 50%, and the probability that they will be female (XX) is 50%. Even if the parents have already had three female children, the chance that the fourth child will be a female is 50% (or $\frac{1}{2}$). The probability "resets" with every fertilisation.

Study tip

You can use highlighters to easily identify phenotypes. Use a different colour (or a capital letter) for each dominant phenotype.

		Possible female gametes: X	Possible female gametes: X
Possible male gametes: X		XX Female	XX Female
Possible male gametes: Y		XY Male	XY Male

FIGURE 2 Of the four possible combinations of gametes from the egg and the sperm, two are XX (female) and two are XY (male). So each outcome (male or female) has a 50 per cent chance.

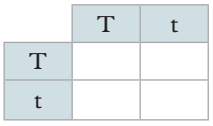
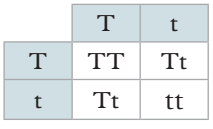
FIGURE 3 A Punnet square shows that there is an equal chance of a baby being born male or female.

Worked example 10.1A

Monohybrid Punnett square

A person's ability to taste the bitter synthetic chemical phenylthiocarbamide (PTC) is coded for by a single gene, *TAS2R38*. A person who has the dominant allele (T) for the gene can taste the bitterness of PTC, while someone who is homozygous recessive (tt) cannot. Although PTC is not found naturally in foods, there are similar compounds in foods such as Brussels sprouts and broccoli. People with at least one copy of the PTC dominant allele typically find these foods bitter in taste.

Using a Punnett square, **predict** the genotype and phenotype frequencies for the offspring of two individuals who are heterozygous for the PTC tasting gene. (4 marks)

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking.	To "predict" means to forecast an expected result.
Step 2: Determine the possible genotype of each parental gamete.	Both parents are heterozygous, so both parents have the genotype Tt. (1 mark)
Step 3: Draw a Punnett square showing the parental genotypes.	
Step 4: Determine the possible genotypes of the offspring.	 (1 mark)
Step 5: Determine the probability of possible genotypes of the offspring.	TT: 1 of 4 = 1/4 = 25% Tt: 2 of 4 = 1/2 = 50% tt: 1 of 4 = 1/4 = 25% (1 mark)
Step 6: Determine the probability of possible phenotypes of the offspring.	TT and Tt have the dominant trait (can taste PTC). TT and Tt = 3 of 4 = 3/4 = 75% tt has the recessive trait (cannot taste PTC). tt = 1 of 4 = 1/4 = 25%
Step 7: State the final solution.	75% of the offspring of two individuals heterozygous for the PTC tasting gene will be able to taste PTC, while 25% will not be able to taste PTC. (1 mark)

Your turn

Using a Punnett square, **predict** the genotype and phenotype frequencies for the offspring of a homozygous dominant individual and a homozygous recessive individual for the PTC tasting gene. (4 marks)

Worked example 10.1B

Dihybrid Punnett square

The trait of having dimples (D) is dominant to having no dimples (d). Being able to roll your tongue (T) is dominant to not being able to roll (t). The genes for the two traits are located on different chromosomes. A parent who is heterozygous for both traits (DdTt) could produce the gametes DT, Dt, dT or dt, whereas a parent who is homozygous dominant for both traits (DDTT) would only produce gametes DT.

If both parents are heterozygous, **determine** the probability that one of the offspring will have dimples *and* be able to roll their tongue. (4 marks)

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking.	To "determine" means to establish, conclude or ascertain after consideration, observation, investigation or calculation.
Step 2: Determine the possible genotype of each parental gamete.	Both parents are heterozygous for both traits (DdTt), so the possible gamete combinations they can pass to offspring are DT, Dt, dT and dt. (1 mark)
Step 3: Draw a Punnett square showing the parental gametes.	
Step 4: Determine the possible genotypes of the offspring.	

	DT	Dt	dT	dt
DT				
Dt				
dT				
dt				

	DT	Dt	dT	dt
DT	DDTT	DDTt	DdTT	DdTt
Dt	DDTt	DDtt	DdTt	Ddtt
dT	DdTT	DdTt	ddTT	ddTt
dt	DdTt	Ddtt	ddTt	ddtt

(1 mark)

Think	Do
Step 5: Determine the probability of each possible phenotype.	Possible gametes from female: DT, Dt, dT, dt Possible gametes from male: DT, Dt, dT, dt DT × DT: DDTT, Dimples & can roll tongue DT × Dt: DDTt, Dimples & can roll tongue DT × dT: DdTT, Dimples & can roll tongue DT × dt: DdTt, Dimples & can roll tongue Dt × DT: DDTt, Dimples & can roll tongue Dt × Dt: DDtt, Dimples & cannot roll tongue Dt × dT: DdTt, Dimples & can roll tongue Dt × dt: Ddtt, Dimples & cannot roll tongue dT × DT: DdTT, Dimples & can roll tongue dT × Dt: DdTt, Dimples & can roll tongue dT × dT: ddTT, No dimples but can roll tongue dT × dt: ddTt, No dimples but can roll tongue dt × DT: DdTt, Dimples & can roll tongue dt × Dt: Ddtt, Dimples & cannot roll tongue dt × dT: ddTt, No dimples but can roll tongue dt × dt: ddtt, No dimples & cannot roll tongue Possible offspring genotypes and phenotypes (1 mark for phenotypes, 1 mark for genotypes) From the Punnett square, indicate the **dihybrid ratio** for the possible phenotypes of the offspring. Dimples & can roll tongue : Dimples & cannot roll tongue : No dimples & can roll tongue : No dimples & cannot roll tongue 9 : 3 : 3 : 1
Step 6: State the final solution.	Of the 16 possible outcomes, nine have dimples *and* can roll their tongue. This means there is a 9/16 probability of an offspring having dimples and being able to roll their tongue. (1 mark)

Your turn

Determine the probable genotype and phenotype frequencies of the offspring of an individual who is heterozygous for the dimples and tongue rolling trait, and an individual who has no dimples and can't roll their tongue. (4 marks)

Laws of probability

Mendel's laws are based on mathematical principles known as the laws of probability. One of these laws is the **product rule**, which states:

The chance of two independent events occurring together is equal to the chance of one event occurring alone multiplied by the chance of the other event occurring alone.

In Worked example 10.1B, this means the individual probabilities of inheriting dimples and rolling the tongue could be determined independently, and then multiplied.

FIGURE 4 The chance that a child will have dimples and be able to roll their tongue can be determined mathematically using the laws of probability.

dihybrid ratio
a predicted ratio of the offspring of a cross between individuals simultaneously heterozygous for two characteristics

product rule
a law of probability; states that the chance of two independent events occurring together equals the chance of one event occurring alone multiplied by the chance of the other event occurring alone

Worked example 10.1C

Law of probability

The trait of having dimples (D) is dominant to no dimples (d), and tongue rolling (T) is dominant to cannot roll (t). The genes for the two traits are located on different chromosomes. A parent who is heterozygous for both traits (DdTt) will produce the gametes DT, Dt, dT and dt, whereas a parent who is homozygous dominant for both traits (DDTT) will only produce gametes DT.

If both parents are heterozygous, **determine** the probability of one of the offspring having dimples *and* being able to roll their tongue. (4 marks)

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking.	To "determine" means to establish, conclude or ascertain after consideration, observation, investigation or calculation.
Step 2: Determine the possible genotype of each parental gamete.	Both parents are heterozygous for both traits, so both parents have the genotype Dd for dimples, and Tt for tongue rolling. (1 mark)
Step 3: Draw a Punnett square showing the parental gametes.	Dimples: D, d / D, d Tongue rolling: T, t / T, t
Step 4: Determine the possible genotypes of the offspring.	D, d / D: DD, Dd / d: Dd, dd T, t / T: TT, Tt / t: Tt, tt (1 mark)
Step 5: Determine the probability of each phenotype.	Identify the probability of dimples, then identify the probability of rolling tongue. Chance of dimples = $\frac{3}{4}$ Chance of rolling tongue = $\frac{3}{4}$ (1 mark)
Step 6: State the final solution.	Chance of having dimples and rolling tongue: $= \frac{3}{4} \times \frac{3}{4}$ $= \frac{3 \times 3}{4 \times 4}$ $= \frac{9}{16}$ (1 mark)

Your turn

Determine the genotype and phenotype frequencies of the offspring of a cross between an individual who is heterozygous for the dimples and tongue rolling trait, and an individual who has no dimples and is heterozygous for tongue rolling. (4 marks)

Test crosses

It can sometimes be difficult to determine the genotype of an individual with a dominant phenotype. This is because the genotype could be heterozygous (Bb) or homozygous (BB) for the dominant trait. In animal and plant breeding, because of the short time between generations and the large number of offspring in each generation, a **test cross** can be done to determine the genotype of an individual.

A test cross involves the individual with the unknown genotype being crossed with an individual that is homozygous for the recessive trait. If a large number of offspring are produced, there are two possible outcomes.

- All the offspring have the dominant phenotype. This means the unknown parent was homozygous for the dominant trait.
- At least one offspring has the recessive trait. This means the unknown parent is heterozygous.

test cross
a cross between an organism that displays the recessive trait of a characteristic and one that displays the dominant trait, to determine whether the dominant phenotype is due to a homozygous or heterozygous genotype; this only applies if a large number of offspring are produced

Worked example 10.1D

Test crosses

In Persian cats, the long-hair trait (H) is dominant to the short-hair trait (h). The owners of a cat with the dominant phenotype want to determine their cat's genotype. **Explain** how they could do this.
(4 marks)

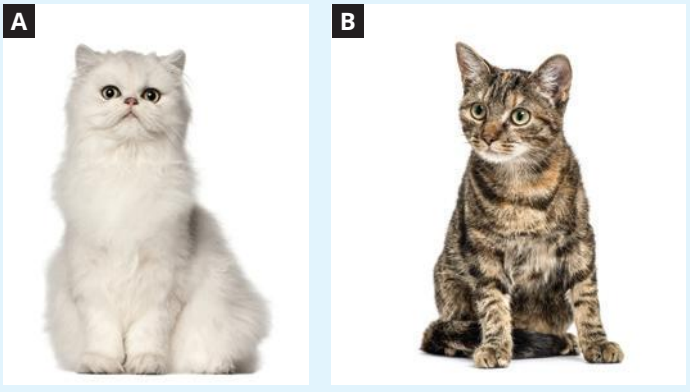


FIGURE 5 Hair length in (A) a Persian long-haired cat and (B) a domestic short-haired cat

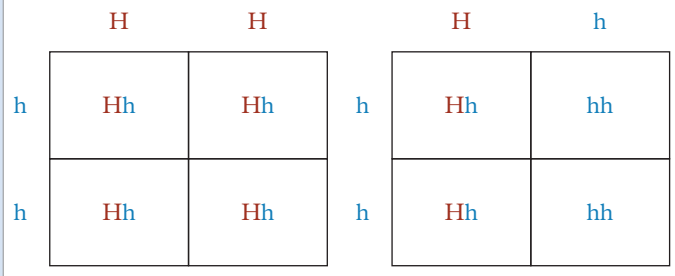
Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking.	To "explain" means to make an idea or situation plain or clear by describing it in more detail or revealing relevant facts.
Step 2: Determine the possible genotype of each parental gamete.	The cat could be HH or Hh. It must have at least one allele for the dominant trait (H); the other is unknown. A short-haired cat would have the genotype hh. (1 mark)
Step 3: Draw a Punnett square showing the parental gametes.	Two possible crosses must be considered, because there are two possible genotypes for the long-haired cat. Possibility 1: The cat is homozygous dominant. Possibility 2: The cat is heterozygous dominant.

Possibility 1:

	H	H
h		
h		

Possibility 2:

	H	h
h		
h		

Think	Do
Step 4: Determine the possible genotypes of the offspring.	 (1 mark)
Step 5: Determine the probability of each phenotype.	Possibility 1: The cat is homozygous dominant. All offspring (100%) would have long hair. Possibility 2: The cat is heterozygous. Half (50%) the offspring would have long hair and half (50%) would have short hair. (1 mark)
Step 6: State the final solution.	If the owner did a test cross between their cat and a cat that had the alleles for the recessive short-haired trait (hh), there are two possible outcomes. If their cat's unknown allele is for the dominant long-haired trait (HH), there will be no offspring with the recessive short hair phenotype. If their cat's unknown allele is for the recessive short-haired trait (Hh), some offspring with this phenotype will be produced. (1 mark)

Your turn

The allele for green peas (G) is dominant over the allele for yellow peas (g). **Explain** how a farmer wanting to grow green peas could use a test cross to determine which pea plants to use to reproduce to grow green peas. (4 marks)

Pedigrees

pedigree
a chart showing the ancestry, descent and relationships between all members of a family or other genealogical group

Pedigrees are often used to determine whether an allele is dominant or recessive, or whether it is autosomal or sex-linked. In a pedigree (also known as a family tree), a female is represented by a circle and a male by a square. The expression of the trait is indicated by shading. If only males exhibit a particular trait, this strongly suggests that the trait is sex-linked. If a son displays the trait but the mother does not, it is X-linked recessive. If both males and females show the trait in approximately equal ratios, it is most likely an autosomal gene.

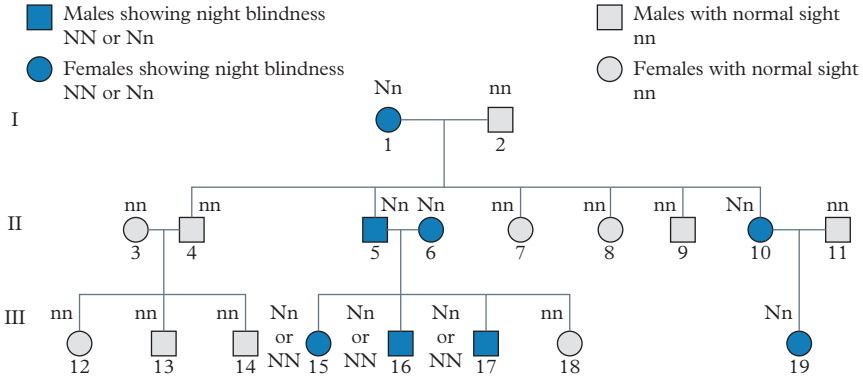


FIGURE 6 Family pedigree showing inheritance of night blindness

In the pedigree shown in Figure 6, both males and females show night blindness. Female 1, who is night blind, has sons who have normal vision. Therefore, night blindness is inherited autosomally. Individual 18 is the offspring of two individuals with night blindness, and is normal, so the trait for night blindness is dominant. The possible genotypes can then be determined and are shown in Figure 6.

Worked example 10.1E

Pedigrees

Huntington's disease is a neurodegenerative genetic disorder that causes the progressive breaking down of nerve cells in the brain. Inheritance of Huntington's disease is autosomal dominant in humans. If an individual receives the dominant allele (H), they will exhibit the dominant traits of Huntington's disease. Figure 7 shows the inheritance pattern of Huntington's disease.

a **Identify** one piece of evidence to support the conclusion that Huntington's is an autosomal dominant trait. **Justify** your response using a Punnett square. (4 marks)

b **Infer** the genotype of individual 3, giving reasons for your response. (3 marks)

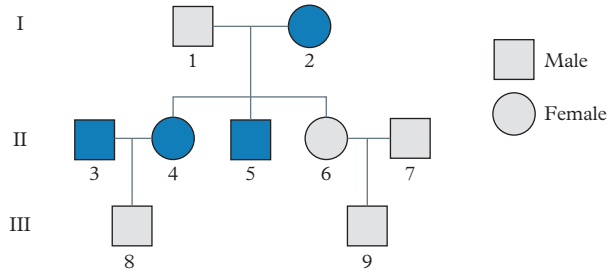


FIGURE 7 Pedigree showing the inheritance pattern for Huntington's disease

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking.	To "identify" means to locate, recognise and name. To "justify" means to give reasons or evidence to support an answer. To "infer" means to draw a conclusion based on evidence and reasoning.
Step 2: Identify a piece of evidence on the pedigree.	**a** If Huntington's disease is autosomal dominant, then individual 1 must be homozygous recessive for the trait (hh). Individual 2 has passed the dominant allele to individuals 4 and 5, but not to individual 6. So individual 2 must have at least one copy of the recessive allele for the trait, and therefore they must be heterozygous (Hh). (1 mark)
Step 3: Draw a Punnett square showing the parental gametes.	<table><tr><td></td><td>H</td><td>h</td></tr><tr><td>h</td><td></td><td></td></tr><tr><td>h</td><td></td><td></td></tr></table>
Step 4: Determine the possible genotypes of the offspring.	<table><tr><td></td><td>H</td><td>h</td></tr><tr><td>h</td><td>Hh</td><td>hh</td></tr><tr><td>h</td><td>Hh</td><td>hh</td></tr></table> (1 mark)
Step 5: Determine the probability of each phenotype.	Half (50%) the offspring would have Huntington's disease, and half (50%) would not have Huntington's disease. (1 mark)
Step 6: State the final solution.	The expected phenotype frequencies match those of the pedigree, therefore supporting the statement that Huntington's disease is an autosomal dominant trait. (1 mark)
Step 7: Identify evidence on the pedigree to determine genotypes.	**b** Individual 8, offspring of individual 3, is homozygous recessive (hh) for the trait, and therefore must have received the recessive allele from both parents.
Step 8: Apply evidence to infer genotypes and state the final solution.	Individual 3 must have a recessive allele for the trait in order to pass this on to his offspring (individual 8). (1 mark) Individual 3 also has the disease, so he must have a copy of the dominant allele. (1 mark) Therefore individual 3 must be heterozygous. (1 mark)

Your turn

Sickle cell anaemia is an autosomal recessive genetic disease in humans. The inheritance pattern for sickle cell anaemia is shown in Figure 7.

a **Identify** one piece of evidence to support the conclusion that sickle cell anaemia is an autosomal dominant trait. **Justify** your response using a Punnett square. (4 marks)

b **Infer** the genotype of individual 3, giving reasons for your response. (3 marks)

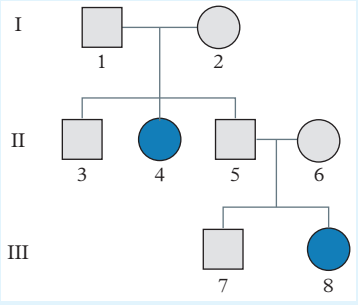


FIGURE 8 Pedigree showing the inheritance pattern for sickle cell anaemia

Check your learning 10.1

Check your learning 10.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the following terms: (1 mark each)
- **a** allele
- **b** gene
- **c** genotype
- **d** phenotype
- **e** monohybrid cross
- **f** dihybrid cross
- **g** heterozygous
- **h** homozygous.

2 **Define** the product rule (1 mark)

3 **Explain** the purpose of a Punnett square. Illustrate your answer by showing how you would determine the expected offspring of a cross between a heterozygous tall-stemmed pea plant (Tt) and a dwarf-stemmed pea plant (tt). (3 marks)

Knowledge utilisation

4 In pea plants, purple flower colour is dominant to white. If two heterozygous tall purple pea plants were crossed and produced 100 offspring, **predict** the numbers of purple- and white-flowered offspring. (3 marks)

5 In guinea pigs, black (B) is dominant to white (b), and rough coat (R) is dominant to smooth coat (r). A homozygous rough black guinea pig (RRBB) is mated with a smooth white one (rrbb).

- **a** **Describe** what the F_1 generation will look like. (1 mark)
- **b** **Infer** the phenotypes that you would expect to see in the F_2 generation, and predict the proportions of each type. (3 marks)
- **c** **Predict** the ratios of phenotypes in the offspring of the following crosses. (3 marks each)
  - **i** RrBb × rrbb
  - **ii** Rrbb × RrBb
  - **iii** Rrbb × rrBB
- **d** A black, rough-coated male guinea pig was crossed with a white, smooth-coated female. Several litters from the pair resulted. Of these offspring, $\frac{1}{4}$ had black smooth coats, $\frac{1}{4}$ had white smooth, $\frac{1}{4}$ had white rough and $\frac{1}{4}$ had black rough. **Predict** the probable genotypes of the parents. **Explain** your response using a Punnett square. (4 marks)
- **e** Suppose you were given a pure-breeding female guinea pig with rough, black fur and a male with smooth, white fur.
  - **i** **Explain** how you could produce a strain of pure-breeding smooth, white-furred guinea pigs. (2 marks)
  - **ii** **Discuss** whether it is possible to produce a strain of pure-breeding rough, black-furred guinea pigs. **Explain** your method. (3 marks)

FIGURE 9 Guinea pigs: (A) black rough-coated and (B) white smooth-coated

Lesson 10.2
Multiple-allele and polygenic inheritance

Key ideas

- → Codominant inheritance results in both alleles being equally expressed in the phenotype.
- → Multiple allele inheritance, like the ABO blood group, involve more than two alleles influencing the trait.
- → Polygenic traits, controlled by multiple alleles, show continuous variation, and can be graphed using a histogram to show variation in a population.

Modifier genes and environmental effects on inheritance

Learning intentions and success criteria

Each coding gene is responsible for the production of a protein. The expression of these genes can be modified by transcription factors or the environment (Module 7). This suggests that not all traits are inherited as a straightforward dominant–recessive involving two alternative expressions of a gene. For example, human eye colour was previously described as being controlled by one gene with two alleles: brown (B), which is dominant to blue (b). A heterozygote (Bb) was considered brown-eyed, while blue-eyed people were described as lacking the melanin pigment in the front layer of the iris.

Eye colour, however, exhibits endless variations in hue. This is a result of other genes – **modifier genes** – influencing the amount of pigment in the iris, the tone of the pigment (e.g. light yellow, dark brown) and the distribution of the pigment (e.g. even, scattered, or forming a definite pattern such as a ring around the outer iris).

modifier genes genes that influence the expression of another gene

The expression of a simple dominant–recessive phenotype may also be greatly influenced by the environment in which the organism is reared. For example, a genetically tall plant growing in a rocky, nutrient-depleted soil may not attain its full genetic potential. Hydrangeas have flowers that can be blue, pink or white. Typically, blue flowers develop if the plant is grown in an acid soil, but white or pink flowers develop if the soil is alkaline.

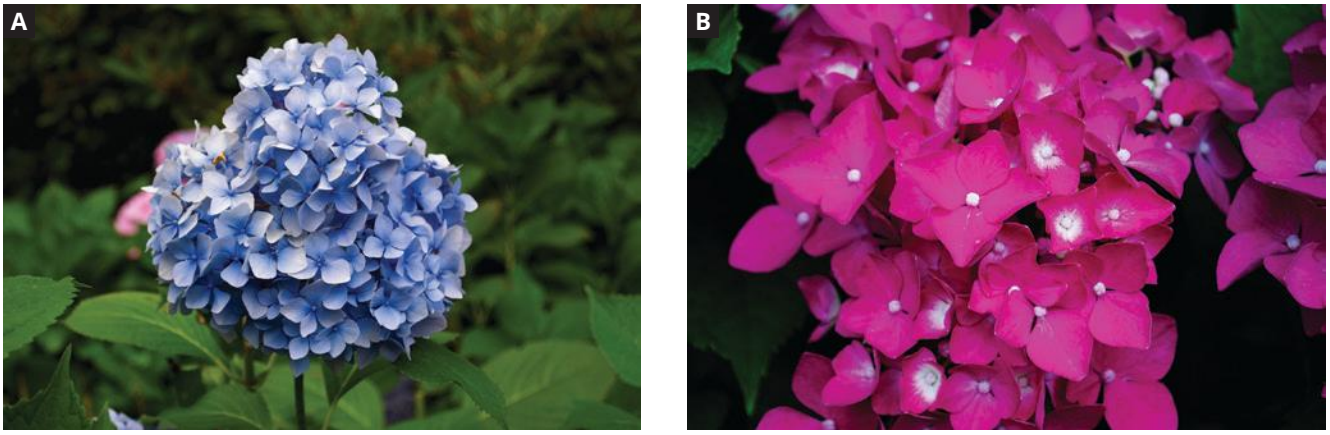


FIGURE 1 (A) Hydrangeas grown in acidic soil produce blue flowers, while (B) hydrangeas grown in alkaline soil produce pink flowers.

Codominance

codominance
the genetic inheritance of two or more traits of a characteristic, both of which are expressed in the phenotype

In **codominant** phenotypes, each allele is expressed equally in the phenotype. This means each allele produces an unchanged amount of protein.

In cattle, a single point substitution in the *KIT* ligand gene can result in a change in a single amino acid in the resulting protein. This results in two alleles for hair colour: an unchanged allele that produces red-coloured hair (C^R) and a mutated allele for white-coloured hair (C^W). When cattle inherit both alleles (heterozygote, $C^R\,C^W$), both alleles are expressed separately. This codominance of the alleles produces a roan-coloured coat, where both white and red hairs are produced (Figure 2).

FIGURE 2 Codominance between red and white alleles in cattle: (A) red-coloured, (B) roan-coloured and (C) white-coloured

	C^R	C^W
C^R	$C^R\,C^R$ Red hair colour	$C^R\,C^W$ Roan hair colour
C^W	$C^R\,C^W$ Roan hair colour	$C^W\,C^W$ White hair colour

FIGURE 3 Punnett square showing the possible genotypes and phenotypes of offspring produced when two roan-coloured cattle are crossed

If two roan-coloured cattle are crossed ($C^R\,C^W \times C^R\,C^W$), the offspring will have the following hair colours:

$\frac{1}{4}$ red ($C^R\,C^R$) : $\frac{1}{2}$ roan ($C^R\,C^W$) : $\frac{1}{4}$ white ($C^W\,C^W$) (Figure 3).

Therefore the ratio is 1 red : 2 roan : 1 white.

Intermediate dominance

Sometimes heterozygous alleles result in a phenotype that is in between the two traits. For example, some flowers, such as the snapdragon, have an allele for red flowers (R_1) and an allele for white flowers (R_2). In the heterozygous condition ($R_1\,R_2$), the flowers are pink – that is, they are intermediate between red and white.

If two pink-flowered plants are crossed ($R_1R_2 \times R_1R_2$), the offspring will be:
$\frac{1}{4}$ red (R_1R_1) : $\frac{1}{2}$ pink (R_1R_2) : $\frac{1}{4}$ white (R_2R_2) (Figure 4)
Therefore the ratio is: 1 red : 2 pink : 1 white.

Although neither trait is dominant over the other, one of the alleles has a stronger influence than the other. The phenotype is an intermediate between complete dominance and codominance. This situation is termed **intermediate dominance**. Other names for this type of inheritance are partial dominance and incomplete dominance. There are many blends of intermediate dominance, and thus a wide range of intermediate varieties between two extremes.

If a flower has two alleles for colour but three phenotypes, codominance or intermediate dominance may be involved.

	R_1	R_2
R_1	R_1R_1 Red	R_1R_2 Pink
R_2	R_1R_2 Pink	R_2R_2 White

FIGURE 4 Punnett square showing the possible genotypes and phenotypes of offspring produced when two pink-flowered plants are crossed

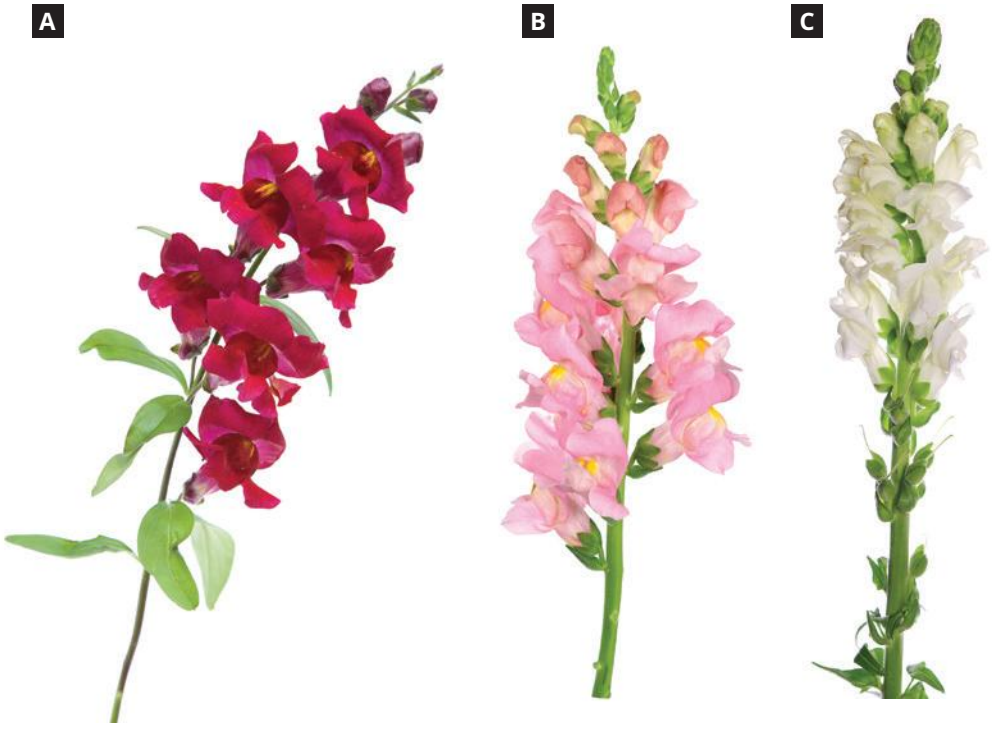


FIGURE 5 Intermediate dominance between red and white flowers: (A) red snapdragon, (B) pink snapdragon and (C) white snapdragon

intermediate dominance
a pattern of inheritance in which neither allele for a characteristic completely masks the effects of the other; results in a blending of traits for the characteristic; also known as partial dominance or incomplete dominance

Multiple-allele inheritance

Many characteristics are governed by more than two alleles, in which case inheritance is said to be controlled by **multiple alleles**, or poly alleles. Although more than two alleles may control the characteristic, there are only ever two alleles present in an individual, one allele inherited from each parent.

The human ABO blood groups, for example, are governed by three alleles: I^A, I^B and i. Alleles I^A and I^B are both dominant to i, but I^A and I^B are codominant. The allele I^A contains the code for an enzyme that produces molecule A (a sugar) on the membrane of red blood cells (blood type A). The allele I^B codes for an enzyme that produces molecule B (blood type B). In contrast, allele i does not produce a functional enzyme at all. This means that a heterozygous individual I^AI^B will produce both enzymes, and hence both sugars A and B on their red blood cells (blood type AB). In contrast, heterozygous individual ii will not produce either enzyme (or sugar) and will therefore be blood type O.

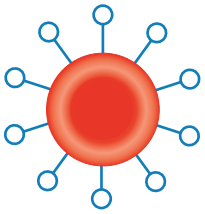
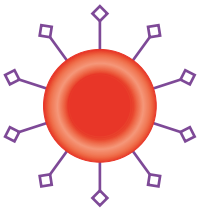
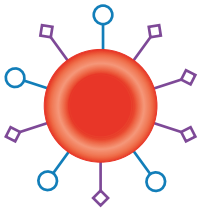
multiple alleles
the inheritance of a characteristic governed by more than two allelic forms (e.g. blood groups); also known as poly alleles

Study tip

Codominant and incomplete dominant traits are given a capital letter to represent the gene, and a superscript to indicate the allele. For blood groups, the I represents the gene for blood grouping and the superscript A (I^A) represents the allele that produces the enzyme for sugar A.

There are four possible phenotypic expressions of human blood types (Table 1).

TABLE 1 The phenotypes and genotypes of human blood types

Phenotype	Type A	Type B	Type AB	Type O
				
Genotype	I^AI^A or I^Ai	$I^B I^B$ or I^Bi	I^AI^B	ii

The membrane sugars A and B can act as antigens if the blood is transfused into another person with a different blood type. This means red blood cells with an A sugar will activate an immune response in a person with type B blood. The person who receives the type A blood (the recipient) will produce protein antibodies against the (donor) A sugar, causing the donated red blood cells to clump together (**agglutinate**) and potentially kill the recipient. A person with blood type O has neither A nor B sugars on their red blood cells. This means their immune system will recognise the A and B sugars as foreign and produce anti-A and anti-B antibodies (Table 2).

agglutination
the sticking together of incompatible cells, e.g. red blood cells of different "groups"

TABLE 2 Compatibility of human blood groups

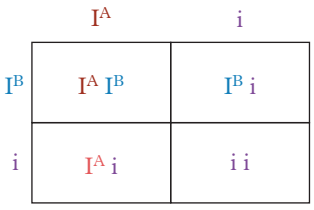
Genotype	Antigens	Blood group	Antibodies	Can donate to:	Can receive from:
I^AI^A or I^Ai	A	A	anti-B	A and AB	O and A
I^BI^B or I^Bi	B	B	anti-A	B and AB	O and B
I^AI^B	A and B	AB	none	AB	O, A, AB, B
ii	none	O	anti-A and anti-B	A, O, AB, B	O

Worked example 10.2A

Multiple-allele inheritance

A woman who is heterozygous for blood type A had a child with a heterozygous male who is blood type B. **Determine** whether it is possible for the child to have a blood type that is different from both their mother and their father. (4 marks)

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking.	To "determine" means to establish, conclude or ascertain after consideration, observation, investigation or calculation.
Step 2: Determine the possible genotype of each parental gamete.	The genotype of the heterozygous mother must be I^Ai and the genotype of the heterozygous father must be I^Bi. (1 mark)

Think	Do
Step 3: Draw a Punnett square showing the parental gametes.	 (1 mark)
Step 4: Determine the probability of each phenotype.	Blood type A = 25% Blood type AB = 25% Blood type B = 25% Blood type O = 25% (1 mark)
Step 5: State the final solution.	Yes, it is possible. Half the children produced could have a blood type that is different from either parent. (1 mark)

Your turn

A woman with type O blood is having a child with a man with type AB blood. **Predict** the genotype and phenotype frequencies for blood types of their offspring, using a Punnett square to support your response. (4 marks)

Blood donors and Rhesus proteins

Because type O blood has neither A nor B sugars on the red blood cells, a person with type O blood can donate to all other blood groups (**universal donor**). Although type O blood contains both antibodies A and B, when transfused into a recipient these antibodies produce very little agglutination, due to their dilution by the host's blood. Because type AB blood does not produce anti-A or anti-B antibodies, a person with type AB blood can receive from all blood groups (**universal recipient**).

Red blood cells can also have a number of Rhesus proteins on their surface. The Rhesus D protein is important in blood transfusions. For example, a person who does not have the Rhesus D protein (Rh^-) on the surface of their red blood cells will produce anti-D antibodies if they are exposed to the D protein on transfused blood cells (Rh^+). As a result, the transfused red blood cells will agglutinate, and the recipient will die.

Occasionally, the Rhesus status of parents can cause problems in pregnancy. A Rhesus D negative (Rh^-) mother is capable of producing anti-Rh antibodies if she is exposed to the Rhesus D protein. During the first pregnancy of an Rh^- mother and an Rh^+ father, an Rh^+ foetus may develop. During this first pregnancy, the placenta will prevent the Rhesus D protein from mixing with the mother's blood. When the mother gives birth, some of the baby's red blood cells can pass into the mother's bloodstream, resulting in the mother producing anti-Rh antibodies (and memory cells). The next time the mother is pregnant with an Rh^+ baby, the anti-Rh antibodies can pass from the mother into the baby, resulting in miscarriage. Most newly pregnant mothers have their blood type tested to determine whether they are Rhesus D negative and therefore whether the pregnancy is at risk. If there is a risk, immediately after delivery the mother will be injected with anti-Rh antibodies to passively remove any of the baby's red blood cells, which might otherwise trigger an immune reaction. This prevents a build-up of the antibodies that might put future pregnancies at risk.

universal donor
a person with type O blood, which has no antibodies to antigens A and B and therefore can be donated in small quantities to individuals of any other blood group

universal recipient
a person with type AB blood, which has both A and B antigens and therefore can receive small quantities of any other blood group

Continuous variation

polygenic inheritance
inheritance of a set of genes that together control a quantitative character such as height; also known as multiple gene inheritance

continuous variation
a variety of phenotypes resulting from more than one gene contributing to a characteristic

Within a population, a gradation of expression for characteristics is often seen. Many people are neither tall nor short; many mice are neither fat nor thin. There are variations between the two extremes. These situations are explained by **polygenic inheritance** (also known as multiple gene inheritance), where two or more pairs of alleles control a single trait. Each allele pair works according to the laws of dominance and segregation. The organism's phenotype depends on the combined effect of the alleles.

The cob or ear length of corn is an example of **continuous variation**. It is believed that two pairs of alleles are responsible, with a series of dominant trait alleles each contributing to length, and the recessive trait alleles not adding any length. The shortest possible length would be represented by the double recessive condition (aabb). Each dominant trait allele adds to the length, so the longest possible ear has the genotype AABB. A cross between AABB and aabb parents results in F_1 offspring that are AaBb and intermediate in length. If these offspring are interbred, a broad range of genotypes and phenotypes results (Figure 6).

Genotypic ratio

$\frac{1}{16}$ AABB : $\frac{1}{8}$ AABb : $\frac{1}{8}$ AaBB : $\frac{1}{4}$ AaBb : $\frac{1}{16}$ AAbb : $\frac{1}{16}$ aaBB : $\frac{1}{8}$ Aabb : $\frac{1}{8}$ aaBb : $\frac{1}{16}$ aabb

Phenotypic ratio

$\frac{1}{16}$ longest : $\frac{1}{4}$ long : $\frac{3}{8}$ medium : $\frac{1}{4}$ short : $\frac{1}{16}$ shortest

or

$\frac{1}{16}$ longest : $\frac{4}{16}$ long : $\frac{6}{16}$ medium : $\frac{4}{16}$ short : $\frac{1}{16}$ shortest

This can be represented graphically (Figure 7).

AaBb × AaBb

	AB	Ab	aB	ab
AB	AABB longest	AABb long	AaBB long	AaBb medium
Ab	AABb long	AAbb medium	AaBb medium	Aabb short
aB	AaBB long	AaBb medium	aaBB medium	aaBb short
ab	AaBb medium	Aabb short	aaBb short	aabb shortest

FIGURE 6 Punnett square showing the broad range of phenotypes and genotypes in the offspring from a cross between AaBb and AaBb corn

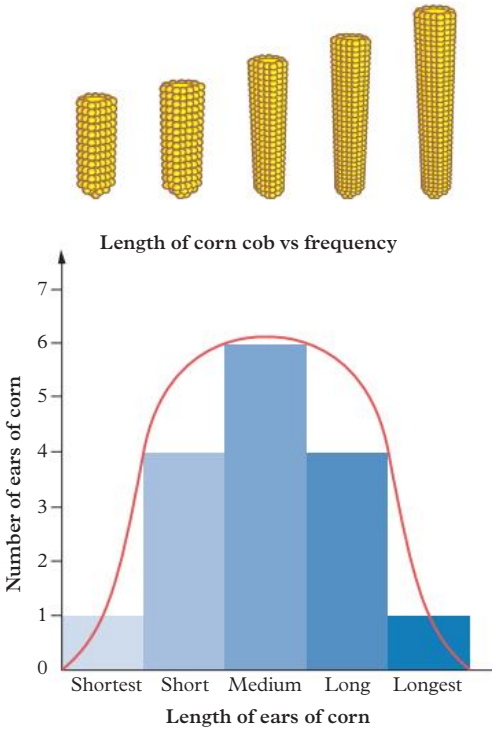


FIGURE 7 Distribution of cob lengths of corn (*Zea mays*)

Human height is believed to be controlled by four pairs of alleles, and skin colour by up to seven pairs. Figure 8 shows the variations that can occur if two pairs of alleles determine human skin colour (i.e. production of the pigment melanin).

FIGURE 8 Human skin pigments are controlled by two pairs of alleles. The dominant trait allele of each gene contributes to melanin production, while the recessive does not.

The colour of wheat grain is also a polygenetic trait, with three genes contributing to the red colour of the seed. If all six alleles for the dominant colour trait are present, the wheat seed will be a dark red. If all alleles for the recessive white trait are present, the seed will appear white. Most seeds have intermediate red colours.

Frequency histograms

A **frequency histogram** is a bar graph showing the frequency of particular characteristics seen in a sample. The frequency of occurrence of each single set of data is shown on the vertical *y*-axis. The name of each data type is shown on the *x*-axis. The general rules of graphing (including an appropriate title, axis labels and units, and using a ruler and pencil) also apply.

frequency histogram
an accurate representation of the distribution of numerical data, and an estimate of the probability frequency distribution of a continuous variable (quantitative variable)

Worked example 10.2B

Frequency histograms

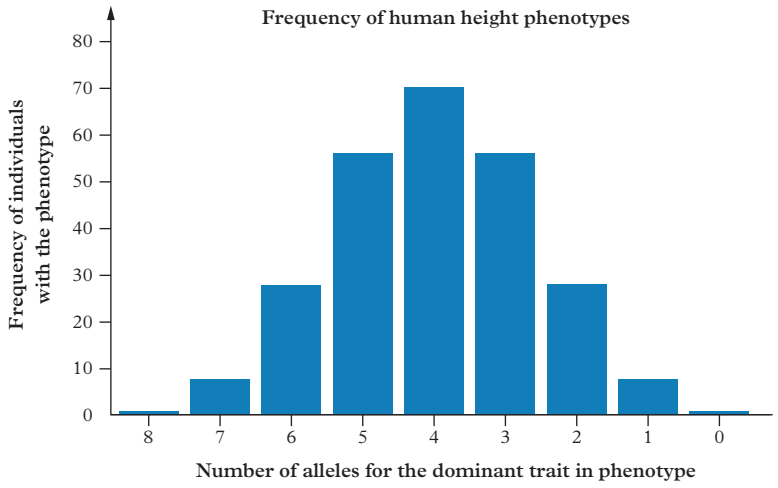
Human height is controlled by four autosomal genes (polygenetic), where each allele for the dominant trait increases the height of the individual. The more alleles for the dominant height trait an individual has, the taller that person will be. If there are no environmental influences (e.g. lack of food), there are nine possible phenotypes, ranging from eight alleles for the dominant height trait to no alleles for the dominant height trait (i.e. all alleles are for the recessive short trait) in the genotype.

a **Use** the data in Table 3 to draw a frequency histogram that shows the relative frequency of the phenotypes resulting from dominant trait alleles for height. (2 marks)

b If the individuals recorded in Table 3 who have six alleles for the dominant trait are the offspring of the cross (AaBbCcDd × AaBbCcDd), **predict** the genotype combinations of alleles in these offspring that would have produced their height. (1 mark)

TABLE 3 Frequency of phenotypes resulting from dominant trait alleles for height

No. alleles for dominant trait	8	7	6	5	4	3	2	1	0
No. individuals with resulting height phenotype	1	8	28	56	70	56	28	8	1

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking.	To "use" means to apply knowledge or rules to put theory into practice. To "predict" means to give an expected result.
Step 2: Construct a histogram from the data provided.	**a**  (1 mark for correct representation of data in histogram, 1 mark for correct axes)
Step 3: Determine the genotype combinations from the parental genotypes containing six dominant alleles.	**b** The parent genotype is AaBbCcDd × AaBbCcDd, so the possible combinations that can have six (capital letter) alleles for the dominant trait are: AABBCCdd AABBccDD AABBCcDd AABbCCDd AABbCcDD AAbbCCDD AaBBCCDd AaBBCcDD AaBbCCDD aaBBCCDD (1 mark)

Your turn

Skin pigmentation in humans is controlled by three autosomal genes (polygenic), where each dominant allele increases melanin production, leading to darker skin pigmentation. The more dominant alleles in an individual's genotype, the darker their skin pigmentation. In the absence of environmental influences (e.g. UV exposure), there are seven possible phenotypes, ranging from six dominant alleles to no dominant alleles in the genotype (i.e. all recessive alleles for lighter pigmentation).

a **Use** the data in Table 4 to draw a frequency histogram that shows the relative frequency of phenotypes resulting from dominant trait alleles for skin pigmentation. (2 marks)

b If the individuals recorded in Table 4 who have four dominant alleles are the offspring of the cross (AaBbCc × AaBbCc), **predict** the genotype combinations of alleles that produced this phenotype. (1 mark)

TABLE 4 Frequency of phenotypes resulting from dominant trait alleles for skin pigmentation

No. dominant alleles	6	5	4	3	2	1	0
No. individuals	1	6	15	20	15	6	1

gene complex when two or more genes interact to determine the phenotypic expression of a characteristic

Gene interactions

Sometimes two or more genes interact in determining the phenotypic expression of a characteristic. These are termed **gene complexes**. An example of a gene complex is the coat colour of labrador dogs, where gene B controls the production of melanin in hair (allele B for

black hair, allele b for brown hair; Table 5). Gene D controls the dispersion and deposition of the pigment into the hair. This is an example of **epistasis**, where the phenotypic expression of one gene is masked by another gene.

epistasis
when the phenotypic expression of one gene is masked by another gene; means "standing upon"

TABLE 5 How genes interact in dihybrid crosses with labrador coat colours

	Yellow labrador	Brown labrador	Black labrador
Effect on pigment	Pigment produced but not dispersed	Brown pigment produced, dispersed and deposited	Black pigment produced, dispersed and deposited
Allele combinations	BBdd Bbdd bbdd	bbDD bbDd	BBDD BbDD BBDd BbDd
Effect on phenotype	Black or brown pigment may be formed, but it is not dispersed (recessive allele dd only). This colour ranges from almost white through yellow to a copper colour, due to other genetic influences.	Brown pigment is produced because of the homozygous recessive form of gene B (bb), and it is dispersed to the hair because there is at least one dominant allele D, and so the dog is brown.	There is one allele for each dominant trait (gene B and gene D), so black pigment is formed and it is dispersed to the hair, and the dog is black.
Phenotypic ratio	4	3	9

Epistasis is significant in coding for enzymes in biochemical pathways. In humans, the recessive condition **phenylketonuria (PKU)** results from alleles being unable to form an enzyme (due to a homozygous recessive epistatic gene) that normally brings about the breakdown of phenylalanine to tyrosine in humans. Even though enzymes for subsequent reactions in the metabolic pathway are present, the series of reactions cannot occur. As a result, phenylalanine is converted to phenylpyruvic acid, but cannot be further processed, which causes severe intellectual disability in the individual. The phenylpyruvic acid is ultimately excreted in the urine, so tests can easily be conducted to detect PKU. Treatment involves a special diet from infancy to diminish the formation of phenylalanine.

phenylketonuria (PKU)
a homozygous recessive genetic disease in which one enzyme required for the normal breakdown of phenylalanine is lacking

Skill drill

Predicting genotypes and phenotypes

Science inquiry skill: Lesson 1.7 Processing and analysing

A species of plant has two traits controlled by different inheritance patterns: flower colour and leaf pattern.

The colour of the flowers is controlled by two genes, each with two alleles (R = red, r = white). The more dominant alleles (R) an individual has, the redder the flowers will be. The following combinations are possible for the flower colour phenotype:

- 4 dominant alleles (RRRR) → very red flowers
- 3 dominant alleles (RRRr) → dark red flowers
- 2 dominant alleles (RRrr) → light red flowers
- 1 dominant allele (Rrrr) → pale pink flowers
- 0 dominant alleles (rrrr) → white flowers

The pattern on the leaves is controlled by three alleles at a single gene locus: P^a (spotted), P^b (striped) and p (no pattern). P^a and P^b are codominant, meaning both will be expressed when present together. p is recessive and is only expressed when present in the homozygous condition.

Practise your skills

1 Using a dihybrid cross between two plants with the genotypes $RrRrP^aP^b \times RrRrP^bp$, **predict** the genotypic and phenotypic frequencies of the traits in their offspring. (3 marks)

2 The data shown in the table was collected from 1,000 plants.

Using this data, **construct** histograms to represent the relative frequency of flower colours and leaf patterns in the plants. (2 marks)

3 Based on your histograms, **infer** the possible genotypes of the parents, giving reasons to support your response. (3 marks)

Flower colour	Number
Very red	200
Dark red	300
Light red	250
Pale pink	150
White	100
Leaf pattern	**Number**
Spotted & striped	400
Spotted	300
Striped	250
No pattern	50

Challenge

Nature vs nurture

Polygenic inheritance explains how complex traits, such as human height, are influenced by multiple genes. Height is not determined by a single gene but by the cumulative effect of several genes, each contributing a small amount to the final phenotype. However, environmental factors, such as nutrition and overall health, also play a significant role in determining height.

Explain how polygenic inheritance contributes to variation in human height, and how environmental factors can influence the expression of these traits. (3 marks)

Check your learning 10.2

Check your learning 10.2: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the following terms: (1 mark each)

- **a** continuous variation
- **b** partial dominance
- **c** codominance
- **d** modifier gene
- **e** multiple alleles
- **f** recipient.

2 When red shorthorn cattle are mated with white shorthorns, all the offspring are roan (a combination of red and white). When two red cattle are mated, they produce only red offspring. When two white cattle are mated, they produce only white offspring. When two roans are mated, half the offspring are roan, a quarter are red and a quarter are white.

- **a** **Explain** this phenomenon. (2 marks)
- **b** **Explain** what genotypes the parents of a red calf must have, using a Punnett square to support your response. (2 marks)

Analytical processes

3 In snapdragons, tallness (T) is dominant to dwarf-ness (t) and red flower colour (R1) shows intermediate dominance to white flower colour (R2). The hybrid condition results in tall plants with pink flowers.

A dwarf red snapdragon is crossed with a plant pure-breeding for tallness and white flowers.

- **a** **Determine** the expected proportions of genotypes and phenotypes in the offspring. (2 marks)
- **b** **Determine** the probable genotypes of the parents. (2 marks)

4 If a litter resulting from the mating of two short-tailed cats contains three kittens without tails, two with long tails and six with short tails, **deduce** the simplest way of explaining the inheritance of tail lengths in these cats. **Describe** the genotypes involved. (4 marks)

5 If a man with blood type B, one of whose parents had blood type O, has children with a woman with blood type AB, **determine** the theoretical percentage of their children with blood type B. (4 marks)

6 Mrs Hockings and Mrs Colless both had babies on the same day in the same hospital. Mrs Hockings took home a baby girl, named Katie. Mrs Colless took home a baby girl, named Emma. Mrs Colless began to suspect, however, that her child had been accidentally switched with the Hockings baby in the nursery. Blood tests were done, and Mr Hockings was found to be type A, Mrs Hockings type B, Mr Colless type A, Mrs Colless type A, baby Katie type O and baby Emma type B. **Determine** whether a mishap has occurred, using Punnett squares and a pedigree to support your response. (5 marks)

Lesson 10.3
Sex-linked inheritance

Key ideas

- → Sex-linked inheritance refers to inheritance of genes on the sex chromosomes (X and Y).
- → X-linked traits are more common in males, due to their single X chromosome inheritance.
- → Pedigrees visually represent genetic inheritance patterns, helping predict trait transmission across generations.

Sex chromosomes

Learning intentions and success criteria

The sex of an individual is determined by specific sex chromosomes. All other chromosomes are termed autosomes. In humans, and in some other species, the female has two X chromosomes and the male has an X and a Y chromosome.

Sex-linked genes

Genes located on the sex chromosomes are termed **sex-linked genes**. Those on the X chromosome are termed X-linked, meaning an equivalent allele is not carried on the Y chromosome. Similarly, genes that are located only on the Y chromosome are called Y-linked genes.

sex-linked gene
a gene located on a sex chromosome

In male offspring (XY), the X chromosome must come from the mother and the Y chromosome must come from the father. Because males have only one X chromosome, there is only one possible set of genes for that chromosome. If the X chromosome in a male has an allele for a recessive trait, the trait will appear in the phenotype. In contrast, females have two X chromosomes and therefore need two copies of the recessive trait allele before it is expressed in the phenotype. A heterozygous female for a sex-linked recessive gene is called a **carrier**.

carrier
an individual (female in humans) who is heterozygous for a sex-linked gene, or an individual who is infected by a pathogen but does not display the symptoms

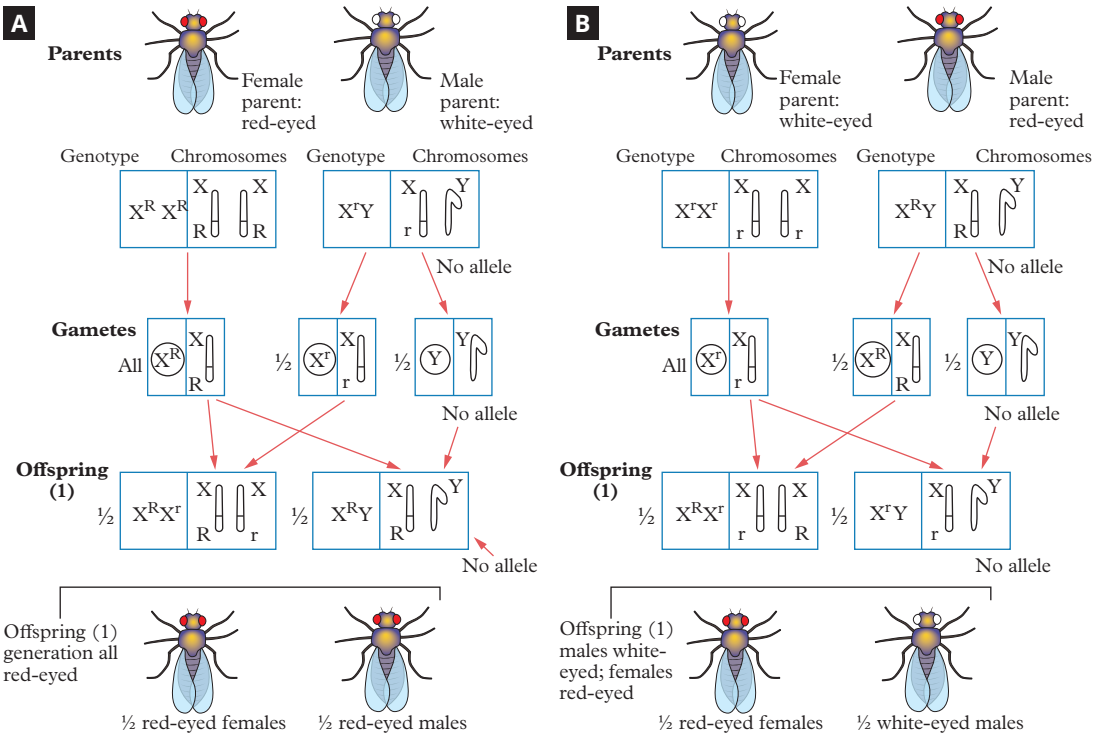


FIGURE 1 Sex-linked genes in *Drosophila*. (A) Normal eye colour in fruit flies is red, which is dominant to white eyes. If a white-eyed individual is crossed with a pure-breeding red-eyed fly, all the offspring are red-eyed. (B) When a male and a female from this cross are mated, only males exhibit the white eye trait. If this gene were autosomal, an equal number of males and females would be white-eyed.

Real-world Biology

Sex determination

Studies of the inheritance of eye colour in the fruit fly, *Drosophila melanogaster*, by American geneticist T.H. Morgan in 1910 led to the discovery of chromosomes specifically involved in determination of the sex of the individual. Female flies were discovered to have four pairs of homologous chromosomes, but the males had three homologous pairs plus one pair of two different chromosomes. One of these chromosomes is similar to the fourth pair of the female and is called the X chromosome. The other chromosome, which has a different shape, is called the Y chromosome. In the fruit fly, the fourth pair of chromosomes are the sex chromosomes. The female has two X chromosomes and the male has one X and one Y chromosome (Figure 2). Thus, both the male and female fruit fly have three pairs of autosomes and one pair of sex chromosomes. All the gametes of the female must have an X chromosome. Although they differ, the sex chromosomes of the male act as a homologous pair during meiosis. Therefore, half the male gametes will contain an X chromosome and half will contain a Y chromosome.

The pattern is different in some organisms. In grasshoppers, for example, there is no Y chromosome. Females have two X chromosomes and males have only one X chromosome. In birds, butterflies, most reptiles and some fish, the male is XX and the female is XY. In mammals (including humans), the female is XX and the male is XY.

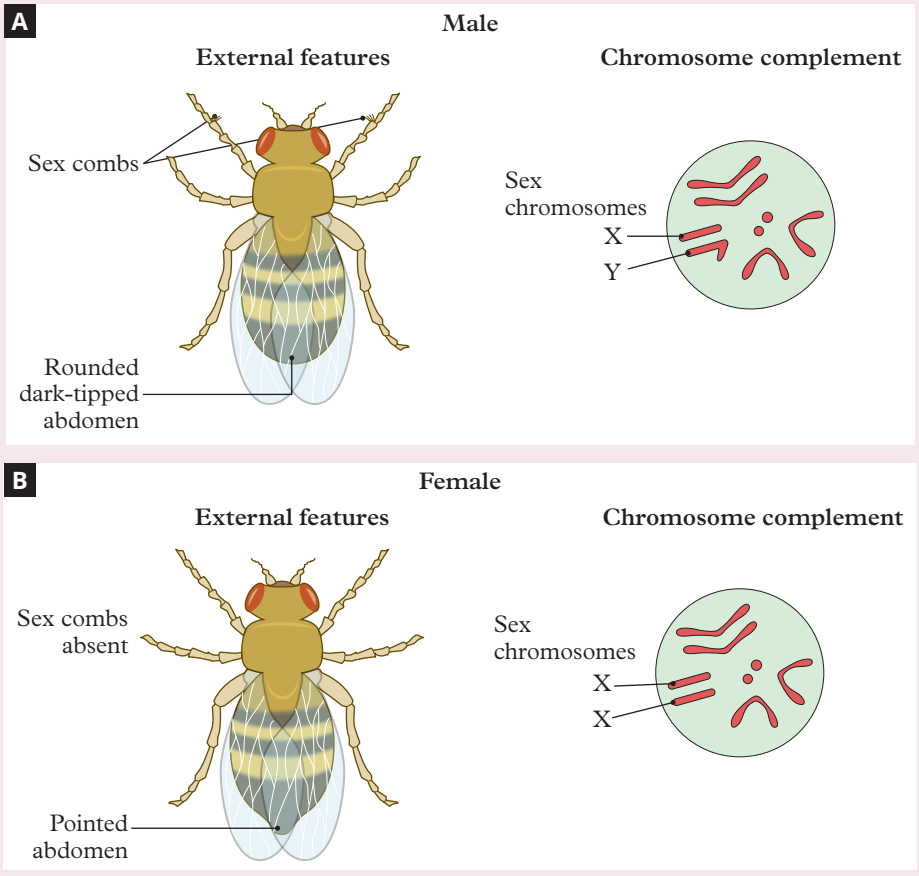


FIGURE 2 (A) Male and (B) female *Drosophila melanogaster*

Apply your understanding

1 **Compare** the composition of sex chromosomes between male and female *Drosophila melanogaster*. (2 marks)

2 **Describe** the role of homologous chromosome pairing during meiosis in male *Drosophila melanogaster* and how it leads to the production of gametes with either an X or a Y chromosome. (2 marks)

Sex-linked conditions

In humans, **colour-defective vision** (red–green colour blindness) and haemophilia are two examples of inherited, recessive sex-linked diseases. Colour-defective vision in humans is caused by a defect in the pigments in the retina of the eye that are sensitive to red and green light. These two colours, therefore, cannot be distinguished by a person with the recessive trait. Few females have colour-defective vision because it is rare for females to have two alleles for the recessive trait. In contrast, 1 in 10 males have colour-defective vision.

Haemophilia is a group of disorders in which the blood does not clot normally. Blood clotting involves a series of chemical reactions in which each reaction depends upon a specific protein factor in the blood. The most common form of haemophilia results from the absence of one of these proteins. The gene for this protein is carried on the X chromosome. Haemophiliacs may bleed to death with even minor injuries. Most people who have been diagnosed with haemophilia are now provided with the missing protein factor (produced

colour-defective vision
in humans, the inability to distinguish between the colours red and green; also known as red–green colour blindness

haemophilia
a group of disorders in which the blood does not clot normally

through a genetically modified bacterium), enabling them to lead near-normal lives. This treatment does not prevent the haemophilia allele being passed on to offspring.

A classic example of haemophilia is that of the British royal family. Neither Queen Victoria nor Prince Albert had the disease, but their descendants did, indicating that the allele on the X chromosome came from Queen Victoria (carrier). Because none of Queen Victoria's predecessors were known to have the disease, it has been hypothesised that this recessive trait allele arose in her as a result of a mutation.

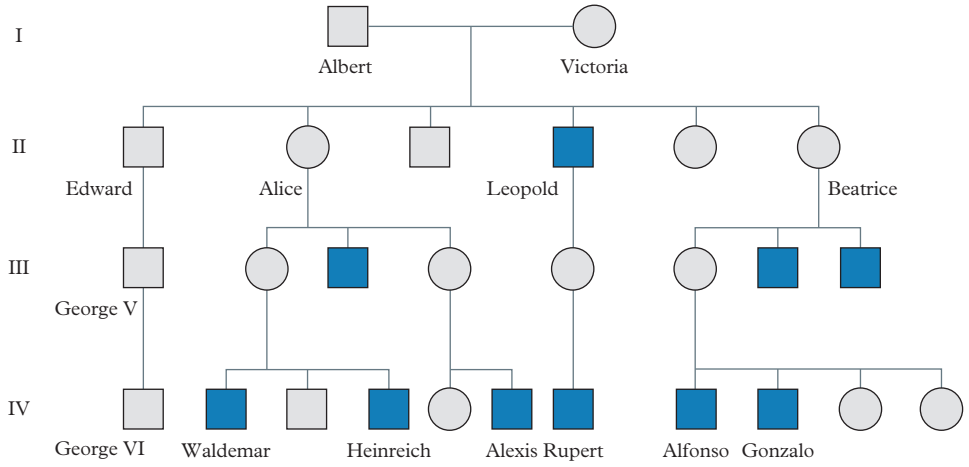


FIGURE 3 Pedigree showing inheritance of haemophilia in the descendants of Queen Victoria

Although mammals carry two alleles for sex-linked genes, it has been found that, in most somatic cells, one of the X chromosomes condenses out into a tiny dark object, called a **Barr body**. The genes on this condensed X chromosome are inactivated, so in a normally functioning female cell there is only one active X chromosome. Barr body formation is therefore a process of **inactivation**.

Barr body
an inactivated X chromosome in the cells of female mammals

X inactivation
the condensation, and thus inhibition, of one of the pairs of X chromosomes in female vertebrates

Because the condensation of each X chromosome is random, in the body as a whole approximately half the cells will contain an active X chromosome from the mother and half will contain an active chromosome from the father. Females, therefore, can be considered genetic mosaics for sex-linked genes. It appears that, for most characteristics, as long as half the cells in a heterozygous female are normal, she will show the normal phenotype. This means a woman who is heterozygous for colour-defective vision will show normal vision.

One characteristic that does not follow this rule is that of coat colour in cats. Ginger and black hair in cats is a sex-linked and codominant trait. A ginger female mated with a black male will produce male offspring that are all ginger, and female offspring that are all tortoiseshell – a mixture of black and ginger fur colours (Figure 4).

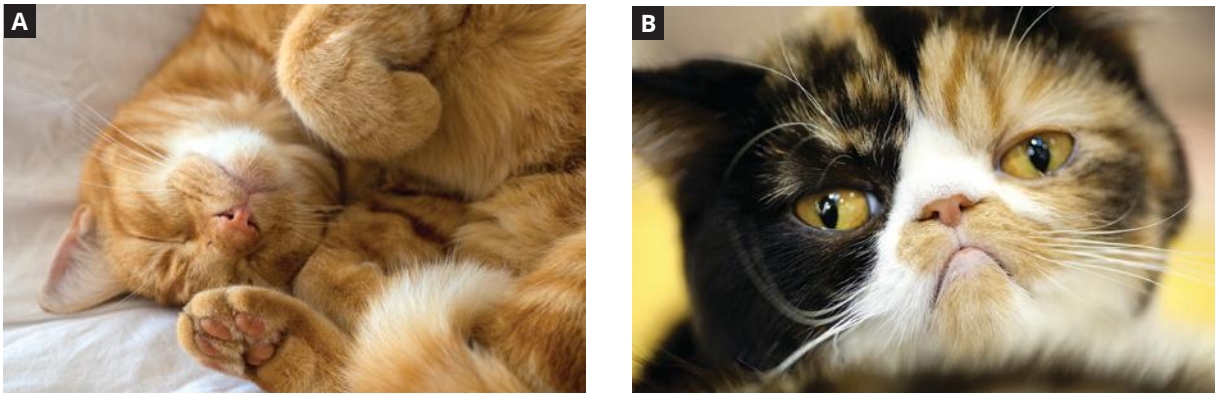


FIGURE 4 Sex-linked coat colour in cats: (A) male ginger cat, (B) female tortoiseshell cat

In female cats, hair follicle cells that have an active black X chromosome will produce black hairs, and those with an active ginger X chromosome will produce ginger hairs. The mixture of black and ginger hairs creates the tortoiseshell condition. This means tortoiseshell colouration is found only in females, because only females have two X chromosomes (with potentially different alleles for hair colour). If a tortoiseshell female is mated with a black male, the progeny will be black or tortoiseshell females, and ginger or black males.

holandric gene
a gene located on a vertebrate Y chromosome

Holandric genes

Holandric genes are genes that are carried on the Y chromosome and inherited by male offspring – this is referred to as Y-linked inheritance. Examples are the *SRY* genes that are the male sex determiners in humans. Phenotypic traits controlled by these genes are found only in males. It appears that the occurrence of human hairy pinnae, a tuft of hair sprouting from the ear rim, is probably due to a holandric gene. Investigations are ongoing as to the number of genes responsible for the trait, different degrees of hairiness, the different ages of onset and increase in frequency with age.

FIGURE 5 Example of hairy pinnae

Analysing pedigrees

A pedigree is a diagram used to trace the inheritance of specific traits through multiple generations of a family. It provides a visual representation of relationships between individuals, and highlights which members of the family exhibit or carry the trait in question. Pedigrees are a valuable tool for identifying patterns of inheritance, such as autosomal dominant, autosomal recessive or sex-linked (X-linked, Y-linked), and they help predict the probability of the trait appearing in future generations. By analysing the transmission of traits across generations, we can infer how a trait is inherited, and identify carriers or individuals at risk of inheriting or passing on the trait. Pedigrees can be useful for:

- identifying affected individuals – shading indicates who expresses the trait
- examining gender distribution – if the trait is seen predominantly in one gender, it suggests sex-linked inheritance (e.g. X-linked, Y-linked)
- assessing generational skipping – traits that skip generations are often recessive, while traits seen in every generation are more likely to be dominant
- identifying parent–offspring transmission – if males and females inherit the trait equally, it suggests autosomal inheritance; if it is primarily males who inherit it, it may be X-linked recessive
- testing consistency with inheritance patterns – known inheritance models (e.g. autosomal dominant, autosomal recessive, X-linked, Y-linked) can be used to predict and verify the genotypes of individuals in the pedigree by using a Punnett square.

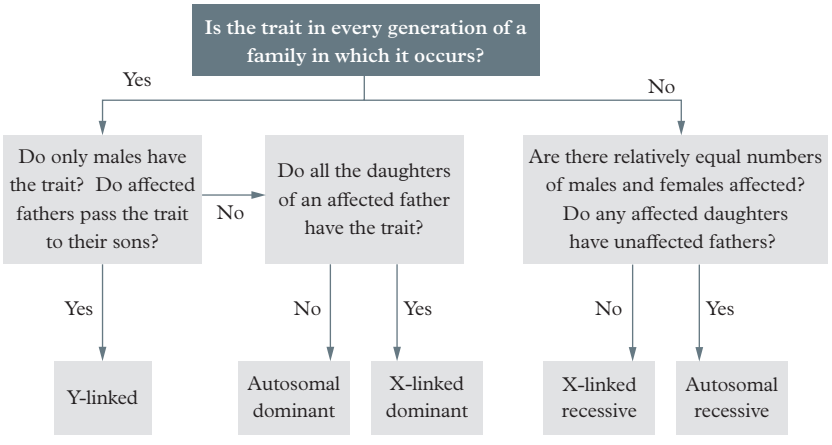


FIGURE 6 The distribution of traits can be analysed to determine the likely mode of inheritance.

Autosomal inheritance

If a gene is inherited on an autosome, males and females are equally likely to inherit the gene. For autosomal recessive traits, the characteristic often skips generations. Affected individuals typically have unaffected parents who are carriers of the recessive allele (Figure 7). Autosomal dominant traits do not skip generations, with affected individuals having at least one affected parent (Figure 8).

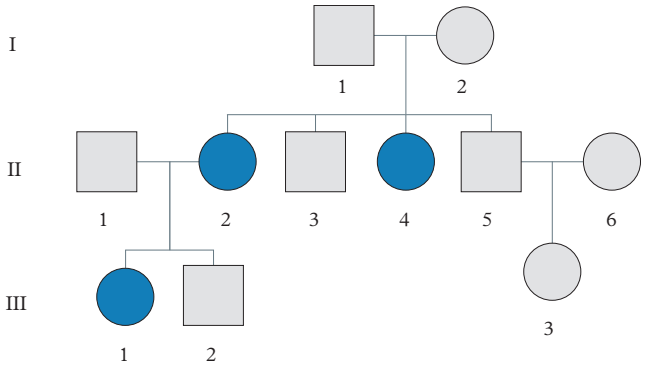


FIGURE 7 Autosomal recessive inheritance: the parents of the affected person are typically unaffected carriers of the allele.

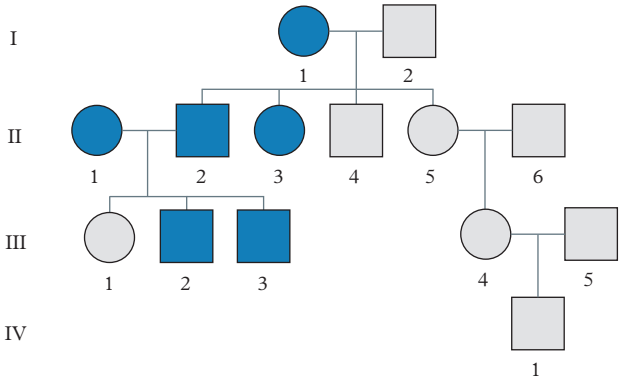


FIGURE 8 Autosomal dominant inheritance: the affected person has at least one affected parent.

Sex-linked inheritance

For X-linked dominant traits, affected males pass the trait to all their daughters but none of their sons (Figure 9). Affected females can transmit the trait to both sons and daughters. These traits do not skip generations and are typically more common in females, as they have two X chromosomes and are more likely to inherit the allele.

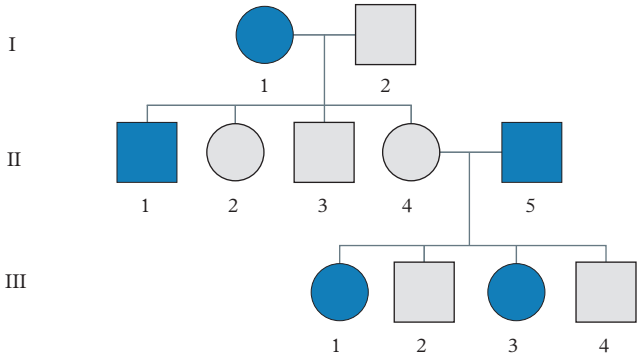


FIGURE 9 In X-linked dominant inheritance, affected males pass the trait to daughters but not sons, while affected females can pass the trait to both.

X-linked recessive traits are more common in males, because males have only one X chromosome (Figure 10). These traits often skip generations and are inherited from carrier mothers. Affected males cannot pass the trait to their sons, but all their daughters are carriers. Carrier females may have affected sons if they pass on the recessive allele.

Y-linked traits are passed exclusively from father to son and never occur in females (Figure 11). These traits do not skip generations (if there are males), and all sons of an affected male inherit the trait.

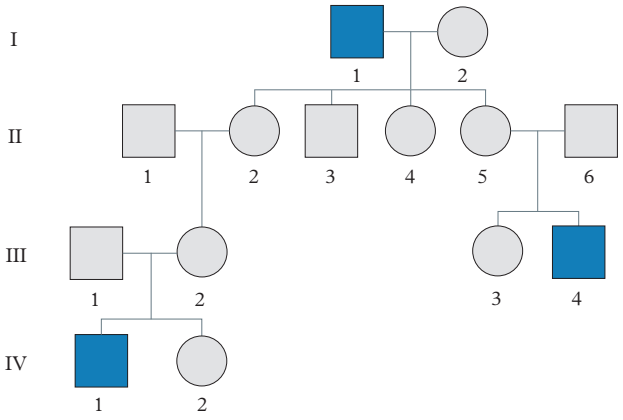


FIGURE 10 X-linked recessive conditions often skip generations, and males are more commonly affected. They can only pass the trait to their daughters, who are carriers.

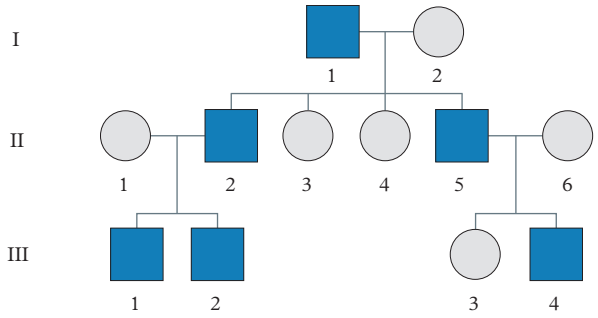


FIGURE 11 Traits inherited on the Y chromosome affect only males, and do not skip generations.

Check your learning 10.3

Check your learning 10.3: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the following terms: (1 mark each)
   - **a** Barr body
   - **b** carrier
   - **c** holandric
   - **d** sex-linked
   - **e** X-inactivation.

2 Colour-defective vision (red–green colour blindness) is inherited as a sex-linked recessive trait. A couple were surprised to learn that one of their sons was colour blind, because neither of the parents showed this trait.
   - **a** **Explain** how this could have occurred. (2 marks)
   - **b** **Explain** which of the boy's grandparents this allele could have come from if none of them showed the trait, using a Punnett square to support your response. (4 marks)

Knowledge utilisation

3 A tortoiseshell cat (genotype X^OX^B) is mated with a ginger cat (X^OY). **Predict** the genotypes and phenotypes you would expect among the offspring. (4 marks)

4 Suppose that, in the cat cross described in question **3**, the female had long hair (H^LH^L) and the male had short hair (H^SH^S). The gene for hair length is autosomal and shows intermediate dominance (H^LH^S giving medium-length hair). **Predict** how many phenotypes you would expect, and in what proportions. (3 marks)

5 Haemophilia is a sex-linked recessive gene in humans.
   - **a** If a father and a son are both haemophiliacs, and the mother is not, **predict** the genotype of the mother, using a Punnett square to support your response (4 marks)
   - **b** **Determine** whether you would expect any of the daughters to be haemophiliacs. **Justify** your response. (3 marks)

MODULE 10

Lesson 10.4
Review: Inheritance

Summary

10.1
- Alternative forms of a gene, called alleles, determine an individual's genotype and traits.
- Dominant alleles mask recessive ones, which only show when an individual is homozygous recessive.
- Punnett squares are used to predict inheritance patterns and offspring traits in monohybrid or dihybrid genetic crosses.
- Inheritance patterns follow Mendel's laws of segregation and independent assortment, governed by probability.
- Pedigrees are used to analyse inheritance patterns, to identify dominant, recessive, autosomal or sex-linked traits in families.

10.2
- Codominant inheritance results in both alleles being equally expressed in the phenotype.
- Multiple allele inheritance (e.g. ABO blood groups) is inheritance that involves more than two alleles influencing a trait.
- Polygenic traits are controlled by multiple alleles, show continuous variation, and can be graphed using a histogram to show variation in a population.

10.3
- Sex-linked inheritance is inheritance of genes that are located on the sex chromosomes (X and Y).
- X-linked traits are more common in males because of their single X chromosome inheritance.
- Pedigrees visually represent genetic inheritance patterns, helping predict trait transmission across generations.

Review questions 10.4A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

1 A gene is best defined as
- **A** a part of a single chromosome in the nucleus.
- **B** a factor responsible for producing a characteristic.
- **C** a portion of a chromosome responsible for several characteristics.
- **D** a part of a chromosome responsible for producing one polypeptide.

2 Chromosomes that are not sex chromosomes are known as
- **A** carriers.
- **C** autosomes.
- **B** genotypes.
- **D** phenotypes.

3 Rabbits may have long or short ears. A long-eared homozygous dominant rabbit is mated with a long-eared heterozygous rabbit.
If L represents the dominant trait allele and l represents the recessive trait allele, the possible genotypes of the offspring would be
- **A** LL and ll.
- **B** LL and Ll.
- **C** all long-eared.
- **D** long-eared and short-eared.

4 The lengths of corn cobs show continuous variation, because they are controlled by two pairs of alleles (A and a, B and b).
Select the genetic combination that would give a short cob but not the shortest cob.
- **A** aabb
- **C** aaBb
- **B** AaBb
- **D** AaBB

5 The coat colour of cats is a trait that is linked to the sex chromosomes. The gene for coat colour is carried on the X chromosome. Suppose that O represents ginger and B represents black, and that tortoiseshell cats show both colours in their coats. A ginger female (X^OX^O) is mated with a black male (X^BY).
Identify the possible litters that this mating could produce.

A Ginger females only
B Ginger females and ginger males
C Ginger females and tortoiseshell males
D Tortoiseshell females and ginger males

6 If a red-flowered plant is crossed with a white-flowered plant, giving all offspring with pink flowers, we would assume that the alleles for red and white showed

A complete dominance.
B incomplete dominance.
C modifier genes present.
D complete recessiveness.

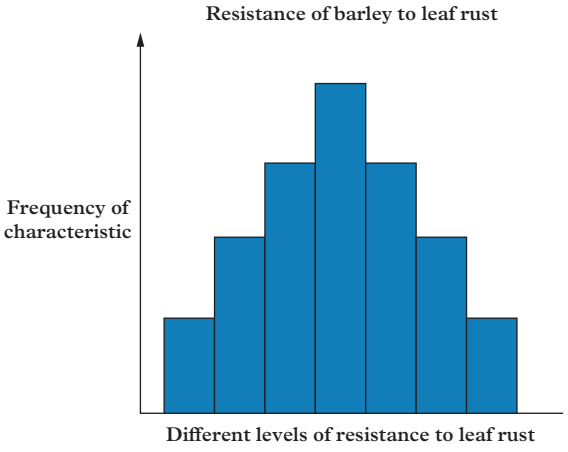
7 A man with an X-linked dominant disorder marries a woman without the disorder.
Determine the proportion of their daughters who will be affected by the disorder.

A 0%
B 25%
C 50%
D 100%

8 The term "holandric gene" refers to genes in humans that

A cross over.
B have displayed non-disjunction.
C are carried on the Y chromosome.
D are sex-linked on the X chromosome.

9 Members of a barley plant species show varying levels of partial resistance to the leaf rust *Puccinia hordei*.
The graph below shows the distribution of a population of barley plants with regard to this characteristic.



With respect to rust resistance, these plants show

A high mutation rates.
B polygenic inheritance.
C discontinuous variation.
D inheritance due to a single pair of alleles.

10 In 1910, Thomas Morgan discovered traits linked to sex chromosomes in the fruit fly. The Punnett square below shows a cross between a red-eyed female and a white-eyed male. Fruit flies usually have red eyes. Predict the most probable combination of offspring.

Red-eyed female	White-eyed male: X^r	White-eyed male: Y
X^R	$X^R X^r$	$X^R Y$
X^R	$X^R X^r$	$X^R Y$

A 2 red-eyed females, 2 red-eyed males
B 2 red-eyed females, 1 red-eyed male, 1 white-eyed male
C 1 red-eyed female, 1 white-eyed female, 2 red-eyed males
D 2 white-eyed females, 1 white-eyed male, 1 red-eyed male

11 In a pedigree, a trait that appears in every generation is most probably

A Y-linked.
B X-linked recessive.
C autosomal recessive.
D autosomal dominant.

12 If a person who is blood type AB (I^AI^B) has a child with a person who is blood type O (ii), what is the probability that the child will have blood type A?

A 0%
B 25%
C 50%
D 100%

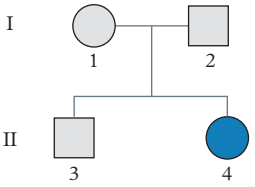
13 A test cross is done with a plant that shows a dominant phenotype for flower colour. If 50% of the offspring have the dominant phenotype and 50% have the recessive phenotype, the genotype of the plant with the dominant phenotype must be

A heterozygous.
B homozygous dominant.
C homozygous recessive.
D none of the above, because the plant has intermediate dominance.

14 In a dihybrid cross, Mendel's law of independent assortment predicts that the two traits being studied will

A show intermediate dominance.
B show a 1:1 ratio in the offspring.
C be inherited together as a single unit.
D segregate independently and form a 9:3:3:1 ratio.

15 In a pedigree such as the one below, the absence of a trait in the offspring of two unaffected parents is most likely due to



A Y-linked inheritance.
B X-linked dominant inheritance.
C autosomal dominant inheritance.
D autosomal recessive inheritance.

Review questions 10.4B Short response

Review questions: Complete these questions online or in your workbook.

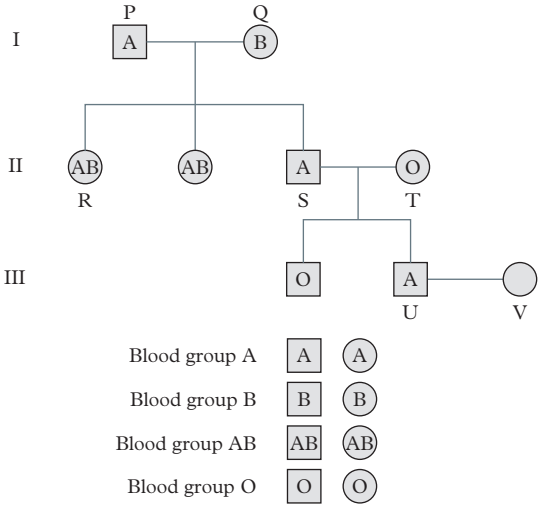
Retrieval and comprehension

16 **Explain** why men express more sex-linked recessive traits than women. (2 marks)

17 **Explain** why some characteristics, such as skin colour, have multiple expressions. (3 marks)

18 In some breeds of dogs, a dominant autosomal trait controls the characteristic of barking while trailing (hunting or tracking game). In these dogs, another independent gene produces erect ears; it is dominant over the allele for drooping ears. Suppose a dog breeder wants to produce a pure-breeding strain of droop-eared barkers, but he knows that the genes for silent trailing and erect ears are present in his kennels. **Describe** how he should proceed. (4 marks)

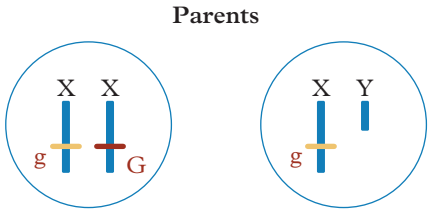
19 The diagram shows three generations of a family tree, with the blood groups (ABO system) of the family members.



a **Identify** the genotypes of person P and person Q. (2 marks)

b Person U and person V have four children, each with a different blood group. **Explain** how this is possible, using Punnett squares to support your response. (4 marks)

20 Drawn below are the sex chromosomes of two parents. There are two alleles, one for normal colour vision, represented by G, and one for red–green colour defective vision, represented by g. **Calculate** the phenotypic and genotypic ratios of their possible offspring. (2 marks)



Analytical processes

21 **Distinguish** between an autosomal dominant trait and a sex-linked dominant trait. (2 marks)

22 In peas, tall plants (T) are dominant to dwarf (t), yellow colour (Y) is dominant to green (y), and smooth seed (S) is dominant to wrinkled seed (s). **Determine** what the phenotypes of the offspring of the following crosses would be.

a TtYySs × ttyyss (2 marks)

b TtyySs × ttYySs (2 marks)

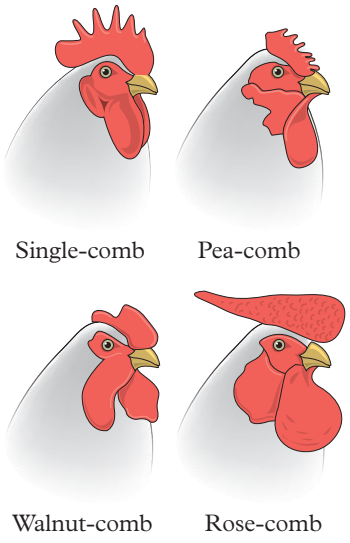
23 The long hair of Persian cats (A) is recessive to the short hair of Siamese cats (B), but the black coat colour of Persians is dominant to the black-and-tan coat of Siamese. If a pure black, long-haired Persian is mated to a pure black-and-tan, short-haired Siamese, **determine** what the appearance of the F_1 offspring will be. **Calculate** the probability of getting a long-haired black-and-tan cat if two of the F_1 offspring mate. (4 marks)

A

B

24 The bar eye gene in *Drosophila* causes a drastic reduction in eye size. A male with narrow bar eyes crossed with a female with normal eyes produced progeny in which all females had wide bar eyes and all males had normal eyes. **Deduce** whether this cross demonstrates that the bar gene is located on the X chromosome. **Explain** your answer. (4 marks)

25 In domestic fowls, the gene for rose comb (R) and pea-shaped comb (P) together produce the so-called "walnut" comb shape (genotypes RRPP, RrPP, RRPp or RrPp). These are shown below.



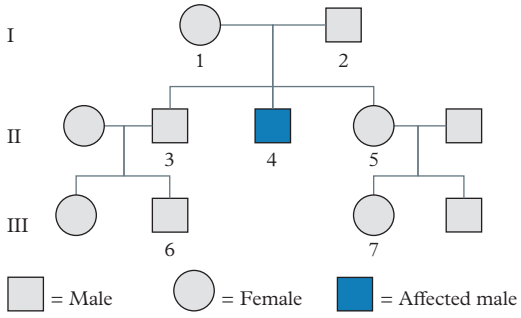
The recessive alleles r and p produce the normal single comb shape (genotype rrpp). **Determine** what phenotypes you would expect from the following crosses, and in what proportions. (2 marks each)

a RRPp × rrPp

b rrPP × RrPp

c RrPp × Rrpp

26 The diagram below represents a family pedigree showing the inheritance of phenylketonuria (PKU), a rare inherited metabolic disorder that can result in neurological issues if left untreated. PKU is controlled by a single pair of alleles, A and a.



a Use this pedigree to **determine** whether the allele for PKU is dominant or recessive. (1 mark)

b **Identify**, with reasons, the genotypes of each of individuals 1, 2 and 4. (3 marks)

c **Deduce** the possible genotypes of each of individuals 3 and 5. (2 marks)

d Individual 7 married a man who is heterozygous for this condition. **Explain** the possible genotypes of their offspring. Illustrate your answer using Punnett squares. (4 marks)

Knowledge utilisation

27 Waxy maize is a specific type of maize that differs from regular maize due to the composition of its starch molecules in its endosperm. Waxy maize contains the highly branched starch molecule called amylopectin. Normal maize contains both amylopectin and amylose, a less-branched starch. The endosperm of the seed develops from a triploid nucleus and so has three genes for each characteristic, not two. A blue–black staining reaction with iodine can be used to indicate the presence of the starch amylose.

Genotype of endosperm	Amylose content (%)
$W_xW_xW_x$	22.0
$W_xW_xw_x$	20.4
$W_xw_xw_x$	18.4
$w_xw_xw_x$	0.0

The table shows the results of different kinds of seeds being analysed for their amylose content.

a **Discuss** evidence from the results to support the conclusion that the non-waxy phenotype is dominant over the waxy phenotype. (2 marks)

b **Discuss** the purpose of adding iodine in determining the genotype of the samples. (2 marks)

28 The frequencies per thousand births of some genetic diseases in populations of northern European origin are shown in the table.

a **Determine** the probable frequency of an individual of northern European origin simultaneously having:

i Huntington's disease and albinism (2 marks)

ii achondroplasia, sickle cell anaemia and cystic fibrosis. (2 marks)

b Although the traits for some disease conditions are autosomal dominant, the frequency of the disease in the population is less than that for some recessively inherited diseases. **Propose** possible reasons for this. **Use** examples from the table to support your answer. (4 marks)

c **Explain** why frequencies of sex-linked diseases were recorded for males only. (2 marks)

Inheritance pattern	Frequency (per 1,000 births)	Pathology
	Autosomal dominant	
Huntington's disease	0.1	Progressive dementia from mid-life
Achondroplasia	0.04	Dwarfism
Myotonic dystrophy	0.05	Progressive muscular weakness
Neurofibromatosis	0.25	Tumours of peripheral and other nerves
	Autosomal recessive	
Phenylketonuria	0.1	Intellectual disability
Cystic fibrosis	0.4	Mucoid build-up; lung congestion
Beta thalassaemia	0–10	Severe anaemia
Sickle cell anaemia	0–10	Haemolytic anaemia
Albinism	0.1	Lack of pigment; abnormal vision
Sex-linked	**Frequency (per 1,000 males)**	
Red–green colour blindness	80	Inability to distinguish red and green colours
Haemophilia	0.2	Defect in blood clotting
Muscular dystrophy	0.3	Progressive muscular weakness
Fragile X syndrome	0.9	Intellectual disability
Testicular feminisation	0.02	Sterile XY females; unresponsive to male sex hormones

Data drill

Interpreting pedigrees

Neurofibromatosis type 1 (NF1) is an autosomal dominant genetic disorder that causes swelling and tumours in the nervous system (neurofibromas), as well as flat, light brown spots on the skin, called café au lait spots, freckling, Lisch nodules (lumps on the iris of the eye), optic pathway gliomas (tumours of the optic nerve) and skeletal disorders. A couple have sought medical advice regarding having children. The male (Individual 10) has a family history of NF1, as shown in the pedigree in Figure 1. The percentage frequency of symptoms of NF1 his relatives have experienced is shown in Figure 2.

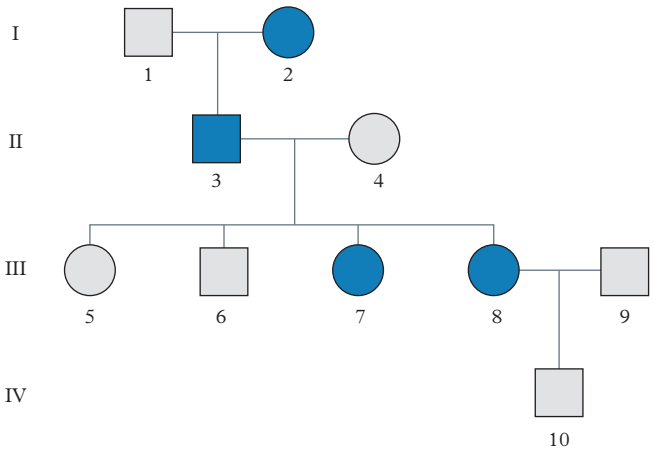


FIGURE 1 Pedigree of the family history of NF1

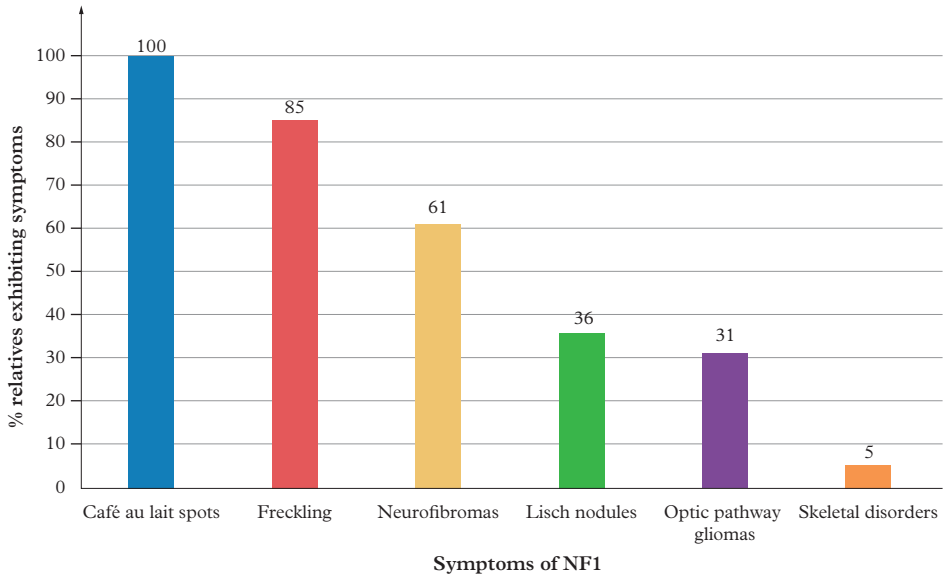


FIGURE 2 Percentage frequency of symptoms of NF1 experienced by group of relatives depicted in the pedigree in Figure 1

Apply understanding

1 **Identify** evidence to support the conclusion that inheritance of the NF1 trait is autosomal dominant, using a Punnett square to support your response. (4 marks)

Analyse data

2 **Contrast** the percentage frequency of relatives experiencing neurofibromas and optic pathway gliomas as symptoms of NF1, using data in your response. (2 marks)

Interpret evidence

3 **Infer** the genotype of the male (Individual 10), using a Punnett square to support your response. (3 marks)

Module 10 checklist: Inheritance

MODULE 11

Biotechnology

Introduction

Biotechnology is the application of biological knowledge to the production of organisms or their products that are useful to humankind. It has been used for thousands of years. Many of the foods we take for granted have been produced using artificial selection and breeding of organisms with desirable characteristics. Genetic principles and techniques have been applied to commercial enterprises, such as genetic engineering of drug- and food-producing organisms, as well as manipulation of some genetic diseases and cloning.

In the twenty-first century, the field of DNA technology is one of the fastest-growing areas of science. Recombinant DNA technology and DNA profiling are major branches of this area. Recombinant DNA (genetic engineering) involves the introduction of new genes by cutting them out of the chromosomes of one species and inserting them into the chromosomes of another species. This modifies organisms, giving them new, desirable characteristics. DNA profiling, also called DNA fingerprinting, is a technique that uses processes such as the polymerase chain reaction to amplify specific segments of DNA, and gel electrophoresis to separate and visualise these fragments, enabling comparison of genetic information between organisms by their unique banding patterns.

Prior knowledge

Prior knowledge quiz Check your understanding of concepts related to biotechnology before you start.

Subject matter

Science understanding

- → Describe the process of making recombinant DNA, including the role of restriction enzymes, plasmids and DNA ligase.
- → Describe how PCR and gel electrophoresis are used in DNA profiling and explain how differences in DNA allow for characteristic banding patterns.
- → Interpret DNA profiles from gel electrophoresis.

Science as a human endeavour

→ Appreciate that
  – the Human Genome Project was an international, collaborative research project which resulted in the publication of the full sequence of the human genome in 2003. The databases associated with the project are freely available via the internet and used extensively by the international scientific community

Science inquiry

→ Interpret DNA profiles from gel electrophoresis

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024

Practicals

oxforddigital **These lessons are available on Oxford Digital.**

Lesson 11.3 Gel electrophoresis

Lesson 11.1
Recombinant DNA

Key ideas

- → Recombinant DNA technology allows for production of specific proteins or traits.
- → Restriction enzymes cut DNA at specific recognition sites.
- → Plasmids act as vectors to carry foreign DNA.
- → DNA ligase joins DNA fragments by forming covalent bonds.

Learning intentions and success criteria

Genetically modified organisms

Deepening our understanding of the structure and function of DNA has raised questions about how we can modify DNA, to improve the production of antibiotics and insulin, to "cure" genetic diseases, and to improve the quality and yield of our food production.

Genetically modified organisms (GMOs) are any organisms that have had their DNA modified in some way. Some of these organisms may have had genes activated or inhibited, while others (**transgenic organisms**, such as bacteria) may have had genes from another organism (e.g. a jellyfish) introduced into their DNA.

genetically modified organism (GMO)
an organism whose genetic material has been altered using recombinant DNA technology

transgenic organism
an organism whose genome has been altered using genetic material from another species or breed

FIGURE 1 Canola grown for oil in Australia is a GMO

Genetic engineering toolbox

When an engineer designs and builds a structure, they need a set of tools to cut, copy or stick the pieces together. **Genetic engineering**, like other forms of engineering, requires a set of tools – in this case, molecular tools. All these tools have been isolated from existing organisms. Because the structure of DNA is the same in all species, the enzymes associated with the DNA of one species will work effectively with the DNA of any other species. Therefore, bacterial DNA enzymes can be used in the manipulation of plant and animal DNA. **Recombinant DNA** is DNA formed by combining genes from various sources and can be created in four key steps.

genetic engineering
direct manipulation of an organism's DNA to alter its traits

recombinant DNA
genetically engineered DNA formed by combining genes from different sources

restriction enzyme
an enzyme that cleaves DNA at or near specific recognition sites

1. The target gene in the DNA of the donor organism is isolated using **restriction enzymes**.
2. The bacterial plasmid is cut using the same restriction enzymes.
3. The target gene and the plasmid are joined using DNA ligase.
4. The recombinant DNA vector is transformed into the host cell.

Restriction enzymes

Since 1968, when the first restriction enzyme (nuclease) was isolated from the *Haemophilus influenzae* bacterium, more than 900 types have been discovered from over 230 strains of bacteria. Each of these enzymes cuts DNA molecules at a particular site. Each restriction enzyme is given a name that generally reflects its origin.

- The first letter (upper case) of the name comes from the genus of the bacterial cell from which it was isolated, and the next two letters (in lower case) come from the species (e.g. "Eco" comes from *Escherichia coli*). If there is a fourth letter, it indicates the strain of that species.
- A Roman numeral following the name indicates the order in which the enzyme was isolated from a single strain of the bacterium.

The enzyme EcoRI comes from the *Escherichia coli* RY13 strain, with a target sequence of 5′–G*AATTC–3′ (* indicates where the enzyme cuts in the sequence). EcoRII is derived from *E. coli* R245, with target sequence of 5′–C*CAGG–3′ and 5′–C*CTGG–3′. Because of their action, restriction enzymes are given the general name of **DNA scissors**. Restriction enzymes that break nucleic acid strands somewhere in the interior of the molecule are called **endonucleases**, while those that break the strands at the ends of the molecule are called exonucleases.

TABLE 1 Some restriction enzymes and their sources

Enzyme	Derived from	Target sequence (cut at *) 5′ – 3′
AvaI	*Anabaena variabilis*	C * C/T C G A/G G
BamHI	*Bacillus amyloliquefaciens*	G * G A T C C
BglII	*Bacillus globigii*	A * G A T C T
EcoRI	*Escherichia coli* RY13	G * A A T T C
EcoRII	*Escherichia coli* R245	* C C A/T G G
HaeIII	*Haemophilus aegyptius*	G G * C C
HhaI	*Haemophilus haemolyticus*	G C G * C
HindIII	*Haemophilus influenzae* RD	A * A G C T T
HpaI	*Haemophilus parainfluenzae*	G T T * A A C
KpnI	*Klebsiella pneumoniae*	G G T A C * C
MboI	*Moraxella bovis*	* G A T C
PstI	*Providencia stuartii*	C T G C A * G
SmaI	*Serratia marcescens*	C C C * G G G
SstI	*Streptomyces Stanford*	G A G C T * C
SalI	*Streptomyces albus* G	G * T C G A C
TaqI	*Thermus aquaticus*	T * C G A
XmaI	*Xanthomonas malvacearum*	C * C C G G G

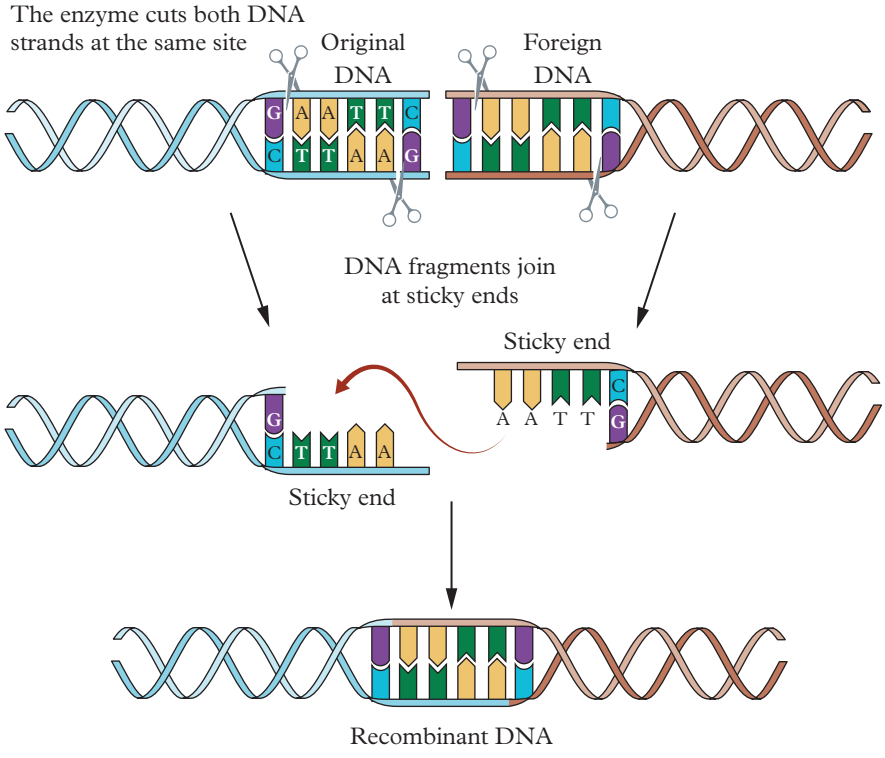


FIGURE 2 Restriction enzyme action of EcoRI

DNA scissors
restriction enzymes that cut DNA into fragments

endonucleases
enzymes that cut internal bonds within DNA or RNA

Study tip

There are both DNA and RNA polymerases and ligases. It can be important to specify which one you are talking about when answering questions. For example, always specify *DNA* ligase or *RNA* polymerase.

Some enzymes, such as SmaI, cut the DNA in the exact centre of the sequence, generating a blunt end with no unexposed bases.

Chain 1: 5′–CCC | GGG3′

Chain 2: 5′–GGG | CCC5′

Other enzymes, such as HindIII, cut asymmetrically. Separation results in fragments, each with a protruding end composed of unpaired bases. These fragmented ends with their unpaired bases are called **sticky ends**. Restriction enzymes that produce sticky ends are more desirable, as the overhangs of these ends facilitate the formation of hydrogen bonds between strands.

Chain 1: 5′–A | AGCTT3′

Chain 2: 3′–TTCGA | A5′

sticky ends
fragments of unpaired DNA bases formed when particular base sequences are cut asymmetrically

DNA ligase

Many cells can repair mistakes made in DNA when undergoing replication. One of the enzymes involved in this repair mechanism is **DNA ligase**. In genetic engineering, scientists exploit this mechanism. DNA that has been cut with a restriction enzyme can be recombined (in different combinations) and the DNA joined together by DNA ligase, which catalyses the formation of the covalent bond in the phosphate–sugar backbone.

DNA ligase
an enzyme that facilitates the joining together of DNA strands

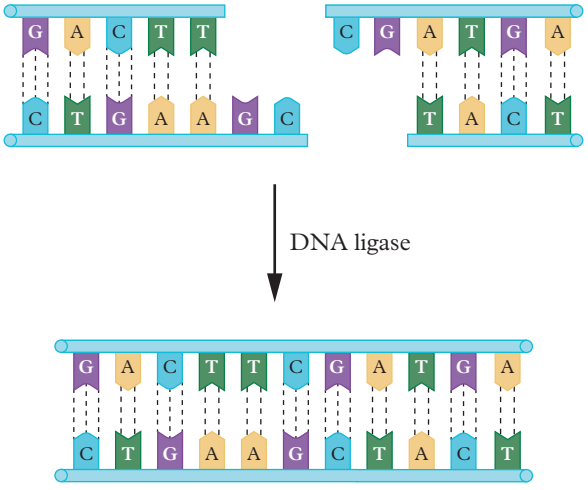


FIGURE 3 DNA ligase acts as molecular "glue", joining segments of DNA together by repairing the covalent bonds in the sugar–phosphate backbone.

recombinant DNA technology
the deliberate modification of the characteristics of an organism, or the production of a new organism, by inserting or deleting genes into the DNA; also known as genetic engineering

Plasmids

The earliest **recombinant DNA technology** experiments were conducted on bacteria. In addition to the circular chromosomal strand of DNA, bacteria have one or more additional small circular segments of DNA, called **plasmids**. The genes on the plasmids give different strains of the same prokaryotic species slightly different characteristics, such as resistance to a particular antibiotic. Scientists use the plasmids to transfer genes from one organism into another (e.g. bacteria). Once in the new cell, these new genes can be translated and transcribed by the normal cell machinery to produce functional proteins.

plasmid
a small DNA molecule that is physically separated from chromosomal DNA and can replicate independently; typically within a bacterial cell

Both the donor DNA and the plasmid DNA are cut with the same restriction enzyme so that it will cut both pieces of the molecule at the site of the specific recognition sequence, producing complementary sticky ends. The donor gene is then added to the cut plasmid, and the DNA ligase can be used to recombine the gene into the plasmid. The plasmid can then act as a **vector** that transfers the donor gene into a prokaryotic cell.

vector
a DNA molecule used in the transfer of foreign genetic material into another cell, where it can be replicated and/or expressed

Bacterial transformation

Once generated, the genetically recombined plasmid is placed with the bacterial cell into a solution of calcium chloride. This makes the bacterial membrane more porous. The plasmid moves into the cell, and the bacterium is transformed. Each time the bacterium divides, the plasmid is replicated and carried in the new bacterial cells. This production of identical copies of the gene is called **gene cloning**.

gene cloning
production of identical copies of a gene

Monitoring recombination

The description of recombinant DNA technology is idealistic and does not always occur without some deviations. For example, some of the plasmids will not splice with the foreign gene. Some uncombined plasmids may reinsert back into the bacterial cell, and some recombined plasmids do not reinsert. To ensure that the required gene has been correctly inserted into the bacterium, scientists use other properties of plasmid genes, such as antibiotic resistance or the ability to produce a fluorescent green protein, to identify the required cells.

Choosing the right molecular tools is important for the success of bacterial transformation. Scientists must be aware of where the restriction enzyme will cut the plasmid and how the inserted gene will affect other genes that are present. For example, one commonly used plasmid contains two genes – one gene (called *ampR*) confers resistance to the antibiotic ampicillin, while the other (*lacZ*) produces the lactose-digesting enzyme β-galactosidase. The *lacZ* gene produces an enzyme that can digest the sugar X-gal to produce a blue protein. If the restriction enzyme EcoRI is used, it will cut the plasmid in the centre of the *lacZ* gene, interrupting this gene so that it cannot be expressed. This means the X-gal sugar cannot be digested, and therefore no blue pigment will be produced.

To separate the transformed bacteria from those without the recombined gene, the colonies are grown on a culture medium containing both ampicillin and the X-gal sugar. Only transformed bacteria will be able to grow on the medium, because they will contain the *ampR* gene within the plasmid, which confers resistance to ampicillin. X-gal is broken down by the enzyme β-galactosidase, encoded by the *lacZ* gene. Bacteria with unrecombined plasmids will express the *lacZ* gene. The colonies containing the recombined gene (and thus non-functional *lacZ*) will not be coloured blue and will appear white. The white colonies can then be isolated and pure cultures of the recombinant bacteria grown.

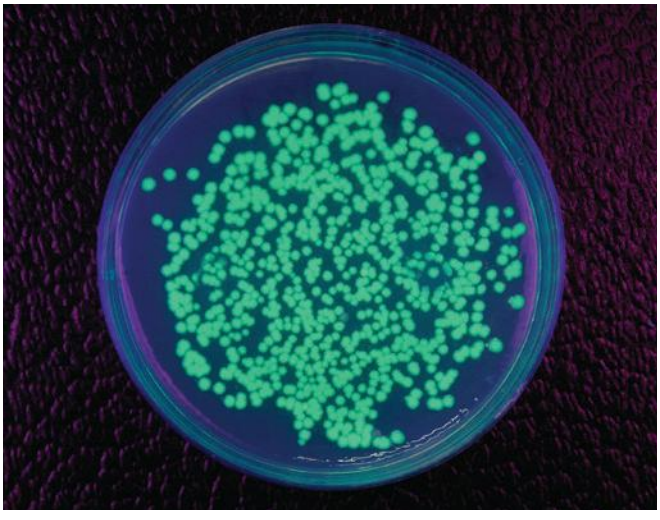


FIGURE 4 The plasmid containing the *pGLO* gene produces a green fluorescent protein in the presence of arabinose sugar. This makes transgenic bacteria glow green in fluorescent light.

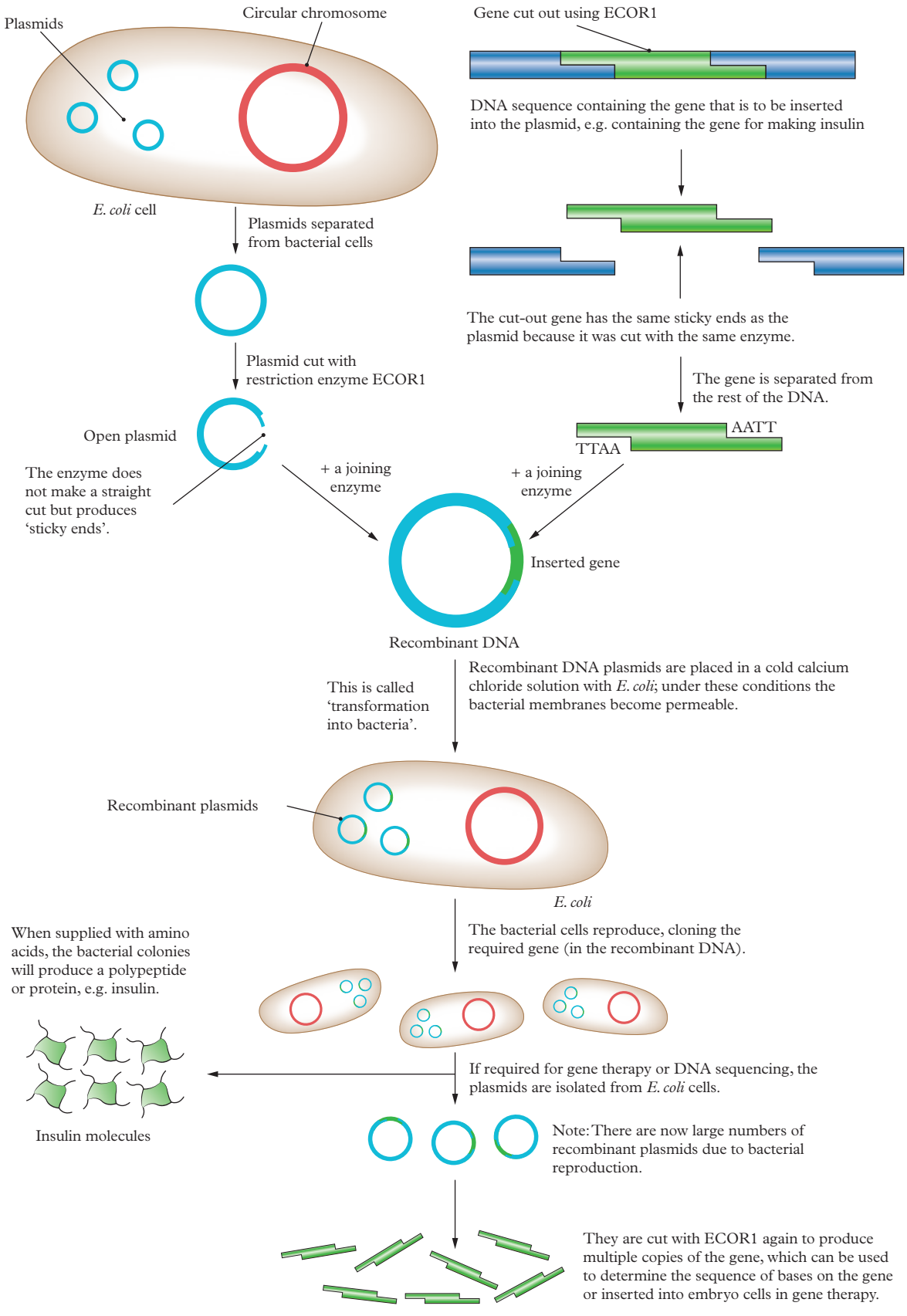
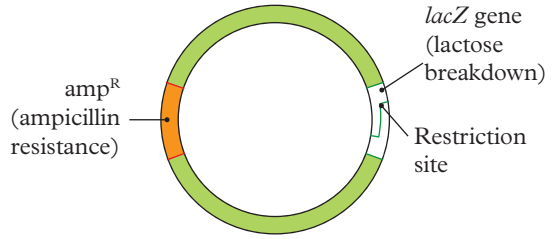


FIGURE 5 Recombinant DNA technology

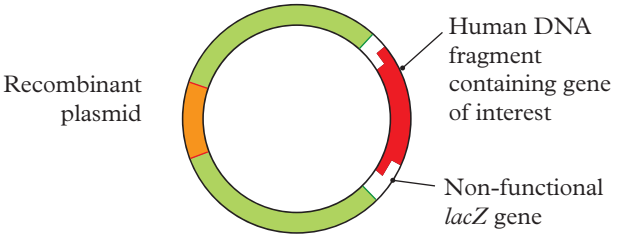
1



Bacterial plasmid before the addition of the foreign gene. The site at which the restriction enzyme cuts is in the middle of the *lacZ* gene; the gene for ampicillin resistance is on the opposite side of the plasmid.

2

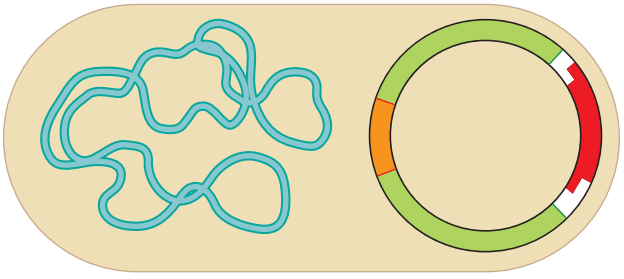
The plasmids are cut with restriction enzymes, then mixed with foreign DNA, e.g. human genes.



The human DNA has been spliced into the plasmid, making the *lacZ* gene non-functional.

3

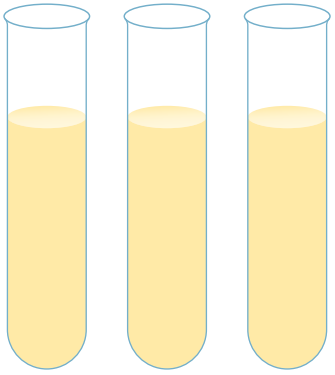
Recombinant plasmid transformed into bacterial cell.



The recombinant plasmids are transformed into the bacteria. Diagram 3 shows a recombinant plasmid in a bacterium but some plasmids will not be recombinant; in other cases, no plasmids will transform into the bacterial cells.

4

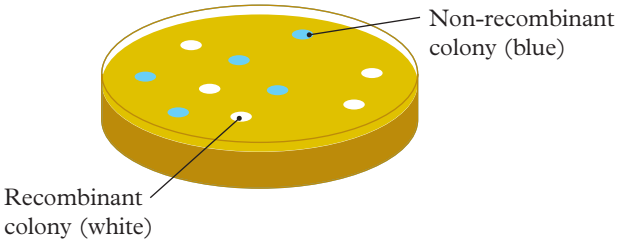
Cloned cells



The bacterial cells are grown in tubes to produce many identical cells (clones).

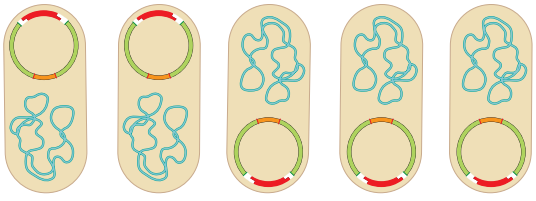
5

The cells are plated onto a growth medium containing ampicillin and X-gal; the clones of cells containing recombinant plasmids are identified by their white colour.



6

Recombinant DNA clones are grown to produce the required product, e.g. insulin.



Note 1: All cells within plasmids will grow because they have the ampicillin-resistant gene.
Note 2: The plasmids have been drawn larger (compared with the bacterial chromosome) than actual size.

FIGURE 6 Identification of recombinant plasmids in bacteria

Uses of recombinant bacteria

Genes that have been recombined into plasmid DNA can be used for a variety of purposes. For example, the gene product (e.g. human insulin) may be required. Because the human insulin gene would not normally be present in the bacterium, it is not automatically expressed when inserted into this organism. **Regulatory genes** may also need to be spliced into the plasmid to promote the expression of the desired gene.

regulator gene
a non-coding segment of DNA that produces transcription factors for gene expression

In addition to human insulin, other substances are now produced in commercial quantities using recombinant DNA techniques. Examples are:

- vaccine antigens for diseases such as malaria and hepatitis
- interferon – used in cancer research and treatment of some viral conditions; previously extracted from infected human blood cells
- hirudin – an anticoagulant used in plastic surgery; previously obtained by "milking" the salivary glands of leeches
- human growth hormone, used to treat stunted growth
- a protein that dissolves blood clots and can be used in the treatment of heart attacks and other heart conditions
- introduction of pest resistance into some plants.

Bacteria can also be used as the vectors for producing large numbers of a particular gene for other purposes, such as **gene therapy**.

gene therapy
the introduction of normal genes into cells in place of missing or defective ones, in order to correct genetic disorders

somatic gene therapy
replacement of defective genes in targeted somatic cells that are affected by a genetic disease

germ cell gene therapy
replacement of a defective gene in a reproductive cell (egg or sperm) with a normal gene, allowing normal development of the embryo and preventing the disease variant from being passed down

Gene therapy

There are two types of gene therapy: **somatic gene therapy** and **germ cell gene therapy**. Somatic gene therapy involves replacing a defective gene in a somatic (body) cell with an intact gene that carries the code for the functioning protein. In this case, a virus is often used as a vector because it can carry the intact gene into the affected cell. For example, in a treatment for cystic fibrosis, the correct gene is first cloned in bacterial plasmids, then inserted into a harmless virus. This virus is sprayed into the lungs, where it enters the lung cells, thereby inserting the correct gene into the DNA of the cells. Human trials of this treatment have had many setbacks, however, because many viral genes display a preference to be inserted into active, regulatory sections of the host cell's DNA. This has led to some instances of the gene therapy patient developing cancerous cells following the treatment.

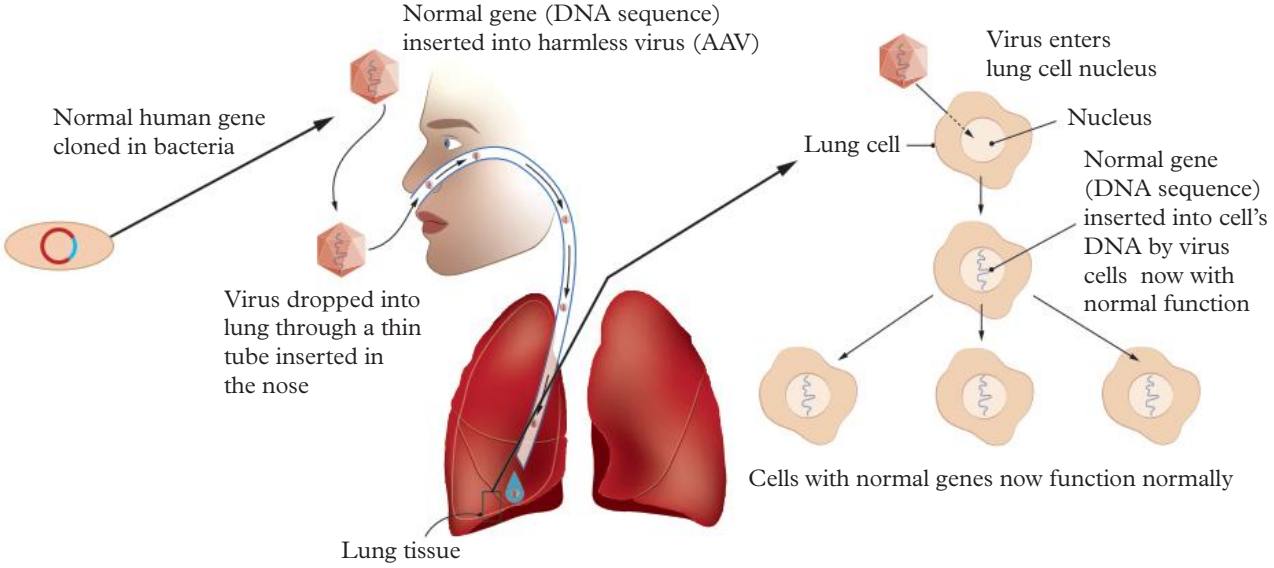


FIGURE 7 Somatic gene therapy treatment of cystic fibrosis

In germ cell gene therapy, a defective gene in the egg or sperm is replaced. Fertilisation of the gametes takes place *in vitro* and the resulting embryo is implanted into the female. This ensures that all the cells of the embryo carry the normal gene, so offspring will not have the disease, and it eliminates the defect permanently in subsequent generations of that family. This technique is controversial, because there is concern about simultaneous accidental introduction of regulatory genes that could affect the individual (and be inherited), and the possibility of genetic manipulation for cosmetic purposes. To date, in most countries, germ cell gene therapy has not been approved for human use.

Challenge

Restriction enzymes

In recombinant DNA technology, restriction enzymes play a crucial role in cutting DNA at specific sequences. However, bacteria have natural defence mechanisms, such as DNA methylation (epigenetic modification), that protect their own DNA from being cleaved by these enzymes.

1 If a restriction enzyme cuts DNA at a specific sequence, **describe** how the presence of methylation in a bacterium's DNA might affect the action of the enzyme during the recombinant DNA process. (2 marks)

2 **Discuss** how bacterial defence mechanisms might influence the success of cloning experiments and what modifications might be necessary to overcome these challenges. (3 marks)

Real-world biology

The Human Genome Project

In 1985, the Human Genome Project (HGP) was conceived in the USA. The project began in 1989 and was scheduled to last for 15 years, with total funding of US$3 billion. The aim of the project was to map and analyse the nucleotide sequences of each of the 100,000 human genes. In 1990, the HGP became a collaborative international project. In 1998, a milestone was passed, with the complete mapping of one human chromosome. The project also aimed to examine the social, ethical and legal implications of the research. Genomic libraries have now been established, where thousands of clones prepared from plants and animals are stored.

The HGP was a multi-institutional project. For example, one group studied Mormon families (which are generally large) over three generations, and focused on gene mapping using recombinants. Another group mapped gene locations with gene markers, and another used recombinant DNA techniques. Other groups directed their efforts towards determining the nucleotide sequencing of specific genes that have been located.

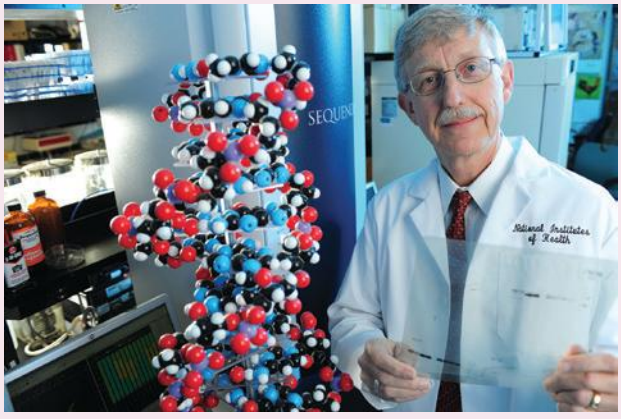


FIGURE 8 Dr Francis Collins led the Human Genome Project

By 2000, a working draft of 90 per cent of the human genome was published, identifying 22,000 potential genes, and screening was made available for 300 genetic diseases. These genetic diseases include the cystic fibrosis gene, adenosine deaminase deficiency, retinitis pigmentosa, severe combined immune deficiency, Duchenne muscular dystrophy, neurofibromatosis and retinoblastoma. In May 2003, the HGP was completed, with 99 per cent of gene-containing regions sequenced to 99.99 per cent accuracy. These 3 billion nucleotide sequences

provide a valuable reference for future medical and human biology research.

This research aimed to determine the possible allelic forms in humans in general, as well as individual genome data. The possible determination of personal genomes raises many issues, particularly that of confidentiality – including, for example, whether insurance companies would be able to request the genetic information of their clients.

Apply your understanding

1 **Describe** the aims of the Human Genome Project. (2 marks)

2 **Propose** three possible ethical issues that could arise from the Human Genome Project. (3 marks)

Check your learning 11.1

Check your learning 11.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** the role of "sticky ends" in recombinant DNA technology and how they are produced. (2 marks)

2 **Describe** the role of DNA ligase in the production of recombinant DNA. (2 marks)

3 **Describe** the process of creating recombinant DNA. (4 marks)

Analytical processes

4 **Distinguish** between plasmids, restriction enzymes and DNA ligase. (1 mark)

5 **Distinguish** between genetically modified organisms and transgenic organisms. (1 mark)

Lesson 11.2
DNA profiling

Learning intentions and success criteria

Key ideas

- → The polymerase chain reaction (PCR) amplifies specific DNA regions for profiling and analysis.
- → Gel electrophoresis separates DNA fragments by size to create banding patterns.
- → Differences in DNA sequences lead to unique banding patterns, which can be compared with other sequences.
- → DNA ladders help interpretation of DNA fragment sizes in gel electrophoresis results.

Polymerase chain reaction

The idea of the **polymerase chain reaction (PCR)** for the **amplification** (rapid copying) of segments of DNA was first conceived in 1983. By 1993, it was a well-established procedure, thereby enabling the Human Genome Project.

polymerase chain reaction (PCR) a technique that enables the amplification of any short sequence of DNA

amplification making multiple copies of a specific DNA segment, typically using PCR, to increase the amount of DNA for analysis or experimentation

The reaction exploits the naturally occurring DNA polymerases that can copy genetic material. There are three key steps in this process, and these must be repeated many times.

1. *Denaturation* – the two strands of DNA are separated by heating to 90–96°C to produce single strands of nucleotide sequences. DNA is synthesised from the 3′ end to the 5′ end.
2. *Annealing* – the mixture is cooled to ~52°C (depending on the primer) so the primers can bind. Primers are short, single strands of nucleotides and must be complementary to the sequences on either side of the DNA to be replicated.
3. *Elongation* – the mixture is heated to 75°C so the DNA polymerase (Taq polymerase) is able to produce new strands of DNA.

The actual temperatures used during each of the above steps are dependent on the type of Taq polymerase and primers used.

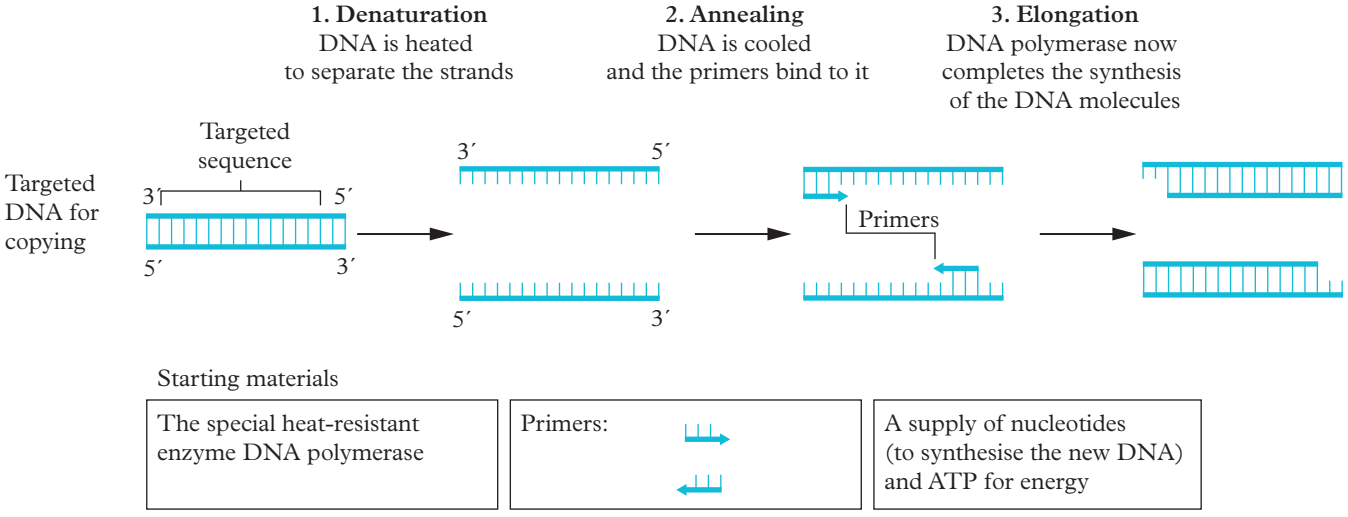


FIGURE 1 The polymerase chain reaction (PCR)

An automated cycle of rapid heating and cooling can take 1 to 3 minutes, depending on the length of nucleic acid being copied. Each time the cycle is repeated, the amount of DNA doubles. Repeating the process for 45 minutes can result in millions of copies of a specific piece of nucleic acid. Most enzymes, which are proteins, are unstable at high temperatures. The polymerase (Taq) used in this process is obtained from the bacterium *Thermus aquaticus*, a **thermophile** that lives in hot springs at temperatures that are lethal to other organisms. This enzyme is stable at high temperatures and is therefore ideal for the fluctuating temperatures of automated PCR.

thermophile a microorganism that can tolerate temperatures higher than 45°C

PCR applications

The PCR technique has a variety of applications. It is a significant tool in the detection of infectious diseases and of variations and mutations in genes. Using primers of known DNA sequences, particular types of DNA can be detected. Because a small fragment of DNA can be amplified rapidly, only a very small amount of DNA is required initially. This means that, for example, detection of the HIV virus after infection is faster because PCR is looking directly for the virus's DNA, whereas the standard test looks for indirect evidence through

antibody formation. PCR has been used to detect the pathogens that cause COVID-19, otitis media (a childhood middle ear infection), Lyme disease (a painful joint inflammation caused by bacteria transmitted in tick bites) and three sexually transmitted diseases (herpes, papilloma viruses and chlamydia), as well as the bacterium *Helicobacter pylori* (which causes stomach ulcers), all on a single swab.

FIGURE 2 PCR was very useful in detecting whether individuals had been infected with COVID-19

Gel electrophoresis

gel electrophoresis
a laboratory method for separating mixtures of DNA, RNA or proteins according to molecular size

short tandem repeats (STRs)
short DNA sequences of a repeating nucleotide sequence, often varying in length between individuals

loci
specific locations or positions of genes or genetic markers on a chromosome; singular *locus*

The technique of **gel electrophoresis** enables the short segments of DNA that have been duplicated via PCR to be used to identify differences between individual organisms. The purpose of gel electrophoresis is to separate DNA fragments based on the size of the fragments, to produce characteristic banding patterns that may be compared.

Although the functions of many alleles and genes have been identified, there are some small differences between the alleles on each individual. Many genes have non-coding areas (called introns) that can have **short tandem repeats (STRs)**, which consist of repeating units of 2–6 DNA base pairs (e.g. "ATCG" repeated multiple times). The number of repeats varies between individuals and is usually passed on from parents. The specific locations of STRs in the genome are known as **loci**.

Loci are highly variable between individuals, meaning that the number of repeats at each locus can differ, resulting in unique patterns of STRs for each person. This variability makes STRs especially useful in DNA profiling for identifying individuals, because the length of the repeated sequence will differ between unrelated people.

These differences can be picked up by first cutting the DNA from two individuals with the same restriction enzyme, and amplifying the STR regions by PCR. The samples are then loaded into a thin sheet of gelatinous material (called a gel) that contains many tangled fibres. An electric current is run across the gel, and because DNA is negatively charged, the sample moves towards the positive terminal (Figure 3A). Small pieces of DNA move through the tangle of gel fibres faster than longer lengths of DNA. This means short strands of DNA travel faster and further than long DNA strands. Staining the DNA

enables the segments of DNA to be identified. A series of specifically measured segments of DNA (called a DNA ladder) are added to an additional well, enabling the length of the DNA strands to be measured. The different genes can be visualised and measured against the DNA ladder under ultraviolet (UV) light (Figure 3B).

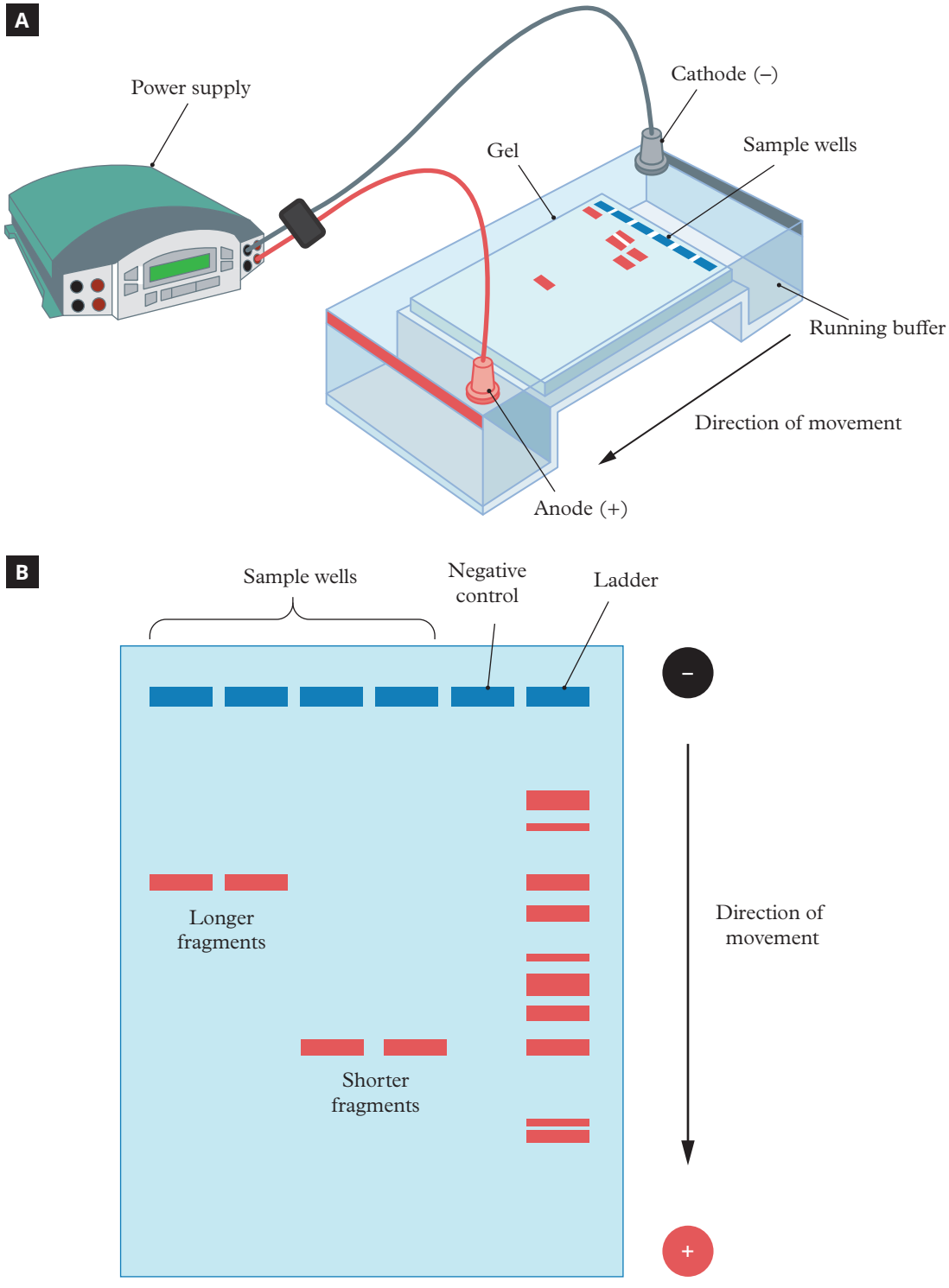


FIGURE 3 Gel electrophoresis. (A) The set-up (B) DNA travels towards the positive end of the gel, and fragments are compared against the DNA ladder

The different lengths of STR fragments reflects the number of repeats in each STR locus. The characteristic banding patterns produced by gel electrophoresis can be compared with other samples and known DNA ladder lengths, allowing analysis of genetic similarities and differences between individuals (Figure 4).

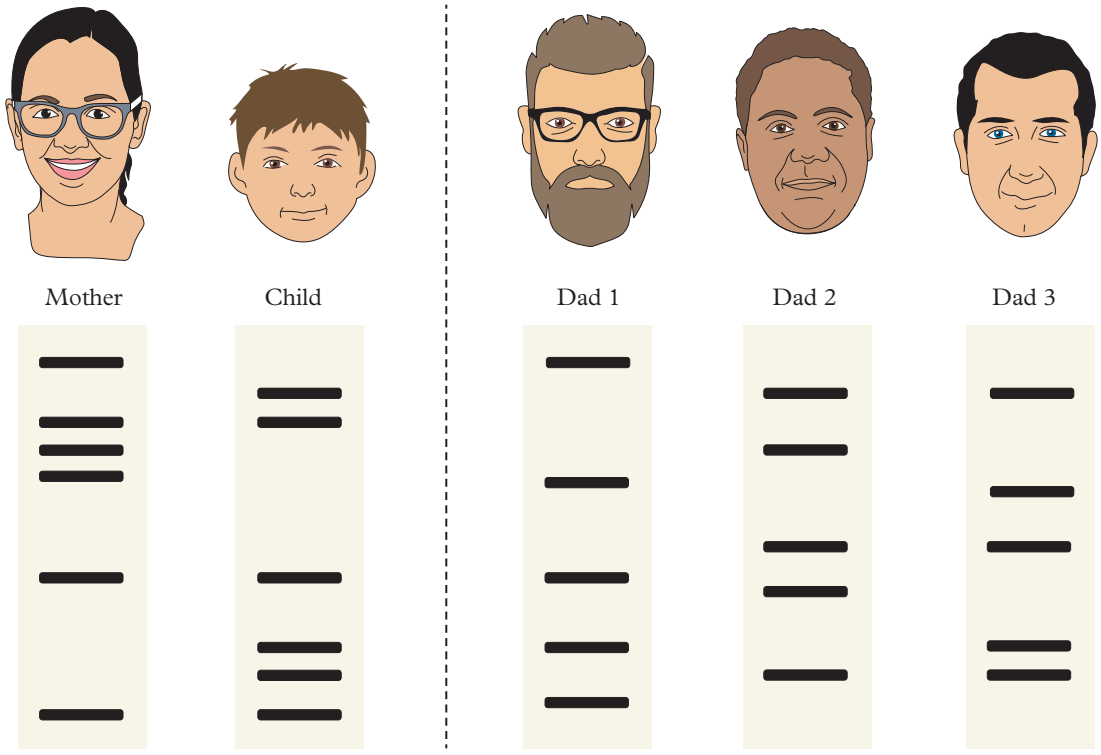


FIGURE 4 Each individual inherits half their chromosomes from their mother and half from their father. In this example, "Dad 3" has provided half the child's genetic material

DNA probes

DNA probes are used to identify the location of a gene on a chromosome (or a gel). A probe is a small section of DNA that is complementary to a sequence on the gene in question. This probe has a dye (either fluorescent or radioactive) attached. When the probe is combined with the single-stranded DNA (hybridised), the probe binds to that short section of DNA in the gene, allowing the location to be identified and isolated.

DNA profiling
a technique used to identify (for forensic purposes) the characteristics of an individual's DNA by extracting and identifying the base-pair pattern of their DNA; also known as DNA fingerprinting

DNA hybridisation
a technique that measures the degree of genetic similarity between DNA sequences of different individuals

DNA profiling

PCR and gel electrophoresis are important in the process of forensic DNA typing, commonly called **DNA profiling** (or DNA fingerprinting).

The method involves taking a DNA sample (e.g. from a crime scene) and using PCR to increase the size of the sample so it can be used for gel electrophoresis. This is followed by Southern blotting, **DNA hybridisation** and autoradiography (Figure 5).

1
Preparation of restriction fragments – three DNA samples from different sources, labelled A, B and C, are treated with restriction enzyme. DNA fragments are produced.

2
Gel electrophoresis – the mixtures of restriction fragments from the three samples are separated; each sample forms a pattern of bonds.

3
Southern blotting – the alkaline solution is pulled upward by capillary action. The DNA fragments are transferred from the gel to the paper in exactly the same positions as they were on the gel. The alkaline solution also unwinds (denatures) the DNA into single strands.

4
DNA hybridisation – the nitrocellulose paper is transferred to a plastic bag and a solution of selected radioactive probes is added. The probes will bind to some of the fragments by complementary base pairing.

5
Autoradiography – after rinsing off unattached probes, the paper is overlaid with a sheet of photographic film. The radioactivity in the bound probes exposes the film, and the probes with their complementary DNA fragments from the samples appear as dark bands.

The patterns can then be compared. In this case, samples A and B are identical but C is different.

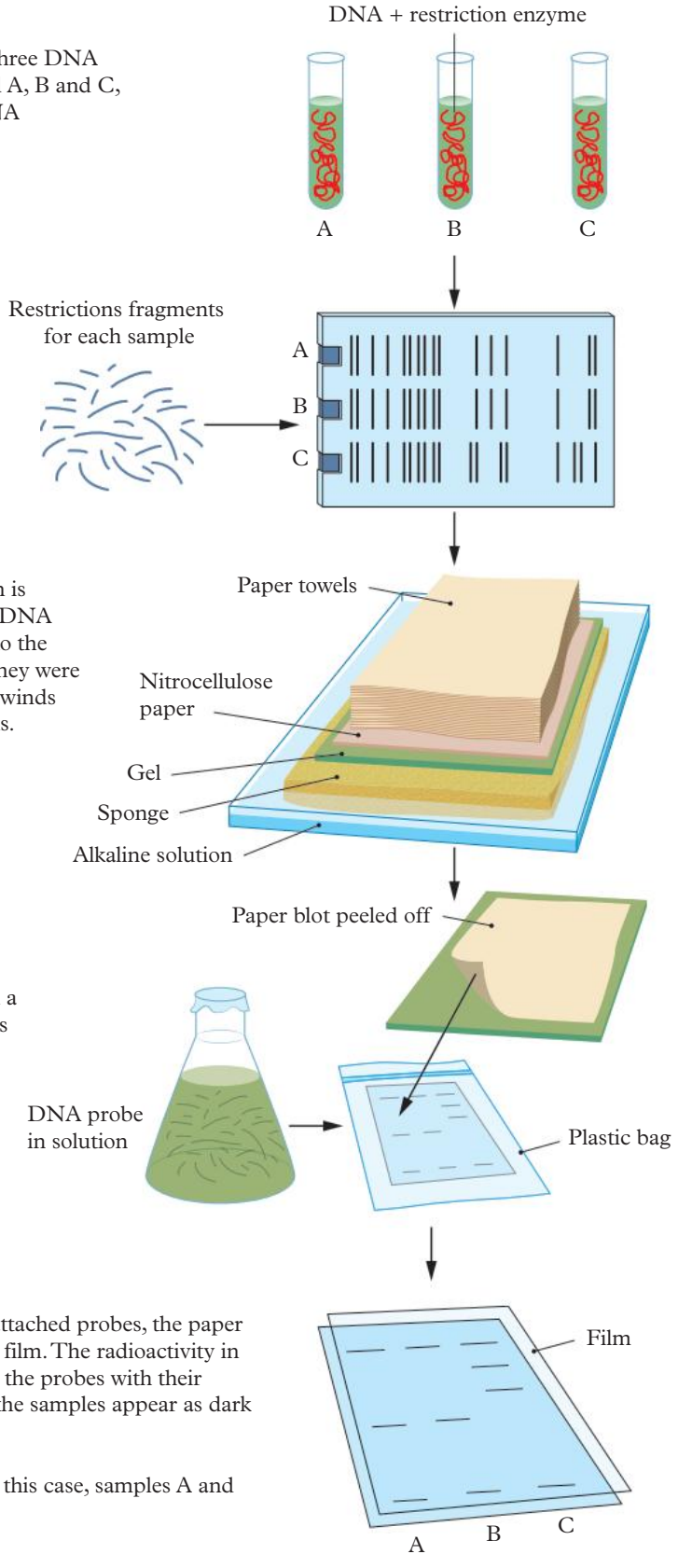


FIGURE 5 The steps in genetic profiling

This crime scene sample of DNA is then compared to that of a suspect (Figure 6). If all the STRs are matched, then it can act as evidence that the suspect has visited the crime location. It cannot, however, identify when the visit was made.

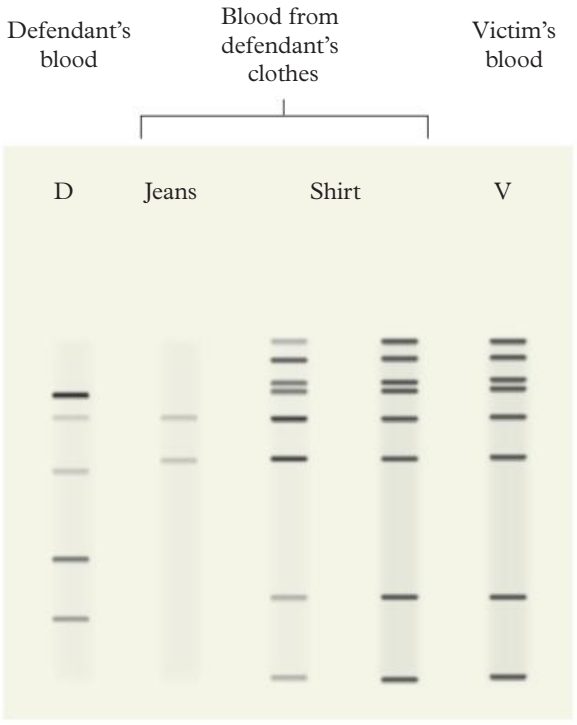


FIGURE 6 A DNA profile output. This DNA profile (fingerprint) shows that the blood on the defendant's clothes is that of the victim (V), not the defendant (D)

Skill drill

Interpreting DNA profiles

Science inquiry skill: Processing and analysing data (Lesson 1.7)

In a genetics lab, researchers are studying the genetic diversity of a population of plants. DNA samples from five plants (labelled A, B, C, D and E) were collected and analysed using gel electrophoresis. The researchers are interested in comparing the genetic variation between these plants by looking at the banding patterns produced from their DNA samples. A DNA ladder is used to estimate the size of the DNA fragments.

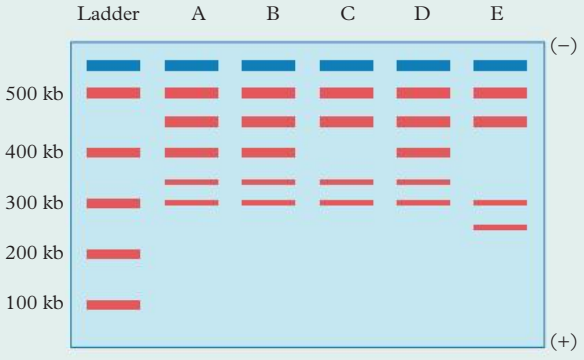


FIGURE 7 DNA profiles of the five plants

Practise your skills

1 **Identify** which plants show the most genetic similarity based on their banding patterns. (2 marks)
2 Based on the gel, **identify** which plant has the most unique genetic profile, giving reasons for your response. (2 marks)
3 **Determine** the length (bp) of the longest DNA fragment for Plant D. (1 mark)

Challenge

CRISPR-Cas9

CRISPR-Cas9 is gene-editing technology that allows precise modifications to an organism's DNA. It was adapted from a naturally occurring bacterial defence mechanism against viruses. For gene editing, the system is repurposed to target specific sequences in an organism's genome (e.g. human, plant or animal DNA). Scientists design a synthetic guide RNA that matches the target DNA sequence in the organism to be edited. The attached Cas9 protein acts as "scissors" to cut DNA at specific sites. CRISPR technology enables genes to be disabled, inserted or corrected, making it valuable in gene therapy, agriculture and research. However, there are concerns about "off-target" effects, where unintended genes may be edited, and ethical questions about editing the human germline, potentially altering future generations.

1 **Discuss** the potential benefits and risks of using CRISPR-Cas9 technology for treating genetic diseases. (3 marks)

2 **Propose** possible ethical implications of using CRISPR-Cas9 for human germline editing. (3 marks)

Check your learning 11.2

Check your learning 11.2: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** the key steps in the polymerase chain reaction. (3 marks)

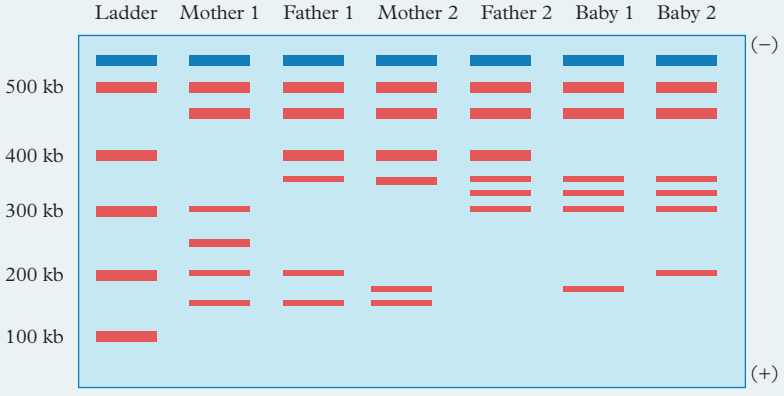
2 **Explain** the purpose of PCR. (2 marks)

3 **Describe** two applications of PCR. (2 marks)

4 **Define** "DNA profile". (1 mark)

Analytical processes

5 DNA samples are taken from two mothers, two fathers and two babies. The samples are analysed using gel electrophoresis, and the banding patterns are compared, to determine which baby belongs to which set of parents. The results are shown here.



a **Determine** the length of the longest fragment of Mother 2. (1 mark)

b Based on the gel electrophoresis results, **determine** which baby belongs to which parents, explaining your reasoning. (4 marks)

Practical

Lesson 11.3
Gel electrophoresis

oxforddigital **This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.**

Learning intentions and success criteria

MODULE 11

Lesson 11.4
Review: Biotechnology

Summary

11.1
- Recombinant DNA technology allows production of specific proteins or traits.
- Restriction enzymes cut DNA at specific recognition sites.
- Plasmids act as vectors to carry foreign DNA.
- DNA ligase joins DNA fragments by forming covalent bonds.

11.2
- PCR amplifies specific DNA regions for profiling and analysis.
- Gel electrophoresis separates DNA fragments by size to create banding patterns.
- Differences in DNA sequences lead to unique banding patterns that can be compared with other sequences.
- DNA ladders help interpretation of DNA fragment sizes in gel electrophoresis results.

11.3
- Practical lesson: Gel electrophoresis.

Review questions 11.4A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

1 The use or alteration of cells or biochemicals to provide a useful product is known as
- **A** transgenesis.
- **B** biotechnology.
- **C** gene targeting.
- **D** genetic modification technology.

2 Manufacturing recombinant DNA molecules involves cutting a gene from its normal location, inserting it into a circular piece of DNA from a bacterial cell, and then transferring it to cells of another species. Which tool is used to cut the gene from its normal location?
- **A** Vector
- **B** Plasmid
- **C** DNA ligase
- **D** Restriction enzyme

3 In genetic engineering, gene products are manipulated at the level of
- **A** DNA.
- **B** RNA.
- **C** proteins.
- **D** amino acids.

4 Restriction endonucleases are most widely used in recombinant DNA technology. They are obtained from
- **A** yeasts.
- **B** plasmids.
- **C** bacterial cells.
- **D** all prokaryotic cells.

5 The role of DNA ligase in creating recombinant DNA is to
- **A** amplify the DNA strand.
- **B** join DNA into a single strand.
- **C** cut DNA at specific locations.
- **D** add nucleotides to elongate the DNA strand.

6 Optimal cutting of target DNA by restriction enzymes produces
- **A** plasmids.
- **B** target sites.
- **C** sticky ends.
- **D** DNA polymerase.

7 A nucleic acid segment tagged with a radioactive molecule is called a
A clone. **B** probe.
C vector. **D** plasmid.

8 Taq polymerase is used for PCR because it
A serves as a selectable marker.
B cuts DNA at specific sequences.
C is used to ligate introduced DNA in recipient cells.
D functions at high temperatures without denaturing.

9 Gel electrophoresis is used for
A isolating DNA molecules.
B cutting DNA into fragments.
C separating DNA fragments by their size.
D constructing recombinant DNA by joining cloning vectors.

10 An electric current is applied during gel electrophoresis in order to
A denature the DNA.
B stain the DNA fragments.
C cut the DNA into smaller fragments.
D move the DNA fragments through the gel.

11 In order to amplify a DNA sample, the PCR mix must contain
A DNA primers.
B RNA polymerase.
C gel electrophoresis.
D restriction enzymes.

12 DNA fragments migrate towards the positive electrode in gel electrophoresis because they are
A hydrophobic.
B neutral in charge.
C positively charged.
D negatively charged.

13 The likelihood of a recombinant plasmid being successfully taken up by a bacterial cell is increased by
A reducing the temperature during the ligation reaction.
B removing antibiotic resistance genes from the plasmid.
C adding restriction enzymes directly to the bacterial culture.
D treating the bacteria with heat shock or chemical transformation agents.

14 The best explanation for why smaller DNA fragments migrate faster through the gel is that
A larger fragments are positively charged and move more slowly.
B smaller fragments are more strongly attracted to the negative electrode.
C smaller fragments experience less resistance when moving through the gel matrix.
D gel electrophoresis selectively slows down fragments with higher molecular weight.

15 A short tandem repeat (STR) inherited from the mother will differ from one inherited from the father, because
A STRs from the mother are typically longer.
B STRs are only inherited from mitochondrial DNA.
C STRs from the father are located in coding regions.
D each parent contributes a unique allele at a given locus.

Review questions 11.4A Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

16 **Describe** the processes involved in producing recombinant DNA. (4 marks)

17 **Describe** how gel electrophoresis contributes to DNA profiling in a forensic context. (3 marks)

18 **Describe** the purpose of genetic profiling. (2 marks)

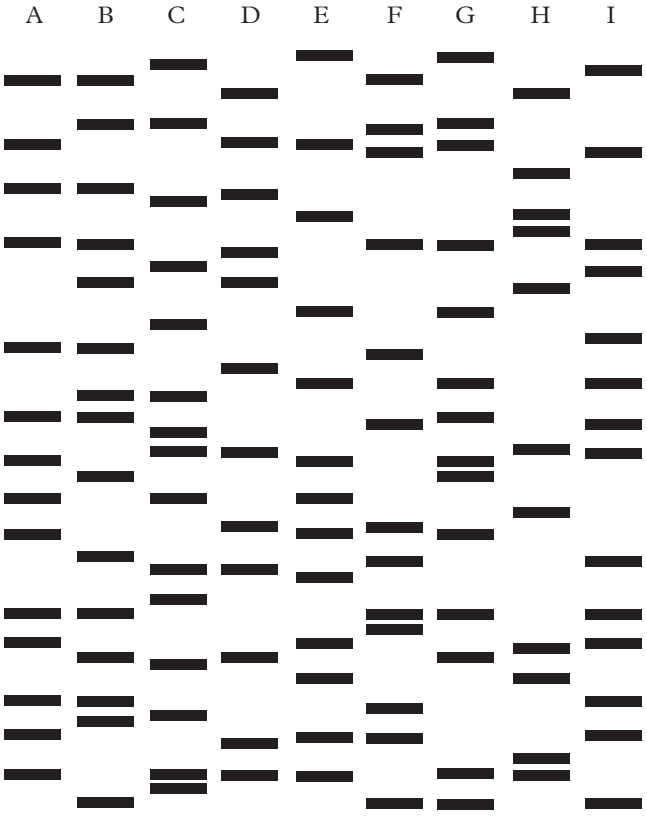
19 **Explain** why plasmids are suitable for use in recombination experiments. (2 marks)

20 **Explain** why it would be especially vital to use a positive control for a PCR analysis. (2 marks)

Analytical processes

21 **Compare** a plasmid with bacterial chromosomes. (2 marks)

22 Shown below is the DNA fingerprint of a girl (A), her parents, her sister and a number of other individuals, two of whom are brothers and are unrelated to the girl's family. Any band present in the DNA fingerprint of a child must also be present in at least one of the parents.

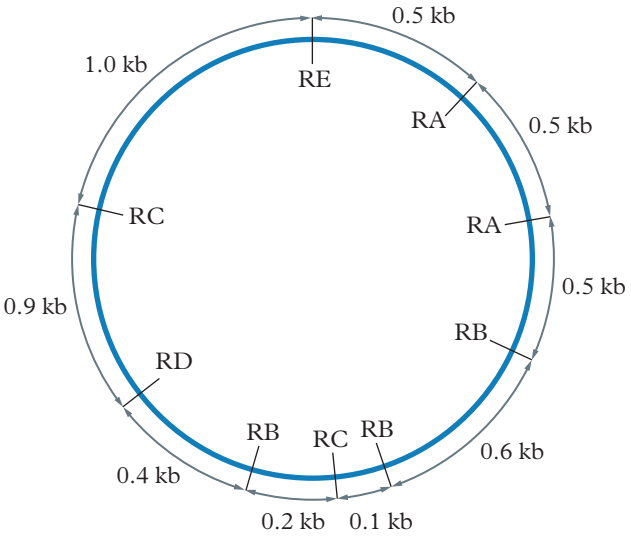


Determine:

a the parents of the girl (A) (1 mark)

b the girl's sister. (1 mark)

23 A scientist wants to cut a bacterial plasmid into five pieces, each of a particular base length (kilobase = kb). She has five restriction nucleases available (RA, RB, RC, RD and RE). The diagram shows how a plasmid 4.7 kb in length can be cut by these five restriction enzymes.



Analyse the data to determine which three enzymes she could use to obtain the five pieces of DNA, of lengths 1.5 kb, 1.2 kb, 0.9 kb, 0.6 kb and 0.5 kb. **Explain** your answer. (4 marks)

Data drill

Using gel electrophoresis data to determine genetic predispositions

Coeliac disease, an autoimmune disorder triggered by the ingestion of gluten, is strongly linked to genetic factors, particularly the presence of specific alleles in the HLA-DQ2 and HLA-DQ8 genes. PCR can be a useful tool for determining genetic predisposition to coeliac disease. PCR is used to amplify particular DNA regions associated with the HLA-DQ2 and HLA-DQ8 alleles. Primers complementary to these gene regions are added to target them specifically. The amplified DNA is analysed to detect the presence of HLA-DQ2 and/or HLA-DQ8 alleles. Individuals lacking both alleles are unlikely to develop coeliac disease, whereas those with the alleles have a genetic predisposition, though not all will develop the condition.

A laboratory is testing three patients (patient A, patient B and patient C) for genetic predisposition to coeliac disease. The HLA-DQ2 and HLA-DQ8 alleles associated with coeliac disease have been amplified using PCR and analysed using gel electrophoresis. The results of the gel electrophoresis of the DNA amplified using PCR are shown in the table.

Lane	1	2	3	4	5	6
Sample	DNA ladder	Patient A	Patient B	Patient C	Positive control (HLA-DQ2, HLA-DQ8 alleles)	Negative control (no alleles)
Visible band lengths (bp)	100, 200, 300, 400	200, 300	200	No bands visible	200, 300	No bands visible

Apply understanding

1 **Identify** which alleles are present for each patient, based on the gel results. (3 marks)

Analyse data

2 **Determine** which patient(s) have a genetic predisposition to coeliac disease, justifying your response. (2 marks)

Interpret evidence

3 **Comment** on the purpose of the positive and negative controls in this analysis. (2 marks)

4 **Discuss** one potential limitation of using PCR and gel electrophoresis alone for diagnosing coeliac disease. (2 marks)

Module 11 checklist: Biotechnology

UNIT 4

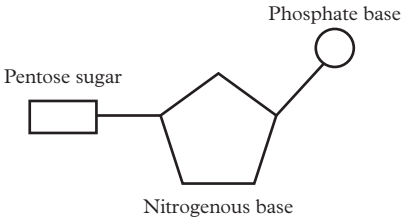
Topic 1 review

Multiple choice

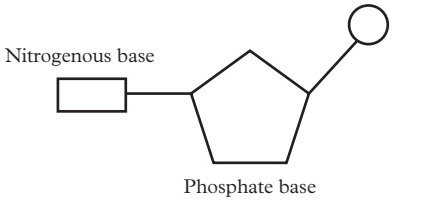
(1 mark each)

1 Identify the correct structure of a nucleotide.

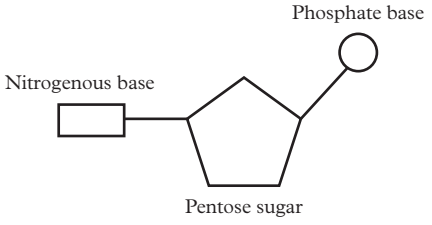
A



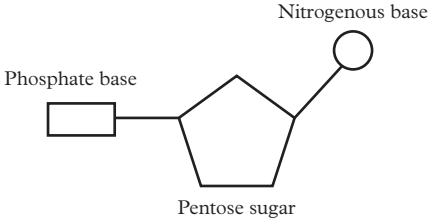
B



C



D



2 Determine the genotype and phenotype ratios for the cross BB × Bb (B = black, b = white)

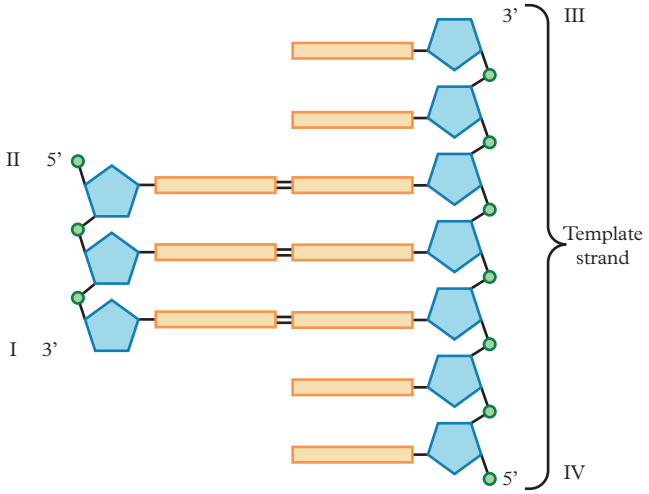
A genotype: 100% homozygous dominant; phenotype: all black

B genotype: 50% homozygous dominant, 50% heterozygous; phenotype: all black

C genotype: 50% homozygous dominant, 50% heterozygous; phenotype: all white

D genotype: 50% homozygous dominant, 50% heterozygous; phenotype: 50% black, 50% white

3 The diagram below shows a DNA molecule being replicated. Identify where DNA polymerase would attach the next nucleotide.



A I **B** II **C** III **D** IV

4 In red pandas, there are 36 chromosomes in each autosomal cell. Determine the number of chromosomes in the sperm cell of a red panda.

A 13 **B** 18 **C** 36 **D** 72

5 A segment of DNA undergoes a block mutation in which the segment is turned back to front and reintegrated into the chromosome. This type of block mutation is an example of

A deletion.

B inversion.

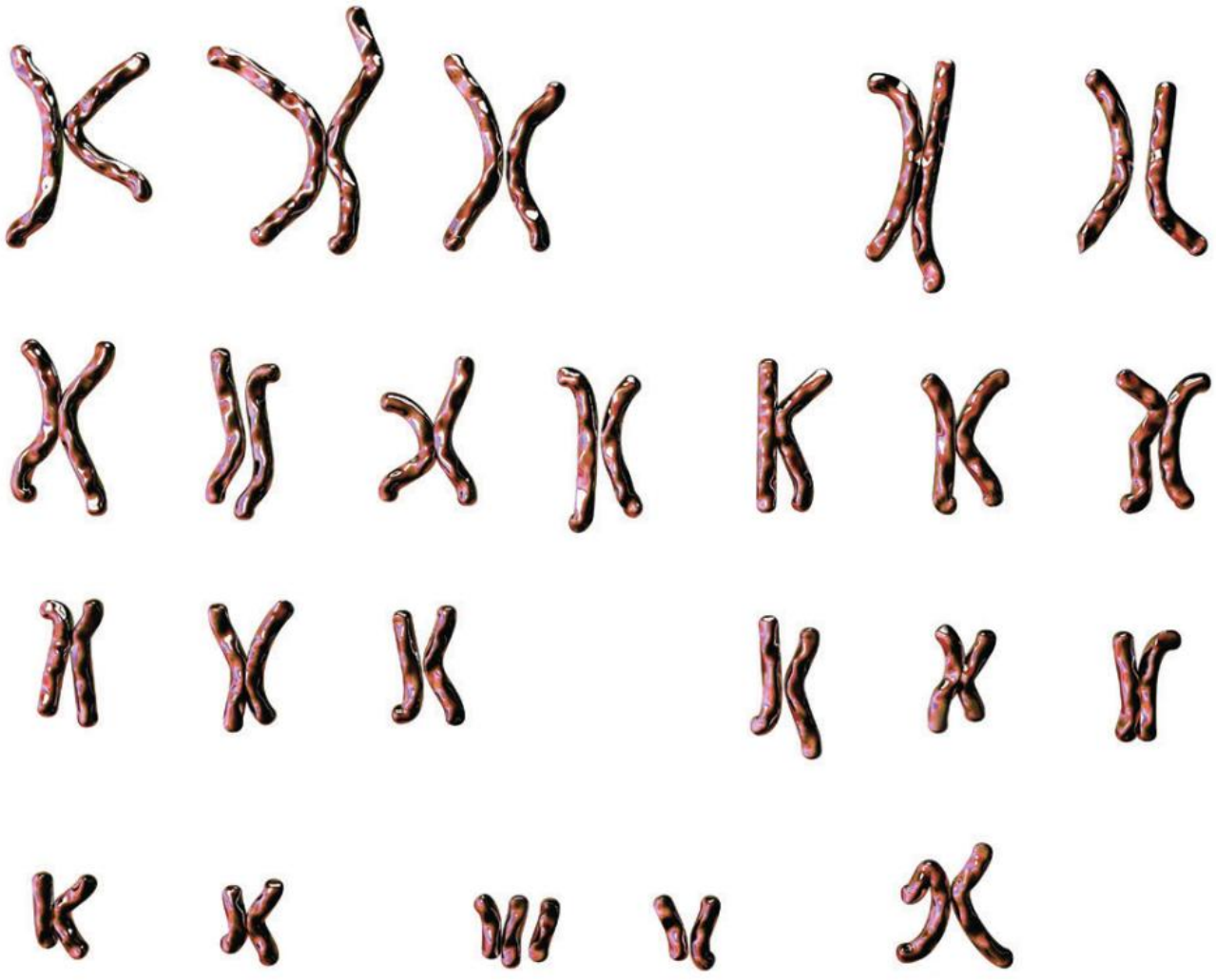
C duplication.

D translocation.

6 The table shows a list of genetic conditions.

Genetic condition	Common name
Monosomy X	Turner syndrome
Monosomy 5	Cri-du-chat syndrome
Trisomy 18	Edwards syndrome
Trisomy 21	Down syndrome

Use the information in the table to identify the genetic condition depicted in the karyotype shown below.



A Down syndrome

C Edwards syndrome

B Turner syndrome

D Cri-du-chat syndrome

7 Epigenetic factors have been found to influence the expression of genes in various ways. Some types of epigenetic factors control the replication of DNA by binding to the tails of a histone protein. These epigenetic factors affect DNA replication by
- **A** inhibiting the unwinding of DNA.
- **B** binding to DNA and "unzipping"' it.
- **C** accelerating the unwinding of DNA.
- **D** repairing DNA mutations during replication.

8 The role of mRNA in protein synthesis is to
- **A** carry amino acids to the ribosome.
- **B** store genetic material in the nucleus.
- **C** replicate the DNA strand during cell division.
- **D** deliver genetic instructions from DNA to ribosomes.

9 Sex-linked traits are more common in males because
- **A** females have fewer sex-linked genes.
- **B** males inherit traits from only one parent.
- **C** the Y chromosome carries more genes than the X chromosome.
- **D** males have only one X chromosome, so recessive alleles are expressed.

10 In recombinant DNA technology, DNA ligase is used to
- **A** cut DNA at specific restriction sites.
- **B** amplify the DNA fragments of interest.
- **C** join DNA fragments by forming covalent bonds.
- **D** separate DNA fragments in gel electrophoresis.

11 Short tandem repeats (STRs) are useful in DNA profiling because they are
- **A** identical across all individuals.
- **B** inherited only from the mother.
- **C** highly variable between individuals.
- **D** found only in coding regions of DNA.

12 Non-coding DNA can block the trimming, capping and tailing of mRNA, leaving it vulnerable to degradation by enzymes. This controls the amount of protein produced. This type of control is described as
- **A** epigenetic control.
- **B** translational control.
- **C** pre-transcriptional control.
- **D** post-transcriptional control.

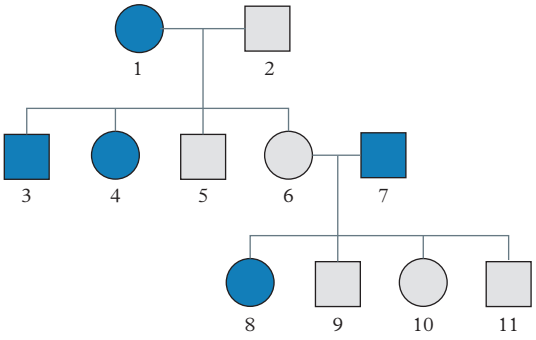
13 Polygenic inheritance occurs when
- **A** alleles are incompletely dominant.
- **B** multiple genes influence a single trait.
- **C** a single gene influences multiple traits.
- **D** a gene is located on a sex chromosome.

14 During meiosis, independent assortment contributes to genetic diversity by
- **A** mutating alleles to create new traits.
- **B** duplicating DNA to produce identical chromatids.
- **C** crossing over between homologous chromosomes.
- **D** randomly aligning homologous pairs during metaphase I.

15 During the polymerase chain reaction (PCR), denaturation occurs when
- **A** DNA is heated to separate strands.
- **B** primers anneal to the DNA template.
- **C** DNA fragments are separated by size.
- **D** DNA polymerase extends the new strand.

Short response

16 The pedigree below depicts the inheritance of a disorder across three generations.



- **a** **Determine** the mode of inheritance for the disorder, using evidence from the pedigree and a Punnett square to justify your response. (4 marks)
- **b** **Infer** the genotype of individual 1, explaining your reasoning. (2 marks)

17 **Define** the term "allele". (1 mark)

18 **Explain** the role of *HOX* genes in regulating body morphology. (3 marks)

19 **Explain** the process of protein synthesis in terms of transcription and translation. (4 marks)

20 A man who is heterozygous for blood type A (I^A allele and i allele) fathers a child with a woman who is heterozygous AB (I^A and I^B alleles). **Predict** the possible genotypes and phenotypes of any offspring. (4 marks)

21 Scientists use recombinant DNA technology to produce genetically modified organisms (GMOs). **Describe** the process of creating recombinant DNA, including the roles of restriction enzymes and DNA ligase. (4 marks)

22 **Explain** the process of RNA processing prior to translation during protein synthesis. (4 marks)

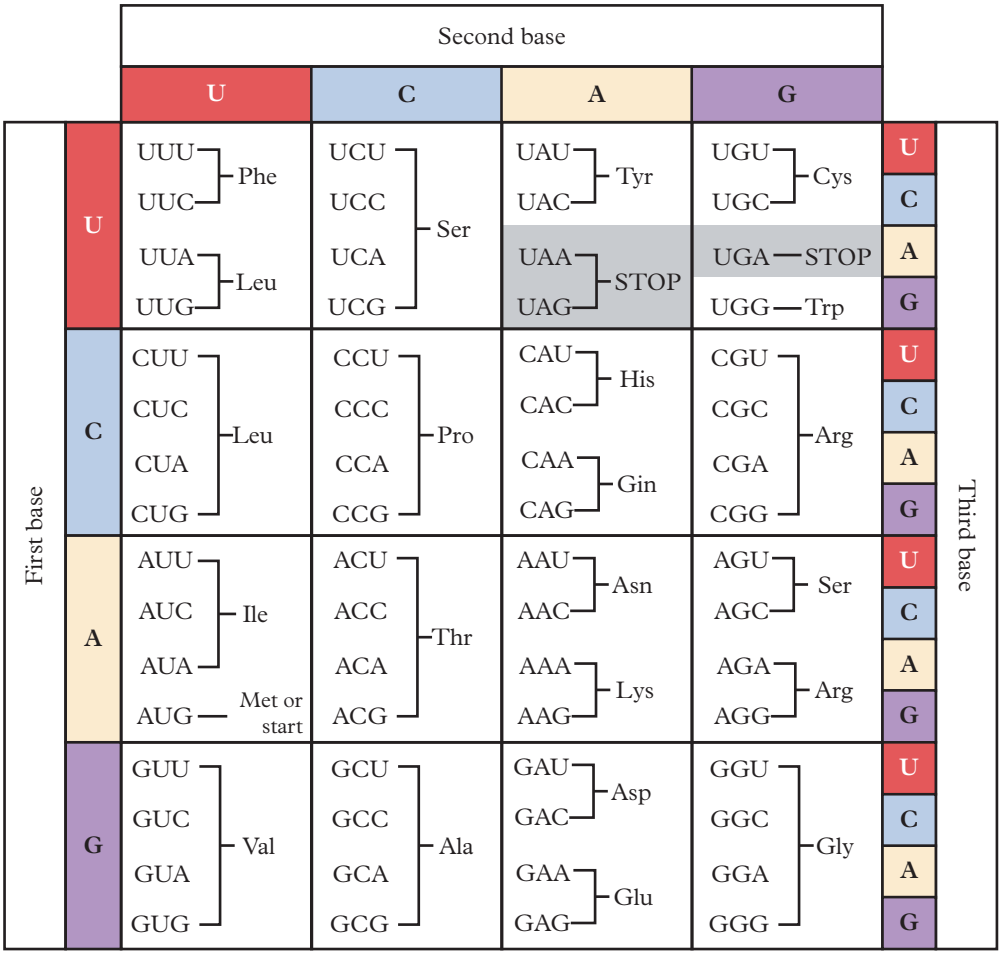
23 **Describe** how environmental factors such as UV radiation can cause mutations in DNA. (2 marks)

24 The table shows a segment of DNA coding for a gene before and after a mutation has occurred.

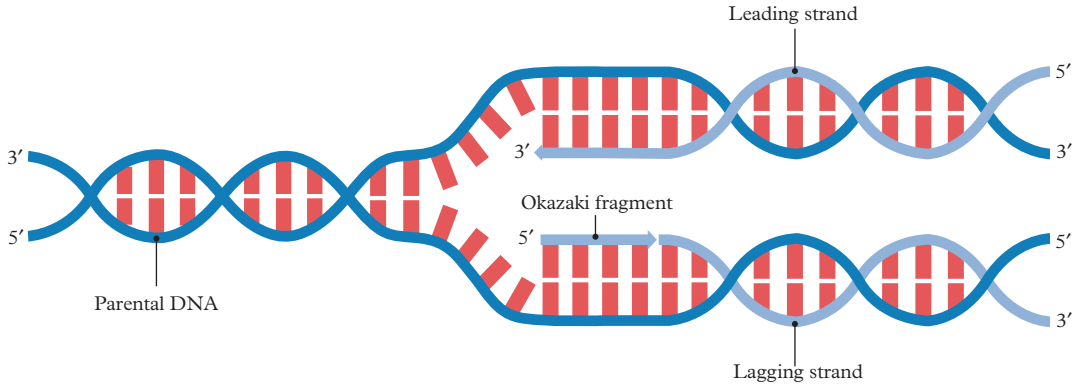
Original code	TACATGTTGTGCCAAATT
Altered code	TACATGTTCTGCCAAATT

a **Determine** the type of mutation that has affected this sequence, giving reasons to support your response. (2 marks)

b If the last thymine base were mutated to an adenine, **describe** the effect this would have on the amino acid sequence transcribed by this gene. (2 marks)



25 The diagram below depicts a segment of DNA being replicated.

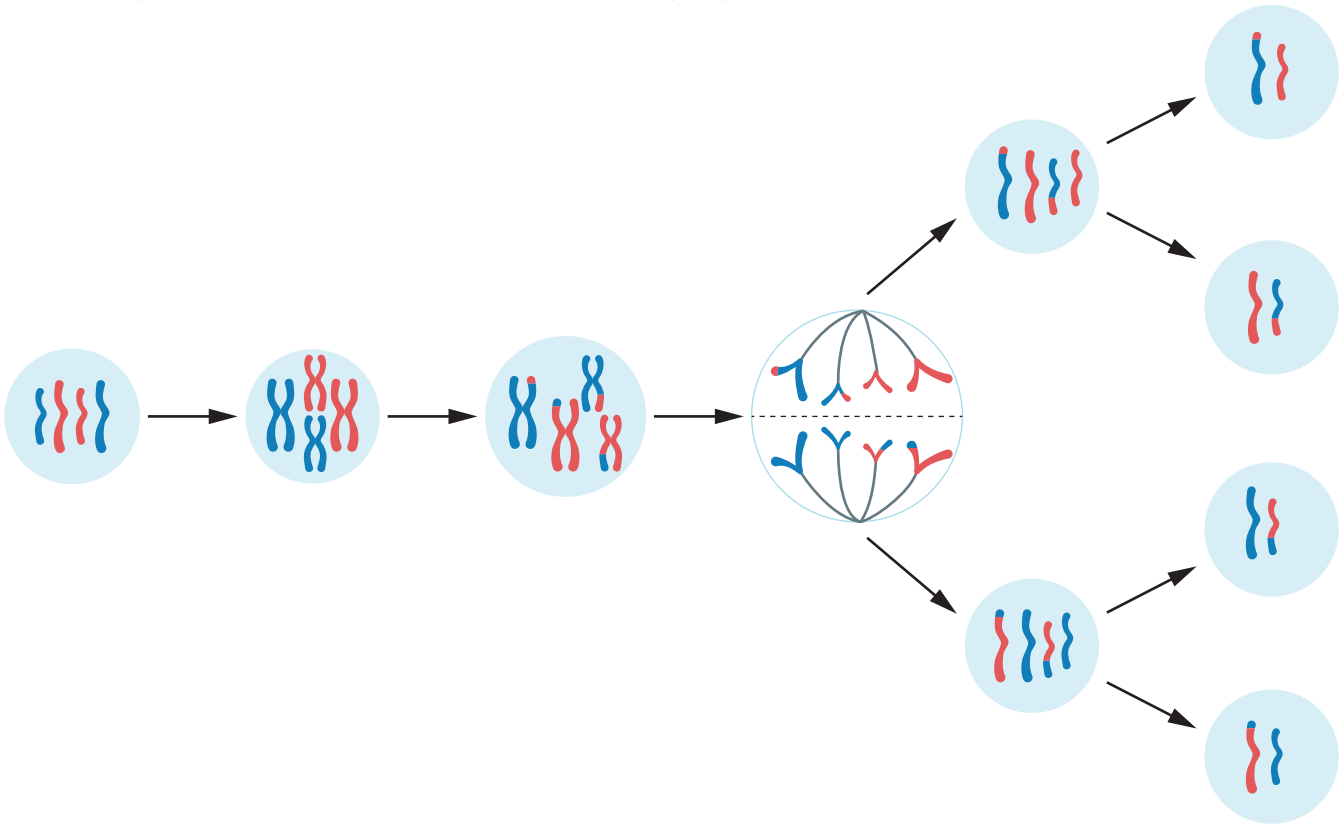


a **Describe** the structure of DNA in the nucleus of a eukaryote. (2 marks)

b **Describe** the roles of the enzymes helicase, DNA polymerase and ligase in DNA replication. (3 marks)

c **Explain** how errors in replication can result in mutations. (2 marks)

26 The diagram below shows the nucleus of a cell undergoing meiosis.

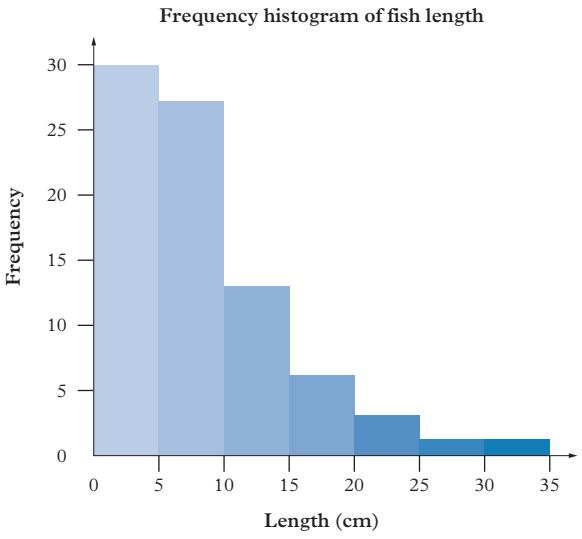


a **Compare** the processes of spermatogenesis and oogenesis. (2 marks)

b **Describe** how crossing over and independent assortment contribute to the genetic diversity of offspring. (4 marks)

c **Predict** the consequences of a non-disjunction event occurring during meiosis I on the resulting gametes. (2 marks)

27 The histogram below depicts the frequency of fish length in a population of whitebait (*Galaxias maculatus*). The continuous variation of body length in whitebait is controlled by three genes – A, B and C. The more recessive alleles the fish inherits for these genes, the shorter its body length.



a **Identify** the inheritance pattern that contributes to the trait of body length in whitebait. (1 mark)

b Using the histogram, **infer** the most common genotype in this population of whitebait. (2 marks)

c **Predict** the length of a whitebait with the genotype AabbCC. (1 mark)

28 **Explain** how chemical modifications of histones influence chromatin structure and gene activation. (4 marks)

29 Sickle cell anaemia is caused by a mutation in the HBB gene, which encodes the beta-globin subunit of haemoglobin. The wild-type allele (H) is dominant, and the mutated allele (h) is recessive. The mutation in sickle cell anaemia is typically a single point mutation, but frameshift mutations can also occur in the same gene.

a **Construct** a Punnett square to determine the possible genotype and phenotype frequencies of offspring if both parents are carriers of the sickle cell trait. (4 marks)

b **Explain** how the point mutation in the HBB gene leads to the production of a dysfunctional protein. (3 marks)

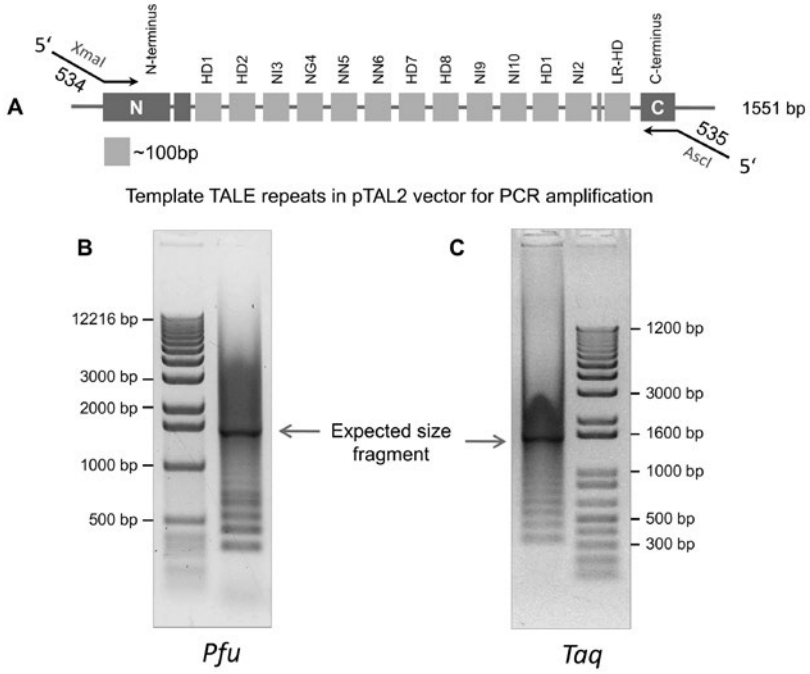
c **Compare** the effects of the point mutation causing sickle cell anaemia with a potential frameshift mutation in the HBB gene on protein structure and function. (2 marks)

30 The image shows a DNA profile generated using PCR for a target DNA fragment.

a **Describe** the role of PCR in DNA profiling. (2 marks)

b **Identify** the length of the target fragment in base pairs (bp). (1 mark)

c **Explain** how gel electrophoresis separates DNA fragments. (3 marks)



TOTAL MARKS

/85

MODULE 12

Evolution

Introduction

All living things that exist on Earth today are here as a result of their ancestors' survival over billions of years. Thanks to their ancestors' resilience and adaptations, each species has physical and behavioural traits that make it suited to surviving in its environment. Each species forms a population of individuals who are able to reproduce together to produce viable and fertile offspring. This population has a common gene pool that can be shared among the individuals of that species. Different patterns of evolution result in speciation, the emergence of a new species.

Prior knowledge

Prior knowledge quiz

Check your understanding of concepts related to evolution before you start.

Subject matter

Science understanding

→ Distinguish between microevolution and macroevolution.
→ Explain microevolutionary change through the main processes of mutation, gene flow and genetic drift.
→ Explain why populations with reduced genetic diversity face increased risk of extinction.
→ Explain natural selection and identify the three main types of phenotypic selection: stabilising, directional and disruptive.
→ Calculate allele frequencies from genotype data.
→ Analyse data to determine the effect of a selection pressure on a population, recognising that selection for an allele can be positive or negative.
→ Describe how macroevolutionary changes result from the accumulation of microevolutionary changes using examples of divergent, convergent, parallel and coevolution.
→ Explain how geographic, temporal and spatial isolation influence gene flow and may lead to allopatric, sympatric and parapatric speciation.

Science inquiry

→ Analyse genotypic changes for a selective pressure in a gene pool (laboratory work or computer simulation).
→ Investigate how different selection pressures (e.g. human activities, changes in climate) are affecting evolution

Practicals

oxforddigital **These lessons are available on Oxford Digital.**

Lesson 12.5 Changes in the gene pool due to selection pressure

Lesson 12.1
Microevolution and macroevolution

Key ideas

- → Evolution explains the physical and behavioural characteristics of all life on Earth, including development of each species from its ancestors over billions of years.
- → Natural selection acts on the phenotype of an organism and selects for the traits most suited to the environment at that point in time.
- → Microevolution is a change in allele frequency within the population of a species.
- → Macroevolution is the accumulation of microevolutionary changes that results in a new species.

Learning intentions and success criteria

Darwin's theory of evolution

Charles Darwin's **theory of evolution by natural selection** was based on his observations of the natural world, and experiments he conducted. Darwin found:

- Within a population there is variation in physical form (traits).
- Individuals with traits that make them better suited to their environment are more likely to survive to reproduce. Those that are less suited do not survive. This process is known as **natural selection** (or "survival of the fittest").
- The traits that give an individual its survival advantage are inherited by its offspring.
- These traits accumulate over many generations, making the population more "specialised", eventually resulting in a new species.

Darwin was not able to explain how advantageous traits were passed on from one generation to the next. Modern evolutionary theory explains it in genetic terms.

theory of evolution by natural selection the theory, originally proposed by Charles Darwin, that all species of organisms arise and develop through a process known as natural selection, whereby small, inherited variations in individuals increase their ability to compete, survive and reproduce, and these variations are passed on to the next generation

natural selection a mechanism of evolution in which species selectively reproduce, resulting in genotypic changes

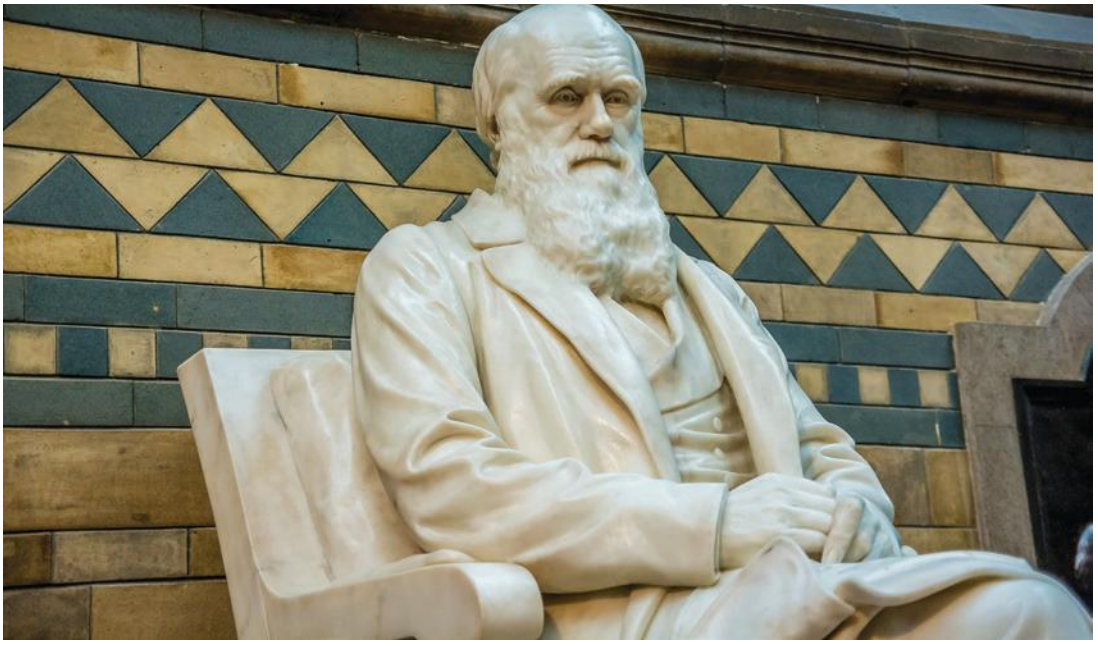


FIGURE 1 Edgar Boehm's marble statue of Charles Darwin at the Natural History Museum in London

Modern evolutionary theory

Phenotypic variation exists within a population. Selection pressure from the environment selects *for* the "fittest" individuals (those with advantageous phenotypes), who have a better chance of surviving to reproductive age and passing on their advantageous alleles to the next generation. Disadvantageous phenotypes are selected *against*, so individuals with these phenotypes often die before reaching reproductive age, and therefore their genes are not passed on to the next generation. This process of natural selection leads to more robust individuals within the population that can survive in their environment.

Modern evolutionary theory defines evolution as change that occurs in the genes of a population during successive generations, which may result in the development of a new species. This means:

- Organisms produce far more offspring than can possibly survive.
- Organisms have a variety of phenotypes.
- Many variations within an organism are controlled by genes.
- Natural selection keeps species adapted to their environment.
- New species may arise by isolation of populations with different selection pressures.

Evolutionary studies tend to focus on the variations of genes within a population (known as the **gene pool**). **Microevolution** is the study of small-scale variations in gene frequency within a species or a population, with descendants being in the same taxonomic group as their ancestors. Conversely, **macroevolution** is the study of variations in allele frequencies at or above the level of species over geological time. These variations result in the divergence of taxonomic groups, with descendants being in a different taxonomic group than their ancestors.

gene pool
all alleles for every gene in a population at a given point in time

microevolution
the change in allele frequencies within a population over a short period; does not result in a new species but genetic change within a species

macroevolution
evolutionary change at or above the species level resulting from the accumulation of microevolutionary changes

Check your learning 12.1

Check your learning 12.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Explain** how microevolutionary changes contribute to the evolution of a new species. (2 marks)

2 **Describe** three of the main observations or ideas on which the theory of evolution by natural selection is based. (3 marks)

3 According to modern evolutionary theory, **explain** how the sources of variation arise. (3 marks)

Analytical processes

4 **Contrast** microevolution and macroevolution. (2 marks)

5 The largest antler span of any living animal belongs to a species of moose. The male's antlers have a span of about three metres. **Determine** how Darwin might have explained the enormous antlers of this species. (3 marks)

6 Darwin recognised the existence of variation and the fact that variations are inherited. However, he knew nothing about genetics. **Describe** how the following support his theory:

- **a** knowledge of the inheritance of characteristics (1 mark)
- **b** events of mitosis, meiosis and fertilisation (2 marks)
- **c** mutation and crossing over of chromatids (2 marks)
- **d** the role of DNA. (2 marks)

Lesson 12.2
Microevolutionary changes

Key ideas

- → The main drivers of microevolution are mutation, gene flow and genetic drift.
- → A genetic bottleneck occurs when a large percentage of a population is wiped out, reducing the variation of alleles in the gene pool.
- → Genetic bottlenecks reduce the genetic diversity of a population, leaving the population vulnerable to extinction.

Learning intentions and success criteria

Microevolution

Microevolution is the change in allele frequency of a population over a short period of time. Microevolutionary changes accumulate to produce macroevolution, or the emergence of a new species over a long period of time.

Through natural selection, individuals with phenotypes better suited to the environment at that time survive and reproduce, while individuals with less-suited phenotypes are less likely to reproduce. Because individuals with viable phenotypes are likely to increase in number, the beneficial alleles they carry also increase in the population. Through this process of natural selection, favourable alleles are increased in the gene pool, and non-beneficial alleles are decreased. This change in allelic frequency results in microevolution of the population.

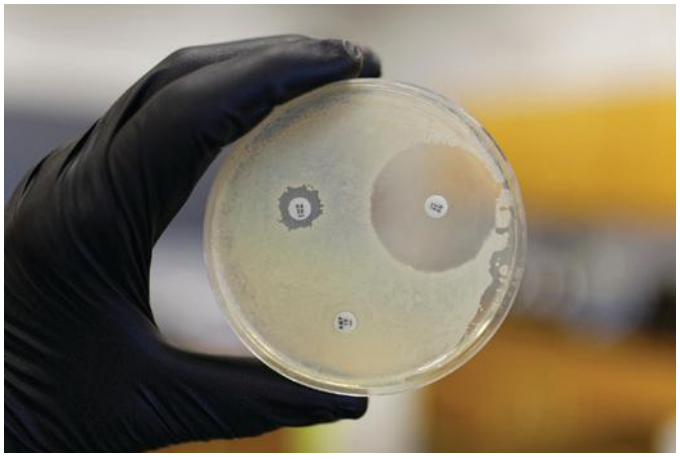


FIGURE 1 Antibiotic resistance is an example of microevolution

Natural selection can have both positive and negative effects on a species over a long period of time. Because natural selection acts on the phenotypes of the members of a population, favouring those phenotypes that best suit the environment at a particular time, this can lead to the population losing alleles that might have been useful in different environmental conditions. A reduction in allele variation like this can leave organisms at a disadvantage if environmental conditions change.

Mutations

Genetic equilibrium is disturbed by selection pressures when these pressures increase the frequency of alleles that are better suited to the environment. In sexually reproducing populations, selection determines the direction of change, largely by altering the frequencies of alleles that arose originally through random mutation many generations before. Through mutation, new allele combinations and allele activities that produce new phenotypes are established. A key role of new mutations is to increase variability in the gene pool. This provides the variation upon which future natural selection will act. These mutations may be important for the survival of the species in a changing environment and may lead to a dramatic change in the gene pool as a result of natural selection.

Gene flow

Individuals within some animal populations interact and breed with other, nearby populations of the same species, causing alleles to be introduced from one population to another. This movement of alleles into or out of a population is termed **gene flow**. Fish, and many other aquatic animals that are external fertilisers, experience gene flow when their gametes float freely in the water and can move between geographically separated populations. Gene flow also occurs in plants, as pollen can be transferred between populations through wind dispersal or through pollination by birds or insects. Immigration or emigration leads to a gain or a loss of alleles in the population. Most natural populations usually experience a small amount of migration, which enhances variation and changes the genetic equilibrium. However, genetic equilibrium is maintained in some populations if no migration, or an insignificant amount, occurs.

gene flow
the movement and exchange of alleles between populations of a species

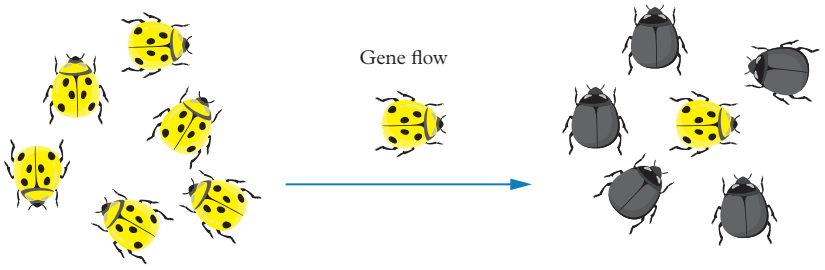


FIGURE 2 Genetic material moving into a population through gene flow

Genetic drift

Small populations of a species are susceptible to random and sudden changes in the gene pool, sometimes resulting in the loss of an allele from the population. If a sudden catastrophic event occurs, such as a volcanic eruption or forest clearing, all individuals carrying a particular gene may be killed. The absence of this allele in the population stops it being passed on to future generations and can change evolutionary patterns in a short time period. Additionally, an existing allele's frequency may increase in the gene pool following a chance event. For example, if most of the surviving individuals of a population carry a specific allele, it is likely that this allele's frequency will increase, which may then contribute to an increase in the allele's frequency in future generations. Both these processes of sudden change to the gene pool of a population are called **genetic drift**. Unlike gene flow, which is the introduction of a new allele or the loss of an existing allele, genetic drift refers exclusively to a change in the frequency of existing alleles that occurs following a chance event.

genetic drift
changes to the frequency of existing alleles within a gene pool, caused by chance

A research project was undertaken in South Australia to study the frequencies of alleles of a gene controlling an enzyme in the heart and the kidney, in thirteen populations of bush rats (*Rattus fuscipes greyi*, Figure 3). This research revealed that small, isolated island populations tended to be homozygous for one or the other allele, whereas the mainland populations exhibited both allelic forms. This genetic drift in the island forms could ultimately lead to their demise, because a population is at risk if the environment changes when there is a low level of genetic variation.

FIGURE 3 *Rattus fuscipes greyi*, the bush rat

Founder effect

founder effect
reduced genetic diversity as a result of a population having descended from a small number of colonising ancestors

The **founder effect** is a cause of genetic drift that results from a small subgroup within a "parent" population colonising a new area. Because this subgroup may not be genetically representative of the original parent population from which it was derived, it will have a limited number of alleles in its population (Figure 4). As the small population increases in size, there will be continued drift that is different from that of the parent population.

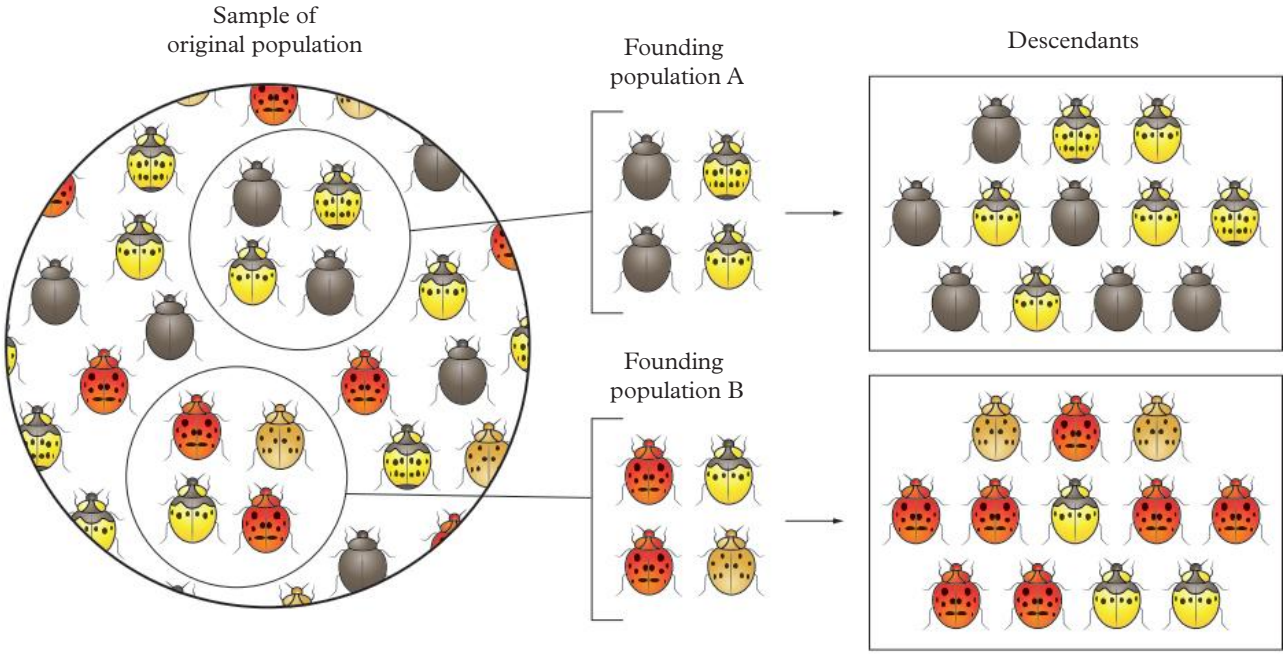


FIGURE 4 An example of the founder effect, where populations A and B have less genetic diversity than the original population

Population bottleneck

population bottleneck
a significant reduction in genetic diversity of a population, caused by a sudden and drastic reduction of that population

Changes in allele frequency caused by genetic drift have a disproportionately large effect on small populations. In a large population, there are more individuals to balance out random allele increases or decreases. When a large population of a species rapidly decreases in number, leaving a much smaller population, the remaining alleles have a disproportionately large effect. Rapid reductions in population may be caused by sudden environmental changes, such as bushfire or flooding – this process is called a **population bottleneck**. When the population recovers in number, it does so with increased homozygosity (a greater proportion of homozygotes) and a reduction in genetic diversity (Figure 5). This decrease in variation of available alleles means the population is vulnerable to future changes in the environment and at increased risk of extinction.

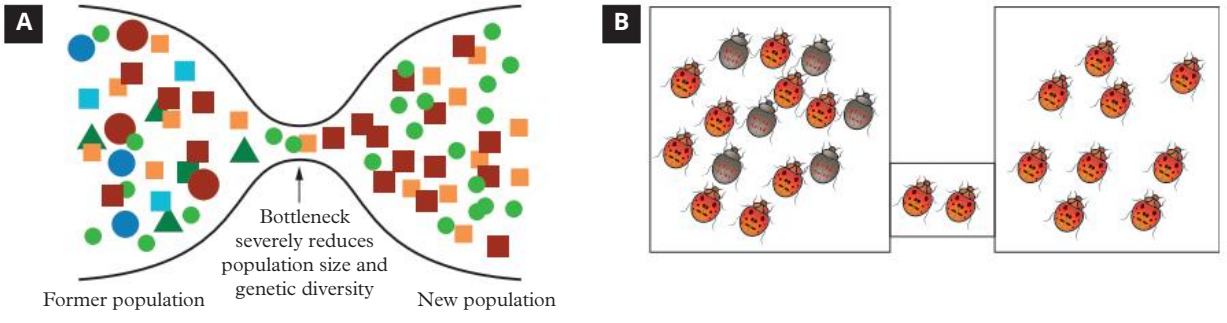


FIGURE 5 An evolutionary bottleneck: (A) the effect on alleles; (B) the effect on phenotypes

The extinction of Tasmanian devils (*Sarcophilus harrisii*) on mainland Australia more than 3,000 years ago caused a population bottleneck in the surviving island population. This smaller population had a limited variety of alleles to pass on to offspring, increasing the similarity of the gene pool of the devils in the time since then. As a result of this population bottleneck, the devils in Tasmania today are genetically similar, with very similar protein markers on their cells. This results in their vulnerability to a mouth cancer called devil facial tumour disease, which is spread by biting during mating or fighting (Figure 6). Because of the similarity of the protein markers, their immune systems do not recognise the cancer cells as foreign, and the disease spreads.

FIGURE 6 A Tasmanian devil with a facial tumour that its immune system does not recognise, due to a population bottleneck that occurred around 3,000 years ago

Skill drill

Interpreting population graphs

Science inquiry skill: Processing and analysing data (Lesson 1.7)

The graph in Figure 7 shows the population size of a species before and after a bottleneck event.

Practise your skills

1 Copy the graph and **identify** the point where the bottleneck event occurred. (1 mark)

2 **Explain** how the bottleneck event is likely to have affected the allele frequencies in the recovering population. (2 marks)

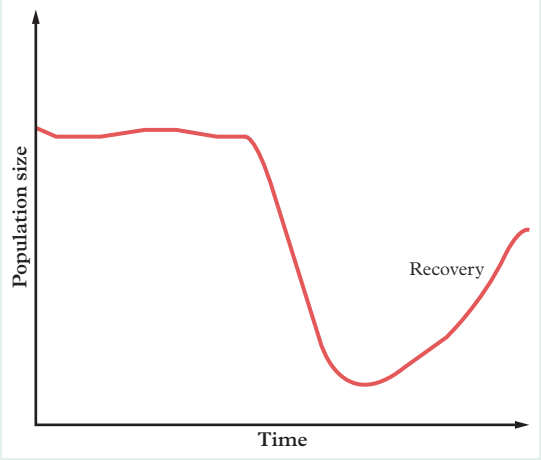


FIGURE 7 Change in population size caused by a bottleneck event

Challenge

The population bottleneck of greater prairie chickens

Greater prairie chickens are birds from the grouse family that live in the grasslands of the USA. They have become critically endangered due to habitat loss caused by widespread repurposing of grasslands for agriculture in the early 1900s. As a result, greater prairie chickens experienced a population bottleneck, significantly reducing their genetic diversity.

1 **Explain** how the population bottleneck has caused a lack of genetic diversity several generations later, in today's populations of greater prairie chickens. (3 marks)

2 **Describe** the role played by genetic drift, when genetic diversity is reduced by a population bottleneck. (2 marks)

FIGURE 8 A male greater prairie chicken inflates the orange air sac on the sides of its head as part of a mating ritual

Check your learning 12.2

Check your learning 12.2: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Explain** the founder effect. (3 marks)
2 **Define** "microevolution". (1 mark)
3 If natural selection acts on individuals, **describe** how this results in changes to the allelic frequencies of a population. (2 marks)
4 **Explain** how natural selection could have a negative effect on a population. (3 marks)
5 **Explain** how genetic drift occurs. (3 marks)

Analytical processes

6 **Contrast** "gene flow" and "genetic drift". (1 mark)

Lesson 12.3
Natural selection

Key ideas

- → Natural selection acts on the phenotypes of organisms and selects the most suitable phenotype for survival in the environment at that time.
- → Genetic mutations occur spontaneously and randomly, and may be neutral, advantageous or disadvantageous.
- → Stabilising selection occurs when an environment is stable for a long period of time and the mean phenotype remains the same, while the phenotypic range becomes narrower.
- → Directional selection occurs when a phenotype at one end of the distribution is selected for, and over time the mean phenotype shifts.
- → Disruptive selection occurs when the mean phenotype is selected against, and alleles at the extremes of the phenotypic distribution are advantageous.

Learning intentions and success criteria

Natural selection

Natural selection is the mechanism of evolution and acts directly on the phenotypes of organisms. Genetic mutations cause variability in the genotype and, therefore, the phenotypic traits of a population. Phenotypic traits are "selected for" if they give an individual an advantage that enables it to survive to reproductive age, so it can reproduce and pass on its advantageous traits to its offspring. Natural selection relies on variation in the phenotypes of a population. Individuals with advantageous traits survive and are able to contribute their advantageous alleles to the gene pool. Individuals without the advantageous alleles are less likely to survive, and therefore their disadvantageous alleles gradually decrease in frequency in the population's gene pool. This is why natural selection is often described as "survival of the fittest" – the fittest organisms are those with alleles that increase their chances of survival and reproduction.

An individual with advantageous phenotypic traits is more likely to survive; this ability to survive; and reproduce is called **viability**. An organism is viable if it is likely to survive to reproductive age and produce offspring. These viable traits are passed on to the offspring, who also benefit from increased viability in their environment. The measure of an organism's ability to produce offspring in one season or throughout its life is called **fecundity**. Species with high fecundity, such as insects or rodents, are characterised by their ability to produce many eggs or live offspring. In comparison, large mammals, such as humans or elephants, have low fecundity and produce only one or two offspring per pregnancy, and have few pregnancies across the lifespan. It is important to understand the difference between viability and fecundity when studying natural selection.

viability
an organism's ability to survive to reproductive age and produce offspring

fecundity
the number of eggs or offspring an organism can produce, measured per pregnancy or over an individual's lifetime

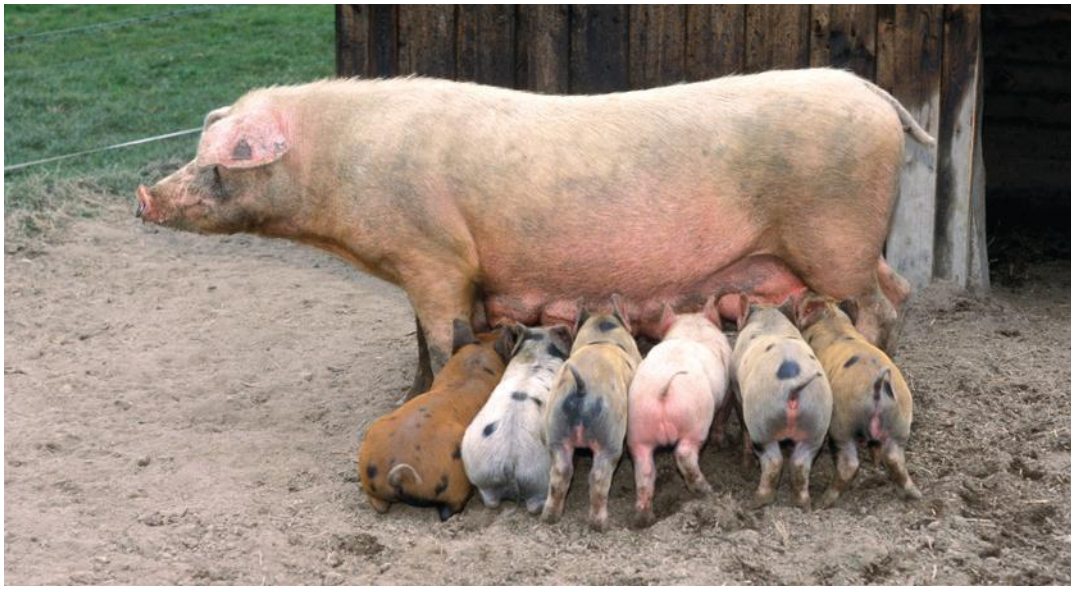


FIGURE 1 Some individuals have high fecundity – they produce a large number of viable offspring

Each individual organism in a population only carries a sample of the gene pool, with two alleles of each gene. This is a relatively small representation of the gene pool, particularly if the organism is part of a large population. However, if the organism is part of a small population, the individual carries a larger relative representation of the gene pool.

Genetic mutations occur randomly and most occur spontaneously. However, the genes that mutate and the rate of mutation can be influenced by environmental factors such as radiation and chemical exposure.

When a gene mutates, producing a new allele, the allele may be:

- neutral – having no impact on survival (e.g. rough or smooth hair in dogs)
- harmful – reducing an individual's chances of survival (e.g. albinism reducing the organism's protection from the sun's heat and radiation)
- advantageous – increasing an individual's chances of survival (e.g. faster reaction time assisting in avoiding predators).

FIGURE 2 Genetic mutations are responsible for the wide variation in lovebird (*Agapornis* spp.) plumage colour

Sexual reproduction results in recombination of alleles, increasing the variety of genotypes and phenotypes in the population. Because natural selection acts on the phenotype, the genotype must be expressed as a phenotype before the organism is advantaged. The somatic cells of an individual are not gametes that contribute to offspring, so any mutations in somatic cells do not contribute to evolution because they are not passed on through generations. A mutation in the somatic cells may provide an advantage or disadvantage to the individual's viability, or have no impact if it is a neutral mutation.

FIGURE 3 Heart cockles (*Corculum cardissa*) have a variety of colour and pattern phenotypes

Natural selection acts on the entire combination of phenotypes of an organism. Selection can occur in different patterns and can be categorised into three main types: stabilising selection, directional selection and disruptive selection.

Stabilising selection

Variation exists within populations for a variety of anatomical and physiological traits and behaviours. The variation of these phenotypes is determined by variations in alleles, or genotype.

When plotted on a histogram, the frequency of these phenotypic variations usually results in a normal distribution curve (Figure 4). The distribution curve is approximately symmetrical around the allele with the mode average (most frequently appearing allele).

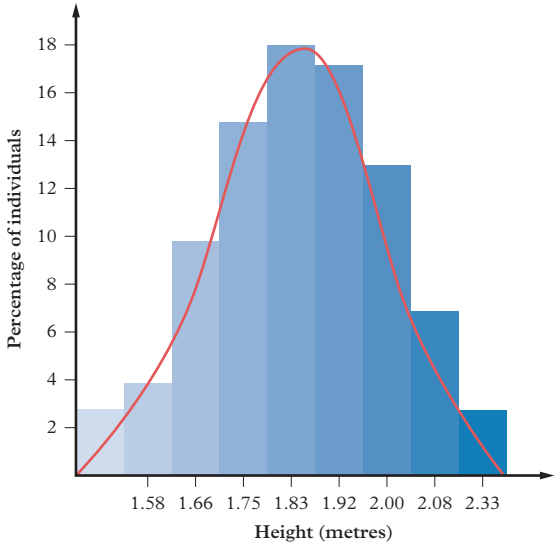


FIGURE 4 A histogram showing the distribution of heights in the human adult population. The line curve shows the approximate normal distribution of the population

When an environment is particularly stable for hundreds or thousands of years, the same phenotypes remain advantageous and are selected for in the population. The traits best adapted to the environment represent the mean phenotype. Individuals with phenotypes furthest in either direction from the mean will have difficulty surviving and reproducing in the environmental conditions. Traits at the extremes of the distribution are removed from the gene pool altogether. This is called **stabilising selection**, because the average phenotypic trait and distribution of traits from the mean remains stable over long periods in unchanging environmental conditions. When plotted on a distribution curve, stabilising selection has an average phenotype and a narrow range (Figure 5).

stabilising selection selection that favours the central alleles in a distribution, eliminating alleles in both the upper and lower extremes of the distribution

Stabilising selection does not mean that all species in a habitat stay the same. Newly established and newly vacant ecological niches will always be filled by some members of a population, who can take advantage of newly opened opportunities. Stability in nature is sometimes short-lived, and organisms will always take advantage of available opportunities.

Directional selection

Abiotic and biotic changes in an organism's environment cause changes to the selection pressures exerted on the organism. For example, a decrease in light intensity would make it advantageous to have larger eyes that let in more light for better vision. Individuals with slightly larger eyes would have a survival advantage in the new environmental conditions and become more viable than those with smaller eyes. As a result, the frequency curve for large eyes would shift to the right, and the mean eye size of the population would increase. This is called **directional selection** and is characterised by new phenotypes at the extreme of the range. Once environmental conditions settle, the new phenotypes become common in the population and are maintained by stabilising selection (Figure 5).

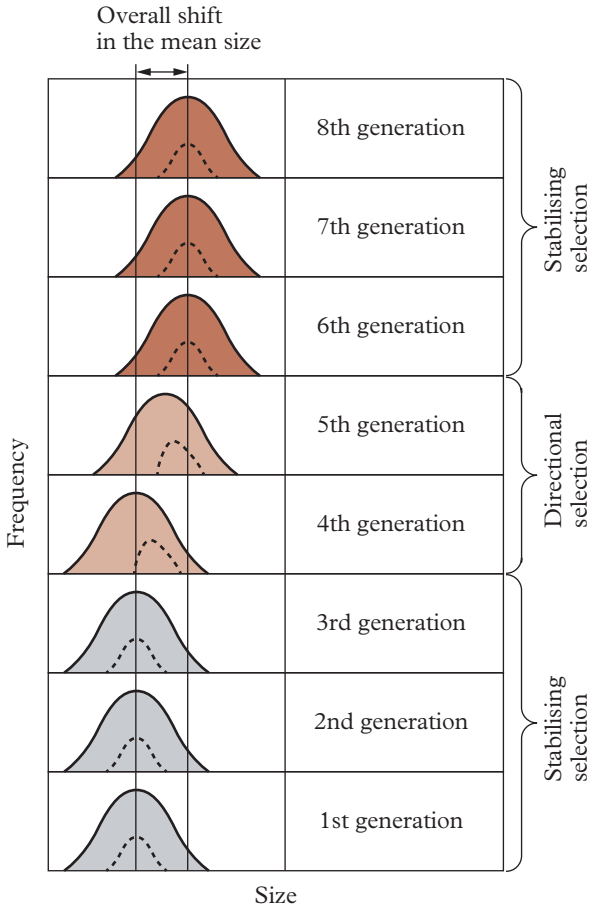


FIGURE 5 The shift from stabilising selection to directional selection and back to stabilising selection with the new phenotype

directional selection selection that favours alleles in one direction, at either the upper or the lower end of the distribution

Directional selection helps us to understand nectar production in flowering plants. Individuals that produced more nectar attracted more insects and birds, which acted as pollinators. They more likely to be visited by pollinators and their genes passed on to the next generation. Individuals that did not produce as much nectar were less likely to be visited and pollinated, resulting in their genes being less likely to be passed on to subsequent generations. Eventually, this trait stabilised, and nectar production became characteristic of the species.

FIGURE 6 Evolution of hominid skulls. Individuals who were smarter survived to reproductive age to pass on their genes to their offspring. As brain size increased, skull size increased, allowing for a larger, more intelligent brain

Disruptive selection

Because the results of natural selection at any given moment depend upon the interaction of phenotypic and environmental variables, a situation could arise where there is an increase in the frequencies of the extreme types in a population and the intermediate (modal) types are eliminated (Figure 7). This is referred to as **disruptive selection**.

disruptive selection
selection that disrupts the normal distribution of an allele, favouring both the lower and upper extremes and eliminating the central alleles of the distribution

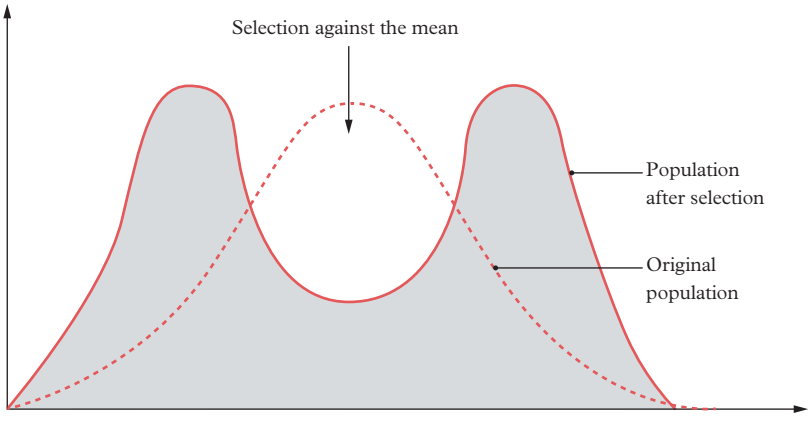


FIGURE 7 Disruptive selection

FIGURE 8 Grass growing on contaminated soil

Plants growing on soil previously contaminated by mining operations often show disruptive selection. Examples are the grasses *Festuca ovina* and *Agrostis capillaris*. There is often a sharp boundary between contaminated and uncontaminated soil. Some of the plants have allelic variations that enable them to live on contaminated soils, unlike "normal" plants. While these allelic combinations allow them to survive on contaminated soils, it makes them less competitive on uncontaminated soil. This leads to intermediate phenotypes being selected against, resulting in the development of two populations with marked differences.

Natural selection perpetuates constancy, as long as the environment remains constant, but it promotes the emergence of new forms if and when the environment changes.

Real-world biology

Antibiotic resistance

In 2018, Melbourne researchers uncovered a common bacterium that had developed resistance to many of the antibiotics in use in Australian hospitals. *Staphylococcus epidermidis* is commonly found on the skin of all humans and often contaminates samples taken from infected wounds. This meant it was frequently dismissed as a false positive on diagnostic tests taken of wounds that failed to heal. Genetic testing by the Peter Doherty Institute for Infection and Immunity found that three strains of this bacterium have spread globally and are resistant to nearly all antibiotic types. They found that *S. epidermidis* had developed a random mutation that led to resistance to two major antibiotics. The frequent impregnation of catheters and other implanted devices with antibiotics has led to a selection advantage for these resistant bacteria. This has resulted in an increase in their frequency, especially in intensive care environments where strong antibiotics are often prescribed.

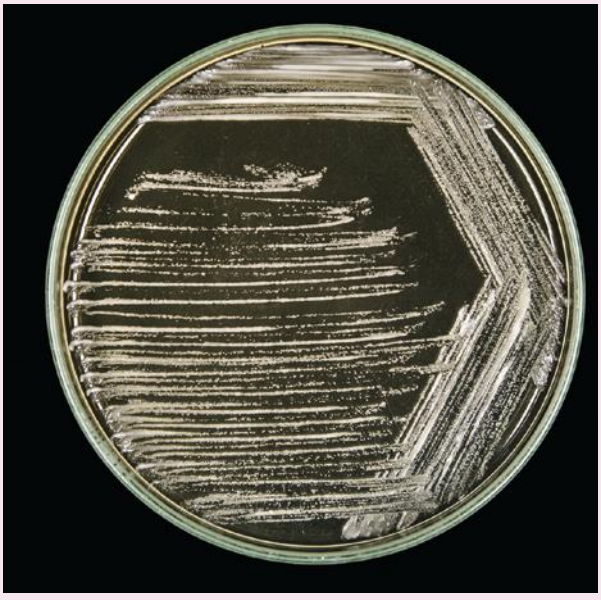


FIGURE 9 *Staphylococcus epidermidis* on an agar plate

Apply understanding

1 **Explain** how *Staphylococcus epidermidis* could have become resistant to antibiotics. (2 marks)
2 **Explain** what is meant by "selection advantage" in this scenario. (2 marks)

Check your learning 12.3

Check your learning 12.3: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** the terms "viability" and "fecundity". (2 marks)
2 **Explain** how the fecundity of one generation affects the viability of the next. (2 marks)
3 **Explain** how natural selection acts on individuals, but evolution occurs at the population level. (4 marks)
4 Although the frequency of alleles in a population is changed as a result of natural selection, **explain** why natural selection only acts directly on phenotypes. (3 marks)
5 **Describe** how natural selection results in adaptation of a population. (4 marks)
6 **Describe** the conditions under which each type of selection (stabilising, directional, disruptive) is likely to be found. (6 marks)
7 **Describe** why "survival of the fittest" is an indication of natural selection, not evolution. (3 marks)

Analytical processes

8 **Contrast** stabilising, disruptive and directional selection. (1 mark)

Knowledge utilisation

9 **Evaluate** the following claim.
"The use of a new antibacterial drug may result in the development of new types of bacteria that are resistant to the drug." (2 marks)

Lesson 12.4
Allele frequencies

Key ideas

- → Allele frequency is a measure of particular alleles in a population.
- → Allele frequency can be calculated using the Hardy–Weinberg equation.
- → Genetic equilibrium occurs when allele frequency remains stable in a population over a long period of time.
- → The frequencies of alleles for a gene in a population over a period of time can be analysed to determine whether there are changes in the gene pool or the population is in genetic equilibrium.

Learning intentions and success criteria

Frequency of alleles in a population

The frequency of an allele in a population may increase or decrease, depending on the selection pressures in the environment. Alleles that produce a phenotype that is favourable for survival in that environment will be selected for and will increase in frequency, while unfavourable alleles will be selected against and will decrease in frequency.

Some heterozygous genotypes produce a more advantageous phenotype than homozygous phenotypes, for the same gene. Sickle cell disease is an example of a heterozygous phenotype advantage. The homozygous dominant genotype is the only variant that does not result in sickle cell disease; however, individuals with this genotype are vulnerable to the deadly mosquito-borne disease, malaria. Individuals with a homozygous recessive genotype are affected by sickle cell disease, which can be fatal. Individuals with the heterozygous genotype also suffer from sickle cell disease, but with much milder symptoms and a much higher rate of survival. While mild sickle cell disease still causes suffering, the heterozygous genotype's advantage is that it confers partial malaria resistance. Because malaria can be fatal in humans, the heterozygous genotype is most advantageous for humans living in malaria-affected areas. Therefore, human populations that evolved in these areas, such as the equatorial region of Africa, retain the sickle cell allele.

Allelic frequency

Two scientists, Godfrey Hardy and Wilhelm Weinberg, independently determined that the frequencies of the alleles of any gene in a population can be calculated using the following formula (known as the Hardy–Weinberg equation):

$$(p + q)^2 = 1$$

where:
p = frequency of the dominant allele in the population
q = frequency of the recessive allele.

This formula can be expanded to:

$$p^2 + 2pq + q^2 = 1$$

where:
p^2 represents the ratio of homozygous dominants in the population
$2pq$ represents heterozygotes
q^2 represents homozygous recessives.

Whether or not an allele for a characteristic is recessive can be determined from a pedigree (Figure 1). If two parents show one phenotype for the characteristic (e.g. both can roll their tongues) but an offspring shows a different phenotype (e.g. cannot roll their tongue), the parents must be heterozygotes and that offspring must be homozygous recessive (i.e. q^2) for the characteristic.

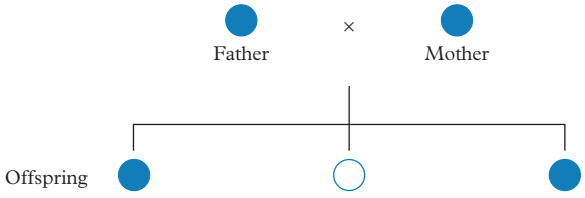


FIGURE 1 A pedigree can help determine whether an allele for a characteristic is recessive

FIGURE 2 The ability to roll your tongue is an inherited trait. The dominant allele gives the ability to roll your tongue, so only those with the homozygous recessive genotype are unable to do so

The proportion of homozygous recessives in the population can then be determined using the equation:

$$\text{Proportion of homozygous recessives in population} = \frac{\text{No. individuals showing recessive phenotype}}{\text{Total no. individuals in population}}$$

As: $(p + q)^2 = 1$, then: $(p + q) = 1$

If the proportion of q^2 is known, the frequency of q can be determined: $q = \sqrt{q^2}$
Additionally, if q is known, the frequency of p can be calculated from: $p = 1 - q$
Using the expansion equation: $p^2 + 2pq + q^2 = 1$, the proportion of homozygous dominants and heterozygotes can be determined for that characteristic. The genotype of any allele in a population can be determined using Table 1.

TABLE 1 Frequency of alleles in a population

First allele	Second allele	Frequency
T	T	$p \times p = p^2$
T	t	$p \times q = pq$
t	T	$q \times p = pq$
t	t	$q \times q = q^2$

By analysing the frequencies of alleles for any particular gene in a population over a period of time, changes in the gene pool can be determined. If there are no changes, the population is said to be in **genetic equilibrium** for those alleles.

The sum of all the allelic frequencies in a population will always equal 1.

genetic equilibrium describes the condition of an allele or genotype in a population when the frequency remains stable over time

Worked example 12.4A

Calculating frequency of lip thickness alleles

In humans, the thickness of the lips is controlled by a single, dominant/recessive gene. In a population of 1,000 individuals, 910 had thick lips and 90 had thin lips. Examination of these phenotypes in family groups showed that thin-lipped parents always had offspring with thin lips, while offspring of parents with thick lips could have either thick or thin lips.

a **Determine**, with reasons, which allele is recessive. (1 mark)

b **Calculate**, using the Hardy–Weinberg equation, the frequency of homozygous dominant, heterozygous and homozygous recessive individuals in this population. (3 marks)

c **Determine** the proportion of homozygous dominant, heterozygous and homozygous recessive individuals in this population. (3 marks)

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the questions are asking you to do.	To "determine" means to establish, conclude or ascertain after consideration, observation, investigation or calculation. To "calculate" means to determine or find a number or answer by using mathematical processes.
Step 2: Write a statement about the impact of allele dominance on each phenotype in this scenario.	**a** The recessive allele results in thin lips in the offspring, because homozygous recessive thin-lipped parents cannot produce thick-lipped offspring, whereas two heterozygous thick-lipped parents can produce thin-lipped offspring. (1 mark)
Step 3: Calculate proportion of homozygous recessives (q^2) in the population.	**b** $q^2 = \frac{90}{100}$ $= 0.09$ $q = 0.3$
Step 4: Substitute the provided values into the Hardy–Weinberg equation.	$(p + q)^2 = 1$ $p + q = 1$ $q = 0.3$ $p = 0.7$
Step 5: Calculate the frequency of each genotype.	$p^2 + 2pq + q^2 = 1$ Homozygous dominant $= p^2$ $= 0.7 \times 0.7$ $= 0.49$ (1 mark) Heterozygous $= 2pq$ $= 2 \times 0.7 \times 0.3$ $= 0.42$ (1 mark) Homozygous recessive $= q^2$ $= 0.3 \times 0.3$ $= 0.09$ (1 mark)
Step 6: Convert decimals to percentages and state the proportion of each genotype.	**c** Homozygous dominant = 49% (1 mark) Heterozygous = 42% (1 mark) Homozygous recessive = 9% (1 mark)

Your turn

In humans, a "widow's peak" is a hairline that comes to a point in the middle of the forehead (Figure 3). This characteristic is thought to be controlled by a dominant/recessive gene. A Japanese study found that of 335 women, 99 had a widow's peak, while the remaining 236 did not.

Examination of these phenotypes in family groups showed that, when both parents had a widow's peak, their offspring always had a widow's peak. However, when at least one parent had no widow's peak, the offspring could have either phenotype.

FIGURE 3 A girl with a widow's peak hairline

a **Determine** which allele is recessive. (1 mark)

b **Calculate**, using the Hardy–Weinberg equation, the frequency of homozygous dominant, heterozygous and homozygous recessive individuals in this population. (3 marks)

c **Determine** the proportion of homozygous dominant, heterozygous and homozygous recessive individuals in this population. (3 marks)

d Similar studies conducted in Nigeria found that 16 per cent of women had a widow's peak phenotype. **Infer** why the results of studies done in different countries may produce different results despite the participants being the same species. (2 marks)

Genetic equilibrium

The stability of an allele in a gene pool from generation to generation is described as genetic equilibrium. When genetic equilibrium is disrupted by something, such as a large migration of individuals in or out of a population, a change in allele frequencies occurs, resulting in microevolution. This concept is summarised by the **Hardy–Weinberg law**.

Hardy–Weinberg law
a principle stating that, when there are no other evolutionary influences, the allele and genotype frequencies in a population will remain constant across generations

Allele frequencies do not change from generation to generation in large, randomly mating populations unless there is migration, mutation and/or selection.

For genetic equilibrium to exist in a population, four conditions must be met.

1 The population is large enough to rule out chance as the only cause of changes to the allele frequencies.

The death of a large number of individuals of a population may occur through random environmental events, such as drought or fire. Large losses of alleles from a gene pool can occur when many individuals are simultaneously wiped out, regardless of whether their phenotypes are advantageous or not.

2 Mutations do not occur, or a state of mutational equilibrium is maintained.

These conditions are not met in any population. Mutations occur constantly and mutational equilibrium, where the emergence of harmful mutations is equal to the elimination of harmful mutations, is very rare.

Changes usually occur in one direction, resulting in mutations changing the allele frequencies of a population. As mutation occurs slowly and randomly, it is rarely a major driver in changes to allele frequency within a population.

3 Immigration and/or emigration does not occur.

4 Reproduction is completely random.

Reproduction refers to mate selection, mating effectiveness and frequency, individual fertility, and survival to reproductive age of offspring. These factors are assumed to be random (i.e. independent of genotype).

It is no surprise that evolution occurs, given that it is next to impossible that these four conditions for genetic equilibrium can be met.

FIGURE 4 Mate selection in zebra finches is not random. Male zebra finches (*Taeniopygia guttata*) show preference for females based on size, whereas females show preference based on beak colour and song

Check your learning 12.4

Check your learning 12.4: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** the impact of immigration and emigration on genetic equilibrium. (3 marks)

2 **Explain** how allele frequency can influence phenotypes in populations. (2 marks)

3 **Explain** how having the sickle cell allele can provide protection against malaria. (4 marks)

Knowledge utilisation

4 **Discuss** why genetic equilibrium existing in a population is almost impossible. (4 marks)

Practical

Lesson 12.5

Changes in the gene pool due to selection pressure

Learning intentions and success criteria

This practical lesson is available on Oxford Digital. It is also provided as part of a printable resource that can be used in class.

Lesson 12.6
Macroevolutionary changes

Key ideas

- → Macroevolution occurs as the result of an accumulation of microevolutionary changes, and produces new species.
- → Divergent evolution is the result of a single population splitting into two or more populations that evolve according to different selection pressures.
- → Parallel evolution occurs when species that share a recent common ancestor face similar environmental selection pressures and develop similar phenotypic traits in homologous structures.
- → Convergent evolution occurs when very distantly related species develop similar phenotypic traits as a result of living in environments with the same selection pressures.
- → Coevolution is the result of two or more species developing an increasingly dependent symbiotic relationship and exerting a selection influence on each other's phenotypic traits.

Macroevolution

Learning intentions and success criteria

Over both short and long periods of time, Earth's climate, geology and ecosystems change. Events such as these change the selection pressures on a species and may result in its evolution.

The variety of circumstances, timing and location of these changes causes evolution to occur in different ways. Initially, microevolution is the result of natural selection, where traits that are best suited to the environment of an organism are selected for. The accumulation of these microevolutionary changes sometimes results in macroevolution – the formation of a new species. Natural selection can only act on the phenotypes available. The phenotypes selected for are rarely perfect for the environment, but they are the most suitable from those available in the gene pool at that point in time.

Macroevolution occurs in four key ways: divergent evolution, parallel evolution, convergent evolution and coevolution.

Divergent evolution

Divergent evolution occurs when a population of a single species separates (diverges) into two species. In most cases, the single population becomes separated into two or more populations that cannot mix and interbreed, and face different survival pressures. The individuals that survive within each population are those with the greatest fitness for their particular environment. Those with advantageous phenotypes survive to reproduce and pass on their genes, and the gene pool of the population subsequently changes in favour of the advantageous genes. Eventually, the separated populations become different enough that they can no longer breed if brought together. Divergent evolution has occurred, resulting in a new species.

divergent evolution
the evolution of a new species as the result of a population splitting into two and adapting to different selection pressures in the environment

Different species can have some common structures inherited from their common ancestor. The appearance and function of the structures will vary according to the organism's needs for survival in its environment. These are referred to as homologous structures. Homologous structures can be seen in the varying form and function of plants. Some rainforest plants have evolved large, dark green leaves that maximise their ability to photosynthesise on the dark forest floor, while some plants in arid climates have evolved small, waxy leaves that minimise water loss. Geographic isolation and mass extinctions are two of the main drivers of divergent evolution.

FIGURE 1 The different leaves of (A) a pitcher plant and (B) a poinsettia. Differing environmental selection pressures have caused these plants to diverge over time into separate species, as shown in their different leaves

Parallel evolution

parallel evolution the independent evolution of similar traits in species that once shared a common ancestor

Parallel evolution occurs when two geographically separated species develop similar phenotypic traits in response to similar environmental selection pressures. Species that shared a common ancestor, and then became geographically separated and evolved to become different species, can evolve to have very similar traits if they face similar selection pressures in their environment. Suppose that two fish species occupy separate geographic locations but share a common ancestor. A new predator enters both their environments. The predator has excellent vision and seeks prey by detecting movement in the water, so fish that move the most are more likely to be caught and eaten. As a result, fish that have slightly larger gills with more surface area are more likely to evade predation, because they are able to extract more oxygen while remaining stationary in the water. This phenotypic trait gives a survival advantage and is passed on to surviving offspring. Eventually, both species have much larger gills than their common ancestor because they have both had to adapt to the same selection pressure.

The parallel evolution of two very similar-looking snakes separated by the Pacific Ocean is an example of this type of evolution. The emerald tree boa, found along the Amazon River in South America, has a very similar appearance to the green tree python, which lives more than 15,000 kilometres away in the rainforests of Far North Queensland (Figure 2). These two snakes are descended from a common ancestor that lived at the time of the dinosaurs around 70 million years ago, yet they look so similar that it would be easy to confuse them. Both species have adapted to their respective rainforest ecosystems with camouflaging, coiled body position and green body colouring.

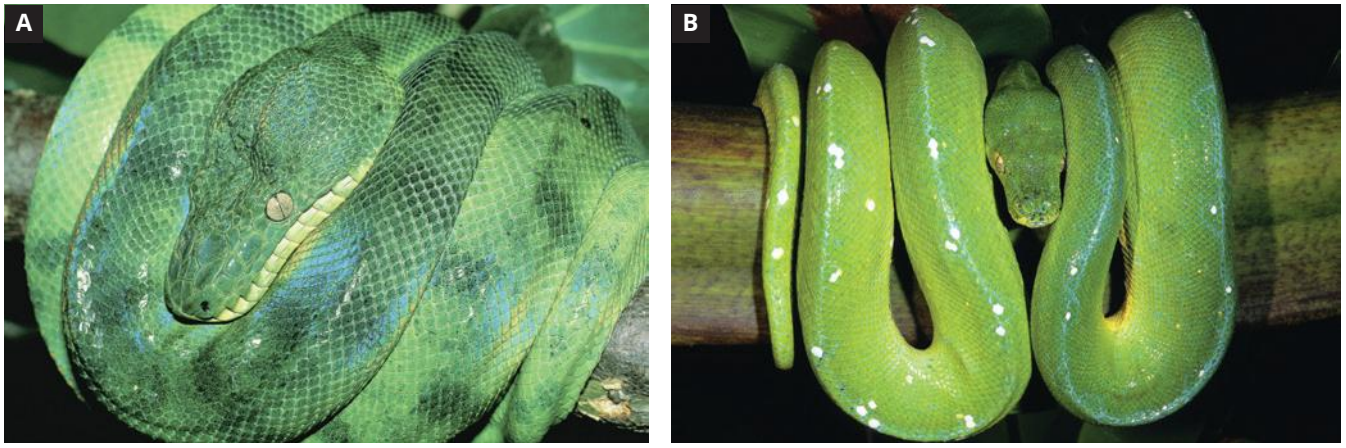


FIGURE 2 Through parallel evolution, the emerald tree boa (*Corallus caninus*) (A) and the green tree python (*Morelia viridis*) (B) have evolved with a very similar appearance

Convergent evolution

Species evolve according to the selection pressures of their environment, and so it stands to reason that similar traits may benefit and evolve in unrelated species. This occurs in **convergent evolution**, where unrelated or distantly related species respond to the same environmental pressures by evolving the same advantageous traits. The key difference between parallel evolution and convergent evolution is the closeness of the ancestral relationship. Parallel evolution occurs in species that share a recent common ancestor and have homologous structures, whereas convergent evolution occurs in species that are only distantly related. In parallel evolution, similarities occur in homologous structures, whereas in convergent evolution, similarities are evident in analogous structures.

convergent evolution
the evolution of similar traits in unrelated or distantly related species due to similar selection pressures in their environment

The many similar traits of dolphins and sharks is an example of convergent evolution (Figure 3). Dolphins and sharks share a common ancestor that existed around 300 million years ago and did not have the appearance of either of these animals. It was advantageous for both animals in their marine environments to develop streamlined bodies for moving easily through the water, pectoral fins for stabilisation, and flat tail fins to propel them through the water. Although their appearance is similar, these traits in dolphins and sharks have evolved independently, making them analogous structures.

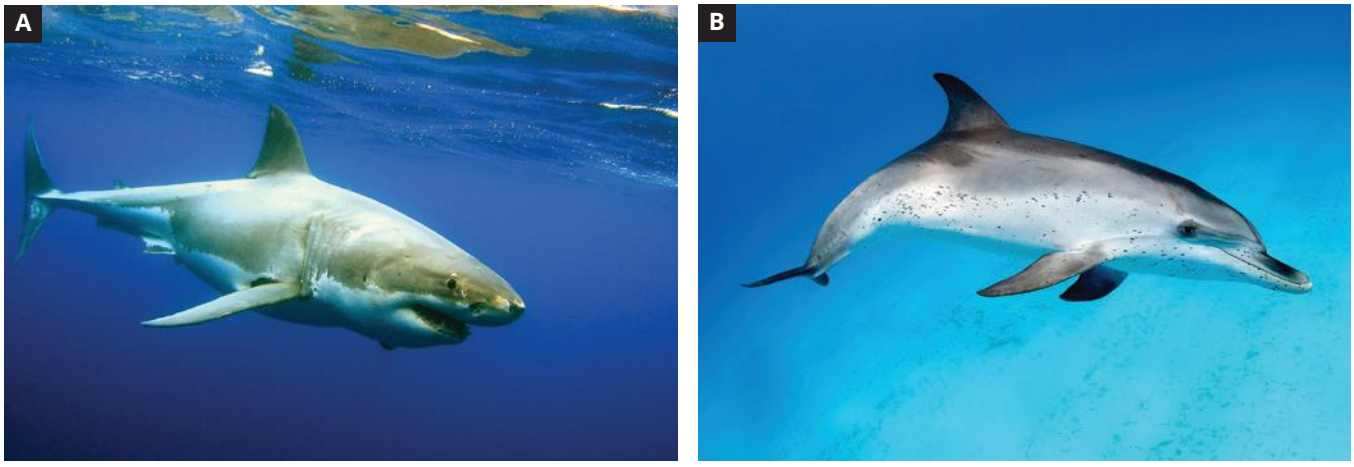


FIGURE 3 (A) Sharks and (B) dolphins are an example of convergent evolution, as they have many physical similarities but do not share a recent common ancestor

Coevolution

Two species living in the same community sometimes forge an extremely close symbiotic relationship that extends to simultaneous phenotypic changes that strengthen this relationship even further. Two species that become increasingly dependent on each other also exert a strong selective force on each other. Often these relationships are between predator (or parasite) and prey. Initially, these are microevolutionary changes to phenotypes in one species that cause selection pressure in the other species, which responds with its own phenotypic changes. This results in the gene pool of both populations changing in a particular direction, and is referred to as **coevolution**.

coevolution
evolution that occurs when two or more species influence each other's evolutionary changes due to a symbiotic relationship

Benefits are often experienced by all organisms involved in a coevolutionary relationship. Animal pollination provides flowering plants with a reproductive advantage over those that rely on ideal weather conditions. When flowers have formed, selection pressures favour flowers that are attractive to pollinators. Flowers that mimic a particular insect pollinator, and flowers with nectar or large amounts of pollen, improve the chance of cross-pollination and genetic variability of offspring. More energy- or nutrient-dense and abundant sources of food (pollen and nectar) benefit the pollinator. Similarly, coevolution has been observed between fruiting plants and the animals that disperse their seeds.

An example of coevolution is the symbiotic relationship between the sword-billed hummingbird and the passionflower plant, in the Andes mountains of South America (Figure 4). The hummingbird's beak has evolved to become longer and longer, to reach the nectar of the passionflower plant, whose corolla (a tube formed by petals) has also become longer and longer. This coevolution has given the hummingbird the unique characteristic of being the only bird with a longer beak than its body (excluding the tail), and having to groom itself with its feet because its beak is too long to reach. There are benefits and risks associated with this codependent relationship, for both the hummingbird and the flower. The hummingbird is dependent on the flower for food, because its long beak makes it difficult to feed on other species, and the flower is dependent on the hummingbird's existence for pollination, because no other bird has a beak long enough to reach the nectar. This means that if one species declines, the other is also affected. The benefits for the hummingbird are reduced competition for food as it is the only bird that can access the nectar, while the flower benefits from a reliable pollinator.

FIGURE 4 A coevolutionary relationship exists between the sword-billed hummingbird (*Ensifera ensifera*) and the passionflower (*Passiflora mixta*)

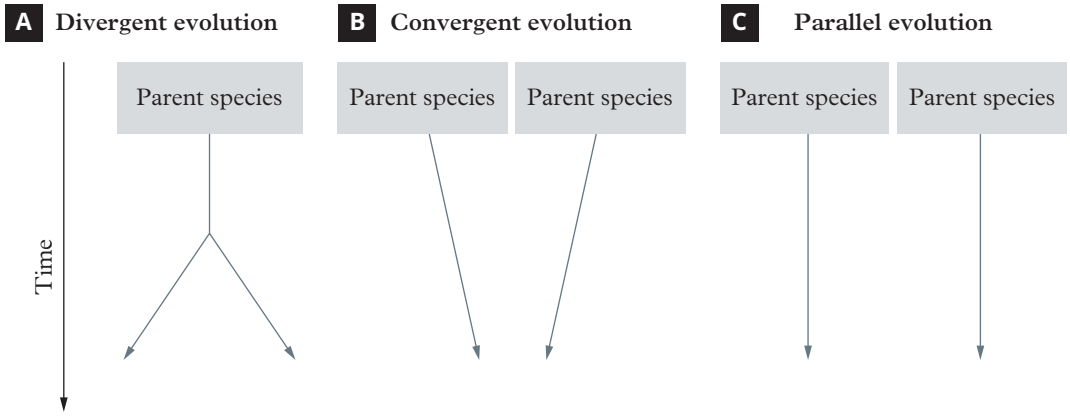


FIGURE 5 Three of the four modes of evolution: (A) divergent evolution, (B) convergent evolution, and (C) parallel evolution

Check your learning 12.6

Check your learning 12.6: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** the means by which divergent evolution may occur. (2 marks)
2 **Define** the term "coevolution". (1 mark)
3 **Infer** a disadvantage of coevolution. (1 mark)
4 **Identify** two specific examples of coevolution between plants and animals. (2 marks)
5 **Construct** a table to compare parallel, convergent and divergent evolution. (3 marks)

Analytical processes

6 **Constrast** divergent and convergent evolution. (1 mark)

Knowledge utilisation

7 **Discuss** the ways in which coevolution differs from convergent evolution. (2 marks)

Lesson 12.7
Speciation

Key ideas

- → Speciation is the evolutionary development of a new species.
- → Allopatric speciation occurs when two populations of a species are geographically separated.
- → Parapatric speciation occurs when species within the same population face differing selection pressures due to their location within a large geographic range.
- → Sympatric speciation occurs when populations are not physically separated, but a genetic or chromosomal abnormality creates a difference between individuals within a population that prevents them from interbreeding.

Learning intentions and success criteria

The emergence of a new species

Individuals of the same species are able to reproduce with each other to produce viable and fertile offspring. They share a common gene pool that includes all the alleles for all the genes in the species. When the gene pool of a population of a species becomes significantly different from the rest of the species, a new species is produced – this process is called **speciation**. The new species can no longer reproduce with the individuals from the original population because they have become reproductively isolated from each other.

speciation
the evolutionary process by which new, distinct species are formed

Individuals within a population carry only a sample of all of the alleles of the species' gene pool. These alleles are expressed as the individual's phenotype, which is acted on by natural selection. Natural selection acts on the phenotypes of the population, selecting individuals who have phenotypes most suited to surviving in the environment. The organisms that are 'fittest' for the environment have a greater chance of reproducing and passing on the alleles they carry. In this way, the frequency of alleles in the population can change. Some alleles will be lost from the population, some will become less prevalent and others will become more prevalent. Over time, these changes in the phenotypes within a single species may accumulate until they form a distinct new species.

This type of speciation commonly occurs because a population has become separated into two or more groups that evolve independently of each other, due to different environmental pressures.

Allopatric speciation

allopatric speciation
the divergence of a species into two separate species, driven by geographical isolation of populations

The most common cause of speciation is geographic separation of a population, termed **allopatric speciation**. Physical barriers such as a newly formed river or sudden habitat fragmentation can separate a single population into two or more physically separated populations. The separated populations can no longer breed and so gene flow between them no longer occurs. Over time, the separated populations experience different selection pressures, and both selected alleles and random mutations accumulate until significantly different phenotypes are established. Eventually, the separated populations become so genetically different that they would be unable to breed even if they were reintroduced to each other.

An example is the two most common Australian octopuses, the western rock octopus (in New South Wales) and the gloomy octopus (in Western Australia; Figure 2). Until recently, both octopuses were considered to be separate populations of the same species, *Octopus tetricus*. However, in 2021, scientists found a difference in the number of suckers on the arms of the males of each population. This, along with differences in DNA sequences between the populations, is enough evidence to support the identification of a new species in the Western Australian population. The new species was named *Octopus djinda*, with "djinda" meaning "star" in the language of the original inhabitants of the south-west of Western Australia, the Noongar peoples. These two species are thought to have diverged from a single population more than 3 million years ago, due to changes in environmental factors such as sea currents, temperature and rainfall.

FIGURE 1 A gloomy octopus (*Octopus tetricus*) on the sea floor

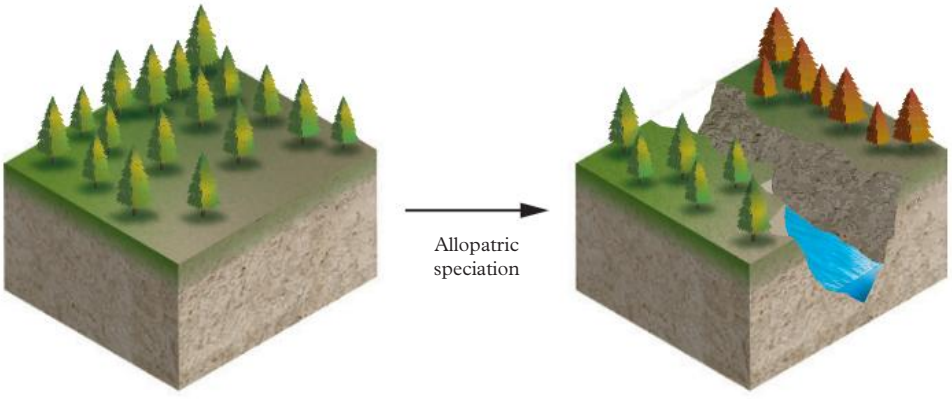


FIGURE 2 Allopatric speciation is driven by geographic isolation

Parapatric speciation

Speciation sometimes occurs in populations that remain in the same geographical location without any barrier to mating and gene flow. This is called **parapatric speciation**. It often takes place when a population is spread over a large area, with individuals subject to differing pressures due to environmental variation across the distribution range. Take, for example, a species of butterfly that has a population distributed evenly throughout a national park. If the park has a busy motorway passing one area, the individuals living in this area find it more difficult to fly, due to the increased wind currents created by the passing traffic. The individuals with the biggest wings can fly better, allowing them to find mates more easily than individuals with smaller wings. The alleles for larger wings are more successful in this small pocket of the population and over time, these butterflies adapt to other local selection pressures and become different enough from the rest of the population that they become a new species. The population was never physically separated, but those living in one small area adapted to different selection pressures. Another example is the great grey shrike and the steppe grey shrike (Figure 3).

parapatric speciation
the evolution of a new species from within a population that is not geographically separated; individuals on the periphery of a population are subjected to slightly different selection pressures, causing speciation within one population

FIGURE 3 (A) The great grey shrike and (B) the steppe grey shrike evolved through parapatric speciation due to different selection pressures within the same population

Sympatric speciation

sympatric speciation
the divergence of a species into two separate species while the populations are not geographically isolated from each other; driven by reproductive isolation due to spontaneous chromosomal or genetic changes

Sometimes populations become reproductively isolated from each other through chromosomal changes – this is called **sympatric speciation**. Sympatric speciation is rare, and usually the result of polyploidy. Polyploidy is a condition that occurs when chromosomes in gametes do not separate correctly during meiosis, resulting in offspring with an incorrect number of chromosomes (Figure 4). This change in chromosome number acts as a barrier that prevents the parent species from reproducing with the new polyploid species.

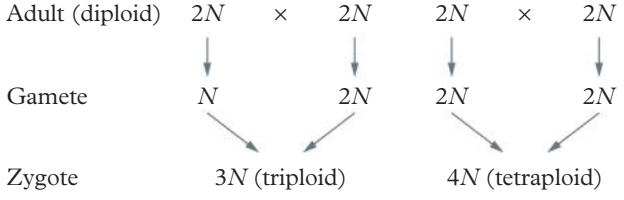


FIGURE 4 Polyploidy results in offspring with an incorrect number of chromosomes

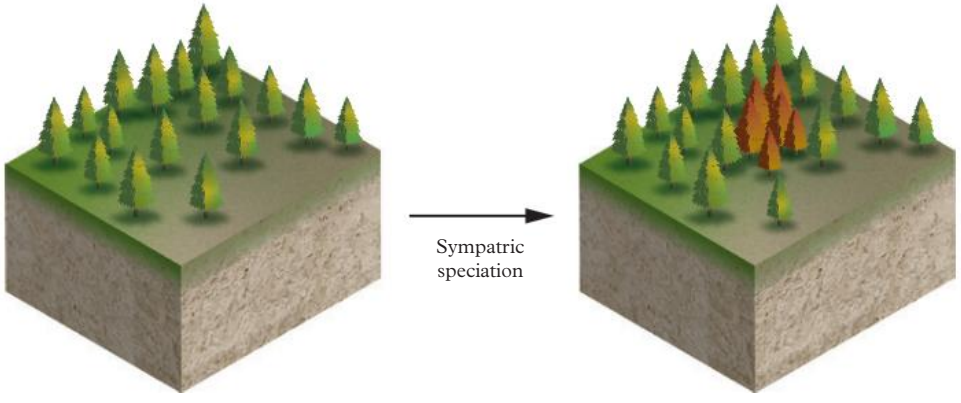


FIGURE 5 Sympatric speciation is driven by polyploidy rather than geographic isolation

Gene flow and calculating allele frequency

If the geographic range of a population is very large, different environmental conditions may exist at either end of the range, resulting in differing selection pressures on some of the population. When migration between the different ends of the range occurs, gene flow is influenced according to the rate of individuals migrating.

FIGURE 6 The leopard's large geographic range (>20 million square kilometres) spans Africa, the Middle-East and Asia

Worked example 12.7A

Calculating allele frequency

A proportion of insects in each of two populations is resistant to a toxin produced by a plant on which the insects feed. Area 1 (where Population 1 lives) contains few of these plants. Area 2 (which contains Population 2) has a large proportion of the plants. Organisms that have allele A are able to resist the toxin. Before migration, the frequency of allele A (f(A)) was:

f(A) in Population 1 = 0.3

f(A) in Population 2 = 0.9

A number of insects migrated from Area 2 to Area 1. As a result, the population in Area 1 now contains 90 per cent original residents and 10 per cent migrants (from Area 2).

Determine the new allelic frequency for toxin resistance in Population 1. (1 mark)

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking you to do.	To "determine" means to establish, conclude or ascertain after consideration, observation, investigation or calculation.
Step 2: Convert 90% original residents to $\frac{90}{100}$ and multiply by the Population 1 frequency before migration.	$\frac{90}{100} \times 0.3$ $= 0.9 \times 0.3$
Step 3: Convert the 10% migrant population to $\frac{10}{100}$ and multiply by the Population 2 frequency before migration.	$\frac{10}{100} \times 0.9$ $= 0.1 \times 0.9$

Think	Do
Step 4: Add the two together.	(0.9 × 0.3) + (0.1 × 0.9)
Step 5: Show your working.	(0.9 × 0.3) + (0.1 × 0.9) = 0.27 + 0.09 = 0.36
Step 6: State the final solution.	= 0.36 (1 mark)
Step 7: Make a statement about the results.	The allele frequency of toxin resistance has increased from 0.3 to 0.36. In this case, migration has had little impact on the allele frequency in Population 1.

Your turn

Capybaras (*Hydrochoerus hydrochaeris*) are a species of semi-aquatic, herbivorous rodent native to South America. As part of a conservation program to improve genetic diversity, a herd of capybaras were relocated from a flooded area in Colombia to join a herd in the south of Argentina. DNA samples were taken from both herds prior to their introduction. A gene that contributes to gigantism was studied, with the frequency of one particular version of the gene, allele Q, recorded. Before relocation, the frequency of allele Q was found to be:

f(Q) in Colombian population = 0.8

f(Q) in Argentinian population = 0.1

Determine the new allele frequency for allele Q in the merged population. (1 mark)

Check your learning 12.7

Check your learning 12.7: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Define** "speciation". (1 mark)

2 **Explain** the circumstances under which allopatric speciation could occur, using examples. (3 marks)

Analytical processes

3 **Contrast** allopatric, parapatric and sympatric speciation. (1 mark)

4 **Evaluate** the following statement: "All speciation is driven by geographic isolation." (2 marks)

MODULE 12

Lesson 12.8
Review: Evolution

Summary

12.1
- Evolution explains the physical and behavioural characteristics of all life on Earth, including their development from their ancestors over billions of years.
- Natural selection acts on the phenotype of an organism and selects for the traits most suited to the environment at that point in time.
- Microevolution is a change in allele frequency within the population of a species.
- Macroevolution is the accumulation of microevolutionary changes that results in a new species.

12.2
- The main drivers of microevolution are mutation, gene flow and genetic drift.
- A genetic bottleneck occurs when a large percentage of a population are wiped out, reducing the variation of alleles in the gene pool.
- Genetic bottlenecks reduce the genetic diversity of a population, leaving them vulnerable to extinction.

12.3
- Natural selection acts on the phenotype of organisms and selects in favour of the most suitable phenotype for survival in the environment at that time.
- Genetic mutations occur spontaneously and randomly, and may be neutral, advantageous or disadvantageous.
- Stabilising selection occurs when an environment is stable for a long period of time and the mean phenotype remains the same, with the phenotypic range becoming narrower.
- Directional selection is the result of a phenotype at one end of the distribution being selected and, over time, the mean phenotype shifting.
- Disruptive selection occurs when the average phenotype is selected against, and alleles at the extremes of the phenotypic distribution are advantageous.

12.4
- Allele frequency is a measure of particular alleles in a population.
- Genetic equilibrium occurs when allele frequencies remain stable in a population over a long period of time.
- Genetic equilibrium can be quantitatively calculated using the Hardy–Weinberg law.
- Allele frequency can be calculated using the Hardy–Weinberg formula.

12.5
- Practical: Changes in the gene pool due to selection pressure

12.6
- Macroevolution occurs as a result of an accumulation of microevolutionary changes, and produces new species.
- Divergent evolution is the result of a single population splitting into two or more populations that evolve according to different selection pressures.
- Parallel evolution occurs when species that share a recent common ancestor face similar environmental selection pressures and develop similar phenotypic traits in homologous structures.
- Convergent evolution occurs when very distantly related species develop similar phenotypic traits as a result of living in environments with the same selection pressures.
- Coevolution is the result of two or more species developing an increasingly dependent symbiotic relationship and exerting a selection influence on each other's phenotypic traits.

12.7
- Speciation is the evolutionary development of a new, unique species.
- Allopatric speciation occurs when two populations of a species are geographically separated.
- Parapatric speciation occurs when species within the same population face differing selection pressures due to their location within a large geographic range.

- Sympatric speciation occurs when populations are not separated but a genetic or chromosomal abnormality creates a difference between individuals within a population that prevents them interbreeding.

Key formulas

Hardy–Weinberg equation	$(p + q^2) = 1$
Expanded Hardy–Weinberg equation	$p^2 + 2pq + q^2 = 1$
Proportion of homozygous recessives in a population	$= \frac{\text{No. individuals showing recessive phenotype}}{\text{Total no. individuals in population}}$

Review questions 12.8A Multiple choice

Review questions: Complete these questions online or in your workbook.

(1 mark each)

1 If there are no mutations and no selection acting on a large population, the phenotype frequency will
   - **A** always decrease.
   - **B** change slowly and predictably.
   - **C** change rapidly and unpredictably.
   - **D** remain approximately the same indefinitely.

2 In which of the following cell types would the presence of a mutation possibly result in evolutionary change?
   - **A** Stem cells
   - **B** Sperm cells
   - **C** Somatic cells
   - **D** White blood cells

3 When an environment changes slowly, a population may continue to survive by
   - **A** having no disadvantageous mutations occurring within the population.
   - **B** increasing its rate of reproduction during times of environmental pressure.
   - **C** interbreeding with individuals from nearby populations of the same species.
   - **D** spontaneously producing advantageous alleles suited to the new environmental conditions.

4 Allele frequencies in a population are a direct result of
   - **A** habitat size.
   - **B** recessive traits.
   - **C** genotypes of individuals.
   - **D** environmental pressures.

5 Although some alleles produce harmful effects, they persist in natural populations. Which one of the following is *not* a possible explanation for this?
   - **A** Even if alleles are being lost by selection, new mutations can be produced.
   - **B** Different alleles may give an advantage to individuals at different times or in different places.
   - **C** Mutated alleles are retained because they may give individuals an advantage if the environment changes.
   - **D** Heterozygous individuals may be at an advantage over either kind of homozygous individual.

6 Calculating allele frequencies helps scientists to
   - **A** eliminate undesirable traits.
   - **B** control the characteristics of future generations.
   - **C** identify individuals that carry undesirable alleles.
   - **D** understand how traits are distributed among the population.

7 Which of the following conditions could explain the long-term stability of the gene pool of a population?
- **A** Genetic drift has occurred often.
- **B** Mating has always been random.
- **C** The population has lower mortality than other populations.
- **D** Interbreeding with other populations has been commonly practised.

8 Allopatric speciation occurs when populations cannot interbreed, due to
- **A** genetic polymorphism.
- **B** lack of mates in the area.
- **C** distance between the populations.
- **D** formation of a geographic barrier that separates two or more populations of a species.

9 The golden marmoset of Madagascar eats only bamboo stalks. It is the only animal known to eat the entire stalk. The pith of the bamboo contains high levels of cyanide. The amount of cyanide in one meal for the marmoset is enough to kill a much larger mammal, and yet the golden marmoset experiences no ill effects from this diet. The evolutionary relationship between the golden marmoset and the bamboo would be best described as
- **A** coevolution.
- **B** divergent evolution.
- **C** convergent evolution.
- **D** punctuated evolution.

Review questions 12.8B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

10 **Describe** the conditions under which stabilising selection acts, and its effect on the phenotypes of the population. (3 marks)

11 **Explain** how immigration of individuals into a population or emigration of individuals out of a population changes its genetic equilibrium. (2 marks)

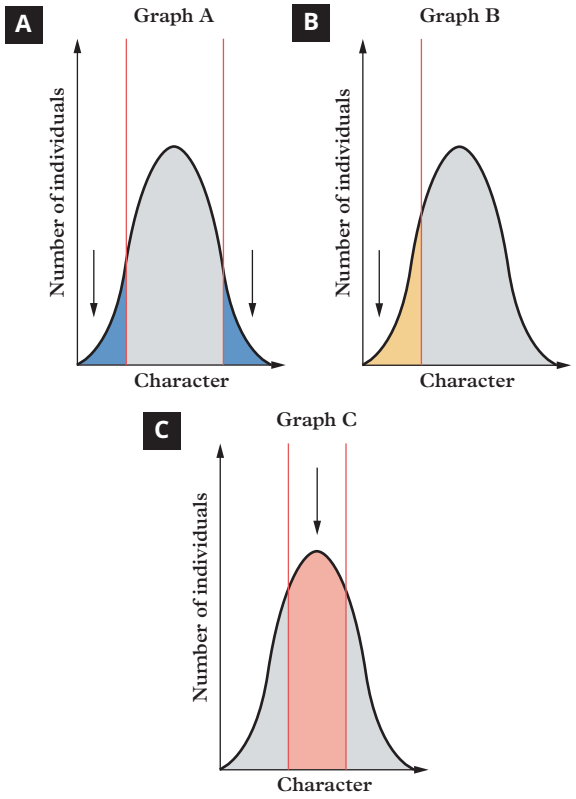
12 **Explain** how a genetic bottleneck occurs and the negative results of this process on the population of a species. (4 marks)

13 **Explain** the founder effect and the conditions that could lead to this occurring. (2 marks)

14 **Contrast** microevolution and macroevolution. (2 marks)

15 **Describe**, with examples, the circumstances under which divergent evolution could occur. (2 marks)

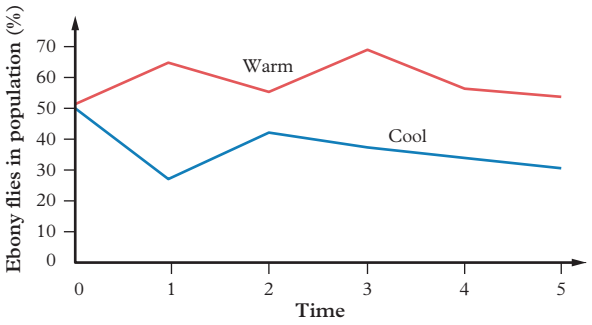
16 In the graphs shown, the areas marked with arrows show the individuals in each population that are being selected against.
- **a** **Identify** the type of selection exhibited in each graph. (1 mark)
- **b** **Explain** the consequences for future generations as a result of the type of selection shown in:
  - **i** graph B (2 marks)
  - **ii** graph C. (2 marks)



17 **Explain** why migrants must interbreed and produce offspring with residents for gene flow between populations to have an evolutionary impact. (3 marks)

Analytical processes

18 Two populations of *Drosophila*, initially containing an equal number of wild type individuals and individuals that have the gene for ebony (dark body colour), were kept in two containers under different temperature conditions. The graph shows the changes with time in the relative proportions of ebony flies. **Analyse** these results. (2 marks)



19 Tongue rolling is a dominant trait. Those who can roll their tongue are homozygous dominant or heterozygous, and those who cannot roll are homozygous recessive for this allele.
A tongue-rolling survey of 5,000 people was conducted, and the results showed that 3,200 could roll their tongues, while 1,800 could not.

- **a** **Calculate** the percentage of people in this sample who are homozygous recessive for tongue rolling. (2 marks)
- **b** **Calculate** the frequency of the recessive allele in the population. (2 marks)
- **c** **Calculate** the frequency of the dominant allele in the population. (2 marks)
- **d** **Calculate** the percentage of people in this sample who are homozygous dominant for tongue rolling. (2 marks)
- **e** **Calculate** the percentage of people who are heterozygous for tongue rolling. (2 marks)
- **f** **Infer** whether you would expect the same percentages (that you calculated in parts **a**, **d**, **e**) in the next generation. **Explain** your response. (3 marks)

20 In Population 1 of a species, the frequency of a particular allele (X) is 0.6. In Population 2 of the same species, the frequency of this allele is 0.2. A single migration occurs from Population 1 to Population 2.

- **a** If migrants account for 15 per cent of Population 2, **calculate** the frequency of this allele in Population 2 immediately after migration. Show your working. (2 marks)

Population 1 immigrants also had another allele (Y) with a frequency of 0.5 that did not occur in Population 2.

- **b** **Determine** the frequency of allele Y in Population 2 immediately after migration. (1 mark)
- **c** If the migrants freely interbred with the residents:
  - **i** **calculate** the frequencies of alleles X and Y in the first generation (1 mark)
  - **ii** **calculate** the frequencies of alleles X and Y in the second generation. (1 mark)
- **d** If allele Y confers a selective advantage to Population 2 individuals in its range, but not to individuals in the Population 1 range, **deduce**:
  - **i** a possible fate for members of Population 2 over a period of many generations if interbreeding between migrants and residents occurred. (1 mark)
  - **ii** a possible fate for members of Population 2 over a period of many generations if no interbreeding between migrants and residents occurred. (1 mark)

Knowledge utilisation

21 Cystic fibrosis is a hereditary disorder of humans caused by a recessive allele. As many as 1 in 29 people are carriers of the recessive allele, but as few as 1 in 2,500 develop the disease. Those affected have a homozygous recessive genotype.
The allele for the normal dominant trait controls the amount of a protein (CFTR) in the membranes of the cells lining the intestine and lungs. In turn, CFTR controls the secretion of ions and fluid through those linings. Cystic fibrosis carriers have only half as much normal CFTR as those who are not carriers.
In cystic fibrosis patients, there is no secretion of chloride ions because the cell membranes have no CFTR. No fluid is secreted into the airways of the lungs, so the mucus that accumulates there becomes sticky and dehydrated, forming an ideal breeding ground for bacteria and viruses. Cystic fibrosis patients suffer from repeated infections. The bacterium *Vibrio cholerae*, which causes cholera, colonises the small intestine, triggering the CFTR mechanism. Patients suffer severe dehydration and electrolyte loss by diarrhoea, and can die if untreated.

a **Propose** an advantage a cystic fibrosis carrier would have if infected with the cholera bacterium. **Justify** your answer. (3 marks)

b **Infer** why the cystic fibrosis allele has remained so common in some parts of the world (e.g. northern Europe). **Explain** your answer. (3 marks)

Data drill

Calculating allele frequencies

Allele frequencies of a population of snails in a temperate forest were recorded over a period of 8 years following the introduction of a green corridor between two previously isolated sections of forest. The results are shown in the data set below.

Year	Genotype			Allele frequency	
	QQ	*Q*	*q*	*Qq*	*qq*
2017	0	0	240	0.00	1.00
2018	0	0	240	0.00	1.00
2019	0	0	240	0.00	1.00
2020	0	7	233	0.03	0.97
2021	4	52	184	Question **1**	Question **1**
2022	29	89	122	0.49	0.51
2023	40	120	80	Question **1**	Question **1**
2024	51	132	57	0.76	0.24

Apply understanding

1 **Calculate** the allele frequencies for 2021 and 2023. (4 marks)

Analyse data

2 **Contrast** the allele frequency in 2017 with that in 2024, using data from the table to support your response. (2 marks)

Interpret evidence

3 **Infer** possible reasons for the introduction of a new allele and the rapid changes in allele frequency. (2 marks)

Module 12 checklist: Evolution

MODULE 13

Evidence of evolution

Introduction

Based on the foundational theories of Darwin and Wallace, modern evolutionary theory explains the changes in living organisms over time, using our understanding of genetics, molecular biology and other emerging techniques. Evolutionary pathways can be tracked through microevolutionary changes in allele frequency to macroevolutionary changes in the formation of new species and taxa.

Geological evidence shows a timeline of life on Earth with evidence of the emergence and extinction of a great number of species. Periods of mass extinction and evolutionary radiation are evident, associated with global changes in climate or the geosphere.

Prior knowledge

Prior knowledge quiz

Check your understanding of concepts related to evidence of evolution before you start.

Subject matter

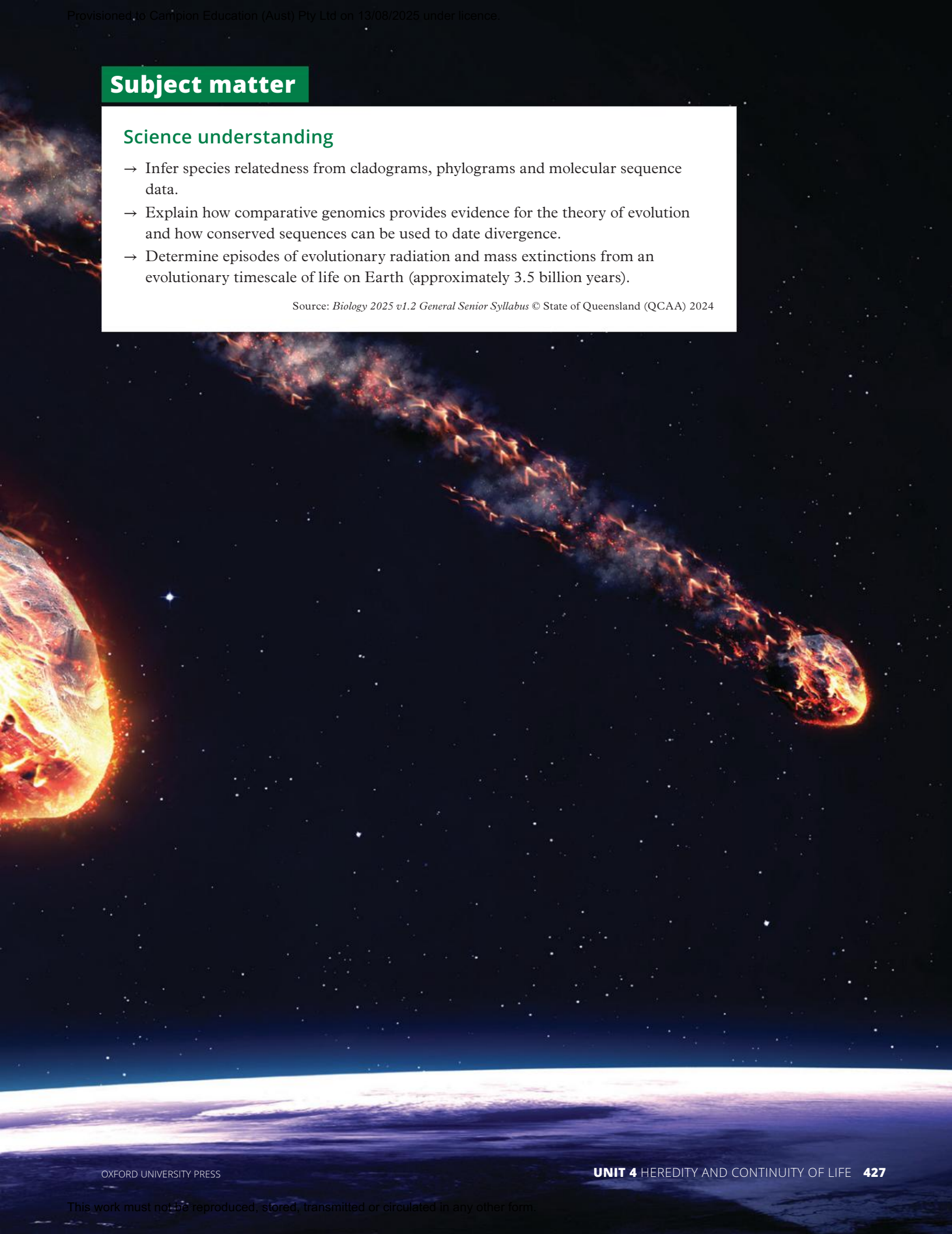
Science understanding

→ Infer species relatedness from cladograms, phylograms and molecular sequence data.

→ Explain how comparative genomics provides evidence for the theory of evolution and how conserved sequences can be used to date divergence.

→ Determine episodes of evolutionary radiation and mass extinctions from an evolutionary timescale of life on Earth (approximately 3.5 billion years).

Source: *Biology 2025 v1.2 General Senior Syllabus* © State of Queensland (QCAA) 2024



Lesson 13.1
Inferring species relatedness

Key ideas

- → Evolutionary relatedness between species is important in understanding species' adaptations and genetic similarities.
- → Cladograms show the evolutionary relationships between species based on shared characteristics.
- → Phylograms show the evolutionary relationships between species based on a quantitative measure of genetic mutations.
- → Molecular sequencing takes a DNA sample and sequences either amino acids or nitrogenous bases in genetic material that can be read or compared, to gain insights into evolutionary relationships and processes.
- → Comparative genomics supports the theory of evolution and aids in estimating evolutionary timing.
- → Significant geological and evolutionary events on Earth can be determined by looking at evolutionary timescales of life on Earth.

Learning intentions and success criteria

cladistics
a classification method based on organisms' traits shared with or derived from a common ancestor; these classifications are often represented on a diagram called a cladogram

shared characteristic
a characteristic that all members of a group or clade share; evidence of a common ancestor

derived characteristic
a characteristic unique to a clade or species that allows it to be identified as different from others

cladogram
a branching diagram that shows evolutionary relationships, using a combination of DNA, physical traits and fossil records as evidence

Relatedness using cladistics

The phylogenetic classification system shows the evolutionary history of a species or group. It shows the points where different groups separated from a recent common ancestor. While Linnaean classification acknowledges the evolutionary development of organisms, its focus is on the description and comparison of an organism's physical structures.

In 1966, Willi Hennig developed **cladistics**, a system of phylogenetic analysis that uses **shared** or **derived characteristics** as the only criteria for grouping taxa. In this system, it is assumed that, as groups of organisms diverge and evolve from a common ancestral group, they retain some unique common characteristics. For example, all mammals have hair, and carnivorous mammals are meat eaters with common tooth and intestinal structures. The domestic cat and the leopard are more closely related to each other than to the wolf because they can both purr. A derived characteristic is a feature that evolved only within the group under consideration (e.g. the ability to purr). The basic idea behind cladistics is that members of a group share a common evolutionary history and are more closely related than members of another group.

In this system, organisms are classified according to the order in which groups arise along a phylogenetic tree. The tree (or **cladogram**) (Figure 1) is composed of a series of branches, with each separation defined by a new feature. For example, the reptile, horse, seal, dog and cat are all vertebrates with pentadactyl limbs (limbs with five digits), a characteristic that existed in their shared common ancestor. At one point in the evolutionary history, the ancestor of the mammals (horse, seal, dog and cat) evolved hair and mammary glands, while the ancestor of the reptiles did not. In the more recent evolutionary history, the ancestor of the seal, dog and cat evolved skeletal changes that the horse ancestor did not. This continued until the early ancestors of each organism diverged from each other.

Cladistics relies on three primary assumptions.

- Life arose on Earth only once, and therefore all living organisms on Earth are the result of reproduction of their ancestors. Groups of organisms share a common ancestor.
- There is a bifurcating pattern in **cladogenesis**. This means that new kinds of organisms may arise when existing populations divide into exactly two groups. Although some biologists suggest that many new species can diverge from a common ancestor within a short time, there are only a limited number of cases of this occurring. This assumption also does not consider the possibility of interbreeding between distinct groups.
- Changes in phenotypic traits change over time through lineages from common ancestor to descendants.

cladogenesis
the making of a clade by means of an ancestor species evolving into two or more new species

There are two main types of cladograms. Most cladistic analysis focuses on identifying groups showing a given species and all its direct descendants – **clades** – that do not include any other lineages. Other cladograms show a group of species with its most recent common ancestor but do not show all the descendants of the ancestor.

clade
a group of organisms that includes a common ancestor and all its descendants; often identifiable on a cladogram as a node and species branching from it

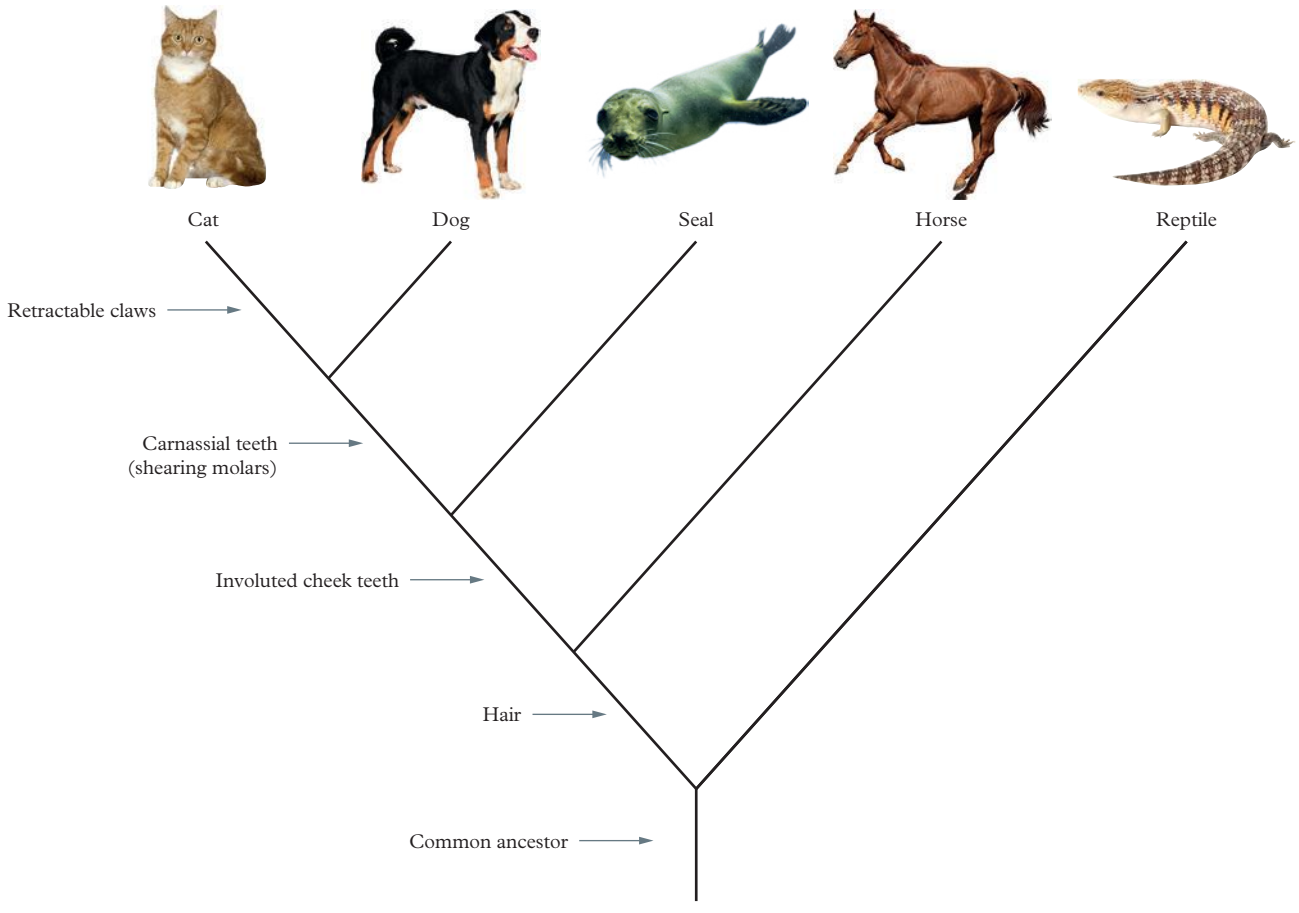


FIGURE 1 A cladogram is a sequence of branches based on derived characteristics from a common ancestor. The features shown are illustrative only and are not the only ones that would be used in determining the branching points. The beginning of the tree, called the root, is the last common ancestor.

Worked example 13.1A

Identifying clades

Analyse the cladogram in Figure 2 to **identify** the organism that forms a clade with birds, crocodiles and rodents. (1 mark)

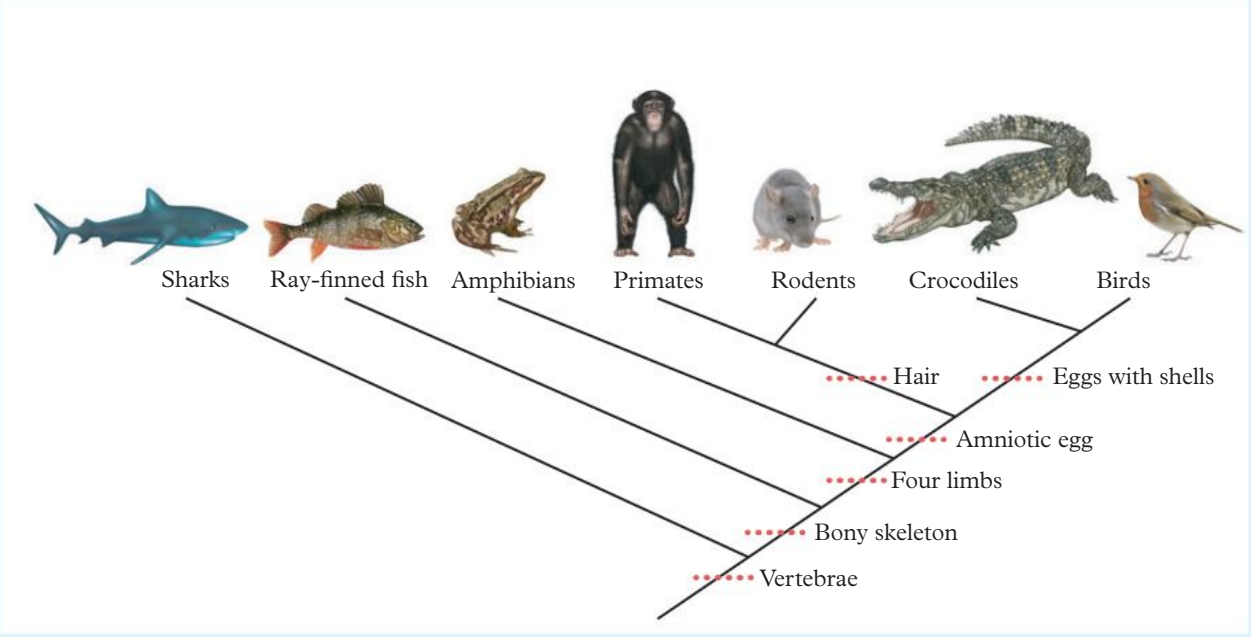
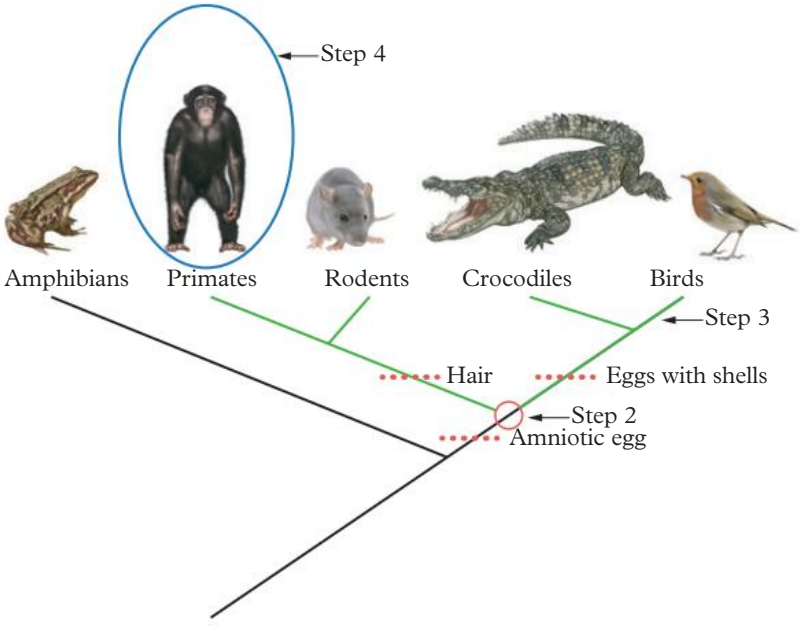


FIGURE 2 A cladogram showing evolutionary relationships between seven species

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking you to do.	To "identify" means to locate, recognise and name.
Step 2: Locate the node representing the common ancestor of the organisms provided.	
Step 3: Identify all organisms branching from that common ancestor.	
Step 4: Determine the missing organism not identified in the list.	

Think	Do
Step 5: Write a statement directly answering the question.	Primates form a clade with birds, crocodiles and rodents. (1 mark)

Your turn

Analyse the cladogram in Figure 3 to **identify** the dinosaur that forms a clade with Ankylosaurus, Stegosaurus and Thyreophora. (1 mark)

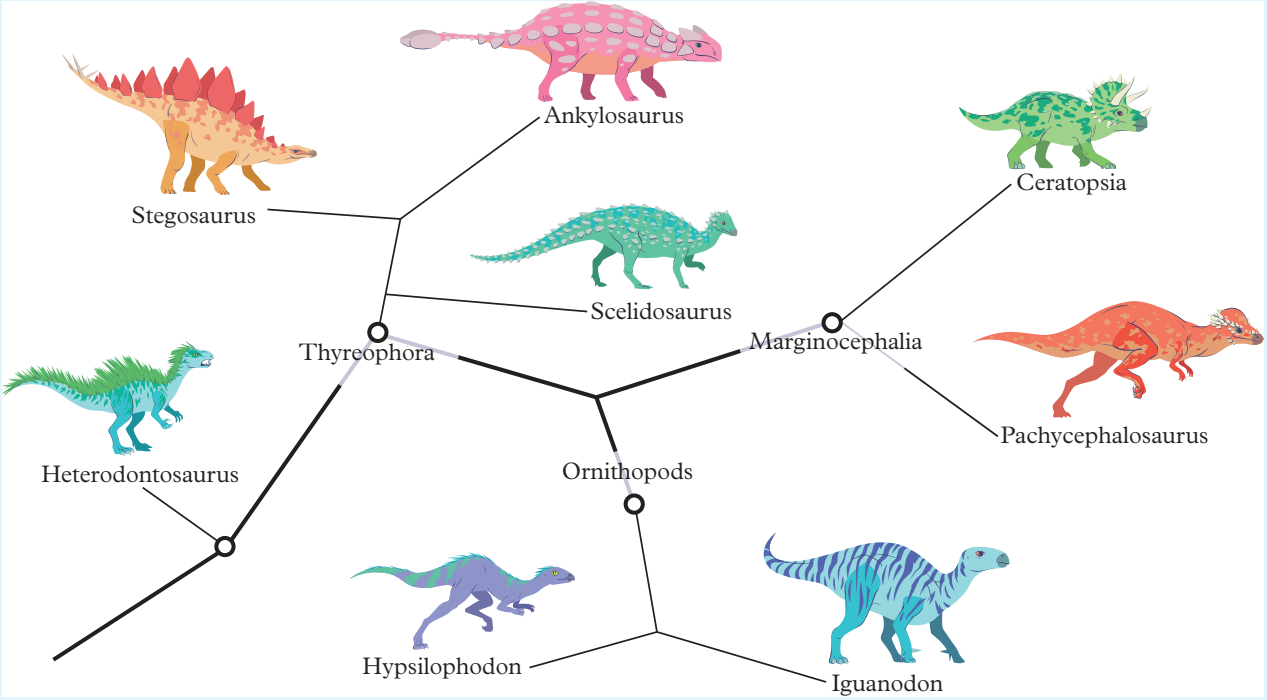


FIGURE 3 A cladogram showing the evolutionary relationships between Ornithischian dinosaurs

Chromosome and DNA analyses

karyotype
the number and visual appearance of the chromosomes in the cell nuclei of an organism or species

The **karyotype** of an organism is a description of the number of chromosomes, and the arrangement of DNA in the chromosomes, in the organism's cells. Each species has a set number of chromosomes in each cell of its body.

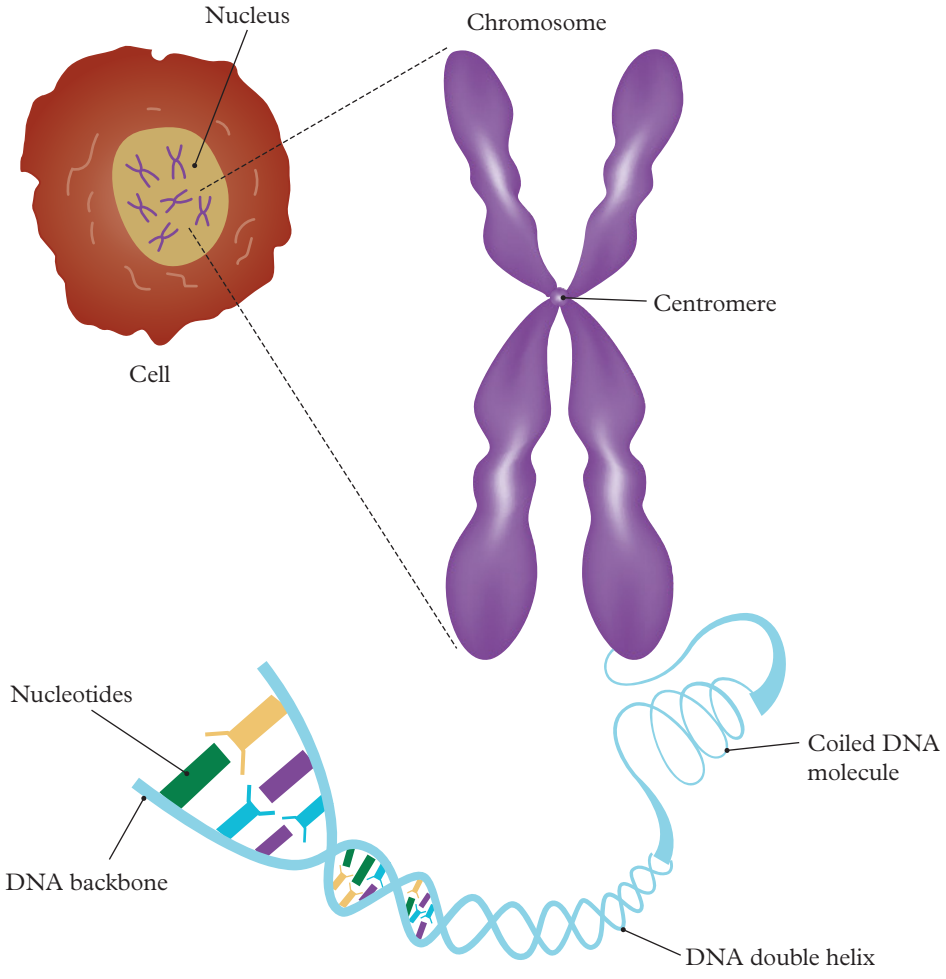


FIGURE 4 Every body cell (somatic cell) in an organism contains a set of chromosomes in pairs. Chromosomes are made up of DNA and replicate before cell division (mitosis). Replicated chromosomes stay connected by a specialised structure made up of DNA and proteins, called a centromere.

Differences between chromosomes in any species can be observed in the position of the centromere and chromosomal banding. Chromosomes can be stained to show a banding pattern similar to a barcode. These bands are unique to each chromosome, making them easy to identify and compare (Figure 5). For example, in humans, chromosome 4 has a different banding pattern to chromosome 5 and chromosome 16. Thus, if samples are collected from two individuals, it is easy to identify and compare chromosome 4 from each individual. Similarities and differences between individuals or species can be identified by comparing their entire karyotype, containing all their chromosomes. Differences in karyotype between species can sometimes be explained by chromosomal mutations (permanent changes in the number or arrangement of chromosomes).

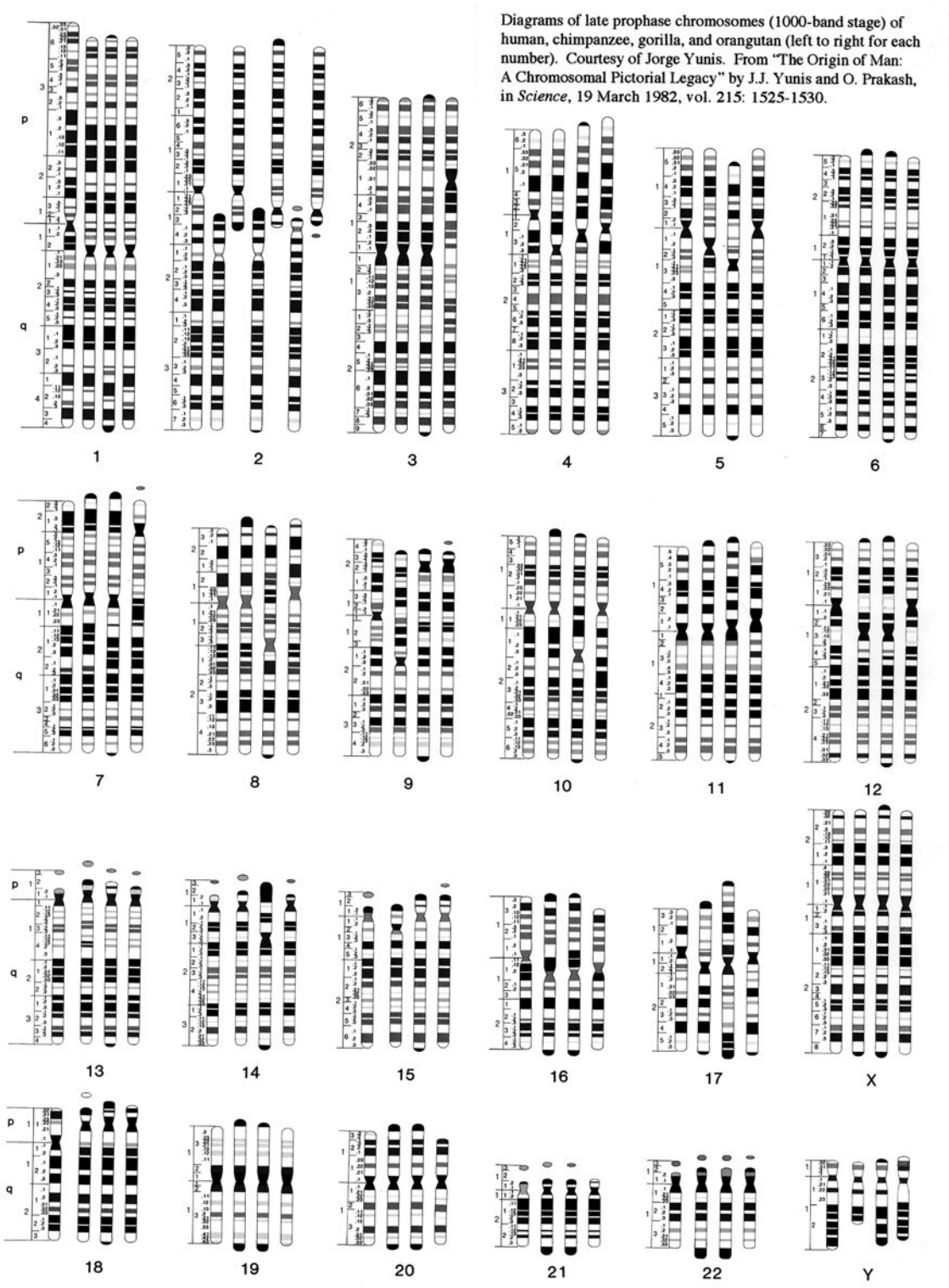


FIGURE 5 Comparison of banding patterns in the chromosomes of (from left to right for each number) humans, chimpanzees, gorillas and orangutans shows many similarities, indicating a relatively recent shared common ancestor.

Each chromosome (made of a DNA molecule wound around histones) contains the genetic code, which can be translated into proteins (the building blocks of all organisms). Any variation in the genetic code can result in a different (and possibly non-functioning) protein being made.

The unravelling of the code contained in each chromosome, and its role in controlling how an organism develops and survives, has led to a greater understanding of relationships between organisms and their evolutionary pathways. Protein comparisons between different organisms are, in effect, a comparison of that part of the chromosome. The greater the number of similar proteins, the closer the relationship between the organisms. If two organisms have very similar proteins, they will have similar nucleic acids, and therefore they may have a common origin. So the analysis of molecules such as DNA or proteins can be used to determine the evolutionary relationship between organisms.

Molecular analysis

molecular analysis
the study and comparison of biological molecules such as DNA, RNA, proteins and genomes

Molecular analysis techniques have become easier and more accessible for scientists. This means the construction of cladograms using molecular data has become more detailed.

As time passes, more mutations accumulate in the DNA. Many of these sections of DNA contain the code for a protein, and the proteins eventually change as these DNA mutations accumulate. The greater the number of changes in DNA or proteins, the more time has passed for these mutations to accumulate. An estimate of real-time differences can be approximated by calibrating the DNA and protein clock with fossil dating.

Amino acid sequences

Each protein collected from a sample is made up of a chain of amino acids (a polypeptide chain) (Figure 6). A change in one amino acid along this chain results in changes to the shape of the final protein. New technologies have resulted in relatively rapid analyses of the sequence of amino acids in the proteins. When the sequences of amino acids for the same protein are compared, the number of differences in the amino acids can be determined. The greater the number of differences in amino acids between two organisms, the more time has passed for changes to accumulate since their common ancestor.

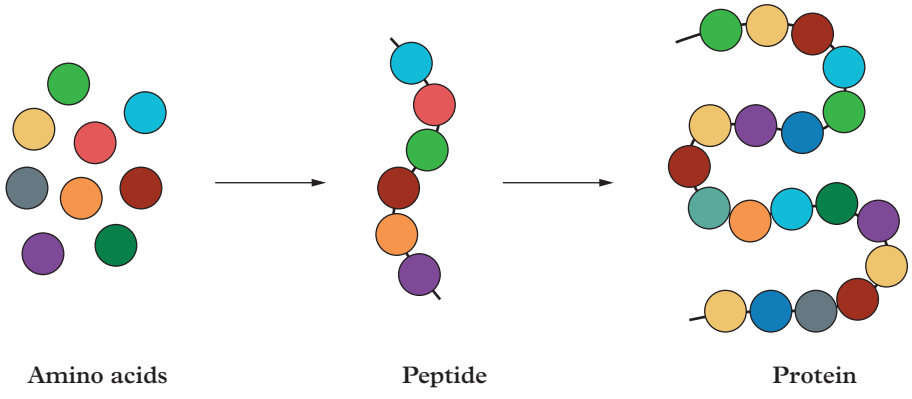


FIGURE 6 Amino acids are the building blocks of proteins.

DNA sequencing

Not every mutation in DNA results in a change in an amino acid. Therefore, two species may have an identical amino acid sequence for a protein but have different DNA sequences. Comparison of these DNA sequences in determining relatedness between species is therefore more powerful than comparison of proteins. Sequencing of DNA is carried out in a laboratory to determine the exact order of the nucleotides that code for amino acids, which make up the protein. DNA is extracted from cells and cut into small sections to allow for targeted sequences to be read. Advanced bioinformatics software is used to analyse and interpret the results of this process, giving detailed insights into genetic relationships between organisms.

FIGURE 7 Preparation of bacterial samples for DNA sequencing

Mitochondrial DNA

Each pair of chromosomes (DNA) in the nucleus of any sexually reproducing individual is composed of one chromosome inherited from the individual's mother and a chromosome inherited from the father.

In mammals, the Y chromosome must be inherited from the father's paternal line. Any mutations in the Y chromosome should be able to be traced through the father's linage.

In all sexually reproducing species, all the mitochondria in the cells of an organism are inherited from the mother only. The mitochondria (like chloroplasts in plants and algae) are able to replicate themselves. Like the bacteria from which they are thought to have originated, mitochondria contain a circular molecule of DNA that contains the code for the enzymes essential for cellular respiration (Figure 8).

In humans, the mitochondrial genome consists of about 16,500 base pairs, which are known to code for 13 proteins, 22 tRNAs and 2 rRNAs. During fertilisation, only the nucleus of the sperm (containing no mitochondria) enters the ovum. Even when sperm cells are injected directly into the cytoplasm of the ovum (during IVF), no paternal **mitochondrial DNA** is found in the zygote.

mitochondrial DNA
a double-stranded DNA found only in mitochondria; in most eukaryotes, circular and maternally inherited

Using the DNA in the mitochondria (mtDNA) to determine the relationship between two groups of organisms has many advantages over using the DNA in the nucleus. For example:

- Direct genetic lines can be traced, because only maternal mtDNA is passed on to offspring.
- mtDNA does not exhibit recombination (swapping bits of chromosome in a pair, one of which is maternal and the other paternal), which creates a garbled genetic history.
- Mitochondria are present in large numbers in each cell, so fewer cell samples are required to obtain large amounts of mtDNA.
- mtDNA has a higher rate of mutations than nuclear DNA, making it easier to identify differences between closely related individuals. By determining the rate at which this mutation occurs, a molecular clock can be calculated that can give the point in time at which groups diverged.

Although the human mitochondrial genome was one of the first human chromosomes to be analysed and sequenced in its entirety, it is only very recently that technology has allowed comparison of the whole sequence.

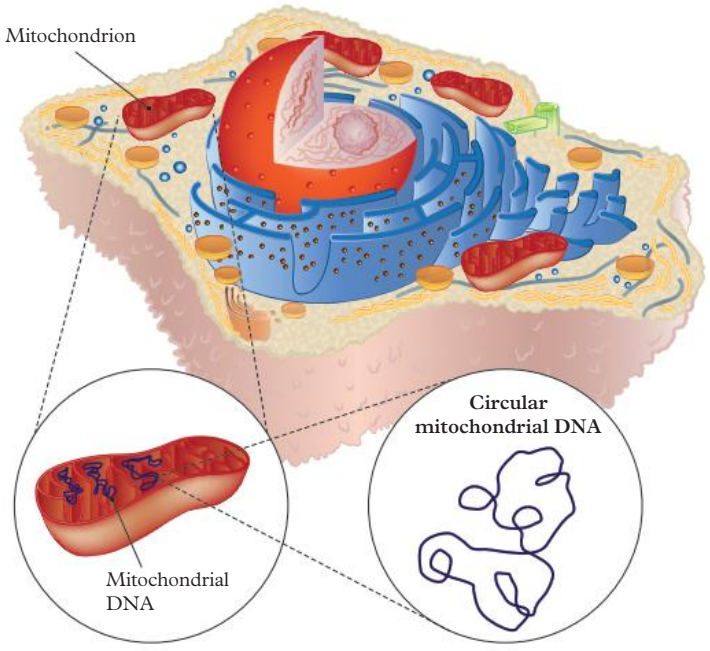


FIGURE 8 A mitochondrion contains circular strands of DNA, called mitochondrial DNA. Sperm do not pass on mitochondria. All mitochondrial DNA is passed on through the maternal lineage.

Skill drill

Comparing molecular sequences

Science inquiry skill: Lesson 1.7
Processing and analysing data

The mitochondrial DNA of three species was analysed and compared, as shown in Table 1. Higher values indicate more differences between the species.

TABLE 1 Nucleotide differences between the mitochondrial DNA of three species

Species	A	B	C
A	0	130	80
B	130	0	170
C	80	170	0

Practise your skills

1 **Identify** the most and least distantly related species. (1 mark)
2 **Explain** why the most recently related species have fewer nucleotide differences in their mitochondrial DNA than the most distantly related species. (3 marks)
3 **Construct** a cladogram to show the possible relatedness of these species with a common ancestor. (4 marks)

Phylograms

The evolutionary relationship between two or more organisms can be quantitatively represented on a phylogram. These diagrams use similarities between the molecular sequences of organisms to represent the length of time that has passed since the species shared a recent common ancestor. The individual taxon group is placed on a "leaf", and the ancestral line is represented by a "branch" (Figure 9). Each common ancestor is represented by a node (the point at which two branches combine). Each group of taxa that evolve from a common ancestor is called a clade. The beginning of the tree is the "root" and represents the last common ancestor. The last common ancestor is typically unidentified on a phylogram. For all life on Earth, the last common ancestor is still unknown, but is postulated to be an archaea.

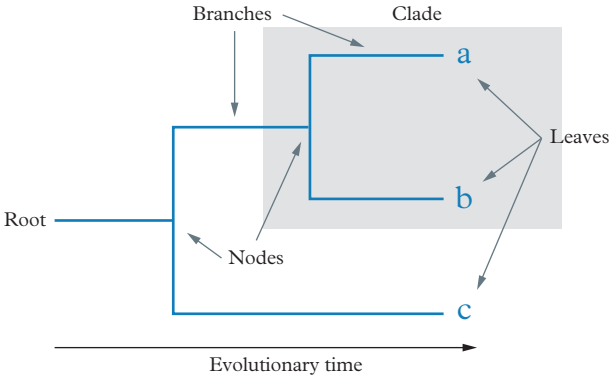


FIGURE 9 The ancestral line of each taxon is represented by a branch, with the taxon named on the leaf. A node represents a common ancestor.

Study tip

All organisms share a common ancestor, if you go back far enough in time. For this reason, it is better to describe the most recent common ancestor when examining evolutionary relationships between organisms.

Worked example 13.1B

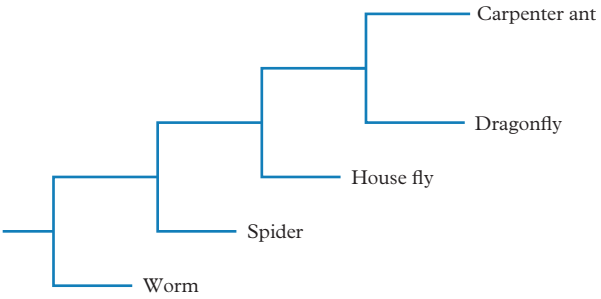
Constructing a phylogram

Construct a phylogram using the characteristics of the organisms in Table 2. (2 marks)

TABLE 2 Characteristics of some organisms

Organism	Cells	Number of legs	Number of antennae	Number of wings
Worm	Yes	0	0	0
Spider	Yes	8	0	0
Carpenter ant	Yes	6	2	4
House fly	Yes	6	2	2
Dragonfly	Yes	6	2	4

Think	Do
Step 1: Look at the cognitive verb and mark allocation to determine what the question is asking you to do.	To "construct" means to display information in a diagrammatic or logical form.
Step 2: List key observations.	• All organisms are multicellular. • All organisms except for worms have legs. • Carpenter ant, housefly and dragonfly have antennae. • Carpenter ant and dragonfly have four wings.

Think	Do
Step 3: Begin with the root and then draw branches for each organism.	
Step 4: Double check that your observations and branches flow logically.	
Step 5: State the final solution.	

(1 mark for showing correct relationship between species, 1 mark for using correct phylogram conventions)

Your turn

Construct a phylogram using the characteristics of the organisms in Table 3. (2 marks)

TABLE 3 Characteristics of some organisms

Organism	Segmented body	Number of legs	Elytra (modified forewings)	Position of wings at rest
Moreton Bay bug (*Thenus orientalis*)	yes	10	–	–
Christmas beetle (*Anoplognathus* spp.)	yes	6	yes	–
Goat moth (*Endoxyla affinis*)	yes	6	no	open
Richmond birdwing butterfly (*Ornithoptera richmondia*)	yes	6	no	closed

Check your learning 13.1

Check your learning 13.1: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Explain** how the cladistic system of classification differs from the Linnaean system. (3 marks)
2 **Describe** a cladogram. (2 marks)
3 **Explain** the assumptions that underpin cladistics. (2 marks)
4 **Describe** the main features of organisms that are used to develop a cladogram. (2 marks)
5 **Define** a "clade". (1 mark)
6 Modern methods of molecular analysis are significant in cladistic analysis. **Describe** two of these methods, and explain how each assists in the development of a cladogram. (4 marks)

Knowledge utilisation

7 The nuclear DNA of three closely related species was examined. The similarity in genes between species was identified as:
- between A and B – 92%
- between A and C – 96%
- between B and C – 99%.

In a particular segment of DNA consisting of 1,000 nucleotides, the number of substitution differences in the bases was:

- between A and B – 6
- between A and C – 4
- between B and C – 2.

When the segments of all three species were analysed, both B and C exhibited a deletion at the same position.

Mitochondrial DNA marker segments were virtually the same, with no differences between species B and C, and one difference shown in species A. This difference was in a non-conserved gene that has a known mutation rate of 1 mutation per thousand years.

a Using this information, **construct** a phylogram showing the divergence of these species from a common ancestor. (2 marks)

b **Determine** the time frame in which the second species diverged after the appearance of the first. **Justify** your answer using data. (2 marks)

Lesson 13.2
Comparative genomics

Key ideas

→ Comparative genomics is the study of similarities and differences in the DNA of organisms to better understand the genetics, function and evolutionary relationships of organisms.

→ Comparative genomics supports the theory of evolution by finding evidence of genetic similarities between organisms.

→ Conserved sequences are useful in estimating time since divergence of a species, because accumulation of mutations is predictable and can act as a clock.

Comparative genomics

Learning intentions and success criteria

Comparative genomics studies the similarities and differences between species' genomes. An understanding of these similarities and differences allows a picture to be built of evolutionary relationships and how organisms function and interact with their environment. Tools for comparative genomics include genome mapping, where the entire genetic sequence of all an organism's chromosomes is identified and labelled, so it can be compared to those of other organisms. Genome mapping may be used to compare individuals of a single species or in cross-species sequence comparisons.

Comparative genomics provides evidence for the theory of evolution by enabling the identification of shared genetic information between species, demonstrating shared ancestry. For example, many human genes for detecting smells have been identified as having originated in an early fish species that lived more than 400 million years ago.

FIGURE 1 Many human genes for smell have been traced to an ancestral fish species.

Conserved sequences

conserved sequence
a gene or sequence of DNA that remains unchanged while evolution influences the surrounding DNA

Some genes and sequences of genes are less likely to accumulate mutations than other genes. These **conserved sequences** and genes are often involved in key roles in the survival of the organism, so any mutations could cause the organism to die, preventing the mutation from being passed on to the next generation. Some examples of these types of genes are:

- regulatory genes that code for the production of hormones
- genes that code for the formation of tRNA
- genes involved in the production of ATP, which is needed for energy.

Molecular clock

When a population of a species becomes separated into two, new selection pressures are exerted on the separated populations and genetic differences begin to accumulate. Some of these differences are molecular, where mutations in the DNA sequences accumulate over time. Differences in the DNA sequence may cause corresponding differences in the amino acid sequences, and eventually in the phenotype of the organism. The number of differences in a molecule between two species is an indication of the amount of time that has passed since they shared a common ancestor. Each gene accumulates mutations at a different rate. If the mutation rate of a particular gene is known, this is called a **molecular clock**.

molecular clock
a technique that uses the rate of genetic mutation to estimate the timing of the evolutionary divergence of two or more organisms

Mitochondrial DNA

Mitochondria are needed by all living cells to produce ATP for energy. Each cell contains multiple mitochondria, each with its own DNA. Because sperm cells only carry genetic information in the form of chromosomes, all mitochondrial DNA is inherited from the egg provided by the mother. There is no recombination in mitochondrial DNA as there is in nuclear DNA. This means any variation is the result of an accumulation of regular mutations, producing a reliable measure of the time that has passed since two individuals shared a common maternal ancestor. This is sometimes referred to as a "mitochondrial clock", because it measures the passing of time.

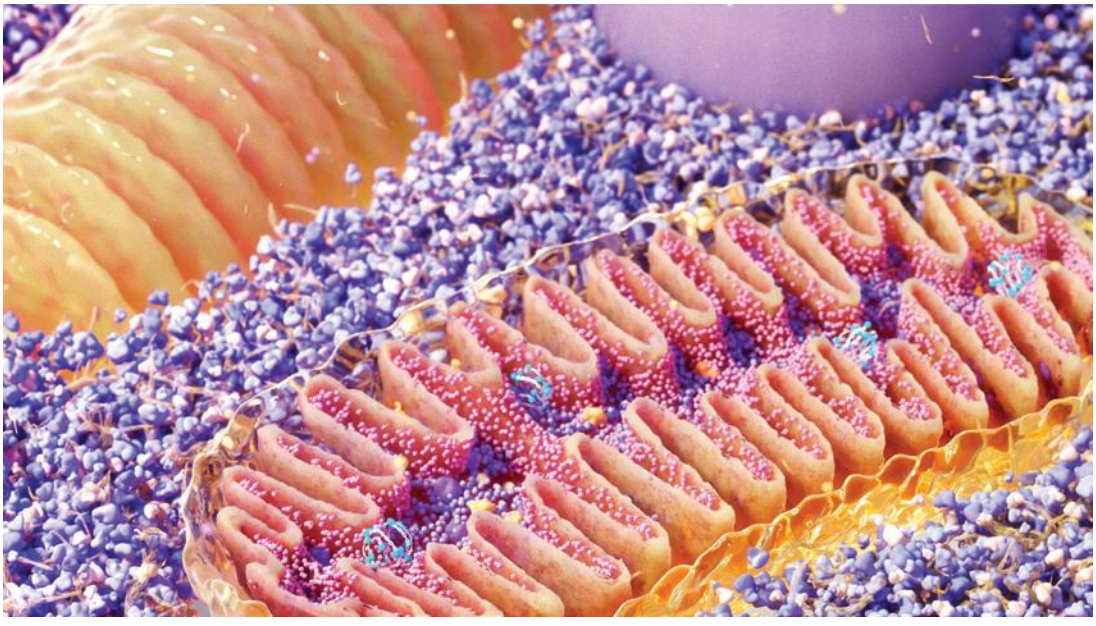


FIGURE 2 An illustration of the internal structure of a mitochondrion

Using the molecular clock

It has been found that mutations occur more readily in non-coding sequences of DNA. The degree of evolutionary divergence of different organisms can be estimated by the number of differences between their comparable base sequences. Using a similar technique, the rate of mutation for any particular gene can be determined. Some genes, for example, have been found to accumulate mutations at a relatively constant rate (e.g. 1 per cent change per million years). These genes can then be used as "molecular clocks" to estimate when species divergence is likely to have occurred.

The reliability of molecular clocks is hindered by:

- different organisms (e.g. animals and plants) having different rates of change
- different genes and proteins having different rates of change
- the possibility that, over long periods of time, early changes may be covered by later changes.

	10	20	30	40	50
Human	AAAGAAGACC	ACGGAGGCCC	TGCTGGAGCT	GAAGGCCGTG	CTGGAGGCCC
Chimpanzee	AAAGAAGACC	ACGGAGGCCC	TGCTGGAGCT	GAAGGCCATG	CTGGAGGCCC
Rat	GGAGAAGACC	AAGGAGGCCC	TACTGGAGCT	AAAGGCCATG	CTGGAGGCCC
Guinea pig	AGAGAAGACC	AAGGAGGCCC	TGCTGGAGCT	GAAGAGCATG	CTGGAAGCTC
Cow	AGAGAAGACC	AAAGAGGCCC	TGCTGGAGCT	GAAGGCCATG	CTGGAGGCGA
Dog	AGAGAAGACC	AAGGAGGCCC	TGCTGGAACT	GAAAGCCATG	CTGGAGGCCC

	60	70	80	90	100
Human	ACCCTGAGGT	GGTGTCCCAC	TACCTGGTGG	GGGTACGCTT	CACCTG–GAG
Chimpanzee	ACCCCGAGGT	GGTGTCCCAC	TACCTGGTGG	GGCTACGCTT	CACCTG–GAG
Rat	ACCCCAAAGT	GGTAGCCCAC	TACCCCGTAG	AGGTGCGCTT	CACCCGAGGC
Guinea pig	ACCCCAAGGT	GGCAGCCCAC	TACCCTGTGG	GGGTGCGCTT	CACCCGGGGG
Cow	GCCCCAAGGT	AGTGGCCCAC	TACCCCGTGG	AGGTACGCTT	CACTCGCGGG
Dog	ACCCCAAGAT	GGTGGCCCAC	TTCCCTGTGG	AGGTCCGCTT	CACCCGCGGG

	110	120	130	140
Human	GATGACATCC	TACTGAGCCC	CTGCTTCCAG	TGGGACAGCCG
Chimpanzee	GATGACATCC	TACTGAGCCC	CTGCTTCCAG	CGGGACAGCCG
Rat	GATGACATTC	TGCTGAGCCC	CTGCTTCCAG	AGGGACAGCTG
Guinea pig	GACGACATCC	TGCTGAGCCC	CTCCTTCCAG	AGGGACAGCTG
Cow	GACGACATCC	TGCTGAGCCC	CTGCTTCCAG	CGAGACAGCTG
Dog	GATGACATCC	TGCTGAGCCC	CTGCTTCCAG	AGGGACAGCTG

FIGURE 3 Differences in the sequence of 140 nucleotides in the same small DNA segment from six mammal species shows 100 per cent similarity between humans and chimpanzees, six differences between humans and rats, and at least one difference between humans and guinea pigs, cows or dogs.

Taken together, information from protein similarity, comparisons of conserved genes, nuclear DNA sequencing and mitochondrial DNA studies provide strong evidence for both divergent evolution and the approximate time of occurrence.

A computer program known as **BLAST** (Basic Local Alignment Search Tool) compares DNA nucleotide or protein sequences to sequence databases and calculates the statistical significance of their matches.

BLAST
Basic Local Alignment Search Tool, a computer program that compares unknown DNA or protein sequences with those of known sequences

Different types of BLAST programs are available according to the sequences under investigation. For example, following the discovery of a previously unknown gene in a mice, a scientist will typically conduct a BLAST search of the human genome to see whether humans carry a similar gene. BLAST will identify sequences in the human genome that resemble the mouse gene based on similarity of sequence.

This powerful system can be used to:

- identify species or find homologous species (e.g. when working with a DNA sequence from an unknown species)
- determine the domain or distinct functional and/or structural units in a protein, using a protein sequence
- generate phylogenetic trees
- determine the chromosomal position of a particular DNA sequence (e.g. of an unknown species)
- compare chromosomal positions of common genes in two related species.

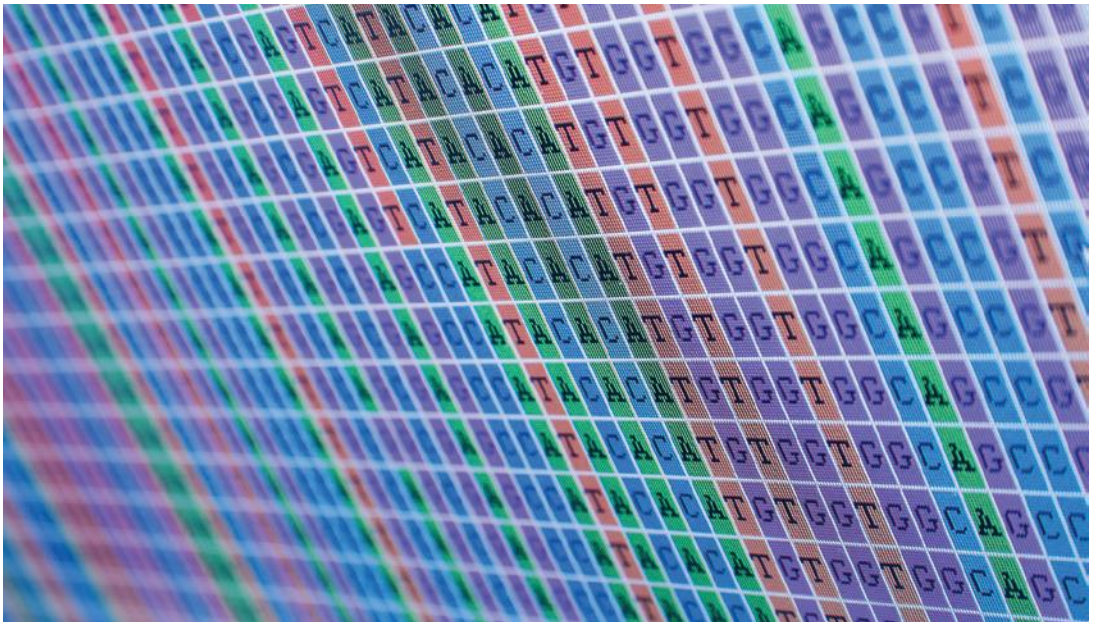


FIGURE 4 In BLAST, DNA bases are aligned to identify similarity between genes.

Check your learning 13.2

Check your learning 13.2: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Describe** what is meant by "conserved sequence". (1 mark)
2 **Explain** how comparative genomics can be used to support a hypothesis that two species are closely related. (2 marks)
3 **Explain** the meaning of a "molecular clock" in the study of evolution. (2 marks)

Analytical processes

4 **Determine** how BLAST technology can improve identification of closely related species. (2 marks)
5 **Determine** whether samples that show 45 differences in their molecular sequence are more closely related or less closely related than samples that show 134 differences in their molecular sequence. (1 mark)
6 **Contrast** mitochondrial DNA and nuclear DNA. (1 mark)

Lesson 13.3
Mass extinctions

Key ideas

- → Endangered species are classified according to their vulnerability to extinction in the future.
- → Species with low genetic diversity are vulnerable to extinction, due to their inability to adapt to a rapidly changing environment.
- → Mass extinctions occur when wide-scale catastrophic environmental events take place, wiping out many species in a short time frame.

Time scales in evolution

Learning intentions and success criteria

It can be difficult for humans to grasp the time scale of evolution. In Australia, our lifespan is on average 82 years, a drop in the ocean compared to the millions of years required for the evolution of new species. To humans in our short lifetimes, Earth seems stable and relatively unchanging, but over longer periods, large-scale changes become apparent. Dramatic climatic changes, such as ice ages, have come and gone, volcanic eruptions have disturbed the atmosphere for years at a time, and tectonic plates have moved around the Earth. All these changes, gradual and sudden, have had an impact on the organisms living on Earth during that time. Some events provided great opportunity for life to thrive, and some signalled the end for many species.

Extinctions

Ecologists and conservationists categorise species in relation to their population size and chances of surviving into the future. In Queensland, species at high risk of extinction in the medium term are classified as "vulnerable", species at very high risk of extinction in the near future are classified as "endangered", and species at extremely high risk of extinction in the immediate future are classified as "critically endangered". More than 1,000 species currently meet one of these classifications in Queensland, including species of marsupials, frogs, birds and plants. These vulnerable, endangered or critically **endangered species** occur in low numbers and are likely to become **extinct species** if the factors exerting pressure on them continue. Some species have become extinct as their environment changed too quickly, meaning they could not survive the changing selection pressures. This is particularly evident in species with limited genetic diversity in their populations. A species is considered extinct if it is unreasonable to doubt that there are no living individuals remaining. The methods for confirming extinction vary depending on the species, due to differences in behaviour, geographic range and habitat.

Natural and physical changes on Earth bring about movement of the continents and variations in climate. These changes affect environmental selection pressures. Evidence from the fossil record shows that throughout the history of life on Earth, many species have become extinct. This was brought about by natural and physical changes in the Earth's ecosystems, geosphere and climate that exert selection pressure on organisms.

Scientists have identified five major extinction events, in which over 75 per cent of the existing species of the time died out. These events are referred to as **mass extinctions** (Figure 1). Most of these extinctions appear to be related to periods of rapid climate change brought on by a variety of factors.

endangered species
a species of animal or plant at threat of extinction through risks to its health, distribution or habitat

extinct species
a species for which there is no reasonable doubt that the last individual has died; a species that is extinct in the wild exists only in captivity, not in its natural habitat

mass extinction
the rapid and widespread extinction of a large number of species more quickly than they can be replaced; often caused by a catastrophic natural event resulting in widespread change to global systems

1 **570 Ma –** Emergence of prokaryotes and eventually eukaryotes. Much later, eukaryotic cells started clumping together and became specialised (multicellular) to aid survival.
2 **520 Ma – Trilobites emerged**.
3 Expansion of marine invertebrates. Emergence of first marine vertebrates.
4 **444 Ma – Mass extinction** Ordovician-Silurian event; 86% of species lost. Sea levels dropped. A short, intense ice age occurred.
5 Recovery of many taxa and expansion of marine vertebrates.
6 **400 Ma – Age of the fish** Expansion of land plants and the emergence of vascular plants and then seed plants. First terrestrial animals. Mild global temperatures.
7 **375–360 Ma – Mass extinction** Late Devonian event; 75% of species lost, mostly marine life and some terrestrial life. Caused by climate cooling (led by reduced CO_2 levels in the atmosphere), tectonic movements and volcanic activity.
8 Marine life flourished and fish and molluscs moved to fresh water. Terrestrial plants flourished (to later form coal beds). Gymnosperms (e.g. *Glossopteris*), insects, vertebrate tetrapods emerged.
9 Reptiles diversified, jaw structures changed, creating more efficient predators. Mammal-like reptiles (therapsids) emerged.
10 **251 Ma – Mass extinction** Permian–Triassic event, 95% of species lost due to extreme global warming from volcanic eruptions near Siberia. Huge release of greenhouse gases. Ocean became acidic and stagnant, and released toxic H_2S.

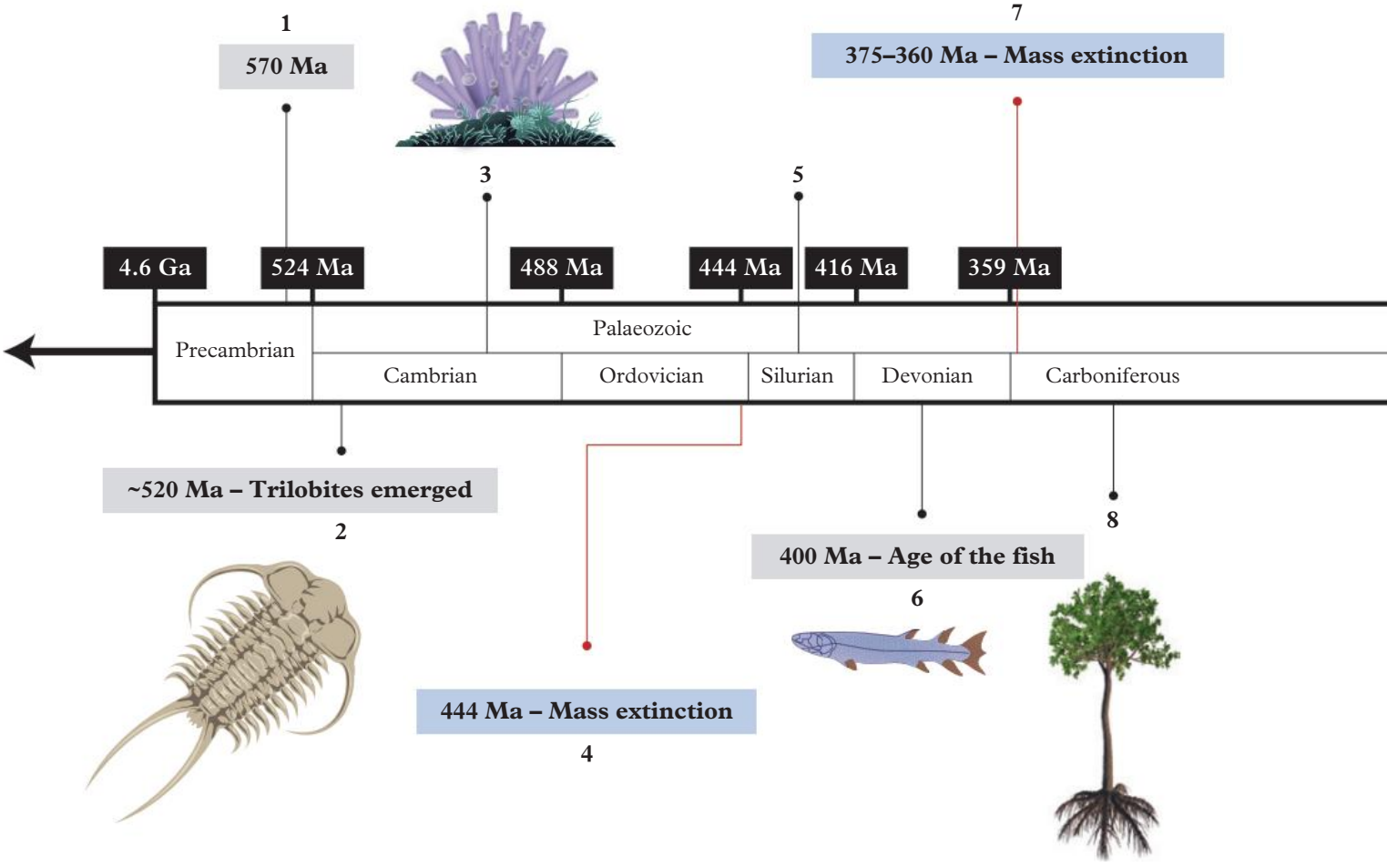


FIGURE 1 Timeline of mass extinction events

11 Reef-building corals evolved. Large fish and reptiles became the main predators. Gymnosperms dominated on land. Small mammals evolved from therapsids. Mass radiation of dinosaurs and first flying reptiles. Frogs established.

12 **199–214 Ma – Mass extinction** Triassic–Jurassic event, 20% of marine animals and many predatory land reptiles caused by Pangaea split into Laurasia and Gondwana, volcanic activity and asteroid collisions driving climate change.

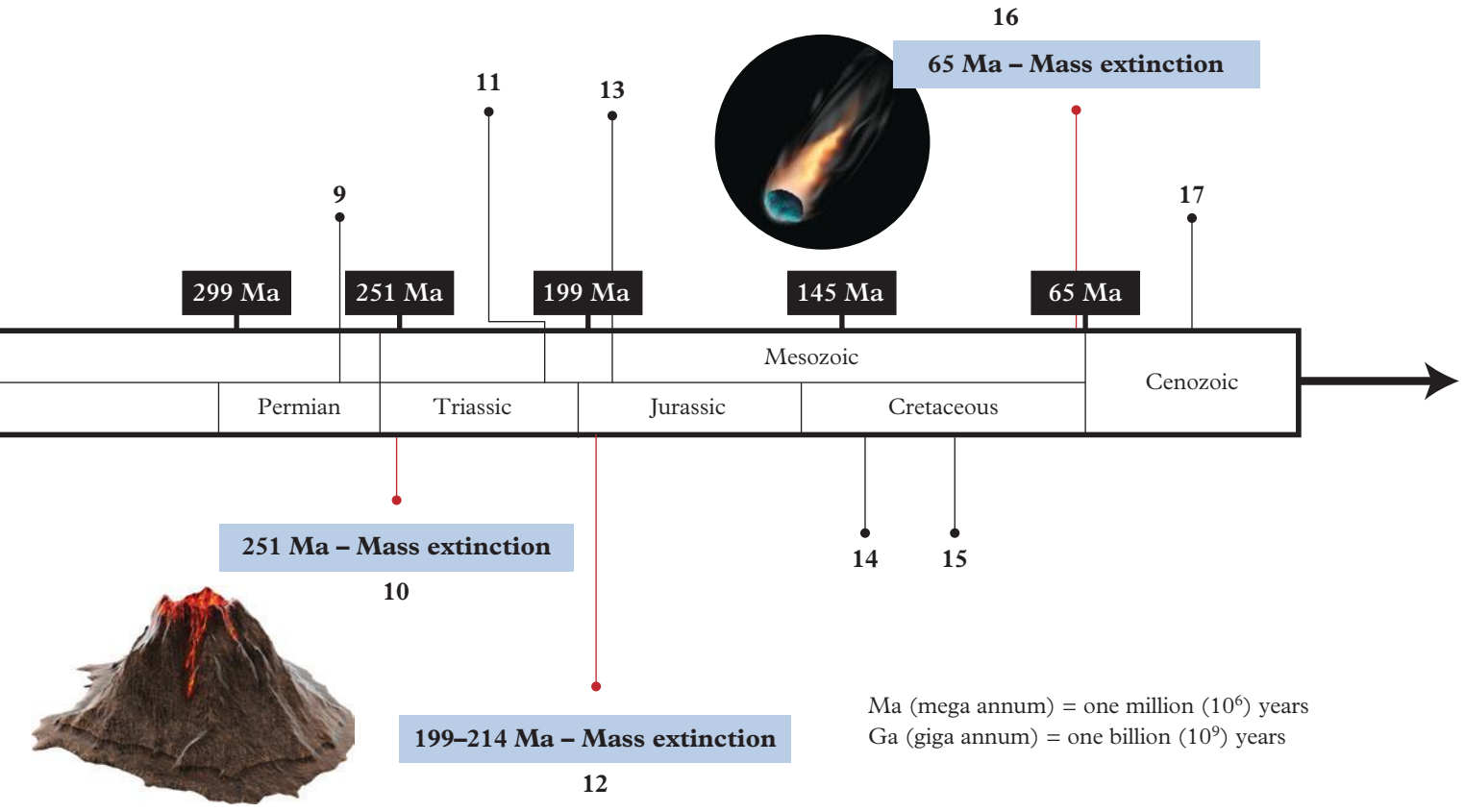
13 Rapid diversity of dinosaurs. First bird, *Archaeopteryx*.

14 Explosion of marine plankton. Seagrasses covered the sea floor. Conifers replaced cycads on land. Flowering plants appeared. Salamanders, turtles, lizards, snakes and crocodiles evolved. The largest reptiles, *Albertosaurus* and *Tyrannosaurus*, evolved. Mammals split into marsupials and placentals. Wading birds and shorebirds evolved.

15 Separation of South America, Africa and India from Antarctica–Australia drove changes to ocean distribution and rain-bearing winds. **90 Ma** – many marine species and large dinosaurs became extinct.

16 **65 Ma – Mass extinction** K–T (Cretaceous–Tertiary) event, 76% of species lost. Caused by meteorite shower and volcanic activity producing enough dust and ash to block out the sun and drive a global winter. Poisonous sulphur gases released into the atmosphere.

17 Modern life with dominance of flowering plants, insects and mammals on land. New array of marine life.



It has been estimated that, although only a small fraction (possibly as few as 0.001 per cent) of the species that have ever lived are currently in existence, species extinction of both plants and animals has increased up to 100 times faster than in the past. The Earth may be facing its sixth mass extinction.

FIGURE 2 *Taudactylus acutirostris*, the sharp-snouted day frog from Queensland, was listed as critically endangered until 2006, when it was deemed extinct.

Challenge

Natural disasters and mass extinctions

Several million years ago, a supervolcano erupted on the North American continent, and continued producing gases and ash for several months. These were carried around the globe by wind currents, blocking sunlight and causing acid rain.

FIGURE 3 Supervolcanoes have erupted several times over Earth's history.

1 **Describe** the possible impact of these ongoing eruptions on the plant life on Earth. (2 marks)
2 **Describe** the possible impact of these eruptions on the Earth's oceans. (2 marks)
3 **Explain** how this environmental disaster could lead to mass extinction of species on Earth. (4 marks)

Check your learning 13.3

Check your learning 13.3: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Explain** why the first mass extinction on Earth only affected marine animals. (2 marks)

2 **Describe** how a shower of meteorites landing on Earth over a relatively short time could bring about mass extinctions. (2 marks)

Analytical processes

3 **Determine** the major contributing factors to past mass extinctions. (2 marks)

4 **Determine** why mammals remained small and were a relatively insignificant group during the age of the dinosaurs, yet they survived the mass extinction of the dinosaurs. (1 mark)

Knowledge utilisation

5 **Hypothesise** how a global temperature rise or drop of 1–2°C could bring about mass extinctions. **Justify** your response from your knowledge of ecosystems and ecosystem change. (4 marks)

Lesson 13.4
Evolutionary radiation

Key ideas

→ Evolutionary radiation is a period of rapid expansion of species on Earth.

→ Evolutionary radiation often follows a period of mass extinction that opens up many ecological niches.

Evolutionary radiation

Learning intentions and success criteria

evolutionary radiation the rapid diversification of species and occurrence of speciation events taking advantage of newly available ecological niches

There have been many rapid expansions in the number and diversity of species, where a single species quickly diversifies into a variety of species to take advantage of newly available ecological niches. This process is called **evolutionary radiation**, and it frequently occurs after a period of mass extinction when the ecological niches abandoned by extinct species become available to other organisms. Random mutations in each population provide new variations that can fill available niches in the environment. Organisms with phenotypes that are suited to the newly available niches will experience reproductive success and pass these traits on to their offspring and future generations.

Evolutionary radiation brings about diverse changes in the morphology of organisms. It may occur as a result of a mutation in an allele providing a new trait that opens up new opportunities for subgroups within the species (and eventually the formation of new species), or it may result from mass extinctions opening up previously occupied niches. This radiation may affect one or many taxonomic groups, and may happen rapidly or gradually.

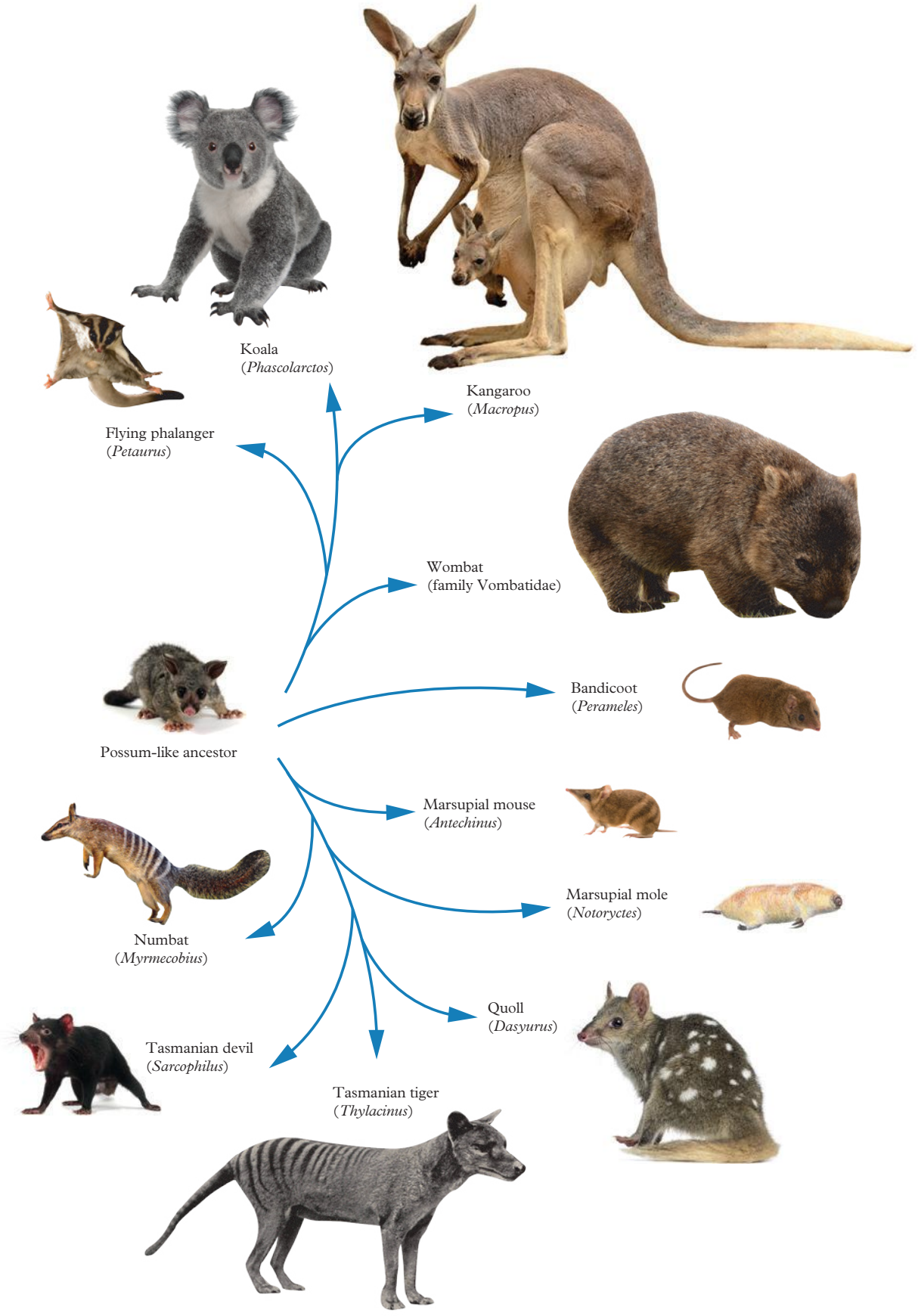
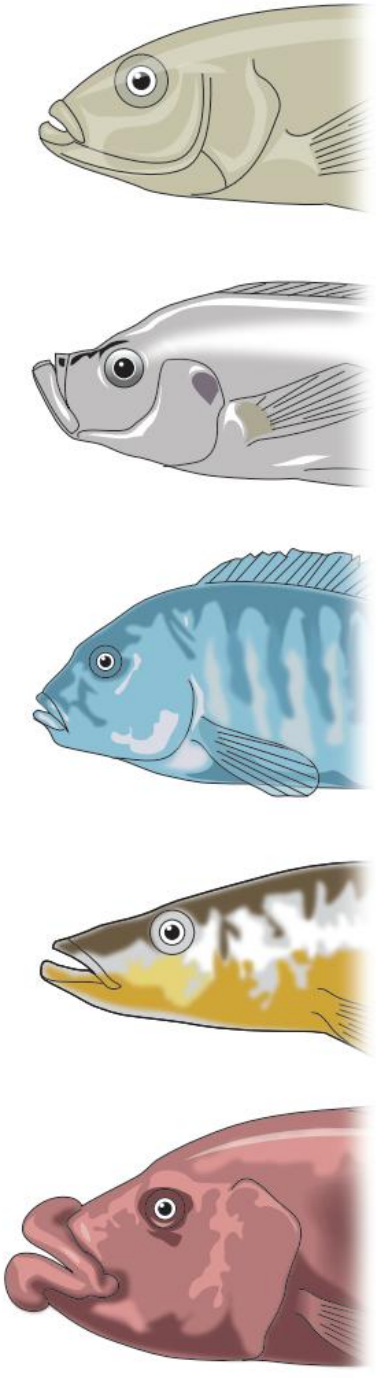


FIGURE 1 Evolutionary radiation can be seen in the diversity of Australian marsupial species.

An example of evolutionary radiation can be seen in the large diversity of cichlid fish species. It is estimated that there are over 2,500 types of cichlid fish species around the world. Many of these are in Lake Victoria, Lake Malawi and Lake Tanganyika in East Africa. It is believed that Lake Victoria, the largest lake in Africa, came close to drying out approximately 12,000 years ago. This period of drying is thought to have resulted in only small pools of water remaining, causing a reduction in the diversity and number of fish species in the lake. As the lake refilled over time, cichlid fish species rapidly diversified from a common ancestor. Approximately 500 species of cichlids are now found in Lake Victoria.



Genyochromis mento
Eats fish scales and fins.

Caprichromis orthognathus
Eats baby fish and eggs.

Trematocranus placodon
Eats molluscs.

Rhamphochromis
Eats small fish.

Abactochromis labrosus
Eats insect larvae.

FIGURE 2 Five species of cichlid fish and their specific diets

Check your learning 13.4

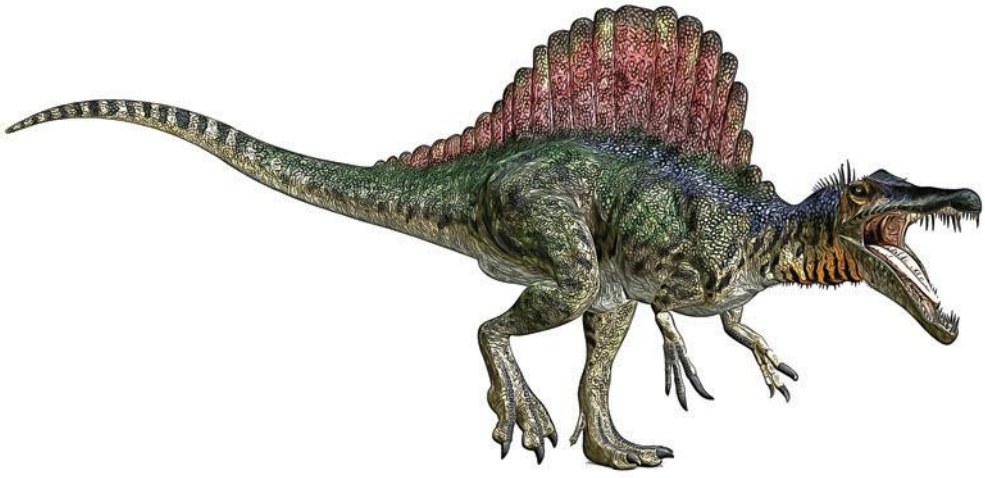
Check your learning 13.4: Complete these questions online or in your workbook.

Retrieval and comprehension

1 **Identify** two causes of evolutionary radiation of species. (2 marks)
2 **Explain** why the presence of key adaptations is important before evolutionary radiation can occur. (2 marks)
3 **Explain** what biologists mean by "ecological niche". (1 mark)
4 **Explain** why some species fill newly created ecological niches, while others do not. (2 marks)
5 **Explain** how the emergence of mammals after the extinction of the dinosaurs is an example of evolutionary radiation. (2 marks)

Analytical processes

6 **Infer** which factors may cause evolutionary radiation to happen quickly or slowly. (2 marks)
7 **Contrast** evolutionary radiation and mass extinction. (1 mark)



MODULE 13

Lesson 13.5
Review: Evidence of evolution

Summary

13.1
- Evolutionary relatedness between species is important in understanding species' adaptations and genetic similarities.
- Cladograms show the evolutionary relationships between species based on shared characteristics.
- Phylograms show the evolutionary relationships between species based on a quantitative measure of genetic mutations.
- Molecular sequencing takes a DNA sample and sequences either amino acids or nitrogenous bases in genetic material that can be read or compared, to gain insights into evolutionary relationships and processes.
- Comparative genomics supports the theory of evolution and aids in estimating evolutionary timing.
- Significant geological and evolutionary events on Earth can be determined by looking at evolutionary timescales of life on Earth.

13.2
- Comparative genomics is the study of similarities and differences in the DNA of organisms to better understand the genetics, function and evolutionary relationships of organisms.
- Comparative genomics supports the theory of evolution by finding evidence of genetic similarities between organisms.
- Conserved sequences are useful in estimating time since divergence of a species, as accumulation of mutations is predictable and can act as a clock.

13.3
- Endangered species are classified using their vulnerability to extinction in the future.
- Species with low genetic diversity are vulnerable to extinction, due to their inability to adapt to a rapidly changing environment.
- Mass extinctions occur when wide-scale catastrophic environmental events take place, wiping out many species in a short timeframe.

13.4
- Evolutionary radiation is a period of rapid expansion of species on Earth.
- Evolutionary radiation often follows a period of mass extinction that opens up many ecological niches.

Review questions 13.5A Multiple choice

Review questions: Complete these questions online or in your workbook

(1 mark each)

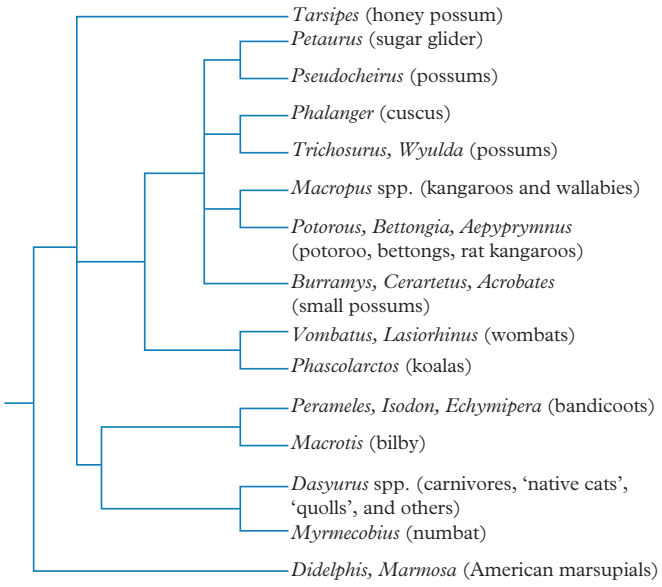
1 Which mass extinction event resulted in the greatest loss of species?

A The late Devonian event
B The Triassic–Jurassic event
C The Permian–Triassic event
D The Ordovician–Silurian event

2 In the cladogram shown in Figure 1, Lesson 13.1, which feature separates a dog from a cat?

A Hair
B Carnassial teeth
C Retractable claws
D Curved cheek teeth

Use the following information to answer questions 3 and 4.
A phylogenetic tree of Australian marsupials is shown.



3 According to the phylogram, the closest relatives to bandicoots are
- **A** bilbies.
- **B** koalas.
- **C** wombats.
- **D** sugar gliders.

4 According to the phylogram, which of the following is the most distant relative of *Petaurus*?
- **A** *Taripes*
- **B** *Potorous*
- **C** *Phalanger*
- **D** *Vombatus*

5 Cladistics is based on
- **A** common physical characteristics.
- **B** similar and dissimilar characteristics.
- **C** evolved and inherited characteristics.
- **D** inherited and common characteristics.

Review questions 13.5B Short response

Review questions: Complete these questions online or in your workbook.

Retrieval and comprehension

6 **Define** "mass extinction". (1 mark)

7 **Explain** two ways scientists can determine evolutionary relatedness. (4 marks)

8 **Define** the term "extinct species". (2 marks)

9 **Define** the term "derived characteristic". **Explain** how it can be used to determine evolutionary relatedness. (3 marks)

10 **Explain** why the different number of mutations in two species helps identify how closely related they are. (2 marks)

11 **Describe** the possible causes of evolutionary radiation. (2 marks)

12 **Describe** how DNA analyses have been significant in tracing evolutionary pathways. (1 mark)

Analytical processes

13 **Infer** why some organisms survived more or less unchanged for millions of years, while others evolved or became extinct. (1 mark)

Knowledge utilisation

14 Populations of pigeons contain both pale grey and dark grey individuals. The difference in colour is genetically determined. There is a higher proportion of dark individuals in city populations and a higher proportion of pale individuals in country populations. All pigeons normally breed in summer. Some characteristics of city and country environments are shown in the table.

	City	Country
Winter temperatures	Warmer	Colder
Winter food supply	Good	Poor
Risk of predation	Similar	Similar

a **Hypothesise**, based on evolutionary theory, what could theoretically account for the observed distribution of colour forms. (1 mark)

b A scientist set out to test the hypothesis that the observed distribution of colour forms existed because dark pigeons, unlike pale ones, are able to breed in winter provided there is adequate food. He proposed carrying out four tests.

i Count the numbers of different-coloured pigeons breeding at different times of the year in both city and country populations.

ii Measure the numbers of deaths caused by predators in both city and country populations.

iii Artificially improve the food supply to a country population.

iv Remove all eggs from the winter nests in a city population.

Propose which of these tests would best provide evidence to support the hypothesis. **Justify** why this test is better than the other three. (2 marks)

15 Current evidence suggests that:

- the first organisms (prokaryotes) appeared on Earth over ~3.5 billion years ago
- the first eukaryotes evolved ~2 billion years ago
- the first multicellular animals evolved ~600,000 years ago.

During that time period, all organisms were marine. Over the past 600,000 years, the increase in eukaryotic marine species and terrestrial plants and animals has expanded enormously despite periods of mass extinctions.

Infer possible reasons for the very slow start in the evolution of life on Earth. **Justify** your response. (3 marks)

16 In 2015, a massive volcanic eruption in Iceland resulted in huge ash clouds over the northern regions of the world that lasted for several weeks. It was so severe that all aircraft in Europe were grounded during that time. A visitor to Iceland shortly after this event noted that large banks (about a metre high) of ash were lined up on either side of all of the roads when the roads had been cleared. She also observed the local people clearing their fields of ash to allow the sparse grasses to grow so their ponies and caribou could graze. Along with seal meat, these animals are the main food sources for the people of Iceland.

Taking into account the characteristics of this ecozone, **discuss** the short-term and long-term consequences for the ecosystem without this human intervention. (4 marks)

17 A comparison of the base sequences of the same section of DNA that codes for ribosomal RNA was carried out for four Australian plant genera: *Eucalyptus*, *Vigna*, *Glycine* (flowering plants, the latter two belonging to the bean family) and *Pinus* (a non-flowering plant). The results are shown below for the first 11 bases in this sequence.

Using this data, **construct** an evolutionary tree showing the relationships between these four plants. **Justify** your response. (3 marks)

	1	2	3	4	5	6	7	8	9	10	11
Eucalyptus	C	C	C	–	T	C	T	T	T	T	T
Vigna	C	T	C	T	T	T	T	T	T	C	A
Glycine	C	T	C	T	T	T	T	A	A	C	G
Pinus	C	C	T	–	C	C	C	C	C	C	C

Data drill

Analysing species relatedness

Mitochondrial DNA (mtDNA) evolves faster than nuclear DNA, making it a powerful tool for evolutionary research. The base sequences of the same section of mtDNA were collected from the remains of three extinct species of hominid: *Homo neanderthalensis*, *Homo erectus* and *Homo habilis*. These base sequences were then compared with the mtDNA of *Homo sapiens* (modern humans). The results are shown in the table below for the first 11 bases in this sequence.

Hominid species	Base sequence											
	1	2	3	4	5	6	7	8	9	10	11	12
Homo neanderthalensis	T	A	C	G	A	G	T	C	C	G	G	A
Homo erectus	T	A	C	G	A	G	T	T	C	G	G	A
Homo habilis	T	A	C	G	A	G	T	T	C	C	G	A
Homo sapiens	T	A	C	G	A	G	T	A	C	G	G	T

Apply understanding

1 **Identify** the bases unique to *Homo sapiens*. (1 mark)

2 **Determine** which two species are most closely related, based on this sequence. (1 mark)

Analyse data

3 **Contrast** the base sequences of *Homo neanderthalensis* and *Homo habilis*. (1 mark)

Interpret evidence

4 Using this data, **construct** an evolutionary tree showing the relationships between these four species of hominid. (3 marks)

Module 13 checklist: Evidence of evolution

UNIT 4

Topic 2 review

Multiple choice

1 Gene flow can be defined as the
- **A** number of times a gene appears in a population.
- **B** inheritance of a genetic trait from parents to offspring.
- **C** random change in the frequency of an allele in a population.
- **D** movement of genes from one population to another through sexual reproduction.

2 Widespread extinction of a large number of species due to a catastrophic environmental change is referred to as
- **A** evolution.
- **B** mass extinction.
- **C** species extinction.
- **D** a population bottleneck.

3 Microevolution occurs
- **A** at species level.
- **B** within a species.
- **C** over geological time.
- **D** during evolutionary radiation.

4 The Kaibab squirrel and Albert's squirrel are two species of squirrel that share a common ancestor. The formation of the Grand Canyon is thought to have geographically isolated populations of the common ancestor which led to the evolution of the two squirrel species.
This is an example of
- **A** coevolution.
- **B** allopatric speciation.
- **C** parapatric speciation.
- **D** sympatric speciation.

5 Which of the following mechanisms is most likely to be responsible for the development of resistance to an infectious disease over several generations?
- **A** genetic drift
- **B** allele frequency
- **C** natural selection
- **D** the bottleneck effect

6 The advantage of using mitochondrial DNA (mtDNA) in tracing ancestry is that
- **A** mtDNA has a lower rate of mutation than nuclear DNA.
- **B** there is less mtDNA in a cell and so contamination of material is low.
- **C** direct gene lines can be traced because only maternal mtDNA is passed onto offspring.
- **D** direct gene lines can be traced because only paternal mtDNA is passed onto offspring.

7 Evolutionary radiation most often occurs
- **A** after a catastrophic event that wipes out a large number of species.
- **B** as a result of the geographical separation of two populations of a species.
- **C** when different organisms are subjected to the same environmental pressures.
- **D** when opportunities for new ecological niches are created by environmental change.

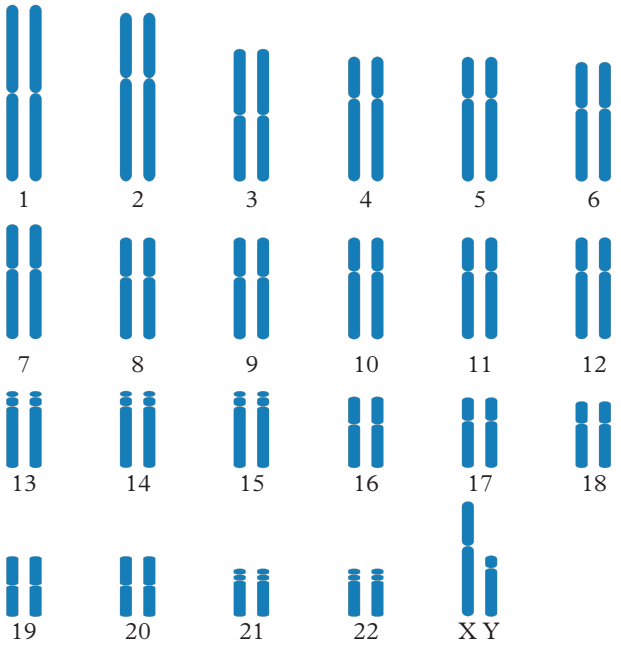
8 Convergent evolution occurs when
- **A** different species evolve together due to a symbiotic relationship.
- **B** a new species evolves from a population although they occupy the same geographic area.
- **C** two species living in the same environment evolve similar traits due to exposure to the same selection pressures.
- **D** individuals within a population are separated geographically due to a natural disaster, such as a volcanic eruption.

9 The inability of two species to occupy the same ecological niche for a long period of time is called
- **A** extinction.
- **B** competition.
- **C** competitive exclusion.
- **D** evolutionary radiation.

10 Natural selection acts on
- **A** genotypes.
- **B** phenotypes.
- **C** homologous organisms.
- **D** heterozygous organisms.

11 Macroevolution is caused by
- **A** gene flow.
- **B** mass extinctions.
- **C** an accumulation of microevolutionary changes.
- **D** interbreeding between populations of the same species.

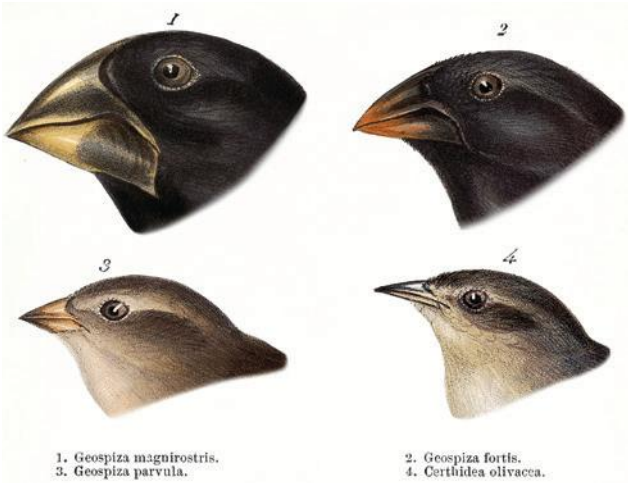
12 The image shows a



- **A** karyotype.
- **B** phylogram.
- **C** cladogram.
- **D** DNA sequence.

13 The most detailed molecular sequencing analysis can be made by comparing sequences of
- **A** proteins.
- **B** nucleotides.
- **C** amino acids.
- **D** chromosomes.

14 The image shows four species of finches living on different islands in the Galapagos that share a recent common ancestor. The beak of each finch is well suited to the type of food available in its environment on the island.



This is an example of
- **A** allopatric speciation.
- **B** temporal speciation.
- **C** sympatric speciation.
- **D** parapatric speciation.

15 The Hardwicke's woolly bat (*Kerivoula hardwickii*) and the pitcher plant (*Nepenthes hemsleyana)*, shown in the image, exert selective pressures on each other.

This is an example of
- **A** coevolution.
- **B** parallel evolution.
- **C** divergent evolution.
- **D** convergent evolution.

Short response

16 One continuous population of a plant species occupies a range that extends all the way around the base of a mountain. On one side of the mountain, the plants grow in a humid environment with high rainfall, while on the other side, the plants grow in an environment with little rainfall and low humidity. Over time, the plants on each side of the mountain become physically different from each other in terms of leaf size and their ability to conserve water.

a If the population eventually becomes two species due to living in different environments, **identify** the type of speciation that will have occurred. (1 mark)

b **Explain** how the plants become more suited to the environment they live in. (3 marks)

17 **Contrast** gene flow and genetic drift. (1 mark)

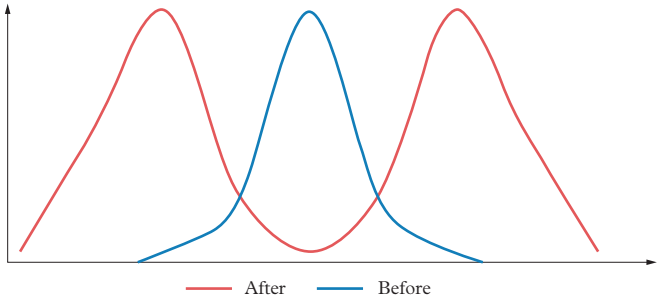
18 **Explain** disruptive selection. (3 marks)

19 **Infer** why some species remain largely unchanged over time, while others evolve into different species or become extinct. (4 marks)

20 Some butterflies and moths have wing spots that have evolved to resemble the eyes of a much larger animal, as shown here.

Explain the evolutionary processes that are likely to have led to this phenotype. (4 marks)

21 The graph shows a population before and after selection. **Identify** the type of selection shown in the graph. (1 mark)



22 **Compare** genetic drift and natural selection in terms of their influence on allele frequencies in small populations. (2 marks)

23 **Compare** allopatric speciation and parapatric speciation. (2 marks)

24 The data shows changes in frequency of two alleles, Q and q, over 45 years in a population of organisms.

Year	Q frequency	q frequency
1975	0.49	0.51
1980	0.47	0.53
1985	0.50	0.50
1990	0.59	0.41
1995	0.65	0.35
2000	0.69	0.31
2005	0.70	0.30
2010	0.72	0.28
2015	0.75	0.25
2020	0.76	0.24

a **Describe** the type of selection acting on allele q in the population (1 mark)

b **Identify** the year in which selection pressures changed in this organism's environment. (1 mark)

c **Predict** what will happen to the allele frequency of Q and q if selection pressures return to their 1975 level. (2 marks)

25 **Explain** how geographic isolation can lead to the development of new species. (4 marks)

26 Scientists observed that, in a population of hares living in Canada, the number of individuals with thicker fur increased over several generations. This increase coincides with several years of colder than usual winters, where rabbits with thicker fur are more likely to survive to produce offspring.

a **Determine** whether this is an example of macroevolution or microevolution (1 mark)

b **Identify** the process driving this change in the rabbits' fur phenotype. (1 mark)

TOTAL MARKS

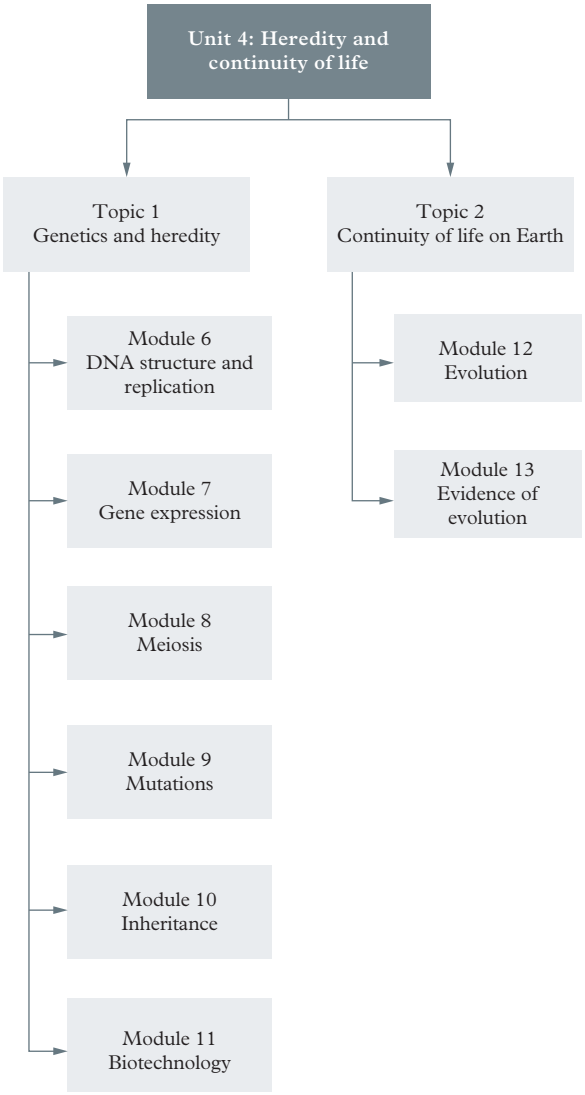
/46

UNIT 4

Review

Part A – Revisit and revise

Part A of the Unit review asks you to reflect on your learning and identify areas in which you need more work.



Part B – Exam essentials

Now that you've completed your revision for Unit 4, it's time to learn and practise some of the skills you'll need to answer exam questions like a pro! Our expert authors have created the following tips and advice to help you maximise your results on the end-of-year examination.

Exam tip 1: Check that you are addressing the subject matter being asked about in the question

Each external assessment item is written for an individual subject matter dot point. Questions do not always contain the same words or terms as the subject matter dot point they are assessing. In fact, some questions might look like they could be addressing a few different parts of the subject matter. For this reason, it is important to check that you are answering the question with the subject matter required. Even if you write some correct information, if it's not the response required by the external assessment marking guide (EAMG), you won't receive the marks. Taking the time to determine exactly which content the question requires will help you avoid silly (and costly) mistakes.

See it in action

Read the exam question below and the two responses that follow. See how the tip has made a difference between a response that has been awarded full marks and a response that has been awarded no marks because it addresses the wrong content.

Question 9 (3 marks)

A computer simulation was used to observe genotypic changes in the gene pool of 20 randomly selected rabbits. The simulation was set with these parameters:

- each rabbit's coat colour was either black or white
- black alleles were dominant; white alleles were recessive
- the number of rabbits was constant in each generation and breeding was random throughout the population
- an environmental factor was chosen in the simulation to provide selection pressure.

The table shows the results of the simulation at the start and after 20 generations.

Initial population genotypes	Population genotypes after 20 generations
BB BB BB BB BB BB Bb Bb Bb Bb Bb Bb Bb Bb Bb Bb bb bb bb bb	BB BB Bb Bb Bb Bb Bb Bb Bb Bb bb bb bb bb bb bb bb bb bb bb

Contrast the initial allele frequency with the allele frequency after 20 generations to draw a conclusion about the effect of the selection pressure on the rabbit population.

Source: *QCAA Biology 2021, Paper 2* © State of Queensland (QCAA)

Complete response

Provides the correct initial and final allele frequencies [1 mark]

Initial allelic frequencies were B 0.55 and b 0.45. Allelic frequencies after 20 generations were B 0.3 and b 0.7. B decreased (from 0.55 to to 0.3) and b increased (from 0.45 to 0.7). This selection pressure was in favour of white rabbits as both genotype and allelic frequencies shifted toward the white phenotype and the white allele.

Identifies consequentially correct change in allele frequency [1 mark]

States a consequentially valid conclusion [1 mark]

Incomplete response

The student has seen the genotypes and assumed that a Punnett square is required in the response to address subject matter from Unit 4 Topic 3 "Infer patterns of inheritance and predict frequencies of genotypes and phenotypes from genetic data including Punnett squares". However, the question asks the student to calculate allele frequency, which addresses subject matter from Unit 4 Topic 4 "Calculate allele frequencies from genotype data".

Bb × Bb

	B	B
b	Bb	Bb
b	Bb	Bb

The allele frequency is 100% heterozygous Bb

The student has correctly completed the Punnett square, but it does not answer the question, so it receives no marks [0 marks]

Think like an assessor

To maximise your marks on an exam, it can help to think like a QCAA assessor. Consider how many marks each question is worth and what information the assessor is looking for.

Read the exam question below and the response that follows. Imagine you are a QCAA assessor and use the marking guide below to mark the response.

Question 23 (3 marks)

In rabbits, black fur is dominant to white fur. A male that is heterozygous for black fur is crossed with a female with white fur, producing 12 offspring.

Predict the number of offspring with white fur. Justify your response using a Punnett square.

Source: *QCAA Biology 2024, Paper 1* © State of Queensland (QCAA)

The parental genotypes are Bb and bb. This means 50% of offspring will have black fur and 50% will have white fur.

Marking guide

Question 23	• Identifies parental genotype [1 mark] • Provides an appropriate Punnett square [1 mark] • Predicts the number of offspring with white fur [1 mark]

Fix the response

Consider where you did or did not award marks in the above response. How could the response be improved? Write your own response to the same question to receive full marks from a QCAA assessor.

Exam tip 2: Don't expect multiple-choice questions to be quick, easy or obvious

Multiple-choice questions offer the correct answer on the page, and so many students expect to be able to recognise it quickly, or for it to be obvious. This is not always the case. Many multiple-choice questions require careful consideration and quite a bit of time. In the example that follows, many students look for the change in the mRNA code before and after the error. They find that G (guanine) has been deleted and look for the option "deletion of guanine". They are then surprised when they find that this is not one of the available options, so they go back and check again. The key to this problem lies in the wording of the question: "An error during DNA replication ...". The question asks for the error that occurred during DNA replication, but the sequences show mRNA strands, which have been transcribed from the DNA. Once you have been through the process of finding the obvious and then seeing that it is not an option, and then re-reading the question and problem solving, it is not a quick or easy question at all.

See it in action

Read the exam question below and the two responses that follow. See how the tip has made a difference between a response that scores full marks and a response that scores no marks.

Question 13

An error during DNA replication resulted in the following change to mRNA transcripts.

mRNA before	AUGAAGUUUGGCAUC ... (continued)
mRNA after	AUGAAGUUUGCAUCG ... (continued)

The DNA replication error most likely involved

(A) deletion of cytosine.

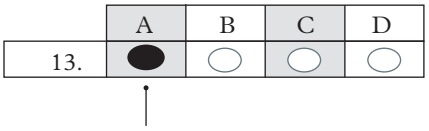
(B) insertion of guanine.

(C) substitution of uracil with guanine.

(D) substitution of guanine with cytosine.

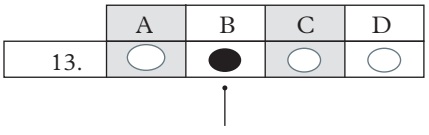
Source: *QCAA Biology 2022, Paper 1* © State of Queensland (QCAA)

Correct response



The question asks for the error during DNA replication, but the sequences show mRNA strands, which have been transcribed from the DNA. Therefore, the correct answer is (A) deletion of cytosine, as this results in the absence of guanine in the transcribed mRNA strand. [1 mark]

Incorrect response



The student finds that G (guanine) has been deleted and looks for the option 'deletion of guanine'. As it is not an option they wonder if it should be an insertion of guanine, which is option B but this is incorrect. [0 marks]

Think like an assessor

To maximise your marks on an exam, it can help to think like a QCAA assessor. Consider how many marks each question is worth and what information the assessor is looking for.

Read the exam question below and the response that follows. Imagine you are a QCAA assessor and use the marking guide below to mark the response.

Question 6

What can introduce new alleles into a population?

(A) point mutations
(B) non-disjunction
(C) random fertilisation
(D) independent assortment

	A	B	C	D
6.	○	○	●	○

Source: *QCAA Biology 2024, Paper 1* © State of Queensland (QCAA)

Marking guide

Question 6 • Identifies the correct option [1 mark]

Fix the response

Consider whether you did or did not award marks in the above response. How could the question be approached to arrive at the correct answer? Provide a response to the same question to receive full marks from a QCAA assessor.

Part C – Practice exam questions

Now it's time to put the tips and advice you've learned into practice while you complete these exam-style questions!

Multiple choice

(1 mark each)

1 Cladograms are based on
- **A** observable features only.
- **B** hierarchal groupings of organisms.
- **C** immunological differences between organisms.
- **D** both observable features and molecular analyses.

2 The Hardy-Weinberg equilibrium assumes which of the following conditions?
- **A** an evolving population
- **B** that regular genetic mutations are occurring
- **C** that natural selection is acting on the population
- **D** that there is no migration in or out of the population

3 Which of the following best describes an adaptation?
- **A** a random change in allele frequencies
- **B** a mutation in the somatic cells of an organism
- **C** an inherited trait that provides a survival advantage
- **D** a behaviour exhibited by organisms in the face of environmental changes

4 Which type of selection is the result of an extreme phenotype being favoured?
- **A** directional selection
- **B** disruptive selection
- **C** dominant selection
- **D** stabilising selection

5 Which of the following is unlikely to result in speciation?
- **A** high genetic variation in a population
- **B** reduced gene flow between two populations
- **C** stable abiotic and biotic environmental conditions
- **D** geographic isolation of two populations of the same species

6 A crop is sprayed with a pesticide to kill the beetle larvae feeding on it. Over several generations, the pesticide no longer works, as the beetles have become resistant. This is an example of
- **A** genetic drift.
- **B** macroevolution.
- **C** natural selection.
- **D** disruptive selection.

7 Genetic drift is best described as
- **A** allele movement between populations.
- **B** increased genetic diversity, caused by mutations.
- **C** a decrease in populations due to selection pressure.
- **D** random changes in allele frequencies within a population of a species.

8 Which of the following observations is central to Darwin's theory of evolution?
- **A** Populations remain stable over time.
- **B** All species produce the same number of offspring.
- **C** Species retain the same traits over long periods of time.
- **D** Individuals better suited to their environment are more likely to survive and produce offspring.

9 Polyploidy is a driver of
- **A** genetic equilibrium.
- **B** allopatric speciation.
- **C** parapatric speciation.
- **D** sympatric speciation.

10 Mitochondrial DNA
- **A** is prone to recombination.
- **B** is passed on from the father to offspring.
- **C** show higher rates of mutation than nuclear DNA.
- **D** requires a larger collection of cell samples than DNA from the nucleus.

11 Which of the following statements about the structure of genetic material is correct?
- **A** genes are made of chromosomes.
- **B** non-coding sections of DNA are called histones.
- **C** DNA is a molecule found only in the nucleus of eukaryotic organisms.
- **D** DNA is wound around proteins called histones to make chromosomes.

12 Which of the following describes sympatric speciation?
- **A** Two populations of the same species evolve to become different species due to genetic drift.
- **B** The sudden reduction in population size caused by a catastrophic event leads to a new species.
- **C** Reproductively isolated species in the same geographic location evolve into two new species.
- **D** A population is separated into two by the formation of a physical barrier, leading to the development of a new species.

13 Which of the following statements about polypeptide chains is true?
- **A** They are produced by the Golgi apparatus.
- **B** They are the building blocks of amino acids.
- **C** They are folded into tertiary or quaternary structures to form proteins.
- **D** They contain codons that can be read by ribosomes to build a protein.

14 Advantageous phenotypic traits in an individual result in
- **A** microevolution.
- **B** macroevolution.
- **C** dominant alleles.
- **D** survival to reproductive age.

15 The Okazaki fragment is necessary in DNA replication for
- **A** checking for errors in matching of nucleotides.
- **B** joining free-floating nucleotides to the exposed DNA strand.
- **C** creating a starting point for DNA replication on the lagging strand.
- **D** unzipping the double-stranded DNA molecule to expose nucleotides.

16 In the DNA double helix, nitrogenous base pairs are held together by
- **A** purines.
- **B** DNA ligase.
- **C** pyrimidines.
- **D** hydrogen bonds.

17 Population bottlenecks often result in a reduction in the diversity of the gene pool as a result of
- **A** mutations.
- **B** genetic drift.
- **C** natural selection.
- **D** geographic isolation.

18 A frameshift mutation is best described as
- **A** a mutation that changes the DNA sequence at the point of mutation only.
- **B** the introduction of a stop codon to a gene that prematurely ends translation.
- **C** an error that occurs during meiosis, causing non-disjunction of chromosomes.
- **D** a mutation that changes the DNA sequence from the point of mutation to the end of the gene.

19 Macroevolution is the result of
- **A** mass extinction.
- **B** an accumulation of microevolutionary changes.
- **C** a disturbance in the ecosystem of an organism.
- **D** the number of ecological niches available in an environment.

20 A difference between DNA and RNA is that
- **A** DNA contains thymine, while RNA contains uracil.
- **B** DNA is a double helix, while RNA is a circular molecule.
- **C** DNA is found in the nucleus, while RNA is found in the mitochondria.
- **D** DNA is necessary for translation only, while RNA is necessary for both transcription and translation.

Short response

21 **Explain** how a population bottleneck can place a species at risk of extinction. (4 marks)

22 **Explain** how ribosomes can translate the information from mRNA to produce a polypeptide chain. (5 marks)

23 **Explain** the role of natural selection in the evolution of a new species of animal. (4 marks)

24 **Describe** the structure of DNA double helix molecules. (3 marks)

25 **Describe** the role of the DNA helicase enzyme in DNA replication. (2 marks)

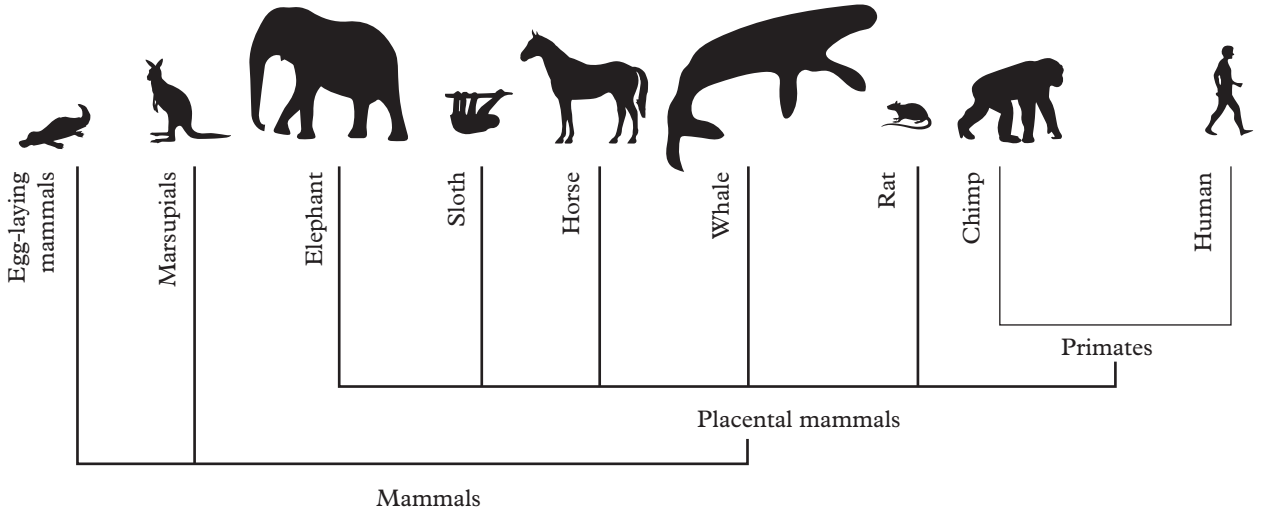
26 **Contrast** the processes of transcription and translation. (1 mark)

27 **Explain** how karyotypes can be used to diagnose aneuploidy. (4 marks)

28 **Describe** the structure of a chromosome. (3 marks)

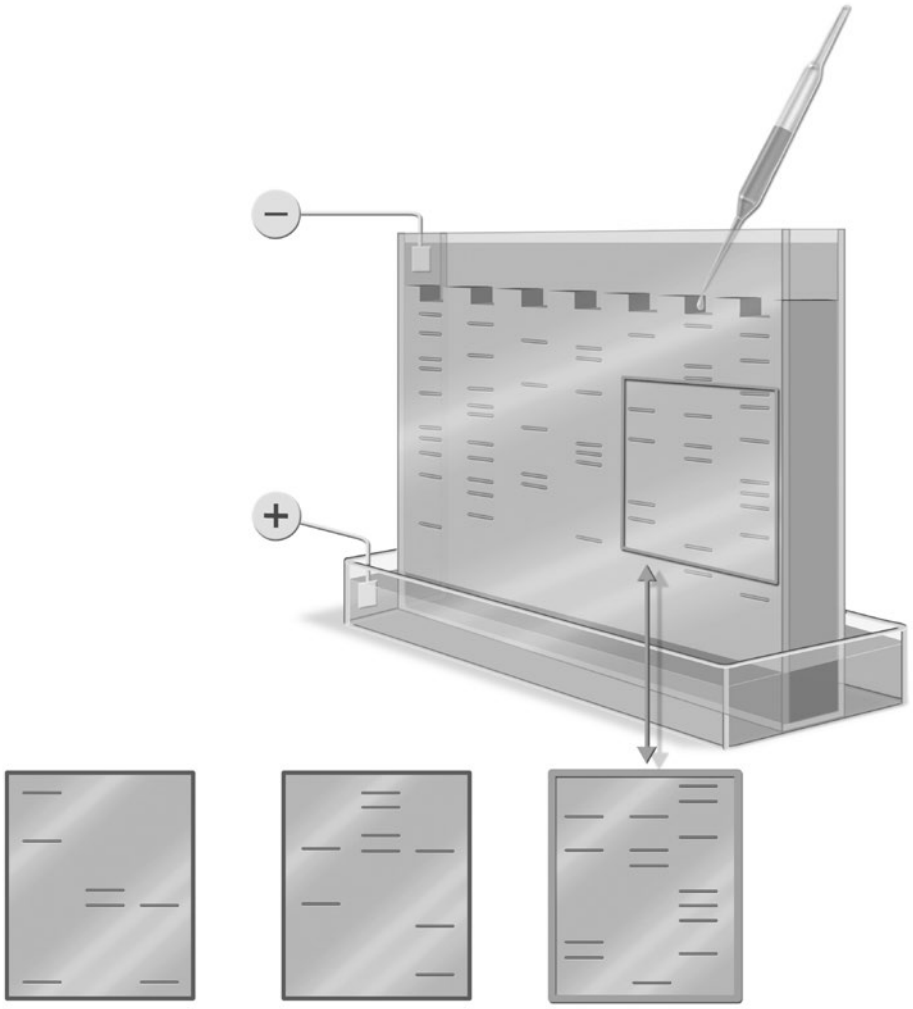
29 **Explain** how two species that share a common ancestor can survive today, while their common ancestor has become extinct. (4 marks)

30 Consider the image below.
- **a** **Identify** the organism that forms a clade with whales, rats, elephants and horses. (1 mark)
- **b** **Determine** whether humans are more closely related to chimps or sloths. (1 mark)
- **c** **Explain** what makes placental mammals a clade. (2 marks)



Source: adapted from https://www.sciencephoto.com/media/1032927/view

31 Examine the image below and answer the questions that follow.



a **Identify** the name of the technique being used in the image above. (1 mark)

b **Describe** how samples of DNA are cut to be used in this technique. (2 marks)

c **Explain** how this technique can be used to compare DNA samples left at a crime scene with samples taken from suspects. (5 marks)

32 During anaphase I of meiosis, non-disjunction occurred and produced an egg that resulted in a genetic condition when the egg was fertilised by a normal sperm and a child was born.

a **Determine** what technique could be used to diagnose this condition after the baby was born. (1 mark)

b **Compare** non-disjunction to the normal process that occurs in anaphase I of meiosis. (2 marks)

c **Contrast** this type of chromosomal error with a genetic mutation. (1 mark)

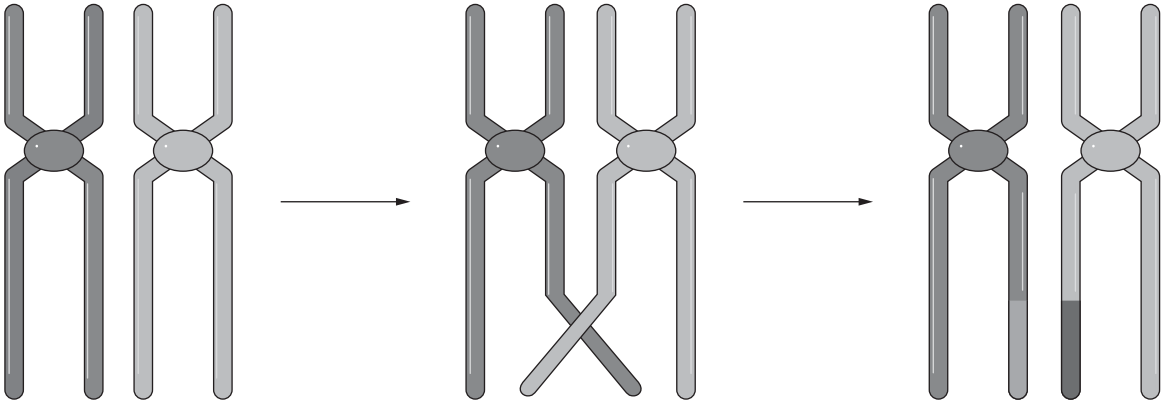
33 After a volcanic eruption, a species of duck is separated into two populations when they can no longer intermingle due to a barren, rocky landscape created by lava flow. In the following years, the two populations are subjected to different environmental pressures.

a **Determine** the type of evolution that is likely to occur in the populations in the 50 years following the eruption. (1 mark)

b If the populations remain separated long enough, they will eventually become different species. **Determine** what type of isolation would have caused this speciation event. (1 mark)

c **Identify** the type of speciation that would result from this separation of the populations caused by the volcanic eruption. (1 mark)

34 The diagram below shows chromosomes during meiosis.



a **Identify** the process that is occurring in this diagram. (1 mark)

b **Explain** why this process is important for the survival of species. (3 marks)

c **Suggest** the effect on the offspring of parents if this process did not occur during meiosis. (2 marks)

MODULE 14

Practical manual

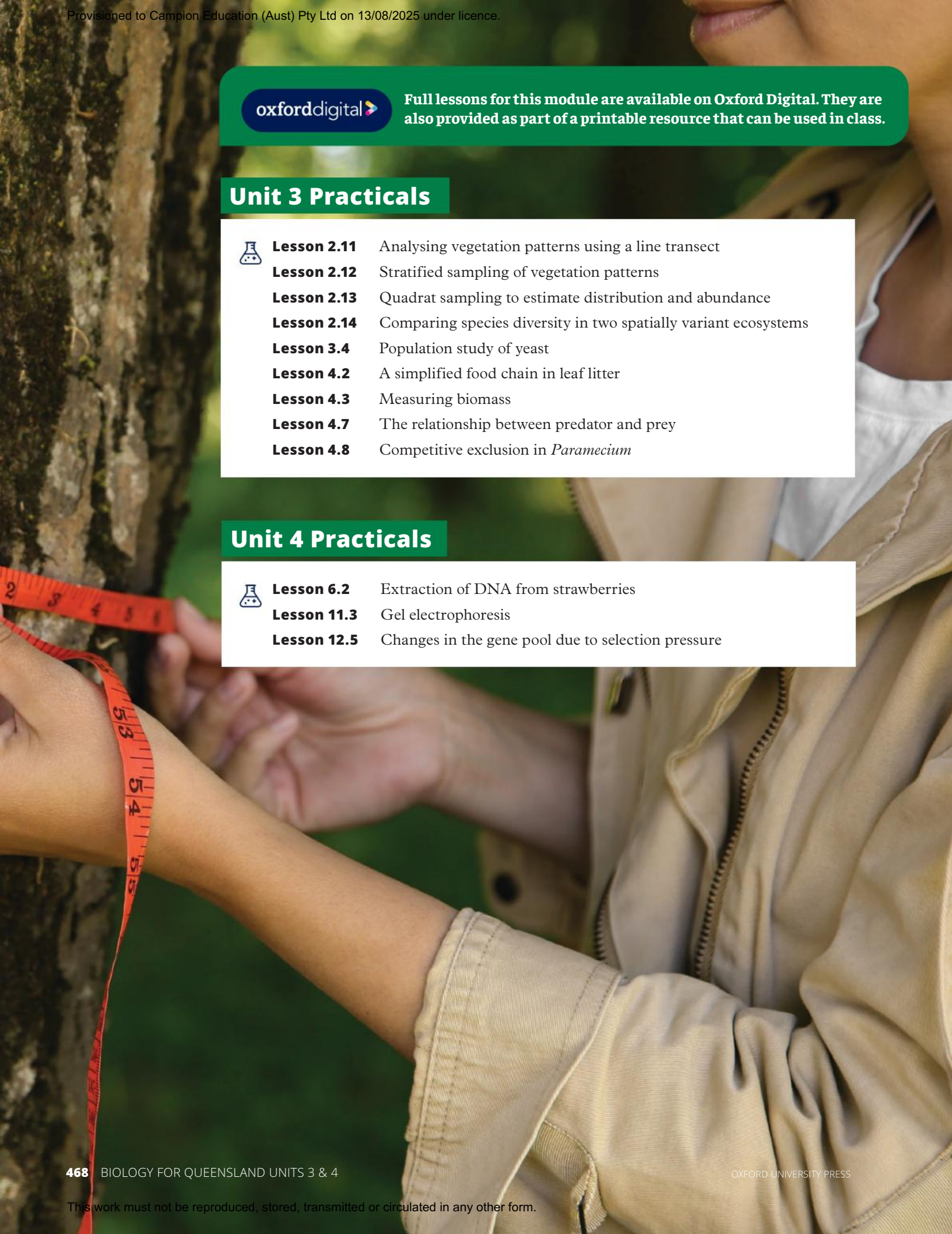
Introduction

The 2025 QCAA Biology General Senior Syllabus does not mandate any particular practicals but requires integration of Science Inquiry Skills into school-selected practicals. The methodologies and materials supplied in this module are suggestions only and not prescriptive. Schools may modify these suggestions or use other methodologies to meet the syllabus requirements and learning needs of students.

The experiments in this module have been selected because they are appropriate for most school laboratories. However, complete risk assessments should be undertaken by teachers according to the legal requirements and considering aspects such as teacher experience, student capability and the school context.

All work undertaken in a laboratory or field setting should take place only after a risk assessment has been completed. The following safety considerations are some of many that should be implemented.

- → Do not bring in or consume food or drink in a laboratory.
- → Wear personal protective equipment (e.g. lab coat, safety glasses, gloves) when necessary.
- → In a laboratory, always wear closed-in shoes and tie back long hair.
- → When conducting practical activities, behave sensibly and with consideration for peers and supervisors.
- → Familiarise yourself with the school's safety procedures and the locations of eye wash, shower, spill kits and first aid kits.
- → When working with chemicals, carefully follow the teacher's direction, handling procedures and risk assessments.
- → Before using electrical equipment, check that the cables are not damaged.
- → Keep flammable materials away from open flames and fuel sources.
- → When handling hot materials, use the appropriate equipment (heat-resistant gloves or tongs).
- → Complete field work in groups and consider risks to participants and the natural environment.
- → If you are unsure about any procedures or equipment in the laboratory, ask a teacher or science technician for clarification.



oxforddigital

Full lessons for this module are available on Oxford Digital. They are also provided as part of a printable resource that can be used in class.

Unit 3 Practicals

⚗	**Lesson 2.11**	Analysing vegetation patterns using a line transect
	Lesson 2.12	Stratified sampling of vegetation patterns
	Lesson 2.13	Quadrat sampling to estimate distribution and abundance
	Lesson 2.14	Comparing species diversity in two spatially variant ecosystems
	Lesson 3.4	Population study of yeast
	Lesson 4.2	A simplified food chain in leaf litter
	Lesson 4.3	Measuring biomass
	Lesson 4.7	The relationship between predator and prey
	Lesson 4.8	Competitive exclusion in *Paramecium*

Unit 4 Practicals

⚗	**Lesson 6.2**	Extraction of DNA from strawberries
	Lesson 11.3	Gel electrophoresis
	Lesson 12.5	Changes in the gene pool due to selection pressure

Glossary

3' (three-prime) end
one end of a DNA strand in which the C_3 carbon atom of the sugar molecule in the DNA's sugar backbone has a "free" OH (hydroxyl) group that is not linked to another chemical group

5' (five-prime) end
one end of a DNA strand in which the C_5 carbon atom of the sugar molecule in the DNA's sugar backbone has a "free" phosphate group that is not linked to another chemical group

A

abiotic
describes the non-living physical factors that affect an organism's ability to survive

abundance
the number of individuals in a population, within a given area

abyssal zone
the deep-water zone (depth 4000–6000 m)

accuracy
how close a measurement is to its true value

adaptation
a physical or behavioural feature of an organism that enhances its ability to survive and reproduce in a particular environment

agglutination
the sticking together of incompatible cells, e.g. red blood cells of different "groups"

allele
a different version of a gene that occupies a particular position (gene locus) on a chromosome

allopatric speciation
the divergence of a species into two separate species, driven by geographical isolation of populations

alternative hypothesis
a hypothesis that predicts an effect or relationship between variables

amplification
making multiple copies of a specific DNA segment, typically using PCR, to increase the amount of DNA for analysis or experimentation

aneuploidy
the presence of an abnormal number of chromosomes in a cell

anticodon
a triplet of nitrogen bases on tRNA

antiparallel
the arrangement of DNA strands where one strand runs in the 5' to 3' direction while the complementary strand runs in the opposite (3' to 5') direction.

apomixis
in plants, asexual development of seeds or embryos

asexual reproduction
reproduction without fertilisation, leading to the formation of offspring that are genetically identical to the parent

autosomal aneuploidy
the presence of an abnormal number of autosomal chromosomes in a cell

autosomal dominant trait
a trait due to an allele on an autosome that overrides the effects of the recessive allele, in the heterozygous condition

autosomal recessive trait
a trait due to an allele on an autosome that is masked by the dominant allele, in the heterozygous condition

autosome
a non-sex chromosome

B

Barr body
an inactivated X chromosome in the cells of female mammals

belt transect
an elongated area of known length and width through a particular environment in which specific community parameters are measured and recorded

benthic ecosystem
the ecosystem at the lowest level of a body of water; includes the sediment surface and some subsurface layers

bias
the occurrence of systematic errors or inclinations, which can lead to incorrect conclusions

bibliography
a detailed list of all references used

binomial nomenclature
a method of naming species of organisms with two parts: the generic and specific names, following particular formatting conventions (e.g. *Eucalyptus crebra*)

biodiversity
the range of living organisms and their environments

biofilm
a layer on a solid matrix composed of microscopic bacteria, algae and protozoa in a complex polymer-linked assemblage

biogeochemical cycles
the circulation of chemical elements in the biosphere

biological magnification
the concentration of substances within the tissues of organisms as they pass along a food chain

biological oxygen demand (BOD)
a measure of the quantity of oxygen used by microorganisms (e.g. aerobic bacteria) in the oxidation of organic matter in aquatic environments; the higher the BOD, the less oxygen available for other organisms

biological species concept
a concept that defines a species as a group of similar organisms that are able to interbreed to produce viable, fertile offspring

biology
the study of all living and once-living organisms on Earth

biomass
the amount of organic matter in a selected system

biomass pyramid
a model of the amount of living matter transferred through a food chain

biome
the living organisms of a large area defined by its climate and dominant plant species (e.g. a desert community)

biosphere
the part of the Earth that supports life

biotemperature
the average annual temperature in an area, adjusting all temperatures below 0°C or above 30°C due to plant dormancy at these temperatures.

biotic
describes the living components of an ecosystem

biotic potential
the number of offspring capable of being produced by individuals of a species

BLAST
Basic Local Alignment Search Tool, a computer program that compares unknown DNA or protein sequences with those of known sequences

block mutation
a type of genetic mutation involving a segment of a chromosome, rather than a single nucleotide

C

canopy
the upper layer or habitat zone, formed by mature tree crowns

capping
the addition of methyl-guanine at the start of the trimmed mRNA

capture–recapture
a method of estimating population density of animals where animals are captured, marked and released; the proportion of tagged individuals in subsequent trapping is used to estimate population size

carcinogen
a substance or agent that can cause cells to become cancerous, by altering their genetic structure so that they multiply continuously and become malignant

carrier
an individual (female in humans) who is heterozygous for a sex-linked gene, or an individual who is infected by a pathogen but does not display the symptoms

carrying capacity
the largest population that can be maintained within a given area without collapsing, determined by the limiting resources within the ecosystem

case study
a detailed investigation that focuses on a specific individual, group or occurrence to better understand it

causation
a cause–effect relationship in which a change in one variable directly results in change in another variable

cellular differentiation
the process of different cell types developing due to different sets of genes being turned on or off

centromere
the region of a chromosome where two sister chromatids are joined together and where spindle fibres attach during cell division

character displacement
the evolutionary divergence of characteristics displayed by two or more species with the same niche in a particular habitat

chiasma
the connection between non-sister chromatids of homologous chromosomes during meiosis, where interchange occurs during crossing over; plural *chiasmata*

chromatid
a replicated chromosome, still attached to the original at the centromere

chromatin
a DNA–protein complex in the nucleus, where DNA wraps around histones to form nucleosomes, helping package and regulate genes

chromosome
tightly wound strands of DNA and protein

chromosome mutation
a change in the chromosome structure or number, often due to an error in pairing during the crossing over stage of meiosis

clade
a group of organisms that includes a common ancestor and all its descendants; often identifiable on a cladogram as a node and species branching from it

cladistics
a classification method based on organisms' traits shared with or derived from a common ancestor; these classifications are often represented on a diagram called a cladogram

cladogenesis
the making of a clade by means of an ancestor species evolving into two or more new species

cladogram
a branching diagram that shows evolutionary relationships, using a combination of DNA, physical traits and fossil records as evidence

class
one of the groups used in the classification of organisms; consists of a number of orders (e.g. animals in class Mammalia all share specific characteristics)

classification
the grouping of organisms based on their similarities in morphology, anatomy and biochemistry

climax community
a relatively stable plant community

clumping
a pattern of distribution in which individuals are clustered in groups in particular parts of the habitat

codominance
the genetic inheritance of two or more traits of a characteristic, both of which are expressed in the phenotype

codon
a triplet of nucleotides on mRNA that codes for a particular amino acid

coevolution
evolution that occurs when two or more species influence each other's evolutionary changes due to a symbiotic relationship

colour-defective vision
in humans, the inability to distinguish between the colours red and green; also known as red–green colour blindness

commensalism
a symbiotic relationship in which one organism benefits and the other is either unaffected or only minimally affected

community
all the species that occupy a particular place at a given time

community structure
the composition and relative abundance of organisms in a community

comparative investigation
an investigation that compares two or more conditions to identify similarities and/or differences

competition
rivalry between individuals, of the same or different species, for a specific resource

competitive exclusion principle
the principle that, when two species compete for the same ecological niche, both cannot occupy the niche simultaneously; one species will have an advantage (even if it is small) and outcompete the other

conclusion
a summary of the findings and results obtained from an investigation

concordance
the extent to which both twins exhibit the same trait or condition, indicating the influence of genetic and environmental factors

condensation polymerisation
the formation of a polymer by the reaction between two monomers, with the loss of a small molecule (e.g. water)

confounding factor
an uncontrolled variable that has a systematic effect on the value of the dependent variable; if a confounding variable exists, no valid conclusions about the research can be drawn

conserved sequence
a gene or sequence of DNA that remains unchanged while evolution influences the surrounding DNA

consumer
an organism that eats another living organism (or part of an organism) for nutrition

continuous variation
a variety of phenotypes resulting from more than one gene contributing to a characteristic

controlled experiment
an experiment in which a control group or standard acts as a reference for the experimental group, in which only one variable is different from that in the control group

controlled variable
a variable that is kept constant by the experimenter to negate any effects it may have on the dependent variable

convergent evolution
the evolution of similar traits in unrelated or distantly related species due to similar selection pressures in their environment

correlation
the relationship between two variables

correlational investigation
an investigation that is run to determine whether a statistical relationship exists between two variables

crossing over
the breaking and rejoining, with exchange of DNA, of non-sister adjacent chromatids of homologous chromosomes during meiosis I

D

data
quantitative or qualitative information; facts and statistics

database
a large, organised collection of data

decomposer
an organism (e.g. bacteria and fungi) that uses dead organisms or waste matter for its nutrients, releasing simple inorganic molecules back to the soil to be reused

deletion
loss of a part of a chromosome during DNA replication

denitrifying bacteria
bacteria that convert nitrate to nitrite, or atmospheric nitrogen or nitrite to ammonia

density-dependent factor
a factor that has a greater impact on the population as the population size increases

density-independent factor
an abiotic factor that is independent of the density of the population, that affects the size of a population

deoxyribonucleic acid (DNA)
a thread-like chain of nucleotides carrying genetic instructions in a double helix of antiparallel strands

dependent variable
a variable whose value is dependent on another variable

derived characteristic
a characteristic unique to a clade or species that allows it to be identified as different from others

descriptive investigation
an investigation that aims to describe the characteristics of a phenomenon

desertification
the formation of desert conditions, usually resulting from overgrazing of susceptible areas

detritivore
an organism that feeds on detritus

detritus
organic debris from decomposing plants and animals

dichotomous key
an identification key with two alternatives at each stage

dihybrid cross
a genetic cross between two individuals, both heterozygous for two specific traits

dihybrid ratio
a predicted ratio of the offspring of a cross between individuals simultaneously heterozygous for two characteristics

diploid
the cellular condition in which there are two of each type of chromosome in the nucleus

directional selection
selection that favours alleles in one direction, at either the upper or the lower end of the distribution

disclimax community
the final community formed after succession as a result of degrading environmental factors

disruptive selection
selection that disrupts the normal distribution of an allele, favouring both the lower and upper extremes and eliminating the central alleles of the distribution

distribution
the density and pattern of spread of a population

divergent evolution
the evolution of a new species as the result of a population splitting into two and adapting to different selection pressures in the environment

division
a major classification group of the plants, fungi and plant-like protists

dizygotic twins
twins that develop from two separate eggs, each egg having been fertilised by a different sperm cell; also known as fraternal twins

DNA helicase
an enzyme that breaks down the hydrogen bonds holding two DNA strands together

DNA hybridisation
a technique that measures the degree of genetic similarity between DNA sequences of different individuals

DNA ligase
an enzyme that facilitates the joining together of DNA strands

DNA methylation
the addition of a chemical tag (a methyl group) to the start of a structural gene, to block transcription

DNA polymerase
a type of enzyme that assembles nucleotides to form new copies of DNA

DNA profiling
a technique used to identify (as for forensic purposes) the characteristics of an individual's DNA by extracting and identifying the base-pair pattern of their DNA; also known as DNA fingerprinting

DNA scissors
restriction enzymes that cut DNA into fragments

domain
the broadest taxonomic group, based on cellular-level differences

dominant allele
an allele for a gene that overrides the effects of the recessive allele in the heterozygous condition; can be autosomal or sex-linked

dominant species
the most common species in a community

dominant trait
the particular trait of a characteristic that is expressed in the phenotype of a heterozygous individual

double helix
the structure of DNA; two linked strands that are twisted on their axis, forming the shape of a helical (spiralled) ladder

duplication
a repetition of a region of DNA that contains one or more genes

E

ecological pyramid
a model of the relationships between different organisms in a food chain

ecological sampling
methods used to study the abundance and distribution of organisms in an ecosystem, particularly to look for correlations with biotic or abiotic factors and when developing effective ecosystem management

ecological succession
the gradual change in the species composition of an ecosystem over time

ecologically dominant layer
the layer of vegetation with the greatest biomass in a given area (the most common canopy height), ignoring emergent plants

ecology
the study of relationships between organisms and their environment

ecoregion
a subdivision of an ecozone; a geographically distinct community based on geology, soils, climate and predominant vegetation

ecosystem
a biological community of interacting organisms and their physical environment

ecosystem diversity
the variety of habitats, communities and ecological processes within and between ecosystems

ecosystem function
the interactions between the biological, geological, meteorological and physical factors that sustain an ecosystem

ecozone
a large area in which organisms have been evolving in relative isolation over a long period of time

electron microscope
a microscope that uses a beam of electrons to form an image of the viewed specimen

endangered species
a species of animal or plant at threat of extinction through risks to their health, distribution or habitat

endonucleases
enzymes that cut internal bonds within DNA or RNA

energy pyramid
a model of the amount of energy transferred through a food chain

environment
the conditions (biotic and abiotic) in which an organism lives

environmental limiting factor
any factor that limits the growth of a population

environmental resistance
the sum of all environmental limiting factors

epigenetic factors
a chemical tag that determines the degree of coiling of the DNA around the nucleosome and thus gene expression

epigenome
a system of gene control that extends beyond DNA ("above the genome")

epistasis
when the phenotypic expression of one gene is masked by another gene; means "standing upon"

equilibrium
the point at which a system can be maintained, e.g. population size for a specific environment; also known as set point

euchromatin
"relaxed" chromatin that is loosely coiled around histone proteins in the nucleosome; contains genes that can be accessed for transcription

eutrophication
a build-up of nutrients in water; may result in oxygen depletion

evidence
data, observations or facts obtained from research

evolutionary radiation
the rapid diversification of species and occurrence of speciation events taking advantage of newly available ecological niches

exon
a segment of DNA or RNA within a gene that contains the code for producing a protein

experimental investigation
an investigation that involves manipulating one or more variables to determine whether this results in a change in another variable

experimental test
an experiment in which a single variable is compared with that of a control group

experimental variable
the single factor under investigation in a controlled experiment; also known as an independent variable

exponential growth
population growth where the reproductive rate of the individuals in a population remains constant, but the number of mature individuals increases due to no limiting factors, causing the population to grow faster and faster

extant
currently living or existing

externally valid
in relation to investigation results, applicable to other settings outside the investigation

extinct species
a species for which there is no reasonable doubt that the last individual has died; a species that is extinct in the wild exists only in captivity, not in its natural habitat

extraneous variable
a variable other than the independent variable that may cause changes in the value of the dependent variable

extrapolation
an estimation of a value based on extending a known sequence of values beyond the values that are certainly known

extremophiles
organisms that live in extreme environments

F

fact
information that has been verified by observation or experimentation

family
a subdivision within an order in the classification of living things

fecundity
the number of eggs or offspring an organism can produce, measured per pregnancy or over an individual's lifetime

food chain
a simple linear arrangement of organisms showing the flow of matter and energy from one organism to another through feeding relationships

food web
all the possible feeding relations in an ecosystem

founder effect
reduced genetic diversity as a result of a population having descended from a small number of colonising ancestors

frameshift mutation
the deletion or insertion of a single nucleotide, or a non-multiple of three nucleotides, into DNA

frequency histogram
an accurate representation of the distribution of numerical data, and an estimate of the probability frequency distribution of a continuous variable (quantitative variable)

G

gametogenesis
the formation of gametes

gel electrophoresis
a laboratory method for separating mixtures of DNA, RNA or proteins according to molecular size

gene
a segment of DNA that is passed from parent to offspring and determines an attribute of an individual

gene cloning
production of identical copies of a gene

gene complex
when two or more genes interact to determine the phenotypic expression of a characteristic

gene expression
the process of information encoded in a gene being used to produce a functional product, such as a protein

gene flow
the movement and exchange of alleles between populations of a species

gene linkage
the location of genes on the same chromosome

gene locus
a specific, fixed position on a chromosome where a particular gene is located; plural *gene loci*

gene pool
all alleles for every gene in a population at a given point in time

gene regulation
the process that controls when, where and how much a gene is expressed in a cell

gene therapy
the introduction of normal genes into cells in place of missing or defective ones, in order to correct genetic disorders

generalisability
the extent to which findings can be applied to other situations or populations

generalist feeder
a heterotroph with a varied diet

genetic code
a code used by the body to convert instructions contained in DNA into the proteins essential for life

genetic diversity
the variety of different genes and alleles in a species or population

genetic drift
changes to the frequency of existing alleles within a gene pool, caused by chance.

genetic engineering
direct manipulation of an organism's DNA to alter its traits

genetic equilibrium
describes the condition of an allele or genotype in a population when the frequency remains stable over time

genetically modified organism (GMO)
an organism whose genetic material has been altered using recombinant DNA technology

genome
the complete set of nucleotide sequences encoded in the total DNA of an organism

genotype
the genetic make-up of an organism, including the specific set of genes and their alleles (different versions of a gene) that it carries

genus
a classification category between family and species; the first part of the scientific name of an organism; plural *genera*

geographic isolation
when a physical barrier prevents interbreeding between members of different populations of a species

germ cell gene therapy
replacement of a defective gene in a reproductive cell (egg or sperm) with a normal gene, allowing normal development of the embryo and preventing the disease variant from being passed down

germline mutation
a heritable change in DNA that occurs in a germ cell (a cell destined to become an egg or a sperm) or in a zygote at the single-cell stage and so is incorporated into every cell of the body

graph
a pictorial representation that displays values and data in an organised way

gross primary production
the total amount of organic matter in an ecosystem produced as a result of photosynthesis

H

habitat
a specific location, with a particular set of biotic and abiotic conditions; where an organism lives

habitat fragmentation
the division of a habitat into smaller, isolated portions as a result of human activities in the intervening spaces

haemophilia
a group of disorders in which the blood does not clot normally

haploid
the cellular condition in which there is one of each type of chromosome in the nucleus

Hardy–Weinberg law
a principle stating that, when there are no other evolutionary influences, the allele and genotype frequencies in a population will remain constant across generations

hereditary mutation
a gene change in a body's reproductive cell that can be passed from parent to offspring

heterochromatin
chromatin that is tightly coiled around histone proteins in the nucleosome, making the genes inaccessible, so they cannot be transcribed

heterozygous
describes a condition in which the two alleles for a gene each exhibit a different expression

hierarchical
relating to grouping things from general to very specific subgroups

histone
a protein that DNA is wound around, to package and organise DNA and regulate gene activity

histone modification
the addition of chemical tags that vary the width between nucleosomes and thereby determine whether a gene can be transcribed

holandric gene
a gene located on a vertebrate Y chromosome

Holdridge life zone system
a system of classifying areas of land, based on climate and ecological types

homeobox
DNA sequence (of about 180 base pairs) contained in a gene (e.g. the *HOX* gene) that is highly conserved and can bind to DNA to control gene expression

homeobox (*HOX*) genes
a subgroup of homeotic genes that control the body plan of an embryo along the head–tail axis

homeotic gene
any of a group of related genes that control the body plan of an embryo along the head–tail axis during early embryonic development

homologous chromosomes
pairs of chromosomes, one inherited from each parent, that are similar in size, shape and gene content, although they may carry different versions of those genes

homologues
two chromosomes that are homologous; during meiosis, the set of pairing maternal and paternal chromosomes; both have the same genes at the same loci but they may have different alleles

homozygous
describes a condition in which both alleles for a gene are the same

HOX protein
a transcription factor produced by a *HOX* gene

hybrid (genetic)
a plant or animal that is heterozygous for a particular trait; results from a cross between parents that are genetically unalike for that trait

hypothesis
a statement that attempts to answer questions raised by observations and can be tested by experimentation

I

independent variable
the variable that is changed or controlled in a scientific experiment

index
a composite measure that summarises and compares multiple variables and presents these factors as a single number

information and communication technologies
(ICT) computer and other technologies that process information to perform a range of tasks

insertion
the addition of a segment of one chromosome into another chromosome

intermediate dominance
a pattern of inheritance in which neither allele for a characteristic completely masks the effects of the other; results in a blending of traits for the characteristic; also known as partial dominance or incomplete dominance

interpolation
an estimation of a value within two known values in a sequence of values

interspecific
between different species

in-text references
references that appear in the flow of body text; also known as citations

intraspecific
within a species; between individuals of the same species

intron
a segment of DNA or RNA within a gene that does not code for proteins and is removed during RNA processing

inversion
a chromosome rearrangement in which a segment of a chromosome is reversed end-to-end

J

J-shaped population curve
the graphical representation of the change in population density of an organism as it increases rapidly and then stops suddenly, due to environmental or other factors

K

karyotype
the number and visual appearance of the chromosomes in the cell nuclei of an organism or species

keystone species
a species that has a disproportionately large effect on its environment relative to its abundance by maintaining local biodiversity within a community, either by controlling populations of other species that would otherwise dominate the community or by providing critical resources

kingdom
a subdivision within a domain; a group of organisms with very general common features

***K*-selected species**
a species whose population fluctuates at or near the carrying capacity (K) of the environment in which it resides

L

lagging strand
a DNA template from the fork to the middle of the replication bubble (point of origin)

law of conservation of matter and energy
a law stating that matter and energy cannot be created or destroyed but can be changed to other forms

law of independent assortment
a Mendelian law that states that each allele pair segregates independently during gamete formation; applies when genes for two traits are located on different pairs of homologous chromosomes

law of segregation
a Mendelian law that states that genes for a characteristic occur in pairs in an individual, one inherited from each parent, and these pairs are separated when the reproductive cells are formed

leading strand
a DNA template from the middle of the replication bubble (point of origin) to the fork

light microscope
a microscope that uses visible light and lenses to magnify viewed specimens

limitation
a factor or condition that can affect the validity and/or reliability of results

limiting factors
conditions that limit the growth, abundance or distribution of an organism or a population of organisms

Lincoln index (*N*)
a method used to estimate the size of closed populations sampled using the capture–recapture method

line graph
a graph of data linking two variables, where one variable is plotted on the y-axis and the other on the x-axis and the points are connected in a line

line of best fit
a trendline that gives an approximation of the linear relationship between two variables

line transect
an estimate of the numbers of organisms in an area by counting individuals observed along a predetermined line

littoral zone
the zone between water and land, which may be affected by tidal action

loci
specific locations or positions of genes or genetic markers on a chromosome; singular locus

logbook
an organised record of investigation ideas, events, results and interpretations

M

macroevolution
evolutionary change at or above the species level resulting from the accumulation of microevolutionary changes

mass extinction
the rapid and widespread extinction of a large number of species more quickly than they can be replaced; often caused by a catastrophic natural event resulting in widespread change to global systems

mean
the average of a set of numbers in a data set

measure of central tendency
summary statistic that represents a central point in a data set

measure of variability
summary statistic that describes the spread of data in a data set

meiosis
nuclear division resulting in daughter cells that have half as many chromosomes, but the same types, as the parent cell; a reduction division, from the diploid to the haploid condition

messenger RNA (mRNA)
a type of RNA molecule formed during transcription

microenvironment
an area within a general habitat with specialised environmental conditions, e.g. a hollow log

microevolution
the change in allele frequencies within a population over a short period; does not result in a new species but genetic change within a species

microhabitat
a small habitat that may be different from the surrounding larger habitat

mitochondrial DNA
a double-stranded DNA found only in mitochondria; in most eukaryotes, circular and maternally inherited

mitosis
nuclear division resulting in daughter cells that have the same number and type of chromosomes as the parent cell

modifier genes
genes that influence the expression of another gene

molecular analysis
the study and comparison of biological molecules such as DNA, RNA, proteins and genomes

molecular clock
a technique that uses the rate of genetic mutation to estimate the timing of the evolutionary divergence of two or more organisms

monoculture
a system that has very low species diversity; in agriculture, a crop that consists of a single species, with any other species eliminated as weeds

monohybrid cross
a genetic cross between two individuals, both heterozygous for a specific trait

monozygotic twins
twins that develop from one zygote, when it splits and forms two embryos; because both twins have the same genotype, they are considered identical

motile
able to move around freely

multiple alleles
the inheritance of a characteristic governed by more than two allelic forms (e.g. blood groups); also known as poly alleles

mutagen
a physical or chemical agent that changes the genetic material of an organism

mutation
a small, permanent change in the DNA of an organism

mutualism
a symbiotic relationship between individuals of two species that is beneficial for both

N

natural selection
a mechanism of evolution in which species selectively reproduce, resulting in genotypic changes

nekton
free-swimming organisms of surface waters

neritic zone
the shallow region of the ocean overlying the continental shelves

net primary production
the amount of energy available for herbivores in an ecosystem

niche
the particular role of an organism, including its interactions with the abiotic and biotic factors in the ecosystem

nitrifying bacteria
bacteria that convert ammonia to nitrite, and nitrite to nitrate

nitrogen fixation
the conversion of atmospheric nitrogen to nitrate by bacteria and cyanobacteria

non-coding DNA
the part of the DNA molecule that does not contain structural genes; most DNA is non-coding

non-disjunction
the failure of homologous chromosomes or sister chromatids to separate during meiosis

non-scientific idea
an idea or theory that is not based on empirical evidence and has not been tested or supported by the scientific method

nucleosome
the basic unit of chromatin, consisting of a length of DNA coiled around a core of eight histone protein molecules

null hypothesis
a hypothesis that predicts no effect or no relationship between variables

nutrient cycle
the cycling of a particular element between biotic and abiotic ecosystem components

O

Okazaki fragments
fragments of DNA that are formed on the lagging strand of replicating DNA

oogenesis
the formation of ova in animals

oogonium
a small diploid cell in the ovary that forms a primary oocyte in a female foetus; plural *oogonia*

optimal range
the level of an abiotic factor at which an organism will best survive, grow and reproduce

order
a subdivision within a class in the classification of living things

organism
an individual living thing, such as a plant, animal or bacterium

origin of replication
a particular sequence in the DNA molecule at which replication is initiated

ovulation
the release of the secondary oocyte that has started meiosis II from the ovary

ovum
a haploid female gamete; plural *ova*

P

parallel evolution
the independent evolution of similar traits in species that once shared a common ancestor

parapatric speciation
the evolution of a new species from within a population that is not geographically separated; individuals on the periphery of a population are subjected to slightly different selection pressures, causing speciation within one population

parasitism
a symbiotic relationship in which one organism (the parasite) obtains benefit and the other organism (the host) is harmed

parthenogenesis
in animals, development of an embryo from an ovum without fertilisation

Pearson's correlation coefficient (*r*)
a measure of the strength of the linear relationship between two continuous variables

pedigree
a chart showing the ancestry, descent and relationships between all members of a family or other genealogical group

peer review
the process in which experts evaluate the quality, relevance and validity of another researcher's work prior to its publication

percentage
a number expressed as a fraction of 100

percentage cover
the estimated percentage of a quadrat that is covered by one species

percentage frequency
the percentage of quadrats in which a species is found divided by the total number of quadrats in a sample

phenotype
the observable traits or characteristics of an organism, resulting from the interaction of its genotype with the environment

phenylketonuria (PKU)
a homozygous recessive genetic disease in which one enzyme required for the normal break-down of phenylalanine is lacking

photosynthetic efficiency
the percentage of light energy that photosynthetic organisms convert into chemical energy during photosynthesis

phylum
a major classification group of the animal kingdom; plural *phyla*

physiological stress
the inability of an organism to function at maximum efficiency as a result of some factor, impacting the growth and reproduction of the organism

pioneer species
species of plants that colonise bare ground

plan sketch
an aerial view showing position and canopy cover of species

plankton–nekton ecosystem
the ecosystem of the ocean surface, consisting of nekton (free swimmers) and plankton (microscopic organisms)

plasmid
a small DNA molecule that is physically separated from chromosomal DNA and can replicate independently; typically within a bacterial cell

plot
an area under investigation, generally a subset of a larger area

point mutation
a change in a single nucleotide in the DNA code that may result in translation of one different amino acid in a polypeptide sequence

polar body
a small haploid cell produced during both meiosis I and II during oogenesis as a result of uneven cell division

polygenic inheritance
inheritance of a set of genes that together control a quantitative character such as height; also known as multiple gene inheritance

polymerase chain reaction (PCR)
a technique that enables the amplification of any short sequence of DNA

polysome
a chain of ribosomes that 'read' mRNA

population
a number of individuals of one species living in a particular place at a particular time; in statistics, the group that scientists wish to draw conclusions about

population bottleneck
a significant reduction in genetic diversity of a population, caused by a sudden and drastic reduction of that population

population density
the number of individuals of a given species per unit area

population growth
the change in the number of individuals in a population in a particular habitat

population growth rate
the rate of change of a population over a particular range of time

population pyramid
a model of the numbers of organisms at each trophic level of a food chain

precision
how close a set of data values are to each other

predator
an organism that catches, kills and feeds on another animal

prediction
forecast of a future event based on similar known events

primary data
data collected by the researcher from their own experiment designed to answer the specific research question

primary follicle
a single-layered structure in the mammalian ovary that contains the primary oocyte

primary forest
a climax forest formed through primary succession

primary oocyte
a diploid cell developed by an ovarian germ cell in mammals, which may later develop into an ovum

primary spermatocyte
a diploid cell formed by mitosis of a spermatogonium; undergoes meiosis I to produce two haploid secondary spermatocytes

primary succession
the process of development and change in plant communities over time, leading eventually from bare ground to a climax community

product rule
a law of probability; states that the chance of two independent events occurring together equals the chance of one event occurring alone multiplied by the chance of the other event occurring alone

productivity
the amount of energy fixed in organic compounds; measured by the increase in biomass per unit of time

profile
slope of the terrain, position and height of vegetation types, and canopy cover

promotor region
a DNA sequence located before a gene that helps initiate the process of transcribing the gene into RNA.

Punnett square
a mathematical device used to calculate probable genotype and phenotype outcomes of genetic crosses

pure-bred
describes an organism that is homozygous for a trait and thus has the same phenotype as the parents

Q

quadrat
a defined area (usually square) with a fixed size, used to count organisms within an area

qualitative
descriptive

quantitative
measured

R

random distribution
an unpredictable spacing of individuals of a species, where the position of each individual is independent of the other individuals of the species in a given environment

random error
an error due to the limitations (uncertainty) of the measurement equipment, and the uncontrollable effects of the method and the environment on the measurement

random fertilisation
the process in sexual reproduction where any of the genetically unique sperm may fuse with a genetically unique ovum, and the combination is entirely up to chance

random sampling
a sampling procedure in which every member of the population has an equal chance of being selected for the sample

ratio
a measure that compares the magnitude of two quantities in terms of how many times one value is contained within the other

recessive allele
an allele on a chromosome that can be masked by its dominant form in the heterozygous condition; can be autosomal or sex-linked

recessive trait
a trait due to an allele that is masked by the dominant allele in the heterozygous condition but expressed in the homozygous condition

recombinant DNA
genetically engineered DNA formed by combining genes from different sources

recombinant DNA technology
the deliberate modification of the characteristics of an organism, or the production of a new organism, by inserting or deleting genes into the DNA; also known as genetic engineering

recombinant gametes
gametes produced as a result of crossing over of the chromatids of homologous chromosomes during meiosis

refute
contradict or not support (in relation to the hypothesis)

regulatory gene
a non-coding segment of DNA that controls the expression of other genes, by producing transcription factors for gene expression

reliability
the extent to which a measurement, test or investigation produces consistent results

repeatability
the extent to which the same results can be produced by a researcher when the experiment is performed again under the same conditions

replicate
a result obtained by repeating a measurement using the same methodology, conditions and materials

replication bubble
an unwound and open region of DNA in which DNA replication occurs, created when the enzyme DNA helicase separates the two strands of DNA

replication fork
a structure with two branching sections that is created when DNA helicases break the hydrogen bonds holding two DNA strands together at a certain point

reproducibility
the degree to which the same results can be generated by other researchers using different equipment and methods in different laboratory settings

reproductive isolation
the inability of different populations or species to interbreed due to behavioural, structural or physiological differences between the organisms

resource partitioning
the division of environmental resources by coexisting species populations, to avoid competition for resources

restriction enzyme
an enzyme that cleaves DNA at or near specific recognition sites

ribonucleic acid (RNA)
a thread-like chain of nucleotides carrying the genetic instructions for forming a protein in a cell

ribosomal RNA (rRNA)
the RNA component of a ribosome

ring species
a series of populations within a species where each population interbreeds with the neighbouring populations, but the end populations differ significantly and are unable to interbreed.

RNA primer
a short strand of RNA that acts as an initiation point for DNA synthesis

***r*-selected species**
a species that occupies an unstable environment and uses the evolutionary strategy of maintaining a high growth rate, occupying less crowded ecological niches and producing many offspring

S

sample
a subset of the population of interest in a study

scale
the relationship between the actual size of an object/specimen/area and how it is presented in a depiction

scatterplot
a graph in which the values of two variables are plotted along two axes, the pattern of the resulting points revealing whether a relationship (correlation) exists

scientific idea
an idea or theory that is based on empirical evidence and has been tested or supported by the scientific method

scientific law
a scientific theory that has been continually upheld by experimentation; a statement based on repeated experimental observations

scientific method
the testing of hypotheses by controlled experimentation

scientific theory
a well-substantiated explanation of some aspect of the natural world, based on a body of facts that have been repeatedly confirmed through observation and experiment

secondary data
secondhand data obtained from other sources

secondary forest
a climax forest formed due to secondary succession

secondary oocyte
a large haploid cell produced during meiosis I of the primary oocyte

secondary spermatocyte
a haploid cell that undergoes meiosis II to form spermatids

secondary succession
successive, natural changes in plant communities in an area where a previous community has been removed

semiconservative replication
replication of DNA resulting in two copies that each contain one of the original strands and one new strand

sere
an intermediate community in ecological succession in an ecosystem advancing towards its climax community

Sertoli cell
a type of cell in the epithelium of tubules of the mammalian tests that protects and nourishes the developing spermatozoa

sessile
fixed in one place; not mobile

sex chromosomes
chromosomes carrying information that determines the sex of the individual

sex-linked gene
a gene located on a sex chromosome

sexual aneuploidy
the presence of an abnormal number of sex chromosomes in a cell

shared characteristic
a characteristic that all members of a group or clade share; evidence of a common ancestor

short tandem repeats (STRs)
short DNA sequences of a repeating nucleotide sequence, often varying in length between individuals

Simpson's diversity index (*SDI*)
the probability that two individuals randomly selected from a sample will belong to different species (or groups)

somatic gene therapy
replacement of defective genes in targeted somatic cells that are affected by a genetic disease

somatic mutation
a mutation in a non-reproductive cell and therefore non-inheritable, affecting only the individual

spatial scale
the size of an area at which an event or process occurs

Spearman's rank (*p*)
a measure of the strength and direction of a monotonic relationship between two variables

Specht's classification system
an Australian system of classification of vegetation based on the height and coverage of the dominant layer

specialist feeder
a heterotroph that can thrive only on a limited diet

speciation
the evolutionary process by which new, distinct species are formed

species
the most specific taxonomic group containing very closely related organisms; allocated two (genus and specific) names; members of the same species can produce fertile offspring when mating under natural conditions

species diversity
the number of species, and the relative abundance of each species, in a community

species evenness
a comparison of the relative abundance of different species in a community

species richness
a measure of the number of species in an ecosystem

specific name
the descriptive name of a species

spermatid
an immature spermatozoon

spermatogenesis
the formation of spermatozoa in animals

spermatogonium
a germ (stem) cell in a layer of cells lining the tubules in the testes; plural *spermatogonia*

spermatozoon
a small, motile male gamete; plural *spermatozoa*

splicing
a post-transcriptional process in which introns are removed and exons are connected, to produce mature mRNA

split gene
a gene that contains coding regions, called exons (expressed as RNA and protein), interrupted by non-coding regions, called introns

S-shaped population curve
the graphical representation of the change in population density of an organism when it initially increases slowly and then rapidly as it approaches an exponential growth rate, but then decreases and levels off as the environmental carrying capacity is reached

stabilising selection
selection that favours the central alleles in a distribution, eliminating alleles in both the upper and lower extremes of the distribution

standard deviation
a measure that describes how far, on average, scores are different from the mean

standard error
the standard deviation of the sampling distribution of a statistic

sticky ends
fragments of unpaired DNA bases formed when particular base sequences are cut asymmetrically

strata
distinct layers or zones within an ecosystem, based on vegetation type or abiotic factors

stratification
the division of the physical environment into smaller components for sampling

stratified sampling
a sampling procedure in which the population is divided into strata and random samples are selected from each stratum

structural gene
a section of DNA that carries the instructions for production of a protein

student's *t*-test
a statistical test used to determine whether the difference between the means of two groups is statistically significant

subspecies
a taxonomic rank immediately below a species; a population that is genetically isolated from other populations of the same species in a particular geographic region, often capable of interbreeding successfully where ranges overlap

sugar–phosphate backbone
the structural framework of nucleic acids, composed of alternating sugar and phosphate groups

summary statistic
a value that provides a summary of a data set

support
agree with (in relation to the hypothesis)

symbiosis
a relationship between two individuals of different species over a long time, where at least benefits from the interactions.

sympatric speciation
the divergence of a species into two separate species while the populations are not geographically isolated from each other; driven by reproductive isolation due to spontaneous chromosomal or genetic changes

systematic error
an error that causes readings to deviate from the true value by a consistent amount and in the same direction each time a measurement is made; it is affected by the accuracy of the measurement process

systematic sampling
a sampling procedure in which samples are selected based on a systematic interval from a randomly chosen starting point

T

table
a format for presenting data in rows and columns

tailing
the addition of a long tail of adenines at the end of mRNA

taxon
any group in a biological classification into which related organisms are classified (e.g. phylum, class); plural *taxa*

taxonomy
the science of naming and classifying living things

telomeres
repetitive DNA sequences at the ends of chromosomes that protect the chromosome from degradation and maintain genomic stability

temporal scale
the time period in which an event or process occurs

test cross
a cross between an organism that displays the recessive trait of a characteristic and one that displays the dominant trait, to determine whether the dominant phenotype is due to a homozygous or heterozygous genotype; this only applies if a large number of offspring are produced

tetrad
two homologous chromosomes, each consisting of two chromatids, lying side by side

theory of evolution
the theory, originally proposed by Charles Darwin, that all species of organisms arise and develop through a process known as natural selection, whereby small, inherited variations in individuals increase their ability to compete, survive and reproduce, and these variations are passed on to the next generation

thermophile
a microorganism that can tolerate temperatures higher than 45°C

tolerance range
the range of a particular abiotic factor within which an organism can survive

transcription
the first step of gene expression, in which a particular segment of DNA is copied into mRNA

transcription factor
a protein produced by regulatory genes that regulates the phenotypic expression of structural genes

transect
a line, often laid across an ecological gradient, along which the abundance of organisms is recorded, either within the whole area or at specified intervals

transfer RNA (tRNA)
small segments of RNA that transport specific amino acids to the mRNA attached to a ribosome during translation

transgenic organism
an organism whose genome has been altered using genetic material from another species or breed

translation
the production of a polypeptide sequence from a sequence of mRNA codons

translocation
the exchange of chromosomal segments from one position to another, either within the same chromosome or to another chromosome

trimming
the removal of non-coding sections at the beginning and end of mRNA

trisomy
a condition in which a diploid organism has three copies of one of its chromosomes instead of two

trophic level
one of the levels of a food chain, e.g. first-order consumer

true value
the value of a measurement if it were measured perfectly

U

uncertainty
the degree to which the result of a measurement does not reflect the exact (true) value of what is being measured

uniform distribution
a pattern of distribution in which individuals are more or less equally spaced throughout the entire area

universal donor
a person with type O blood, which has no antibodies to antigens A and B and therefore can be donated in small quantities to individuals of any other blood group

universal recipient
a person with type AB blood, which has both A and B antigens and therefore can receive small quantities of any other blood group

V

validity
the extent to which a test measures what was intended

variance
a measure of how spread data is from the mean

variety
a group that has a set of characteristics distinct from other varieties within the same species, e.g. a poodle and a Great Dane

vector
a DNA molecule used in the transfer of foreign genetic material into another cell, where it can be replicated and/or expressed

vertical stratification
the vertical arrangement of vegetation into layers (strata), providing a variety of niches

viability
an organism's ability to survive to reproductive age and produce offspring

W

wild type
the most common phenotype for a feature in a population

working hypothesis
the most successful hypothesis of a particular investigation

X

X chromosome
one of the two sex chromosomes in vertebrates and some other animals; females typically have two X chromosomes, while males have one X and one Y chromosome

X inactivation
the condensation, and thus inhibition, of one of the pairs of X chromosomes in female vertebrates

Y

Y chromosome
one of the two sex chromosomes in vertebrates and some other animals; males have one copy

Z

zonation
the breaking of the biome into habitat zones

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Acknowledgements

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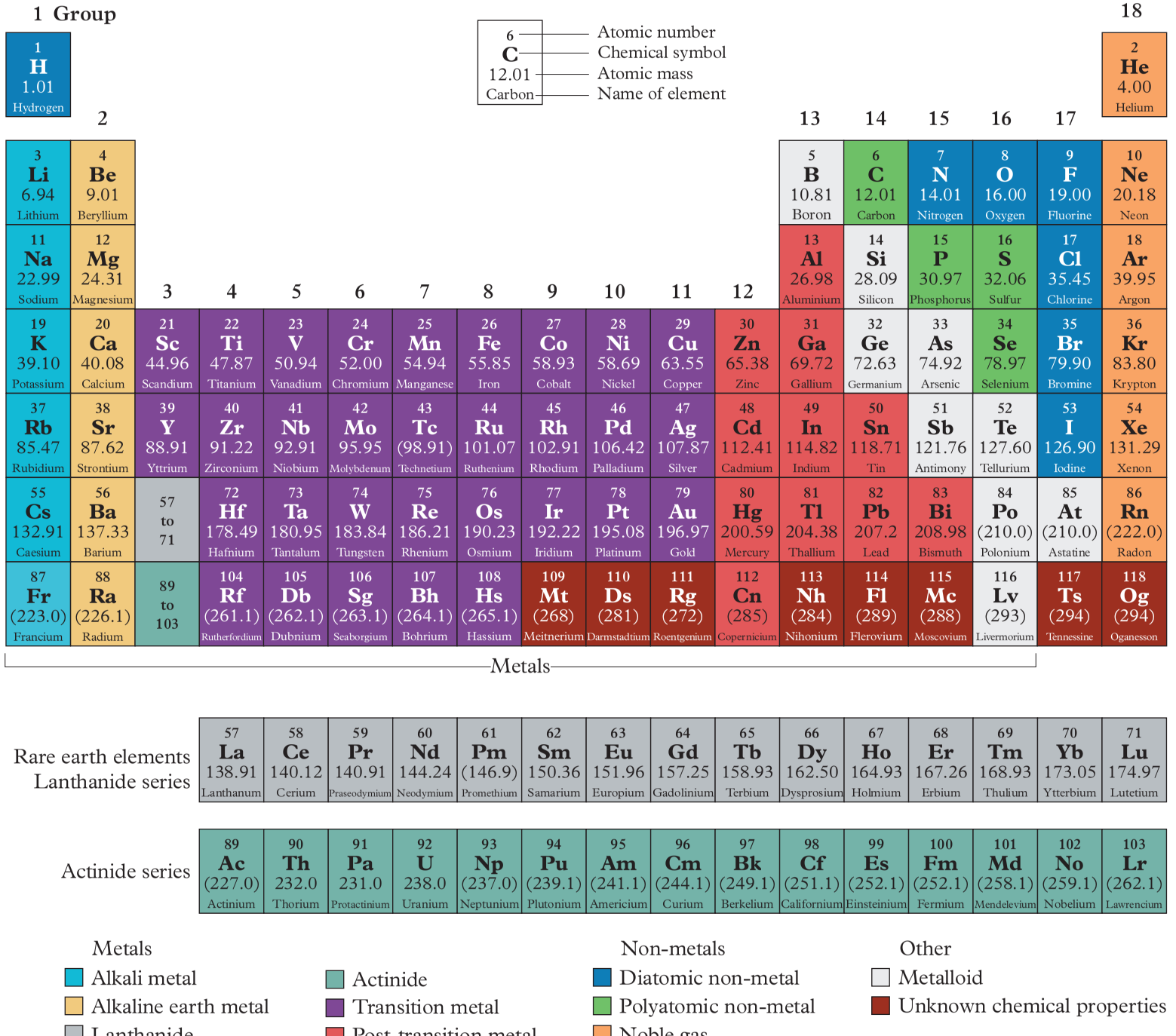

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