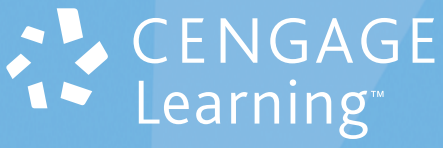
NELSON

QCE Biology

UNITS 3 4

Wendy Cook
Louise Munro



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NELSON

QCE Biology

UNITS 3 4

LEARNING DISCOVERY

CHRYSANTHEMUMS

Adam Nixon/Stocksy

Chrysanthemums are plants that belong to the genus *Chrysanthemum*. The genus includes approximately 40 species and is native to East Asia and northeastern Europe. Chrysanthemums are polyploids, which contributes to their high genetic diversity. Although they appear as a single flower, they are actually made up of many tiny flowers called florets.

Wendy Cook
Louise Munro

Nelson QCE Biology Units 3 & 4
1st Edition
Wendy Cook
Louise Munro

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CONTENTS

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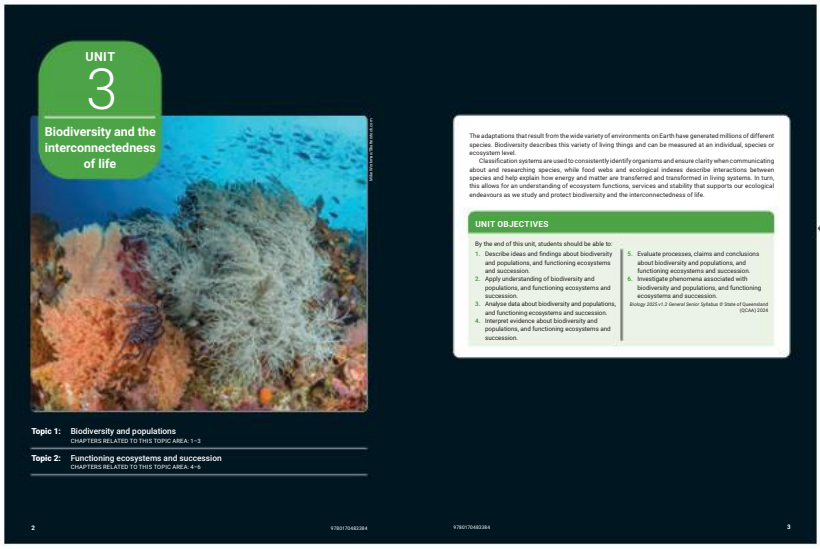
ABOUT THIS BOOK

Nelson QCE Biology Units 3 & 4 is a comprehensive textbook specifically tailored to align with the 2025 QCAA Senior Secondary Science Syllabus – Biology v1.2. It has been thoughtfully developed to empower students by providing a strong foundation in essential concepts and equipping them with the necessary skills to excel in their studies. Emphasising the importance of making connections between topics and practising exam techniques, this edition is designed to support students in unlocking their full potential and achieving success in their journey.

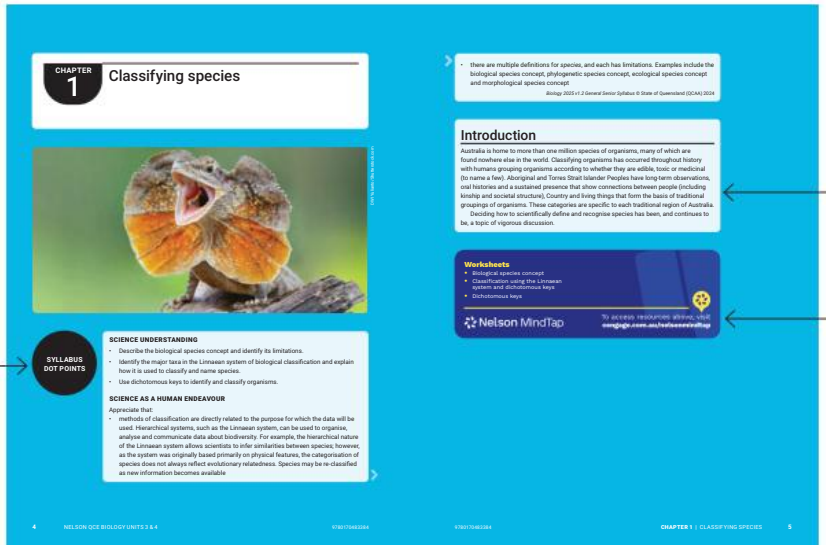
At the beginning of Unit and Topic

- Unit introductions are an overview of the key content in the unit.



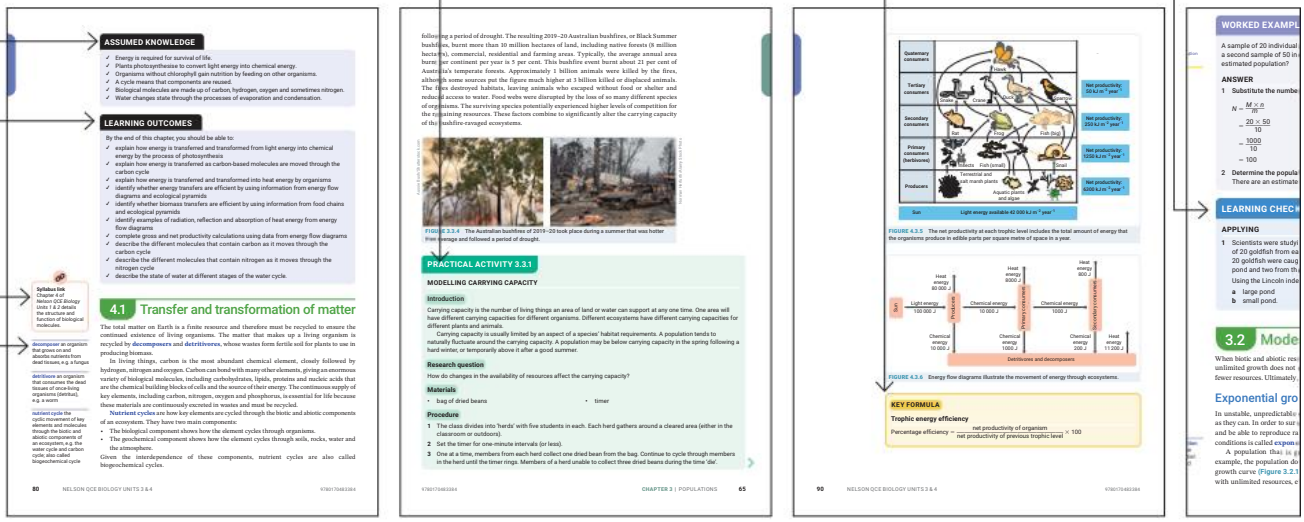
At the beginning of each chapter

- Chapter introduction to set the context of the upcoming key content
- List of syllabus dot points being covered in the chapter
- List of resources available on Nelson MindTap



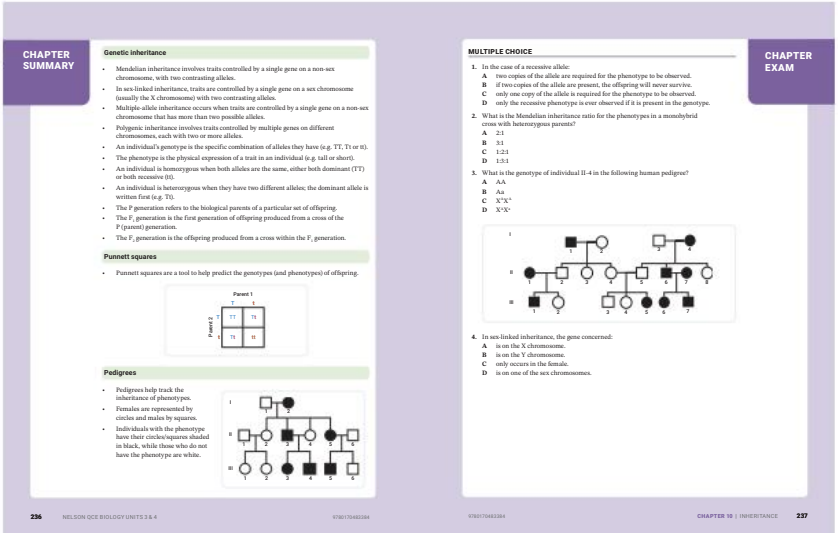
In each chapter

- **Assumed knowledge** – knowledge and skills students are expected to know coming into the chapter that relate to the chapter content
- **Learning outcomes** – highlights the key outcomes from chapter
- **Key terms** – defined in situ to help students deconstruct scientific language
- **Learning check** – written to the developmental levels highlighted in the syllabus objectives
- **Syllabus links** – highlighting links to other areas in the syllabus to help students make connections
- **Key formulas** – important formulas to remember
- **Practicals** – syllabus-aligned practicals with guided instructions on the materials, procedure, collection and analysis of results, and discussion.



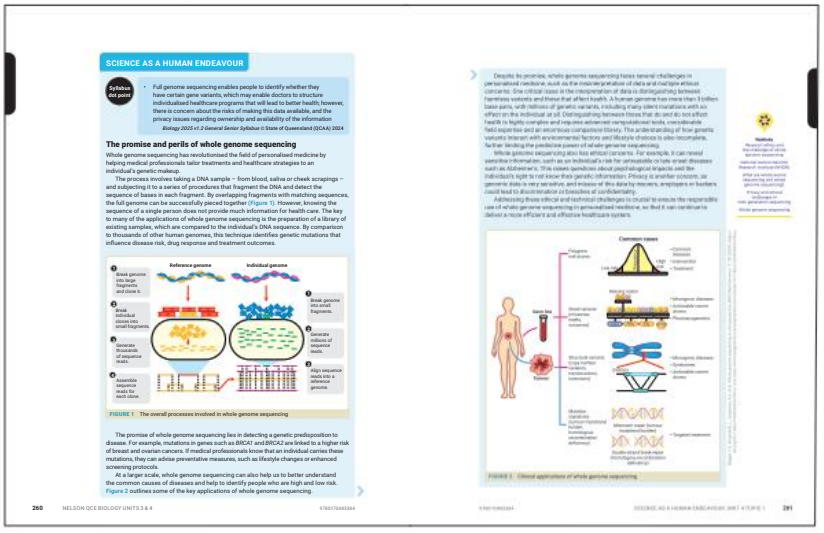
At the end of each chapter

- **Chapter summary** – visual summaries to help summarise key concepts
- **Chapter exam** – exam-style questions to help students develop exam skills, including deliberate practice in data analysis and making connections across content



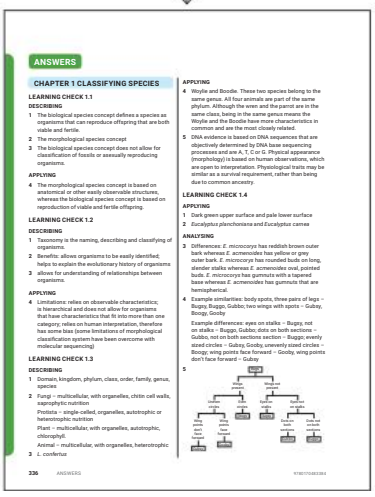
At the end of each topic

- **Science as a Human Endeavour** – a double-page deep dive on the evolution of science and how it has contributed to and influenced society



At the end of the book

- **Glossary** provides explanations of all terms introduced in the text.
- **Answers** provide complete answers for student reference.



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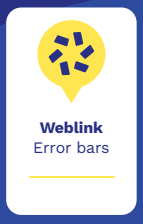
An online learning space that provides students with tailored learning experiences.

- Access tools and content that make learning simpler yet smarter.
- **Flexible formats:** choose how you navigate using either the online eText or offline PDFs.
- Margin links in the student book signpost multimedia student resources found on Nelson MindTap.



For students:

- **Engage** with the **online eText** by adding notes, highlights and bookmarks and using the **Search** and **Read Aloud** (in Australian voice) functions.
- **Check** your understanding with assumed knowledge reviews.*
- **Explore** key concepts with worksheets and additional online-only practicals.
- Access **supporting materials** such as the chapter summary pack and weblinks.
- **Revise** with chapter tests to practise your skills and build confidence.*
- **Navigate** your own learning path, accessing the content and support resources as you need it.

* Available if assigned by your teacher in Cognero Assess.

For teachers**:

- Use **teaching plans** and curriculum guides to support easy program and assessment planning.
- **Prepare** students for assessment with practice versions of data tests, unit-level exams and the external assessment.
- **Answers** to student book questions help you grade efficiently.
- **Risk assessments** and technical notes are provided for each practical activity to ensure the safety of students.
- **Chapter summary** presentations provided in Powerpoint format let you edit and build on them.
- Help build your students' exam readiness with **Cognero Assess** – a test bank containing hundreds of questions and answers to create, assign or export formative and summative tests.

** Complementary access to these resources is only available to teachers who use this book as part of a class set, book hire or booklist. Not available for single purchases. Alternatively, teacher access can be purchased as a separate subscription for schools. Contact your Cengage learning consultant for information about access and conditions

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CHAPTER DC

Science research

Ground Picture/Shutterstock.com

SYLLABUS DOT POINTS

SCIENCE INQUIRY SKILLS

Throughout the course of the study, students will:

- identify, research and construct questions for investigation
- propose hypotheses and/or predict possible outcomes
- 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
- identify and implement strategies to manage risks, ethics and environmental impact, e.g.
  - ethical guidelines
  - cultural guidelines, protocols for working with the knowledges of First Nations peoples

  - material safety data sheets
  - workplace health and safety guidelines
  - appropriate disposal methods
  - standard operating procedures
  - acknowledgement of sources and referencing
- 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
- 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 R^2)
  - 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
- select, synthesise and use evidence to construct scientific arguments and draw conclusions
- extrapolate findings to determine unknown values, predict outcomes and evaluate claims
- 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
- 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
- appreciate the role of peer review in scientific research.

Introduction

Conducting structured experiments is an important part of science because it allows for the gathering of information to help develop a greater appreciation and understanding of the world.

Researching topics and the process of developing and implementing experimental methods form a large part of the scientific studies throughout this course. In fact, the Student Experiment (IA2) and Research Investigation (IA3) make up a significant portion of the internal assessments, incorporating both primary and secondary data. Furthermore, the scientific thinking acquired through these processes is regularly examined in the external assessment. As such, it is important to develop these skills not just for this course, but also to improve critical thinking.

ASSUMED KNOWLEDGE

- ✓ The purpose of experiments is to collect information about a key idea or to answer a question.
- ✓ Controlled experiments have a general structure.
- ✓ Variables are factors or conditions that can be changed, controlled or measured and which can influence the result of an investigation.
- ✓ The data collected from an experiment needs to be related to the question being investigated.
- ✓ Data collected from an experiment can be presented in different ways depending on the nature of the data.
- ✓ Data can be classified as primary or secondary.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ develop research questions for research
- ✓ identify the importance of peer review in scientific research and compare different ideas and information from scientific texts
- ✓ plan and modify investigations, including the materials and methods needed to collect valid and reliable data (both primary and secondary data)
- ✓ consider safety, ethics and the environment when conducting scientific investigations
- ✓ determine the best method to present data; for example, tables and graphs
- ✓ use scientific language and visual representations to organise and present information accurately
- ✓ identify and minimise errors in measurements
- ✓ calculate uncertainties and other measures of data accuracy and describe their impact on data
- ✓ select and construct the most appropriate data presentation technique
- ✓ make predictions based on trends observed in the data
- ✓ use mathematical techniques to analyse data to find patterns, trends and relationships, taking into account any limitations or sources of error or uncertainty
- ✓ draw conclusions based on evidence, comparing findings to expected results
- ✓ communicate scientific information in a clear and appropriate manner for different audiences, while acknowledging sources and using proper referencing
- ✓ reflect on investigations and suggest ways to improve the quality and accuracy of data and findings.

DC.1 Student experiment

Forming

The research question

research question a question that directs the scientific inquiry activity; it focuses the research investigation or experiment, informing the direction of the research, and guiding all stages of inquiry, analysis, interpretation and evaluation

For your Student Experiment (IA2), you will be required to design an experiment to answer a **research question** related to a topic in the syllabus. In science, the design of experiments is guided by the scientific method **(Figure DC.1.1)** – a systematic and structured approach that ensures that the results are objective, accurate and reliable.

A research question is the question you are trying to answer with your research, and by doing so it helps to guide and refine the research and experimental method. For example, a research question could be 'How does a fever of more than 38°C affect the function of enzymes

in the body?' Remember to make the research question both specific and relevant. Including units for the independent and dependent variables will help with this.

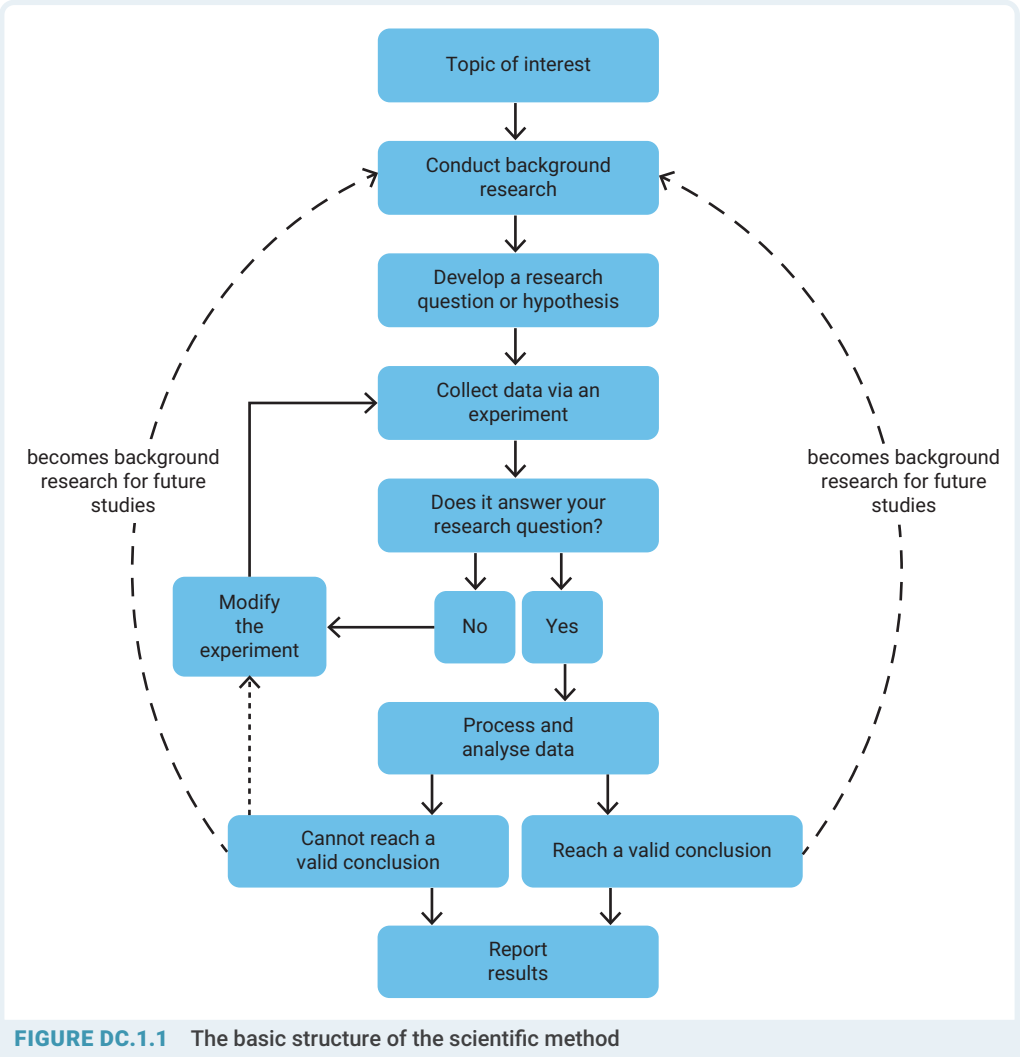

FIGURE DC.1.1 The basic structure of the scientific method

Rationale

When developing a research question, it is important to demonstrate an understanding of the underlying theory related to the topic. This is described in the rationale of your experiment and is also implied through your research question. In the example above, the research question explores the relationship between enzymes and temperature. Given that it is known that the function of enzymes can be affected by changes in temperature, exploring the impact of an increase in temperature (because of a fever) expands our understanding of enzymes.

With an understanding of the topic, it is likely that you have developed a possible answer to the research question. As you know, this is the hypothesis. The hypothesis highlights the relationship between the **independent** and **dependent variables**, showing the directional impact that one would have on the other. A possible hypothesis to the example above is 'As the temperature of the fever increases, enzyme function would be reduced'. In this case, the independent variable is the change in temperature and the dependent variable is the level of enzyme function, which can be measured by the amount of product produced over time.

independent variable the variable that is changed or manipulated in an experiment

dependent variable the variable that changes because of changes to the independent variable

Methodology

For your experiment, you will need to modify an existing method from previous studies. During your research, you may have encountered various studies conducted by scientists who were interested in investigating a similar topic. These studies can serve as a valuable foundation for you to build on and refine your own approach. How and what you modify in the experiment will depend on:

- the variables you are testing
- sources of error and bias in the previous method
- the type of data being collected (**quantitative** or **qualitative**)
- how much data you will need to collect to ensure that there is sufficient data for analysis
- access to resources.

qualitative data
information that is not numerical in nature

quantitative data
numerical information

In Biology, scientists often use different types of investigations. These can be categorised into five main types:

- Descriptive
- Comparative
- Correlational
- Experimental
- Case studies

Table DC.1.1 summarises the five main types of investigations.

TABLE DC.1.1 The five main types of investigation techniques used in Biology

Investigation type	Description	Example
Descriptive	Researchers collect data through surveys, interviews or observations to gain a better understanding of the subject being investigated.	Describing the distribution of a species in an ecosystem
Comparative	Two or more groups or variables are compared to identify similarities and differences between them. Researchers can use this information to investigate the impact of factors on the groups being investigated.	Comparing the growth of different plants under different environmental conditions
Correlational	These investigations focus on identifying the relationship between variables. Data collected in these investigations is used to determine whether changes in one variable are associated with a change in another variable. Note: Correlation does not mean causation.	Identifying the relationship between temperature and plant growth
Experimental	Variables are manipulated to determine whether there is a cause-and-effect relationship between the variables.	Testing the effect of a fertiliser on plant growth
Case study	These involve analysis of a particular individual, group or situation.	Studying the behaviour of a particular type of frog in a specific ecosystem

Once you have your base experiment (which could be one that you completed in class), you will be required to make some modifications to design your own student experiment. A modification may be one of three different types (see Table DC.1.2).

Although you will not need to write your entire methodology in your experiment, it is important that you can justify the modifications that you made and how they improve the validity and/or reliability of the experiment. For example, if you decided to refine an experiment by using a digital thermometer instead of an analogue alcohol thermometer, you could justify this by saying that your refinement will improve the accuracy of your data collection because the digital thermometer has a smaller uncertainty and removes human error.

TABLE DC.1.2 Types of modifications that can be made to methodologies for the Student Experiment (IA2)

Type of modification	Explanation	Instruction	Example
Refine	To make subtle changes to improve the accuracy or precision of the data	• Make improvements without changing the independent or dependent variables.	• Use equipment with a higher level of precision. • Improve the methodology or way of measuring the independent variable. • Change the sample size.
Redirect	To gain further insight by changing the course or direction of the data	• Change the independent variable.	• Measure pH instead of temperature. • Use a different species. • Use different chemicals.
Extend	To change or extend the scope of the current data range	• Change the range of the independent variable. • Extend the range of the independent variable.	• Use more concentrations of solution. • Use more sample categories or data ranges.

Essentially, any modifications to the methodology are done to improve the reliability of data and validity of the experiment. Although you will not need to show your full methodology, you will need to explain and justify any modifications and refinements in your final presentation of your experiment (Table DC.1.2). The justifications need to be specific to your modifications and making statements such as 'this makes the data more accurate' is not sufficient.

Sampling methods

In a biological experiment, it is often not feasible to collect information about a whole population or ecosystem. So, we need to select a subset or sample from the larger population that can be considered representative of the population. The way we select the sample is known as the sampling method. The main sampling techniques are summarised in **Table DC.1.3**.

TABLE DC.1.3 A summary of different sampling methods

Technique	Description	Example
Random sampling	Samples are selected randomly from the population. There is an equal chance of being selected. This helps minimise bias. It is generally used when there are time constraints and/or the samples appear relatively uniform in species composition.	Randomly selecting trees from a forest to study the biodiversity within the forest
Systematic sampling	Samples are selected at fixed intervals in a particular pattern.	Determining the species of fish in a river by collecting data at regular intervals at a point along the river
Stratified sampling	Groups in a population are divided into subgroups based on certain characteristics. Samples are randomly selected from each subgroup as a representative of their population. Samples are taken in proportion to the different strata present (i.e. if it is 30% field and 70% scrub, 30% of the quadrats are placed in the field and 70% in the scrub).	Studying the diversity of bird species across different forest canopy layers

Depending on the nature of the experiment, you need to be familiar with the techniques and measuring instruments involved. Surveying techniques are the methods used to gather information and/or data for your investigation. **Table DC.1.4** summarises common sampling techniques often used to gather information for biological investigations.

TABLE DC.1.4 A summary of different types of sampling techniques

Sampling technique	Description	Example
Quadrats	Square or rectangular frames used to sample an area. Data is measured from within the frame.	Investigating the abundance of a particular species of weed in an area.
Transects	A line is drawn through the area of interest from one point to another. Data is collected along this transect line at specific points or intervals. Transects can be categorised as line or belt transects. Belt transects have a wider line than line transects, and can have quadrats placed along the transect lines at particular points (interrupted belt transects).	Examining the changes in vegetation along a walking path of a mountain or in relation to an environmental gradient.
Capture–recapture	A sample of a species is captured, marked and release back into their environment. After a period of time, another sample is captured, including marked and unmarked individuals. This is used to estimate the total population size.	Researchers capture kangaroos, mark them with ear tags and release them back to their habitat. After a period of time, researchers capture another sample and count the number of kangaroos with ear tags. This is used to estimate the population of kangaroos.

Regardless of the type of sampling method technique, misreading the instruments used to collect the data results in inaccurate results. For example, when reading the volume of a liquid in a measuring cylinder, the measurement must be taken at eye level and measured from the bottom of the meniscus **(Figure DC.1.2)**.

When collecting and recording data, ensure that it is measured in the appropriate units. For example, the concentration of solutions can be measured using different units such as $g\,L^{-1}$, $mol\,L^{-1}$ or ppm (parts per million). However, this will depend on the nature of the experiment. Since there are different units to express the same measurement, you will often need to convert between units, especially when analysing results. **Table DC.1.5** shows common unit conversions.

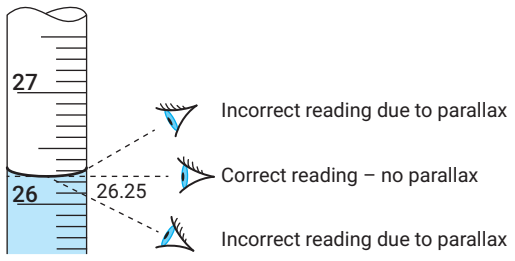

FIGURE DC.1.2 How to read measurements from a measuring cylinder

TABLE DC.1.5 Common unit conversions

Measurement	Common conversions
Distance	1 km = 1000 m = 100 000 cm = 1 000 000 mm
Mass	1 kg = 1000 g = 1 000 000 mg
Volume	1 L = 1000 mL = 1000 cm^3

If the proposed experiment involves exploring knowledges of First Nations peoples, it is extremely important to understand all the cultural guidelines and protocols involved in conducting such research. For example, the *Traditional Knowledge Guidelines – Biodiscovery Act 2004* released by the Queensland Government helps to identify the measures that need to be taken for biodiscovery.

Weblinks

Traditional Knowledge Guidelines – Biodiscovery Act 2004

Guidelines for Ethical Research in Australian Indigenous Studies

Finding

Health and safety

Health and safety are important considerations for practical exercises in all sciences. When undertaking your own practical research investigations, you must consider any relevant workplace health and safety guidelines. In Queensland, this includes the *Work Health and Safety Act 2011*. As the researcher, you must ensure safe laboratory practices when planning and conducting investigations by using risk assessments, supported by material safety data sheets (MSDSs), and accounting for risks. MSDSs are important when you are using chemicals as part of your investigation. This includes both the use and the disposal of any potentially harmful materials used and produced in your experiment. Even if your research does not use chemicals but requires participants to take some actions that may cause harm, you will still need to complete a risk assessment form (Figure DC.1.3). Your school is likely to have one of these documents for

Science investigation risk assessment for *Nelson Science 10*

Nelson MindTap

Chapter 2

School			
Name of teacher/technician			
Date		**Year level/class**	

Name of investigation/activity	Modelling natural selection
Book reference	*Nelson Science 10*, Chapter 2, Module 2.4, downloadable/PDF science investigation
Activity type	Demonstration Student activity
Description of activity	

Equipment

Equipment to be used	Potential hazards	Control measures/safe handling procedures
	Electrical Radiation Thermal Sharps Projectile Glass Gravity – Weights or magnets Other –	Safety glasses Sharps container Thermally insulated gloves Signage Safety shield Other –

Chemicals

Chemicals to be used	Potential hazards		Control measures/safe handling procedures
	Explosive Flammable Oxidising Gases under pressure Corrosive	Acute toxicity Chronic health hazards Health hazards Environmental Other –	Ventilation Fume cupboard Safety shield Safety glasses Lab coat Gloves Limit concentration/quantity Other –

FIGURE DC.1.3 A section of a risk assessment form

Resource

Risk assessment

you to complete when you conduct your experiment. If you are unsure of either the ethical, environmental or the health and safety aspects of your experiment, check with your teacher.

Any risks that you identify need to be highlighted in your experiment, including the steps to mitigate these risks.

1.4 Management of risks

The overall experiment was given a low–medium risk due to several safety hazards. An over-heating power supply may cause melting to outer-plastic and can shut down – affected connected outlets to the supply (Hill, 2021). Consequently, the power supply was shut off every 2 minutes and was placed over a heat-resistant mat to eliminate heat-transfer and to allow a risk-free 8 V supply. Furthermore, many power cables were connected to walls, computers and other equipment throughout the procedure, hence a safety hazard for a potential 'trips and falls' in the laboratory-safety-procedure section (Safety, 2013). Thereby, chairs were placed over all wires – to caution anyone near the premises. Finally, gloves and sanitisation of equipment were also utilised for COVID-19 regulations to prevent cross-contamination.

FIGURE DC.1.4 An example of the inclusion of risks in an experiment

Apart from highlighting any potential dangers, another way to reduce the risk of injury and improve safety is to clearly outline the procedures in the experiment. This also includes the proper use and disposal of any materials involved in the experiment. This can be referred to as the standard operating procedures of an experiment.

Ethics

Ethics is a guiding framework that all research investigations must follow. Ethical concepts provide moral guidance for making decisions about the design and implementation of a research investigation. Examples of ethical concepts are shown in Table DC.1.6.

TABLE DC.1.6 Descriptions of different ethical concepts

Concept	Description
Beneficence	Having a commitment to do good (and minimise risk and harm)
Integrity	Acting with honesty and transparency
Justice	Ensuring fair distribution of benefits, risks, costs and resources
Non-maleficence	Avoiding harm or ensuring that potential harm is outweighed by benefits
Respect	Respecting individual differences and ensuring the right to autonomy and choice

You must apply your ethical understanding throughout your study of science, particularly for your own research.

Analysing data

The **primary data** collected in the experiment should be first organised into a raw data table. When constructing these tables, the independent variable is usually expressed in the first column and the dependent variables from the trials in the experiment are placed in the subsequent columns. For example, when measuring the time taken for a current to pass through a solution of different concentrations, the different concentrations (the independent variable) are presented in the first column, and the time measurements (dependent variable) are presented in subsequent columns (Table DC.1.7). It is often suggested that you record everything in your **logbook**; however, a logbook is not a mandatory component of your investigation.

primary data data collected directly by a person or group

logbook a complete, permanent record of how an experiment or research project was conducted; it shows what was done at every step along the way

TABLE DC.1.7 An example of a table of raw data from an experiment

Concentration (mol L^{-1})	Time (±0.5 s)		
	Trial 1	Trial 2	Trial 3
0.2	359.5	368.5	364.5
0.4	360.0	345.5	327.5
0.6	325.5	339.5	333.5
0.8	343.5	307.0	327.5
1.0	307.0	339.5	326.5

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As shown in Table DC.1.7, the units for each measurement are included in the column headings.

Once the data has been collected, the next step is to analyse it. As part of this, we need to make a judgement on the quality of the data in terms of:

- accuracy
- precision
- reliability
- validity
- sources of error.

It is important to note that each senior subject will have different and specific forms of mathematical analysis. What is appropriate for one type of data in one subject may not be appropriate for another. For example, calculated means and uncertainties might be appropriate for a Chemistry or Physics experiment, but mean and standard deviations might be more appropriate for Psychology or Biology experimental data. The following information is a general overview of the types of analysis you could undertake, but it is best to check that the type of analysis you choose is appropriate for your data.

Accuracy and precision

accuracy the degree to which the result of a measurement, calculation or specification conforms to the correct value or a standard

accepted value the value of a substance or quantity that is universally agreed as being a best estimate due to multiple and highly accurate measurements

percentage error the difference between a measured result and an accepted value, expressed as a percentage of the accepted value

In science, the **accuracy** of a measurement is how close it is to the true value of the quantity being measured. Even when the true value is unknown, scientists can rely on the best available **accepted value** to compare with the experimental measurement result to determine its accuracy. Often the accepted value is the theoretical value calculated for the measurement.

A way to help indicate the accuracy of a measurement is to calculate **percentage error**. Percentage error shows us how close the measured value is to the true or accepted value:

$$\text{Percentage error (\%)} = \left|\frac{\text{measured value} - \text{true value}}{\text{true value}}\right| \times \frac{100}{1}$$

KEY FORMULA

Percentage error

$$\text{Percentage error (\%)} = \left|\frac{\text{measured value} - \text{true value}}{\text{true value}}\right| \times \frac{100}{1}$$

WORKED EXAMPLE DC.1.1

A student used a ruler to measure the height of a 100 mL beaker. These beakers are known to have a height of 7.2 cm. The measured value was 6.8 cm.
Calculate the percentage error of the measurement.

ANSWER

1 **Determine the measured and true values.**
Measured value: 6.8 cm
True value: 7.2 cm

2 **Substitute and calculate the percentage error.**

$$\text{Percentage error} = \left|\frac{6.8 - 7.2}{7.2}\right| \times 100$$
$$= 5.6\%$$

This suggests that the measurement is slightly lower than the true value.

A low percentage error indicates a high degree of accuracy, whereas a high percentage error indicates a low degree of accuracy.

In contrast, **precision** describes how close a set of measured values are to each other. For single measurements, precision is about the level of detail given by the measurement usually based on the instrument used to take the measurement. For example, 0.3 g is less precise than 0.312 g. Note that precision can apply to the type of instrument used to take the measurement (instrument precision) or as a measure of reliability of the data collected (data precision).

precision the closeness of several independent measurements of the same quantity to each other

Measurements that are precise are not necessarily accurate **(Figure DC.1.5)**.

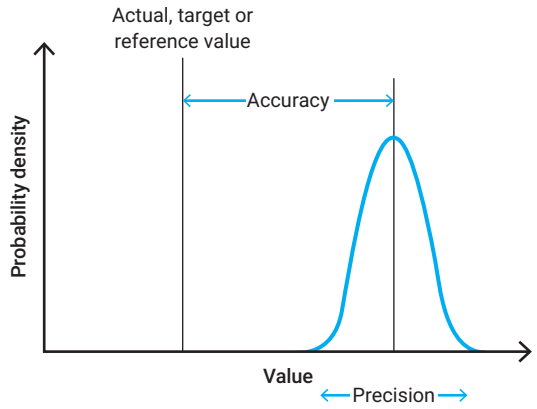


FIGURE DC.1.5 A graph showing the difference between accuracy and precision

Figure DC.1.6 helps further distinguish between accuracy and precision. In parts a and c, the individual indication values cluster closely around the mean; whereas parts b and d show imprecise measurement results as the individual measured values spread significantly around the mean.

For example, for an individual experiencing a fever, having precise measurements of body temperatures of 32.1°C, 33.2°C and 32.0°C does not mean that this is an accurate measure of their body temperature. We know this because humans have a core body temperature of approximately 37.0°C and fevers cause an increase, not a decrease, in body temperature.

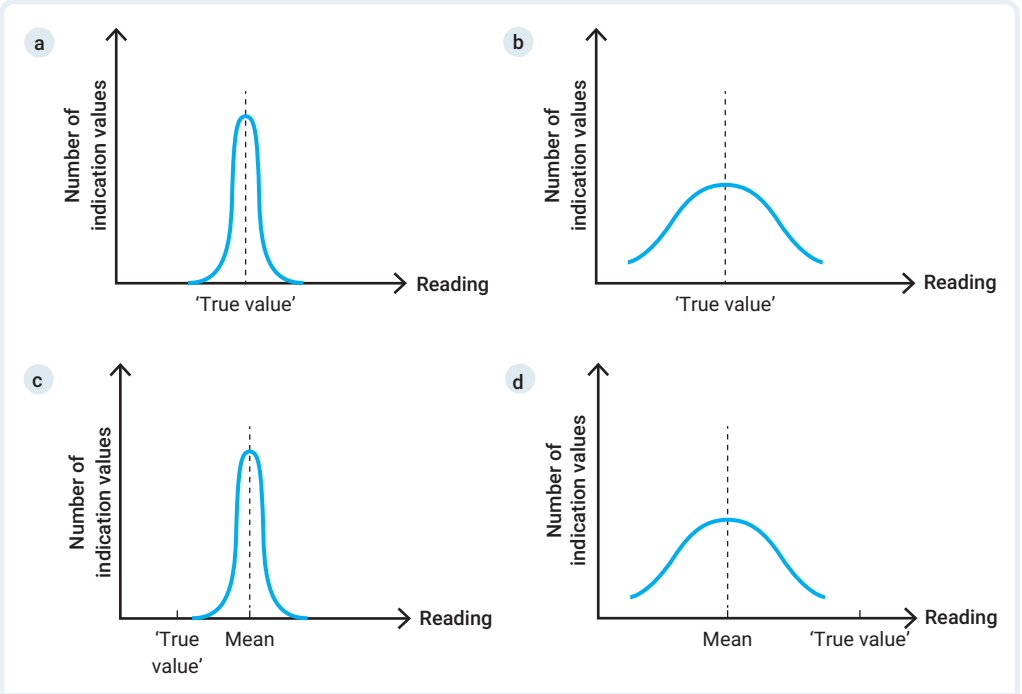


FIGURE DC.1.6 In a plot of measured values versus reading, results can be: (a) accurate and precise, (b) accurate and imprecise, (c) inaccurate and precise or (d) inaccurate and imprecise.

To improve the accuracy of measured values, you could:

- conduct multiple trials and average the results
- ensure that all variables except for the independent variable are controlled (also referred to as fair testing)
- ensure that the measuring tools used in the experiment are appropriate for what is being measured.

This helps to minimise the impact of any errors in the experiment that could affect the accuracy of the measured results. Errors will be discussed in more detail in a later section.

Reliability

reliability the extent to which the results of assessments are consistent, replicable and free from error

If an experiment is repeated, you would expect to obtain very similar results. When this happens, we say that the experimental results are reliable. However, this is not always the case because errors can affect the data collected. **Reliability** can be measured with uncertainty and standard deviation, concepts that will be described in more detail in a later section. The reliability of results can be improved by carefully controlling all variables apart from the independent variable. We will discuss other factors affecting reliability later in this section.

Validity

validity the extent to which the experiment measures what it is intended to measure

extraneous variable any variable that is not directly related to the experiment but could affect the results of the experiment

confounding variable a variable that is related to the independent and dependent variables

The quality of the data affects the **validity** of an experiment. We describe data as being valid if the result is due to the independent variable only and can answer the research question. In the example of measuring the effect of temperature on enzyme function, if variabilities in pH in the environment are not properly controlled, they can also affect enzyme function. As a result, we cannot confidently conclude that the results measured from the experiment are due to the changes in temperature only. This type of variable is known as an **extraneous variable** and can affect the relationship between the dependent and independent variables. In this example, pH is a specific type of extraneous variable known as a **confounding variable** because it

relates to both the independent and dependent variables. This is why it is important to ensure that all variables other than the independent variable are controlled.

Apart from extraneous variables, **errors** can also affect the results of an experiment. The two main types of errors are random and systematic errors.

error the difference between a measured value and the true value

Errors

Random errors are unpredictable variations that can occur during measurement. When taking multiple readings of the same thing, random measurement errors cause small variations so that you end up recording a spread of readings. These errors affect the precision of a set of data and can be caused by limitations of measuring instruments. You can reduce the effect of random errors by taking more or repeated measurements and calculating the **mean** (or average). To calculate the mean, divide the sum of the measured values by the total number of measurements:

random error a variation that affects a measurement in a random way so that successive measured values may show small changes from each other

mean the average value of a set of values

$$\text{Mean} = \frac{\text{sum of measured values}}{\text{total number of measurements taken}}$$

The mean value is then regarded as the most likely or best estimate of the true value. However, we cannot be certain that it is the true value.

KEY FORMULA

Mean

$$\text{Mean} = \frac{\text{sum of measured values}}{\text{total number of measurements taken}}$$

While random errors affect the precision of data, **systematic errors** affect the accuracy of a measurement. These errors cause the readings to differ from the true value by a consistent amount in the same direction. This can occur when measuring instruments are not properly calibrated, so readings differ from the true value by the same amount. Systematic errors can also be caused by observational error if there is a consistent distortion in the way we view things that causes errors that are the same every time. For example, a tall person may read a thermometer from a higher viewpoint and record a lower measure than the true value every time. To minimise the impact of systematic errors, it is important to know how to use measuring tools properly and to calibrate them before use.

systematic error a value that is either consistently above or consistently below an expected value; an error that acts in a predictable manner to give a consistent offset in data

Figure DC.1.7 highlights the differences between random and systematic errors.

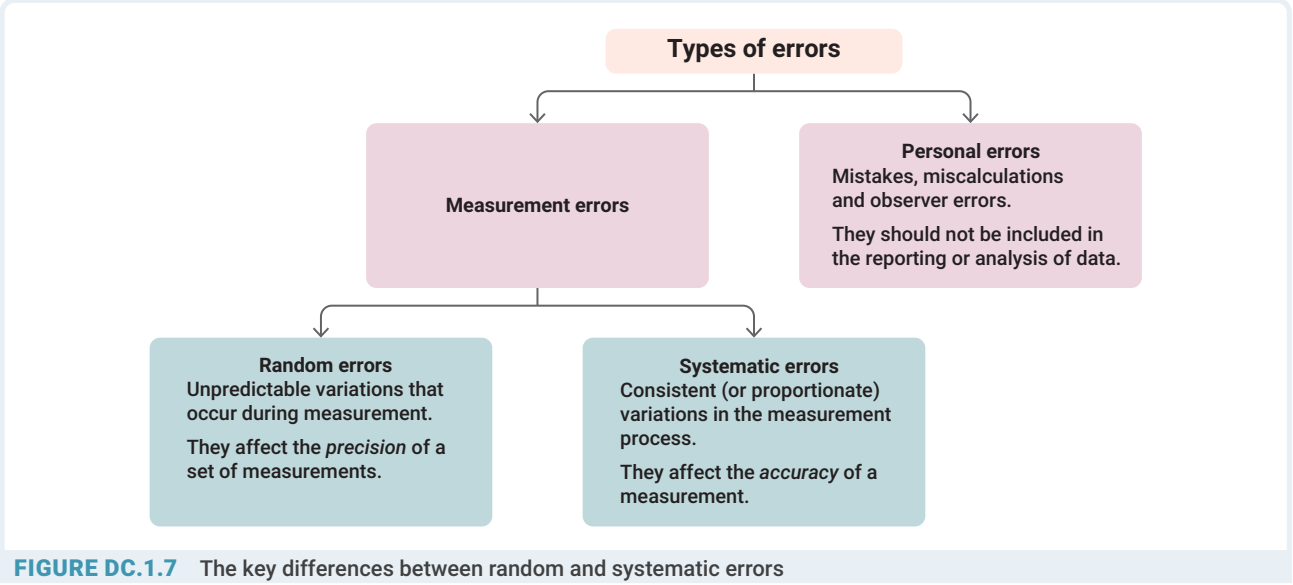


FIGURE DC.1.7 The key differences between random and systematic errors

Uncertainty

uncertainty the range of values for a measurement result, taking account of the likely values that could be attributed to the measurement result given the measurement equipment, procedure and environment

instrument uncertainty the inherent limitations and potential errors associated with the measuring instruments or tools used in scientific experiments or observations

absolute uncertainty the magnitude of the difference between the observed/measured value and the true value

range the difference between the maximum and minimum values of a measured confidence interval

While systematic errors can be accounted for by subtracting or adding the value of the error, random errors contribute to the **uncertainty** of a measurement. This reflects the lack of exact knowledge of the true value of the measurement. All measurements are subject to uncertainty because there are many sources of variation. For example, **instrument uncertainty** in measuring tools can result in variability and imprecision of results due to factors such as sensitivity, calibration and resolution. To minimise the effect of instrument uncertainty, it is important to calibrate tools, ensure that the appropriate tools and techniques are used and consider any limitations when designing the experiment. Uncertainty can also occur because of the way the person taking the reading interacts with the tool.

Uncertainties can sometimes be quantified. We can estimate the uncertainty of a measurement, which is usually expressed as ± a certain value. This is known as **absolute uncertainty**. Most of the time, uncertainty should be recorded using one significant figure.

Absolute uncertainty of repeated measurements

Most experiments require you to take multiple measurements. As mentioned above, doing so and averaging the results can help to reduce the effect of random errors. Imagine you take multiple measurements of your body temperature. The values are 35.6°C, 36.1°C, 35.9°C and 36.4°C. The difference between the maximum and minimum values is called the **range**. The absolute uncertainty of the mean is calculated as the halfway point between the maximum and minimum values, or half of the range:

$$\text{Absolute uncertainty of the mean } \Delta\bar{x} = \pm\frac{\text{maximum} - \text{minimum}}{2}$$

$$= \pm\frac{36.4 - 35.6}{2}$$

$$= \pm 0.4°\text{C}$$

KEY FORMULA

Absolute uncertainty

$$\text{Absolute uncertainty of the mean } \Delta\bar{x} = \pm\frac{(\text{maximum} - \text{minimum})}{2}$$

The measurement result would be the mean of the values:

$$\text{Mean} = \frac{35.6 + 36.1 + 35.9 + 36.4}{4}$$

$$= 36.0°\text{C}$$

The reported value includes both the mean and the absolute uncertainty. In this example, the reported value would be 36.0 ± 0.4°C. In other words, the actual value could lie anywhere between 35.6°C and 36.4°C.

Absolute uncertainty of single measurements/device details

For analogue devices, the uncertainty is normally determined as half of the smallest division on the scale. For example, a glass thermometer with graduations of 1°C has an uncertainty of ±0.5°C.

With digital devices, the uncertainty is normally defined as the smallest division because we cannot see in-between divisions as we can in an analogue device. For example, a digital thermometer that measures in 1°C has an uncertainty of ±1°C. One limitation of this calculation is that it does not indicate the direction of the error; we do not know if we overestimated or underestimated.

Percentage uncertainty

Absolute uncertainty can be used to calculate **percentage uncertainty**. Percentage uncertainty is calculated relative to the measured quantity, and is calculated by:

$$\text{Percentage uncertainty (\%)} = \frac{\text{absolute uncertainty}}{\text{measurement}} \times \frac{100}{1}$$

percentage uncertainty a measure of the uncertainty of a measurement compared with the size of the measurement, given as a percentage

A low percentage uncertainty indicates a more precise measurement, whereas a high percentage uncertainty indicates a less precise measurement because of greater variability.

Once data has been processed in this way, a table can be presented that also includes these measurements of uncertainty (Table DC.1.8)

KEY FORMULA

Percentage uncertainty

$$\text{Percentage uncertainty (\%)} = \frac{\text{absolute uncertainty}}{\text{measurement}} \times \frac{100}{1}$$

TABLE DC.1.8 An example of a summary table showing measurements of uncertainty

Voltaic cell	Cathode metal	Potential difference (±0.05 V)			Mean potential difference (V)	Absolute uncertainty of mean (±V)
		Trial 1	Trial 2	Trial 3		
1	B(s)	2.25	2.40	2.20	2.28	0.10
2	C(s)	1.30	1.28	1.37	1.32	0.45
3	D(s)	3.11	3.15	3.04	3.10	0.55

QCAA Chemistry 2019 v1.3 IA2 sample assessment instrument August 2018 © State of Queensland (QCAA)

Standard deviation

Standard deviation (SD) can give information about the spread of data points measured against the mean of the results. Consider using a mercury thermometer to measure the temperature of the same liquid four times. Given that the resolution of the thermometer is 1°C, the absolute uncertainty is ±0.5°C. Suppose the measurements are 10°C, 9°C, 11°C and 9°C. The standard deviation will show us how much each individual measurement deviates from the mean of 9.75°C. Calculating the standard deviations of measurements involves a series of steps that can become time consuming if completed manually. Software such as Excel and other graphing tools have functions to calculate the standard deviation of given data.

Weblink
Calculating mean and standard deviation

standard deviation (SD) a statistical measure that quantifies the variation in a set of data values

A small standard deviation indicates that the data points are close to the mean, whereas a large standard deviation indicates that the data points are spread out over a larger range, which suggests a low level of precision. A large or small spread is determined by how many raw data points lie within one, two or three SD of the mean (or similar).

For example, an SD of 1 is small if the mean is 400, but an SD of 1 is large if the mean is 4.

Standard error

Where standard deviation measures the variability of data in a single sample, **standard error** shows the variability of the sample data compared to the true population. In other words, it estimates how much the mean differs from the rest of the sample population. To calculate the standard error of the mean:

standard error a statistical measure that describes the variability of sample mean data compared to the population mean

$$\text{Standard error} = \frac{\text{SD}}{\sqrt{n}}$$

where: SD = standard deviation

n = sample size.

Standard error can be considered a measure of accuracy.

KEY FORMULA

Standard error

$$\text{Standard error} = \frac{\text{SD}}{\sqrt{n}}$$

where: SD = standard deviation
n = sample size.

WORKED EXAMPLE DC.1.2

A scientist was investigating the diameter of human red blood cells. They carefully measured 50 samples and the standard deviation is known to be 0.27 µm.
Determine the standard error for this sample.

ANSWER

1 Identify the values for each variable.

$n = 50$
SD = 0.27 µm

2 Use the formula to calculate the standard error.

$$\text{Standard error} = \frac{0.27}{\sqrt{50}}$$
$$= 0.038\ \mu\text{m}$$

Based on the samples, the average diameter is likely to be within ±0.038 µm of the true value.

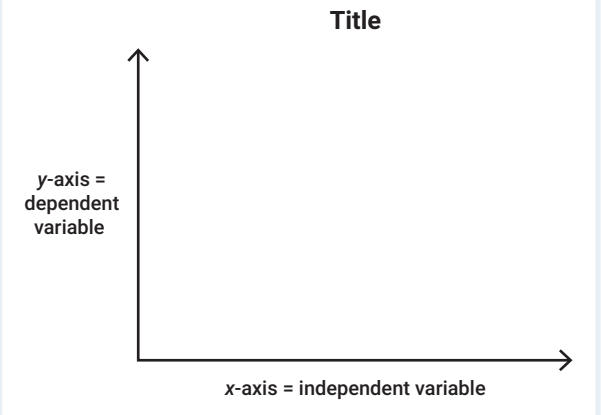


FIGURE DC.1.8 The positive quadrant of cartesian plane showing the variables represented on the *x*-axis and *y*-axis

Graphs

Although tables can be an effective way to collect and record data, it is difficult to visualise any trends or relationships between the independent and dependent variables. Presenting data in graphical form makes it easier to identify if any trends exist between the variables.

Many different types of graphs can be used to represent data; for example, column graphs, pie charts, scatterplots and line graphs. Choosing the right graph depends on the nature of the data collected and what you are trying to show. For graphs that involve an *x*-axis and a *y*-axis, the independent variable is represented by the *x*-axis and the dependent variable is represented by the *y*-axis (Figure DC.1.8).

It is also important to choose an appropriate scale when drawing graphs because it represents the data in a way that can be easily interpreted. It also avoids misleading representations that imply inaccurate relationships between data. All graphs need to have a title that outlines the information being presented.

Pie charts

Pie charts are best used to show parts of a whole and the percentage composition of each different category. For example, pie charts can be used to show the composition of a mixture of air – nitrogen, oxygen and other gases – and the percentage of each **(Figure DC.1.9)**.

A limitation with pie charts is that they become visually cluttered when there are many different categories.

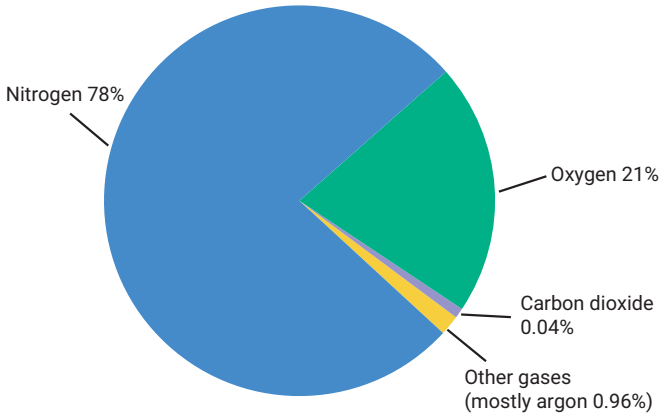


FIGURE DC.1.9 A pie graph representing the composition of air

Column graphs

Column graphs are useful when comparing quantities or different categories of groups **(Figure DC.1.10)**.

These types of graphs are preferred for comparing categories when order or time is important to show changes over time, or when comparing the differences between groups.

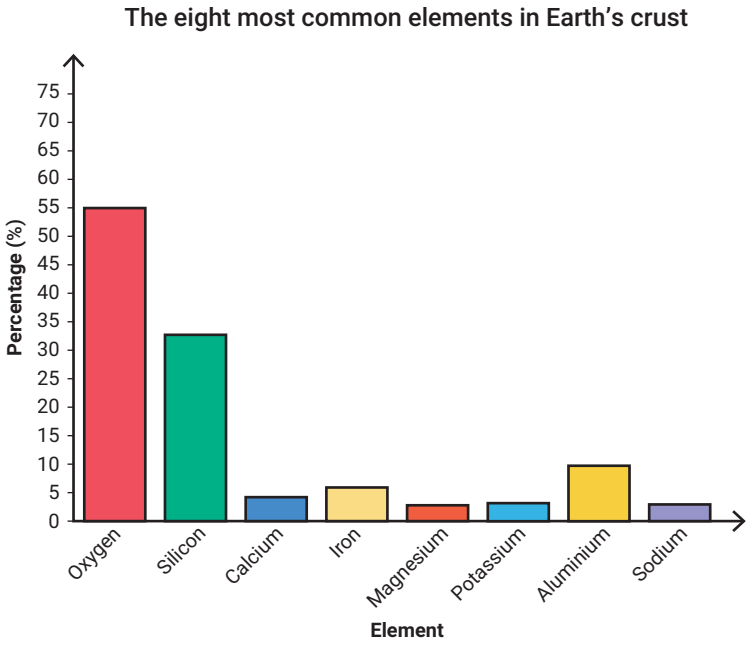


FIGURE DC.1.10 A column graph showing the differences in mineral composition of Earth's crust

Line graphs

Line graphs are ideal for showing trends over time for continuous data, particularly when comparing multiple series over the same period. In line graphs, each data point is connected to the next and the relationship between the two variables can be represented as the equation:

$$y = mx + c$$

where: m = the gradient

c = the y intercept.

For example, the calibration curve measuring the absorbance of light based on concentration of a solution can be represented by a linear graph, as shown in **Figure DC.1.11**.

If using Excel to draw these graphs, it is sometimes useful to use the x,y scatterplot.

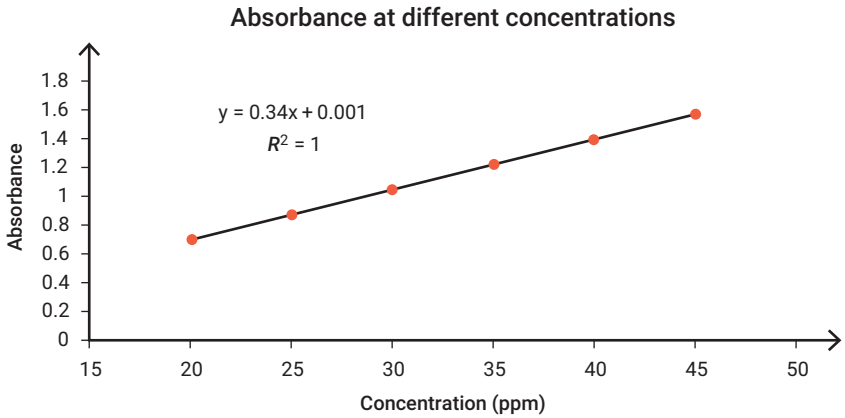


FIGURE DC.1.11 A line graph showing the absorbance at different concentrations

The gradient is a useful piece of information that helps to describe the relationship between the independent and dependent variables. For linear relationships, the gradient of the slope helps to identify the nature of the relationship between the independent and dependent variables. To calculate the gradient of a linear graph, m, where the equation is $y = mx + c$:

$$\text{Gradient } (m) = \frac{\Delta y}{\Delta x}$$

Determining the gradient in this way only requires two data points, where the difference in the y values is divided by the x values of the same two points. Depending on the value of the gradient, a:

- positive gradient **(Figure DC.1.12a)** indicates that as the x value (independent variable) increases, so does the y value (dependent variable)
- negative gradient **(Figure DC.1.12b)** indicates that as the x value (independent variable) increases, the y value (dependent variable) decreases
- gradient of zero **(Figure DC.1.12c)** indicates that as the x value (independent variable) increases, there is no change in the y value (dependent variable). As such, there is a constant relationship between the two variables.

Analysing the gradient for non-linear relationships is a bit more complicated and requires us to calculate the gradient of different tangents at specific points along the graph and compare the changes.

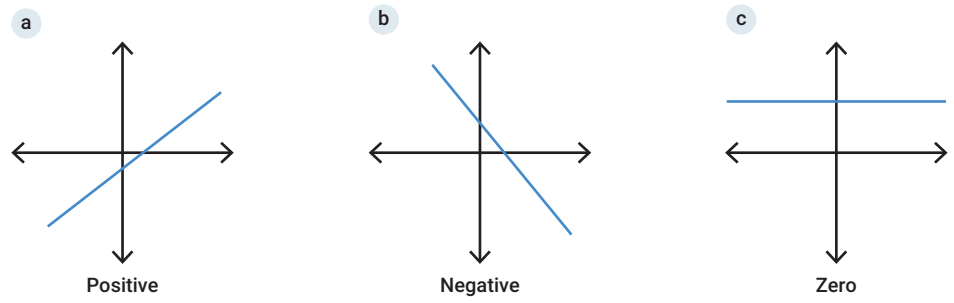


FIGURE DC.1.12 Linear graphs with (a) a positive gradient, (b) a negative gradient and (c) zero gradient

Scatterplots

Scatterplots are similar to linear graphs in that they show individual data points, highlighting the relationship between the independent and dependent variables. However, unlike line graphs, the data points in scatterplots are not connected **(Figure DC.1.13)**

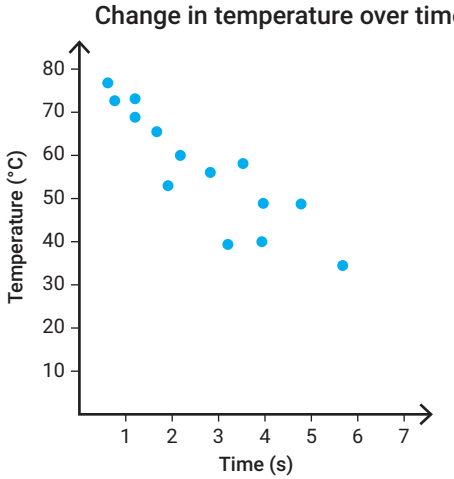


FIGURE DC.1.13 A scatterplot of change in temperature over time

Although the points are not connected, organisation of the data points relative to each other in these graphs can identify a relationship between the variables. **Trendlines** can be drawn through or near the datapoints to help make the relationship between the independent and dependent variable more visible (Figure DC.1.14) while also showing the strength of this relationship.

Although it is possible to draw trendlines manually, it is more accurate to use software. When adding trendlines manually, the line should be drawn so that it minimises the distance between the line and the data points.

If a trend does exist, we can often easily identify whether it is positive (positive correlation) or negative (negative correlation). In a positive trend, the dependent variable increases as the independent variable increases, whereas in a negative trend, the dependent variable decreases as the independent variable increases (Figure DC.1.15).

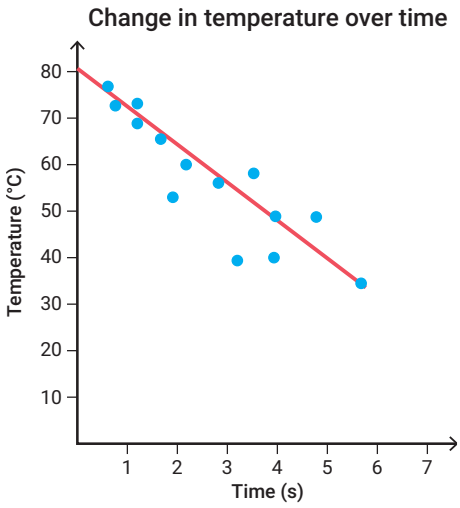


FIGURE DC.1.14 A scatterplot of change in temperature over time, including a trendline (red)

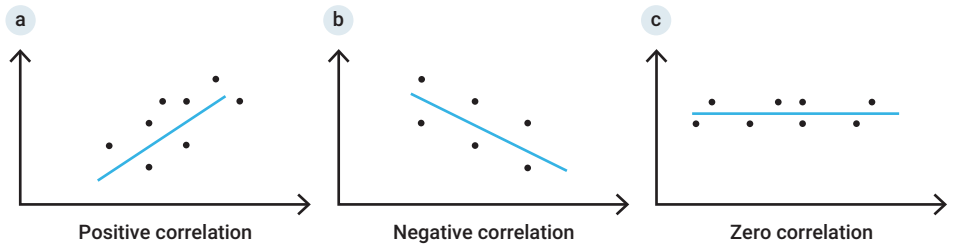


FIGURE DC.1.15 Scatterplots with trendlines showing (a) a positive trend, (b) a negative trend and (c) zero trend

trendline a line that represents the general direction or pattern of data points

Maximum and **minimum trendlines** are visual representations of the strength of the relationship between the variables (Figure DC.1.16). A wider range between the two suggests a greater variability of uncertainty in the data, whereas a narrow range suggests a lower variability in the measured values.

maximum trendline a trendline with the greatest gradient that fits within the data within the uncertainty values

minimum trendline a trendline with the smallest gradient that fits within the data within the uncertainty values

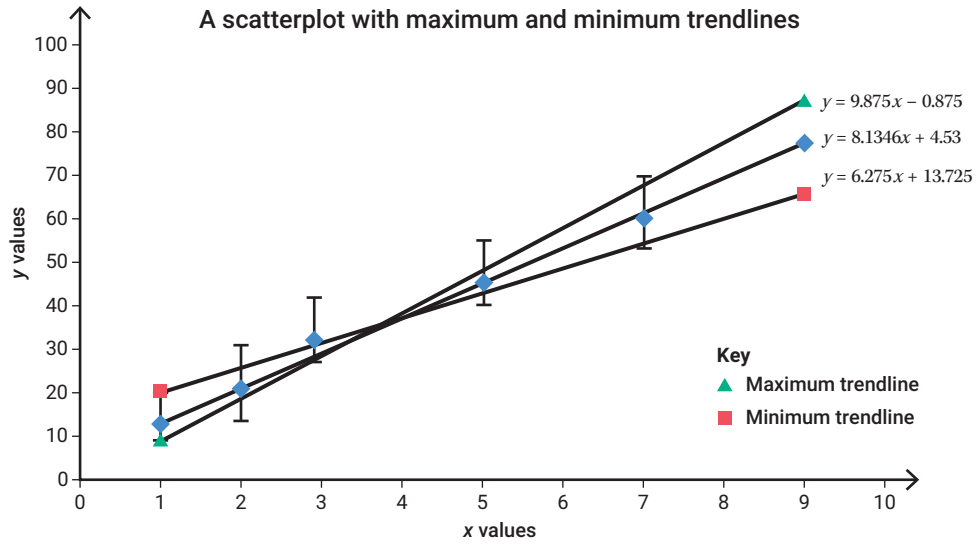


FIGURE DC.1.16 An example of a scatterplot that includes a maximum and minimum trendline

Analysing maximum and minimum trendlines together can help us predict the potential range of outcomes. For example, using trendlines to forecast temperature changes as a result of emissions can help us predict and prepare for worst-case scenarios. Maximum and minimum trendlines can also help identify potential errors in the experiment. Values that fall significantly outside the area between the maximum and minimum trendlines suggest an outlier that may have been due to a random error.

Greater variability in certain areas of the graph may also suggest error. For example, when measuring the rate of a reaction at different temperatures, it may be evident that there is a large variability in the rates at higher temperatures. This could imply an error in temperature control at higher temperatures.

A common strategy used to draw a:

- maximum trendline involves drawing a line from the bottom of the error bar of the starting data point to the top of the error bar of the last data point
- minimum trendline involves drawing a line from the top of the error bar of the starting data point to the bottom of the error bar of the last data point.

line of best fit a straight line through data points in a graph that best expresses the relationship shown in a scatterplot

Although trendlines are more general and can be used for different types of graphs with linear and non-linear data, the **line of best fit** is better suited for linear relationships. Since the line of best fit is used for linear relationships, the data points can be used to establish the relationship expressed as $y = mx + c$.

Although this can be done manually, the calculations can become complex and therefore it is often easier (and more accurate) to use software such as Excel, which can both draw the graph and establish the corresponding equation for the line of best fit. Lines of best fit can be used to predict values not measured in the experiment (extrapolation) or estimate values within the range of data collected (interpolation) that were not directly measured **(Figure DC.1.17)**

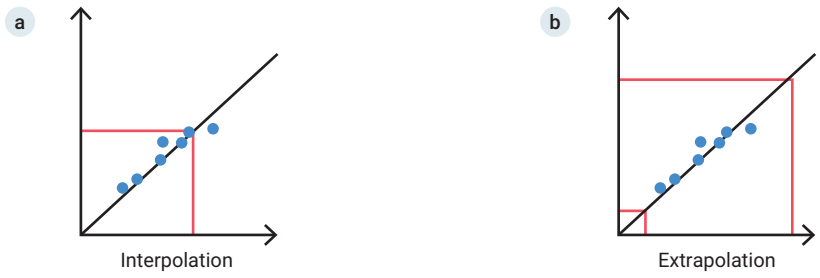


FIGURE DC.1.17 Using a line of best fit to (a) interpolate a data point within the measured values and (b) extrapolate a data point outside of the measured values

Drawing the line of best fit involves specific statistical models such as linear regression and is often accompanied by a quantifiable level of certainty, known as the *R*-squared value (R^2) (also referred to as the coefficient of determination). Regression analysis provides an equation for a graph so that predictions can be made about the data.

Weblink
Linear regression and Excel

Linear regression is a basic and commonly used type of predictive analysis. The overall idea of regression is to examine two things:

1. Does a set of predictor variables do a good job at predicting an outcome (dependent) variable?
2. Which variables in particular are significant predictors of the outcome variable?

These regression estimates are used to explain the relationship between one dependent variable and one or more independent variables.

This can be calculated in Excel using raw data (not averages).

Regression, R^2, is the coefficient of determination as calculated by a linear regression.

$$\text{Equation: } \frac{\text{regression sum of squares}}{\text{total sum of squares}}$$

It ranges from 0 to 1, with higher values meaning that most of the change in the dependent variable is accounted for by a linear model.

To understand R^2 values, we must understand the significance of R values.

A **Pearson correlation coefficient (R)** measures the correlation between two sets of data. R values can be between –1 and 1, where:

- $R = 0$ suggests no correlation
- $R = 1$ suggests a strong positive correlation
- $R = -1$ suggests a strong negative correlation.

Pearson correlation coefficient (R) a statistical measure that quantifies the direction and strength of a relationship between two variables

The formula to calculate the R value is complicated and therefore it is much easier to use software to help with this calculation. Programs such as Excel have options for calculating R when plotting a graph.

Squaring the R gives us the R^2 value. The square of the correlation shows the proportion of variation in the y-axis that is predicted by the x-axis. This value indicates the strength of the correlation of the linear relationship between two sets of data. In simple terms, it answers the question, 'Can I draw a line graph to represent the data?' Calculating this coefficient does not allow you to fit a line to your data (use a regression analysis for this). The value is also not able to tell the difference between the independent and dependent variables; for example, investigating a high-calorie diet causing diabetes might give a correlation of 0.8. However, you could also get the same result with the variables switched around – diabetes causes a high-calorie diet. Therefore, as a researcher you must be aware of the data you are putting in and note the difference between correlation and causation:

- $R > 0.8$ = *strong* correlation.
- $R < 0.5$ = *weak* correlation.

Non-linear graphs

Not all trends show a linear pattern. For example, a graph showing the solubility of substances at different temperatures shows a non-linear relationship (Figure DC.1.18).

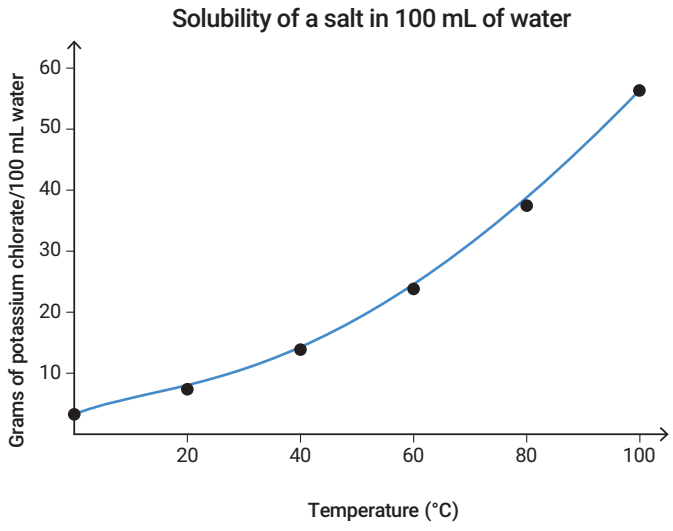


FIGURE DC.1.18 The solubility of a particular salt in 100 mL of water at different temperatures shows a non-linear relationship.

The simplest way to identify whether a relationship between two variables is linear or non-linear is to plot the data points on a graph to identify the overall trend. Gradient analysis can be conducted on non-linear graphs by calculating the instantaneous gradient of the tangent line at each data point and comparing the extent of the changes between each point. The tangent line

is a straight line that 'touches' the data point and has the same gradient as the curve at the given data point (Figure DC.1.19).

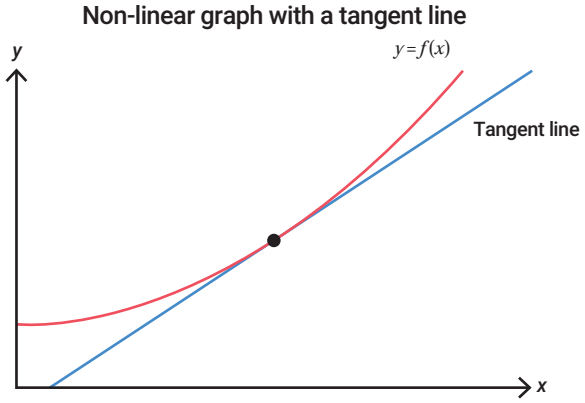


FIGURE DC.1.19 An example of a tangent touching a data point on a non-linear graph

Error bars

To illustrate uncertainty, your graphs should incorporate error bars. These extend from data points to demonstrate the uncertainty of the measurement (Figure DC.1.20).

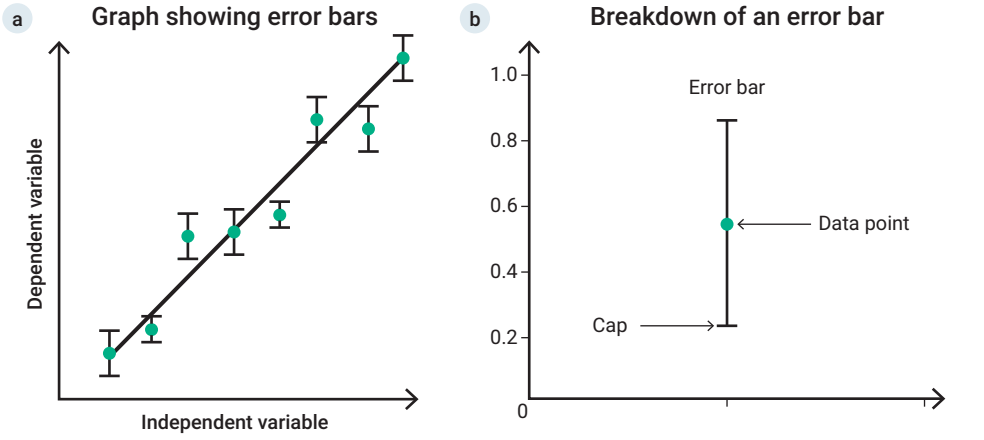


FIGURE DC.1.20 (a) A scatterplot that has incorporated error bars. (b) The structure of an error bar.

Weblinks
Error bars

Drawing graphs with error bars

The upper and lower limits of the error bars can be determined by using descriptive statistics such as standard deviation or absolute uncertainty. (Note: There are different types error bars; e.g. standard deviation, confidence intervals, absolute uncertainty, percentage uncertainty.) To draw error bars on graphs:

1. Identify the data point.
2. Calculate the uncertainty of the mean or standard deviation for the data point. This determines the upper and lower limits of the error bar.
3. Use the values from step 2 to identify the maximum and minimum value for the data point. Use this to draw the error bar. Ensure that the statistical value represented by the error bar is clearly stated.

Graphing applications such as Excel have an option to include error bars in graphs. This is a faster and often more accurate method for generating graphs with error bars. Note that Excel usually puts on average error bars. If the error for each independent variable value is different, you will need to manually adjust the error bars in Excel.

A larger error bar indicates that the values are spread out and suggests greater uncertainty than a smaller error bar, which signals that the measurements are clustered around the data point. Error bars can be drawn for different types of graphs (Figure DC.1.21).

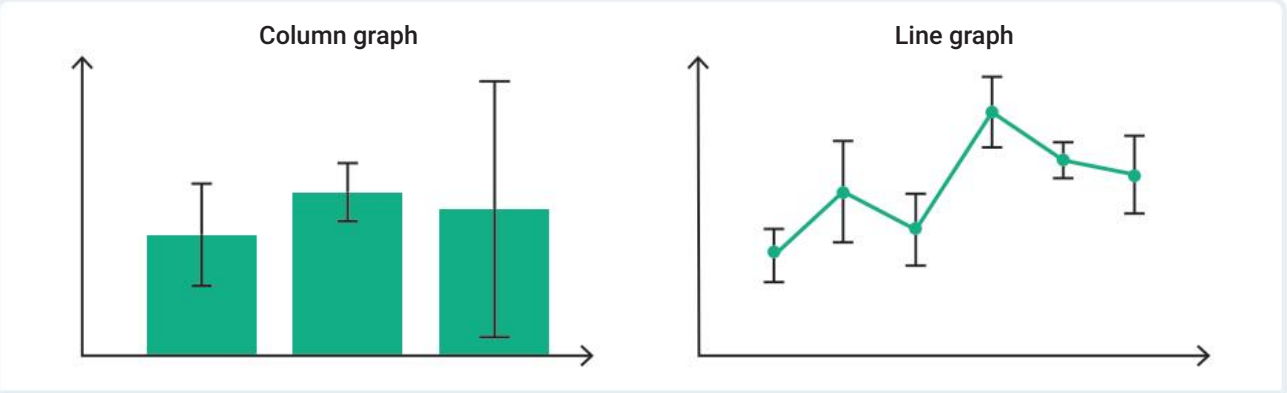


FIGURE DC.1.21 A column graph and a line graph with error bars

Other representations of data

Profile diagrams

Profile diagrams help to visually show the different layers or sections of an ecosystem and how they vary from one another. These diagrams help us understand how things such as plant and animal species, as well as their heights or population sizes, change as we move along a specific line or area. For example, soil profile diagrams are side-view cross-sections that show the different layers of soil in an area (Figure DC.1.22).

profile diagram a visual representation that shows a cross-sectional view or side view of a specific aspect of an ecosystem or organism

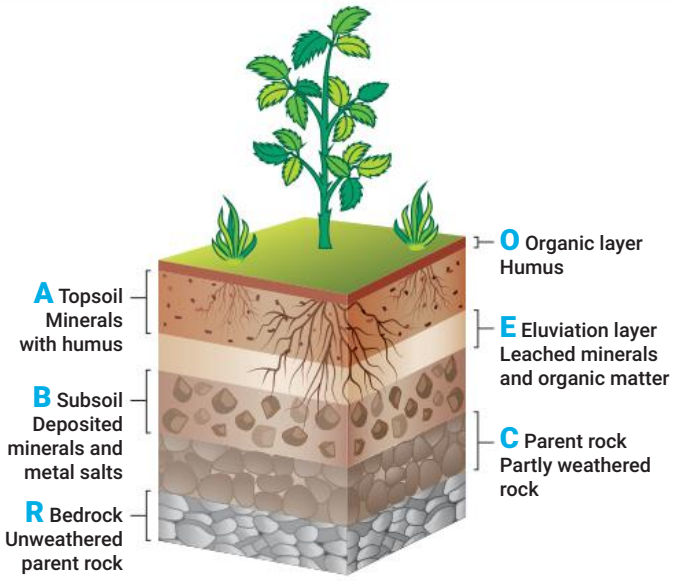
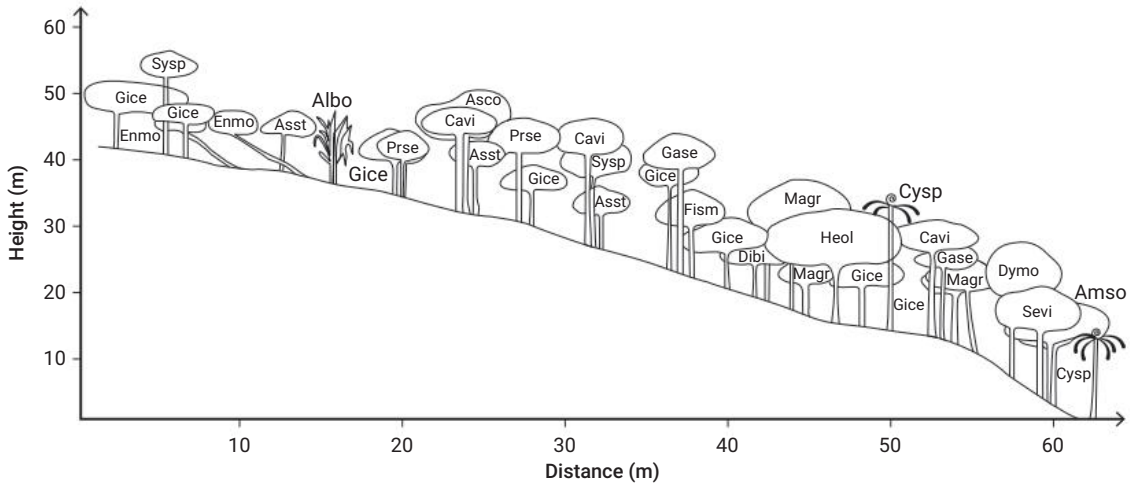


FIGURE DC.1.22 A soil profile diagram showing the different layers of soil in an area

Forest profile diagrams are effective for visually representing the distribution of plant and tree species, as well as their varying heights, along a transect line (Figure DC.1.23). By examining profile diagrams, we can get a better understanding of how the ecosystem has changed and the factors influencing these changes.

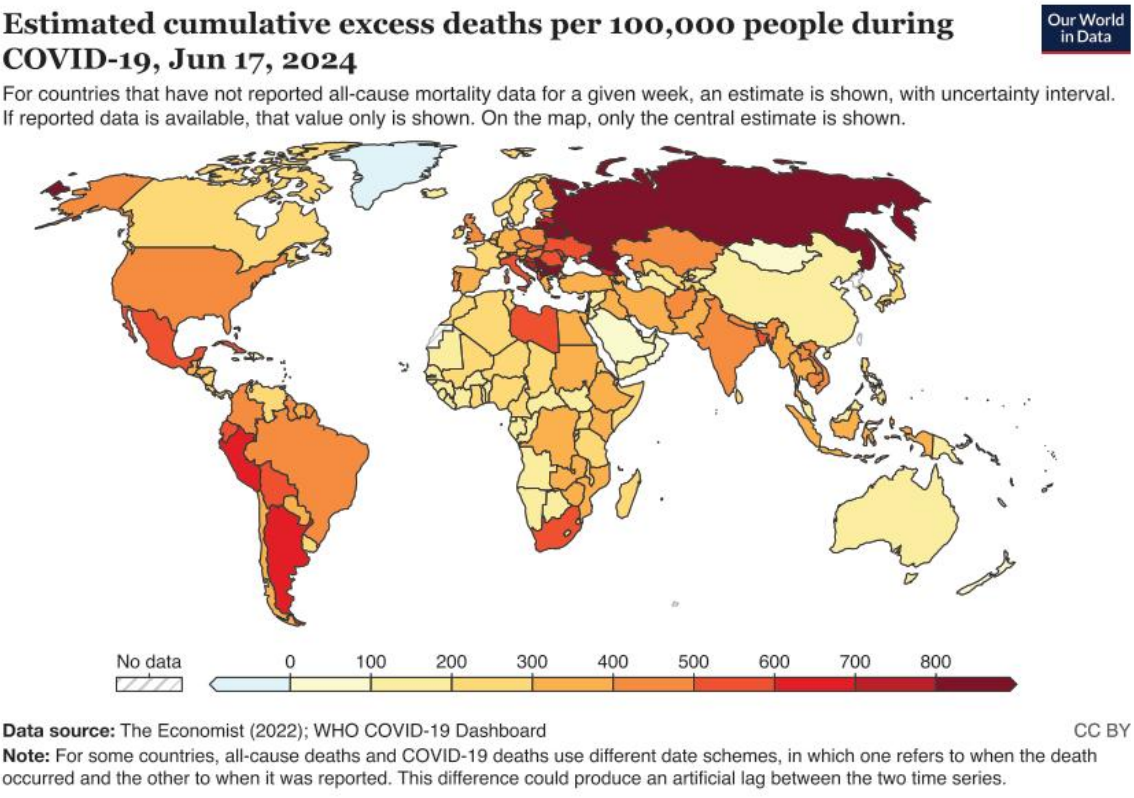


Tuiwawa, Marika & Pene, Sarah & Winder, Linton. (2021). Vegetation Patterns in Waisoi Primary Rainforest, Southeast Viti Levu, Fiji1. *Pacific Science*. 74. 10.2984/74.3.2.

FIGURE DC.1.23 A forest profile diagram of a slope rain forest in Viti Levu, Fiji

Maps

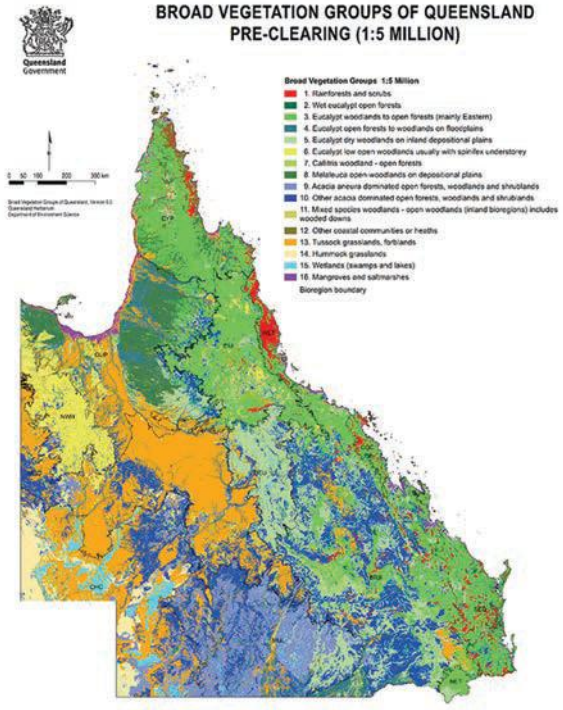
Like profile diagrams, maps are visual representations of data. Maps can represent complex data in a way that is easy to understand and identify trends and relationships. For example, governments often use maps to track the causalities of COVID-19 across the world **(Figure DC.1.24)**.



Edouard Mathieu, Hannah Ritchie, Lucas Rodés-Guirao, Cameron Appel, Charlie Giattino, Joe Hasell, Bobbie Macdonald, Saloni Dattani, Diana Beltekian, and Esteban Ortiz-Ospina (2020) - "Coronavirus Pandemic (COVID-19)". Published online at OurWorldinData.org. Retrieved from: 'https://ourworldindata.org/coronavirus' [Online Resource]

FIGURE DC.1.24 A map showing the worldwide cumulative deaths due to COVID-19

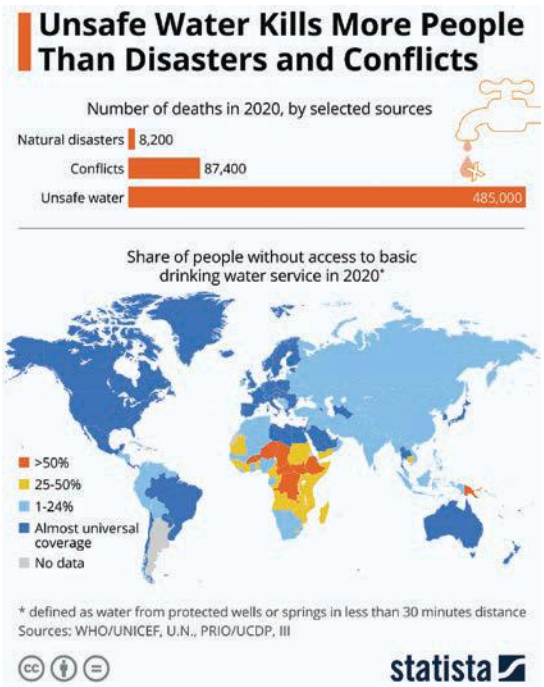
The Queensland Government uses maps to monitor the state's vegetation and regional ecosystems **(Figure DC.1.25)**



The State of Queensland

FIGURE DC.1.25 A map of Queensland's regional ecosystems and vegetation

Sometimes, especially in infographics, maps and charts can be used together to illustrate trends and relationships about a topic **(Figure DC.1.26)**.



Katharina Buchholz, Unsafe Water Kills More People Than Disasters and Conflicts, Statista, Mar 22, 2022. Licensed under CC BY-ND 3.0.

FIGURE DC.1.26 An infographic combining a chart and map to show the impact of unsafe water

Scientific drawings

Textbooks are full of scientific drawings that represent structures, organisms and processes. These drawings are highly detailed, accurate and clear. For example, examine the detailed drawing of an animal cell in **Figure DC.1.27**.

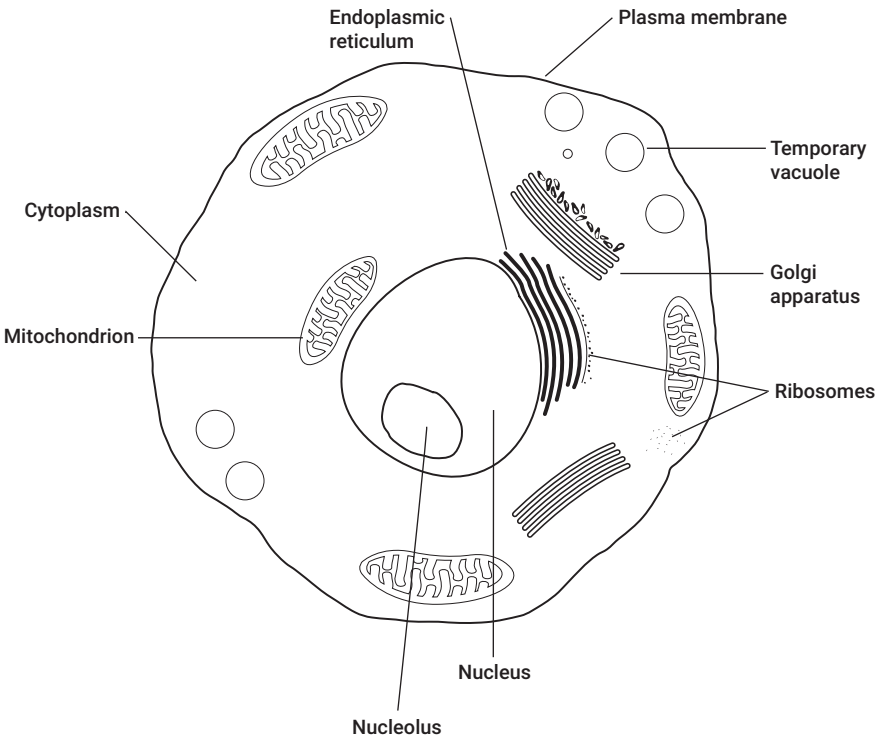


FIGURE DC.1.27 (a) A eukaryotic animal cell showing its plasma membrane and other organelles; (b) A line drawing of a cell

Scientific drawings include labels and annotations and are drawn to scale to show the relative proportions of the elements involved.

Identifying trends, relationships and patterns

The purpose of an experiment is to collect relevant data that can be analysed and used to understand the relationship between the independent and dependent variables.

Analysing graphs

When analysing graphs, it is important to consider all aspects presented in the graph. Consider the graph shown in **Figure DC.1.28**. What we tend to notice first is the overall trend in the data. The graph shows a negative trend where the cell potential decreases as the concentration of Zn^{2+} increases. We determine this visually based on the shape of the line; however, it is possible to also measure the negative gradient for the line. The large R^2 value of 0.9723 (very close to 1) can confidently predict cell potential using Zn^{2+} concentration since R^2 is high.

The graph in Figure DC.1.28 also contains error bars showing the overlap of all data points. When this happens, it suggests that the differences between the overlapping data points are statistically insignificant and are due to random errors. As such, the trend shown may not reflect the true relationship between the concentration and cell potential.

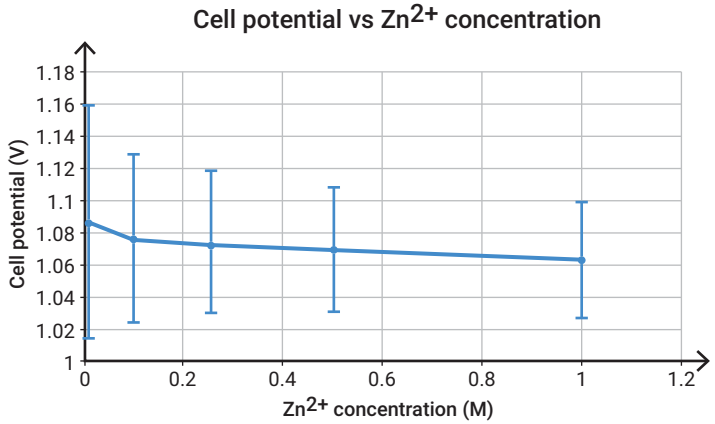


FIGURE DC.1.28 A graph showing the effect of the concentration of Zn^{2+} on cell voltage

Although not as easy to visually identify as graphs are, raw data tables can also be interpreted to identify the relationship between two variables. Consider the raw data table for the graph above **(Table DC.1.9)**.

TABLE DC.1.9 A data table for an experiment testing the effect of the concentration of Zn^{2+} on cell voltage

$ZnSO_4$ conc. (M)	Mean cell potential (V)	Absolute uncertainty (V)	Percentage uncertainty (%)	Theoretical E_{cell} (V)	Percentage error (%)
0.01	1.087	±0.005	0.460	1.159	6.249
0.10	1.077	±0.005	0.464	1.129	4.681
0.25	1.073	±0.005	0.465	1.117	3.977
0.50	1.070	±0	0	1.108	3.506
1.00	1.063	±0.005	0.470	1.100	3.333

All results have an overall low percentage error, suggesting that the experiment has high validity.

Spearman's rank

Data that is ranked – there is an order or sequence – is often analysed using **Spearman's rank** correlation coefficient (rho, ρ). The value calculated lies between –1 and +1, which indicates the strength of the relationship between two sets of ranked data. Values that are closer to +1 show a strong positive correlation between the variables, whereas values closer to –1 indicate a strong negative correlation between the variables. Similar to some of the tests already mentioned, calculating rho can be complicated and is best done using software such as Excel or Spearman's rank calculators (see weblink).

Spearman's rank a statistical measure that quantifies how closely two datasets (ranked data) are related

Weblinks
Spearman's rank calculator
P-value | Hypothesis testing

Student's *t*-test

The student's *t*-test, often shortened to *t*-test, is used to compare the means of different groups of samples. The value generated from the test, also known as the *p*-value, measures the probability

of the results being due to chance. We measure *p*-values between 0 and 1.0. A value of 0.05 or less is considered statistically significant and the observed data is considered to have a low probability of occurring due to chance. Again, software such as Excel can be used to calculate the *p*-value from *t*-tests.

Interpreting

You need to scientifically justify the argument. This is done by referencing theory and previous studies to explain the phenomena being shown through the data. For example, in an experiment measuring the effect of temperature on enzyme function, we would want to refer to the theory relating to the current understanding of enzyme function and use that to justify the arguments made from the trends identified in the data.

The culmination of this allows us to draw well-informed conclusions that help to answer the research question.

Evaluating

In your evaluation, you need to comment on the reliability and validity of the relationships using your calculations of errors and uncertainty. Although it sounds counterintuitive, highlighting sources of error in your experiment and describing its effect on your results strengthens your argument. It also allows you to identify any limitations and offer suggestions for improvements and/or extensions to your experiment. By doing so, you are demonstrating an ability to critically analyse data, which helps to develop well-informed arguments.

LEARNING CHECK DC.1

DESCRIBING

1 **Describe** the difference between:
   - **a** accuracy and precision
   - **b** reliability and validity.

2 **Identify** two strategies to improve the accuracy of data.

3 **Identify** the type of data most suited to:
   - **a** pie charts
   - **b** line graphs
   - **c** column graphs.

4 **Describe** the importance of:
   - **a** a logbook
   - **b** an MSDS
   - **c** ethics in experiments.

5 Put these steps of the scientific method in the correct order:

   methods, materials, discussion, research question

APPLYING

6 **Consider** the following research question.

'How does increasing light exposure (hrs per day) affect the rate of plant growth (cm/day)?'

Identify the:

a dependent variable
b independent variable.

7 A student wanted to conduct an experiment to see whether eating food before running had any effect on how far she could run. Write a research question for this experiment.

8 A student is conducting an experiment involving the use of a glass measuring cylinder to measure and pour a sample of acid into a 100 mL glass beaker. **Identify** one safety concern associated with the experiment and how the risk can be minimised.

9 In a medical experiment, a participant was asked to undergo a series of additional tests that could reveal sensitive information about their health situation. The participant refused to give consent to the tests. However, the experimenter ignored this and requested for the tests to be conducted anyway. Which ethical concept has the experimenter breached? **Explain** your answer.

10 A student measured a value of 20 cm in their experiment with an absolute uncertainty of 1 cm.

a **Calculate** the percentage uncertainty.
b What does this value suggest about the precision of the measurement?

11 A group of students designed an experiment to measure the effect of water on plant growth. The plants were kept in the same room and the growth of the plants was measured daily.

a **Identify** an extraneous variable for this experiment.
b Each student took turns measuring the growth of the plant. Students used their own rulers to measure the growth, and it was noticed that all rulers had different resolutions (graduations). **Identify** the type of error that occurred as a result of this.

12 In a particular set of measurements, a student recorded the following measurements: 14.2, 14.1 and 14.3 cm. **Calculate** the absolute uncertainty.

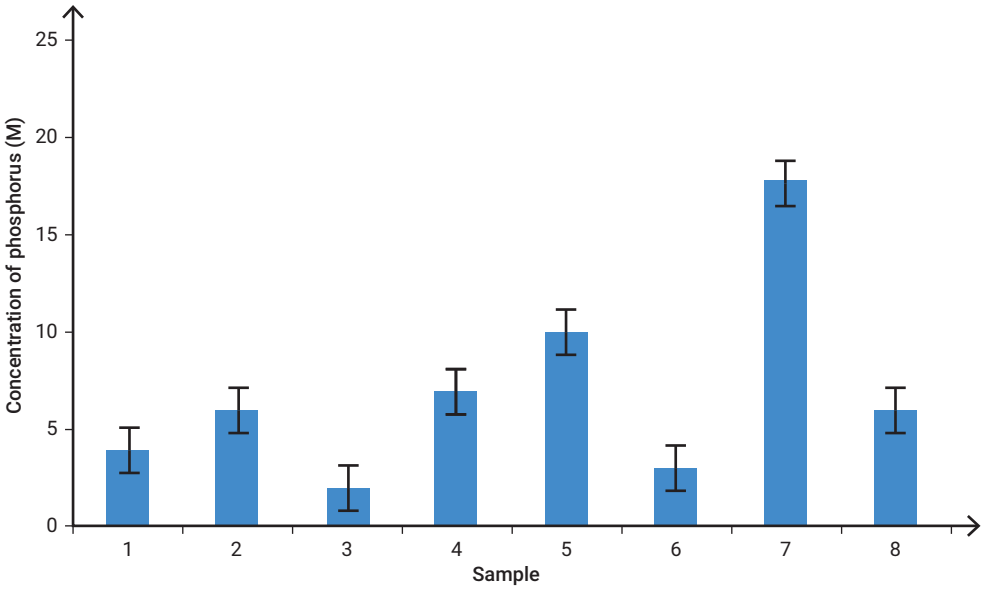
ANALYSING

13 The results from a student's experiment are shown below.

Concentration of nutrient solution (%)	Plant height (cm)		
	Day 10	Day 20	Day 30
0	5	8	10
5	7	10	12
10	9	13	15
15	12	16	20
20	15	19	25
25	17	22	28
30	18	24	30

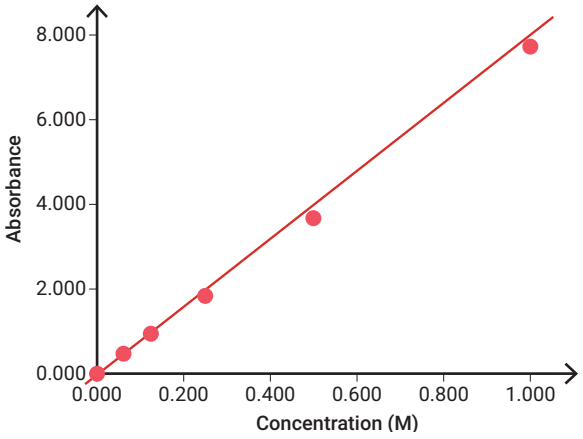
a **Identify** the dependent and independent variables for this experiment.
b **Calculate** the mean value for each concentration.
c Use the values to draw a graph to represent this data.
d **Determine** the correlation (if any) between the independent and dependent variables.

14 Consider the following graph.



a **Determine** the dependent variable.
b **Determine** which sample shows the greatest variability.

15 The following graph was drawn for an experiment measuring the change of absorbance as a result of a change of concentration.



a **Identify** the name of the type of graph drawn.
b **Identify** the name given to the line drawn in the graph.
c **Calculate** the gradient (m) of the line.
d **Determine** the approximate absorbance at a concentration of 0.200 M.
e On the basis of the graph, would you expect the R value to be closer to 1 or to 0? **Explain** your response.

DC.2 Research investigation

To help prompt your Research Investigation (IA3) assessment, your teacher will provide a list of claims that you can investigate. These claims will be related to particular topics outlined in the syllabus. After selecting a claim, you will be required to choose a research question to investigate. Unlike the student experiment, the research investigation requires you to collect and analyse **secondary data** about your topic and particular research question.

secondary data data that is collected by someone else

Forming and finding

Researching to write a rationale

As with the student experiment, you will need to conduct research before developing a research question. This involves reading scientific articles and books and investigating other resources to develop a solid understanding of the topic. From blogs to scientific journals, there are many resources available to help develop your understanding. These sources may be available through open access (e.g. Google Scholar) or through organisations such as government websites and local or national libraries; for example, the State Library of Queensland. For scientific research, it is important to use a variety of credible resources. Therefore, you will need to be able to assess the reliability of the sources you are using. For example, blogs that can be written by anyone are not as reliable as a scientific article from a peer-reviewed journal (Figure DC.2.1).

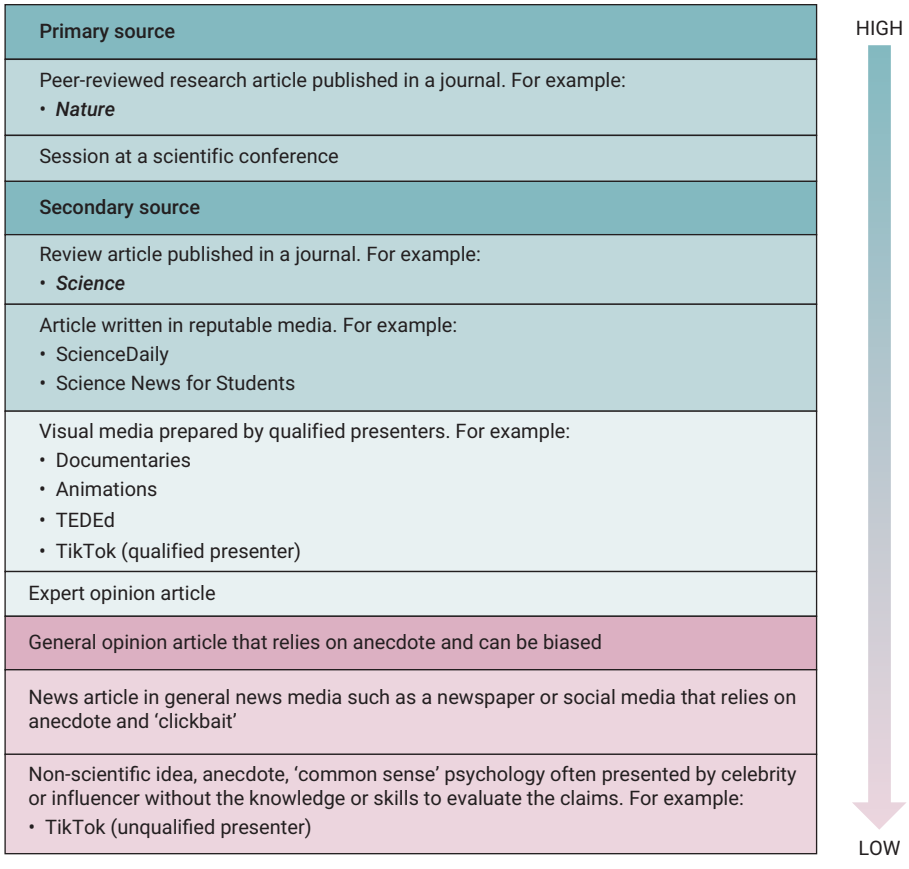


FIGURE DC.2.1 Sources of information based on their reliability

This is why the peer review process in scientific research is so important **(Figure DC.2.2)**. For an article to be published in a journal, it must be reviewed by multiple experts, who evaluate it and make suggestions for further improvement. Before it can be resubmitted, the author must review and respond to the suggestions. This process can take months. Only once this process has been completed is the article accepted by the journal.

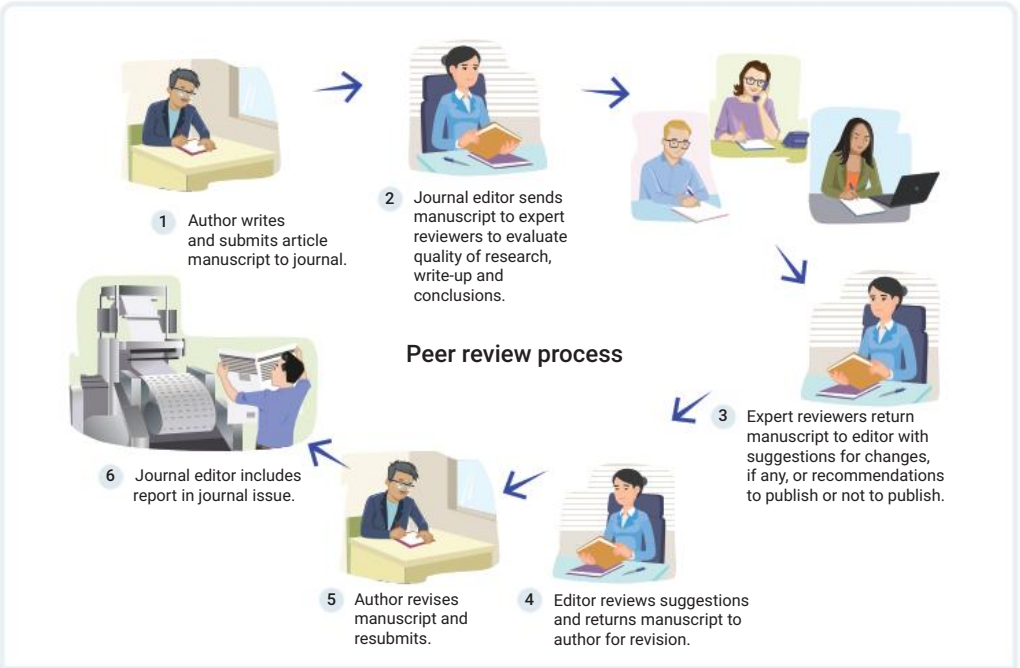


FIGURE DC.2.2 The peer review process

Weblink
Evaluating the information you find

When using sources that are not from peer-reviewed journals, it is important to assess the reliability and validity of the information. It is helpful to ask yourself question such as:

- Is the author(s) an expert in this domain?
- Does the author use evidence to support their claims?
- Is the methodology valid?
- If evidence is used, where does the data come from?
- Is this publication trustworthy?
- Is there any bias? For example, is there a conflict of interest among the researchers?

It is also a good idea to cross-reference the information presented by these resources with other sources such as primary sources and textbooks. This initial research helps you to develop a rationale for your investigation, and as a result helps to craft a research question that is relevant to the claim. As with the student experiment, the research question needs to be able to be tested.

To help the reader have the necessary context for the research investigation, you need to provide a level of background. The background needs to include enough of a foundation that the reader can understand the theoretical underpinnings of the research while also showing that you have used scientific evidence to develop a research question that aligns with the claim.

Referencing conventions

Since experiments and scientific research draw on the knowledge, thoughts and ideas developed by others, we need to appropriately acknowledge sources of information. The referencing format that is required depends on the discipline; however, in most cases, science uses the APA (American Psychological Association) referencing style.

Analysing evidence

As part of your assessment, you will need to find scientific evidence from previous research related to your research question. The data derived from these studies is used in the same way as the data collected from your student experiment; to identify trends, patterns and relationships between variables to answer the research question.

Because there are multiple data points, it is important to re-organise the data and present it in a way that can be analysed. For example, **Table DC.2.1** shows data collected from two different scientific experiments that measured the prevalence of lactase persistence-associated alleles of populations in Finland.

Additionally, the data can be used to construct graphs. Organising data in this way makes it easier to identify any trends, patterns or relationships that exist between the variables being tested. As in your student experiment, you would also need to identify any sources of error and levels of uncertainty that can affect the results.

TABLE DC.2.1 Comparison of results between different studies

Population	Long.	Lat.	*N*	–14010 G>C	–13915 T>G	–13907 C>G	–13910 C>T	Sum of all LP associated alleles	Predicted lactase persistence frequency
Finns	28.00	65.00	1876	0.00	0.00	0.00	0.58	0.58	0.82
Saami	39.00	69.00	60	–	–	–	0.17	0.17	0.31

Table 2: Lactase persistence-associated alleles frequencies in populations of Finland, viewed in https://www.qcaa.qld.edu.au/downloads/senior-qce/sciences/snr_biology_19_ia3_asr_high.pdf, source: Source: Enattah et al 2008 Am J Hum Genet. (via Global Lactase persistence association database).

Interpreting evidence

Weblinks

Referencing style guides

Referencing sources

As you now know, presenting data and describing trends and relationships on their own is not sufficient. We need to be able use the evidence and scientific theory to justify the argument being made and to draw a conclusion.

When developing your conclusion, ensure that it directly answers the research question. Sometimes when assessing studies at an individual level, the data may point towards a particular conclusion. However, when studies in the same area are evaluated together, an overall analysis may suggest a different conclusion. If your investigation shows a different conclusion from the studies used, that in itself is an important conclusion. It highlights that further investigation is required to develop a deeper understanding of the area.

Scientific language

The ability to communicate scientific understanding to an audience is often an overlooked skill. How we present the information depends on what we are sharing and the audience we are sharing with. For example, when communicating to a younger audience who are unfamiliar with many scientific concepts, it is important to use accessible language and visuals to help foster a foundational understanding of the topic. When communicating findings to those in the scientific community, we need to make sure to use scientific language, including correct nomenclature, units and symbols specific to the scientific theory.

Evaluating evidence

The quality of the evidence can impact the reproducibility of the research and strength of the conclusions drawn. We can assess the quality of the evidence by identifying any limitations caused by errors and/or uncertainty **(Figure DC.2.3)**. This may include assessing the:

- appropriateness of the method (where possible)
- sample size
- sources of error
- degree of uncertainty of the data.

> Collected evidence supports the claim that genetic modification increases crop productivity. However – given only soybeans genetically modified to improve crop seed yield were investigated — the conclusions cannot be extrapolated to the claim in its entirety to assume that observed trends are evident for all crops; all genetic modification; and all crop productivity measures. To provide a more insightful and relevant answer to the claim through source comparability, the investigation could be improved by ensuring that data compares the same transgenic cultivars against the same parameters. Furthermore, only data covering several years should be considered, ensuring interpretations validly consider long-term crop performance.
>
> This could further be extended by conducting studies on a greater variety of GMO crops and their non-GMO counterparts — such as cotton, alfalfa and corn — to determine whether the same trends are evident. Moreover, to provide a more balanced depiction of GMO crops and their applications, the investigation should be extended to include more measures of crop productivity, such as disease resistance and biochemical properties. Finally, information should be consistently collected over several consecutive years across crops grown in a variety of countries to determine the effect of environmental conditions, thereby ensuring relevance and reliability of collected data in lieu of a rapidly changing climate.

FIGURE DC.2.3 An excerpt evaluating the evidence provided by previous scientific studies

It's also important to consider any bias (e.g. is the funding from a particular company?), recency of data as well as qualifications of the author(s). Identifying limitations also helps you to make interpolations or extrapolations of the findings, to further analyse the research claim.

It is also important to suggest any further improvements for future studies related to this area. For example, you could identify any changes that you would make to the methodology to improve the validity or reliability of the data from the experiment. Suggestions for improvement should also address any limitations present in the experiment, including any:

- experimental limitations; for example, time available to conduct the experiment, errors
- methodological limitations; for example, accuracy and reliability of measurement techniques, ethical constraints
- external limitations; for example, environmental factors that can introduce variability, access to proper equipment.

As you can appreciate, being able to interpret and evaluate data is crucial for reaching informed conclusions about your research.

Resource
Sample research investigation

LEARNING CHECK DC.2

DESCRIBING

1 **Identify** the difference between primary data and secondary data.

2 **Describe** the role of the peer review process in scientific research.

APPLYING

3 A student conducted an experiment to investigate the effect of different fertilisers on the growth of tomato plants. The student divided the tomato plants into four groups and assigned each group a different type of fertiliser: A, B, C and D. The plants were placed under identical conditions, receiving the same amount of water and sunlight. The student measured the height of the plants every week for 4 weeks. **Identify** one possible experimental and one methodological limitation of this experiment.

4 **Consider** the following passage.

The rate of reaction is a fundamental concept in science. Enzymes function to increase the rate of reaction by providing an alternative pathway for a reaction to occur.

Rewrite the passage so that it can be read and understood by a primary school student who is studying science.

5 A student used the following source for their research investigation.

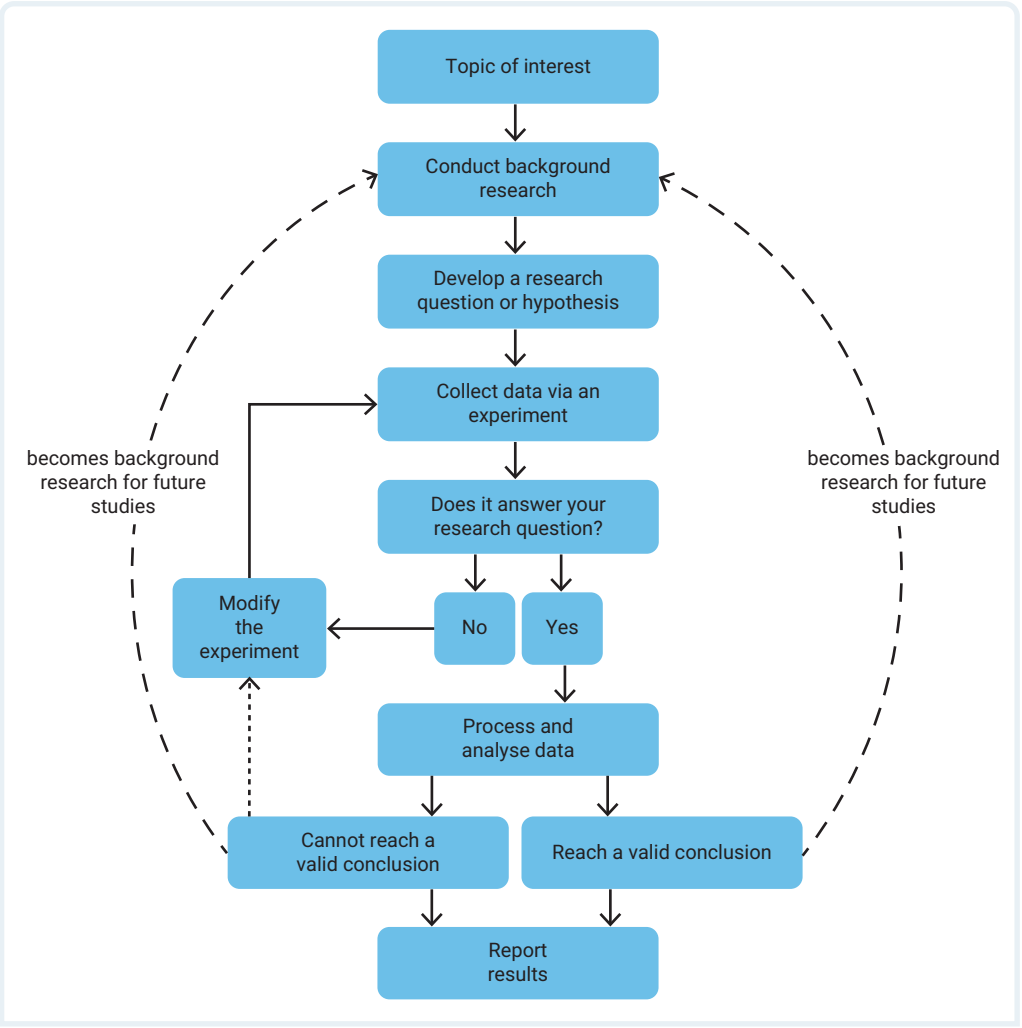
Cruzan, J. (2012). 'The most important solvent'. Retrieved from http://www.drcruzan.com/Water.html.

Use information from the 'Referencing sources' weblink to show how this resource would be referenced in the text.

CHAPTER SUMMARY

Conducting research

- The scientific method follows a particular process aimed to maximise accuracy, reliability and objectivity while minimising uncertainty and error.



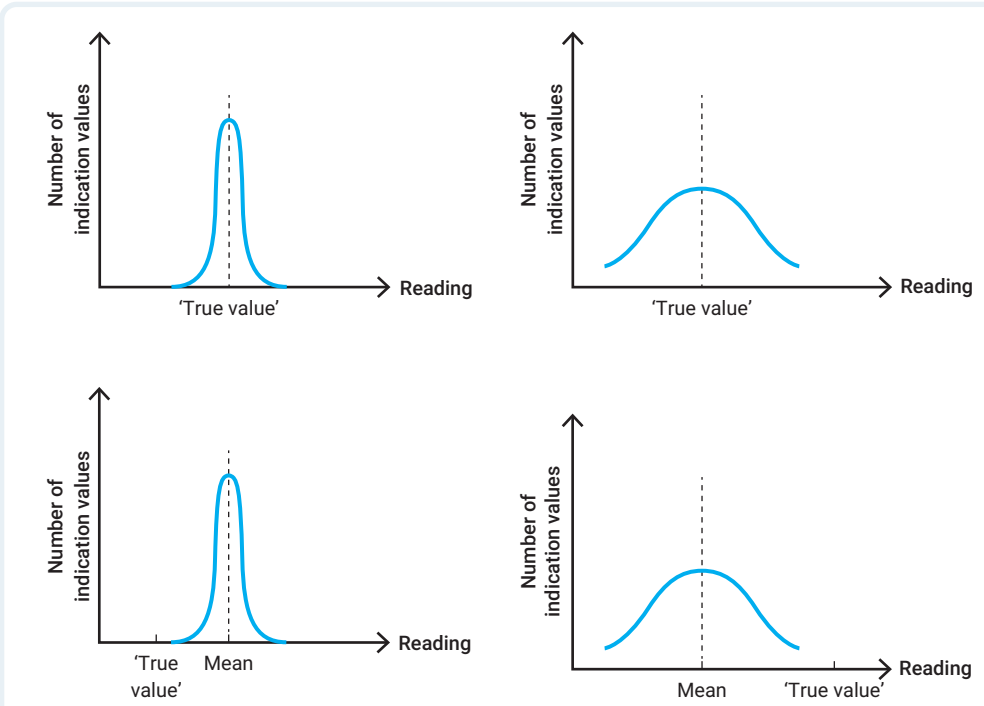
- There are five main types of investigations:
  - Descriptive
  - Comparative
  - Correlational
  - Experimental
  - Case study

Investigation type	Description	Example
Descriptive	Researchers collect data through surveys, interviews or observations to gain a better understanding of the subject being investigated.	Describing the distribution of a species in an ecosystem
Comparative	Two or more groups or variables are compared to identify similarities and differences between them. Researchers can use this information to investigate the impact of factors on the groups being investigated.	Comparing the growth of different plants under different environmental conditions
Correlational	These investigations focus on identifying the relationship between variables. Data collected in these investigations is used to determine whether changes in one variable are associated with a change in another variable. Note: Correlation does not mean causation.	Identifying the relationship between temperature and plant growth
Experimental	Variables are manipulated to determine whether there is a cause-and-effect relationship between the variables.	Testing the effect of a fertiliser on plant growth
Case study	Analysis of a particular individual, group or situation.	Studying the behaviour of a particular type of frog in a specific ecosystem

- Different sampling techniques are better suited to certain types of investigation.

Analysing data

- Precision describes the closeness of data, whereas accuracy describes how close the measured value is to the true value.
- The quality of data affects the validity of the experiment.



- Percentage error helps to indicate the accuracy of a measurement.

$$\text{Percentage error (\%)} = \left|\frac{\text{measured value} - \text{true value}}{\text{true value}}\right| \times \frac{100}{1}$$

- Errors affect the accuracy and precision of data. These can be categorised into:
  - random errors
  - systematic errors.
- Uncertainty describes the variability in the measured results:

$$\text{Absolute uncertainty} = \frac{\text{maximum} - \text{minimum}}{2}$$

$$\text{Percentage uncertainty} = \frac{\text{absolute uncertainty}}{\text{measured value}} \times 100$$

- Standard deviation and standard error can be used to quantify variability of data. This is best calculated using software such as Excel:

$$\text{Standard error} = \frac{\text{SD}}{\sqrt{n}}$$

where: SD is the standard deviation, and n is the sample size.

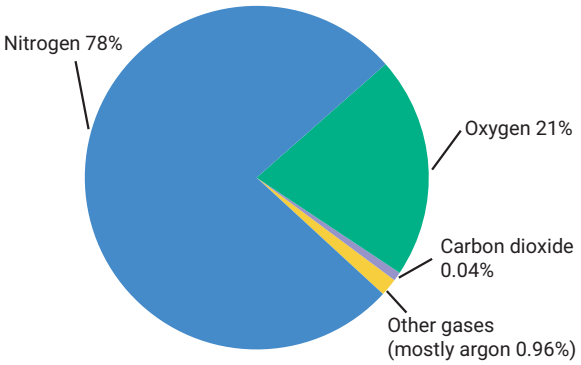
- The student's t-test measures the probability of results occurring due to probability. A $p < 0.05$ is considered statistically significant
- Pearson's correlation (R) coefficient helps quantify the direction and strength of the relationships between the measured variables.
  - $R = 0$ suggests no correlation.
  - $R = 1$ suggests a strong positive correlation.
  - $R = -1$ suggests a strong negative correlation.

- Spearman's rank (rho) quantifies how closely data (ranked data) are related.
  - Values that are closer to +1 indicate a strong positive correlation between the variables
  - Values closer to −1 indicate a strong negative correlation between the variables.

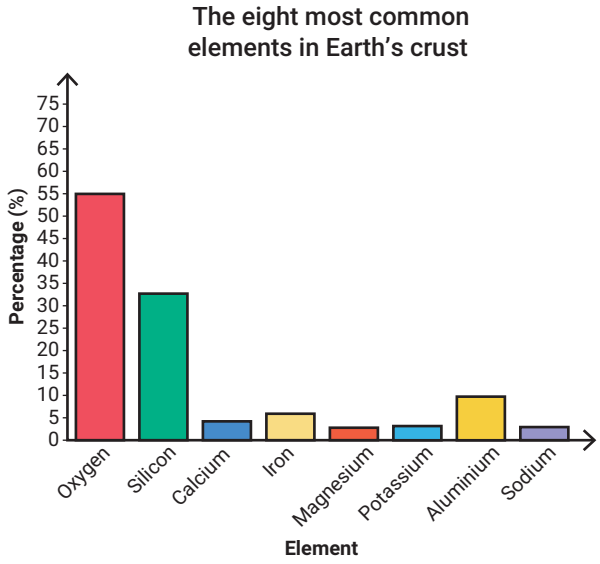
Graphs

- There are many different graphical representations of data, including:
  - linear graphs
  - column graphs
  - pie charts
  - scatterplots.

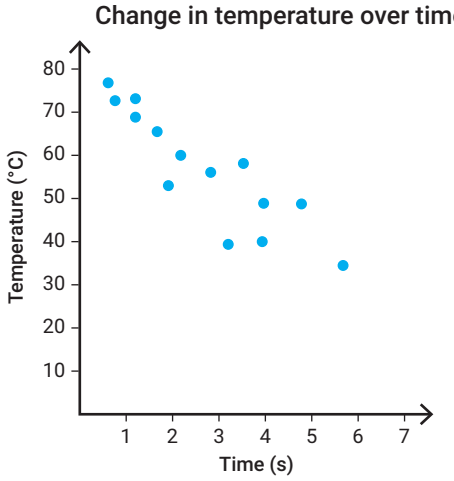
Pie charts



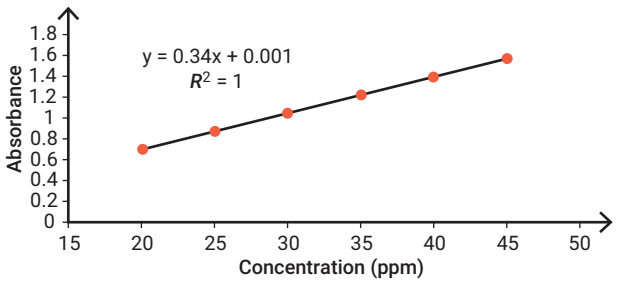
Column graphs



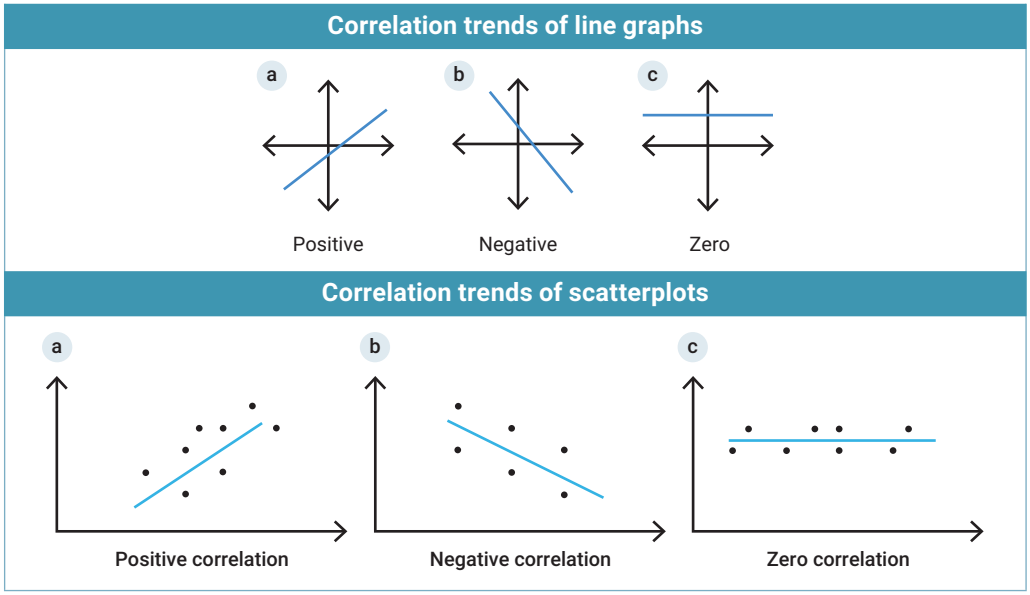
Scatterplots



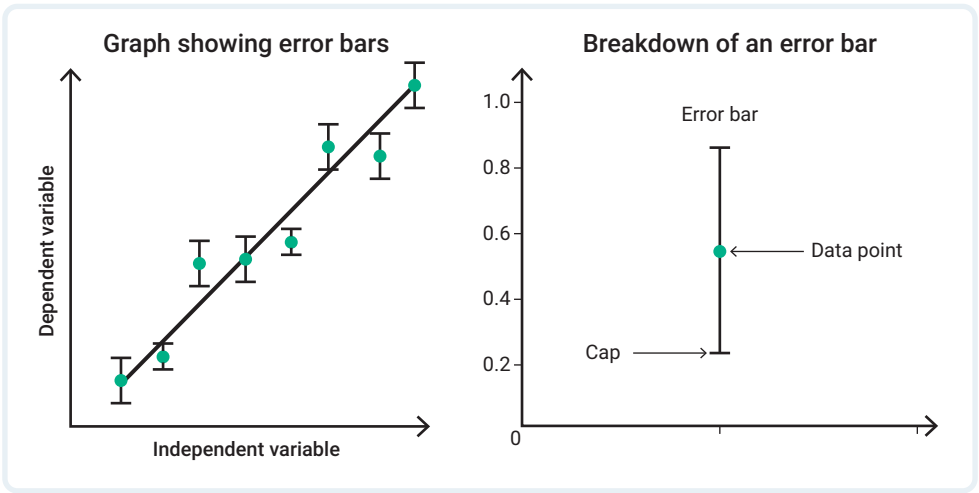
Line graphs



- Graphs help to show the relationship between variables. Although they can show correlation, this does not mean causation.



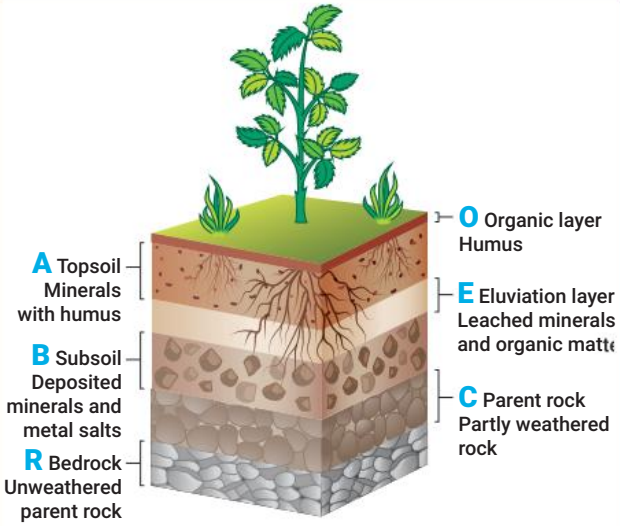
- Error bars on graphs help to visualise variability of measurements around the mean.
  - The central point shows the data point.
  - The upper and lower limits show the variability of the measured values.



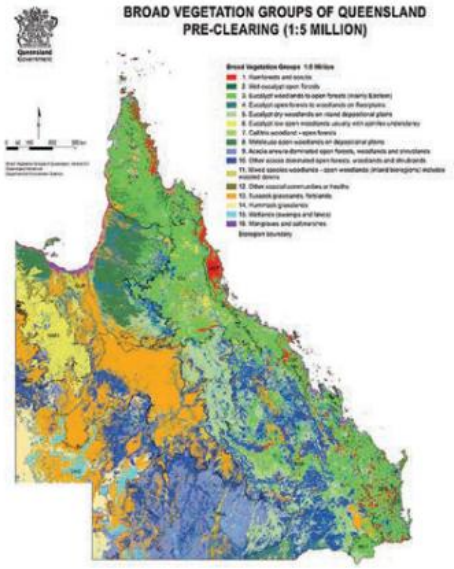
Other visual data representations

- Data can also be represented using profile diagrams, maps, or a combination of maps and charts.

Profile diagrams

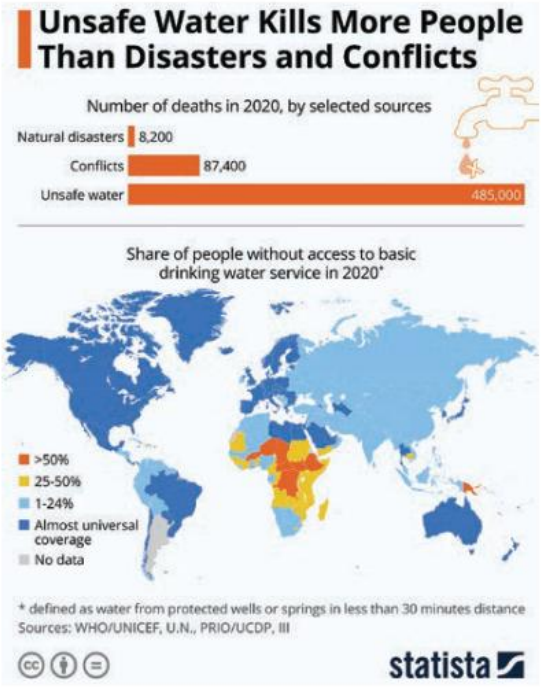


Maps



The State of Queensland

Combination of maps and charts

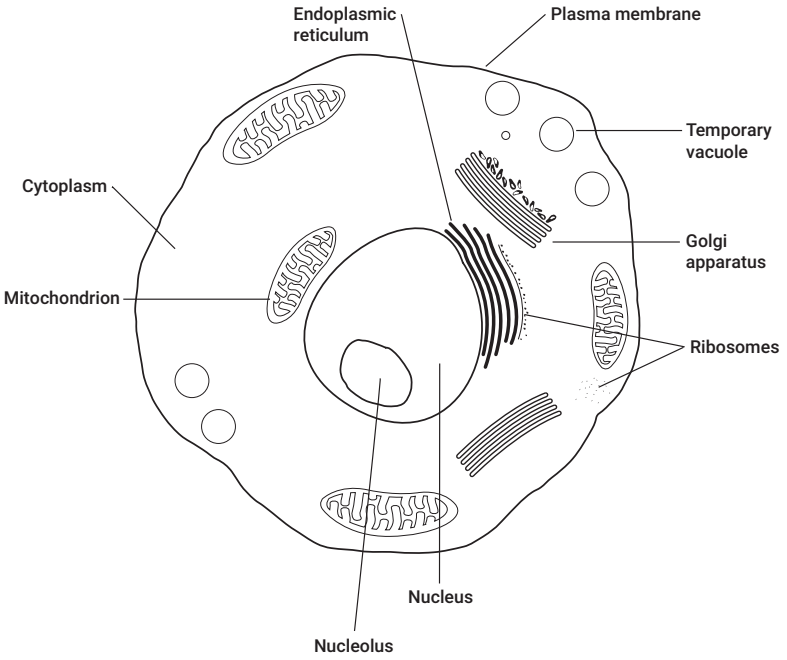


Katharina Buchholz, Unsafe Water Kills More People Than Disasters and Conflicts, Statista, Mar 22, 2022. Licensed under CC BY-ND 3.0.

Scientific drawings

- Scientific drawings are representations of scientific concepts.

Basic structure of a eukaryotic animal cell



Interpreting, analysing and evaluating evidence

- Apart from speaking to the trends shown in the data, when analysing data it is also important to assess the:
  - appropriateness of the method
  - sample size
  - sources of error
  - degree of uncertainty of the data.
- When evaluating evidence, make sure to also address any limitations present in the experiment, including:
  - experimental limitations; for example, time available to conduct the experiment, errors
  - methodological limitations; for example, accuracy and reliability of measurement techniques, ethical constraints
  - external limitations; for example, environmental factors that can introduce variability, access to proper equipment.

Communicating findings

- When communicating findings, make sure to:
  - use appropriate conventions and nomenclature
  - use language appropriate to the audience
  - reference appropriately using the relevant referencing system.

CHAPTER EXAM

MULTIPLE CHOICE

1. Which measure provides information about the spread or variability of data points in a dataset?

A Mean
B Mode
C Outlier
D Standard error

2. Which of the following datasets would be considered precise but not accurate?

A Measuring a flower's height with a ruler missing the mm markings (Readings: 22, 21, 23 cm)
B Measuring water temperature that is constantly 3° higher than the actual temperature (Readings: 15°C, 15°C, 16°C)
C Measurements made by different students of the width of leaves (Readings: 11.4, 15.8, 13.2 cm)
D Measuring how long it takes a ball to roll down a hill (Readings: 11.14, 10.59, 10.77 s)

3. A student measures the length of a plant stem to be 12.5 cm, using a ruler. The actual length of the stem, as determined by a more precise instrument, is 12.9 cm. The percentage error in the student's measurement is:

A 1.5%
B 2.4%
C 2.6%
D 3.1%

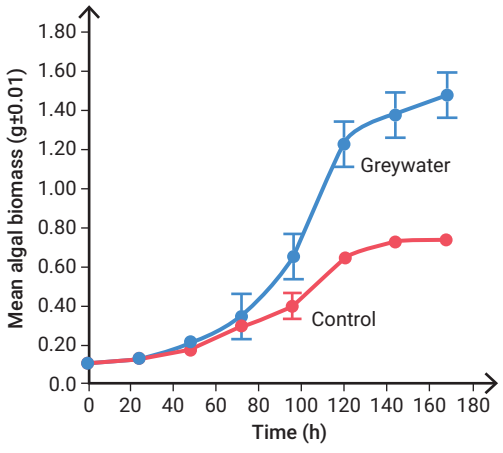
4. Which of the following would not be considered a type of investigation?

A Comparative
B Correlational
C Descriptive
D Relative

5. In a Biology experiment, students investigated the effect of light intensity on plant growth. Which of the following can be considered an extraneous variable?

A Type of plant species
B Soil moisture
C Light intensity
D Temperature

Questions 6–8 relate to the following information.
A student conducted an experiment to measure the change in mean algal mass over a 168-hour period, as shown in the graph.



6. The independent variable for this experiment is:

A control.
B greywater.
C mean biomass.
D time (h).

7. Comparing the algal biomass growth, the algal biomass in:

A the control experiences the greatest overall change.
B greywater grows faster than in the control throughout the experiment.
C greywater grows slower than in the control throughout the experiment.
D greywater and the control show similar growth rates initially, but the greywater condition eventually surpasses the control.

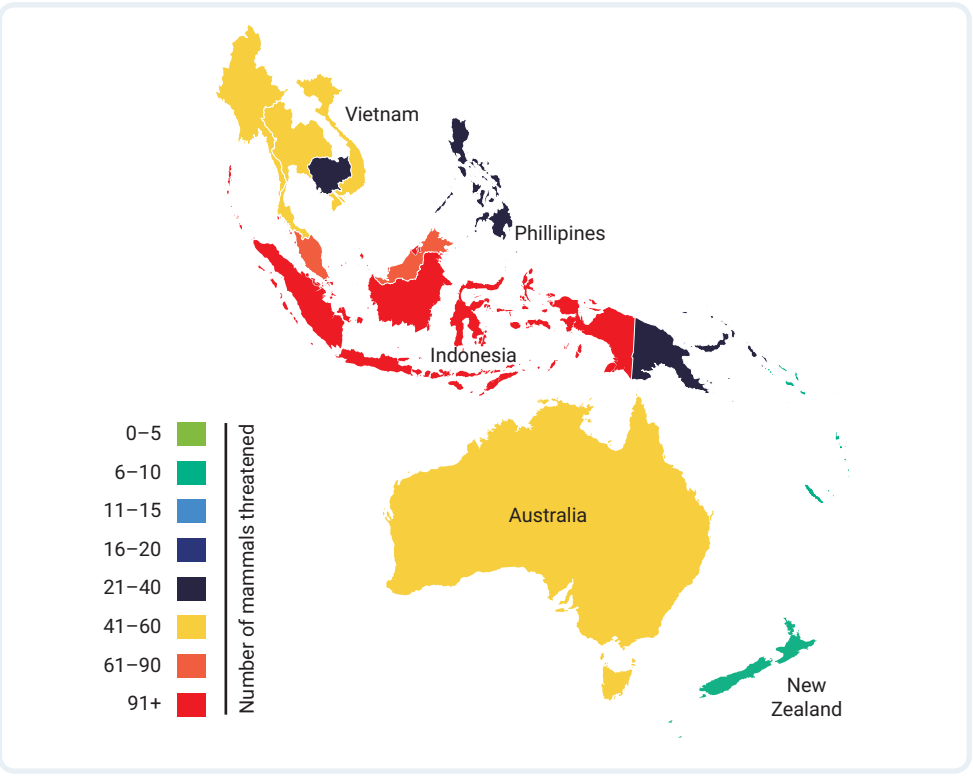
8. The data point showing the greatest variability is:

A control at 66 hours.
B control at 142 hours.
C greywater at 88 hours.
D greywater at 120 hours.

9. Based on the map below, the area with the least number of mammals threatened is:

A Australia.
B New Zealand.
C Philippines.
D Vietnam.

Adapted from: The Eco Experts



10. Which of the following cannot improve the reliability of results in an experiment measuring soil acidity levels in different areas?

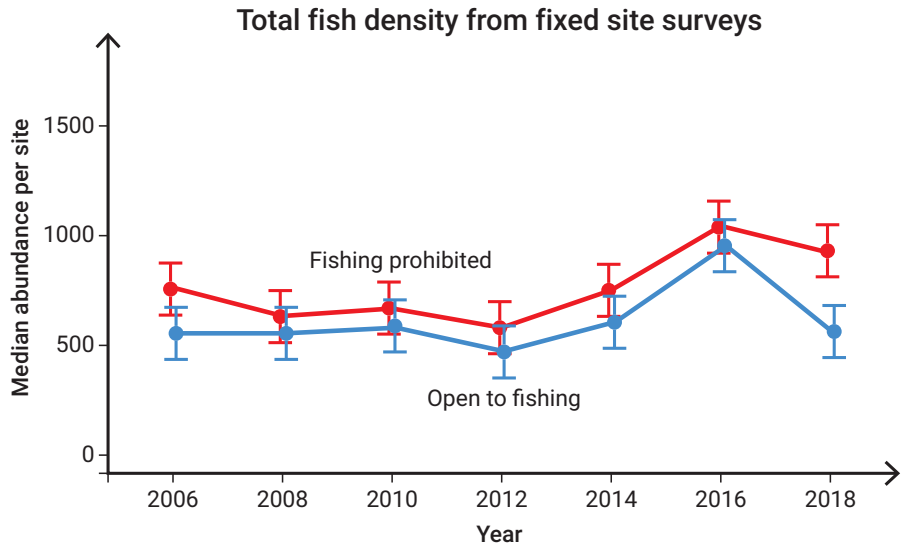
A Increasing the replicates in each area
B Use various measurement techniques
C Calibrating the pH meters before taking measurements
D Reducing the number of data points collected in each area

SHORT RESPONSE

11. The following is a description of an experiment.

For this experiment, students are given sets of bean plants to investigate how different light conditions affect plant growth. In the experiment, the plants are exposed to three conditions: full sunlight, partial shade and artificial light.
All plants are given sufficient water and growth is measured weekly.
Write an appropriate research question for this experiment.

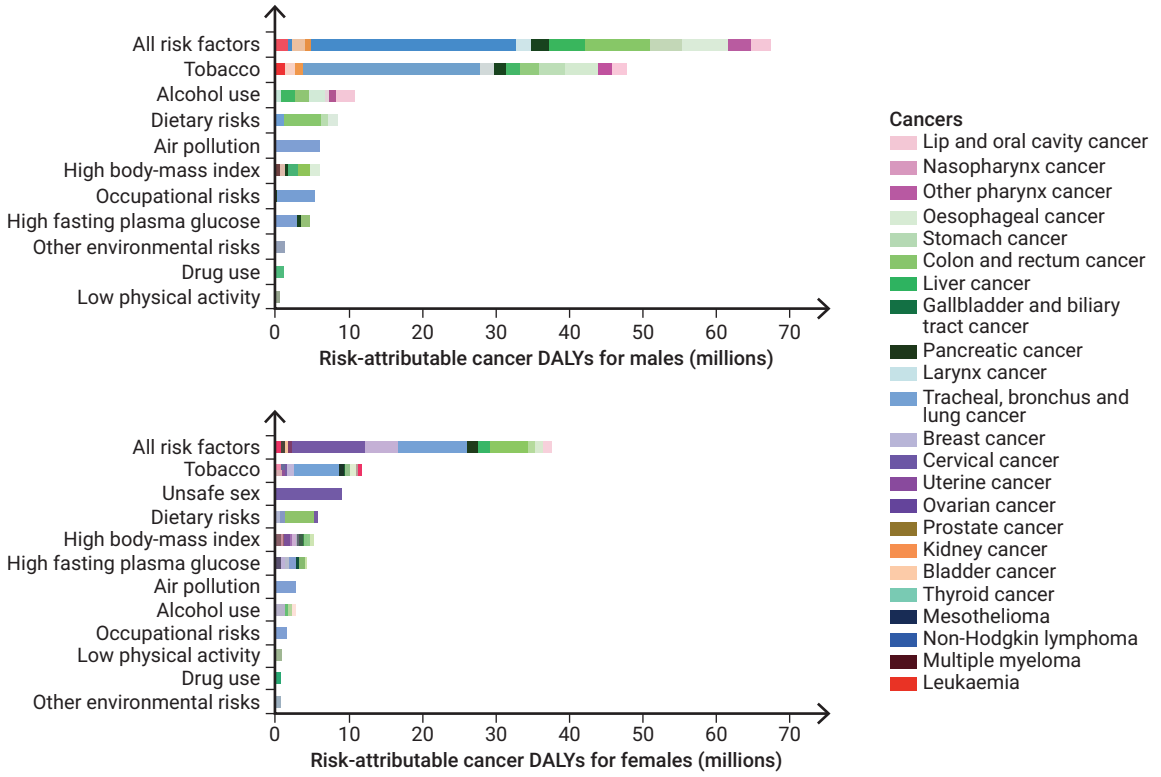
12. The graph below shows the impact of marine park zoning in reefs close to Townsville.



a **Identify** the independent variable in the experiment.
b **Compare** the effect of the two conditions on the density of fish.
c **Comment** on the reliability of the results.

13. The Global Burden of Disease Study in 2019 set out to understand the magnitude of cancer burden attributed to different risk factors. The goal was to use this information to develop effective prevention and mitigation strategies. Selected graphs from the study are shown below.

On analysing these graphs, a student made the following statement.
'For both sexes, occupational risks were the highest leading factor causing tracheal, bronchus and lung cancer.'
Assess the accuracy of this statement.



*DALY = the sum of years of life lost as a result of premature deaths and years lived with disability. One DALY represents the loss of one year of health.

14. The following data was collected from an experiment testing the effect of light intensities on plant growth over a 4-week period.

Week	Low-intensity light		Medium-intensity light		High-intensity light	
	Mean height (cm)	Error (%)	Mean height (cm)	Error (%)	Mean height (cm)	Error (%)
1	2.0	5	3.0	5	4.5	5
2	3.8	5	5.7	5	8.0	5
3	6.0	5	8.5	5	12.0	5
4	7.5	5	11.0	5	15.5	5

Sketch an appropriate graph to represent this data.

ANSWERS

CHAPTER DC SCIENCE RESEARCH

LEARNING CHECK DC.1

DESCRIBING

1 a Accuracy refers to how close a value is to the true value, whereas precision describes how close a set of measurements are to each other.

b Reliability refers to the consistency of measurements upon repeat experiments, whereas validity describes the extent to which the experiment measures what it is intended to measure.

2 Calibrate measuring instruments. Take multiple measurements and take an average.

3 a Data that is in categories

b Continuous data or measurements taken over time

c Data that is in categories or discrete data

4 a A logbook contains detailed notes relating to the experiment, including observations, results and methodology. This information is important during the analysis of the results of the experiment.

b MSDS contain information about the safe handling of any chemicals or substances used in an experiment. This ensures the safety of the researchers.

c Ethics help to ensure the safety of participants in the experiment, the integrity of the experiment and the proper use of the experimental results.

5 Research question, materials, methods, discussion

APPLYING

6 a Rate of plant growth

b Light exposure

7 Does the consumption of food (g) before running affect the total distance(km) a person can run?

8 Potential risk: The student could drop the measuring cylinder, causing it to break and shatter. The pieces of glass could damage the skin.

Risk minimisation: Wear gloves and closed toe shoes to protect against pieces of broken glass.

9 The experimenter breached informed consent. The experimenter ignored the participant's refusal to be tested and performed the procedure anyway. Participants need to give formal consent to participate in experiments and the experimenter must respect their wishes, not go against them.

10 a $\text{Percentage uncertainty} = \frac{1}{20} \times 100$

$= 5\%$

b This suggests that the measurements are relatively imprecise.

11 a Where the plant is placed and therefore the amount of sunlight exposure

b Random error

12 $\text{Absolute uncertainty} = \frac{14.3 - 14.1}{2}$

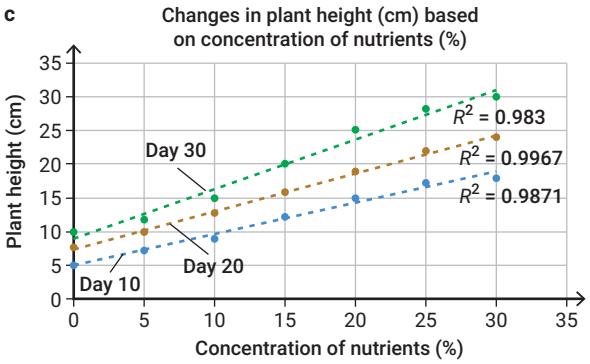
$= \pm 0.1\,\text{cm}$

13 a Independent: concentration of nutrients (%); dependent: plant height

b

Concentration of nutrient solution (%)	Mean height (cm)
0	7.7
5	9.7
10	12.3
15	16.0
20	19.7
25	22.3
30	24.0

c



d There is a positive correlation between the concentration of nutrients in the solution and the plant height. It is >0.98 on each measurement day.

ANALYSING

14 a Concentration of phosphorus

b Sample 3

15 a Scatterplot

b Line of best fit

c $\text{Gradient} = \frac{\Delta y}{\Delta x}$

$= \frac{4 - 2}{0.480 - 0.250}$

$= 8.70\,\text{(approximately)}$

d Approximately 1.500

e Since there is a strong positive correlation between the two variables, the *R* value is likely to be closer to 1 than to 0.

LEARNING CHECK DC.2

DESCRIBING

1 Primary data is firsthand data collected by the researcher, whereas secondary data refers to information collected from an experiment conducted by someone else.

2 The peer review process helps to ensure the quality of the research and the results. It also helps to add credibility to the research investigation.

3 Experimental: How different tomato plant types respond to the particular fertiliser used

Methodological: The consistent timing of when the plant heights are measured

4 How quickly a reaction occurs is important in science. Enzymes can make reactions occur in less time by providing a different pathway for the reaction to take place.

5 (Cruzan, 2012)

CHAPTER EXAM

MULTIPLE CHOICE

1	D	**3**	D	**5**	B	**7**	D	**9**	B
2	B	**4**	D	**6**	D	**8**	C	**10**	D

SHORT RESPONSE

11 How does exposure to light (hr) affect the growth of bean plants (cm)?

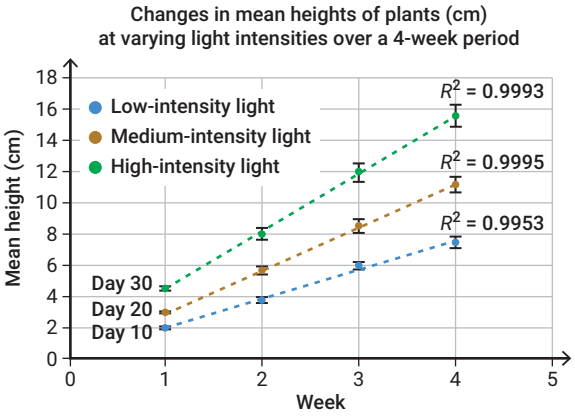
12 **a** Year

b In general, in areas where fishing is prohibited, there is a larger density of fish than in areas that are open to fishing. However, both conditions have similar fluctuations, with a peak in 2016.

c The graph shows relatively large error bars for both conditions and, at times, the error bars overlap for both the fishing prohibited as well as open to fishing conditions. As such, it's not certain that there was a difference in fish density between both conditions.

13 The statement is not accurate. According to the graph, tobacco was the leading risk for tracheal, bronchus and lung cancer for both male and females.

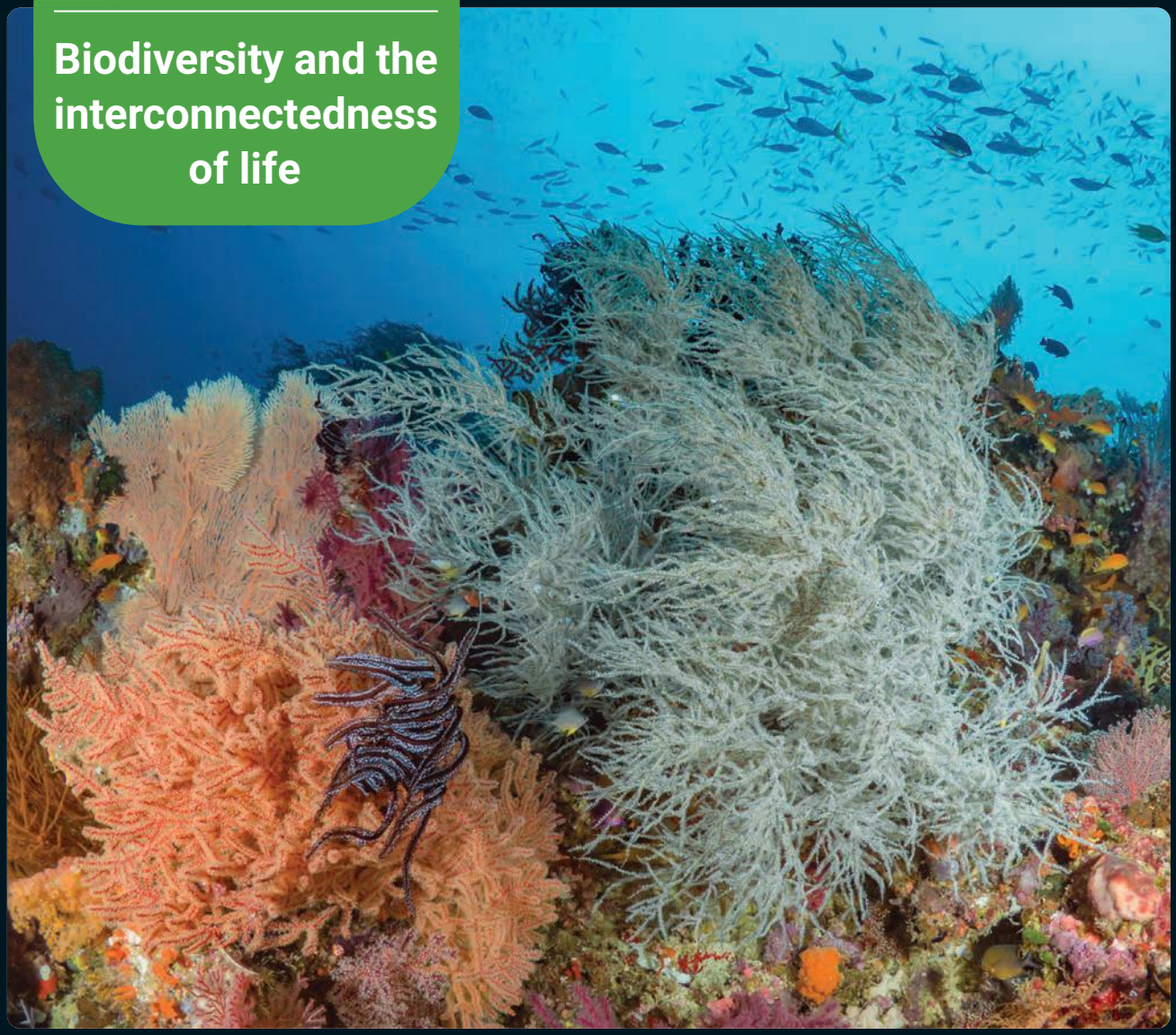
14



UNIT

3

Biodiversity and the interconnectedness of life



Mike Workman/Shutterstock.com

Topic 1: Biodiversity and populations
CHAPTERS RELATED TO THIS TOPIC AREA: 1–3

Topic 2: Functioning ecosystems and succession
CHAPTERS RELATED TO THIS TOPIC AREA: 4–6

9780170483384

The adaptations that result from the wide variety of environments on Earth have generated millions of different species. Biodiversity describes this variety of living things and can be measured at an individual, species or ecosystem level.

Classification systems are used to consistently identify organisms and ensure clarity when communicating about and researching species, while food webs and ecological indexes describe interactions between species and help explain how energy and matter are transferred and transformed in living systems. In turn, this allows for an understanding of ecosystem functions, services and stability that supports our ecological endeavours as we study and protect biodiversity and the interconnectedness of life.

UNIT OBJECTIVES

By the end of this unit, students should be able to:

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.

CHAPTER 1

Classifying species

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SYLLABUS DOT POINTS

SCIENCE UNDERSTANDING

- 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.

SCIENCE AS A HUMAN ENDEAVOUR

Appreciate that:

- methods of classification are directly related to the purpose for which the data will be used. Hierarchical systems, such as the Linnaean system, can be used to organise, analyse and communicate data about biodiversity. For example, the hierarchical nature of the Linnaean system allows scientists to infer similarities between species; however, as the system was originally based primarily on physical features, the categorisation of species does not always reflect evolutionary relatedness. Species may be re-classified as new information becomes available

- 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

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Introduction

Australia is home to more than one million species of organisms, many of which are found nowhere else in the world. Classifying organisms has occurred throughout history with humans grouping organisms according to whether they are edible, toxic or medicinal (to name a few). Aboriginal and Torres Strait Islander Peoples have long-term observations, oral histories and a sustained presence that show connections between people (including kinship and societal structure), Country and living things that form the basis of traditional groupings of organisms. These categories are specific to each traditional region of Australia.

Deciding how to scientifically define and recognise species has been, and continues to be, a topic of vigorous discussion.

ASSUMED KNOWLEDGE

- ✓ Living things have similarities and differences in their morphology and physiology.
- ✓ It is possible to group living things on the basis of similarities.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ describe how the ability to reproduce fertile offspring is one accepted definition for species concept
- ✓ describe, with examples, the organisms that this species concept cannot be applied to
- ✓ explain how an organism is classified according to the Linnaean system
- ✓ explain how an organism is named according to the Linnaean system and binomial nomenclature
- ✓ classify an organism by using the attributes listed on a dichotomous key.

1.1 What is a species?

A species concept provides a set of criteria for determining what constitutes a species. Species concepts are typically based on reproduction, morphology or shared evolutionary history. There are several different species concepts, each with its own advantages, assumptions and limitations. The most commonly used species concept is the biological species concept.

Biological species concept

biological species concept a definition of species as groups of actual, or potentially, interbreeding natural populations that are reproductively isolated from other such populations

gene pool the range of genes and all their alleles present in a population

Syllabus link
Chapters 13 and 14 discuss gene pools and speciation.

hybrid an organism resulting from the interbreeding of two different species

Charles Darwin (1809–82) considered species as the fundamental units of evolution, starting a new era of species definition. In the early 1940s, Ernst Mayr proposed that species are groups of actual, or potentially, interbreeding natural populations that are reproductively isolated from other such populations. This is the **biological species concept**. According to this model, individuals from the same species can produce viable offspring under natural conditions. This definition represents a species as an isolated **gene pool**. The biological species concept is the most widely used in biology.

However, it has the following limitations:

- Fossils: It is impossible to know which individuals could interbreed by studying only the fossilised remains of an extinct organism, or whether physical differences between specimens are just variations between individuals or significant enough to denote a new species.
- Proof of mating: It can be difficult to observe organisms mating in certain environments (e.g. deep ocean environments) and determine whether or not the offspring are fertile.
- Hybrids: Often, where populations of two identified species overlap to some extent, there are zones where **hybrid** organisms exist. Hybrids are difficult to classify because they are the result of interbreeding between individuals from two different species. They generally do not survive well outside restricted hybrid zones, nor do they displace either of the parent species.

  The existence of hybrids offers evidence that the parents are the same species, even though all other markers (e.g. behaviour and physiology) indicate that the parents are different species. Sometimes, the resulting hybrid offspring seem to survive quite well in the wild, such as the polar–grizzly bear hybrid (grolar bears) that have been observed in the Arctic regions of

Canada. However, the resulting mix of features such as coat colour or dentition (tooth structure and arrangement) may not be well suited to either the forest (grizzly bear) or marine (polar bear) environments. Other hybrids are often sterile (unable to produce offspring); for example, infertile mules that result from the interbreeding of a horse and a donkey.

Other species definitions

When the biological species concept is not appropriate, other species definitions can be considered that address some of the limitations provided (note that these specific species concepts are not stated in the syllabus subject matter. They are listed under Science as a human endeavour.).

The **morphological species concept** states that 'a species is a community, or a number of related communities, whose distinctive morphological characters are, in the opinion of a competent systematist, sufficiently definite to entitle it, or them, to a specific name' (Regan, 1926). In simpler terms, this concept characterises a species by its morphology (the shape and arrangement of the parts of an organism), including size, shape and/or structure. These morphological features are used when there is limited information about reproductive behaviours or genetic information. It can be applied to sexually and asexually reproducing organisms. It is most often used when examining fossils.

FIGURE 1.1.1 The ancestral platypus *Obdurodon dicksoni*

Riversleigh is a fossil fauna site in north-west Queensland (south-western boundary of the Waanyi Peoples) that has altered scientific understanding of Australia's vertebrate history. For example, the discovery of an ancestral platypus (*Obdurodon dicksoni*) skull **(Figure 1.1.1)**, one of the most complete fossil skulls found, improved the understanding of relationships between members of the platypus family. One of these fossilised species is the ancestor of the current toothless platypus, *Ornithorhynchus*.

The morphological species concept has the following limitations:

- Scientists often disagree about which morphological features should be used, and when the features are different enough to justify creating a new group.
- Morphology can be misleading because organisms can develop similar structures as a result of being in similar environments rather than having a recent shared genetic history.

The **phylogenetic species concept** (similar to the evolutionary species concept or the lineage species concept when looking at just one branch of a phylogenetic tree) identifies a species as the smallest clade, or smallest group of organisms, who can all trace their origins to a single common ancestor. This concept increasingly uses genetic techniques to determine historical branching points and current groups, and most phylogenetic trees produced today are based almost solely on these. It can be applied to asexual species and those for which detailed reproductive behavioural data is unavailable.

The phylogenetic species concept has the following limitations:

- The reliance on genetic data makes it difficult to apply to long-extinct species whose DNA is badly degraded or non-existent; it is rarely possible to reconstruct with certainty the past evolutionary pathway and, if so, it is difficult to devise a satisfactory branching pattern.

The **ecological species concept** states that two similar individuals are more likely to be of the same species when they have similar survival requirements; therefore, their distribution in the ecosystem is more likely to overlap. Limitations include difficulties in determining the degree of competition between individuals and the similarity in life history of the individuals.

morphological species concept a definition of species that is based on physical characteristics

phylogenetic species concept a definition of species that is based on the smallest group of individuals having a common ancestor, often determined through genetic analysis

Syllabus links
Chapter 13 discusses the evolution of similar structures in unrelated species.

Chapter 14 details the construction of phylogenetic trees.

Weblinks
What is a species?
Why should we care about species?
Ecological species concept
Genetic species concept

Worksheet
Biological species concept

ecological species concept a definition of species that is based on occupying the same ecological niche and similar interactions with the environment

LEARNING CHECK 1.1

DESCRIBING

1 **Describe** the biological species concept.
2 State which species concept is most useful for fossil classification.
3 **Describe** two limitations of the biological species concept.

APPLYING

4 **Explain** the differences between the morphological species concept and the biological species concept.

1.2 Taxonomy

taxonomy a system of classification, particularly biological; or the study of these systems

hierarchy a system categorised by the specific arrangement of information into layers

Weblink
A brief history of the kingdoms of life

Biological classification systems or **taxonomies** are methods of naming, describing and organising living things, so that similar or related organisms are grouped together. The diversity of life on Earth is so large that to organise such vast amounts of information, organisms need to be classified first. By grouping similar organisms together, it can be easier to observe and understand patterns, trends and relationships between organisms and groups of organisms.

Classification systems are often hierarchical. Organising the information into layers provides a clear structure for understanding relationships between organisms. In **hierarchies**, the highest ranks or levels are larger and more inclusive. They incorporate general information and a wider variety of organisms than the lower ranks or levels, which are smaller, more specific and contain fewer organisms (Figure 1.2.1). In biological taxonomies, the information is typically based on one species concept. Current biological taxonomies are based primarily on the biological species concept and updated using genetic information as it becomes available.

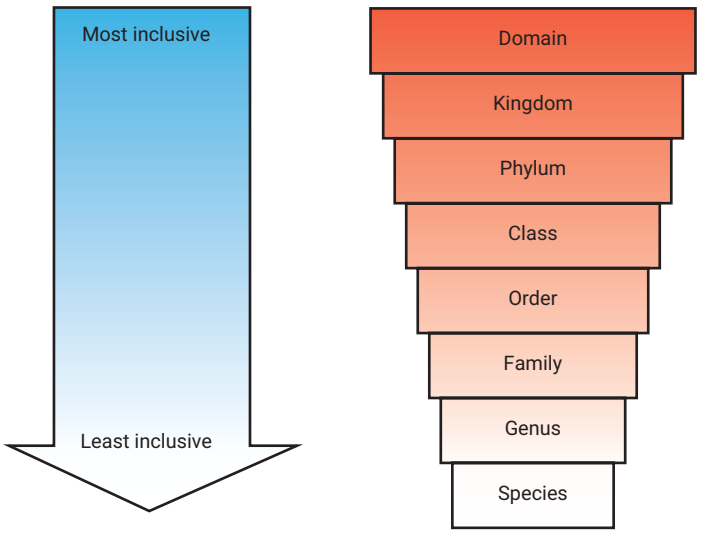


FIGURE 1.2.1 Hierarchies become more specific and less general as you go from the top to the bottom.

Building a standard taxonomy allows biologists around the world to communicate with one another in a common language and to compare findings. It supports the identification of organisms that have already been discovered and consistently absorbs information about entirely new organisms. It would be beyond the capabilities of a single scientist to classify the breadth of life on Earth, but through global collaboration, a standard taxonomy is very effective.

Weblink
Introductory classification activity

Limitations of classification

Classification systems have limitations, just as species concepts do, because many of the same attributes are being used to develop the taxonomy. Groupings can be interpreted differently according to the choices made when classifying organisms. Classifying also requires biologists to emphasise major similarities, which means reducing the importance of or ignoring minor differences in individuals.

A taxonomy is built to organise the data for analysis and is directly related to the purpose for which the data will be used. If the data or the purpose changes, so does the taxonomy. This has been shown where DNA information has been used to update classification systems previously based on morphology. For example, **Figure 1.2.2** shows a pangolin. Pangolins were initially classified with armadillos and anteaters but are now classified in a separate order: Pholidota.

2630ben/Shutterstock.com

FIGURE 1.2.2 An African pangolin

LEARNING CHECK 1.2

DESCRIBING

1 **Define** 'taxonomy'.
2 **Identify** two benefits of classifying organisms.

APPLYING

3 **Explain** two limitations of classification.

1.3 Linnaean classification

binomial nomenclature a naming system in which each individual is given a two-part name; in biology this is genus and species

Currently, the most widely accepted standard taxonomy is Linnaean classification. Carl Linnaeus was the first scientist to consistently use **binomial nomenclature**, a two-part naming system using Latin words, the first being the genus (general name) and the second being the species (specific name). He wrote the first version – *Systema Naturae* – in the 1730s, using a systematic approach to naming six classes of animals based on shared physical traits (morphology). It detailed both a framework of taxonomic levels to organise the known species and the rules for its use. The agreed starting point for the nomenclature of plants is Linnaeus' first edition of *Species Plantarum* (1753) and for animals his 10th edition of *Systema Naturae* (1758). The current rules are stated below.

BINOMIAL NOMENCLATURE – THE RULES

COMMON CONVENTIONS IN NOMENCLATURE

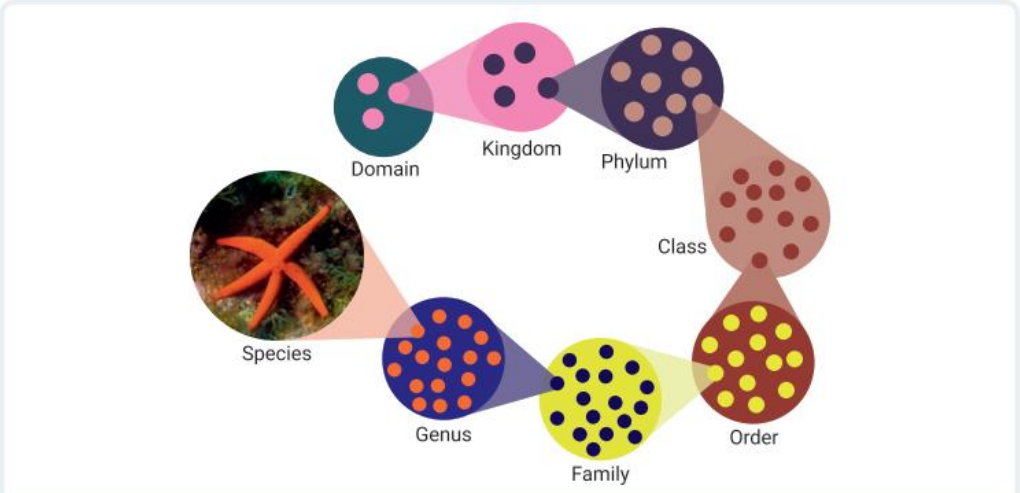
- Scientific names are written in italics. The genus starts with a capital letter; the species starts with a lower-case letter.
  Escherichia coli
- When handwritten, the scientific name is underlined instead of italicised.
  Escherichia coli
- After the full name of a species has been mentioned, the genus can be abbreviated to its initial and a full stop.
  First mention: *Escherichia coli*
  Subsequent mentions: *E. coli*
- When referring to members of a genus in a general sense, rather than to a particular species, the abbreviations 'sp.' (a singular species) and 'spp.' (more than one species) can be used. These abbreviations are not italicised.
  Escherichia sp. (a member of the genus *Escherichia*)
  Escherichia spp. (members of the genus *Escherichia*)

Bildagentur Zoonar GmbH/Shutterstock.com

FIGURE 1.3.1 At one point, the common wild briar rose was known alternatively as *Rosa sylvestris alba cum rubore, folio glabro* or *Rosa sylvestris inodora seu canina*. In Linnaeus' binomial taxonomy, it became *Rosa canina*.

Linnaean taxa

Linnaeus originally envisioned all life in three domains – Animal, Vegetable and Mineral – with several subordinate taxa (singular: **taxon**) grouping life into more and more specific subsets. Today, the precise name and number of domains has been updated by evolutionary biology and molecular science, but the taxa still stand (Figure 1.3.2). The names of the major taxa, from largest to smallest, are **domain**, **kingdom**, **phylum** (plural: phyla) or **division**, **class**, **order**, **family**, **genus** (plural: genera) and **species**. At each taxonomic level, organisms can be further grouped according to features that they share, either morphological, DNA sequences and/or protein structure. Therefore, each organism can be defined by the taxa to which it belongs.



Alain Machet (4)/Alamy Stock Photo

FIGURE 1.3.2 The hierarchy of Linnaean classification involves eight taxa. Thus, each organism on Earth can be identified with just eight words that indicate which taxa it belongs to.

Domains and kingdoms

Although Linnaeus did not have access to cellular information, it is now used to categorise life into three domains (Figure 1.3.3). In members of domain Eukarya, called eukaryotes, the DNA is contained within a nucleus and there are other **organelles** within their cells. Domains Archaea and Bacteria include prokaryotes: organisms that lack some of these features. Despite this superficial similarity, organisms in Archaea and Bacteria differ in how DNA is stored and how proteins are synthesised, which means that they are classified in separate domains (formerly considered to be in one kingdom – Monera). Many members of Archaea live in extreme environments, such as areas of high salt concentration or temperature.

There are four kingdoms in domain Eukarya: Animalia, Plantae, Protista and Fungi. Animals (kingdom Animalia) are multicellular organisms that are heterotrophic. Plants (kingdom Plantae) are multicellular organisms that have cell walls that contain cellulose and are autotrophs, obtaining energy from the Sun, using organelles called chloroplasts. Yeasts, mushrooms and moulds all belong to kingdom Fungi and are characterised by having cell walls made of a specific polysaccharide (chitin). The protists (kingdom Protista) are a diverse group of mostly single-celled organisms and live in aquatic or moist environments.

taxon a level of a hierarchical classification system, e.g. kingdom, family or species

domain the highest ranking taxon in Linnaean classification, e.g. Eukarya

kingdom the second-highest taxon in Linnaean classification, e.g. Animalia

phylum the third-highest taxon in Linnaean classification of animals, e.g. Chordata

division the third-highest taxon in Linnaean classification of plants, e.g. Tracheophyta (vascular plants)

class the fourth-highest taxon in Linnaean classification, e.g. Mammalia

order the fifth-highest taxon in Linnaean classification, e.g. Carnivora

family the sixth-highest (third lowest) taxon in Linnaean classification, e.g. Felidae

genus the seventh-highest (second lowest) taxon in Linnaean classification; it is always italicised, e.g. *Felis*

species the lowest taxon in Linnaean classification; it is always italicised and combined with genus, e.g. *catus* in *Felis catus*

organelle a cellular structure that performs a specific function in a partitioned space within the cell

Syllabus link
Chapter 1 of ***Nelson QCE Biology Units 1 & 2*** details prokaryotic and eukaryotic cells, including plants, animals and fungi.

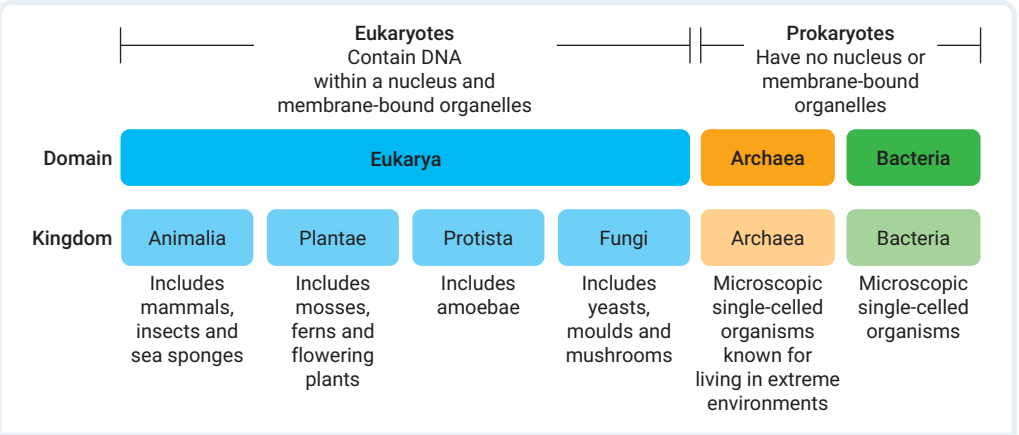


FIGURE 1.3.3 Organisms are classified into three domains on the basis of cell structure (eukaryote/prokaryote) and cell function (Archaea/Bacteria).

LEARNING CHECK 1.3

DESCRIBING

1 State the eight taxa of Linnaean classification.

2 **Describe** the four kingdoms in domain Eukarya.

3 State the abbreviated binomial name of *Lophostemon confertus*.

APPLYING

4 **Explain** which two organisms in the following table are the most closely related.

Common name	Orange-bellied parrot	Purple-crowned fairy wren	Woylie	Boodie
				
Kingdom	Animalia	Animalia	Animalia	Animalia
Phylum	Chordata	Chordata	Chordata	Chordata
Class	Aves	Aves	Mammalia	Mammalia
Order	Psittacidae	Passeriformes	Diprotodontia	Diprotodontia
Family	Psittaculidae	Maluridae	Potoroidae	Potoroidae
Genus	*Neophema*	*Malurus*	*Bettongia*	*Bettongia*
Species	*Neophema chrysogaster*	*Malurus coronatus*	*Bettongia penicillata*	*Bettongia lesueur*

5 Comparative genomics is reclassifying several organisms that had previously been grouped according to physical and physiological traits. **Explain** why DNA evidence could be considered superior evidence of relatedness compared to physical appearance.

1.4 Dichotomous keys

Once a taxonomy has been created that allows an organism to be classified on the basis of easily observable traits that do not change, the information can be used to generate a **dichotomous key**. This allows biologists to identify the organism as belonging to an existing taxon, or it may identify the need for a new taxon. The term 'dichotomous' comes from the Greek *dikhotomos* (from *dikho* for 'in two' and *temnein* for 'to cut'). It describes a key that consists of a sequence of paired statements about an observable trait that are mutually exclusive.

dichotomous key a series of choices between two options that results in the classification of an organism

The key repeatedly divides into two categories. After selecting and following one branch from each pair, more information about the organism is revealed. Once the organism shares no more of the characteristics described in the key with another organism, it has been identified. The two categories are usually presented as either a branching flow chart or a numbered sequence of paired statements. Dichotomous keys may be written to suit a higher level of taxonomy, such as 'class' (Figure 1.4.1), or be written to be very specific for lower levels, resulting in species name (Figure 1.4.2).

When developing a dichotomous key:

- make enough observations of the organisms being identified; look for key characteristics or traits, and note how these differ between organisms. Remember that some traits are not visible all the time; for example, flowers
- use observable and objective traits; for example, 'Longer than 10 cm', 'Equal to or shorter than 10 cm' rather than 'Long' and 'Short'
- start with the most general traits, then the more specific ones
- make sure the choice has only two options. The two options are often 'Have this feature' and 'Does not have this feature'. It can become problematic if the key is initially developed for specific numbers; for example, two legs or four legs, and subsequently an organism with six legs is identified.

Worksheets
Classification using the Linnaean system and dichotomous keys
Dichotomous keys

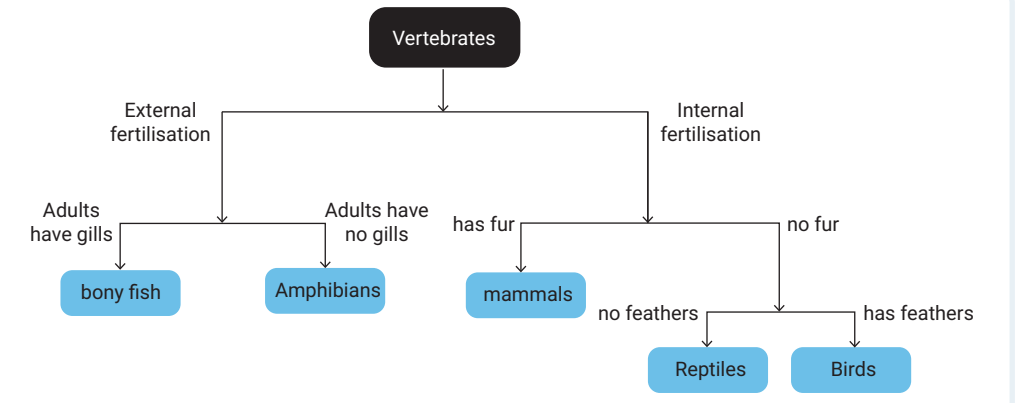


FIGURE 1.4.1 A typical dichotomous key: a branching flow chart classifying up to the class level

1a. Lower surface of the leaf is pale with a darker green upper surface . . . . . go to 2

1b. Both leaf surfaces are the same colour . . . . . go to 3

2a. Leaves generally pointed at each end and adult leaves 3–8 cm wide. Coarse, spongy bark that crumbles to dust without fibres. Gumnuts are usually cylindrical with fused valves at the opening . . . . . *Eucalyptus robusta*

2b. Adult leaves are <4 cm wide. Gumnut valves are not fused . . . . . go to 4

3a. Rough, fibrous, splintery bark covering most of the tree. Gumnuts are 1.5–2.5 cm long with ridges on the outside with buds up to 3 cm . . . . . *Eucalyptus planchoniana*

3b. Gumnuts and buds are not ridged and <1.5 cm long . . . . . go to 5

4a. Bark is slightly creased, grey on the surface and reddish underneath. Pointed buds about 2 cm long. Gumnuts have protruding valves . . . . . *Eucalyptus resinifera*

4b. Gumnuts have valves at or below rim level with rounded buds <1 cm long . . . . . go to 6

5a. Rough, fibrous bark in strips (not stringy). Buds are 7–11 mm long with gumnuts that have a stalk and a narrow rim. Leaves have a blueish tinge of colour and a symmetrical base . . . . . *Eucalyptus carnea*

5b. Fibrous and stringy bark that is grey with a red/brown base colour. Buds are 6 mm long and gumnuts have little or no stalk. Leaves are a silvery grey-green without a symmetrical base . . . . . *Eucalyptus tindaliae*

6a. Outer bark is reddish-brown and may have circular swellings with central holes. Long, slender stalks on rounded buds, while gumnuts have a tapered base . . . . . *Eucalyptus microcorys*

6b. Outer bark is grey or yellow with brown inner bark. Buds are oval and pointed 5 –7 mm long, while gumnuts are hemispherical . . . . . *Eucalyptus acmenoides*

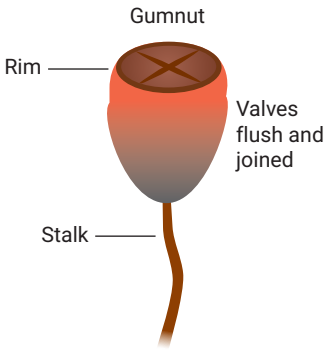


FIGURE 1.4.2 A typical dichotomous key: paired statements classifying to genus and species

WORKED EXAMPLE 1.4.1

Use the key in Figure 1.4.2 to identify the name of this species of plant.

Peter Krisch/Shutterstock.com

Stephanie Jackson/Alamy Stock Photo

Attributes:

- Leaves darker above and lighter below
- Leaves 0.8–4 cm wide
- Gum nuts with separate valves
- Blunt buds less than 1 cm long
- Gum nuts with valves below rim level
- Bark reddish-brown
- Outer bark with minute holes
- Buds rounded
- Gum nuts tapered at the base

ANSWER

Using the attributes to follow the key in Figure 1.4.2:
Read each pair of sentences, beginning with 1a and 1b. Decide which sentence best fits the listed attributes and follow the stated path to the next number.
1a → 2b → 4b → 6a. *Eucalyptus microcorys*

WORKED EXAMPLE 1.4.2

Use the following information to develop a dichotomous key using paired statements.
This will be a simple key.
The attributes to use are identified below.

Attributes:

- Body ≤5 mm long body OR body >5 mm long body
- Has stripes along wings OR does not have stripes
- Has dots all over wings OR does not have dots not all over wings

Cocon/Shutterstock.com; Tomasz Klejdysz/Shutterstock.com; Bdp Studio/Shutterstock.com; ABS Natural History/Shutterstock.com

Micraspis frenata
4 mm long

Illeis galbula
4–5 mm long

Hippodamia variegate
5.5 mm long

Harmonia conformis
6–7 mm long

ANSWER

1a. Body ≤5 mm long …… Go to 2.
1b. Body >5 mm long …… Go to 3.
2a. Has stripes along wings …… *Micraspis frenata*
2b. Does not have stripes along wings …… *Illeis galbula*
3a. Has dots all over wings …… *Harmonia conformis*
3b. Does not have dots all over wings …… *Hippodamia variegate*
Challenge: Is there an alternative sequence for the attributes that still results in a workable dichotomous key?

LEARNING CHECK 1.4

APPLYING

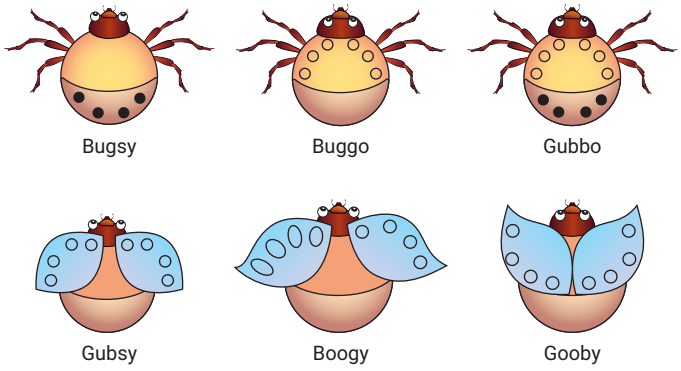
1 Identify what colour leaves *Eucalyptus robusta* has.

2 Identify which species of eucalypt have rough fibrous bark.

ANALYSING

3 **Analyse** the key in Figure 1.4.2 to identify trait differences between *Eucalyptus microcorys* and *Eucalyptus acmeniodes*.

Questions 4–6 refer to the following image, which shows six bizarre bugs found in a backyard.



4 **Compare** these bugs to state enough traits to construct a dichotomous key that identifies them.

5 **Organise** these traits to produce a dichotomous key for these bugs.

INTERPRETING

6 A seventh bizarre bug is found. **Determine** whether this bug can be classified using the dichotomous key designed in Question 4.

CHAPTER SUMMARY

Biological species concept

- Species are groups of actual (or potentially) interbreeding natural populations that are reproductively isolated from other such populations.

Taxonomies and classification

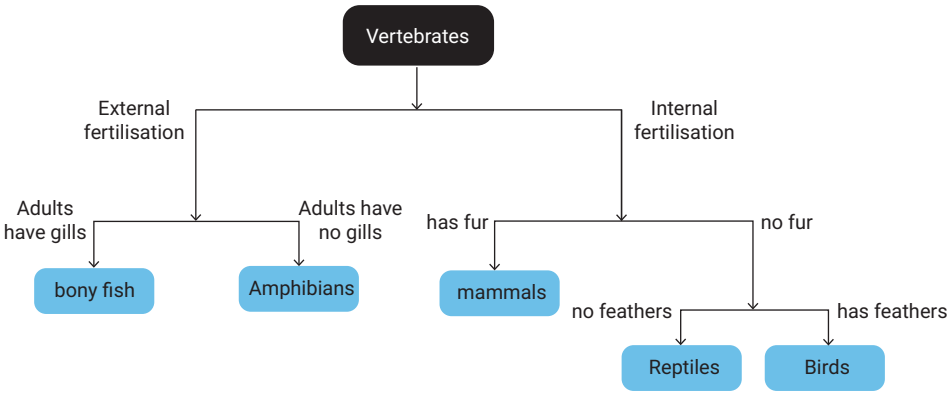
- Linnaean taxonomy is a hierarchical system of organisation that uses shared characteristics to group individual species together.
- Binomial nomenclature allows all organisms to be named according to a two-part naming system, based on Latin terms.
  - The name of the genus always begins with a capital letter.
  - The species name begins with a small letter.
  - The scientific names are always italicised.
  - When handwritten, the genus name and species name have to be underlined.

Crbellette/Shutterstock.com

Linnaean taxonomy of the platypus		
Domain	Three divisions of life based on cell structure	Eukarya
Kingdom	Highest level of organisation within domain Eukarya	Animalia
Phylum/division	Levels that become increasingly specific as organisms have more characteristics in common	Chordata
Class		Mammalia
Order		Monotremata
Family		Ornithorhynchidae
Genus	First part of binomial name. Name for closely related species	*Ornithorhynchus*
Species	Second part of binomial name. Organisms that share common characteristics and are capable of interbreeding	*anatinus*

Dichotomous keys

- A dichotomous key provides a sequence of paired statements about an observable trait that are mutually exclusive.



1a. Lower surface of the leaf is pale with a darker green upper surface . . . . . go to 2

1b. Both leaf surfaces are the same colour . . . . . go to 3

2a. Leaves generally pointed at each end and adult leaves 3–8 cm wide. Coarse, spongy bark that crumbles to dust without fibres. Gumnuts are usually cylindrical with fused valves at the opening . . . . . *Eucalyptus robusta*

2b. Adult leaves are <4 cm wide. Gumnut valves are not fused . . . . . go to 4

3a. Rough, fibrous, splintery bark covering most of the tree. Gumnuts are 1.5–2.5 cm long with ridges on the outside with buds up to 3 cm . . . . . *Eucalyptus planchoniana*

3b. Gumnuts and buds are not ridged and <1.5 cm long . . . . . go to 5

4a. Bark is slightly creased, grey on the surface and reddish underneath. Pointed buds about 2 cm long. Gumnuts have protruding valves . . . . . *Eucalyptus resinifera*

4b. Gumnuts have valves at or below rim level with rounded buds <1 cm long . . . . . go to 6

5a. Rough, fibrous bark in strips (not stringy). Buds are 7–11 mm long with gumnuts that have a stalk and a narrow rim. Leaves have a blueish tinge of colour and a symmetrical base . . . . . *Eucalyptus carnea*

5b. Fibrous and stringy bark that is grey with a red/brown base colour. Buds are 6 mm long and gumnuts have little or no stalk. Leaves are a silvery grey-green without a symmetrical base . . . . . *Eucalyptus tindaliae*

6a. Outer bark is reddish-brown and may have circular swellings with central holes. Long, slender stalks on rounded buds, while gumnuts have a tapered base . . . . . *Eucalyptus microcorys*

6b. Outer bark is grey or yellow with brown inner bark. Buds are oval and pointed 5 –7 mm long, while gumnuts are hemispherical . . . . . *Eucalyptus acmenoides*

CHAPTER EXAM

MULTIPLE CHOICE

1. Which of the following is not one of Linnaeus' taxa?
   - **A** Clade
   - **B** Family
   - **C** Phylum
   - **D** Species

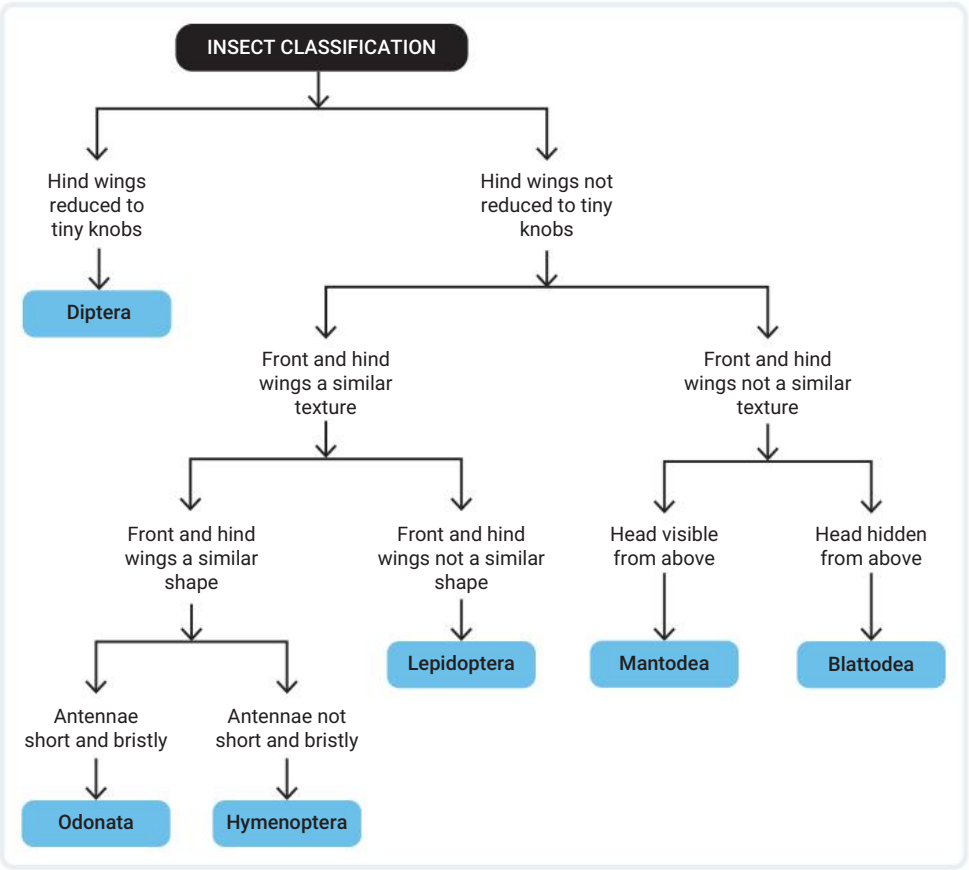
2. What is an infertile organism produced by the interbreeding of different species called?
   - **A** Hybrid
   - **B** Hubris
   - **C** Humus
   - **D** Heterozygote

3. The naming system initially developed by Linnaeus is:
   - **A** binomial nomenclature.
   - **B** genus nomenclature.
   - **C** Latin nomenclature.
   - **D** species nomenclature.

4. Which is the most general grouping in Linnaeus' taxa in the following list?
   - **A** Clade
   - **B** Family
   - **C** Phylum
   - **D** Species

5. Archaebacteria and Eubacteria are now considered to be separate domains because:
   - **A** Archaebacteria are multicellular.
   - **B** both have ribosomes.
   - **C** Eubacteria have a nucleus.
   - **D** there are differences in how DNA is stored.

Questions 6–10 refer to the following information.



6. What is the insect pictured on the right correctly classified as?

A Diptera
B Hymenoptera
C Lepidoptera
D Odonata

7. What is the insect pictured on the right correctly classified as?

A Diptera
B Hymenoptera
C Lepidoptera
D Odonata

8. Which feature would you expect to see in both Mantodea and Blattodea?

A Short, bristly antennae
B Head visible from above
C Tiny knobs for hind wings
D Front and hind wings a different texture

9. A feature that Odonata and Lepidoptera share is:
   - **A** short, bristly antennae.
   - **B** head not visible from above.
   - **C** front and hind wings a similar shape.
   - **D** front and hind wings a similar texture.

10. What should an insect with two obvious pairs of wings, wings of different textures with its head visible from above be classified as?
   - **A** Blattodea
   - **B** Diptera
   - **C** Mantodea
   - **D** Odonata

SHORT RESPONSE

11. **Explain** why one species concept is not able to account for all species, both living and extinct.

12. **Explain** why using attributes such as 'big' or 'small' are not suitable to use when developing a dichotomous key.

CROSS-CHAPTER QUESTION

13. **Predict** what changes would need to happen to Linnaean taxonomy if an Archaebacteria species was found to have mitochondria.

DATA ANALYSIS

Questions 14 and 15 refer to the following information.

puyalroyo/Shutterstock.com; Ken Griffiths/Shutterstock.com

Kingdom	Animalia	Animalia
Phylum	Arthropoda	Arthropoda
Class	Insecta	Insecta
Order	Lepidoptera	Lepidoptera
Family	Papilionidae	Papilionidae
Genus and species	*Papilio ulysses*	*Ornithoptera richmondia*

14. **Analyse evidence**
Compare the images and the information below the images for these two butterflies.

15. **Interpret evidence**
Deduce whether these two butterflies would be able to produce fertile offspring.

CHAPTER 2

Ecosystem diversity

Destinations Journey/Shutterstock.com

SYLLABUS DOT POINTS

SCIENCE UNDERSTANDING

- Describe genetic, species and ecosystem diversity.
- 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.

Introduction

Biodiversity refers to the variety of life on Earth, from genes to species to ecosystems. Not only do genes within species vary, but the types of species in an ecosystem and the ecosystems themselves also vary. The environmental conditions in an area can affect the survival, type, number and distribution of organisms that can live there. Some changes are cyclical, while others are caused by natural disasters and human activities. Measuring the types, abundance and distribution of species allows scientists to analyse species interactions, species diversity and ecosystem diversity. These measurements are useful when comparing and managing ecosystems across different areas and over time.

ASSUMED KNOWLEDGE

- ✓ Species are defined by a species concept, typically the biological species concept.
- ✓ A group of one type of species in an area is a population.
- ✓ If it is not possible to count every individual, a population estimate can be calculated.
- ✓ Abiotic factors are non-living.
- ✓ Biotic factors are living.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ describe the different levels of diversity: genetic, species and ecosystem
- ✓ analyse data to describe species richness and evenness (relative species abundance)
- ✓ analyse data to calculate percentage cover, percentage frequency and Simpson's diversity index (SDI)
- ✓ investigate an ecosystem, using appropriate data collection methods for the diversity measure being used, including sampling method, sampling technique and minimising bias
- ✓ describe how different types of biotic factors – food availability, competition for resources, predation, disease – influence the distribution and abundance of species
- ✓ describe how different types of abiotic factors – space, shelter, availability of water, nutrients, environmental conditions – influence the distribution and abundance of species
- ✓ explain how the uniform, random or clumped distribution of species depends on the availability of the required habitat or microhabitat
- ✓ explain how the uniform, random or clumped distribution of species affects the choice of sampling technique, validity and reliability of data collected
- ✓ when given data, explain how abiotic factors affect the distribution, abundance and/or biodiversity of species in an ecosystem
- ✓ when given data, correctly classify and name ecosystems using Specht's classification system and the Holdridge life zone classification scheme.

Weblinks

What is biodiversity and why is it important?

Australia's biodiversity

Biodiversity in Queensland

2.1 Genetic, species and ecosystem diversity

biodiversity the full range of living things in a particular area or region; it can be described at various levels, including genetic differences, different species or types of ecosystems in a larger area

ecosystem a self-sustaining unit consisting of the interactions between the species present and their environment

The variety of life is called **biodiversity**, and the term can apply to the planet as a whole or to individual locations. Biodiversity is recognised for the vital role it plays in the long-term stability of species, communities and **ecosystems**. Consequences of low biodiversity include inbreeding, vulnerability to disease, over-predation and ecosystem breakdown. In this context, a species is a group of organisms that share a gene pool; all members of the same species can breed with each other to produce fertile offspring as long as they are not prevented by a physical barrier.

Biodiversity can also refer to three different levels of study: genetic, species and ecosystem. Genetic diversity is the range of genes within a species. Species diversity is the range of species in an ecosystem. Ecosystem diversity is the range of ecosystems in a particular location. The level of study most commonly referred to is species diversity.

Genetic diversity

Genetic diversity describes the combined differences in DNA of all the individuals in a species. The resulting variation in characteristics of individuals makes it possible for at least some members of the species to survive when the environment changes. Small, isolated populations typically have lower genetic diversity. Large and well-connected populations are the most effective way to retain genetic diversity.

genetic diversity the combined differences in DNA of all the individuals in a species

Species diversity

Species diversity is the number of different species in an area. Determining the number of species on Earth is extremely challenging. Estimates vary from 500 000 to 10 million, depending on the type of mathematical analysis used. One study on the diversity of microbes estimates that the number of microscopic species could be in the billions. Approximately 1 million animal species, 200 000 plant species and 45 000 species of fungi have been named, described and catalogued so far, with more species discovered every day.

Australia has one of the most diverse ecologies in the world, with more than 7300 species of native vertebrates, including mammals, birds, reptiles, amphibians and fish. There are also more than 21 000 species of native plants, of which 18 700 are flowering plants. More than 80% of these species are endemic – they can only be found in Australia (Figure 2.1.1).

The Natural History Museum/Alamy Stock Photo

FIGURE 2.1.1 British scientist and explorer Joseph Banks (1743–1820) gave scientific names to hundreds of plant genera in Australia. One plant genus was named after him – the banksias, such as this *Banksia serrata*.

Syllabus links
Chapter 12 discusses adaptations and survival.
Chapter 13 discusses genetic diversity in more detail.

Ecosystem diversity

An ecosystem is composed of all the living organisms and their interactions (**biotic factors**) together with the physical environment (**abiotic factors**) in one particular area. Within an ecosystem, the **communities** of organisms and the physical conditions tend to be fairly uniform. All the components of an ecosystem are tightly linked through the cycling of nutrients and raw materials within it. These include carbon dioxide, oxygen, water, nitrogen, phosphorus and many other minerals, as well as the living organisms that transfer energy and matter through the system. In most systems, the energy is initially transformed from light to chemical energy, through photosynthesis, and then transferred between organisms through **food webs**. Each ecosystem may have a different combination of climate, geology, landforms, native vegetation and species. Each of these contribute to the diversity of ecosystems in Australia, including the Great Barrier Reef, reef kelp forests, wet tropical rainforests, mangrove forests, tropical savanna and arid zones.

biotic factor a living component of an ecosystem, including animals, plants and bacteria

abiotic factor a non-living component of an ecosystem, including the physical landscape, minerals and weather conditions

community groups of different species in an area and their interactions

food web a diagram of interconnecting food chains that shows how different organisms feed on each other, thereby transferring energy and matter through an ecosystem

Syllabus link
Chapter 4 discusses cycles of matter and energy.

LEARNING CHECK 2.1

DESCRIBING

1 **Define**:
   - **a** species
   - **b** ecosystem.

2 **Describe** the three types of biodiversity.

APPLYING

3 **Explain** why all types of diversity are important in an ecosystem.

2.2 Determining species diversity

Five common measures are used, often together, to describe the diversity of the species in an ecosystem: species richness, species evenness, percentage cover, percentage frequency and Simpson's diversity index (SDI).

Species richness

species richness the number of species in an ecosystem

Species richness refers to the number of species in an ecosystem and is shown by a whole number. Although this seems like a good measure of diversity, it does not take into account how many of each species are present or the nature of their interactions. For example, an ecosystem that consists almost entirely of one invasive species such as *Lantana* (Figure 2.2.1) but has three other species not yet killed by its presence has a species richness of 4. However, an ecosystem that has three native species with only a small amount of one *Lantana* species, or that has four native species, also has a species richness of 4. To correct this, ecologists also look at species evenness.

Sharohyip/Shutterstock.com

Gurcharan Singh/Shutterstock.com

FIGURE 2.2.1 (a) *Lantana camara* and (b) *Lantana montevidensis*. All *Lantana* species are Category 3 restricted invasive plants under the *Biosecurity Act 2014*.

Species evenness (relative species abundance)

Species evenness (or **relative species abundance**) refers to how many of each species are present. This can be more difficult to count, because many plant species, such as grasses, have runners that make it difficult to decide what an individual plant is (Figure 2.2.2). Regardless, this measure enables ecosystems with one dominant species (the highest number of individuals) to be differentiated from ecosystems with a more numerically equal species distribution. An ecosystem is generally considered healthier if it has similar numbers of individuals in each species.

species evenness (relative species abundance) the number of individuals of each species in an ecosystem

William Edge/Shutterstock.com

FIGURE 2.2.2 Grasses are particularly difficult to count individually.

Percentage cover

Percentage cover is an estimate of the percentage of an area (typically a **quadrat**) being occupied by a particular species or vegetation as a whole. Grasses and other plants that can be difficult to count individually are better approximated with this measure. Vegetation cover is an important indicator because it reflects the amount of soil, water and nutrients available to the plant(s) at a site.

percentage cover the percentage of an area occupied by a species

quadrat a frame used to set a standard area for sampling

Percentage frequency

Frequency is the number of times a plant species occurs in a given area (typically a quadrat) and is usually expressed as a percentage frequency. When **percentage frequency** is provided, it gives the probability that a species will be found within a single quadrat or the proportion of quadrats that contain a particular species. It is most often used to detect changes in vegetation composition over time. Percentage frequency is calculated using the following equation:

percentage frequency the probability that a particular species will occur in a quadrat; the proportion of quadrats that contain a particular species

$$\text{Percentage frequency (\%)} = \frac{\text{number of quadrats in which the species is found}}{\text{total number of quadrats}} \times 100$$

Note that percentage frequency doesn't take into account the size of the plant, so although it is a measure of abundance, it should not be used to compare abundance across sites. By noting how many of the quadrats in a sample have a particular species, ecologists can make a more accurate assessment of how abundant a species is in the ecosystem.

Simpson's diversity index

Simpson's diversity index (SDI) the combined ratio of individuals in each species to the total individuals in an ecosystem – a quantitative measure of biodiversity

Simpson's diversity index (SDI) is a number between zero (no diversity) and one (infinite diversity), and accounts for both species richness and relative species abundance. A value closer to 1 denotes good biodiversity. The value also represents the probability that two randomly selected individuals from a sample belong to different species. Increased richness increases the index, as does greater evenness of individuals.

KEY FORMULA

Simpson's diversity index

$$SDI = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$$

where: n = number of individuals of each species

N = total number of individuals at the site.

Table 2.2.1 shows data gathered for two open forests in Queensland.

TABLE 2.2.1 Data gathered from two open forests in Queensland

Genus	Site 1			Site 2		
	Number of individuals (n)	$n-1$	$n(n-1)$	Number of individuals (n)	$n-1$	$n(n-1)$
Eucalyptus	2	1	2	1	0	0
Melaleuca	6	5	30	0	−1	0
Acacia	3	2	6	3	2	6
Diuris	1	0	0	1	0	0
Grevillea	9	8	72	12	11	132
		$\Sigma n(n-1) = 110$			$\Sigma n(n-1) = 138$	
	N	$N-1$	$N(N-1)$	N	$N-1$	$N(N-1)$
Total individuals (N)	21	20	420	17	16	272
Simpson's diversity index	$SDI = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$ $= 1 - \frac{110}{420}$ $= 0.738$			$SDI = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$ $= 1 - \frac{138}{272}$ $= 0.493$		

When completing the SDI calculation, ensure that at least one step of value substitution is shown in the calculation. In the example given in Table 2.2.1, the Simpson's diversity indices for sites 1 and 2 are 0.738 and 0.493, respectively. This means that site 1 is considerably more biodiverse than site 2. The number of individuals of the five species at site 1 (2, 6, 3, 1, 9) are

more evenly spread than the four species at site 2 (1, 0, 3, 1, 12), which is dominated by *Grevillea*. SDI also considers that species with only one individual present do not contribute to the overall health of the ecosystem. SDI may be presented to two or three decimal places.

LEARNING CHECK 2.2

DESCRIBING

1 State the five indicators used to determine diversity of species.

APPLYING

2 **Explain** the difference between species richness and species evenness.

3 **Explain** why percentage cover can be a better indicator than species evenness for plants such as grass.

4 **Calculate** the Simpson's diversity index for a section of Moreton Bay with 36 flathead, 720 Australian bass, 934 garfish, 60 pearl perch and 14 tailor.

habitat a location that meets all of the conditions for an organism's survival

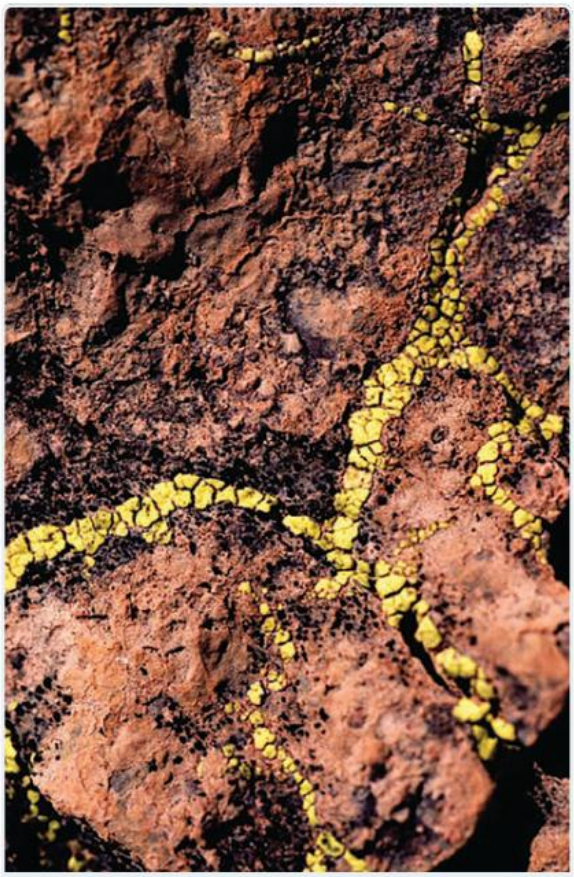
microhabitat a smaller location within a habitat

Weblink
Habitats

2.3 Habitats

An ecosystem encompasses both living and non-living (biotic and abiotic) parts, including the interactions among species and the environment. Ecosystems are composed of various **habitats**. A habitat is a geographic location that meets all of the conditions an organism needs to survive including shelter, food, water and appropriate physical environment. Some organisms have very specific habitat requirements while others have a broad set of survival conditions.

A **microhabitat** is a smaller part of the habitat that experiences different amounts of factors such as light, temperature and humidity, making this smaller part of the larger habitat suitable for a specific organism. An example can be seen in the Australian desert, where lichens grow in the microhabitats of rock crevices (Figure 2.3.1), because the cracks funnel and collect water in a way that is not possible on the top smooth surface of the rock.



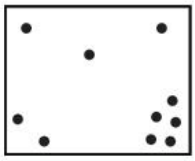
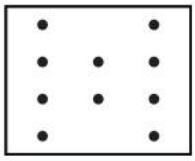
Atlas of Living Australia/Fagg, M.

FIGURE 2.3.1 Yellow 'veins' of the lichen *Acarospora citrina* and brownish-orange 'veins' of a species of the lichen *Caloplaca* growing along microhabitats in cracks or surface irregularities on rock in semi-arid Australia

Factors affecting distribution and abundance within a habitat

Abundance is the number of individuals of a species in a habitat. Distribution is the spatial location of organisms in the habitat. Environmental conditions such as pH, temperature, salinity, light intensity and wind speed/direction affect the ability of organisms to survive in a particular area, depending on their unique needs and tolerance limits, affecting their abundance and distribution. Distribution patterns typically fit into three categories: random, uniform and clumped **(Table 2.3.1)**.

TABLE 2.3.1 A summary of factors affecting distribution

	Random	Uniform	Clumped
Diagram			
Example	Forest  Maralee Park/Shutterstock.com	Territorial animals  Butler Stock Photography/ Shutterstock.com	Schooling fish  Paul Cowell/Shutterstock.com
Description	Individuals are spaced in no predictable pattern – the location of one organism does not affect the location of any other organism. More often seen in plants, especially with wind dispersed seeds.	Individuals are equally spaced apart – the presence of one organism determines how close or far away another organism will be.	Individuals are gathered in groups (the group is often the population).
Biotic factors	• Food is distributed randomly or uniformly. • Competition is sporadic. • Other interactions are limited.	• Food is distributed uniformly. • Territorial defensive behaviours are displayed. • Competition for resources keeps organisms evenly spaced.	• Food is located in one area. • Social behaviours such as herding or pack hunting are displayed. • Disease mostly affects closely packed individuals because transmission of infectious particles is more likely.
Abiotic factors	Resources and the environment change in unpredictable ways.	One or more environmental resources is limiting, and organism distribution maximises individual access to the resource.	Reflects that the required resources exist only in one area of the habitat.

The map in **Figure 2.3.2** shows the distribution of frog species across Australia, based on biotic and abiotic factors, including rainfall, temperature and competitors.

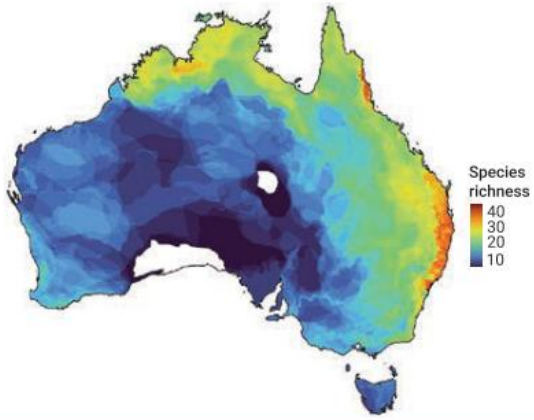


FIGURE 2.3.2 Frog species richness across Australia (the number of species present in each region) changes as biotic and abiotic factors change. The large white areas in southern and central Australia are where no frog species have been documented.

The factors listed in Table 2.3.1 also influence the abundance of organisms, as shown in **Figure 2.3.3**.

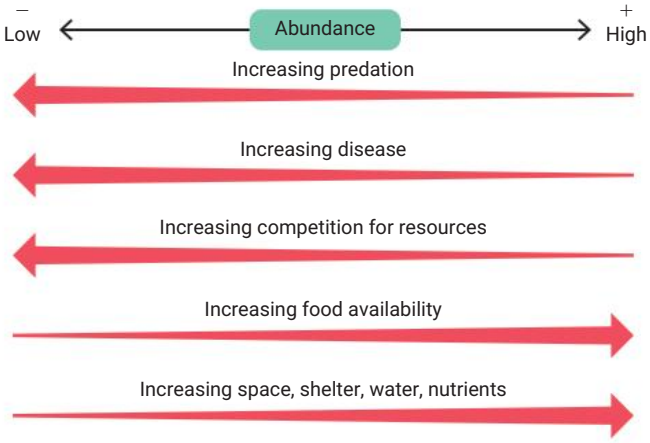


FIGURE 2.3.3 How different factors affect the abundance of organisms

LEARNING CHECK 2.3

DESCRIBING

1 **Describe** the three different ways that organisms can be distributed.

2 List three abiotic factors that affect the distribution of organisms.

APPLYING

3 **Explain** why disease can affect the distribution of organisms.

ANALYSING

4 **Compare** 'habitat' and 'microhabitat'.

2.4 Sampling

Ecological sampling is the process of collecting data to obtain information about ecosystems or habitats to see what species are present, and how they are changing over time. It is impossible to count every organism of every species, so designated areas of ecosystems are sampled in a standard way. The type of sampling depends on the environment and the information needed. Ecologists consider the sampling technique, sampling method, bias minimisation and measure(s) of diversity.

Science Photo Library

FIGURE 2.4.1 Quadrat sampling requires observations of the percentage cover or number of species in the frame.

Sampling techniques

Quadrats

For organisms that are fixed or do not move very much, the quadrat method of sampling can be used to collect data about species richness, evenness, percentage cover and percentage frequency, and allow for SDI to be calculated **(Figure 2.4.1)**. (This method can also be used to calculate density, but this is not stated in the syllabus.)

A quadrat is a fixed area commonly measured at ground level. The size of the quadrat is determined by the organism being studied, although 1 m^2 quadrats are common. For each quadrat, the number of individuals of each species is counted or the percentage of the quadrat covered is determined and then recorded. Quadrats may be used on tree trunks for lichen, under water on coral reefs/sea grasses or in a canopy for epiphyte studies. The use of quadrats does not consider any environmental gradients.

transect a narrow section taken straight across an area, along which observations or measurements are made

Transects

A line **transect** is a line drawn through a community to provide a site for sampling **(Figure 2.4.2)**. The species touching the line are recorded, either the whole way along the line (continuous line transect) or at marked points along the line (point intercept line transect). The information gathered about the

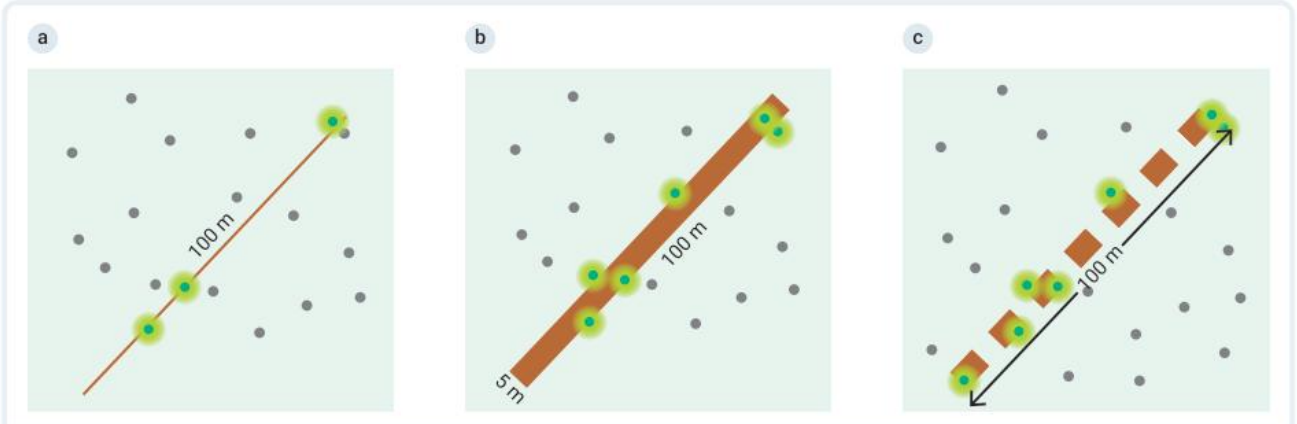


FIGURE 2.4.2 (**a**) A line transect, (**b**) a continuous belt transect and (**c**) an interrupted belt transect. Transects allow ecologists to profile habitats with an environmental gradient.

presence or absence of species on this line is used to determine the distribution of species against an environmental gradient (zonation) and it can give an indication of species richness. Again, this is a useful method when species are fixed in place.

For a belt transect, the line is widened to form a continuous belt transect. A width of 1 m is commonly used. Alternatively, quadrats are placed along the transect line at specific points forming an interrupted belt transect. This allows for data on abundance of species in specific locations to be recorded, as well as species presence or absence along the environmental gradient. However, if the intervals are too large, then some species will not be recorded, and some zonation patterns will be missed. Too small an interval can make the sampling very time consuming, and yield more data than is useful.

Mark Carwardine/Nature Picture Library

FIGURE 2.4.3 The Cook Strait giant weta *(Deinacrida rugosa)* is an insect endemic to New Zealand. It was extinct in the wild for more than 100 years. But since 2007, captive-bred animals have been tagged (blue tag) and re-released. The species is now considered endangered.

Capture–recapture

One of the most common sampling methods for mobile species, such as animals, is capture–recapture. This method involves capturing several individuals, marking them and releasing them (Figure 2.4.3). Later, individuals are recaptured and the proportion of marked to unmarked individuals is used to estimate the population size.

For this technique, animals are captured randomly in cages, pitfall traps, nets or light traps. The markings are usually paint or tags. They must not harm the organism, make the organism obvious to predators or affect its usual ability to survive. The timing of the recapture needs to ensure marked organisms have had the opportunity to mix back into the population but are unlikely to have died or emigrated. The values recorded are used in the Lincoln index to calculate an estimate of the abundance of the organism.

Syllabus link
Chapter 3 discusses the Lincoln index and estimating population numbers from sampling data.

Sampling methods

Random

In **random sampling**, each part of the sample area has an equal chance of being included and counted. It is typically used when the study area is large, there is limited time and/or the species appear to be uniformly distributed. A grid is marked out with an *x*-axis and a *y*-axis. A random-number generator provides coordinates for quadrat placement. This removes observer bias when placing quadrats, but some areas can be difficult to sample this way because of the size of the organisms (e.g. trees in a forest).

Weblink
Sampling techniques

Systematic

Systematic sampling occurs when data is collected at fixed intervals, usually along a line or transect that shows an **environmental gradient**, such as a slope or distance from a source of pollution.

Stratified

Stratified sampling is a method where a proportionate number of observations is taken from each different stratum (zone with similar characteristics) in the sample area. When the abiotic and biotic factors vary widely across an ecosystem, stratified sampling can ensure the data reflects a more accurate portrayal of the area. To begin, the area is divided into relatively similar subsections called **strata** (singular: stratum). The entire area to be analysed must be divided completely and neighbouring strata cannot overlap (Figure 2.4.4).

random sampling a sampling method that ensures each part of the sample area has an equal chance of being counted

systematic sampling a sampling method that occurs at fixed intervals, typically along an environmental gradient

environmental gradient a gradual change in an abiotic factor over distance

stratified sampling a sampling method that divides an area into strata for separate sampling

stratum a layer or subsection of a whole

Worksheet
Ecological sampling

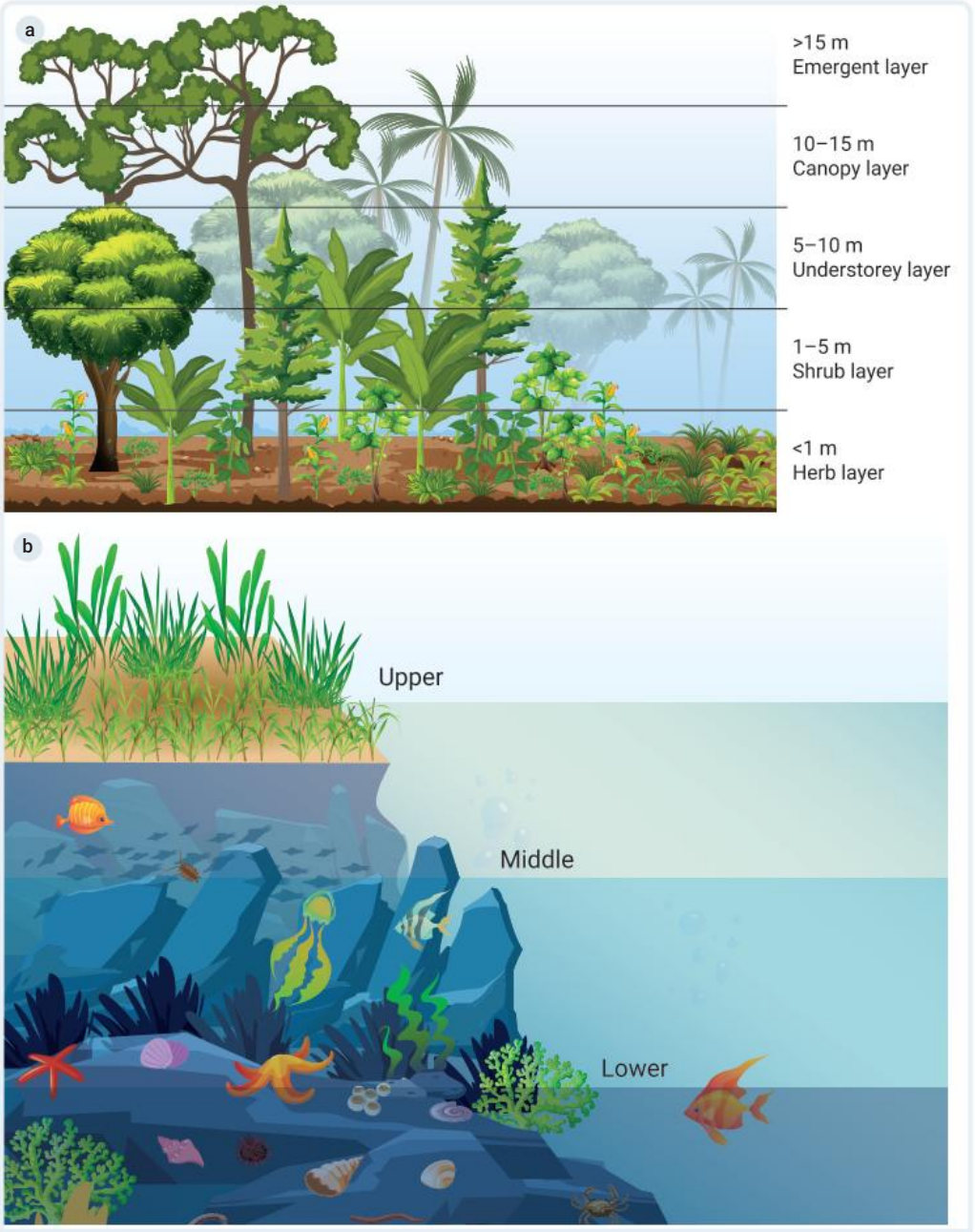


FIGURE 2.4.4 Strata can be arranged (a) vertically or (b) horizontally but cannot overlap or leave gaps.

The number of samples taken from each stratum must match the percentage of the area that the stratum occupies. For example, if vegetation cover in an area of woodland is 60 per cent acacia and 40 per cent bottlebrush, take 60 per cent of the samples from within acacia woodland and 40 per cent of the samples from within bottlebrush (Figure 2.4.5).

This method requires prior knowledge of the environment and selection of an appropriate size of sample area. The boundaries between strata should be as defined as possible. Obvious boundaries make it easier to determine if the sampling is representative of the area.

validity (of sampling) how well a population is accurately represented by the sample collected using the selected methods/techniques

reliability (of sampling) whether the sampling methods/techniques produce the same results when repeated

Validity and reliability

The **validity** and **reliability** of sampling techniques and methods are affected by the distribution of species within a habitat. When deciding how to collect data, consider the species

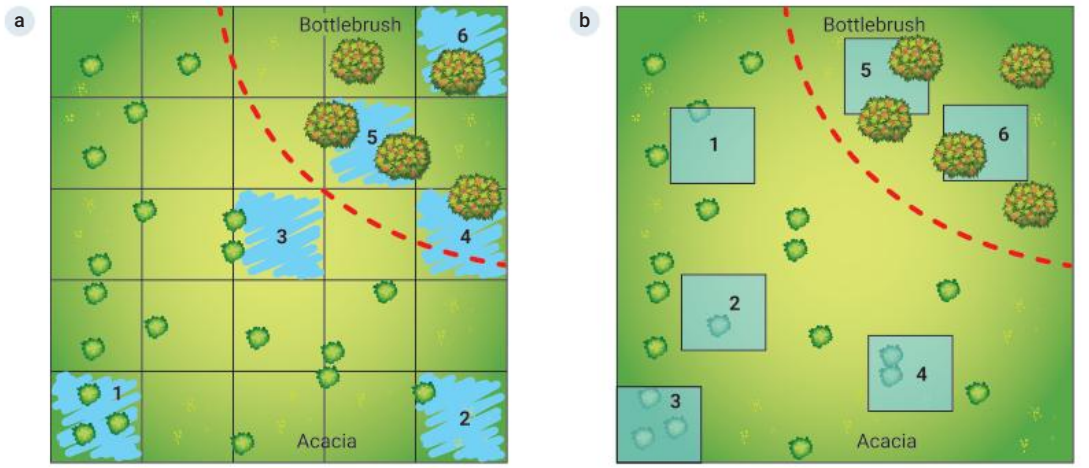


FIGURE 2.4.5 (a) Random sampling often produces quadrats of mixed habitat and ignores the relative sizes of those habitats in the ecosystem. In this case, the bottlebrush will be sampled in three quadrats, while the much larger acacia habitat will also be sampled three times. The data will represent that there are equal proportions of these two habitats despite that not being the case. (b) Stratified sampling divides the area into habitat-based strata and randomly samples from each stratum, which means a more accurate proportion of quadrats can be taken from each habitat area.

distribution. Sampling validity refers to how accurately the sample collected by the selected methods represents the population. For example, if the habitat has distinct strata but stratified sampling is not used, the data collected is not representative of that population or habitat.

Reliability refers to whether the sampling methods or techniques produce the same results when repeated. The more consistent the results are, the more likely the methods or techniques are reliable and not being influenced by unknown factors.

Note that, despite all efforts, sampling may not always be representative of the population or environment. Small or rare habitats may be missed. Other cyclical changes, such as seasonal changes or day and night, may be missed if data is only recorded at one point in time. For example, nocturnal animals such as the Australian boobook owl (*Ninox boobook*) would not be counted in a daytime sampling, and the bulbine lily (*Bulbine bulbosa*) flowers in summer and then dies off in winter and would not be captured with winter sampling.

Strategies to minimise bias

Size and number of samples

The more samples taken, the more likely it is that the data collected is representative of the community. The minimum number of samples required to be representative of a particular habitat can be ascertained by graphing the number of species recorded, as a function of the number of samples examined **(Figure 2.4.6)**. Once the number of species is constant, the ideal number of quadrats can be identified. Make the quadrat big enough to include at least one of the species of interest, but small enough that counting can be done in a reasonable amount of time. Typically, larger quadrats are required for sparse vegetation than for dense vegetation. Fewer and smaller quadrats are required for uniform vegetation distribution than for diverse and varied vegetation. A transect line should span the area or environmental gradient of interest.

Random-number generators

A random-number table or generator removes human bias by choosing random pairs of numbers to use as coordinates on a grid.

Weblinks
Sampling methods
Estimating population size via random sampling

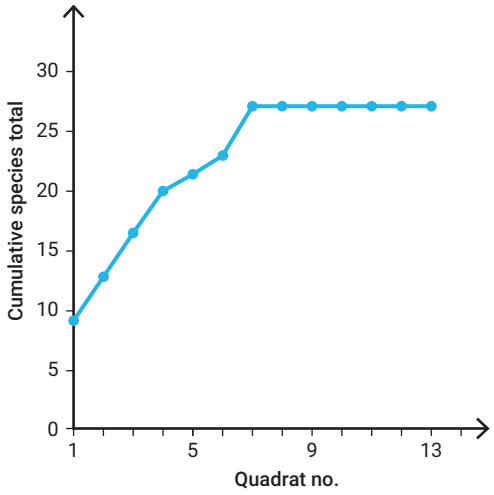


FIGURE 2.4.6 An example of a survey showing cumulative species totals with increasing numbers of quadrats used. This shows that seven or eight quadrats should be sufficient when sampling this area.

Counting criteria

Set strict criteria for how much of the organism must be within the quadrat to include it in a count. For example, count every plant that is touching the left and top quadrat boundaries as well as those entirely within the quadrat. Alternatively, the stem must be inside the quadrat, even if the foliage is not. If it is difficult to determine what constitutes an individual plant, decide what criteria to use for individuality (e.g. for groundcover plants and grass runners) because a percentage cover may be more effective than counting individuals.

Calibrating equipment and noting associated precision

Calibrate equipment for abiotic sampling immediately before use and note the associated precision of the instrument in the data. Correct calibration means ensuring that the device being used to take readings is reading correctly. A precise measuring instrument is one that can measure values in very small increments. The last digit that can be read from the equipment is the first value with measurement uncertainty. The uncertainty of analogue instruments (e.g. a tape measure) is plus or minus half of the smallest division. For digital instruments, the last place value that can be read from the equipment is the measurement uncertainty. For example, an instrument that measures to three decimal places has an uncertainty of ± 0.001.

LEARNING CHECK 2.4

DESCRIBING

1 **Describe** stratified sampling.
2 State the main features of the quadrat and transect sampling methods.
3 State two ways to minimise bias when sampling.

APPLYING

4 **Explain** why quadrat and transect sampling are not generally useful for sampling animals.

5 **Explain** three factors that may contribute to two ecologists sampling the same ecosystem but producing drastically different species diversity measures.

6 **Explain** how species diversity may differ in the same place at different times.

7 Give two reasons why stratified sampling is more accurate than true random sampling for ecosystems with a wide variety of habitats.

2.5 Interpreting data to classify and name ecosystems

Holdridge life zones

The Holdridge model is a system of large-scale zoning of vegetation correlated to simple climatic data. Each unit, or life zone, is based on biotemperature, precipitation (P), potential evapotranspiration (EVP), EVP/P ratio or potential evapotranspiration ratio (PER), latitude and altitude **(Figure 2.5.1)**.

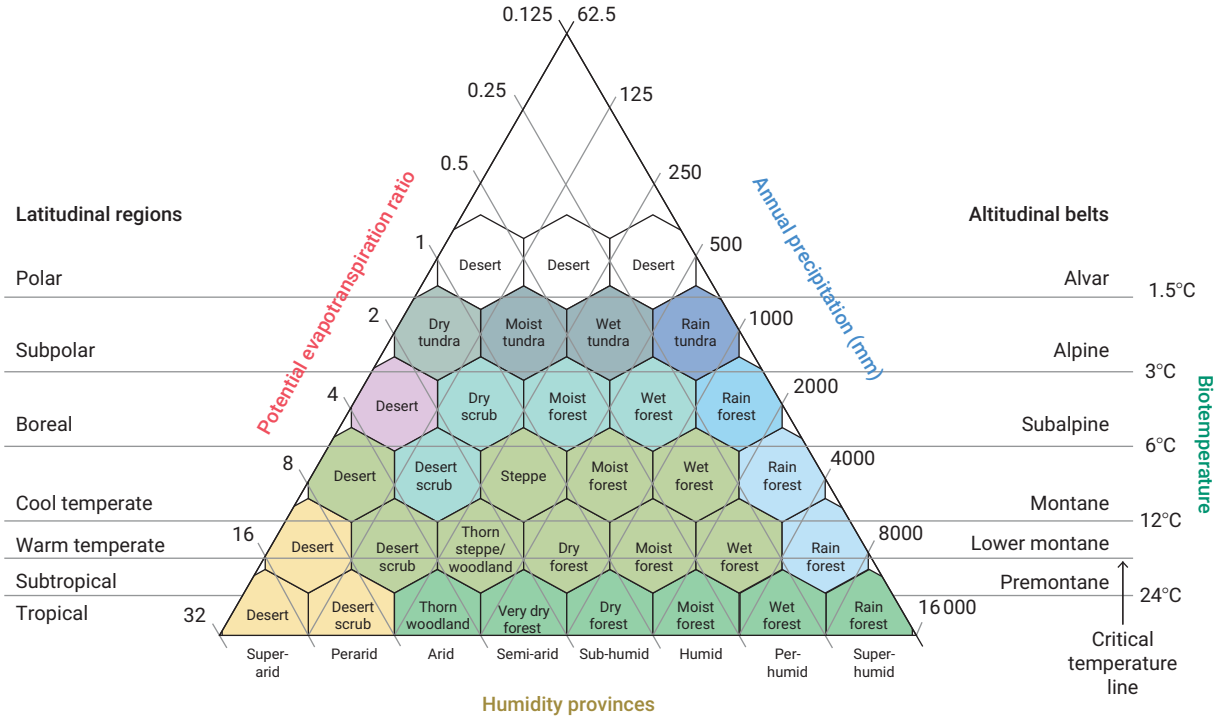
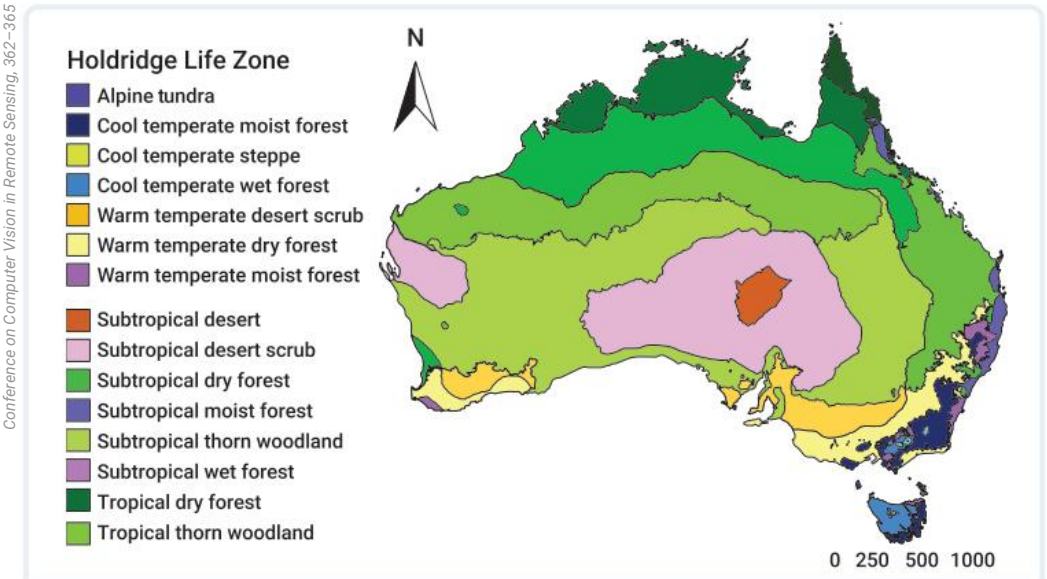


FIGURE 2.5.1 A representation of the Holdridge life zone categories

Using two key climate variables – average annual precipitation (the annual total) and annual average biotemperature (mean monthly temperatures) – it is possible to define an ecological 'life zone'. A third variable, such as PER, may also be used. Note that the choice of measurement may lead to different outcomes when using this information.

The point at which lines drawn parallel to the direction of the chosen climatic data factor intersect will provide the name of the life zone. **Figure 2.5.2** shows Australian life zones.



Jia, M., Liu, D., Song, K., Wang, Z., & Ren, C. (2012). Mapping biomes of Australia based on the Holdridge Life Zone Model. *2012 International Conference on Computer Vision in Remote Sensing*, 362–365

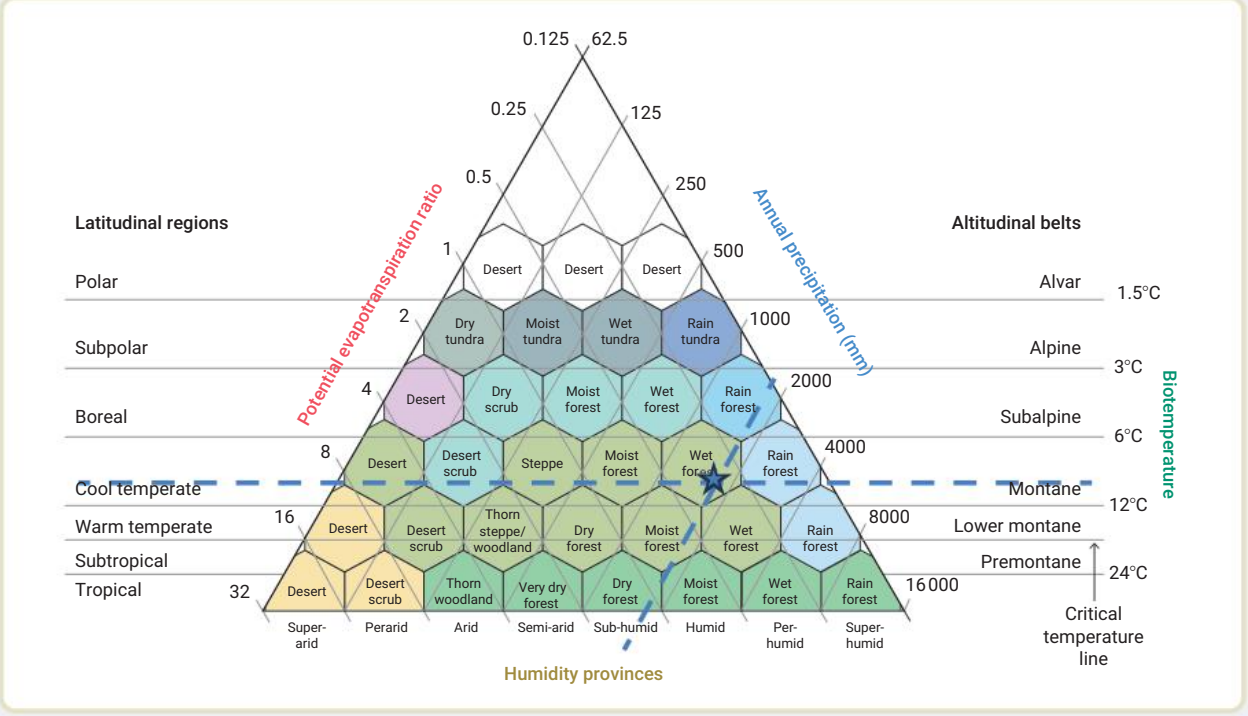
FIGURE 2.5.2 Biomes of Australia based on the Holdridge life zone model

WORKED EXAMPLE 2.5.1

Use Figure 2.5.1 to determine the life zone for an area with mean annual biotemperature of 10°C and annual precipitation of 1800 mm.

ANSWER

A horizontal line at 10°C and a diagonal line at 1800 mm intersect at 'wet forest'.

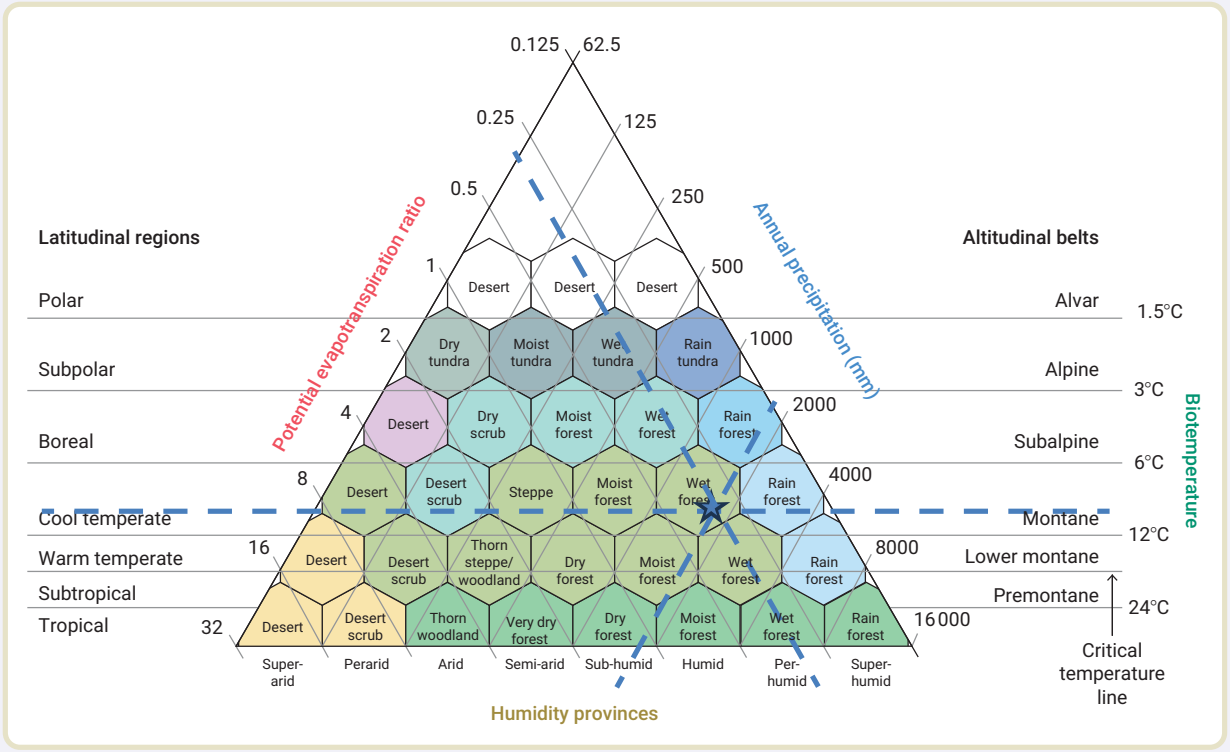


WORKED EXAMPLE 2.5.2

Use Figure 2.5.1 to determine whether the life zone changes if a further factor of PER 0.30 is included.

ANSWER

A diagonal line at 0.30 intersects in the same life zone of 'wet forest'.

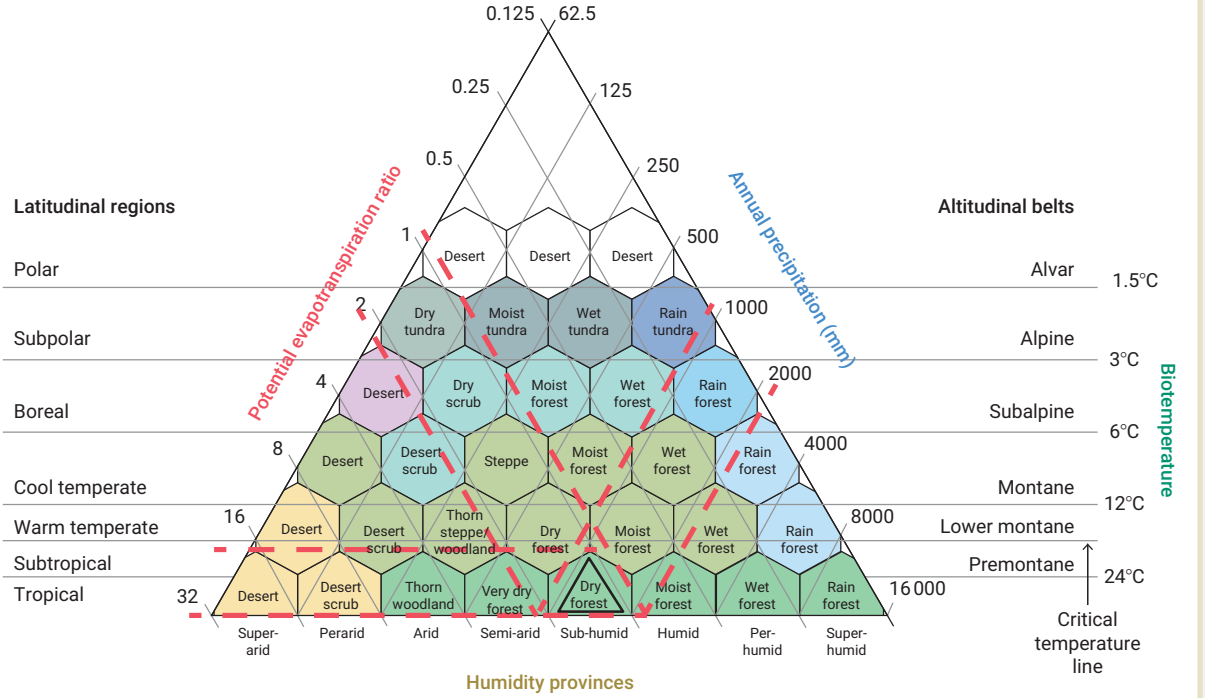


WORKED EXAMPLE 2.5.3

Look at the map of Australian life zones in Figure 2.5.2. With the aid of Figure 2.5.1, identify the mean annual biotemperature, annual precipitation and PER for Far North Queensland (dark green).

ANSWER

This is tropical dry forest: biotemperature >24°C, precipitation 1000–2000 mm, PER 1–2.



Worksheet
Influences on distribution and abundance

Specht's classification

In 1970, Raymond Louis Specht, then Professor of Botany at the University of Queensland, developed an ecological classification system to account for the variation in Australian landscapes. This system relies on two factors: the height of the tallest vegetation layer (or stratum) present and the approximate percentage cover of this layer of foliage. A later modification includes the genus or the common name of the dominant species.

Table 2.5.1 is the key to Specht's classification system. A tree is a woody plant more than 5 m tall, with a single trunk. A shrub is a woody plant less than 8 m tall, frequently with many stems arising at or near the base. **Figure 2.5.3** shows the differences between hummock grasses, tussock grasses and sedges. The map in **Figure 2.5.4** shows the major vegetation types in Australia, based on Specht's classification.

TABLE 2.5.1 Specht's ecological classification system

Tallest vegetation		Approximate foliage cover of tallest vegetation (%)				
		<10	10–30	30–50	50–70	70–100
Trees	>30 m		Tall woodland	Tall open forest	Tall forest	Tall closed forest
	10–30 m	Open woodland	Woodland	Open forest	Forest	Closed forest
	<10 m	Low open woodland	Low woodland	Low open forest	Low forest	Low closed forest
Shrubs	<2 m	Tall open shrubland	Tall shrubland	Open scrub	Scrub	Closed scrub
	0.25–2 m	Open shrubland	Shrubland	Open heathland	Heathland	Closed heathland
	<0.25 m	Dwarf open shrubland	Dwarf shrubland			
Hummock grasses		Open hummock grassland	Hummock grassland			
Tussock grasses		Open grassland		Grassland		Closed grassland
Sedges		Open sedgeland		Sedgeland		Closed sedgeland
Flowers		Open herbland		Herbland		Closed herbland
Ferns				Fernland		Closed fernland

Genevieve Vallee/Alamy Stock Photo

iStock.com/Ykkaa; Auscape/Universal Images Group/Getty Images

FIGURE 2.5.3 (a) Hummock grasses develop as a large, well-defined mound of grass, (b) tussock grasses grow in clumps that are not well defined or in mounds, and (c) sedges grow as individual plants with strong, sharp leaves.

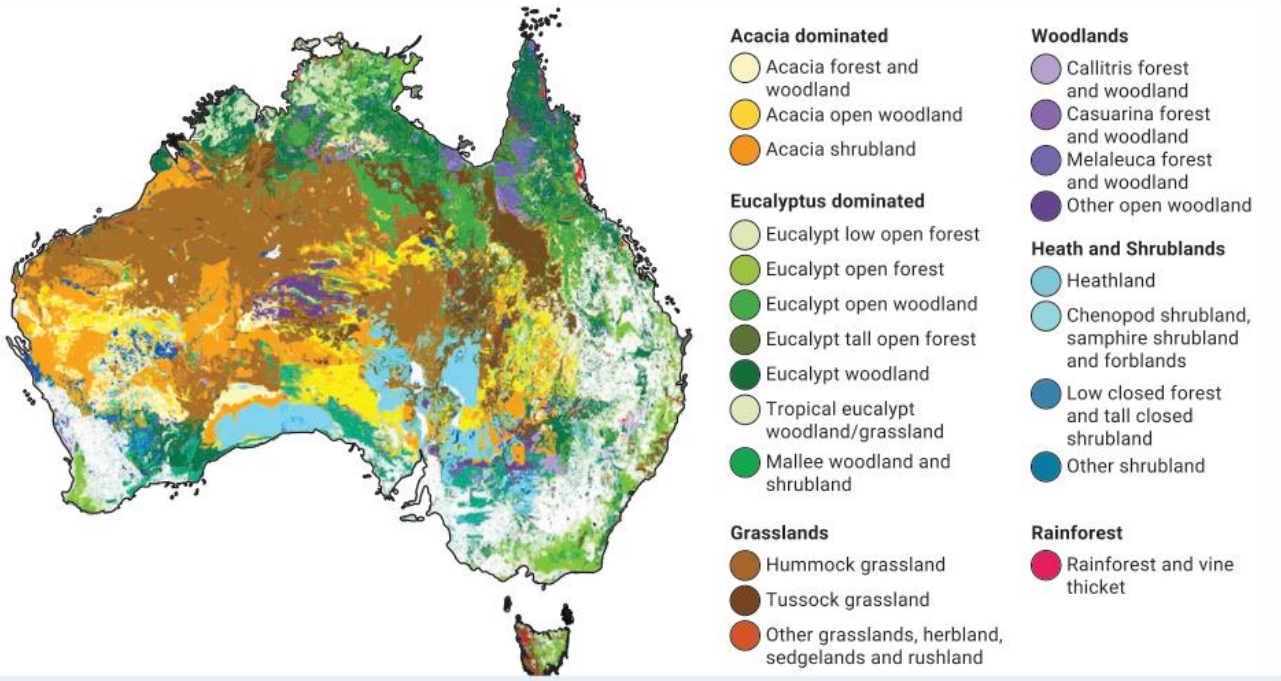


FIGURE 2.5.4 A map of major vegetation types in Australia, based on Specht's classification

WORKED EXAMPLE 2.5.4

Use Table 2.5.1 to determine the ecosystem whose tallest vegetation layer is 2–3 m shrubs that cover 40 per cent of the land area.

ANSWER

Shrubs <2 m (first column, fourth row) and 30–50 per cent cover (top row, third column) intersect at open scrub.

WORKED EXAMPLE 2.5.5

Use Table 2.5.1 and Figure 2.5.4 to identify the tallest vegetation and approximate foliage coverage for Far North Queensland (mid-green).

ANSWER

Mid green is on the key in Figure 2.5.4 as open woodland. The table has only one cell with open woodland; it has 10–30 m trees and 10–30 per cent foliage cover.

WORKED EXAMPLE 2.5.6

Use Table 2.5.1 to determine the ecosystem where the dominant species is *Corymbia clarksoniana* at a height of 15–20 m with 80 per cent cover.

ANSWER

Table 2.5.1 shows that 15–20 m trees with 80 per cent cover intersect at closed forest. When naming ecosystems with Specht's classification, the genus of the dominant species is listed first, so this is a *Corymbia* closed forest.

LEARNING CHECK 2.5

DESCRIBING

1 State two factors that can be used to determine a Holdridge life zone.

2 State two factors that are used to name an ecosystem according to Specht's classification.

INTERPRETING

3 Data was collected from an ecosystem and is summarised in the following table.

Dominant tree	Tree height	Foliage cover	Biotemperature	Annual precipitation	PER
Eucalypt	>30 m	40%	20°C	1800 mm	0.8

Determine the type of ecosystem present according to:

a Holdridge life zones

b Specht's classification.

2.6 Collecting and interpreting environmental data

Instructions for gathering environmental data

The environmental conditions in an area can have a big impact on the type and number of organisms that can live there. Observing the abiotic factors can give ecologists a better idea of how an ecosystem is functioning.

Table 2.6.1 shows common abiotic factors, their measurement instruments and associated units.

TABLE 2.6.1 Some common abiotic factors, instruments and associated units

Abiotic factor	Instrument	Unit
Temperature (air, water, soil)	Thermometer – analogue Thermometer – digital	°C
Light intensity	Lux meter	lux
pH (soil, water)	pH probe, pH indicator	–
Wind speed	anemometer	$m\ s^{-1}$
Wind direction	compass	–
Humidity	Hygrometer or wet/dry bulb thermometer	%
Salinity (soil, water)	Probe	% or ppm
Dissolved O_2	Probe	ppm

PRACTICAL ACTIVITY 2.6.1

DETERMINING BIODIVERSITY

Introduction

Assessing the biodiversity of an ecosystem is an important part of an ecologist's job, particularly when monitoring the ongoing health of an area after development. The five measures of species biodiversity can assist in making accurate, quantifiable assessments.

Research question

How similar are the species diversities of two ecosystems according to a given index by using the five measures of species biodiversity?

Materials

- 2 field sites of vegetation (e.g. grassed yard, bushland, rainforest, crop field, garden)
- quadrat frame
- clipboard
- 6 copies of Table 2.6.2
- 2 copies of Table 2.6.3
- pen

Procedure

1. Choose an area to sample within the first field site. The area should be large enough to require at least three quadrats to sample sufficiently.
2. Lay the quadrat frame over a section of the area. This will be quadrat 1.
3. Identify the first species and note it on Table 2.6.2.
4. Count and record the number of individuals of this species within the quadrat.
5. Estimate the percentage of the quadrat that the individuals take up in total and record this.
6. Repeat steps 3–5 for all the species that can be identified.
7. Repeat steps 2–6 for at least three quadrats in the area.
8. Repeat steps 1–7 for the second field site. In total, complete at least six copies of Table 2.6.2.

What are the risks in doing this experiment?	How can you manage these risks to stay safe?
Insects or spiders living in the natural environment may bite.	Wear gloves when touching plants or soil.
You may get sunburnt.	Wear a hat and sunscreen.
You may damage plants or habitat.	Take care when placing quadrats and transects.

Results

TABLE 2.6.2 Field site #____ Quadrat #____

Species	Number of individuals	Percentage cover

TABLE 2.6.3 Field site #____

Species richness		
Species	**Relative species abundance (average)**	**Percentage cover (average)**

Analysis of results

1 Calculate species richness, species evenness, percentage cover and percentage frequency for each of the field sites and enter them into Table 2.6.3. Calculate the SDI for each site to complete the diversity index summary.

2 Compare the diversity summaries for each of the field sites.

Interpretation

3 Explain what each diversity measure says about the two sites to decide whether the two sites are similar.

Evaluation

4 Identify strategies used to minimise bias in the data collection.

5 Discuss the reliability and validity of the collection methods chosen.

PRACTICAL ACTIVITY 2.6.2

DISTRIBUTION AND ABUNDANCE OF PLANTS

Introduction

Two sampling techniques and methods will be used to determine the distribution and abundance of plant species: one to determine the total number of plants in an area and another to determine the distribution of a range of species within a defined space.

Research questions

How different is the abundance of species between two sites?
How does the distribution of plants change with an environmental factor?

Materials

- 2 × 10 m tape measures
- 1 m² quadrat
- random-number generator
- instrument for recording the environmental factor

RISK ASSESSMENT

What are the risks in doing this experiment?	How can you manage these risks to stay safe?
Insects or spiders living in the natural environment may bite.	Wear gloves when touching plants or soil.
You may get sunburnt.	Wear a hat and sunscreen.
You may damage plants or habitat.	Take care when moving through an environment. Avoid damaging plants and animals.

Part A: Abundance (random quadrats)

Procedure

1. Select two accessible sites to investigate; for example, a school oval and a forested area.
2. Arrange the two tape measures as a 10 m × 10 m grid at the first site so the tape measures form *x*- and *y*-axes.
3. Generate five random-number pairs to place the quadrat randomly.
4. Place the quadrat and count the number and type of species in each quadrat. If the name of the plant species is unknown, refer to them as 'species 1', 'species 2' etc.
5. Repeat steps 2–4 at the second site.

Results

Copy and complete the results tables, adding rows as required.

Site 1

Species	Number in quadrat					Total
	1	2	3	4	5	

Site 2

Species	Number in quadrat					Total
	1	2	3	4	5	

Analysis of results

1. Identify the species richness for each site.
2. Identify the species evenness for each site.
3. Calculate the SDI for each site.

Part B: Distribution (point intercept line transect)

Procedure

1. Select a site that has an environmental gradient (e.g. changing light intensity, soil moisture or distance from a footpath).
2. Set out the two 10 m tapes as transect lines so they follow the environmental gradient. Record the environmental factor in the table.
3. Starting at 0 m on the first transect line, record the plants present at each metre along the transect.
4. Repeat step 3 for the second transect line.

Results

Copy and complete the results table.

Environmental factor	Distance along transect (m)										
	0	1	2	3	4	5	6	7	8	9	10

Analysis of results

1 Identify any trend or relationship along each transect line. Identify whether the environmental factor investigated has an effect on the distribution of any species.

Interpretation

2 Explain any similarities or differences in diversity between the two transect lines.

3 Explain whether the abiotic factor investigated has an effect on the distribution of any species.

Evaluation

4 Compare your results with those of other groups. Is the data reliable? Is the data valid?

CHAPTER SUMMARY

Biodiversity

- Biodiversity is the full range of living things in a particular area or region.
- Genetic diversity is the combined differences in DNA of all the individuals in a species.
- Species diversity is the number of different species in an area.
- Ecosystem diversity includes all the living organisms and their interactions together with the physical environment in one area.

Species diversity

- There are five common measures used to describe species diversity: richness, evenness, percentage frequency, percentage cover and Simpson's diversity index (SDI).

Richness	Total number of species
Evenness	Abundance of each species
Percentage frequency	Percentage frequency (%) $= \frac{\text{number of quadrats in which the species is found}}{\text{total number of quadrats}} \times 100$
Percentage cover	Proportion of sample area covered
Simpson's diversity index (SDI)	$\text{SDI} = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$

Sampling methods and techniques

- Organisms can be distributed in patterns that are random, uniform or clumped.

Random	Uniform	Clumped
		

Maralee Park/Shutterstock.com

Butler Stock Photography/Shutterstock.com

Paul Cowell/Shutterstock.com

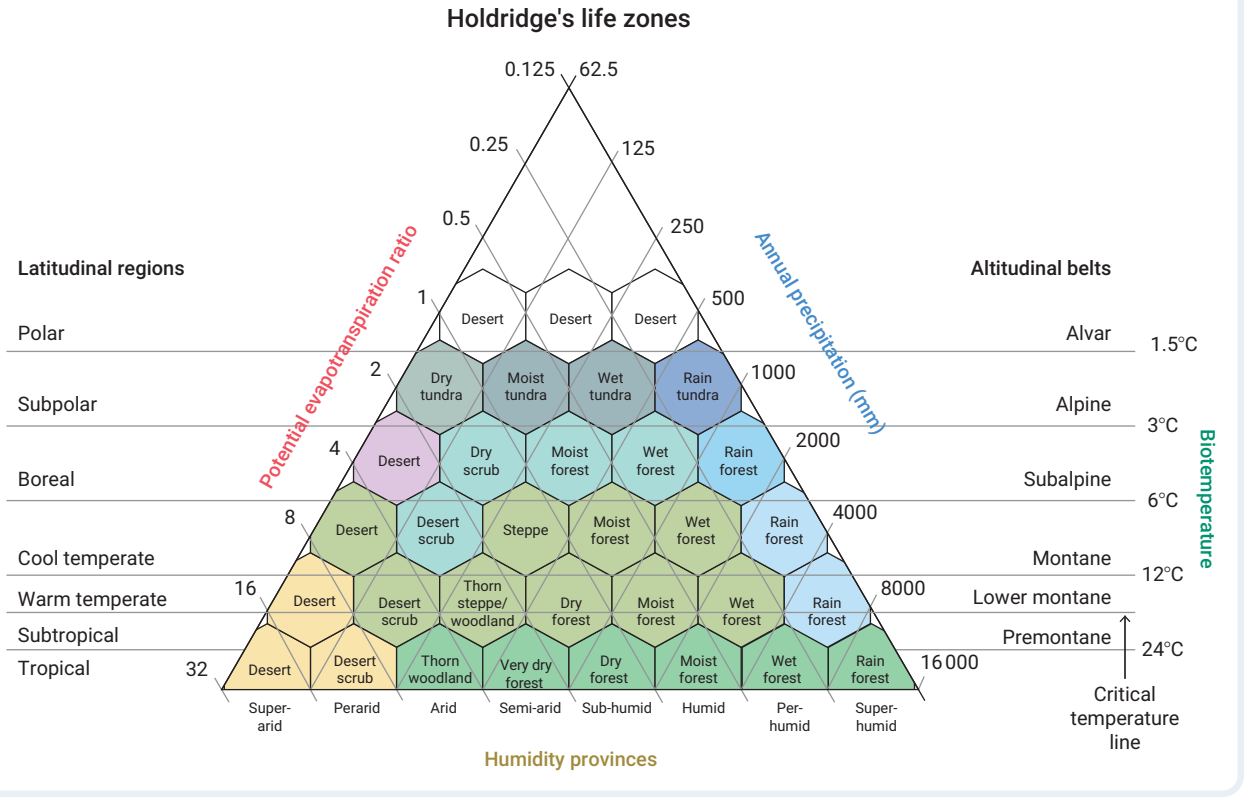
- There are three main sampling methods:
  - Random – each part of the sample area has an equal chance of being included and counted.
  - Systematic – data is collected at fixed intervals.
  - Stratified – a proportionate number of observations is taken from each environment in the sample area.
- There are three main sampling techniques:
  - Quadrats sample a fixed area measured at ground level.
  - Transects include line and belt transects.
  - Capture–recapture involves capturing several individuals, marking them, releasing them and then recapturing them.

Avoiding bias

- Strategies to avoid bias include:
  - size and number of samples
  - random-number generators
  - counting criteria
  - calibrating equipment
  - noting associated precision.

Classifying ecosystems

- Holdridge's life zones and Specht's classification can be used to help classify ecosystems.



Specht's ecological classification system

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	10–30 m	Open woodland	Woodland	Open forest	Forest	Closed forest
	<10 m	Low open woodland	Low woodland	Low open forest	Low forest	Low closed forest
Shrubs	>2 m	Tall open shrubland	Tall shrubland	Open scrub	Scrub	Closed scrub
	0.25–2 m	Open shrubland	Shrubland	Open heathland	Heathland	Closed heathland
	<0.25 m	Dwarf open shrubland	Dwarf shrubland			
Hummock grasses		Open hummock grassland	Hummock grassland			
Tussock grasses		Open grassland		Grassland		Closed grassland
Sedges		Open sedgeland		Sedgeland		Closed sedgeland
Flowers		Open herbland		Herbland		Closed herbland
Ferns				Fernland		Closed fernland

CHAPTER EXAM

MULTIPLE CHOICE

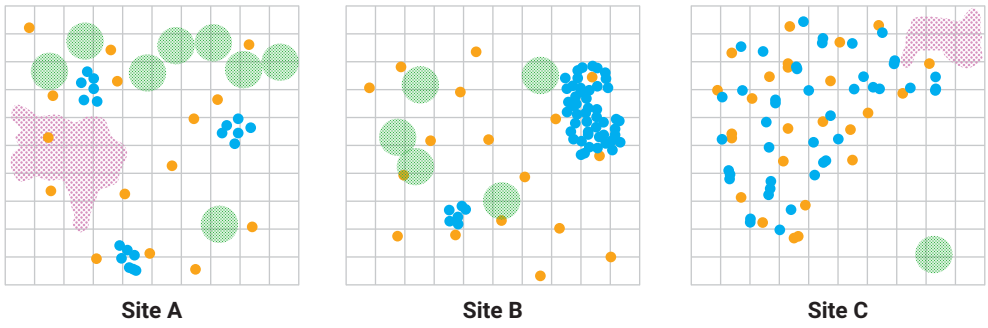
1. Biodiversity is:
   - **A** the number of species in an ecosystem.
   - **B** a group of organisms that share a gene pool.
   - **C** the full range of living things in a particular area.
   - **D** the interactions between a community and the environment.

2. Limiting factors are:
   - **A** biotic factors that restrict population size and diversity.
   - **B** biotic and abiotic factors that control food webs in ecosystems.
   - **C** biotic and abiotic factors that restrict an organism's ability to live in an area.
   - **D** abiotic factors that characterise the environments that an organism can live in.

3. Which of the following is not a measure of biodiversity?
   - **A** Percentage cover
   - **B** Percentage present
   - **C** Relative species abundance
   - **D** Species richness

4. The three levels at which diversity can be studied are:
   - **A** genes, cells, organisms.
   - **B** genes, species, ecosystems.
   - **C** species, organisms, systems.
   - **D** species, systems, communities.

Questions 5–8 relate to the following diagram, which shows average quadrats of three separate areas. Different colours represent different species of plants.



5. What is the species richness of site A?
   - **A** 3
   - **B** 4
   - **C** 5
   - **D** 6

6. Species evenness appears highest in:
   - **A** site A only.
   - **B** sites A and B.
   - **C** site B only.
   - **D** sites B and C.

7. Site A would have the highest SDI, because it has the:
   - **A** lowest species richness and evenness.
   - **B** lowest species richness and highest evenness.
   - **C** highest species richness and lowest evenness.
   - **D** highest species richness and evenness.

8. At site B, the:
   - **A** orange dot and blue dot species both have a random distribution.
   - **B** orange dot and blue dot species both have a clumped distribution.
   - **C** orange dot species has a random distribution, whereas the blue dot species is clumped.
   - **D** orange dot species has a clumped distribution, whereas the blue dot species has a random distribution.

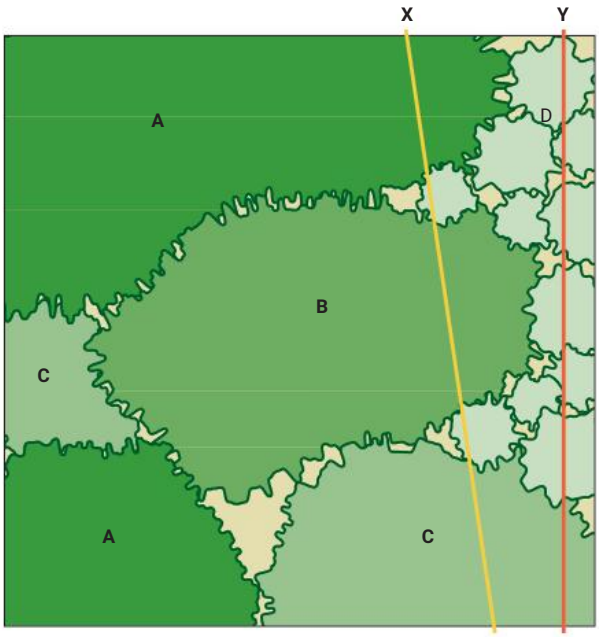
9. A strategy used to minimise sampling bias is:
   - **A** capture–recapture.
   - **C** random-number generators.
   - **B** quadrats.
   - **D** transects.

10. A biotic factor affecting the distribution and abundance of species is:
   - **A** disease.
   - **B** nutrients.
   - **C** shelter.
   - **D** space.

SHORT RESPONSE

11. Modifications to Specht's system include adding the genus or common name of the tallest vegetation. **Describe** a benefit that this modification provides for ecology.

12. Plots of ecosystems often use surface maps to show a rough aerial view of the area. The diagram shown is a rough surface map of an ecosystem.
   - **a** **Identify** the dominant species.
   - **b** Estimate the percentage cover of the dominant species.
   - **c** **Sketch** an image of the transect along line X.
   - **d** Suggest a classification for this ecosystem based on the transect along line Y, using Specht's classification.



Scale 1 cm = 2 m

	Species	Height
A	Eucalypt species A	40 m
B	Eucalypt species B	26 m
C	Eucalypt species C	15 m
D	Species D	Shrubs >2 m

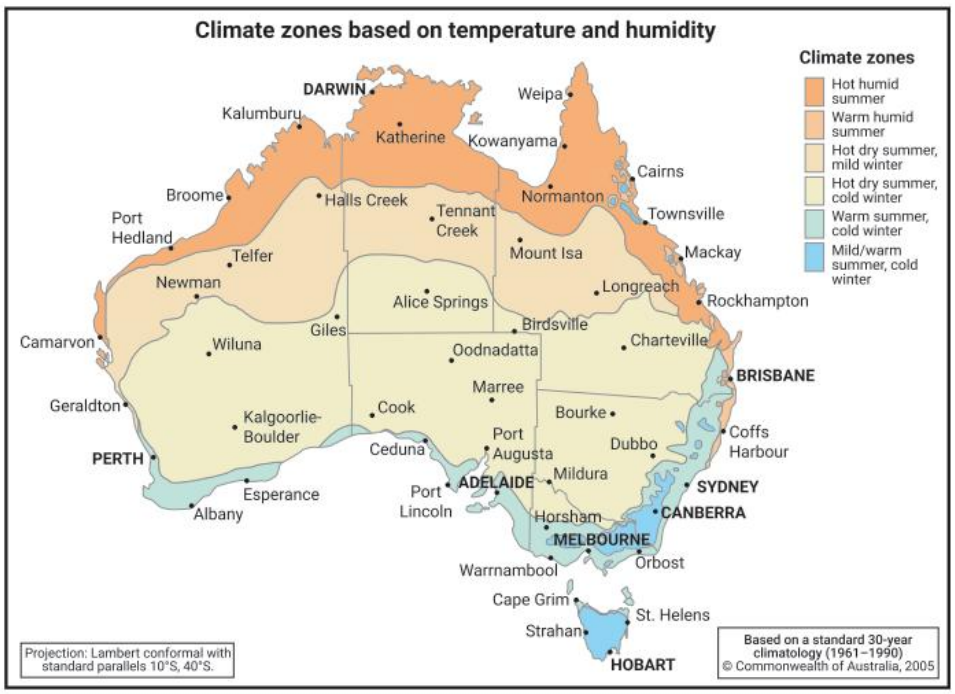
CROSS-CHAPTER QUESTION

13. **Explain** how a dichotomous key would help an ecologist determine the species diversity of an ecosystem.

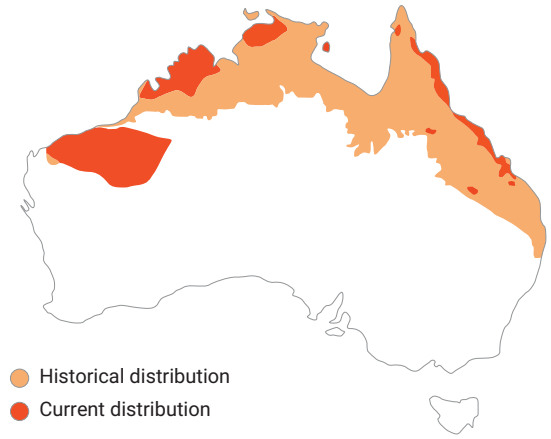
DATA ANALYSIS

Questions 14 and 15 refer to the following figures.

Australian climate zones

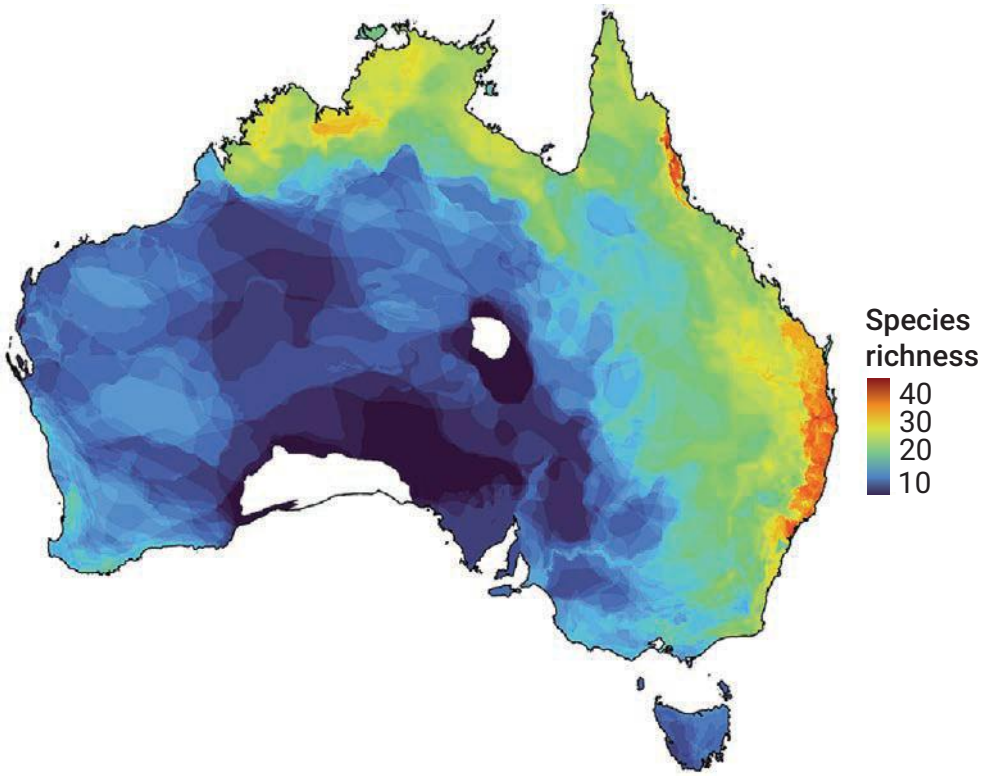


Quoll distribution – historical and current



Adapted from 'Spotlight on quolls: the quest to save Australia's disappearing dasyurids', Australian Wildlife Conservatory, https://www.australianwildlife.org/spotlight-on-quolls/.

Cane toad distribution



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14. Analyse evidence

a **Identify** a relationship between Australian climate zones and frog species distributions.

b **Identify** a relationship between Australian climate zones and quoll distribution.

15. Interpret evidence

Draw a conclusion as to the key difference(s) in abiotic factors affecting the survival of the quoll versus species of frogs in Australia.

CHAPTER 3

Populations

Steven Giles/Shutterstock.com

SYLLABUS DOT POINTS

SCIENCE UNDERSTANDING

- Identify and explain different modes of population growth, including
  - exponential growth (J-curve)
  - logistic growth (S-curve).
- Compare the reproductive strategies and growth curves of K- and r-strategists.
- Use the Lincoln index ($N = \frac{M \times n}{m}$) to estimate the size of a population.
- Calculate population growth rate and change using birth, death, immigration and emigration data.
- Explain how the carrying capacity of an ecosystem can be impacted by changes to biotic and abiotic factors, including climatic events. (Topic 2)

SCIENCE INQUIRY

- Investigate factors affecting carrying capacity. (Topic 2)

Introduction

A population is a group of organisms in the same area and with the potential to interbreed. Populations fluctuate in size and density in response to seasonal and environmental changes. The black swan (*Cygnus atratus*) is a nomadic species of waterbird native to the waterways of Australia. In times of plentiful rain, when food is abundant, adult swans migrate to areas that have received the heaviest rain, and reproduce. These waterways often have a small resident population, which quickly increases in number due to the increased birth and immigration rates. When resources are depleted, most of the swans leave and some die because of the lack of food. The local population size is reduced to a level that the environment can support at that time.

ASSUMED KNOWLEDGE

- ✓ Populations are groups of living organisms.
- ✓ Populations can change size.
- ✓ Quadrat sampling allows for the population size of plant species to be estimated.
- ✓ Capture–recapture sampling allows for the population size of animal species to be estimated.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ calculate an estimated population size for animals, using the Lincoln index formula
- ✓ calculate an estimated population size for plants from density data
- ✓ after looking at a graph of population growth, describe the increase in number of individuals as either exponential growth or logistic growth
- ✓ explain why each mode of population growth occurs
- ✓ explain factors that maintain a population at carrying capacity
- ✓ identify the reproductive strategies used by K-strategists
- ✓ identify the reproductive strategies used by r-strategists
- ✓ identify similarities and differences in the reproductive strategies and growth curves for both r- and K-strategists
- ✓ after looking at a graph of population growth, identify the mode of growth as belonging to a K- or an r-strategist
- ✓ calculate the change in population by using birth (B), death (D), immigration (I) and emigration (E), and birth rate (BR), immigration rate (IR), death rate (DR) and emigration rate (ER)
- ✓ calculate the population growth rate based on the change in population over a period in time.

3.1 Population size

population a group of individuals of the same species living in a particular place at the same time

There are many reasons for determining the size of a **population**. It may be to help understand how a vulnerable species such as the flatback turtle (*Natator depressus*) can survive disturbances from uncontrolled vehicles and coastal development on its Queensland nesting beaches. Or it may be to determine how many minke whales (*Balaenoptera acutorostrata*) can be hunted in one season and still sustain a viable population.

What determines whether a population is thriving, surviving or on the brink of extinction? What is the critical population size and what needs to be considered when working to maintain Earth's biodiversity? The factors to consider vary greatly between species. For example, the *B. acutorostrata* population in any area may be as small as six animals or as large as 50–100 animals where food is plentiful. Even six whales are enough to maintain the population if it consists of two mature females, one mature male and two or three immature animals. Krill (the food of many baleen whales, such as minke whales), experienced a decline in the 1990s and was included in the International Union for Conservation of Nature Red List of Threatened Species in 2015. However, due to the stability of the population, krill is now considered to be of 'least concern'.

Weblink
Antarctic krill

Syllabus link
Chapter 2 explains sampling techniques such as quadrats.

Lincoln index

For stationary species such as plants, population numbers can be estimated from data collected from sampling techniques such as quadrats. For example, to estimate the population size of *Austromyrtus dulcis* (midyim berry) in a 200 m^2 area, 20 quadrats of average size 1 m^2 could be used. If each quadrat contains one *A. dulcis* plant, then the density of *A. dulcis* is one plant per square metre and the estimated population is 200 square metre area × 1 plant per square metre = 200 plants.

For mobile species such as animals, the **Lincoln index (Figure 3.1.1)** is commonly used to estimate population size from data collected by capture–recapture. The Lincoln index method of estimating populations is demonstrated in Worked example 3.1.1.

Lincoln index a formula used to estimate animal population sizes through a mark-and-recapture technique

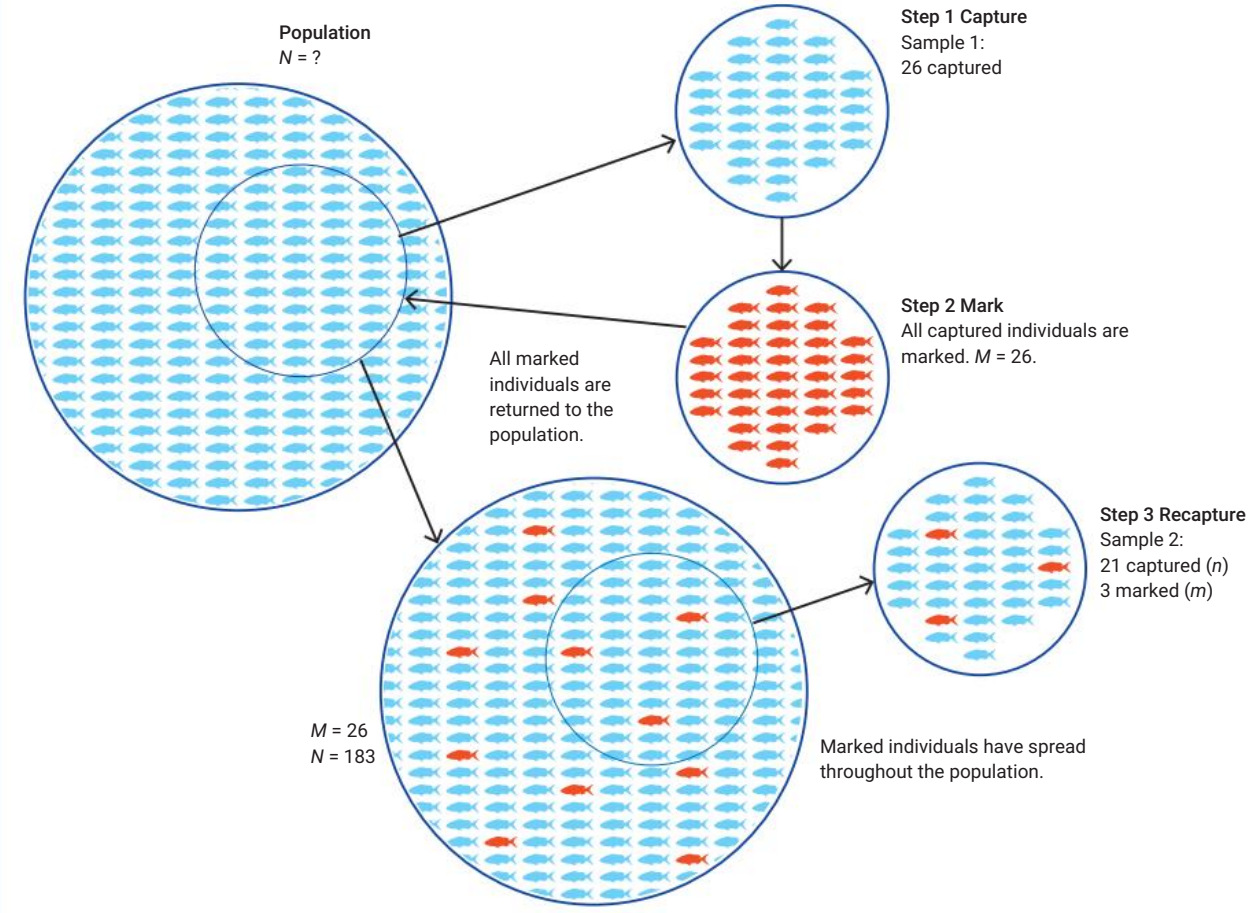


FIGURE 3.1.1 The Lincoln index method of estimating population numbers

KEY FORMULA

Lincoln index

$$N = \frac{M \times n}{m}$$

where N = total population
M = number of individuals caught, marked and released initially
n = number of individuals caught on second sampling
m = number of individuals recaptured that were marked.

Syllabus link
Chapter 2 provides detail about capture–recapture sampling technique.

Practical
Estimation of population size

WORKED EXAMPLE 3.1.1

A sample of 20 individuals from a population were captured, marked and released. Then, a second sample of 50 individuals were captured, 10 of which were marked. What is the estimated population?

ANSWER

1 **Substitute the numbers of individuals caught and marked into the key formula.**

$$N = \frac{M \times n}{m}$$
$$= \frac{20 \times 50}{10}$$
$$= \frac{1000}{10}$$
$$= 100$$

2 **Determine the population.**
There are an estimated 100 individuals in the population.

LEARNING CHECK 3.1

APPLYING

1 Scientists were studying goldfish in two ponds, one large and one small. A total of 20 goldfish from each pond were caught, tagged and released. The next day, 20 goldfish were caught from each pond. There were eight recaptures from the small pond and two from the large pond.

Using the Lincoln index, **calculate** the population estimate for the:

a large pond
b small pond.

3.2 Modes of population growth

When biotic and abiotic resources are abundant, populations can expand rapidly. Normally, this unlimited growth does not occur indefinitely because as the population increases, there will be fewer resources. Ultimately, there is a limit to the number of individuals that can occupy a habitat.

Exponential growth J-curve

In unstable, unpredictable ecosystems, opportunistic species move in and colonise as quickly as they can. In order to survive, these types of species must colonise new environments swiftly, and be able to reproduce rapidly and in relatively large numbers. Population increase in these conditions is called **exponential population growth**.

exponential population growth (J-curve) the growth of a population in an ideal, unlimited environment

A population that is growing exponentially increases at a constant rate per capita; for example, the population doubles each fixed time period. This results in a non-linear J-shaped growth curve (Figure 3.2.1) when population size is plotted over time. Under ideal conditions with unlimited resources, every population has maximum potential for growth.

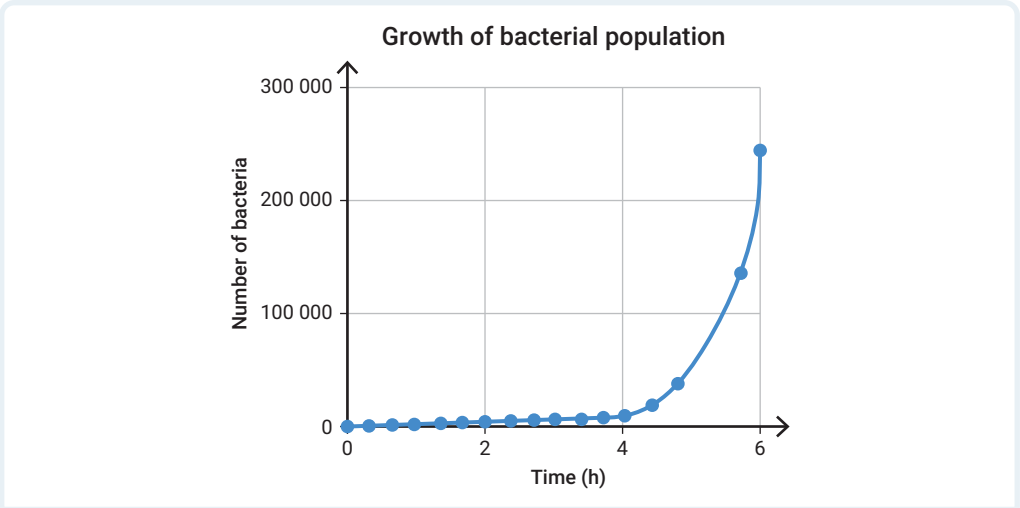


FIGURE 3.2.1 Exponential growth of bacteria

Logistic growth S-curve

Exponential population growth cannot be sustained; as resources are used, the population begins to level off between upper and lower limits. In the **logistic population growth** model, the rate of population increase approaches zero over time, with the population stabilising at a relatively constant size. When logistic growth is graphed, it produces an S-curve (Figure 3.2.2).

logistic population growth (S-curve) the population growth that levels off as population size approaches carrying capacity

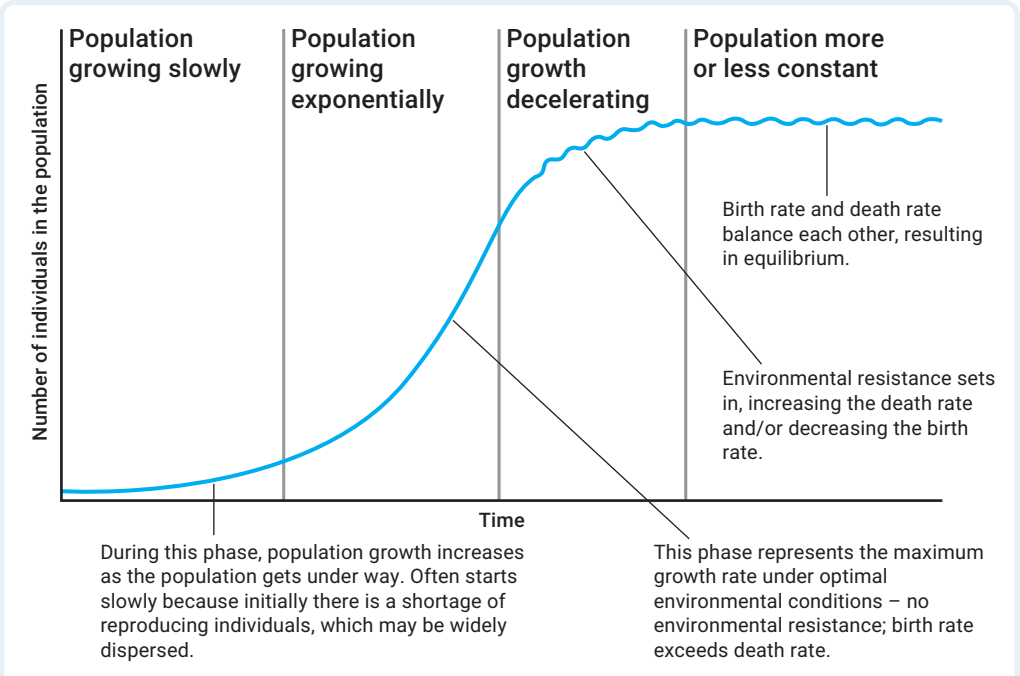


FIGURE 3.2.2 The S-curve is a generalised graph of population growth.

environmental resistance environmental conditions that limit a species population from growing out of control; includes both biotic and abiotic factors

Weblink
How populations grow: the exponential and logistic equations

Factors in the environment, collectively referred to as **environmental resistance**, act on a population. If the population increases above the equilibrium level, competition for resources such as food and space begin to take effect. The increased ability of disease-causing organisms and parasites to spread also increases deaths and possibly reduces breeding, potentially decreasing the population. If the population falls below the equilibrium, there is less competition and the population begins to rise again. This negative feedback process keeps the population relatively constant.

LEARNING CHECK 3.2

DESCRIBING

1 **Describe** the shape of a logistic population growth curve.

APPLYING

2 **Explain** why an exponential growth curve is not typical of an established population.

ANALYSING

3 **Compare** exponential population growth and logistic population growth.

INTERPRETING

4 Consider two areas of forest on Queensland's Central Coast. One area has recently been logged. Another area is undisturbed old-growth forest. **Predict** which area is likely to experience exponential growth and which area will experience logistic growth. Provide reasoning.

3.3 Limiting factors and carrying capacity

carrying capacity the greatest density of organisms that an area or a resource can potentially support

density dependent the effect of a factor increases with an increase in population size

density independent the effect of a factor is the same regardless of population size

The **carrying capacity** is the maximum population size of a species that can be supported in a given environment and is shown on logistic growth curves where the population reaches equilibrium.

Populations rely on balanced relationships between the biotic and abiotic components in their environment. These factors can vary spatially and temporally. The maximum population size that a particular environment can sustain depends on the biotic and abiotic limiting factors at any given place and point in time. Factors that are influenced by the size of the population are described as **density dependent** – the larger the population, the greater the effect. Factors that affect the population in the same way regardless of population size are **density independent**. These are summarised in Table 3.3.1.

TABLE 3.3.1 A summary of density-dependent and density-independent factors affecting population size

	Density dependent	Density independent
Biotic	• Food availability • Competition for resources (including reproductive mates) • Predation • Disease	
Abiotic	• Space • Shelter • Water availability • Nutrients	• Environmental conditions, including weather events and natural disasters

Biotic factors and carrying capacity

Changes to biotic factors can affect the carrying capacity of the ecosystem. Biotic factors that can determine the carrying capacity of an environment are the availability and abundance of foods, number of competitors, number of mates, number of predators, and number and variety of disease-causing organisms.

For example, the availability of food affects the number of young that are born to female kangaroos **(Figure 3.3.1)**. When food is plentiful, a female kangaroo may have up to three young at various stages of development: an older a joey that has mostly left the pouch and no longer depends on her for nourishment; a young joey that is firmly attached to a nipple in the pouch while it completes development; and an embryo whose development and birth have been suspended until there is room in the pouch. If food or other requirements for life become scarce, the female can abandon any one of the three young kangaroos. Without her protection, they perish. This may seem harsh but it ensures that a sustainable population size is maintained. In the long term, this provides stability to the ecosystem and equilibrium to the populations that exist within it.

Structuresxx/Shutterstock.com

FIGURE 3.3.1 The kangaroo-carrying capacity of an environment is affected by the amount of food available.

The loss or introduction of a species can change the carrying capacity for other species in that environment. For example, removing feral cats from an ecosystem increases the survival of plover nests by decreasing the risk of predation and thus increases the number of birds that can survive in this environment **(Figure 3.3.2)**.

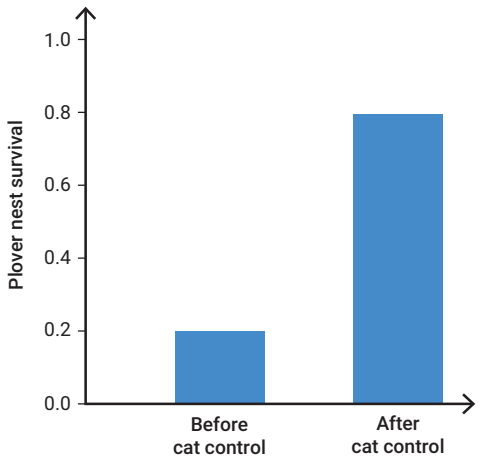


FIGURE 3.3.2 Removing feral cats allows a greater number of plover nests to survive.

AlecTrusler2015/Shutterstock.com

FIGURE 3.3.3 Sturt's desert pea (*Swainsona formosa*) is an opportunistic ephemeral plant, whose population numbers depend on abiotic factors such as water availability.

Abiotic factors and carrying capacity

Availability of nutrients, shelter, refuge from predators, light, water and nesting sites are examples of abiotic limiting factors. If these limiting factors change, the carrying capacity of the ecosystem also changes. If abiotic factors are more favourable, carrying capacity can increase. Alternatively, if abiotic factors are less favourable, carrying capacity is likely to decrease. Abiotic factors can change quickly during natural disasters such as cyclones, floods and fires or more slowly during drought conditions and global temperature change. In most cases, adverse conditions are likely to decrease the carrying capacity.

Sturt's desert pea (*Swainsona formosa*) **(Figure 3.3.3)** has a relatively short flowering season. Its natural habitat includes open desert areas and dry woodlands. It is often described as an opportunistic ephemeral plant because it is short lived, particularly after heavy rains when conditions become temporarily suitable for its growth and reproduction. Most of its life is spent as a seed with a tough, water-resistant coat. Only after drenching rains will the seeds germinate, flower and then set seed all within a matter of days. When conditions become less suitable, the carrying capacity is reduced and the initial population explosion is quickly followed by a crash when resources (such as available water) are depleted or other abiotic conditions alter. This limits the numbers of the plant that can be sustained. The plant's use of existing resources is highly efficient and ensures its ongoing survival in an environment to which it is best suited.

Weblink
How biotic and abiotic factors shape ecosystems and set limits

Climatic events – an Australian example

Bushfires are a regular occurrence in the Australian landscape, especially when temperatures are high and vegetation dies and dries out at the end of a wet season or as a result of a drought. In 2019–20, the summer months had higher than average temperatures,

following a period of drought. The resulting 2019–20 Australian bushfires, or Black Summer bushfires, burnt more than 10 million hectares of land, including native forests (8 million hectares), commercial, residential and farming areas. Typically, the average annual area burnt per continent per year is 5 per cent. This bushfire event burnt about 21 per cent of Australia's temperate forests. Approximately 1 billion animals were killed by the fires, although some sources put the figure much higher at 3 billion killed or displaced animals. The fires destroyed habitats, leaving animals who escaped without food or shelter and reduced access to water. Food webs were disrupted by the loss of so many different species of organisms. The surviving species potentially experienced higher levels of competition for the remaining resources. These factors combine to significantly alter the carrying capacity of the bushfire-ravaged ecosystems.

Aussie Bush/Shutterstock.com

Norman Herfurth/Alamy Stock Photo

FIGURE 3.3.4 The Australian bushfires of 2019–20 took place during a summer that was hotter than average and followed a period of drought.

PRACTICAL ACTIVITY 3.3.1

MODELLING CARRYING CAPACITY

Introduction

Carrying capacity is the number of living things an area of land or water can support at any one time. One area will have different carrying capacities for different organisms. Different ecosystems have different carrying capacities for different plants and animals.

Carrying capacity is usually limited by an aspect of a species' habitat requirements. A population tends to naturally fluctuate around the carrying capacity. A population may be below carrying capacity in the spring following a hard winter, or temporarily above it after a good summer.

Research question

How do changes in the availability of resources affect the carrying capacity?

Materials

- bag of dried beans
- timer

Procedure

1. The class divides into 'herds' with five students in each. Each herd gathers around a cleared area (either in the classroom or outdoors).
2. Set the timer for one-minute intervals (or less).
3. One at a time, members from each herd collect one dried bean from the bag. Continue to cycle through members in the herd until the timer rings. Members of a herd unable to collect three dried beans during the time 'die'.

4 Record the number of survivors after three rounds.
5 In a group, discuss carrying capacity and limiting factors. Identify strategies that could allow more of the population to live. Decide what could be done or might happen to allow more of the population to live through the 'winter' on the food available.
6 Repeat the activity, incorporating an option suggested in step 5.
7 Each herd chooses a member to be a young animal 'born the previous spring'. Repeat the activity, allowing the 'young animal' to take two beans each time.

Analysis of results

1 What effect did the strategy identified in step 5 have on the number of survivors that could live to reproduce the following year?
2 How did introducing young animals affect the population?
3 What happens to the number of survivors that live to reproduce the next year on the introduction of young animals?

PRACTICAL ACTIVITY 3.3.2

MICROSCOPIC COLONIES

Introduction

Populations initially grow exponentially in environments without limiting factors then eventually reach the carrying capacity of their environment.

Research question

Does a yeast population reach carrying capacity on a microscope slide?

Materials

- For the class:
  - 2 teaspoons (10 g) of sugar
  - packet of yeast
  - lukewarm water (1 cup)
  - mixing bowl
- 1% methylene blue solution
- eye dropper (two if using methylene blue)
- microscope with slides and coverslips

Procedure

1 The teacher mixes the sugar, yeast and lukewarm water in a bowl until combined.
2 Using droppers, place a drop of the yeast mixture on a microscope slide, add a drop of methylene blue on top of the yeast, and cover with a coverslip.
3 Allow the slide to sit for 3–10 minutes.
4 Place the slide under a microscope and count the number of yeast cells. Record the information. Dead yeast cells will appear dark blue.
5 Every 5 minutes, count and record the number of cells that are dark blue. If there are too many to count, estimate the number of cells.
6 Identify when the slide has reached its carrying capacity.

Results

Draw a table to represent your results.

Analysis of results

1 Identify a trend in the number of living cells.
2 Identify a trend in the number of dead cells.

Interpretation

3 Explain why the ratio of living to dead cells changed over time.
4 What evidence is there to suggest a carrying capacity was reached?
5 What factors were limiting to the yeast cell population?

Evaluation

6 How reliable is this method for investigating carrying capacity?

LEARNING CHECK 3.3

DESCRIBING

1 **Define**:
   a population
   b carrying capacity.

APPLYING

2 **Identify** two biotic limiting factors that can affect carrying capacity and explain how they affect carrying capacity.
3 **Identify** two abiotic limiting factors that can affect carrying capacity and explain how they affect carrying capacity.

INTERPRETING

4 Figure 3.3.5 is a photo of a track entering the Simpson Desert. **Predict** the effect of the following on the carrying capacity of this area:
   a flood
   b fire.

Terry Lonergan/Shutterstock.com

FIGURE 3.3.5 The Simpson Desert

3.4 Reproductive strategies

The r/K selection theory classifies (or arranges) species on a spectrum on the basis of their reproductive strategies, habitats, behaviours, length of life and survivorship. The K-end of the spectrum is characterised by stability, which includes longer reproductive cycles, longer periods of parental care and social learning, longer lifespans and lower mortality rates. K-selected species tend to live in stable environments and have only a few offspring. These populations often reach and remain at the carrying capacity of an environment.

The other end of the spectrum is the r-end, which is characterised by variability, which includes faster and more frequent reproductive cycles, little to no parental input or social learning, shorter lifespans and higher mortality rates. r-selected species tend to inhabit unpredictable environments and have a large number of offspring. These populations often go through repeated patterns of exponential growth followed by a population crash.

As this is a spectrum, most species exhibit more moderate or mixed characteristics rather than just the two extremes. **Figure 3.4.1** illustrates the impact that each extreme strategy has on the logistic growth curve of a population.

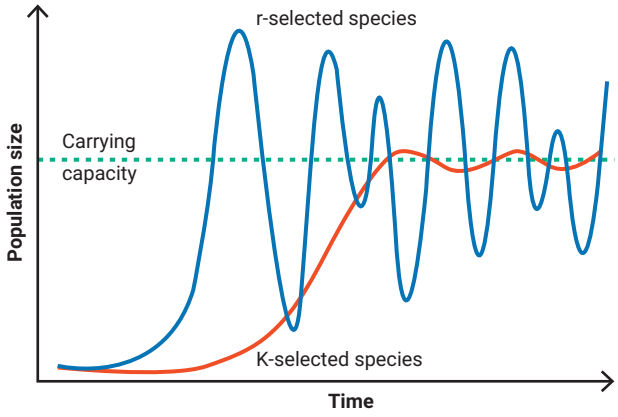


FIGURE 3.4.1 Typical population growth curves for r-selected and K-selected species. Note the repeated cycle of exponential growth followed by a population crash for r-selected species.

Table 3.4.1 summarises the key attributes associated with the r-end and K-end of the spectrum.

TABLE 3.4.1 Key attributes associated with the r-end and K-end of the spectrum

Attribute	r-selected	K-selected
Reproductive rate	High	Low
Lifespan	Short	Long
Reproductive maturity	Early	Late
Level of parental care	Low	High
Dispersal ability	High	Low
Growth rate	High	Low
Niche	Generalist	Specific
Diet	Generalist	Specific

Understanding this theory helps to:

- predict how changes in a species' environment affects population dynamics and responses to environmental changes based on allocation of resources to growth, reproduction and survival. For example, if environmental stability increases, the population of a K-selected species should increase but the population of an r-selected species should decrease
- inform conservation and management strategies to support the high reproductive rate of r-selected species or the survival of low numbers of offspring of K-selected species through resource availability and regulated harvesting.

Worksheet
K- and r-reproductive strategies

LEARNING CHECK 3.4

DESCRIBING

1 **Identify** three attributes of a K-selected species.

2 **Identify** three attributes of an r-selected species.

ANALYSING

3 Copy the r to K continuum and then **analyse** the information in the table to place each organism on the continuum.

r ⟵ ⟶ K

Mosquito	Rabbit	Duck
Lays eggs directly on or near water	Gives birth to live young	Lays eggs
50–200 eggs per clutch	Average seven kits per litter	Up to 12 eggs per clutch
No observed parental input	Parental input for 7–8 weeks	Parental input for about 2 months

INTERPRETING

4 **Justify** your placement of the mosquito, rabbit and duck in Question 3.

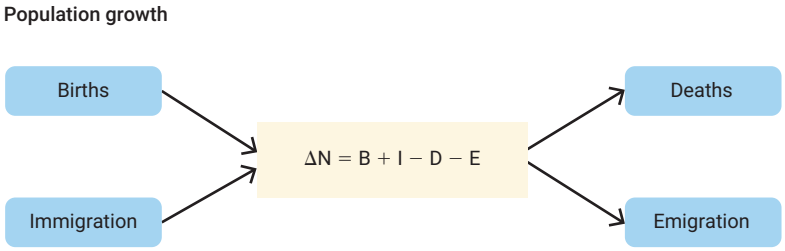
3.5 Population changes

Populations change depending on four factors: births (B), deaths (D), **immigration** (I) and **emigration** (E). Births and immigration cause an increase in a population, deaths and emigration cause a decrease. Therefore, a population increases if the births and immigration exceeds the death and emigration. Conversely, a population decreases when the number of deaths and emigration exceeds the number of births and immigration.

immigration the movement of individuals of a species into a place

emigration the movement of individuals of a species out of a place

Population change (ΔN) may also be calculated as a rate, which takes into account birth rate (BR), immigration rate (IR), death rate (DR) and emigration rate (ER), where rate refers to the number of individuals per hundred, per thousand or whatever unit is appropriate **(Figure 3.5.1)**.



Population growth rate

Population growth rate = (birth rate + immigration rate) − (death rate + emigration rate)
= (BR + IR) − (DR + ER)

FIGURE 3.5.1 Rules for calculating population growth and population growth rate

WORKED EXAMPLE 3.5.1

Bilbies once occupied about 70 per cent of the Australian continent in semi-arid environments before populations were devastated by cats and foxes. Other threats include habitat fragmentation and altered fire patterns. In 2019, the greater bilby was re-introduced to a 2500-hectare predator-free enclosure in Currawinya National Park near the Queensland–New South Wales border.

The starting population was 36 individuals. In the first year, 20 bilbies were born and two died. Two bilbies escaped the enclosure and none joined the population.

Calculate the growth of the population.

Ken Griffiths/Shutterstock.com

ANSWER

1 Substitute the values into the formula.

Growth = (B + I) − (D + E)
= (20 + 0) − (2 + 2)
= 16

2 Determine the answer.

Therefore, the population increased by 16 individuals.

WORKED EXAMPLE 3.5.2

Calculate the growth rate of a population of 400 bilbies where, every year, 100 individuals are born, 65 individuals immigrate into the population, 37 individuals die and 25 individuals emigrate to another population.

ANSWER

1 **Substitute the values into the formula.**

Growth rate requires converting the number of individuals to a rate by dividing each by the population size.

$\text{BR} = \frac{100}{400}$, $\text{IR} = \frac{65}{400}$, $\text{DR} = \frac{37}{400}$, $\text{ER} = \frac{25}{400}$

$$\begin{aligned}\text{Growth rate} &= (\text{BR} + \text{IR}) - (\text{DR} + \text{ER}) \\ &= \frac{165}{400} - \frac{62}{400} \\ &= \frac{103}{400}\end{aligned}$$

The growth is 103 individuals per 400 individuals.

To convert to a percentage:

$$\begin{aligned}\% &= \left(\frac{103}{400}\right) \times 100 \\ &= 25.75 \\ &= 26\% \text{ (round to nearest whole number)}\end{aligned}$$

2 **Determine the answer.**
Therefore, the population grows by 26 individuals per 100 in the population. Growth rates are expressed as a percentage: +26% if there is an increase or −26% if there is a decrease.

Weblinks
The Texas mosquito mystery
Human population growth

LEARNING CHECK 3.5

DESCRIBING

1 State the characteristics of populations that are usually studied when calculating the growth rate.
2 **Describe** what effect biotic factors have on the growth of a population.
3 **Describe** what effect abiotic factors have on the distribution of a population.

APPLYING

4 A particular population of kangaroos has 1000 births during the year; 72 individuals join the population, 108 leave and 345 die. **Calculate** the growth for this population for the year.
5 **Calculate** the growth rate of a population if, for every 1000 individuals, there are 59 births, 105 immigrants, 86 deaths and 40 emigrants.
6 **Calculate** the growth rate of a population if, for every 1000 individuals, there are 150 births, 59 immigrants, 290 deaths and 30 emigrants.

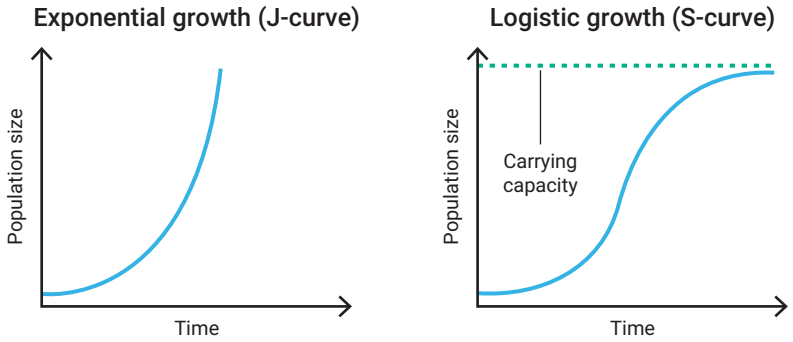
INTEPRETING

7 **Predict** whether a population's size is increasing or decreasing when (BR + IR) is greater than (DR + ER).

CHAPTER SUMMARY

Population growth

- The two main types of population growth are:
  - exponential growth – growth rate per capita stays the same as population increases
  - logistic growth – growth rate decreases as population increases until carrying capacity is reached.



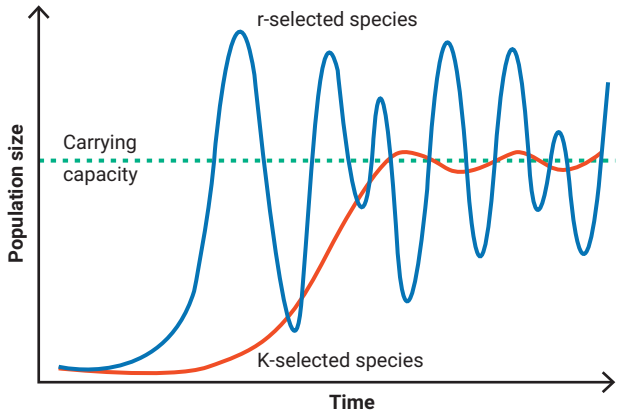
r/K selection theory

- r-selected species and K-selected species have differences in key attributes.

Key attributes associated with the r-end and K-end of the spectrum

Attribute	r-selected	K-selected
Reproductive rate	High	Low
Lifespan	Short	Long
Reproductive maturity	Early	Late
Level of parental care	Low	High
Dispersal ability	High	Low
Growth rate	High	Low
Niche	Generalist	Specific
Diet	Generalist	Specific

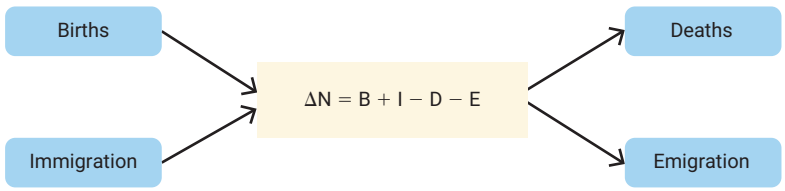
- Typical population growth curves for r-selected and K-selected species



Calculating population changes

Rules for calculating population growth and population growth rate

Population growth



Population growth rate

Population growth rate = (birth rate + immigration rate) − (death rate + emigration rate)
= (BR + IR) − (DR + ER)

CHAPTER EXAM

MULTIPLE CHOICE

1. Carrying capacity is defined as:
   - **A** the movement of individuals of a species into an area.
   - **B** environmental conditions that limit a species population from growing out of control.
   - **C** the maximum population size of a species that can be supported in a given environment.
   - **D** a group of individuals belonging to the same species living in a particular place at the same time.

2. Factors that affect the rate of growth of a population are the birth rate (BR), immigration rate (IR), death rate (DR) and emigration rate (ER). The following must be true if the rate of growth of a population has a negative value.
   - **A** ER is greater than IR.
   - **B** DR is greater than BR.
   - **C** DR + ER is greater than BR + IR.
   - **D** IR + ER is greater than BR + ER.

3. During one year, 282 animals are born into a population, 83 emigrate, 67 immigrate and 92 die. The increase in this population is:
   - **A** 13 individuals.
   - **B** 174 individuals.
   - **C** 187 individual.
   - **D** 200 individual.

4. The Lincoln index is commonly used to find the size of animal populations. In a study of possums in an open forest ecosystem, a random sample of 36 individuals was caught. Each captured animal was marked and released. At a later date, a random sample of 24 animals was found to contain four marked individuals. What is the predicted population of possums?
   - **A** 20 individuals
   - **B** 28 individuals
   - **C** 216 individuals
   - **D** 600 individuals

5. An abiotic factor that affects abundance and distribution is:
   - **A** disease.
   - **B** food availability.
   - **C** predation.
   - **D** shelter.

6. An attribute associated with K-selected species is:
   - **A** high birth rate.
   - **B** low parental input.
   - **C** short gestation.
   - **D** late maturity.

7. An attribute associated with r-selected species is:
   - **A** high parental input.
   - **B** specific niche.
   - **C** long gestation.
   - **D** high reproductive rate.

8. Both r- and K-strategists have a growth curve that shows:
   - **A** a dramatic population drop.
   - **B** a section that remains stable at carrying capacity.
   - **C** a section that fluctuates widely around carrying capacity.
   - **D** an initial exponential growth.

9. A factor that would increase the carrying capacity of an environment for a species is:
   - **A** fewer shelter options.
   - **B** greater food availability.
   - **C** a bushfire.
   - **D** presence of disease.

10. Rabbits were released in Australia in 1853. One reason Australia had a high carrying capacity is:
   - **A** there was not enough food.
   - **B** there was no natural predator.
   - **C** it was difficult for rabbits to find shelter.
   - **D** it was difficult for rabbits to find reproductive mates.

SHORT RESPONSE

11. Australia has about 700 endemic species of grasshoppers and locusts, but the one that usually hits the headlines is the Australian plague locust (*Chortoicetes terminifera*). Locust populations increase enormously under favourable climatic conditions, usually following periods of rainfall. Many minor plagues occur regularly but there have been five major plagues in the past 60 years. Densities of 1000 per square metre have been recorded.
   - **a** Outline the biotic and abiotic conditions that may give rise to locust outbreaks.
   - **b** **Identify** this type of population growth and **describe** the shape of the graph produced when locust numbers are plotted against time.
   - **c** **Explain** why plague numbers are unsustainable for this population.

12. The Lincoln index or capture–recapture is one method used to determine population size. Suggest what problems may arise if too much time is left between the initial capture and the recapture.

CROSS-CHAPTER QUESTION

13. In the following examples, **determine** the resource that is having the most effect on the population distribution.
   - **a** Heath plants in clumps in a field
   - **b** Penguins distributed evenly across an ice sheet
   - **c** Alpine grasses randomly spread along the side of a hill

DATA ANALYSIS

Questions 14 and 15 refer to the following information.

An ecologist records the abundance of turtles in the Great Barrier Reef by using the Lincoln index.

- Location A: In the first sample, 30 individuals were marked. In the second sample, 50 individuals were captured and 10 of these were marked.
- Location B: In the first sample, 100 individuals were marked. In the second sample, 200 individuals were captured and 50 of these were marked.

14. **Apply understanding**

    Calculate the population estimates for Location A and Location B.

15. **Analyse evidence**

    Compare the samples taken at each location.

SCIENCE AS A HUMAN ENDEAVOUR

Syllabus dot point

- Methods of classification are directly related to the purpose for which the data will be used. Hierarchical systems, such as the Linnaean system, can be used to organise, analyse and communicate data about biodiversity. For example, the hierarchical nature of the Linnaean system allows scientists to infer similarities between species; however, as the system was originally based primarily on physical features, the categorisation of species does not always reflect evolutionary relatedness. Species may be re-classified as new information becomes available.
- 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.

Ways of classification

At the time of the arrival of the British and subsequent colonisation of Australia, the science of natural history as practised throughout Europe was emerging. The European naturalists seeing Australia for the first time, who described, collected and classified plants and animals, were amazed by the number of species unknown to European naturalists of the day. However, Australia's rich biodiversity had long been understood and used by the First Nations Peoples, who had lived on and managed these lands for tens of thousands of years. Indigenous communities have extensive knowledge of local plants and animals and have their own longstanding classification systems.

The colonisation of Australia provided opportunities, as well as challenges, for the European naturalists of the 18th and 19th centuries, who often failed to recognise existing Indigenous knowledge.

One such challenge was understanding the flora and fauna in Australia. Initially, they described Australian animals in terms of those they were familiar with, such as referring to dingoes as 'wolves', wombats as 'badgers', and wallabies as 'raccoons' (Figure 1). Over time, these naturalists realised that the plants and animals of Australia were distinct and required their own names. Despite this recognition, the valuable knowledge of First Nations Peoples, who had long classified and named these species and among other things, understood their relatedness and roles within the ecosystem, was largely overlooked in the scientific community of the time.

Mitchell Library, State Library of New South Wales

FIGURE 1 An early drawing of a kangaroo by natural history illustrator Sarah Stone (1760–1844), who drew from specimens brought back to England from Australia

What defines a species is still debated today

Classifying organisms in ecosystems, particularly forests in south-east Queensland, from a First Nations perspective involves understanding the intricate relationships that these Peoples have with the land. Rather than Linnaean systems, which focuses on hierarchial taxonomies, First Nations classification systems are more holistic and emphasises usage, the interconnections between species, landscapes, spirituality and human activity.

Below are a few examples of classification approaches from First Nations perspectives in south-east Queensland forests.

Bill Coster/Alamy Stock PhotoWales

FIGURE 2 The black booyong tree is used for medicine and food and has spiritual significance for some First Nations Peoples of south-east Queensland.

Cultural and ecological connections

First Nations cultures of south-east Queensland, such as the Yugara, Turrbal and Gubbi Gubbi/Kabi Kabi Peoples, often classify forests based on their cultural significance. This includes the spiritual, medicinal and practical uses of organisms. For example, certain trees like the *booyong* (a species of fig) **(Figure 2)** can be seen as a source of medicine or food, but also hold spiritual significance, often being considered as 'living ancestors' of a particular clan or family group. The plants and animals are not merely organised on the basis of their physical traits, but also on their significance in respective cultural narratives including kinship and aspects of daily life.

Natural resources classification

Some First Nations Peoples in south-east Queensland have been recorded to classify forests according to the resources they provide. This includes plant species used for food (e.g. bush tomatoes or yams), tools (e.g. stringybark for ropes) or shelter (e.g. paperbark for roofing). This approach is functional and ecosystem-based, understanding that the resources provided by each species are linked to the health and sustainability of the ecosystem.

Comparing classification systems

The classification systems of First Nations Peoples differ in may ways to the Linnaean system. While the Linnaean system uses a hierarchical system for naming and organising species, systems used by First Nations Peoples include its uses and significance in cultural narratives, where it is about relationship, respect and sustainability rather than hierarchy. In this way, the knowledge passed down through generations provides a detailed and nuanced view of how to live sustainably within ecosystems.

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* Please note that some of the sources listed in the bibliography regarding First Nations Australians are sources of information only.
These are not provided or recommended as classroom resources.

CHAPTER 4

Transfer and transformation

Sara Spohr/Shutterstock.com

SYLLABUS DOT POINTS

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.

Introduction

Wherever life exists, it depends on a source of energy and a supply of matter. Ecosystems across the world are linked in networks of energy and nutrient exchange between living things and their non-living surroundings. This chapter explores the transfer and transformation of this energy and matter as they are cycled and recycled through the biosphere.

Worksheets

- Biogeochemical cycles
- Energy flow
- Transfer and transformation of energy

To access resources above, visit
cengage.com.au/nelsonmindtap

ASSUMED KNOWLEDGE

- ✓ Energy is required for survival of life.
- ✓ Plants photosynthesise to convert light energy into chemical energy.
- ✓ Organisms without chlorophyll gain nutrition by feeding on other organisms.
- ✓ A cycle means that components are reused.
- ✓ Biological molecules are made up of carbon, hydrogen, oxygen and sometimes nitrogen.
- ✓ Water changes state through the processes of evaporation and condensation.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ explain how energy is transferred and transformed from light energy into chemical energy by the process of photosynthesis
- ✓ explain how energy is transferred as carbon-based molecules are moved through the carbon cycle
- ✓ explain how energy is transferred and transformed into heat energy by organisms
- ✓ identify whether energy transfers are efficient by using information from energy flow diagrams and ecological pyramids
- ✓ identify whether biomass transfers are efficient by using information from food chains and ecological pyramids
- ✓ identify examples of radiation, reflection and absorption of heat energy from energy flow diagrams
- ✓ complete gross and net productivity calculations using data from energy flow diagrams
- ✓ describe the different molecules that contain carbon as it moves through the carbon cycle
- ✓ describe the different molecules that contain nitrogen as it moves through the nitrogen cycle
- ✓ describe the state of water at different stages of the water cycle.

Syllabus link
Chapter 4 of *Nelson QCE Biology Units 1 & 2* details the structure and function of biological molecules.

4.1 Transfer and transformation of matter

The total matter on Earth is a finite resource and therefore must be recycled to ensure the continued existence of living organisms. The matter that makes up a living organism is recycled by **decomposers** and **detritivores**, whose wastes form fertile soil for plants to use in producing biomass.

In living things, carbon is the most abundant chemical element, closely followed by hydrogen, nitrogen and oxygen. Carbon can bond with many other elements, giving an enormous variety of biological molecules, including carbohydrates, lipids, proteins and nucleic acids that are the chemical building blocks of cells and the source of their energy. The continuous supply of key elements, including carbon, nitrogen, oxygen and phosphorus, is essential for life because these materials are continuously excreted in wastes and must be recycled.

Nutrient cycles are how key elements are cycled through the biotic and abiotic components of an ecosystem. They have two main components:

- The biological component shows how the element cycles through organisms.
- The geochemical component shows how the element cycles through soils, rocks, water and the atmosphere.

Given the interdependence of these components, nutrient cycles are also called biogeochemical cycles.

decomposer an organism that grows on and absorbs nutrients from dead tissues, e.g. a fungus

detritivore an organism that consumes the dead tissues of once-living organisms (detritus), e.g. a worm

nutrient cycle the cyclic movement of key elements and molecules through the biotic and abiotic components of an ecosystem, e.g. the water cycle and carbon cycle; also called biogeochemical cycle

Carbon cycle

Carbon atoms circulate between the organic compounds of living things and their non-living surroundings through several pathways, and together these form the carbon cycle **(Figure 4.1.1)**.

Weblink
The carbon cycle

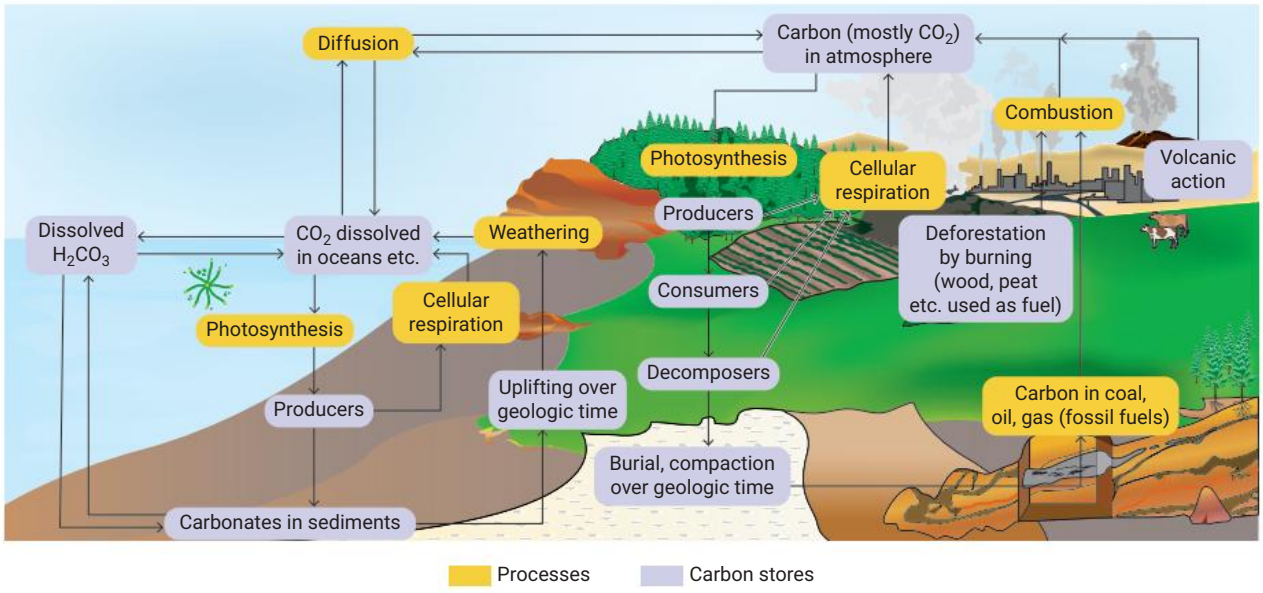


FIGURE 4.1.1 Carbon atoms in atmospheric carbon dioxide are incorporated into carbohydrates during photosynthesis. This carbon is eventually released through cellular respiration or combustion, both of which convert the organic compounds back to carbon dioxide.

The carbon cycle is unique among nutrient cycles because it does not necessarily involve decomposers. Even when decomposers are present, not all dead material decays. Under **anaerobic** or highly acidic conditions, decomposers may be unable to break down all the remains and waste products of organisms. In such situations and over long periods of time, these substances may accumulate to form fossil fuels, such as peat, coal, oil and the gases derived from them. In nature, these deposits represent a **sink**, a place where carbon atoms are densely accumulated and trapped away from the cycle.

Carbon can circulate for some time outside of the sinks because carbon is incorporated into and released from glucose through photosynthesis and cellular respiration. The amount of carbon dioxide in the atmosphere is maintained largely by a balance between photosynthesis, which withdraws it from the atmosphere and stores it as **biomass**, and cellular respiration and combustion, which release it to the atmosphere. Unfortunately, as a result of a number of factors, the level of carbon dioxide in the atmosphere has risen considerably during the last 200 years. Humans remove fossil fuels from sinks for combustion, to generate electricity. This produces CO_2 that is reintroduced to the carbon cycle. The extra carbon in the cycle disrupts the natural balance between photosynthesis and cellular respiration. Even though plants photosynthesise more rapidly when there is more carbon dioxide in the atmosphere, humans have also cleared vast areas of forest over the last century, so the carbon is not being taken in fast enough.

Changes to ocean temperatures have also affected the cycling of carbon. The temperature of ocean water affects how much carbon dioxide can remain dissolved in it. As the temperature increases, the oceans can hold less carbon dioxide, leaving more in the atmosphere.

Syllabus link
Chapters 5 and 6 of *Nelson QCE Biology Units 1 & 2* explore the twin processes of cellular respiration and photosynthesis.

anaerobic in the absence of oxygen

sink an area where atoms naturally accumulate away from the normal nutrient cycle

biomass the total mass of living matter in an ecosystem

Syllabus link
Chapter 4 of *Nelson QCE Biology Units 1 & 2* details the essential role of proteins in cell function.

nitrogen-fixing bacteria bacteria that absorb elemental nitrogen (N_2) from the atmosphere and convert it to nitrites (NO_2^-), nitrates (NO_3^-) or ammonium ions (NH_4^+)

ion an atom or group of atoms that has either lost or gained valence shell electrons, acquiring a net positive or negative charge

Weblink
The nitrogen cycle

Nitrogen cycle

Nitrogen is an essential element for living organisms because it is a key element in making proteins. These molecules have many different roles in cells and play an essential part in controlling cell activities and growth.

Unlike carbon, nitrogen atoms do not have a direct link between the atmosphere and most living organisms. Even though the atmosphere is 78 per cent nitrogen, it is elemental nitrogen (N_2). Plants and animals cannot absorb nitrogen in this form. Instead, plants rely on **nitrogen-fixing bacteria** to convert elemental nitrogen into **ions** such as nitrite (NO_2^-), nitrate (NO_3^-) and ammonium (NH_4^+), which they can absorb. Animals absorb nitrogen from the nitrogen-based compounds in plants.

The nitrogen cycle **(Figure 4.1.2)** is a combination of two cycles:

- In the elemental cycle, N_2 is absorbed from the atmosphere by nitrogen-fixing bacteria and released back to the atmosphere by denitrifying bacteria and volcanic activity.
- In the ionic cycle, nitrogen-containing ions such as nitrite (NO_2^-), nitrate (NO_3^-) and ammonium (NH_4^+) are passed between organisms in the biosphere.

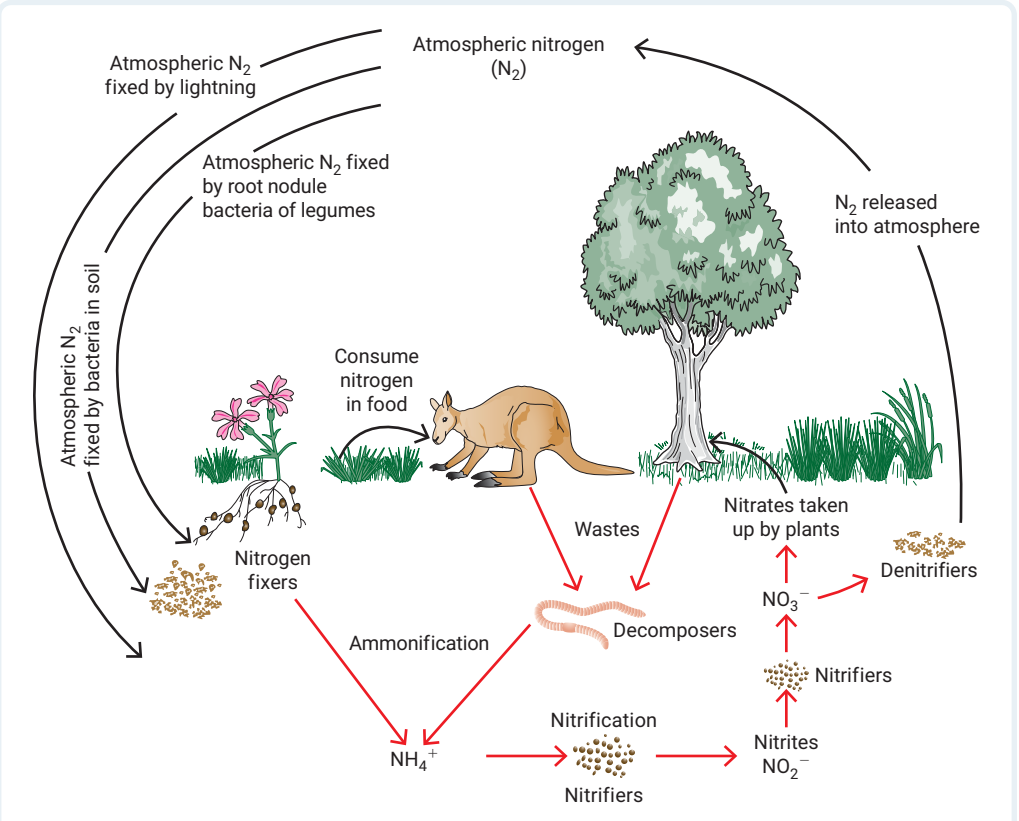


FIGURE 4.1.2 The balance between atmospheric nitrogen (black arrows) and ionic nitrogen (red arrows) is maintained by a set of key bacteria, including nitrogen fixers and denitrifiers.

The nitrogen cycle depends on the metabolic activities of the nitrogen-fixing and nitrogen-releasing bacteria. Some of these bacteria have developed a special symbiotic relationship with plants such as *Casuarina* species, *Acacia* species and legumes, including clover, peas and

beans. Instead of living free in the soil, these bacteria live in special root organs called **nodules** (Figure 4.1.3). In exchange for providing protected living space for the bacteria, the plants have a ready source of ionic nitrogen.

nodule a small swelling or lump

Nigel Cattlin/Alamy Stock Photo

Custom Life Science Images/Alamy Stock Photo

FIGURE 4.1.3 Plants such as beans and peas have a symbiotic relationship with nitrogen-fixing bacteria. The bacteria live in nodules on their root systems and the plants gain a constant source of ionic nitrogen.

Weblink
Interactive water cycle

Worksheet
Biogeochemical cycles

Water cycle

Water is considered a nutrient even though it has no specific nutritional value. In addition to providing a habitat for a diverse range of organisms, the ongoing supply of water is crucial to the processes of photosynthesis and cellular respiration, as well as to the maintenance of internal cellular environments in which all metabolic processes occur. The water cycle (Figure 4.1.4), also known as the hydrological cycle, is the continuous exchange of water between oceans, the atmosphere and the land. This cycle is powered by energy from the Sun. As a result of gains and losses in energy, water changes state as it moves through the cycle and its processes, including:

- evaporation – water changing state from liquid to gas
- condensation – water changing state from gas to liquid
- transpiration – water released from plants as a gas
- precipitation – water falling from the sky as a liquid or solid
- infiltration – liquid soaking into the soil
- percolation – liquid seeping into spaces between rocks and soil underground
- run-off – liquid flowing over Earth's surface.

Syllabus link
Chapter 6 in *Nelson QCE Biology Units 1 & 2* describes transpiration in further detail.

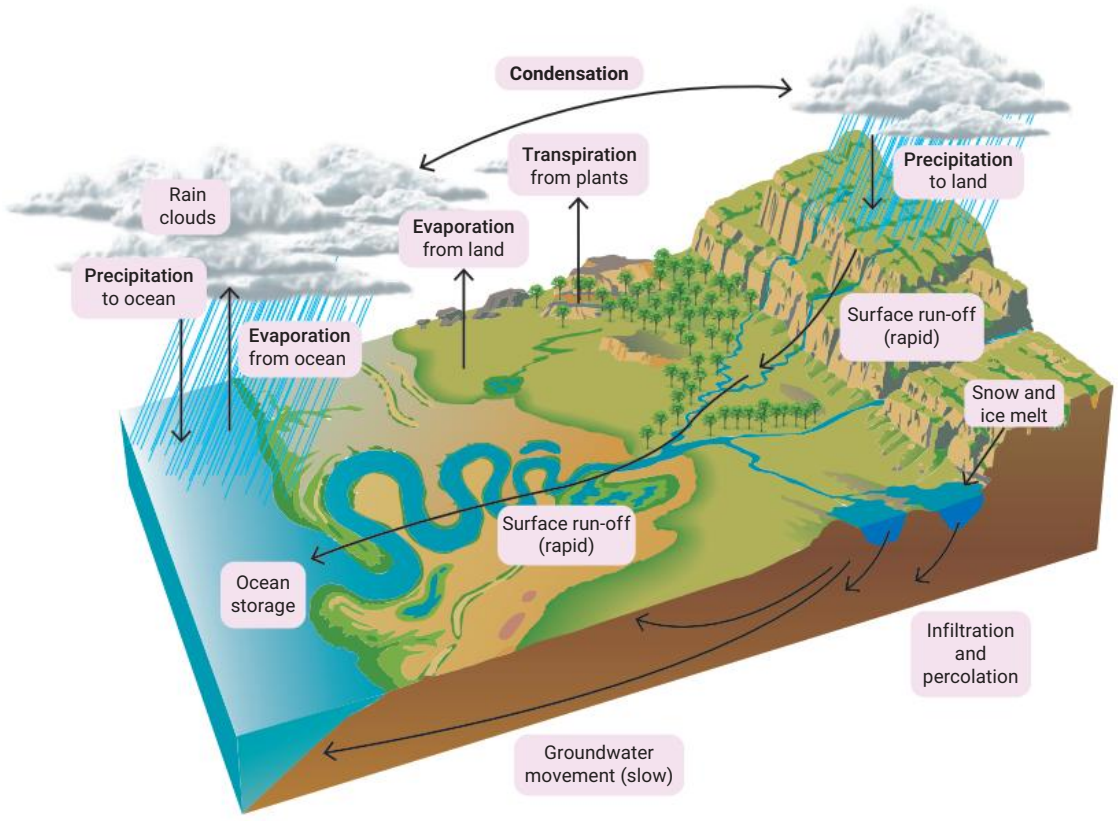


FIGURE 4.1.4 The water cycle follows water molecules between the abiotic and biotic components of an ecosystem, as well as between the three states of matter: solid, liquid and gas.

LEARNING CHECK 4.1

DESCRIBING

1 **Identify** three biogeochemical cycles.
2 **Describe** the two biological processes that cycle carbon between the atmosphere and living organisms.
3 **Identify** the processes involved in the water cycle.

APPLYING

4 **Explain** what would happen if large volumes of nitrogen-fixing bacteria were killed.
5 **Explain** why deforestation and the excavation and burning of fossil fuels are affecting the carbon cycle.

4.2 Transfer and transformation of solar energy

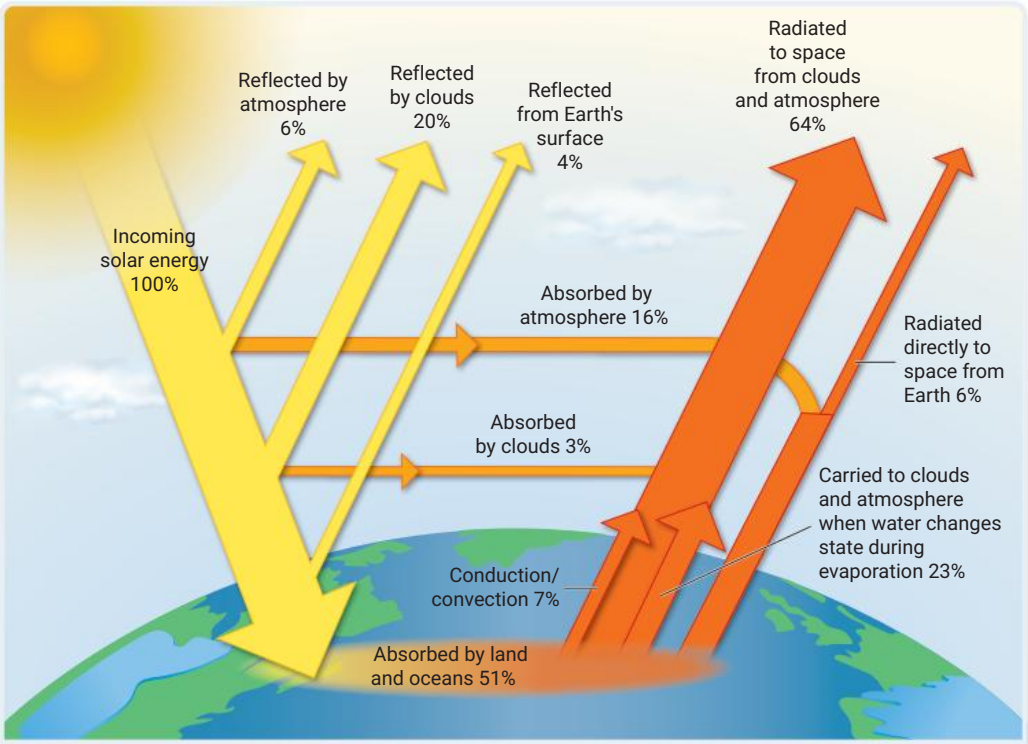
Sources of energy

All complex systems on Earth require a constant supply of energy to drive them. The Sun provides Earth's energy in the forms of light energy and heat energy. Heat energy warms the planet's surface, and this in turn warms the atmosphere that drives all of the geochemical

processes, hydrological cycle, tides, weather systems and ocean currents. The Sun emits all wavelengths of visible, infrared and ultraviolet radiation. The total amount of energy is very large. However, most organisms cannot capture this energy, so it is necessary to **transform** it into a more useful form.

transform to change from one type to another

About 70 per cent of the incoming energy from the Sun is absorbed by the atmosphere and Earth's surface. The remaining 30 per cent is reflected into space **(Figure 4.2.1)**. The absorbed energy drives processes in the atmosphere, hydrosphere and biosphere. Absorption of sunlight causes an increase in temperature, as the molecules of the atmosphere and surface vibrate more, and this energy is reradiated as heat energy. The more sunlight a surface absorbs, the warmer it gets, and the more energy it reradiates as heat.



Based on E. O. Falayi & A. B. Rabiu (2012). Solar Radiation Models and Information for Renewable Energy Applications. InTech. doi: 10.5772/35390

FIGURE 4.2.1 Earth's energy budget – what happens to the incoming solar energy

Weblinks
Solar energy
Earth's radiation budget

Worksheet
Energy flow

Leaves absorb, reflect and transmit most of the visible light and infrared radiation reaching Earth's surface **(Figure 4.2.2)**. The leaf structures, including the cuticle, epidermal cells, waxes and leaf hairs, affect the way light is absorbed or scattered. The variety of leaves among plant species are adapted to absorb and reflect light differently. For example, leaves of one species may be white and shiny or green and smooth to reflect and transmit most of the incoming light, whereas those of another species to reflect and absorb light well while transmitting very little. Light absorption is crucial for plants, as this is the energy source for photosynthesis. Heat energy is also absorbed, transmitted and reflected by leaves.

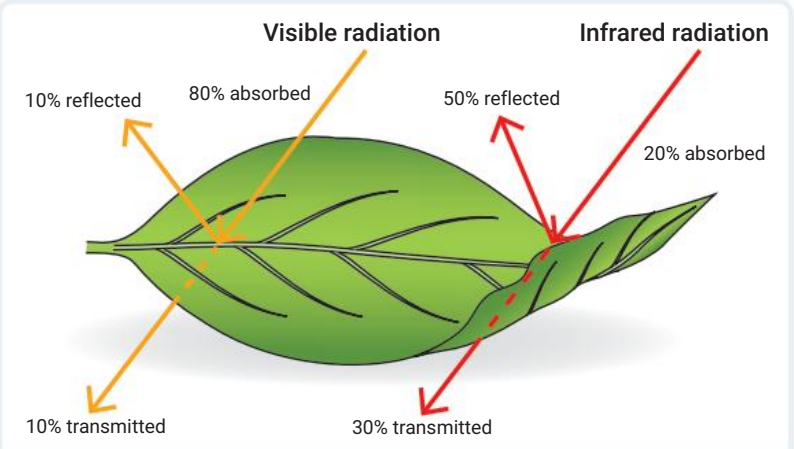


FIGURE 4.2.2 How light and heat energy are absorbed or reflected by leaves

Transformation of light to chemical energy

Plants, algae and some protists undergo photosynthesis and utilise the Sun's energy to combine molecules of water and carbon dioxide to form glucose molecules with oxygen as a by-product. Organisms that can capture the Sun's energy and convert it to sugars are called **autotrophs** because they do not rely on any other organism for their energy needs. The Sun's light energy is transformed into chemical energy during this process and then stored in the high-energy chemical bonds within the glucose molecules. Some of this energy is used by autotrophs for metabolic processes and the rest is stored as biomass in the form of starch or plant structures, such as leaves, stems, roots and fruit. Autotrophs (also known as producers or primary producers) are the basis of all organic matter and the initial source of chemical energy in most ecosystems.

autotroph (producer) an organism that can produce its own organic compounds from sunlight, water and carbon dioxide

Syllabus links
Chapters 5 and 6 in *Nelson QCE Biology Units 1 & 2* describe respiration and photosynthesis.

Chapter 9 of *Nelson QCE Biology Units 1 & 2* explores the regulation of body temperature in endotherms.

Weblink
Biomass energy

Transfer and transformation of chemical energy

Processes that move carbon through living systems, also transferring chemical energy, are summarised below.

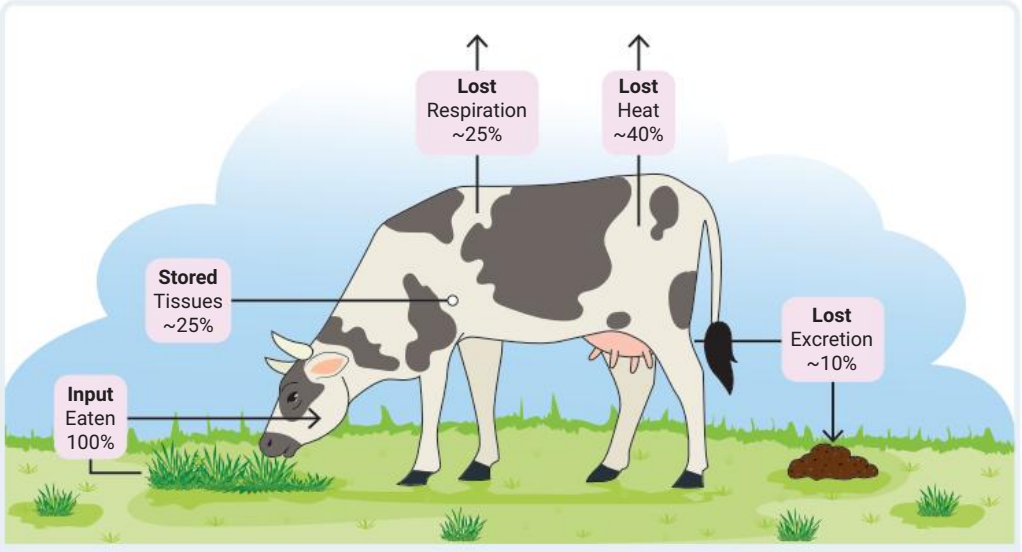
- Consumption – **heterotrophs** are organisms that cannot photosynthesise so must obtain their energy either directly or indirectly from organisms that can. Heterotrophs are also called consumers because they must consume other organisms to transfer the organisms' chemical energy to their own body systems, with carbon being incorporated into parts of their body structure.
- Respiration (aerobic or anaerobic) is the chemical reaction that releases CO_2 while transferring chemical energy from glucose to ATP to power cellular processes. This process also transforms some of the chemical energy to heat energy.
- Decay – wastes and dead organisms are broken down by decomposers and detritivores, such as bacteria, transferring chemical energy from the wastes to nutrients into the soil while releasing CO_2, and transforming part of the energy to heat energy.
- Fire – burning organic matter transforms most of the chemical energy to heat and light energy while also transferring some of it to CO_2.

Carbon is taken out of the atmosphere by photosynthesis, becomes biomass and is moved around by consumption then released via respiration or combustion (page 83). These processes show how closely related the carbon cycle is to ecosystem interactions.

During all transfers of chemical energy, some energy is also transformed into heat (Figure 4.2.3). In **endotherms**, such as mammals and birds, this heat energy maintains

heterotroph (consumer) an organism that cannot convert sunlight to useful energy and must consume other organisms for food

endotherm an organism that regulates and maintains internal body temperature higher than the temperature of the surroundings



Adapted from 'Energy loss', BioNinja, https://old-ib.bioninja.com.au/standard-level/topic-4-ecology/42-energy-flow/energy-loss.html

FIGURE 4.2.3 Transfer and transformation of chemical energy in a living organism. Chemical energy is transferred and stored in tissues. Metabolic processes transform the chemical energy into heat energy, which is lost to the environment.

a constant internal body temperature. However, they also lose energy through heat loss to the environment. **Ectotherms**, such as reptiles, rely on external sources of heat from the environment to regulate their body temperature. Consequently, endotherms require a much higher food consumption than equivalently sized ectotherms to balance out their heat loss.

ectotherm an organism whose internal body temperature reflects and fluctuates along with the surroundings

LEARNING CHECK 4.2

DESCRIBING

1 **Describe** what happens to the energy from the Sun that reaches Earth and its atmosphere.
2 **Describe** four forms of chemical energy transfer and/or transformation in an ecosystem.

APPLYING

3 **Explain** the role of detritivores and decomposers in energy flow.
4 **Explain** why heat energy is important to endotherms.

4.3 Analysing ecosystems

Food chains

Food chains and food webs are two ways to summarise the flow of matter and energy in ecosystems. Food chains have their own internal order, with each organism occupying a position or **trophic level** (Figure 4.3.1), whereas a food web shows the interconnecting food chains in an ecosystem.

food chain a chain of organisms where one organism occupying a trophic level is consumed by the next organism in a higher trophic level

trophic level a level in the food chain of an ecosystem based on feeding relationships

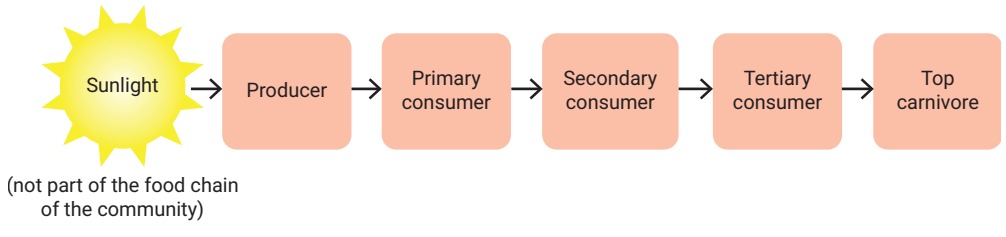


FIGURE 4.3.1 Food chains begin with the Sun as the original source of all energy in the chain.

From the base level of autotrophs or trophic level 1 (TL1), matter and energy move through other trophic levels populated by heterotrophs. Trophic level 2 (TL2) contains herbivores. Trophic level 3 (TL3) and above contain omnivores and carnivores. A food web shows the interconnecting food chains in an ecosystem.

Trophic levels continue to be numbered in order if there are additional feeding levels. Some commonly used terms are summarised in Table 4.3.1.

TABLE 4.3.1 Terms not stated in the syllabus, but commonly used

Trophic level 1	Primary producers	Producers
Trophic level 2	Primary consumers	Herbivores – eat plant material only
Trophic level 3	Secondary consumers	Carnivores – eat animal material only
Trophic level 4	Tertiary consumers	Omnivores – eat plant and animal material

Weblink
Food chains and food webs

The first organism in every food chain receives its energy directly from the Sun, although the Sun is not usually included in the chain because food chains focus on feeding relationships. Arrows represent the flow of energy and matter from one trophic level to another. Each organism in the chain receives energy and matter from the preceding one, generally by eating it (Figure 4.3.2). At each trophic level, a proportion of the available energy is either used to fuel the needs of the organism or lost due to inefficiencies in the process, and the remaining energy is transferred to the next level.

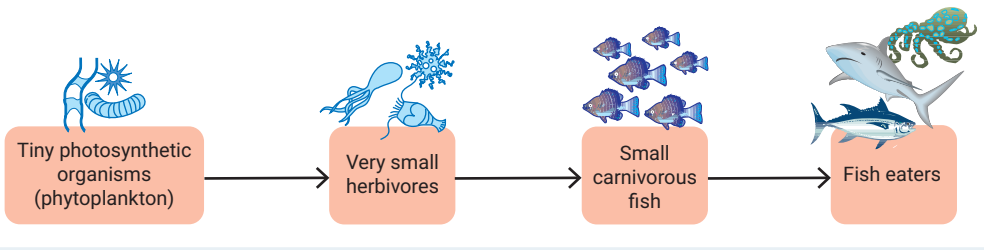


FIGURE 4.3.2 In general, food chains simplify feeding relationships by focusing on one organism or group of organisms at each trophic level.

Productivity: GPP and NPP

Not all producers make the same amount of initial biomass for their ecosystem. This depends on the availability of water, nutrients and sunlight, but also on temperature, light intensity and the nature of the organism and whether the molecules produced are used or stored. For example, an area covered in trees produces significantly more biomass than the same area covered with grass (Figure 4.3.3). Tropical forests cover only about 4 per cent of Earth's surface but contribute about 25 per cent of the world's yearly **gross primary productivity (GPP)** of organic matter. Ocean ecosystems depend on producers such as phytoplankton to transform light energy into vast amounts of organic matter, but this organic matter is not stored in plant structures like those seen in terrestrial plants.

gross primary productivity (GPP) the total organic matter produced annually in an area by photosynthesis

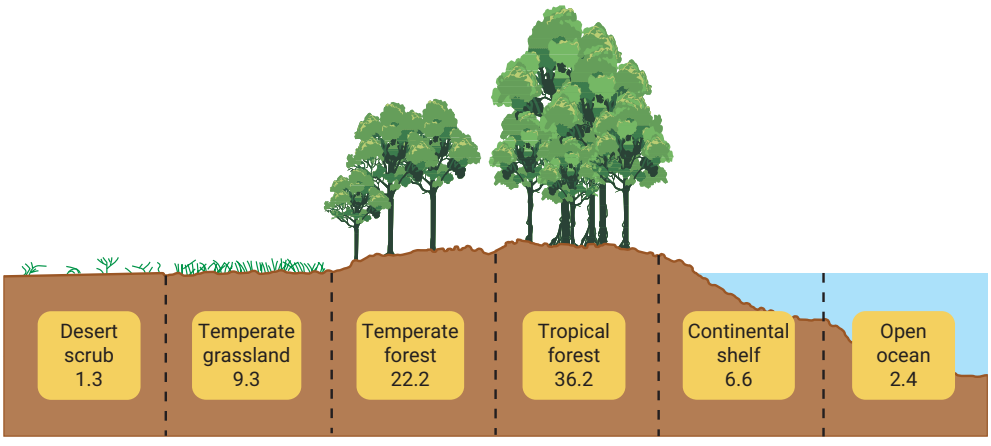


FIGURE 4.3.3 Different autotrophs have different primary productivity rates. The numbers in this diagram refer to the amount of chemical energy converted from sunlight per square metre each year (kJ m^{-2} $year^{-1}$).

net primary productivity (NPP) the amount of organic matter made available to herbivores annually; equals gross primary productivity minus the energy required by the producers themselves

Although GPP refers to the total amount of organic matter made in an ecosystem by producers, not all of this material is available to the consumers for food because the producers use some of it for their own energy needs. The actual amount of energy that is available to support consumers is the amount of energy, or carbon, fixed by producers (GPP), minus that required by the producers for cellular respiration. This remaining amount is called the **net primary productivity (NPP)** of an ecosystem.

Calculating energy efficiency

Consumers differ considerably in how efficiently they convert the energy they receive into biomass, which can then be consumed by organisms at the next trophic level. The ecological efficiency of an ecosystem is low, generally about 10 per cent of the energy at one trophic level is passed on to the next level (the '10 per cent rule'). The remaining 90 per cent is transformed by metabolism into heat energy and lost to the surroundings or remains as chemical energy in both the uneaten portion of an organism and its body waste **(Figure 4.3.4)**. These percentages can vary depending on the organism or ecosystem.

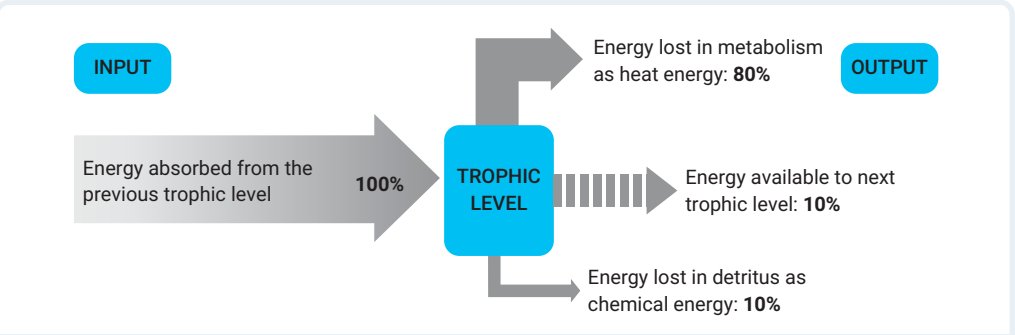


FIGURE 4.3.4 Trophic efficiency describes the proportion of energy that is available to the next trophic level within a food chain.

Understanding energy loss at each trophic level helps to explain why food chains are usually only four to five trophic levels long and why higher trophic levels usually contain fewer organisms and less biomass. The loss of so much energy at each trophic level means there is not enough energy to support organisms at higher levels. Understanding ecological efficiency can help ensure energy flow in ecosystems is not disrupted in a way that is detrimental to the organisms present. Data is gathered on the bulk biomass and energy production of each species, each year, after organising them into trophic levels. This can be quite difficult for complex food webs because some organisms occupy three trophic levels depending on their food source. With simpler food webs, it is considerably easier **(Figure 4.3.5)**.

Energy flow diagrams

Energy flow diagrams map the path of the Sun's energy as it moves through the trophic levels of an ecosystem and is transformed into heat by metabolism. Energy flow through the trophic levels can be presented more clearly in an energy flow diagram **(Figure 4.3.6)**. Several key principles govern the construction of these diagrams.

1. Arrows show the direction of energy flow and are labelled with the form and quantity of energy they carry.
2. Boxes represent trophic levels in sequence. The Sun is included because these diagrams focus on mapping energy, rather than feeding relationships.
3. Heat energy from metabolic processes is lost from each trophic level to the surroundings.
4. Detritivores and decomposers are included as a subtrophic level because they play an important role in energy transformation, because this energy is eventually converted to heat energy.
5. Total heat energy lost must equal the amount of light energy brought into the system by producers.

To calculate energy efficiency, divide the energy produced by the organism by the energy available from the previous trophic level. For clarity, this can be converted from a decimal to a percentage. Worked example 4.3.1 shows how to do this calculation.

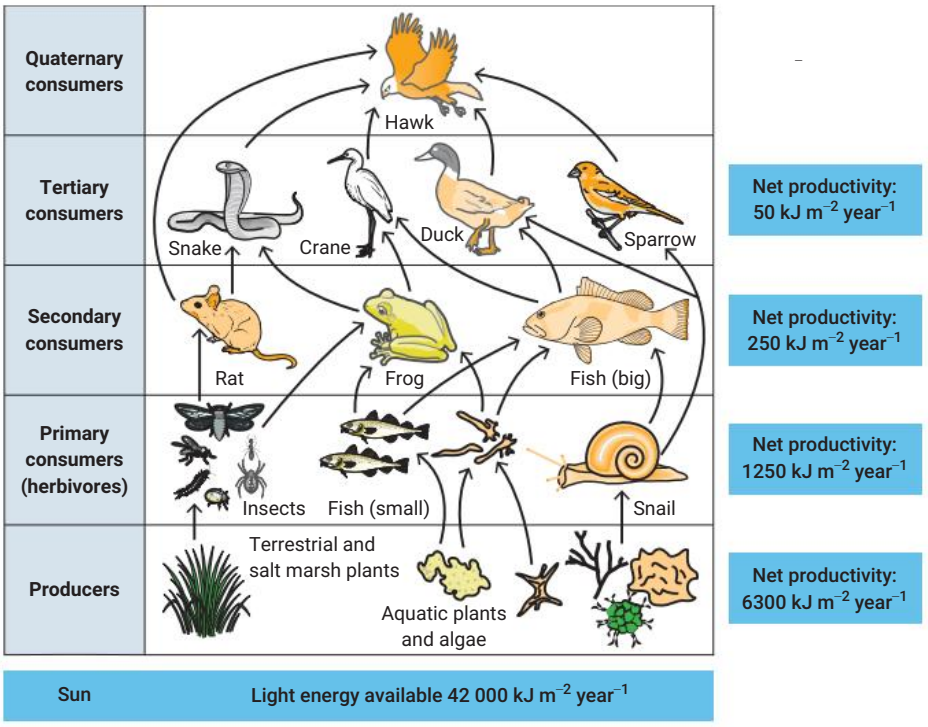


FIGURE 4.3.5 The net productivity at each trophic level includes the total amount of energy that the organisms produce in edible parts per square metre of space in a year.

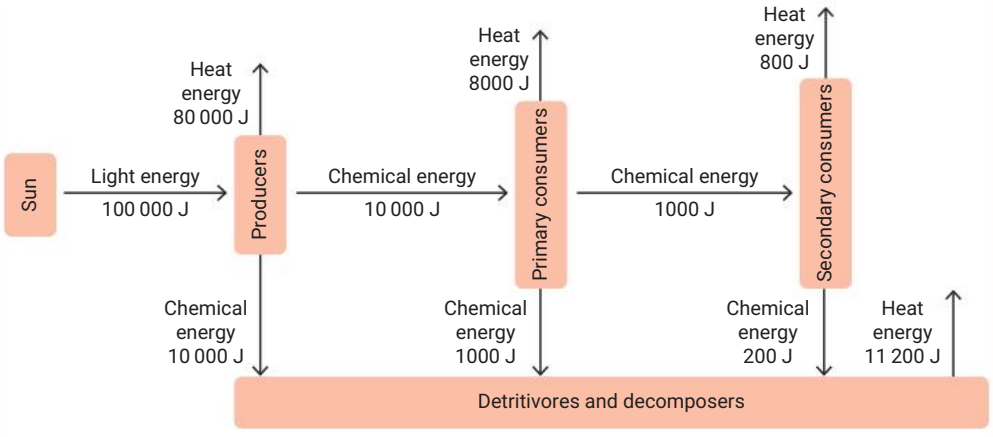


FIGURE 4.3.6 Energy flow diagrams illustrate the movement of energy through ecosystems.

KEY FORMULA

Trophic energy efficiency

$$\text{Percentage efficiency} = \frac{\text{net productivity of organism}}{\text{net productivity of previous trophic level}} \times 100$$

WORKED EXAMPLE 4.3.1

Calculate the percentage efficiency of the producers in Figure 4.3.5.

ANSWER

Substitute the values for producers and available light into the key formula.

$$\text{Percentage efficiency} = \frac{\text{net productivity of organism}}{\text{net productivity of previous trophic level}} \times 100$$

$$= \frac{6300}{42\,000} \times 100$$

$$= 15\%$$

Ecological pyramids

Ecological pyramids are another way to represent the amount of biomass, energy or individual organisms at a particular trophic level. They can represent a single food chain or an entire ecosystem. Figure 4.3.7 shows a food chain from a coastal scrub ecosystem in Queensland. Figure 4.3.8 shows this food chain as different types of ecological pyramids.

ecological pyramid a pyramid diagram that shows the relative proportions of biomass, numbers or energy at each trophic level in an ecosystem

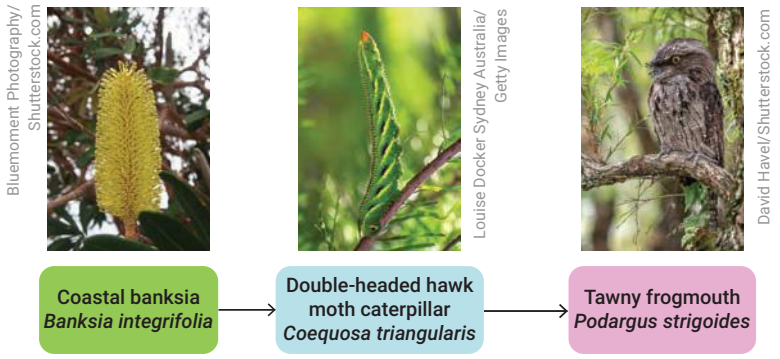


FIGURE 4.3.7 A food chain for a Queensland coastal scrub ecosystem

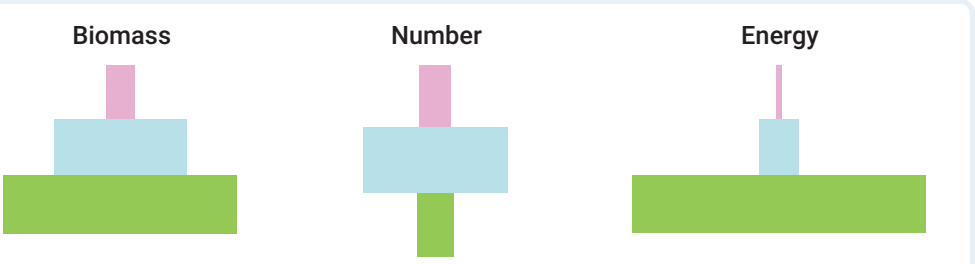


FIGURE 4.3.8 Ecological pyramids: the width of each level in a pyramid indicates the relative biomass, number of individuals or amount of energy available in each trophic level. The bottom level indicates producers, with each successive trophic level stacked on top.

Worksheet
Transfer and transformation of energy

A biomass pyramid shows the relationships between the amounts of autotrophic matter and heterotrophic matter. These pyramids are almost always upright because biomass is lost between trophic levels through waste and as CO_2. Marine ecosystems are an exception because the high reproduction rate of phytoplankton can support a larger mass of zooplankton.

A number pyramid shows the relative numbers of organisms in each trophic level. These are usually upright when the producer species is small, such as grasses or aquatic plants, so herbivores eat many individuals to survive. An exception is shown in Figure 4.3.8 where the relatively large biomass of a producer species, like a tree or shrub, can support many herbivores. In this case, one banksia shrub can support multiple caterpillars.

An energy pyramid shows the relative amount of energy stored at each trophic level. These pyramids are always upright. Each trophic level will be around 10 per cent the size of the previous level, representing the inefficiency of the energy transfer. A balanced and healthy ecosystem must have a stable energy pyramid, with decreasing amounts of energy in each successive trophic level.

Weblink
Pyramids of number and biomass

LEARNING CHECK 4.3

APPLYING

1 **Explain** the difference between GPP and NPP.

2 Biomass pyramids are often constructed as part of the information-gathering process used to inform ecosystem management strategies. **Explain** the benefits and limitations of basing ecological decisions on a biomass pyramid.

3 **Calculate** the total energy lost to metabolism and wastes between TL1 and TL2 in Figure 4.3.5.

4 **Calculate** the percentage efficiency between TL2 and TL3 in Figure 4.3.5.

5 **Calculate** the percentage efficiency between the total energy originally available from the Sun and the amount available to TL4 in Figure 4.3.5.

ANALYSING

6 **Identify** the relationship in the data by drawing a biomass pyramid showing the correct scale of losses in an ecosystem with:

- 2 kg m^{-2} of producers
- 675 g m^{-2} of primary consumers
- 150 g m^{-2} of secondary consumers
- 75 g m^{-2} of tertiary consumers.

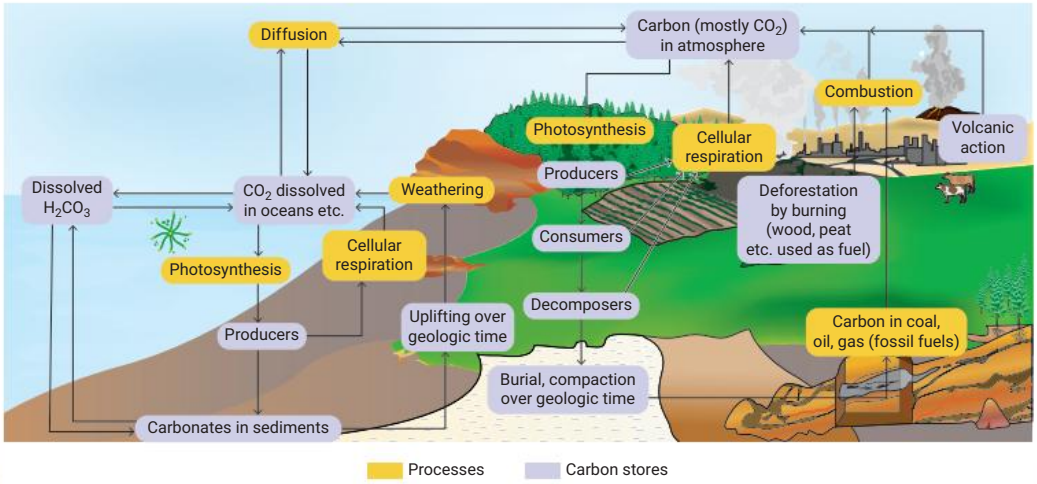
Begin with producers as a bar 20 cm wide and take careful note of the units.

7 **Identify** the relationship in the data by drawing an energy flow diagram for an ecosystem in which 400 000 kJ of light energy is brought into the system by producers that are 13 per cent efficient. The primary consumers are 15 per cent efficient and the secondary consumers are 18 per cent efficient. Heat lost by each trophic level is 10 per cent.

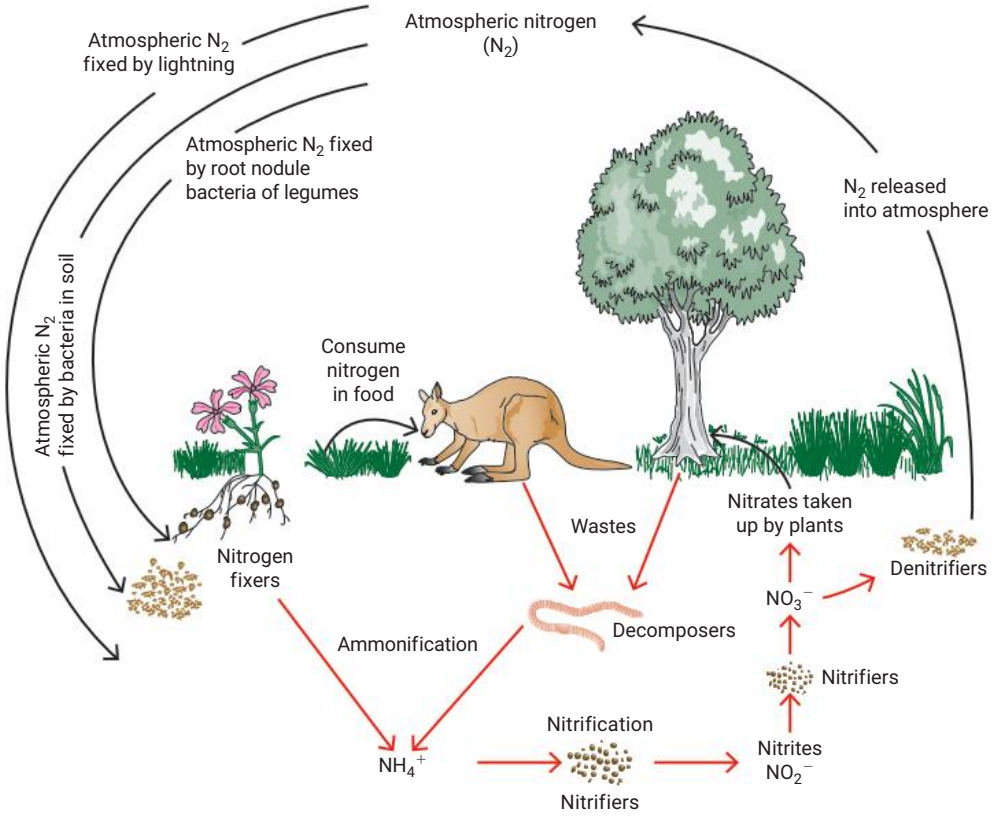
Transfer and transformation of matter

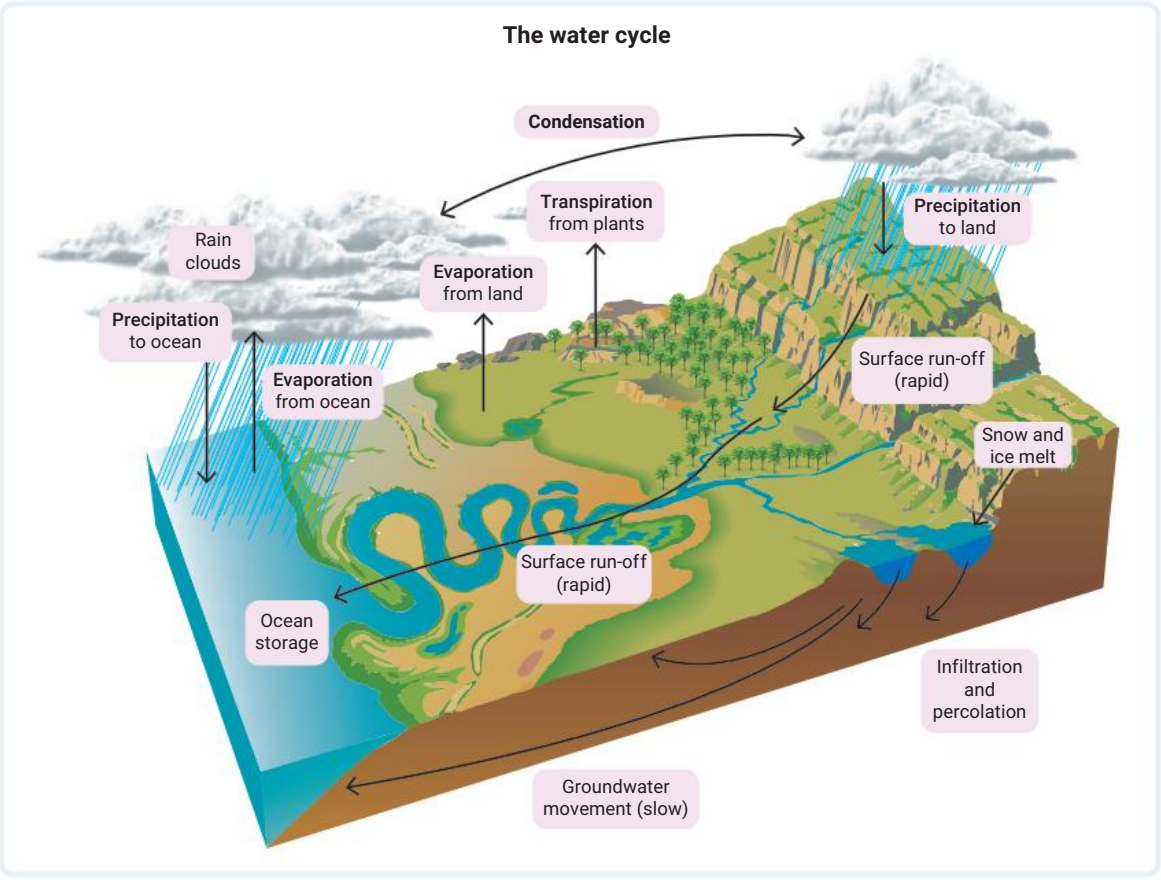
- Important nutrients such as nitrogen, carbon and water can be cycled through systems through the nitrogen, carbon and water cycle respectively.

The carbon cycle



The nitrogen cycle



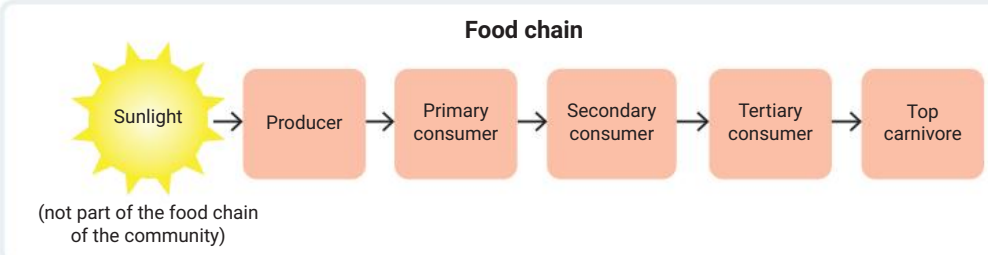


Transfer and transformation of energy

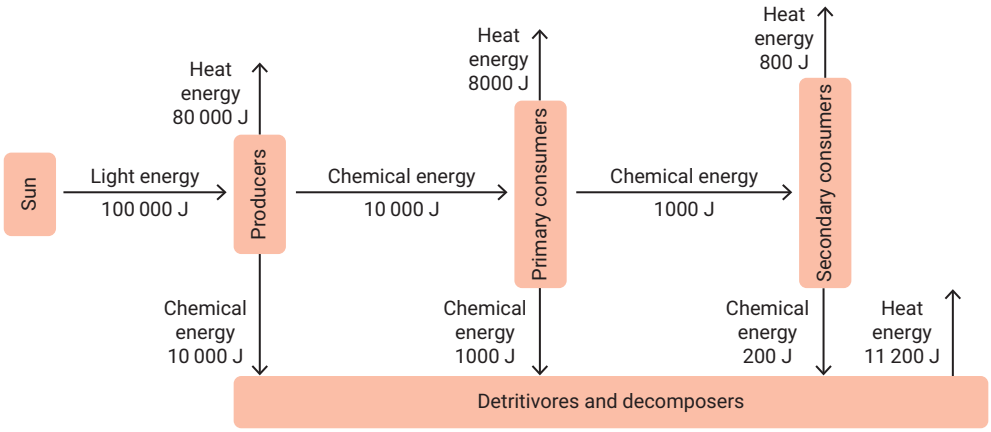
- Energy from the Sun is often transformed into other types of energy. For example, plants convert light energy into chemical energy and organisms convert chemical energy into heat energy.
- Chemical energy is transferred from one organism to another; for example, through consumption.

Showing energy flow

- Food chains, food webs, ecological pyramids and energy flow diagrams show the movement of energy through an ecosystem.
- The transfer of energy is not 100 per cent efficient; only approximately 10 per cent of energy is transferred from one level to the next.



An energy flow diagram



CHAPTER EXAM

MULTIPLE CHOICE

1. Producers can also be categorised as:
   - **A** autotrophs.
   - **B** chemotrophs.
   - **C** heterotrophs.
   - **D** homotrophs.

2. In the nitrogen cycle, which form is nitrogen not found in?
   - **A** N
   - **B** N_2
   - **C** NO_3^-
   - **D** NH_4^+

3. The process of photosynthesis transforms:
   - **A** chemical energy into light energy.
   - **B** chemical energy into heat energy.
   - **C** light energy into chemical energy.
   - **D** light energy into radiant energy.

4. A process that is part of the carbon cycle is:
   - **A** ammonification.
   - **B** breathing.
   - **C** precipitation.
   - **D** respiration.

5. A process that is part of the nitrogen cycle is:
   - **A** ammonification.
   - **B** breathing.
   - **C** respiration.
   - **D** precipitation.

6. A process that is part of the water cycle is:
   - **A** ammonification.
   - **B** breathing.
   - **C** precipitation.
   - **D** respiration.

Questions 7–9 relate to the following table of information.

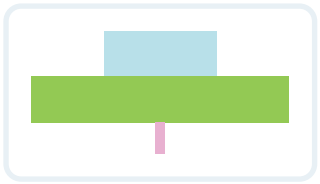
An extract from a food web for a lake ecosystem in Western Australia

Organism	Role/diet
Bulrush	Producer
Coot	Grass, algae, waterweed, bulrush
Gambusia (fish)	Mosquito larvae, midge larvae, water fleas
Grass	Producer
Motorbike frog	Fish, lizards, insects, spiders
Purple swamp hen	Grass, bulrush, waterweed, frogs
Swamp harriers	Coots and other water birds, small mammals, reptiles, frogs, fish
Water flea	Algae, water weed, bulrush, detritus

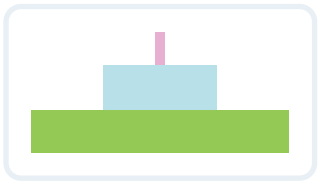
7. Which of the following is a correct food chain?
   - **A** Grass → motorbike frog → gambusia → cane toad
   - **B** Grass → coot → purple swamp hen → motorbike frog
   - **C** Bulrush → coot → swamp harrier → motorbike frog
   - **D** Bulrush → water flea → gambusia → motorbike frog

8. Which of these ecological pyramids is the best representation for three trophic levels of this food web?

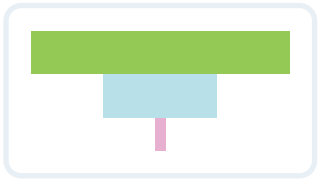
   A Pyramid of energy



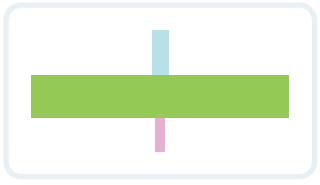
   B Pyramid of energy



   C Pyramid of biomass

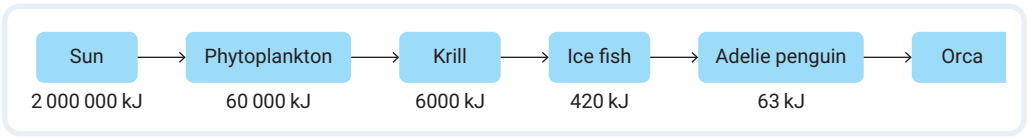


   D Pyramid of biomass



9. Which is the highest trophic level evident in the data in the table?
   - **A** TL3
   - **B** TL4
   - **C** TL5
   - **D** TL6

10. Ocean ecosystems are often less efficient at converting sunlight into chemical energy because of the reduced light intensity below the water's surface.



Odum, H.T. (1957) Tropic Structure and Productivity in the Silver Springs Community, Florida. *Ecological Monographs, 27*(1), pp. 55–112.

The efficiency of energy transfer from TL3 to TL4 in the food chain shown is:
- **A** 3 per cent.
- **B** 7 per cent.
- **C** 10 per cent.
- **D** 15 per cent.

SHORT RESPONSE

11. **Explain** how food webs form part of the carbon cycle, using examples from the food web in Question 7 to support your explanation.

12. In general, humans rarely eat carnivores. Provide an ecological explanation for this observation.

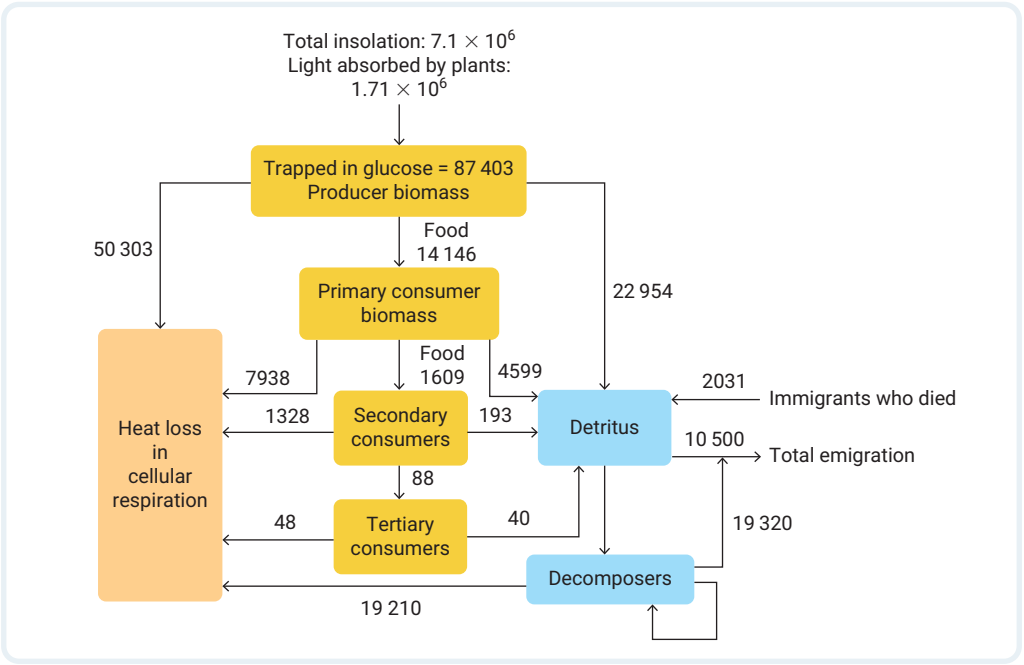
CROSS-CHAPTER QUESTION

13. Including a reference to the carbon cycle, **explain** how biomass production and species diversity would change if another two species that eat bulrushes were introduced into the food web shown in Question 7. Consider short-term and long-term effects.

DATA ANALYSIS

Questions 14 and 15 refer to the following information.

The following energy flow diagram is for a community in Silver Springs – a spring-fed stream in Florida, USA. The Silver Springs community was the first study of trophic efficiency, undertaken by ecologist H.T. Odum in 1957. The units used are kJ m^{-2} $year^{-1}$.



Odum, H. T. (1957) Trophic Structure and Productivity in the Silver Springs Community, Florida. *Ecological Monographs*, *27*(1), pp. 55–112.

14. **Apply understanding**

Calculate the efficiency of the primary consumers in this community.

15. **Interpret evidence**

Determine if heat losses equal the total energy brought into the system by producers. Provide reasoning.

CHAPTER 5

Interactions

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SYLLABUS DOT POINTS

SCIENCE UNDERSTANDING

- 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.
- Explain how overexploitation, habitat destruction, monocultures and pollution affect community structure and ecosystem functioning.

SCIENCE INQUIRY

- Investigate the competitive exclusion principle, e.g. by studying vertical zonation on a tree.

Introduction

The Great Barrier Reef has the most marine diversity in the world with 450 types of hard coral, more than 1500 types of fish and more than 6000 types of molluscs. It is also the world's largest coral reef ecosystem. Organisms within this reef ecosystem depend on each other: fish species depend on corals for food, shelter and safety from predators, and corals depend on the grazing by certain fishes for reproductive success. An understanding of the relationships and interactions helps scientists assess and support community structure and ecosystem functioning in all types of ecosystems.

ASSUMED KNOWLEDGE

- ✓ Organisms are classified as species.
- ✓ Transfer of energy and matter can be represented by food chains, food webs and ecological pyramids.
- ✓ Data about organisms and their environment is collected through sampling.
- ✓ Different environments have biotic and abiotic factors that limit the survival of organisms.
- ✓ The diversity of species can be described using species richness, species evenness and Simpson's diversity index (SDI).

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ explain the role of each organism in the following relationships and whether they are benefited, harmed or not affected: predation, competition, mutualism, commensalism, parasitism
- ✓ describe an ecological niche by the habitat and role of the organism
- ✓ explain why two organisms cannot occupy the same niche because of competitive exclusion
- ✓ explain the effect of removing an organism on community structure
- ✓ after analysing data in the form of food webs and/or population numbers:
  - identify a keystone species as one whose removal has a larger effect than expected on community structure or ecosystem function, and what the effect is
  - explain whether the relationship between two organisms is predation, competition, mutualism, commensalism or parasitism by referring to the relative benefit received, harm caused or the organism being unaffected
- ✓ predict changes (e.g. population numbers, feeding relationships, symbiosis, competition) that could occur in an ecosystem if an organism is removed
- ✓ explain how the diversity of a community (species richness, evenness and/or SDI) and interactions change as a result of overexploitation, habitat destruction, monocultures or pollution
- ✓ explain how the cycles of matter and/or energy change as a result of overexploitation, habitat destruction, monocultures or pollution.

Weblink
Species interactions and competition

5.1 Species interactions

Predation, competition, symbiosis and parasitism are all species interactions that have wide-ranging effects on their ecosystems. Understanding the relationships within and between species can help improve understanding of how an ecosystem works and how it can be classified.

predation a species interaction in which one species kills and eats another

predator an organism that kills and consumes all or part of the body of another organism

prey an organism that is hunted by another organism for food

Predation

One of the most common and overt interactions within an ecosystem is **predation**. In this relationship, one organism feeds on another by consuming it. When considering animal interactions, the **predator** typically hunts, kills and consumes the **prey** organism. Although predators usually have a preferred prey species, it is unusual for a predator to depend solely on one species. If one prey species becomes scarce, the predator can turn to others.

The dynamic relationship that exists between predator and prey (Figure 5.1.1) is usually balanced, but sometimes conditions can change and upset this balance. Under favourable conditions, with increasing availability of prey, the number of predators can increase until there are no longer enough prey to support the increased predator population. Then the number of predators decreases, allowing the prey population to recover and increase again. During a period of adverse conditions, the prey population can decrease. When this occurs, there is increased competition within the predator population. Predators may decrease in number or turn to alternative prey species, and the effect on them can be severe. Predator populations generally remain far below that of the prey because they occupy a higher trophic level in the food chain.

Syllabus link
Chapter 4 discusses food chains.

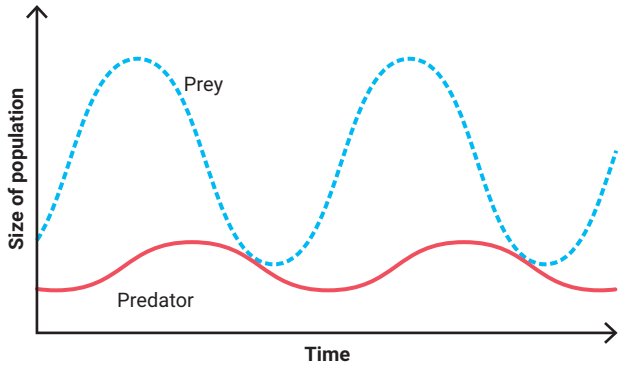

FIGURE 5.1.1 Predator populations are always smaller than their total prey population to enable sufficient energy transfer between trophic levels. A decrease in the availability of prey will result in the starvation of the less effective predators.

Predation of any sort affects the prey population in an ecosystem. The broader definition of predation focuses on consumption of an organism, which usually results in the death of that organism. Therefore, predation can include more than just animals preying on other animals, such as plants preying on animals (e.g. Venus flytrap and pitcher plant) and animals preying on plants (herbivorous predation). For example, seed predators have a large effect on the plant population and their distribution throughout an ecosystem. Seed predators only feed on the seeds of plants (which are considered an entire organism), consuming them entirely or causing the seeds to become unviable or damaged. An indirect effect of predation on the biodiversity of an ecosystem is the release of nutrients into the soil from decomposing organic matter, such as animal carcasses, left behind by predators, allowing for micro-organisms to survive in the ecosystem.

Competition

Individuals compete because they require the same resources for survival, even if they have different roles in an ecosystem. **Competition** is a common feature of all communities and can occur directly (at the same time) or indirectly (e.g. a food source is consumed during the day, so none is available for nocturnal animals). Intraspecific competition occurs between individuals of the same species, whereas interspecific competition occurs between individuals of different species (Figure 5.1.2).

competition a species interaction in which two or more individuals, from the same or different species, compete for the same resource in the same area

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William Edge/Shutterstock.com

FIGURE 5.1.2 (a) Intraspecific competition – kangaroos fighting for a mate. (b) Interspecific competition – feral honeybees outcompeting native birds and mammals for access to tree hollows.

Weblink
Symbiosis: mutualism, commensalism and parasitism

symbiosis a relationship between individuals of two or more species in which at least one organism benefits from the interaction

parasite an organism that causes long-term disease while leaving the host alive, such as protozoa and worms

host an organism that is infected with a pathogen or parasite

Symbiosis

Symbiosis is the general term for the relationship in which at least one species benefits from the interaction. The three main types are:

- parasitism: one species benefits at the expense of the other (+/–)
- mutualism: both species benefit from the interaction (+/+)
- commensalism: one species benefits and the other neither benefits nor is harmed (+/0).

Parasitism (+/–)

Parasitism occurs when an organism, the **parasite**, lives in (endoparasite) or on (ectoparasite) another organism, the **host**, to consume nutrients. Unlike predation, parasites leave their host alive, if unwell. The parasite benefits from the interaction by gaining nutrition and a habitat. Hosts are harmed. Examples of endoparasites are worms, fungi and protozoa. Ectoparasites include ticks and lice, and some plants and fungi. Hosts are usually plants or animals. The host is the parasite's habitat and a parasite must find a new host before the existing one dies.

Mutualism (+/+)

Mutualism occurs when both species involved benefit from any interactions. This could include 'goods' or 'services' that they cannot produce themselves, such as nesting space, nutrition or defence from predators.

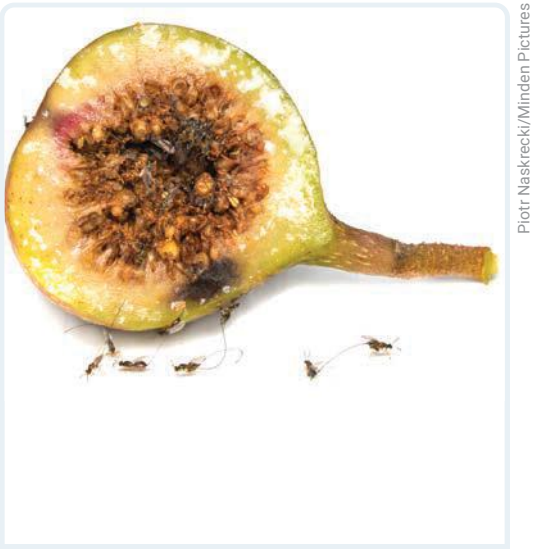
Myrmecodia beccarii is an ant plant (a plant that provides nesting space to ants) native to Australia's mangroves and lowland forests near Cairns and northern Cape York. As it grows, its tuber forms hollow chambers that ants, mainly *Iridomyrmex cordatus*, inhabit. This symbiotic relationship benefits both: the plant offers shelter while the ants provide nutrients from their food leftovers (Figure 5.1.3).

If the species are entirely dependent on each other, it is an example of obligate mutualism (e.g. some species of moth and the flowering plant *Boronia megastigma* (Figure 5.1.4)).

Facultative mutualism occurs when the species benefit by their relationship but could survive without each other; for example, plants that have many different pollinators.

Auscape/Universal Images Group/Getty Images

FIGURE 5.1.3 *Myrmecodia beccarii* provides nesting space to ants, which form and occupy chambers in an example of mutualism.



Piotr Naskrecki/Minden Pictures

FIGURE 5.1.4 An example of obligate mutualism: research suggests only one species of moth can pollinate *Boronia megastigma*.

Commensalism (+/0)

Commensalism is an association between two organisms where one benefits and the other is unaffected, neither benefiting nor being harmed.

Gramastacus insolitus is a very small non-burrowing Australian freshwater crayfish occurring almost exclusively in seasonal habitats throughout its range in Victoria. Research suggests that *G. insolitus* are commensal on other crayfish species, using the burrows made by larger crayfish species to survive the seasonal drying of their habitat.

Austcray.com

FIGURE 5.1.5 *Gramastacus insolitus* is an example of a commensal organism.

Worksheet
Species interactions

Keystone species

keystone species a plant or an animal that plays a unique and crucial role in the way an ecosystem functions

Keystone species help to maintain community structure (types and numbers of species present) by occupying important roles in the ecosystem. They have a disproportionately large influence over the stability and biodiversity of the whole community, including species they do not directly interact with. A keystone species is not necessarily the most abundant species, or the top-level predator, but their presence prevents any one species from monopolising space and resources in the area.

The purple sea star (*Pisaster ochraceus*) is a natural predator of mussels in the intertidal zones of Pacific Ocean seashores **(Figure 5.1.6)**. When researcher Robert Paine removed purple sea stars from this environment, the resident mussels were no longer affected by predation and their population expanded until they displaced species such as barnacles and limpets. The diversity of species in the area decreased from 15–20 invertebrates and algae to fewer than five over a period of 3 years. When the purple sea stars were returned, the mussels were again preyed on and the barnacles, limpets and other species had space to return to.

William Ragosta/Alamy Stock Photo

FIGURE 5.1.6 Purple sea stars (*Pisaster ochraceus*) are a keystone species in intertidal rock pools, where they keep the mussel numbers under control.

In this community, the presence of the predator, *P. ochraceus*, allows the stable coexistence of a large number of species with the same requirements for food and space. The purple sea star in this community is the keystone species.

Other categories of species are foundation, umbrella, flagship, indicator and invasive species. (These are important classifications that help ecologists determine ecosystem functions and services but are not stated explicitly within the 2025 syllabus.)

LEARNING CHECK 5.1

DESCRIBING

1 **Identify** one example of competition within a species and one example of competition between two species.
2 **Identify** the characteristics of a keystone species.
3 **Describe** the role that purple sea stars play in their community.

APPLYING

4 **Explain** why predator and prey populations follow a predictable and repetitive cycle, as in Figure 5.1.1.
5 **Explain** the four species interactions.

ANALYSING

6 African acacia species are often plagued by beetle grubs that destroy their seeds and prevent them from germinating by themselves. This would have dire consequences for the trees, if not for elephants. Many animals, including elephants, feast on their fruits, but elephants don't chew their food much so their dung contains a lot of fibrous matter, including whole, beetle-free acacia seeds. On average, 90 per cent of acacia seeds deposited in elephant dung germinate.

Identify the relationships between acacia trees, beetles and elephants.

5.2 Ecological niche

The organisms that inhabit an ecosystem survive because of the particular set of biotic and abiotic factors present. The way in which species function and their role within their environment (e.g. when they feed, what they feed on, where they live and when they reproduce) is known as an **ecological niche**. To place this concept into context, Eugene Odum (1913–2002) a US biologist at the University of Georgia, made the analogy that if the species' habitat was its home address, then its ecological niche was the combination of its profession and its location. If two species attempt to occupy the same niche (i.e. practise the same profession in the same location), one will eventually out-compete the other until only one remains. Narrow niches, where the role and location of a species is very specialised, are good for biodiversity because they allow the time, space and resources to support a larger number of species in the community.

ecological niche the role and space that an organism fills in an ecosystem, including all its interactions with the biotic and abiotic factors of its environment

The niche of the short-beaked echidna (*Tachyglossus aculeatus*) includes being mainly nocturnal, ground dwelling and feeding on ants, termites and other insects. Echidnas burrow in soil, hide under vegetation and shelter in hollow logs and rock crevices. Their role is 'ecosystem engineers': studies show that they spend up to 12 per cent of their time digging. Echidnas move up to 200 m^3 of soil each year, reducing compaction, improving soil mixing and water penetration, incorporating leaf litter and other organic matter into the soil, and reducing run-off and erosion. Echidnas are one of the remaining mammals that perform this function; therefore, they have one of the widest niches and distributions of any native Australian mammal.

The common wombat (*Vombatus ursinus*) is another solitary native Australian species whose burrowing actions improve soil health by bringing important nutrients to the surface and mixing organic matter and seeds through soil. At dusk, wombats leave burrows to graze on grasses and roots, often travelling kilometres looking for food. They play an important role in the ecosystem of their habitat by grazing and displacing the soil, thus enhancing the plant growth in the area. Despite these role similarities, their diets allow them to occupy a different niche from that of echidnas.

Paul Looyen/Shutterstock.com

jindrich_pavelka/Shutterstock.com

FIGURE 5.2.1 (a) Echidna and (b) wombat distributions often overlap. However, although they have similar digging roles, they occupy different niches, particularly for diet.

Competitive exclusion principle

An organism's **fundamental niche** is defined as the widest potential niche that they could occupy in ideal conditions, including locations that have the necessary abiotic factors for survival and all possible roles. In reality, predation, competition and disease reduce the location and roles an organism actually occupies. This narrower set of interactions and locations is called the **realised niche**.

fundamental niche the widest potential niche that a species could occupy without competitors, predators or parasites

realised niche the actual niche that a species occupies, given the restrictions placed on it by interactions with other species

Competitive exclusion is one of the main reasons for the difference between fundamental and realised niches.

competitive exclusion principle a key ecological principle that states that no two species can occupy exactly the same niche in an ecosystem

resource partitioning the creative use of space and time that reduces competition between species and allows many unique ecological niches to exist in the same area

The **competitive exclusion principle** states that no two species can occupy exactly the same niche in an ecosystem. If two species have overlapping fundamental niches, they will compete with each other in the overlapping areas until one out-competes the other and the other retreats.

In the intertidal zones discussed earlier, the purple sea stars (*P. ochraceus*) preyed on the mussel population. When the sea stars were removed, the mussel population was no longer restricted to this narrow realised niche and expanded into more of their fundamental niche, which overlapped with neighbouring populations of barnacles and limpets. This overlap triggered the competitive exclusion principle and biodiversity plummeted as the mussels outcompeted the other species. The ecosystem re-estabilised after the sea stars were reintroduced and the mussels were forced back into their original realised niche.

Ways to reduce competition include **resource partitioning** where organisms differ in their use of space and even the timing of their activities. For example, different forest birds feed on the same trees at different heights above the ground (Figure 5.2.2), and some animals feed at night while others feed during the day.

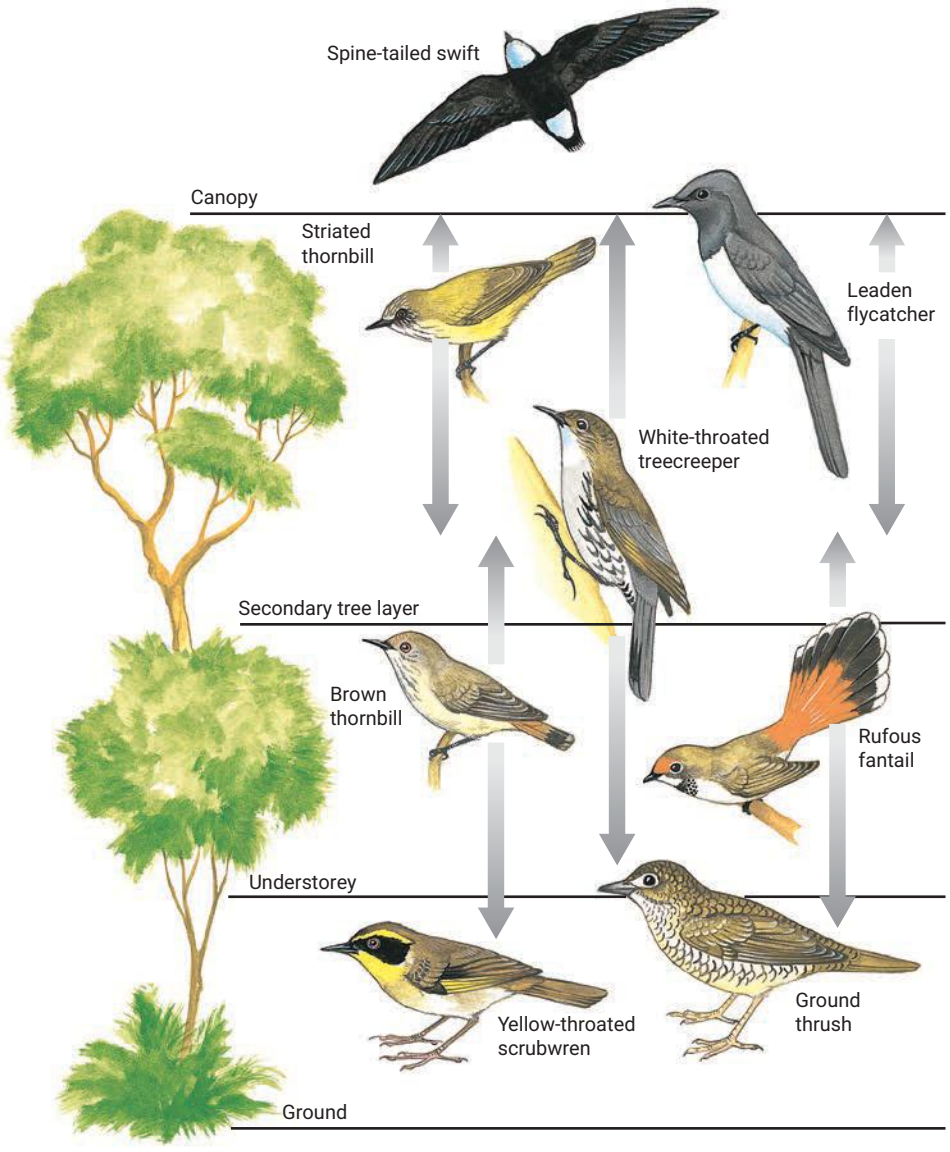


FIGURE 5.2.2 Resource partitioning reduces feeding competition between these bird species, which would otherwise occupy the same ecological niche in an eastern Australian eucalypt forest.

Even with resource partitioning, some species do not occupy their fundamental niche because the limitations that competition, predation, disease and symbiosis place on a species force it to compromise on its fundamental niche, resulting in the much narrower realised niche.

For example, the abiotic factors suitable for the laughing kookaburra (*Dacelo novaeguineae*) extend virtually all the way down the eastern coast of Australia, from Cape York Peninsula in Far North Queensland to the eastern Eyre Peninsula in South Australia, and Tasmania. However, the species is not distributed evenly in Australia because successful competitors, such as the blue-winged kookaburra (*Dacelo leachii*), occupy this niche in central northern and north-western Australia **(Figure 5.2.3)**.

Ken Griffiths/Shutterstock.com

Vaclav Matous/Shutterstock.com

FIGURE 5.2.3 The (a) laughing kookaburra (*Dacelo novaeguineae*) and (b) blue-winged kookaburra (*Dacelo leachii*) have similar fundamental niches.

PRACTICAL ACTIVITY 5.2.1

COMPETITIVE EXCLUSION

Introduction

One form of competitive exclusion in plants is allelopathy, in which chemicals produced by plants affect the growth and distribution of other plants. In Australia, allelopathy is seen in *Casuarina* species, as evidenced by the lack of understorey species that grow under a *Casuarina*.

Research question

Does the presence of alfalfa extract prevent the germination of radish seeds and mung beans?

Materials

- 5 g alfalfa shoots
- 20 radish seeds
- 20 mung beans
- 50 mL distilled water
- 150 mL beaker
- Parafilm or plastic wrap
- marker pen
- 50 mL flask
- 4 petri dishes
- pipette
- filter paper or cotton wool
- cheesecloth or absorbent kitchen cloth

RISK ASSESSMENT

What are the risks in doing this experiment?	How can you manage these risks to stay safe?
Seeds may be poisonous.	Do not consume seeds.
Environmental – seeds are not in their natural environment.	Ensure that seeds are disposed of correctly and not introduced into the local environment.

Procedure

Part A: Alfalfa-leaf extract preparation

1. Cut 5 g of alfalfa shoots into smaller pieces. Place them into the 150 mL beaker.
2. Add 25 mL of distilled water.
3. Press the shoots down so they are completely submerged, and cover the beaker with Parafilm or plastic wrap to prevent evaporation.
4. Let the alfalfa shoot 'tea' steep for 2 days in a cool place. If room temperature is above 22°C, place the 'tea' in a refrigerator.
5. Pour the alfalfa-leaf extract through several layers of cheesecloth or kitchen cloth to remove any suspended matter, and collect the liquid in a 50 mL flask. This extract will be used to treat the seeds.
6. Label the tea 'Alfalfa-leaf extract' (the extract can be stored at 4°C in a refrigerator for a few days).

Part B: Testing germination

7. Label two petri dishes for each seed species – one control and one treatment – with petri dish number, treatment or control, target species, date and your group initials.
8. Line each petri dish with three sheets of filter paper or cotton wool.
9. Add 5 mL of distilled water to each of the control dishes with a 5 mL disposable pipette or syringe.
10. Add 5 mL of leaf extract to each of the treatment dishes with a 5 mL disposable pipette or syringe.
11. Place 10 radish seeds in each of the control petri dish and the treatment petri dish. Spread the seeds evenly in the dish. Cover with the lid.
12. Repeat step 11 with the mung beans.
13. Place all the petri dishes in a warm dark place (remember seeds germinate under soil).
14. Check the petri dishes the following day for evidence of germination or sprouting. Record these observations as Day 1.
15. On Days 2 and 3, record the number of germinated seeds and descriptions of each seedling's appearance in each dish.
16. Dispose of the petri dish contents appropriately – compost if possible.

Results

Group results

Seed	Number of seeds germinated		
	Day 1	Day 2	Day 3
Radish			
Mung bean			

Class total

Seed	Number of seeds germinated		
	Day 1	Day 2	Day 3
Radish			
Mung bean			

Analysis of results

1 Construct a graph to show the number of seeds germinated for each species over 3 days.
2 Identify a trend in the data.
3 Identify a pattern in the data.
4 Calculate the standard deviation or uncertainty of the mean for each seed for Day 3.

Interpretation

5 Explain whether this data provides evidence for competitive exclusion in the form of allelopathy.

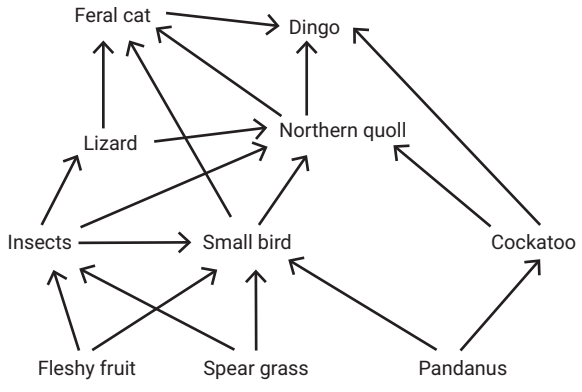
Evaluation

6 Discuss the reliability of this data, with reference to the standard deviation or uncertainty of the mean.
7 Discuss the validity of this data.

LEARNING CHECK 5.2

DESCRIBING

1 **Describe** the difference between a fundamental niche and a realised niche.
2 Northern quolls (*Dasyurus hallucatus*) are nocturnal insectivorous marsupials who occasionally feed on figs and small vertebrates such as lizards and frogs and scavenge on road-kill. Their current range is restricted to small pockets of the northern Australian coastline from Queensland to Western Australia.



Based on Kakadu National Park, http://kakadunatpak.weebly.com/endangered-species.html

FIGURE 5.2.4 A food web showing interactions involving northern quolls

Identify an animal that would:

a competitively exclude this species

b compete with this species in some aspects, but would probably not competitively exclude them.

APPLYING

3 **Explain** why ecologists are so concerned about the impact of feral cats on the continued existence of many Australian native animals and birds.

4 **Explain** how resource partitioning allows more species to inhabit the same area than would otherwise be possible.

INTERPRETING

5 The competitive exclusion principle applies to smaller communities. The channel-billed cuckoo (*Scythrops novaehollandiae*) lives along the northern coast of Australia and is a brood parasite for currawongs, butcherbirds and magpies. Brood parasites do not raise their offspring; instead, they lay their eggs in the nests of other species, who unwittingly raise the intruding chicks.

Predict and **explain** the expected differences in the magpie population between two areas, one with and one without channel-billed cuckoos.

5.3 Analysing ecological data

Analysing data plays an important role in being able to understand more about different ecosystems. Consider the data for the Daintree Rainforest in **Figures 5.3.1 and 5.3.2** and **Table 5.3.1**.

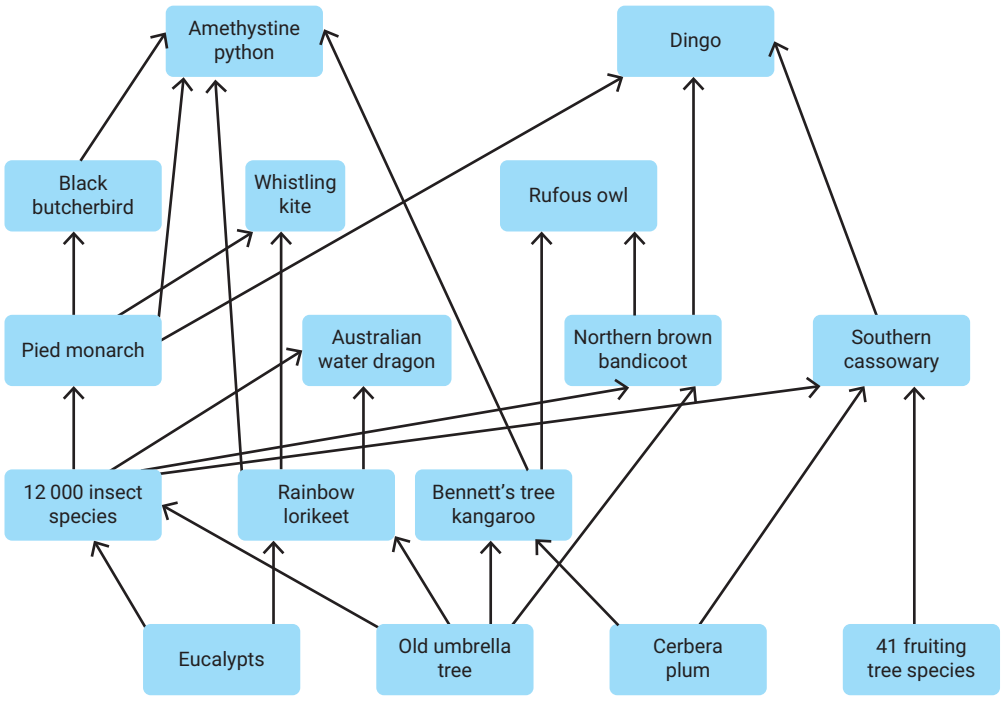


FIGURE 5.3.1 Ecological data for the Daintree Rainforest. The Daintree lowland rainforest in Far North Queensland has an ecosystem too complex to fit in a single food web. Simplified food webs, such as this one, include many of the important components.

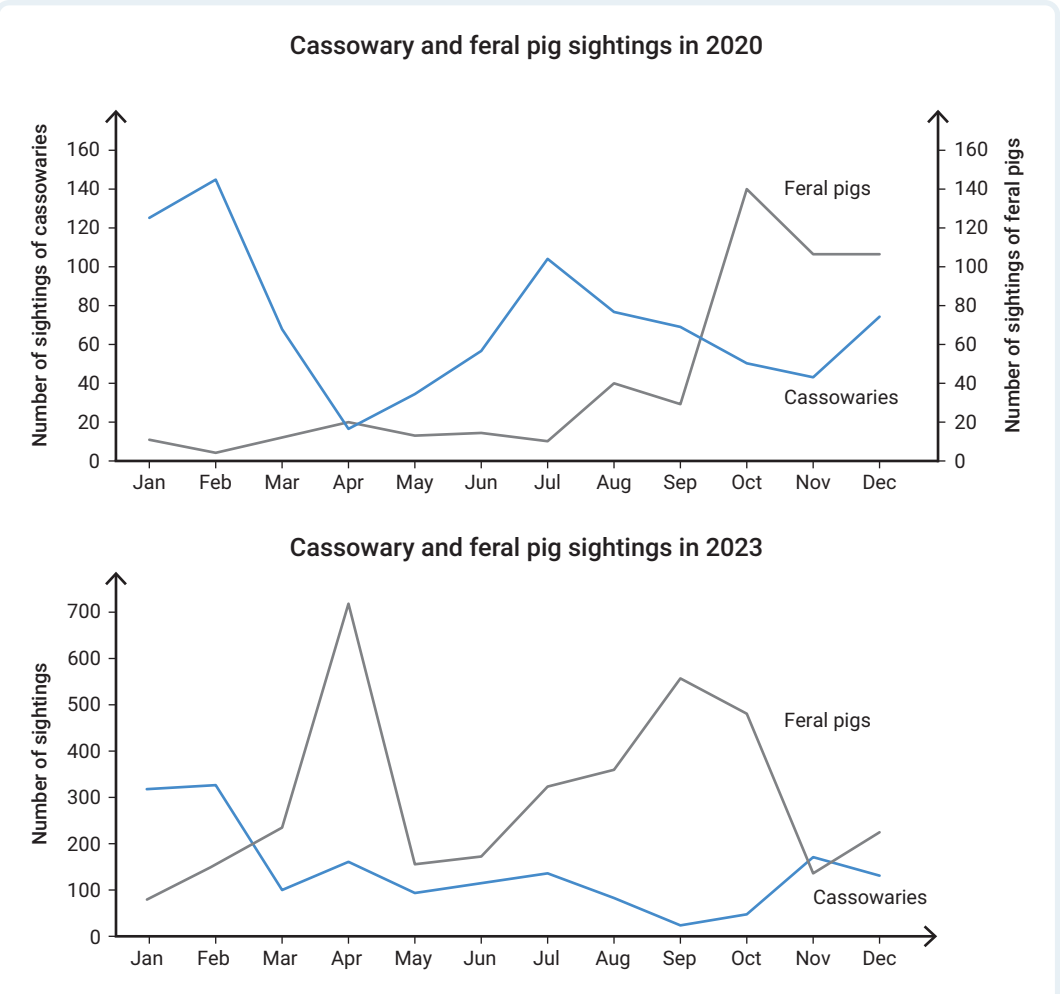


FIGURE 5.3.2 Graphs showing sightings of cassowaries and feral pigs in the Daintree Rainforest area in 2020 and 2023. The feral pig is an introduced species that arrived in 1788, and is believed to have been well established in the Daintree area by the 1930s. Feral pigs are omnivores and have been observed eating cassowary eggs and chicks. Cassowaries have a diet consisting mainly of fruits and berries.

TABLE 5.3.1 Ecological profile of the Daintree Rainforest

Profile component	Comments
Access to shelter	The vast majority of the rainforest consists of long-lived fruiting trees and vines. These provide permanent shelter sites for almost all resident animal and insect species.
Access to water and light	The rainforest receives regular copious rainfall and features a wide network of rivers and streams. The closed canopy limits the amount of light, but not rain, to the forest floor.
Source of soil	A healthy range of fungi, bacteria and detritivores thrive in the thick damp layer of fallen leaves and fruits, which are processed into fertile soil.

The analysis on the following pages is based on the data in Figures 5.3.1 and 5.3.2 and Table 5.3.1.

Identifying keystone species

In the food web in Figure 5.3.1, the southern cassowary interacts with 41 fruiting tree species. This suggests that the southern cassowary plays an important role in distributing the seeds for these trees, as no other animal can do this. Table 5.3.1 states that the fruiting trees provide shelter for resident animals. If seeds for these species are not dispersed by the southern cassowary, then new saplings are unlikely to grow to replace any lost trees. Therefore, the southern cassowary is most likely a keystone species because all the other species that are dependent on the trees for shelter are affected if the cassowary is unable to disperse seeds.

Inferring species interactions

Data can help to infer species interactions such as predation, competition, mutualism, commensalism and parasitism.

Predation

Figure 5.3.1 shows feeding relationships. This makes it easy to identify examples of predation. Three examples are:

- dingo (predator) – northern brown bandicoot (prey)
- Australian water dragon (predator) – rainbow lorikeet (prey)
- rufous owl (predator) – Bennett's tree kangaroo (prey).

The population graphs in Figure 5.3.2 also suggest predation. Looking at the sighting numbers, it can be seen that high sightings of feral pigs, such as during September in 2023, are associated with low sightings of cassowaries in the same period. This could indicate that the feral pig is a predator and the cassowary is prey. Information in Figure 5.3.2 also states that feral pigs have been observed eating cassowary eggs and chicks, further supporting predation.

Competition

Figure 5.3.1 shows organisms that feed on the same food source. If the food source is an animal, then they are competitors. If they are both feeding on a plant, they may occupy different niches (e.g. feeding on leaves rather than feeding on fruit) and this distinction is not evident in this food web; thus they may not be competing. Three examples of competition are:

- whistling kite and black butcher bird competing for the pied monarch
- rufous owl and amethystine python competing for the Bennett's tree kangaroo
- rufous owl and dingo competing for the northern brown bandicoot

The population graphs in Figure 5.3.2 may also suggest competition. The high numbers of feral pigs associated with low numbers of cassowaries could indicate that feral pigs are more effective competitors for a particular resource than cassowaries. Information in Figure 5.3.2 also states that feral pigs are omnivores, which may also include fruit that are preferred by the cassowary, further supporting competition.

Mutualism

None of the data provided gives a clear indication of a mutualistic relationship. It would be reasonable to infer a mutualistic relationship between some of the 12 000 species of insects and eucalypts where the insects act as pollinators and the insects receive food and or shelter.

Commensalism

None of the data provided gives a clear indication of commensalism. It would be reasonable to infer a commensal relationship between Bennett's tree kangaroos and old umbrella trees where the tree kangaroo receives food but neither helps nor harms the umbrella tree.

Parasitism

None of the data provided shows a parasitic relationship.

Predicting the outcomes of removing species from an ecosystem

Removal of a predator

Removing the amethystine python takes away the only predator of the black butcher bird and one of the predators for the Bennett's tree kangaroo, rainbow lorikeet, pied monarch and rainbow lorikeet. This means that the whistling kite and the black butcher bird should have more food (pied monarch) available. Because the black butcher bird is no longer eaten by any organism, the black butcher bird numbers should initially increase significantly. Whistling kite numbers should also increase, due to more food being available (pied monarch and rainbow lorikeet). In the longer term, the numbers of these predators may decrease if they eat the prey species faster than the prey species can reproduce. An increased number of Bennett's tree kangaroos may lead to an increase in rufous owl numbers.

Removal of a feral species

The sightings data (Figure 5.3.2) suggests that the feral pig is a predator and/or competitor of the southern cassowary. Removal of the feral pigs should allow the population of cassowaries to increase. This means they will be able to interact with more of the 41 fruit-bearing species of trees, distributing seeds and contributing to the stability of the ecosystem.

Removal of a producer

The food web shows that 12 000 species of insects depend on eucalypts for food. These insects are not shown to interact with any other producers, so the removal of eucalypts would cause this population to crash. The populations of the four species in trophic level 3 (TL3) that feed on these insects would also probably decrease, especially that of the pied monarch that has no other identified food source. Reduced populations or loss of these TL3 species would then affect other trophic levels as higher trophic levels would have fewer food sources (increasing competition) and lower trophic levels would have fewer predators/consumers, meaning their populations would increase, also leading to increased competition.

LEARNING CHECK 5.3

APPLYING

1 **Explain** why narrow niches are good for biodiversity.

2 **Explain** why the dominant species is not necessarily the keystone species.

INTERPRETING

3 Many ecologists think that keystone species should be central to the efforts to amplify biodiversity. Others speculate that this process could be detrimental to species that are not considered key to biodiversity, and yet are indicators of habitat health (indicator species). Using information from section 5.3, provide a justified decision on whether conservation strategies should be based on keystone species.

4 Look at the data in the 2024 graph (Figure 5.3.3) for cassowary and feral pig sightings. Draw a conclusion as to whether this data continues to support predation, competition or another type of interaction between cassowaries and feral pigs. Refer to Figure 5.3.2 in your response.

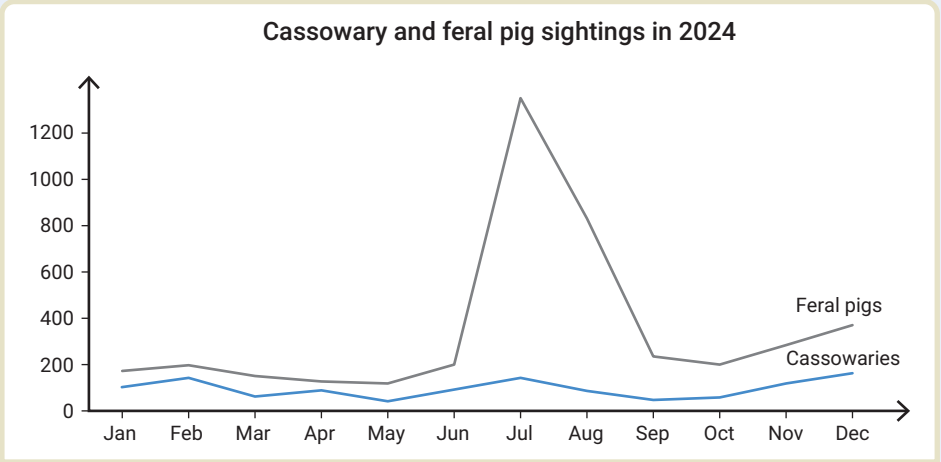


FIGURE 5.3.3 Sightings of cassowaries and feral pigs in the Daintree Rainforest area in 2024

5.4 Effects on community structure and ecosystem functioning

Community structure is described by biotic components, such as species richness and evenness, and influenced by species' interactions. Ecosystem function reflects the cycling of matter and energy through living and non-living systems. When considering the abiotic components as well as the community and biotic interactions, it is possible to measure ecosystem function. Ecosystem function is usually measured by determining standing biomass or change in biomass because it is often difficult to directly measure productivity.

In Australia, introduced species, particularly the feral cat (*Felis catus*) and European red fox (*Vulpes vulpes*), have caused the loss of 64 native species over the last 200 years.

However, many factors affect community structure and ecosystem functioning, including overexploitation, habitat destruction, monoculture and pollution, which represent four of the most urgent impacts in Australia.

Weblink
Biggest threats to Australian endangered plants and animals

Overexploitation

Overexploitation is the unsustainable use of natural resources through hunting, logging, fishing and the gathering of plants, removing these organisms faster than they can be replaced.

In 2016, researchers at the University of Queensland studied 8688 of the world's most-threatened and near-threatened species and analysed the risks. Overexploitation was found to threaten more than 70 per cent of the species assessed. For example, the Australian Leadbeater's possum (*Gymnobelideus leadbeateri*) is critically endangered, being affected by the unsustainable harvesting of mountain ash (*Eucalyptus regnans*) forest. This shows that significant reduction of the population of one species (mountain ash) can have a big impact on species that are not being directly exploited (Leadbeater's possum). Species endangerment does not immediately affect species richness. However, species evenness is significantly reduced. This, in turn, affects food webs and the cycling of matter and energy.

Worksheet
Ecosystem structure and function

Habitat destruction

Both species richness and species evenness are reduced by habitat destruction, with the clearance of native vegetation a significant threat to community structure. Some studies in Australia have shown habitat loss as the number one threat to the environment. Since the mid to late 1700s, deforestation has occurred to clear land for crops and grazing, with various sources stating about 40 per cent of forests have been cleared.

The pattern of native vegetation loss shown in **Figure 5.4.1** reflects that of changed land use. The greatest reductions in native vegetation have been in eastern, south-eastern and south-western Australia, where post-1750 urban and agricultural land use has been the most widespread because of the higher fertility soils. Further damage is due to introduced hard-hooved livestock animals compacting the soil when they graze, unlike soft-footed native animals. Compacted soil leads to invasive, shallow-rooted grasses outcompeting deep-rooted native grasses. Combined with reduced tree cover, this causes the topsoil to become more exposed and easily lost.

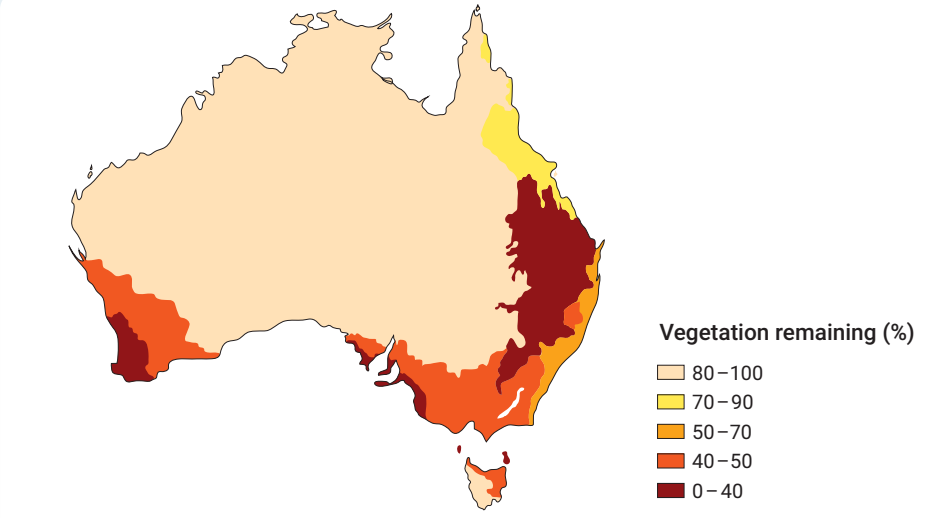


Figure 4 Human footprint map for Australia, 2013, Australia State of the Environment 2021. https://soe.dcceew.gov.au/land/graphs-maps-and-tables

FIGURE 5.4.1 Percentage of Australian native vegetation remaining since 1750.

Clearing native vegetation means habitats that were once continuous become fragmented, isolated from each other by urban settlements, cropland and pasture in a process known as **habitat fragmentation**. Small fragments can support only small populations of fauna and flora that are more vulnerable to extinction. They do not support species that require large home ranges to obtain resources and locate mates. For example, northern hairy-nosed wombat populations are restricted to two locations in Queensland as their preferred environment of eucalypt forests were predominantly cleared for farming in the 19th and 20th centuries. Clearing land of natural vegetation changes the way matter and energy can be cycled through food webs and often paves the way for invasive species to take hold under the changed environmental conditions at the expense of native species.

Monocultures

A biologically diverse ecosystem, such as an old-growth forest or a tropical rainforest, is healthy, complex and stable. However, modern agricultural practices often use low numbers of crop or livestock species, reducing species richness **(Figure 5.4.2)**. This type of farming, resulting in a **monoculture**, often requires the extensive use of fertilisers, pesticides and herbicides to reduce the natural tendency of the community to diversify, and to attempt to replace broken nutrient

Syllabus link
Chapter 2 discusses habitats.

Weblinks
Threatened species and ecological communities in Australia
UN Convention to combat desertification
Land degradation: measuring Australia's progress

habitat fragmentation the process by which areas of a habitat are lost, resulting in a large continuous habitat being broken up into smaller, more isolated habitats

Syllabus link
Chapter 12 discusses the effect of habitat fragmentation on evolution and extinction.

monoculture the agricultural practice of growing a single crop or species over a wide area for many consecutive years

Meryll/Shutterstock.com

FIGURE 5.4.2 A pine plantation is an example of a monoculture.

cycles, such as nitrogen. Another disadvantage of this practice is the fast spread of disease through communities with low species richness and susceptibility to changing environmental conditions. Aquaculture (an aquatic monoculture) can be used to produce a single species at one location, including fish, molluscs, crustaceans and aquatic plants. The escape of exotic species and control of predatory species are also areas of concern in this type of farming.

Maintaining high productivity over time is unlikely to be sustainable in the face of disturbance, disease, soil erosion and overuse of natural resources (e.g. water). Other significant problems associated with replacing natural vegetation with crops is salinity as a result of irrigation requirements. Although farm dams and irrigation channels can become important local sites of biodiversity, irrigation contributes significantly to increasing groundwater. This raises the water table, often high in salt content, to the surface **(Figure 5.4.3)**. Initially, this can

Jo Hanley/Alamy Stock Photo

FIGURE 5.4.3 Salination of land. Dryland salinity caused by a combination of land clearing and irrigation practices can reduce biodiversity and devastate ecosystems.

cause **waterlogging** and then, depending on evaporation and the degree of surface flushing, **salination** (increased salt concentration). Even if the surface is flushed regularly by rain or other water sources, it inevitably ends up in a stream.

Past land clearance practices, the move to shallow-rooted pastoral grasses and the overuse of fertilisers that have affected soil organisms have also placed enormous pressures on the structure of the soil and the ability of the land to hold its topsoil. If pest outbreaks occur, beneficial populations of insects are missing, and if favourable weather conditions happen simultaneously, the effect on the crop can be catastrophic.

waterlogging what happens to plants when the water table rises into the root zone; results in anaerobic conditions that may kill some plants; may also increase salinity levels in the soil

salination increased salt concentration

Pollution

Pollution is the introduction of harmful materials, called pollutants, into the environment. Pollutants damage air, water and land quality. Activities causing pollution may be the result of natural activity (e.g. volcanic activity) or human activity.

pollution the introduction of harmful materials into the environment

Human-induced atmospheric pollution results from burning of fossil fuels, heavy industry, wood-fired heaters and traffic emissions as well as dust storms and bushfire smoke. Greenhouse gases emitted are measured as CO_2 equivalents, which are calculated from the atmospheric concentrations of CO_2, methane, nitrous oxide and other synthetic greenhouse gases. According to the Department of Climate Change, Energy, Environment and Water, Australia released 446.4 million tonnes of CO_2 equivalent in 2024.

Water pollution is also an issue. Australia's shoreline and aquatic ecosystems are affected annually by agricultural run-off estimated to contain about 19 000 tonnes of phosphorus and 141 000 tonnes of nitrogen resulting from intensive farming practices, both agricultural and aquaculture. Organic material also builds up under fish farms, causing changes to water quality and sediment conditions. Water pollution is also considered to be one of the highest risks to the Great Barrier Reef, affecting critical habitats for dugongs, turtles, corals and fish.

Waste discarded by Australian households also contributes to pollution in landfill, including cigarette butts, food waste, single-use plastics, unwanted household items for demolition and hazardous waste. Poorly managed rubbish dumps leak waste and contribute to reducing water quality and the transmission of disease. On average, 100 kg of plastic waste is produced each year per person. Only 13 per cent of this plastic is recycled, while the rest eventually leaks into aquatic environments, where it can kill wildlife through ingestion, bioaccumulation and reduced soil quality. Tiny plastic particles, such as microbeads, cannot be collected or treated once generated because they are too small for current filtration systems. Microbead pollution is increasingly problematic because the beads accumulate in all organisms in the food web and leach toxic chemicals directly into body tissues.

LEARNING CHECK 5.4

DESCRIBING

1 **Identify** one consequence each for air, water and land pollution.
2 **Describe** the effect of habitat destruction on populations.

APPLYING

3 **Explain** how monocultures affect community structure.
4 **Explain** how overexploitation affects ecosystem functioning.

CHAPTER SUMMARY

Interactions between species

- Different species in an ecosystem have different relationships with each other, including:
  - predation (feeding relationships)
  - competition
  - mutualism (+/+)
  - parasitism (+/–)
  - commensalism. (+/0)

Ecological niches

- Each species plays an important role in the ecosystem, also known as the ecological niche.
- No two species can occupy the same niche. An overlap results in competition.
- Reducing competition in the niche improves biodiversity, which could involve resource partitioning.

Analysing ecological data

- Analysing food webs, population data and ecological profiles can help us understand the state of the ecosystem.

Communities and ecosystem functioning

- Communities include the populations of different organisms and their interactions.
- Factors affecting ecosystem functioning include:
  - exploitation of resources
  - destruction of habitats
  - reducing species diversity (e.g. monocultures)
  - pollution.

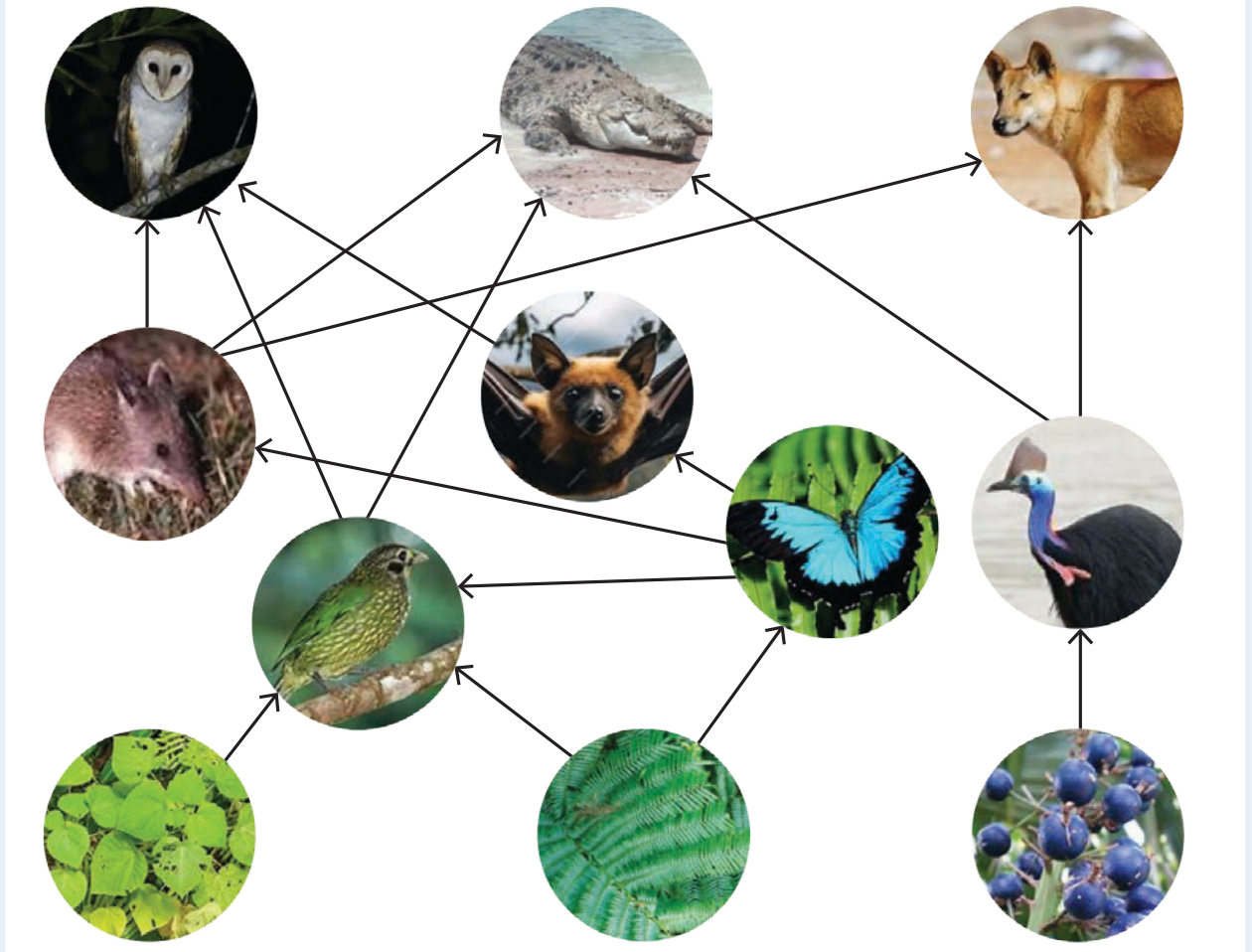
CHAPTER EXAM

MULTIPLE CHOICE

1. Which of the following is an example of predation?
   - **A** A wombat drinking water
   - **B** A tapeworm in intestines
   - **C** A feral cat eating a bilby
   - **D** A bird feeding on nectar

2. An example of symbiosis is:
   - **A** competition.
   - **B** commensalism.
   - **C** predation.
   - **D** succession.

Questions 3–7 relate to the following food web from the Daintree Rainforest.



3. Which pair of organisms are competitors?
   - **A** Bat and dingo
   - **B** Cassowary and marsupial
   - **C** Bat and bird (green)
   - **D** Kookaburra and berry

4. Which pair of organisms are in the same trophic level?
   - **A** Bat and dingo
   - **B** Cassowary and marsupial
   - **C** Bat and bird (green)
   - **D** Kookaburra and berry

5. Which organism is a carnivorous predator?
   - **A** Berry
   - **B** Bird (green)
   - **C** Cassowary
   - **D** Dingo

6. Which organism is least likely to compete with the owl?
   - **A** Berry
   - **B** Cassowary
   - **C** Dingo
   - **D** Crocodile

7. Which of the following shows an accurate food chain from this food web that includes the green bird occupying trophic level 2?
   - **A** Berry → cassowary → dingo
   - **B** Fern → butterfly → bat → owl
   - **C** Fern → green bird → crocodile
   - **D** Fern → butterfly → green bird → owl

8. A niche is the:
   - **A** role that an organism fills in an ecosystem.
   - **B** space that an organism fills in an ecosystem.
   - **C** role that an organism fills in an ecosystem, including all its interactions with the biotic and abiotic factors of its environment.
   - **D** role and space that an organism fills in an ecosystem, including all its interactions with the biotic and abiotic factors of its environment.

9. A crop made up of only one species of wheat is an example of:
   - **A** habitat destruction.
   - **B** monoculture.
   - **C** overexploitation.
   - **D** pollution.

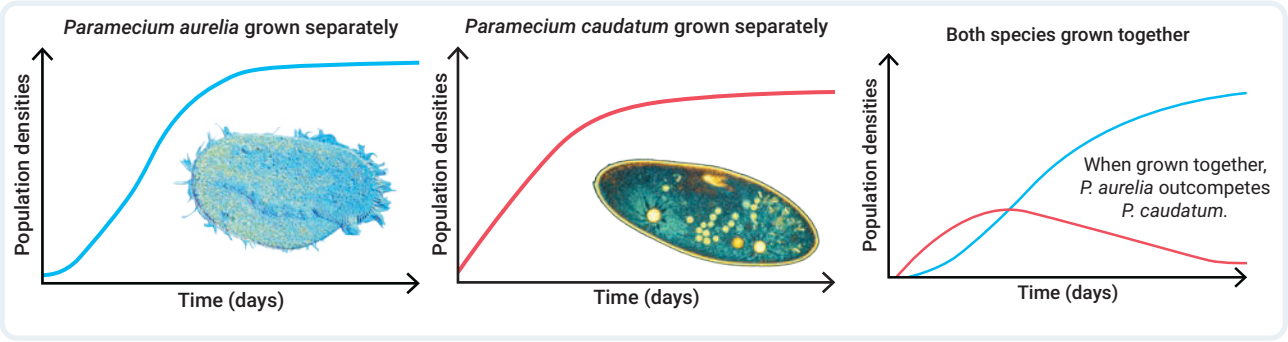
10. When removing one species from an ecosystem leads to a rapid decrease in biodiversity in a short time period, that species is probably:
   - **A** a competitor.
   - **B** an endangered species.
   - **C** a keystone species.
   - **D** a niche species.

SHORT RESPONSE

11. US ecologist Joseph Connell conducted an experiment to determine the fundamental and realised niches of two species of barnacle, *Balanus balanoides* and *Chthamalus stellatus*. The two barnacles inhabited the same rock face, but *C. stellatus* lived on higher rocks and *B. balanoides* lived on the lower rocks. During his experiment, Connell discovered that *B. balanoides* could only live on the lower rocks because exposure to air during low tide caused the barnacle to dry out and die (known as desiccation). When *B. balanoides* was removed from the rock, *C. stellatus* could inhabit the entire area.

Explain, with a diagram, both the realised and fundamental niches of *B. balanoides* and *C. stellatus*.

12. In 1934, Russian ecologist, G.F. Gause completed an experiment on *Paramecium aurelia* and *Paramecium caudatum*, two closely related species of protists. The following graphs summarise Gause's findings.



Explain how the data shown in the graphs provides evidence for competitive exclusion.

CROSS-CHAPTER QUESTION

13. Populations become separated and fragmented because of a number of factors, including urbanisation and deforestation. Use an example to **explain** how population fragmentation is detrimental to the genetic diversity of a species and their continued existence.

DATA ANALYSIS

Questions 14 and 15 refer to the following information.

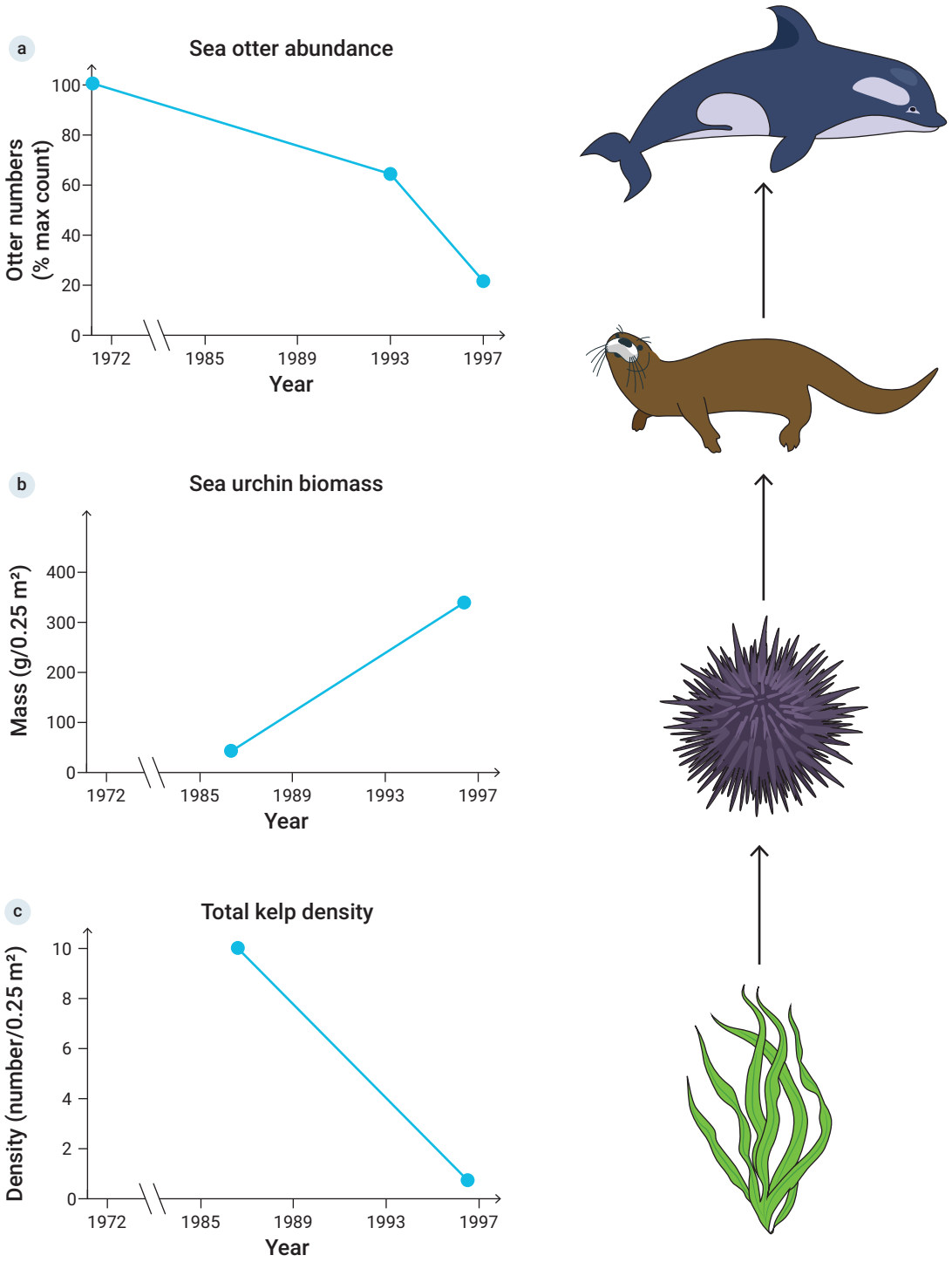
The diagram on page 126 shows a food chain for an aquatic community. The abundance of each species is shown over time in graphs a–c.

14. Analyse evidence

Identify a relationship between kelp and sea urchins shown in the data in graphs b and c.

15. Interpret evidence

Predict which of the four species in the food chain is most likely to be the keystone species. Provide reasons.


a
Sea otter abundance
Otter numbers (% max count)
100
80
60
40
20
0
1972
1985
1989
1993
1997
Year
b
Sea urchin biomass
Mass (g/0.25 m²)
400
300
200
100
0
1972
1985
1989
1993
1997
Year
c
Total kelp density
Density (number/0.25 m²)
10
8
6
4
2
0
1972
1985
1989
1993
1997
Year

CHAPTER 6

Succession

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SYLLABUS DOT POINTS

SCIENCE UNDERSTANDING

- 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.

Introduction

Ecosystems are dynamic, with daily and seasonal changes in abiotic factors associated with variation in number and types of species present. Disturbances occur regularly in ecosystems and can be on a small scale (e.g. a tree falling over) or a large scale (e.g. a bushfire). The changing mix of species and habitat in an area is known as an ecological succession.

Worksheets

- Succession 1
- Succession 2

Nelson MindTap

To access resources above, visit
cengage.com.au/nelsonmindtap

ASSUMED KNOWLEDGE

- ✓ There are many abiotic and biotic factors in an ecosystem that can be observed and measured.
- ✓ A community is an association of two or more populations of different species occupying the same space at the same time.
- ✓ A habitat is the resources present to support the survival of a community or an individual species.
- ✓ Different types of species interactions have positive, neutral or negative outcomes.
- ✓ Reproductive strategies used by species fit on a spectrum from K- selected to r-selected.
- ✓ Biodiversity is the full range of organisms living in a defined area and can be described by the range of species present.
- ✓ Biomass is a measure of the total mass of living matter in an ecosystem.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ state the steps or stages involved in an ecological succession
- ✓ identify the stage by looking at species type and species diversity
- ✓ state the differences between a primary succession and a secondary succession
- ✓ explain how each stage has a different combination of:
  - species interactions
  - abiotic factors
  - K- and r-selected species
  - biodiversity
  - biomass
- ✓ identify similarities and differences between ecosystems at different times (temporal scale)
- ✓ identify similarities and differences between ecosystems at different locations (spatial scale).

6.1 Ecological succession

Change is a natural feature of dynamic ecosystems and occurs on different scales. When a tree falls in a forest or wombats dig, small-scale disturbances occur. On a slightly larger scale, one set of living things can change the environment in such a way that conditions no longer suit them but do suit a different set of living things. Large-scale catastrophic events, such as volcanic eruptions, may completely remove an existing ecosystem. Communities change in structure over time, with one community being replaced (or 'succeeded') by the next in a serial process known as **succession**.

succession the progressive change of communities over time

primary succession the process of a community developing in a barren place

nudation the development of bare sites with no organisms inhabiting them

Primary succession

Primary succession is a series of changes that occur in an area that has not previously been colonised (Figure 6.1.1). Catastrophic events such as volcanic eruptions, cyclones, earthquakes and tsunamis can cause the formation of bare sites with no soil or organisms inhabiting them in a process called **nudation**.


M. Kuehl/Shutterstock.com

ImageBROKER.com/Alamy Stock Photo

FIGURE 6.1.1 About 190 000 years ago, in the Cainozoic era, Undara in north Queensland was an active shield volcano. A massive eruption occurred and lava flowed more than 90 km to the north and 160 km to the north-west from Undara. Over the years, the surface developed into a dry woodland, and the ceilings of the lava tubes have collapsed in many places, allowing vegetation to flourish in the damp interiors, both examples of primary succession.

Pioneer species begin to colonise the area in the first stage of a primary succession. The early colonising pioneer autotrophs are hardy enough that they can live under extreme conditions. They are able to grow in poor soils with low nutrient levels but in high light levels and variable temperatures and, as they grow, they fix nitrogen into the soil. Pioneer species are normally small and photosynthetic, fast-growing and typical of r-selected species, with attributes such as rapid growth and reproduction (sexual or asexual), large numbers of offspring and effective spore or seed dispersal. The seeds or spores are usually adapted to low moisture environments, allowing them to lie dormant for long periods. Although there is an initial rapid increase in population for these species showing exponential growth (J-curve), their populations drop just as rapidly when new species move in because of the changed conditions.

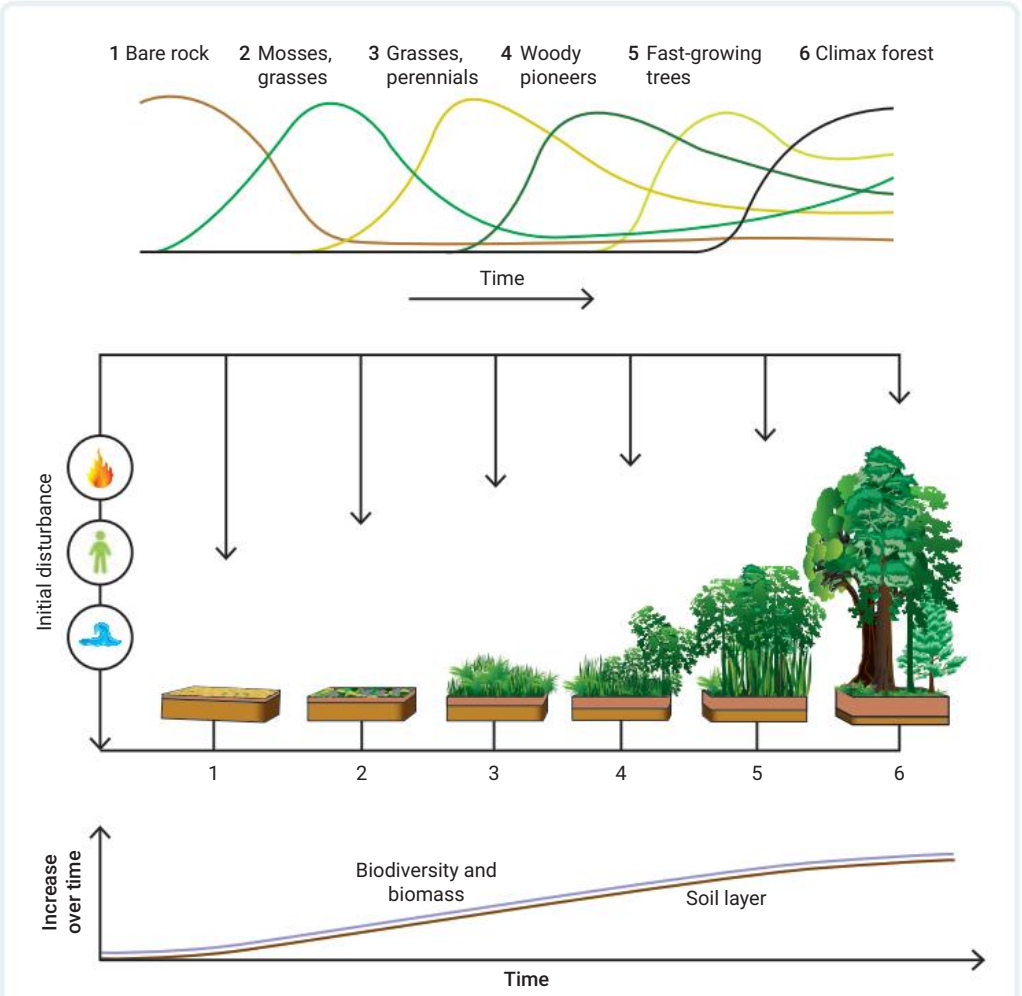
pioneer species an organism capable of invading bare sites and surviving

A key outcome of colonisation is the development of soil. The type of pioneer species depends on the environmental factors in the habitat, such as whether it is coastal sand dunes, rock appearing after glacial retreat or newly formed islands rising from the sea as a result of volcanic activity. Autotrophic organisms such as lichens and algae are usually the first to become established in harsh, bare surroundings. Acids secreted by the lichens attack the rocky surface in the process of weathering, allowing windblown dust particles to settle in the cracks. Decomposition of lichens also contributes to the formation of a thin layer of soil.

The shallow soil makes it possible for mosses to become established. When they die, they add nutrients to the soil. Over time, there is enough soil for grasses, then ferns and/or shrubby herbaceous plants to become established; they grow upwards and outwards, shading those below, their roots speeding up the process of weathering. In this way, succession moves through a series of transitional stages or **seres**, shown as stages 2–5 in **Figure 6.1.2**.

seres transitional stages that are part of a succession

With the establishment of producer organisms (autotrophs), small herbivores such as insects have food and shelter, and they become the next link in the food chains. A new community structure forms at each stage, colonised by immigrants from the surrounding areas. Immigrating organisms survive and stay only if they can occupy a niche that provides the resources they need.



climax community the end-point in a community succession when the community has become relatively stable

FIGURE 6.1.2 Forest succession over time in six stages

AustralianCamera/Shutterstock.com

FIGURE 6.1.3 The rainforests of Queensland are an example of a climax community with high biodiversity, long-lived species and a deep soil layer.

Climax community

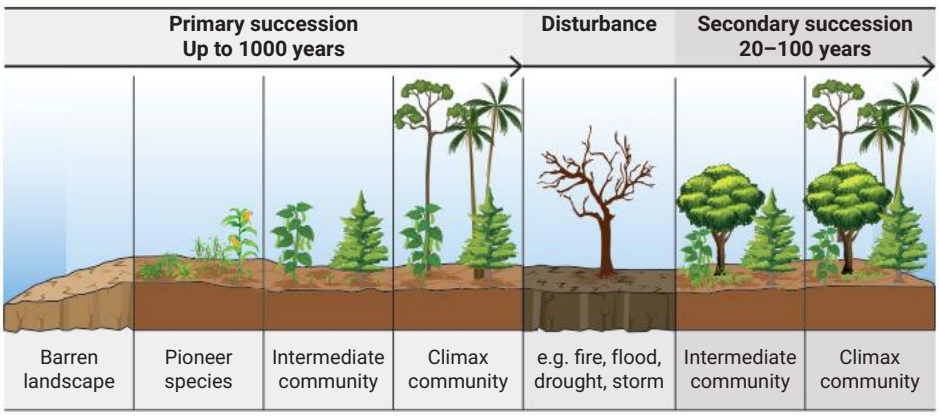
The end of succession is marked by a **climax community**. The old-growth forests of the Daintree Rainforest in north Queensland **(Figure 6.1.3)** and the temperate rainforest pockets scattered throughout the east coast of Australia are examples of climax communities. Such communities remain in relative equilibrium, with limited changes in biotic or abiotic factors until a disturbance restarts the succession process.

Secondary succession

Not all successions remain at or even reach a climax community. A combination of factors such as fire, extreme weather and selective grazing by herbivores helps to create conditions

that allow intermediate stages to persist. Human intervention by logging and land clearing for agriculture also changes the likelihood of a climax community developing. These disruptions alter the cycling of matter and the flow of energy, but do not remove all the organic matter as would occur for a primary succession. Organisms can recolonise recently disturbed communities through **secondary succession**, although the number and kinds of organisms present may be different from the original ecosystem (Figure 6.1.4).

secondary succession the recolonisation of disturbed plant communities



Adapted from Khanolkar RA, et. al. (2020). Ecological Succession of Polymicrobial Communities in the Cystic Fibrosis Airways. mSystems 5:10.1128/msystems.00809-20.

FIGURE 6.1.4 Forest succession showing a primary succession and the effect of a disturbance, causing a secondary succession

Both primary and secondary successions involve changing communities over time in progressive stages called seres, starting with colonisers or pioneer species, then ultimately reaching a climax community.

The differences between primary and secondary succession are summarised in Table 6.1.1.

TABLE 6.1.1 Differences between primary and secondary succession

Attribute	Primary succession	Secondary succession
Starting environment	Pioneer species colonise bare rock	Pioneer species colonise an area with existing soil
Organic matter	Occurs after the removal of any previously existing organic matter	Occurs due to a disruption that leaves organic matter
Abiotic factors	Extreme conditions for pioneer species – least suitable for the survival of life	Favourable conditions exist for pioneer species
Pioneer species	Usually lichen or algae	Usually grasses
Seres	Many intermediate stages	Fewer intermediate stages
Time	Longer time to complete (up to 1000 years)	Shorter time to complete (20–100 years)

Weblink
Primary versus secondary succession

Worksheet
Succession 1

LEARNING CHECK 6.1

DESCRIBING

1 **Describe** factors that may prevent succession from reaching a climax community.

2 **Construct** an annotated timeline to show the sequence of stages in primary succession.

APPLYING

3 **Explain** the differences between primary succession and secondary succession.

4 **Explain** why pioneer species require specific attributes.

Syllabus links
Chapter 2 details the sampling techniques and methods used to collect ecological data.
Chapter 3 discusses r/K selection.

6.2 Successional change

To predict the stage of succession in a habitat, data on a number of features is collected and analysed (Table 6.2.1).

TABLE 6.2.1 Features in a habitat that can be used to predict the stage of succession along with reasoning

Feature	Early stages	Climax community
Type of species present	**r-selected; smaller organisms; fast growing** Unstable environmental conditions, so organisms need to be able to reproduce rapidly. Competitive adaptations offer little advantage because the environment is likely to change suddenly.	**K-selected; larger organisms; slow growing** Stable environmental conditions, so species can have long gestation periods and high parental investment and few offspring. Competitve adaptations are beneficial because of stable environmental conditions.
Biodiversity	**Low** The challenging environmental conditions mean that few species can survive, keeping biodiversity low.	**High** The stable environmental conditions mean that many plants can survive, which supports the survival of a greater variety of organisms, keeping biodiversity high.
Biomass	**Low** Low number of organisms, so biomass is low.	**High** Since many more organisms can survive, biomass is high, until a stable community is reached.
Biotic interactions	**Simple interactions, food chains common** Few types of organisms can survive in the conditions; therefore, few interactions occur (e.g. insects feeding on lichen).	**Complex interactions, food webs operate** High biodiversity, so many types of organisms can interact, through feeding relationships, competition and symbiosis.
Abiotic interactions	**Small amounts of poor-quality soil; low nutrient levels; unused resources and living spaces; conditions unstable** Not enough time has passed for rock to have been weathered to form a deep layer of soil. Few autotrophs have had the opportunity to break down to add nutrients. Therefore, there are few plants to create shade, lower temperatures or trap water. Few habitats are occupied.	**Large amounts of good-quality soil and nutrients; resources and living spaces in demand; stable conditions** Sufficient weathering has occurred and organic matter has broken down to form nutrient-rich soil, allowing plants to grow. These shade the environments, reduce air and soil temperatures and allow for water to be retained in the environment. Habitats are occupied.

These features aren't definitive because communities can be disturbed, changing the stage of succession. Species richness generally increases in cleared areas as individuals move in to occupy newly empty habitats, leading to increased competition, which ultimately reduces species richness, usually because of competitive exclusion.

Worksheet
Succession 2

LEARNING CHECK 6.2

APPLYING

1 **Explain** the characteristic features of r-selected species and K-selected species and how these relate to the stages of succession they are most likely to be found in.

INTERPRETING

2 **Predict** the effect on species diversity of ongoing small-scale disturbances on a succession after it reaches a climax community.

6.3 Interpreting data

The spatial scale of an ecosystem refers to how large an area it covers. Similar ecosystems should be similar, regardless of ecosystem size. Species diversity should be similar because values such as Simpson's diversity index (SDI) are a ratio of the number of individuals present to the number of species. Likewise, the ratio of producers to consumers is similar in similarly diverse ecosystems of different sizes, allowing for interactions such as predation and competition to be compared. However, abiotic factors vary considerably across large spatial scales (e.g. in June, the average temperature range on Mt Wellington, Tasmania, is –5°C to 0°C but in Darwin, Northern Territory, it is 20–30°C), but less so on small scales (e.g. in June on the Sunshine Coast, Queensland, the average temperature range at Noosa is 13–22°C and at Mooloolaba it is 11–21°C).

The temporal scale of an ecosystem refers to the time period of ecosystem investigation. Measures of species diversity can vary at different times of day or year due to organisms being nocturnal or diurnal or hibernating or migrating during winter months. Therefore, species interactions also change considerably over time. Temperature and humidity changes over shorter time scales, but most abiotic factors are relatively constant in an area over time.

To better understand successional changes in ecosystems, ecological data for specific spatial and temporal scales is used to develop models that demonstrate successional changes. The most accurate and comprehensive dataset entails examining every part of the ecosystem, such as in a census collection. However, this is highly impractical for most ecosystems. A more practical approach is to examine parts of the ecosystem through sampling. The reliability of the model is determined by how well the sample represents the ecosystem.

Ecosystem models are also useful for simulating and analysing the long-term dynamics and properties of complex ecosystems. This provides a basis for predicting the impacts of changes in real ecosystems and developing tools for management support and policy advice. For example, the concept of secondary succession is applied to restoration ecology projects worldwide to determine how to restore ecosystems that have suffered natural or human-made disturbances. An understanding of abiotic conditions and the roles of species can be used to predict successional outcomes.

Syllabus link
Chapter 2 discusses the different sampling methods and techniques.

Analysing the ecological succession of abandoned farmland

Figure 6.3.1 shows an example of data collected at a hypothetical location in south-east Queensland of abandoned farmland. The number and types of plants that grow in the field were counted 5, 50 and 100 years after the farmland was abandoned **(Table 6.3.1)**.

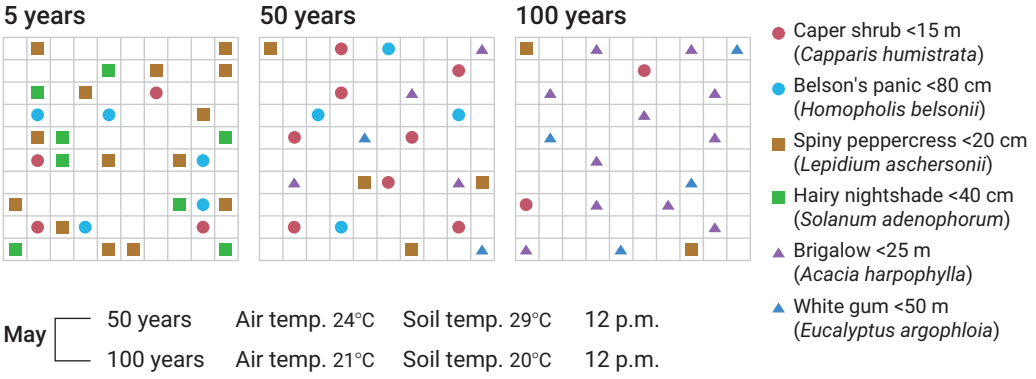


FIGURE 6.3.1 Data for a hypothetical location in south-east Queensland

TABLE 6.3.1 Summarising the percentage of different plant species present over time

Plant	5 years		50 years		100 years	
	Total number	Percentage (%)	Total number	Percentage (%)	Total number	Percentage (%)
Spiny peppercress	14	45	3	14	1	6
Hairy nightshade	8	26	0	0	0	0
Belson's panic	5	16	4	19	0	0
Caper shrub	4	13	8	38	2	11
Brigalow	0	0	4	19	11	61
White gum	0	0	2	10	4	22
Total	31	100	21	100	18	100

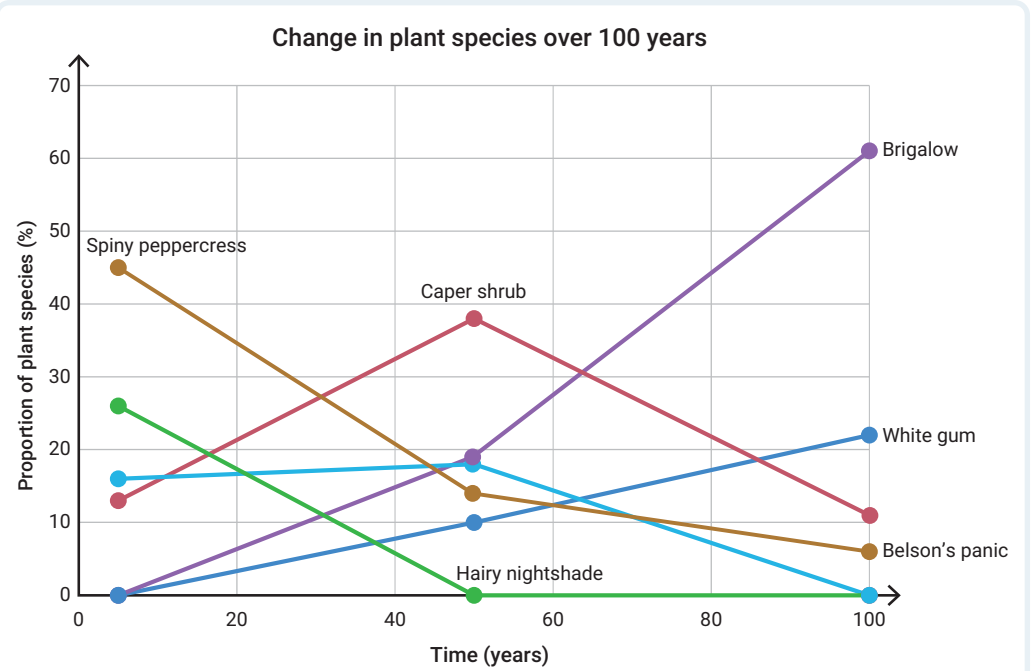


FIGURE 6.3.2 A graph representing the data in Table 6.3.1

Analysis

Trend: From 5 years to 100 years, the proportion of smaller herbaceous species decreases.
Trend: From 5 years to 100 years, the percentage of plants that are trees increases.
Pattern: Both the air and soil temperatures decreased from 50 years to 100 years.

Interpretation

The smaller plants were able to grow in the existing soil (secondary succession). This changed the environment, allowing for shrubs and then trees to become established. As a result of the shade provided by trees, the air temperature and soil temperature were lower at 100 years than at 50 years.

Evidence of changes in past ecosystems

Comparing organisms across very long time scales by using evidence from the fossil record and current biota improves understanding of how the living components of ecosystems change over time. Changes in abiotic factors can also be deduced by studying soils, rocks and even ice cores.

Evidence from the fossil record

The Riversleigh Fossil Site is located in north-west Queensland. Discovery of fossils here improved understanding of the history of many of Australia's vertebrate groups. Scientists can accurately predict and describe Riversleigh's ecosystem 25–15 millions of years ago because

many of the more than 250 sites at Riversleigh that are rich in fossils are well preserved (Figure 6.3.3). The extensive biodiversity seen in the fossil record points to a climate very different from today's dry and hot habitat. Sedimentary rocks at the sites also indicate signs of a wetter climate. Early relatives of today's fauna were preserved in the lime-rich sediments of the wetlands that flourished in this era. This layer lies on top of older limestone that doesn't display the fossil remnants or sedimentation patterns characteristic of a wet climate.

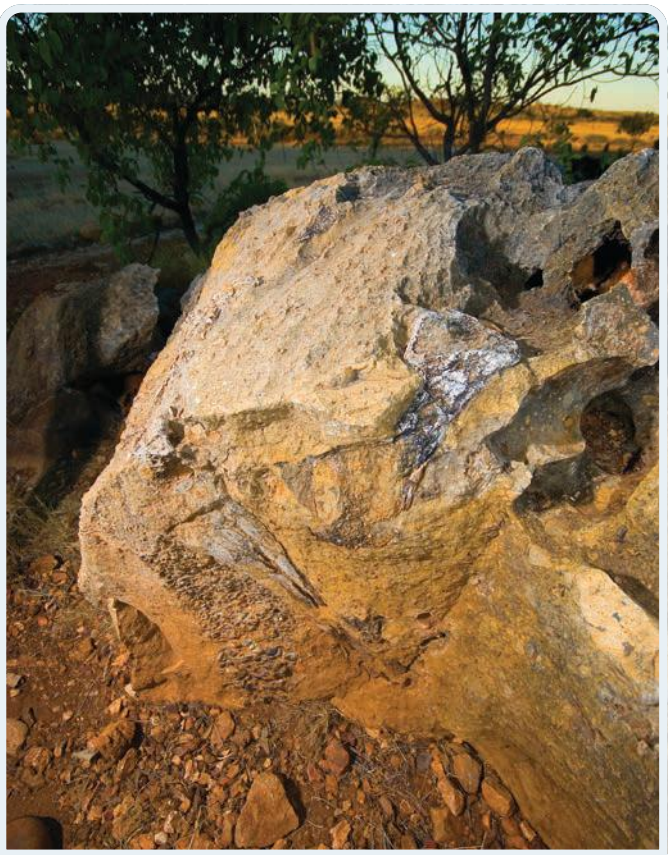


FIGURE 6.3.3 Fossil remains of a crocodile on the Riversleigh Fossil Site

Ice cores as evidence of change

Drilling down into the ice at the poles and within large glaciers produces cores that have preserved a continuous record of past climatic conditions. Trapped gas bubbles and the presence or absence of traces of organisms reveal information about changes in temperature and relative concentrations of atmospheric gases.

Periods of low global temperatures resulted in ice ages – extended periods of time when glaciation occurred over large sections of the northern hemisphere and when the ice sheets expanded at both poles. There have been five major ice ages, the last reaching its maximum 15000–18000 years ago.

Glaciation helped create the deep fertile soils of Europe, but in Australia the story was different. Sea levels dropped and huge expanses of the ocean floor were exposed, providing a land link for species to move between Australia and the islands to the north. Lower global temperatures and evaporation rates also affected the water cycle – lower levels of atmospheric water meant less rainfall (Figure 6.3.4). A little more than 15000 years ago, Australia became a desert: windblown, dry and, for more than three-quarters of the continent, treeless, with two-thirds covered in sand dunes and the topsoil heavily wind-eroded.

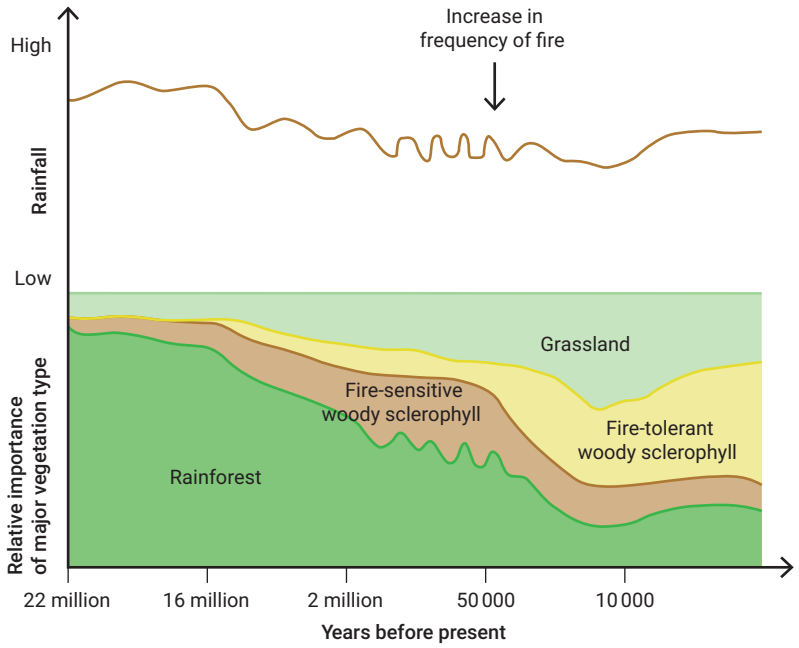


FIGURE 6.3.4 Changes in Australian vegetation over time. With a decrease in rainfall and a cycle of recent ice ages, the vegetation of Australia has changed dramatically over the last 22 million years.

LEARNING CHECK 6.3

DESCRIBING

1 **Describe** a temporal scale change in an ecosystem.

2 **Describe** a spatial scale change in an ecosystem.

APPLYING

3 **Explain** how sampling ice cores can be used to give evidence of climate change.

INTERPRETING

4 Table 6.3.2 shows data for a similar ecosystem to that shown in Figure 6.3.2.

TABLE 6.3.2 The percentage of different plant species present over time in an ecosystem

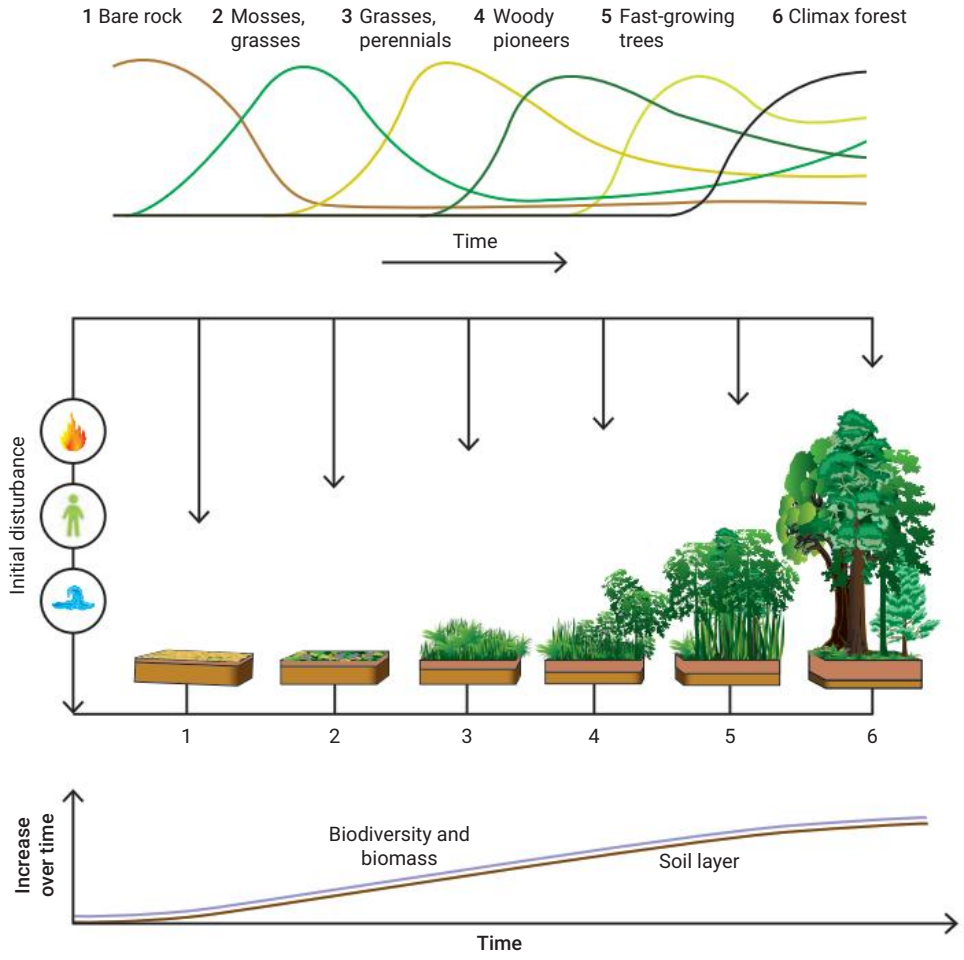
Plant	Percentage (%) of plant species at		
	5 years	50 years	100 years
Spiny peppercress	45	18	40
Hairy nightshade	26	10	30
Belson's panic	16	18	19
Caper shrub	13	36	11
Brigalow	0	18	0
White gum	0	0	0

Deduce what happened in the brigalow scrub system described by the data in Table 6.3.2. Include references to biotic and abiotic factors in your response.

CHAPTER SUMMARY

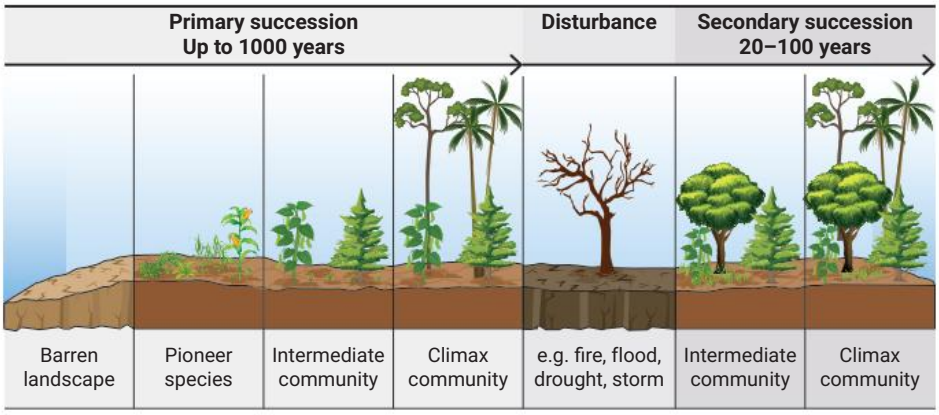
Primary succession

- Primary succession describes changes that happen in an area that has not previously been colonised.
- Pioneer species are the first to colonise the area – this is the first stage of succession.
- The area undergoes additional transitional stages as part of the succession process.
- The end of succession is usually marked by a climax community.



Secondary succession

- Because of some environmental and human activity, some successions do not reach climax communities.
- Secondary succession occurs when organisms recolonise recently disturbed communities.



Adapted from Khanolkar RA, et. al. (2020). Ecological Succession of Polymicrobial Communities in the Cystic Fibrosis Airways. mSystems 5:10.1128/msystems.00809-20.

Interpreting data

- Data can help us to understand the changes that occur in an ecosystem over time.
  For example:
  - Spatial scale can indicate the size of an ecosystem.
  - SDI can indicate species diversity.
  - Ecosystem models can help simulate and analyse long-term dynamics of ecosystems.
  - Plant species type and abundance can give information about succession.

CHAPTER EXAM

MULTIPLE CHOICE

1. When succession occurs, the species present change because:

A the early species exhaust the food supply and die out.
B different species take different lengths of time to develop.
C each community alters the environment, enabling other organisms to become established.
D the change in climate from season to season results in different physical environments, suiting different species.

2. The fossil record, rocks, soils and ice cores provide information on the nature of past ecosystems and changes in the components of those ecosystems. At Riversleigh in Queensland:

A there are rich, well-preserved fossils that demonstrate extensive biodiversity and point to a climate similar to today's dry and hot habitat.
B sedimentary rocks indicate changes in abiotic factors, suggesting that the climate was drier in the past.
C trapped gas bubbles in ice cores reveal information about how the temperature and relative concentrations of atmospheric gases do not change.
D early relatives of today's fauna were preserved in the lime-rich sediments of the wetlands that flourished 25–15 million years ago.

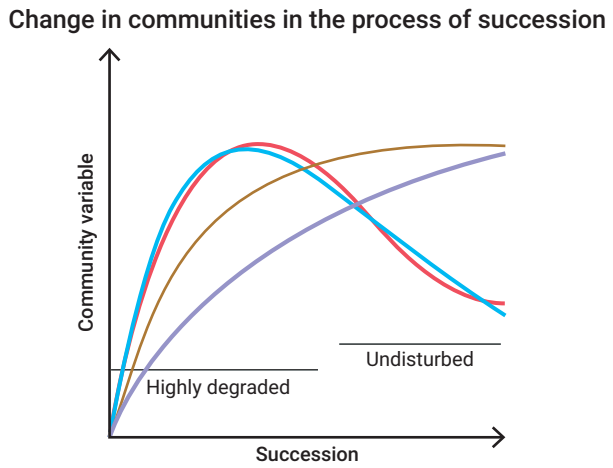
3. Ecosystems and the communities within them are dynamic in nature and are always changing. Succession is a process that occurs progressively over time as one community is replaced by another. Select the best description of succession from the following.

A A plant growing in early succession would have an abundance of resources and would be a K-selected species.
B Few offspring would be produced by a K-selected animal during late succession.
C r-selected species generally take a long time to reach sexual maturity and produce many offspring in their lifetime.
D Plants living in a climax community are likely to show K-selected characteristics, including being fast-growing colonisers.

4. An ecologist sampled two ecosystems. Their findings showed temporal similarities. An example of a similarity is:

A same types of plant species.
B same types of animal species.
C plant species that are found in different locations.
D animal species that feed at the same time.

Questions 5 and 6 relate to the following graph.



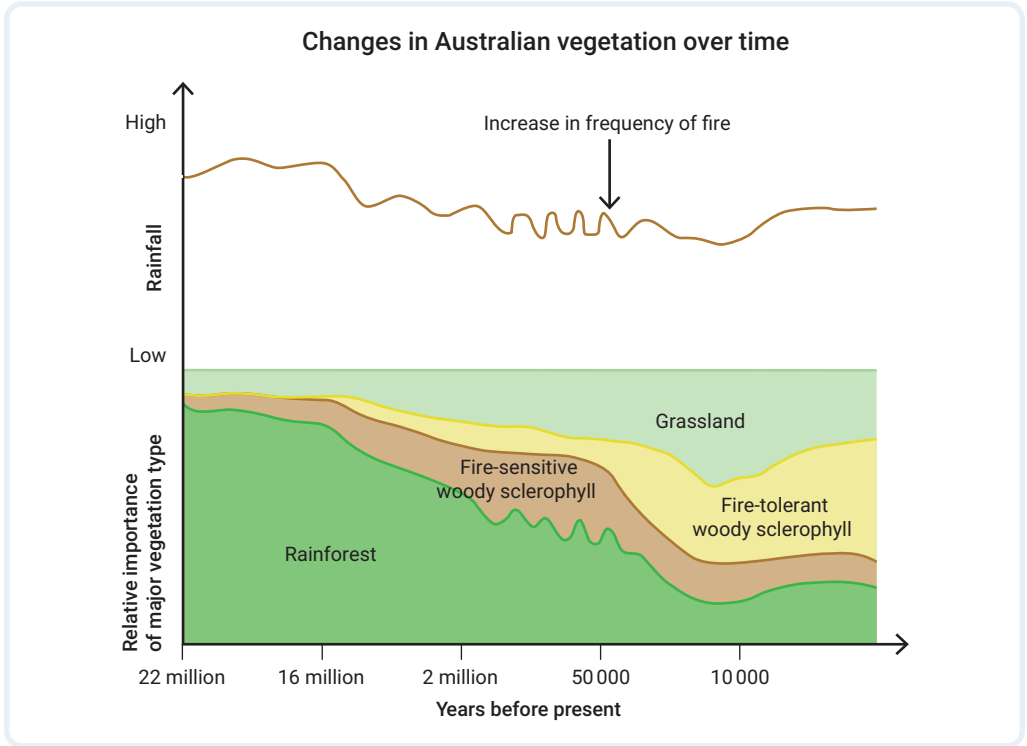
5. The species that are most likely to be r-selected are represented by:
- **A** the blue and red lines.
- **B** the brown and purple lines.
- **C** the blue, red, brown and purple lines.
- **D** none of the lines.

6. The species that are most likely to be K-selected are represented by:
- **A** the blue and red lines.
- **B** the brown and purple lines.
- **C** the blue, red, brown and purple lines.
- **D** none of the lines.

7. An observation that suggests a primary succession is occurring is the presence of:
- **A** bare rock.
- **B** insects.
- **C** soil.
- **D** water.

8. An observation that suggests a secondary succession is occurring is the presence of:
- **A** bare rock.
- **B** insects.
- **C** soil.
- **D** water.

Questions 9 and 10 relate to the following information.
With a decrease in rainfall and a cycle of recent ice ages, the vegetation of Australia has changed dramatically over the last 22 million years.



9. How many years before present was the Australian vegetation predominantly rainforest?

A 0 to 10 000
B 10 000 to 50 000
C 10 000 to 2 million
D 50 000 to 22 million

10. According to the graph, the vegetation currently dominant in Australia is:

A grassland.
B fire-sensitive woody sclerophyll.
C fire-tolerant woody sclerophyll.
D rainforest.

SHORT RESPONSE

11. **Identify** three characteristics of pioneer species that make them effective colonisers.

12. **Explain** how the fossil record and sedimentary rock characteristics provide evidence of past ecosystems.

CROSS-CHAPTER QUESTION

13. Consider the following photo. **Explain** how the complexity of the food web would be expected to change as you move away from the shoreline across the sand dunes.

Ophe/Shutterstock.com

DATA ANALYSIS

Questions 14 and 15 refer to the following information.

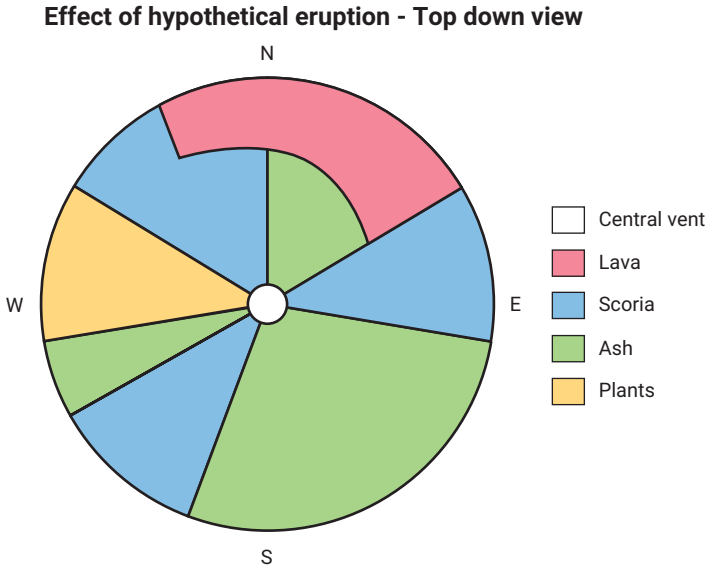
Mt Quincan is a cinder cone volcano in the Atherton Tablelands, Queensland. It is last thought to have erupted 10 000 years ago and is currently considered 'dormant' rather than extinct. When a volcano erupts, rocks, gas and ash are released, along with lava flows. Mt Quincan is now home to a large variety of flora and fauna.

Tom Watson/Getty Images

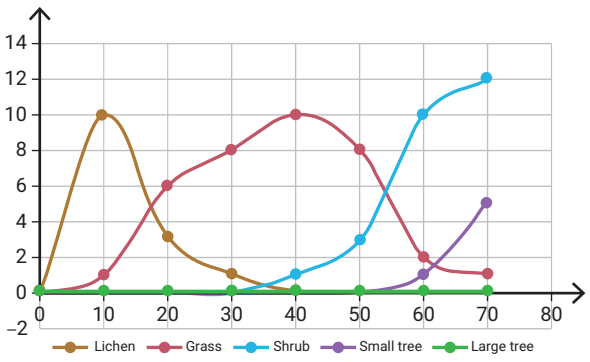
A hypothetical scenario of an eruption generated some data, based on previous cinder cone eruptions:

- A spray of molten rock into the air driven by the gas released from the volcano.
- This forms small scoria rocks or 'cinders' that are >2mm in diameter and ash that is ≤2mm in diameter.
- These fall down around the central vent of the cone.
- Lava emerges towards the base of the cone on the north side.

Hypothetical outcome of an eruption:



Predicted succession for the recovery:



14. Interpret evidence
Deduce whether the same type of succession would occur on all parts of the cinder cone after an eruption, using evidence from the data.

15. Interpret Evidence
Determine whether the predicted succession has returned to a climax community, using evidence from the data.

SCIENCE AS A HUMAN ENDEAVOUR

Syllabus dot point

- 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.

First Nations people's knowledge and management of ecosystems

First Nations Australians have an inherent bond with the land. As explained by Noonuccal woman Karen Martin-Booran Mirraboopa of North Stradbroke Island:

> 'We believe that Country is not only the Land and People, but is also the Entities of Waterways, Animals, Plants, Climate, Skies and Spirits. Within this, one Entity should not be raised above another, as these live in close relationship with one another. So People are no more or less important than the other Entities.' (Martin & Mirraboopa, 2003, p. 207).

For thousands of years, First Nations Australians have studied and developed a deep understanding of interrelationships in the environment. This wealth of knowledge is often called 'traditional ecological knowledge'. This knowledge has led the development of longstanding sustainability of the environment, taking into account the biotic and abiotic elements of ecosystems.

The use of fire to protect and maintain the environment

First Nations Australians have been consciously using fire to support and maintain ecosystems for thousands of years **(Figure 1)**. This practice is often referred to as 'cleaning up the Country' or 'caring for Country'. For example, before colonisation, the Kuku-Yalanji Peoples in north Queensland used fire regimes in certain areas to manage areas of tropical rainforest and sclerophyll forest. These practices are used to support plant life and germination as well as to protect carbohydrate resources in fire-sensitive areas. The Martu Peoples of the Western Desert have also long used fire in certain regions to support the regrowth of plants, to create habitats and as a preventative measure to reduce the occurrence of wildfires.

FIGURE 1 Early dry season burn conducted by Wellesley Islands rangers on Lardil Country.

Indigenous ecological knowledge: The Gunditj Mirring Partnership Project

The Budj Bim Cultural Landscape (Figure 2) in south western Victoria, now a UNESCO World Heritage listed site, is a traditional homeland of the Gunditjmara People. Budj Bim ('High Head') is part of the Eccles volcanic landform. The volcanic explosion forming Mt Eccles is estimated to have occurred 27 000–30 000 years ago and was witnessed by the Gunditjmara People.

FIGURE 2 Lake Condah, which is part of the Budj Bim National Heritage Landscape in south-west Victoria.

The volcanic explosion created a complex landscape of stony rises, wetlands, swamps and adjacent low-lying land prone to flooding, and an excellent habitat for an abundance of flora and fauna that became readily available resources for the Gunditjmara. In addition to this, the Gunditjmara constructed extensive aquaculture centred on the kooyang (short-finned eel) and aqueduct systems at least 6600 years ago to help trap store and harvest kooyang.

The Gunditj Mirring Partnership Project has produced a nine-volume literature review recording traditional and contemporary Gunditjmara land management practices, some refined over thousands of years.

The partnership project is designed as a way of continuing the traditional land ownership strategies, as well as their contemporary techniques, as part of a broader recognition of First Nations communities' contributions and unique viewpoint on land management.

Weblinks
Gunditj Mirring Partnership Project

Field Guide to the Budj Bim Cultural Landscape

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The Martu: https://news.mongabay.com/2024/03/traditional-aboriginal-fire-practices-can-help-promote-plant-diversity-study/

The Gunitj Mirring Partnership: https://www.gunditjmirring.com/indigenous-ecological-knowledg

* Please note that some of the sources listed in the bibliography regarding First Nations Australians are sources of information only.
These are not provided or recommended as classroom resources.

UNIT

4

Heredity and continuity of life

Piyaset/Shutterstock.com

Topic 1: Genetics and heredity

CHAPTERS RELATED TO THIS TOPIC AREA: 7–11

Topic 2: Continuity of life on Earth

CHAPTERS RELATED TO THIS TOPIC AREA: 12–14

9780170483384

All organisms are alike in key respects. They all consist of cells that carry out cellular processes. All organisms need inputs of energy, respond to their surroundings, and have a capacity to grow and reproduce according to instructions contained in DNA. Life on Earth also shows immense diversity. Millions of different organisms exist now, and many more millions lived in the past. Studies of genetic inheritance and theories of evolution help to explain life's unity and diversity.

UNIT OBJECTIVES

By the end of this unit, students should be able to:

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.

CHAPTER 7

DNA structure and function

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SYLLABUS DOT POINTS

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, promoter 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.
- Explain how errors in DNA replication and damage by physical/chemical factors in the environment can lead to point and frameshift mutations.

Introduction

Biologists have known since the time of Gregor Mendel, in the mid-19th century, that organisms inherit their physical characteristics from their parents. However, it is only in the last 70 years that the mechanism of inheritance has been explained. Understanding DNA structure and function has allowed the fields of genetics, epigenetics and genetic engineering to arise and grow into the life-saving fields of study we now rely on for medical diagnosis and treatment. Genetic mutations and errors in DNA replication account for a large percentage of human congenital conditions. Every new discovery brings us closer to providing hope and relief to those who suffer from them.

Worksheets

- DNA structure
- Structure and function of genetic materials
- DNA replication
- Point mutations

Nelson MindTap

To access resources above, visit **cengage.com.au/nelsonmindtap**

ASSUMED KNOWLEDGE

- ✓ All living things inherit deoxyribonucleic acid (DNA) from their parents.
- ✓ DNA is the common genetic material for all organisms and carries the information coded in genes.
- ✓ Prokaryotes are organisms that do not have organelles in their cells, whereas eukaryotes have many organelles.
- ✓ In eukaryotes, DNA exists in the nucleus, chloroplasts and mitochondria.
- ✓ Enzymes are proteins with a specific functional role in the cell.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ identify the major researchers in the development of the DNA double helix model
- ✓ describe the chemical structure of DNA, including nucleotides, directionality, hydrogen bonding and complementary base pairing
- ✓ describe the chemical structure of a nucleotide, including nitrogenous base, sugar and phosphate
- ✓ explain complementary base pairing
- ✓ describe the structural and functional differences between DNA and RNA
- ✓ describe the functional structure of DNA, including centromeres, telomeres, genes and gene loci
- ✓ describe the functional structure of genes, including promoter regions, introns and exons
- ✓ describe the structure and function of chromosomes, including sister chromatids and homologous chromosomes
- ✓ describe the role of histones in the structure and function of euchromatin and heterochromatin
- ✓ describe the structure and function of circular chromosomes and plasmids
- ✓ describe the process of DNA replication, including the formation of the replication bubble and replication fork, synthesis of the leading strand, and synthesis of the lagging strand
- ✓ explain the processes that create Okazaki fragments
- ✓ describe the role of DNA ligase in the joining of Okazaki fragments
- ✓ describe the role of DNA polymerase in both creating and repairing errors in DNA replication
- ✓ explain how chemical and physical factors create errors in the DNA sequence during replication
- ✓ explain how errors in replication become permanent mutations
- ✓ explain the impact of point and frameshift mutations on the functioning of a cell.

7.1 Structure of DNA

deoxyribonucleic acid (DNA) an information molecule that is the universal basis of an organism's genetic material; it contains instructions, in chemical code, for the operation of the cell

Deoxyribonucleic acid (DNA) is the cellular genetic material that contains the instructions for growth, development and functioning of all organisms, whether they are prokaryotes or eukaryotes, unicellular or multicellular. DNA has the same basic structure in all organisms, but small differences in the sequence of subunits make individuals and species distinct from one another.

Developing the helical model of DNA

Maurice Wilkins (1916–2004) began using spectroscopy to study DNA in the late 1940s. In 1950, he and Ray Gosling (1926–2015) obtained the first clear crystalline X-ray diffraction patterns from DNA fibres. Their colleague Alec Stokes (1919–2003) suggested that the patterns indicated that DNA was helical in structure.

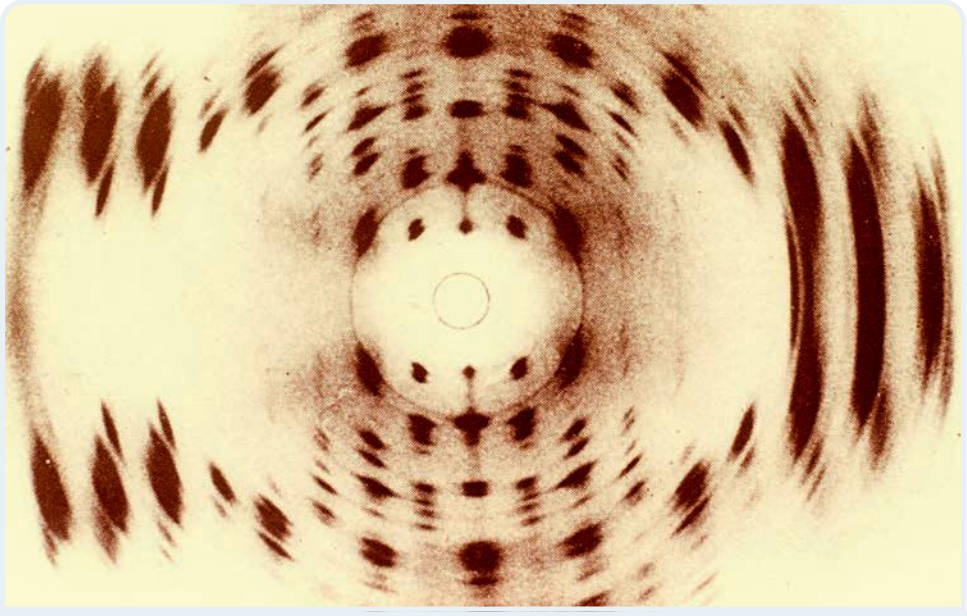
In 1952, Rosalind Franklin (1920–58) **(Figure 7.1.1)**, working alongside Wilkins in his laboratory in England, obtained some clear X-ray diffraction images of DNA **(Figure 7.1.2)**. This was not an easy task because of the complexity and size of DNA and how difficult it was to crystallise.

In 1953, using Franklin's results without her knowledge or consent, US biologist James Watson (1928–) and English physicist Francis Crick (1916–2004) suggested that DNA consisted of the now familiar two chains joined and twisted around each other to form a double helix ladder **(Figure 7.1.3)**.

This was the beginning of a further 7 years of work for Wilkins and his colleagues to check and verify Crick and Watson's hypothetical model. It was for this and his original X-ray diffraction studies that Wilkins was awarded the Nobel Prize for Physiology or Medicine with Crick and Watson in 1962. There is continued debate about whether Rosalind Franklin should also have been awarded this Nobel Prize. However, Franklin had died before the prize was awarded (of cancer caused by the radiation in her research), and Nobel Prizes are not awarded posthumously (after death).

Pictorial Press Ltd/Alamy Stock Photo

FIGURE 7.1.1 Rosalind Franklin, an expert X-ray crystallographer, worked on the structure of DNA in the early 1950s. Her work was pivotal in enabling Watson and Crick to propose their hypothesis for the structure of DNA.



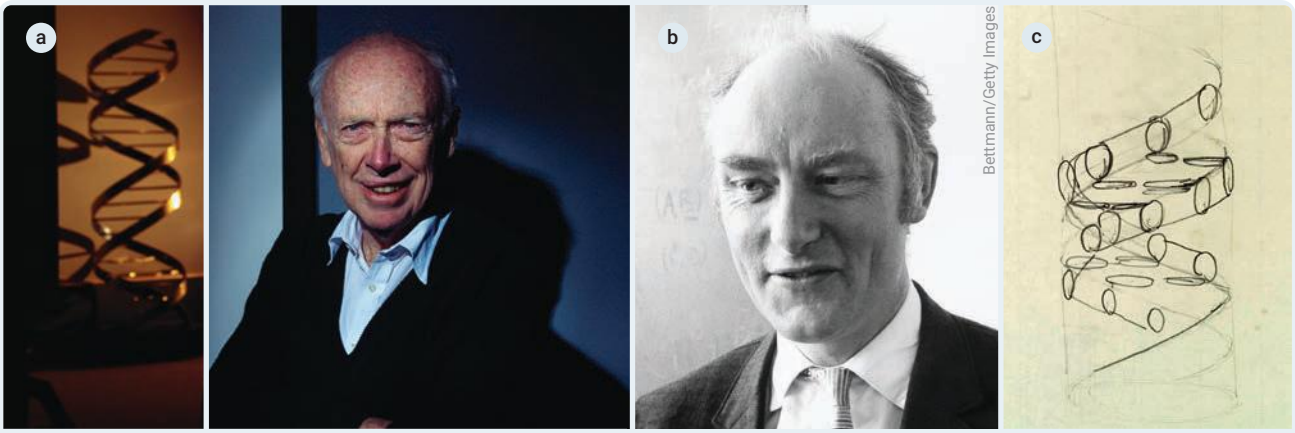
Science History Images/Alamy Stock Photo

FIGURE 7.1.2 An X-ray diffraction photograph of DNA. The DNA molecule was too small to see physically by conventional methods, so X-rays were used. This image shows the regular spacing and paired nature of DNA bases.

Weblinks

Rosalind Franklin: DNA's unsung hero

James Watson: How I discovered DNA



Karen Kasmauski/The Image Bank Unreleased/Getty Images

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FIGURE 7.1.3 (a) James Watson and (b) Francis Crick proposed a structure for DNA. (c) Crick's sketch of a double helix.

The chemical structure of DNA

nucleotide the basic building block of nucleic acids (DNA and RNA) linked together by phosphodiester bonds; each nucleotide is made up of a five-carbon sugar molecule, a phosphate group and a nitrogenous base

A molecule of DNA is composed of two long strands of subunits called **nucleotides**, wound around each other to form a double helix. A nucleotide has three distinct chemical components (Figure 7.1.4):

- a five-carbon sugar molecule
- a negatively charged phosphate group
- an organic nitrogen-containing compound called a base.

There are four kinds of nitrogenous (nitrogen-containing) bases in DNA: adenine (A), thymine (T), guanine (G) and cytosine (C).

In each strand, the sugar molecule of one nucleotide binds to the phosphate group of the next nucleotide, leaving the nitrogenous base sticking out from each sugar–phosphate backbone (Figure 7.1.4c). These bases do not stick out horizontally; instead, they tilt towards the 5′ ('five-prime') end of the strand and away from the 3′ ('three-prime') end of the strand. To ensure that the helix is stable, the two strands are oriented in opposite directions, so that the 3′ end of one strand pairs with the 5′ end of the other strand (Figure 7.1.4b).

Syllabus link
Chapter 11 discusses RNA and its functions in more detail.

Worksheet
DNA structure

complementary bases nitrogenous bases that bind to each other in DNA (A–T and C–G) and in RNA (A–U and C–G)

Hydrogen bonds between pairs of nitrogenous bases hold the two strands of the double helix together. Two features of the structure of these bases ensure that they can only pair with one other base: their size and the number of hydrogen bonds they can form. For example, thymine (T) has only one ring and can form two hydrogen bonds. This means it cannot pair with guanine (G) or cytosine (C) because these both form three hydrogen bonds. It also cannot pair with another thymine (T) because it only has one ring and the distance between the two strands requires a total of three rings across a pair. Adenine (A) has two rings and can form two hydrogen bonds, meaning it can pair with thymine's (T) one ring to form a **complementary base** pair. The structure of the four bases ensures the correct pairing of nucleotides because A can only pair with T and G can only pair with C (Figure 7.1.4b).

ribonucleic acid (RNA) a short-lived molecule consisting of ribonucleotides; it plays an essential role in protein synthesis (as messenger RNA and transfer RNA) and as a structural component of ribosomes

Ribonucleic acid (RNA) is a nucleic acid related to DNA, but has three major differences:

- RNA is usually single stranded.
- The base thymine (T) is replaced by the base uracil (U).
- The nucleotide's sugar is ribose instead of deoxyribose.

RNA is generally a short-lived molecule for copying or transporting information. It degrades far quicker than DNA, which makes it unsuitable for long-term information storage.

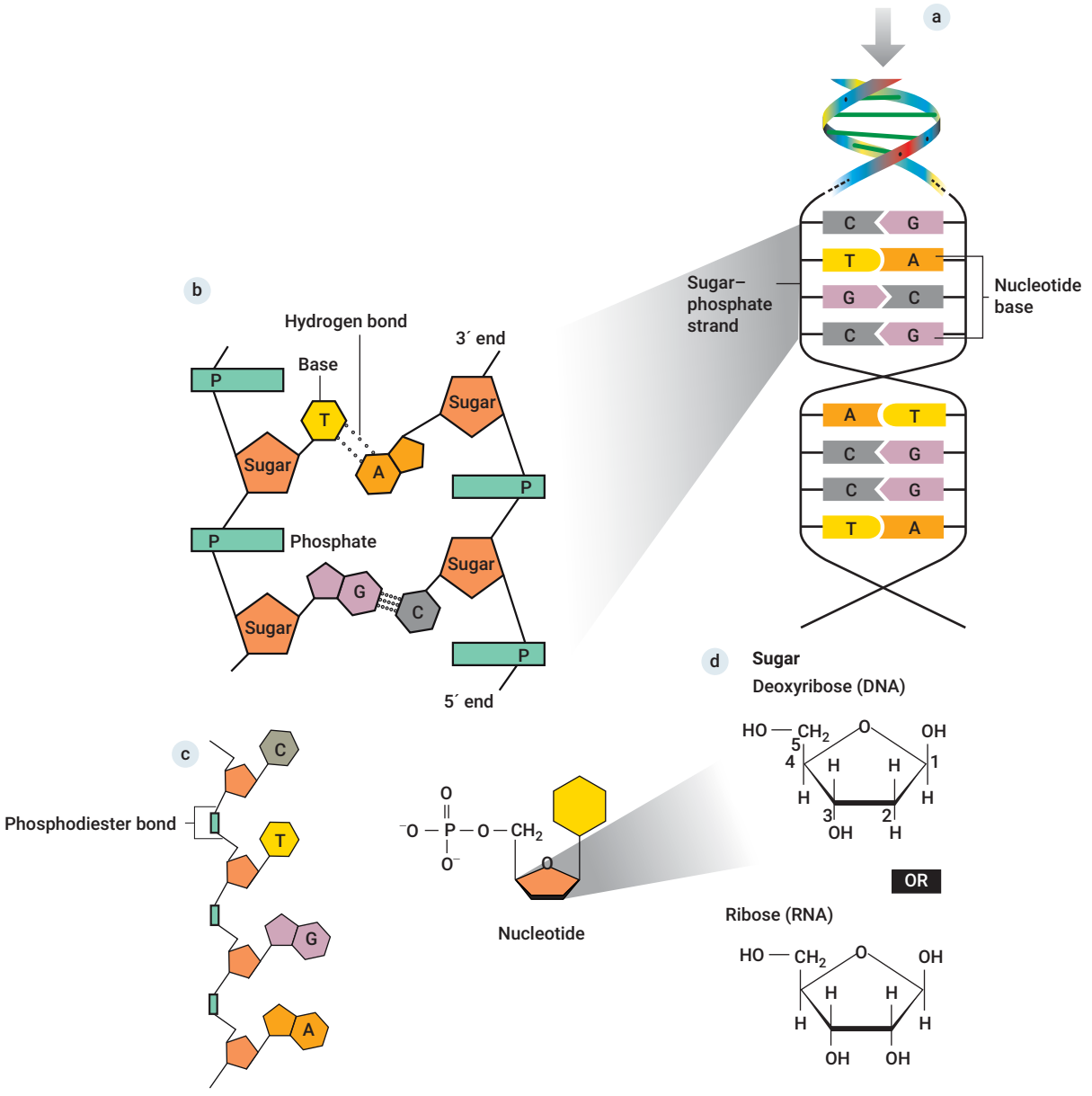


FIGURE 7.1.4 (a) The DNA helix is a double-stranded molecule. (b) The two strands are held together by hydrogen bonding between complementary nitrogenous bases. (c) As well as nitrogenous bases, nucleotides have a sugar–phosphate backbone linked by phosphodiester bonds. (d) DNA contains deoxyribose sugars and RNA contains ribose sugars.

The functional structure of DNA

The sequence of bases along a strand of DNA carries the information required for an organism to be built and function. However, with roughly 3 billion base pairs in the human genome, it requires some sort of organisation to be functional.

Weblink
DNA: the book of you

centromere the waist-like constriction in a duplicated chromosome required for the movement of chromosomes during cell division

Figure 7.1.5 shows the functional structures of DNA. At some point along the strand lies a sequence of DNA that controls the formation of the **centromere**, the connecting point on a **chromosome** for replicated DNA. The centromere divides the DNA strand into two arms, one longer than the other. Along the length of each arm, sections of DNA that code for proteins are called **genes**.

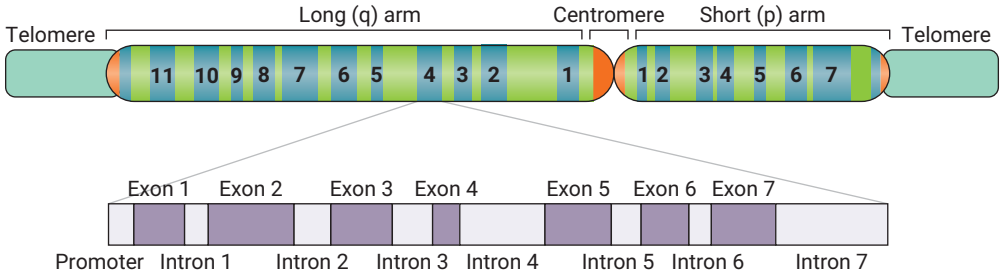


FIGURE 7.1.5 The functional structures of DNA. Genes are located on the long and short arms of a DNA strand and consist of various sections of coding and non-coding DNA. Of all the regions encompassed by a gene, only the exons are coding DNA, and even then, they are spliced together in different combinations to produce several different proteins from the same gene.

chromosome a structure composed of DNA and protein that contains, along its length linear arrays of genes carrying genetic information

gene a region of DNA that encompasses the coding and non-coding DNA for a particular protein or protein family

gene locus the specific physical location of a gene on a chromosome

coding DNA a section of DNA that specifically carries the code for direct translation into a polypeptide

non-coding DNA a section of DNA that carries information for when, where or how often its associated coding DNA is expressed

promoter region a region of DNA upstream of a gene that binds enzymes that initiate transcription

intron a section of DNA or mRNA that does not code for a polypeptide

exon a section of DNA or mRNA that codes for a polypeptide

Genes are of varying lengths and varying distances apart, but the location of each gene (**gene locus** (plural: loci)) are consistent between members of the same species. For example, the gene that is currently suspected to be responsible for the curliness of human hair, *PRSS53*, is located in every human on chromosome 16; specifically, it is within sub-band 11.2 on the short arm of this chromosome. The sequence of DNA bases at this location will determine which variant of hair curliness an individual carries.

Each gene can be read, switched on and switched off independently of other genes. When a gene is switched on, the cellular machinery will read the **coding DNA** to produce a specific protein. The gene is then said to be expressed.

Non-coding DNA mainly exists between genes on a DNA strand. The study of non-coding DNA is part of epigenetics and new discoveries are building a convincing picture of the importance of these in-between sections. They are no longer considered 'junk'. Among other things, non-coding DNA provides instructions for when, where and how often the coding DNA is expressed, such as **promoter regions** that encourage gene expression and inhibitor regions that discourage it.

Some non-coding DNA occurs within the gene itself. These are called **introns** and are generally spliced out of the sequence during protein synthesis. The remaining sections of the gene are coding DNA and are called **exons**. Stitching together different combinations of exons allows for a single gene to produce multiple different effects in the body.

At each end of the DNA strand are several thousand bases of repetitive non-coding DNA called **telomeres**. These protect the fragile ends of the molecule so that if a base or two were to break off, it would not affect the sequence of an important gene. Telomeres become shorter with age, gradually exposing important functional genes to degradation and contributing to the general loss of bodily function associated with ageing.

LEARNING CHECK 7.1

DESCRIBING

1 **Identify** three scientists who contributed to the discovery of the structure of DNA.

2 **Describe** the chemical structure of DNA, including the backbone, directionality, hydrogen bonding and complementary base pairing.

3 **Describe** the structure of a nucleotide.

4 **Describe** the function of telomeres.

5 **Identify** the type of chemical bond that holds two strands of DNA together.

6 **Define**:

a exon **b** centromere.

APPLYING

7 **Identify** the nucleotide sequence for the complementary strand of a fragment of a DNA chain with the nucleotide bases GCCTATTGCA.

Worksheet
Structure and function of genetic material

Syllabus link
Chapter 11 considers the effects of coding and non-coding DNA on protein synthesis and gene expression.

telomere a region at the end of a chromosome, characterised by repeated sequences of non-coding DNA

chromatin the complex of proteins and DNA in eukaryotes

heterochromatin a tightly coiled complex of proteins and DNA that is characterised by few genes and limited transcription activity

euchromatin a loosely coiled complex of proteins and DNA that is characterised by many genes and high transcription activity

7.2 Chromosomes

In most eukaryotic cells, DNA is only visible as a grainy substance without detail. The term **chromatin** describes the combination of the cell's DNA and all of the proteins associated with it. It is generally divided into two forms (Figure 7.2.1): **heterochromatin**, which carries only a few genes, isn't very active and remains tightly condensed most of the time, and **euchromatin**, which is densely populated with genes, highly active and loosely wound to allow frequent transcription.

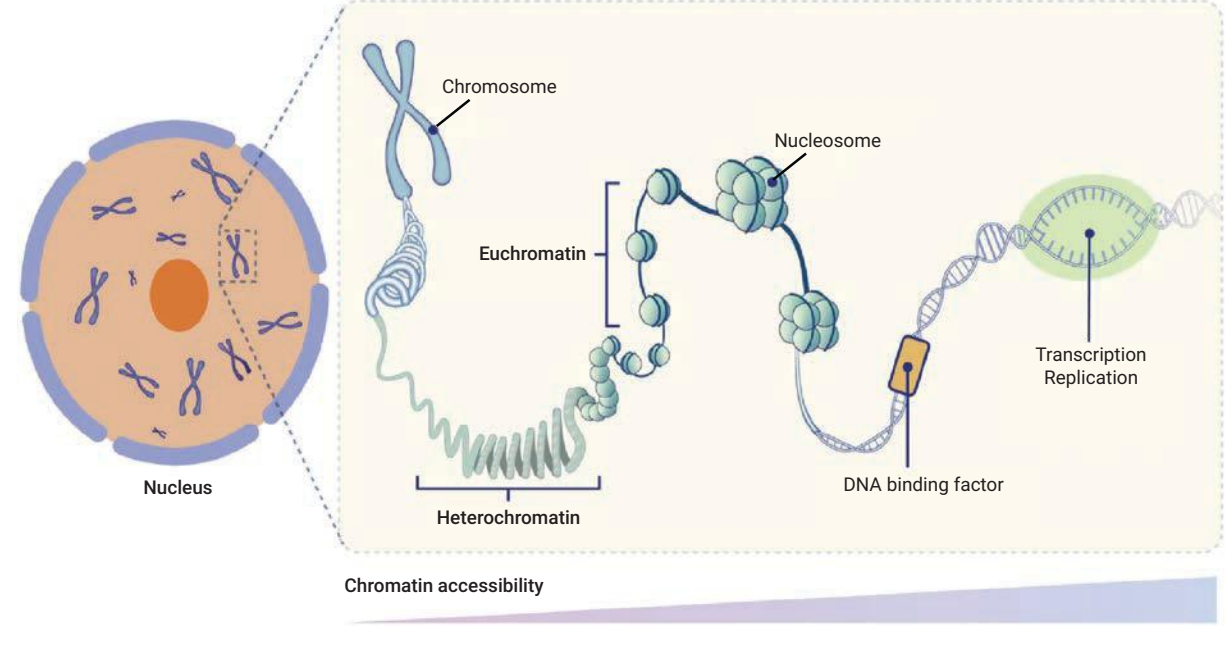


FIGURE 7.2.1 Heterochromatin and euchromatin storage structures in DNA. Euchromatin allows for easier access to DNA, so genes that are highly active are stored in euchromatin.

histone a protein that spools DNA in eukaryotic cells

When the cell prepares to divide, both forms of chromatin condense by coiling tightly around **histone** proteins, eventually becoming thick enough to be seen under a microscope, when stained, as a number of separate chromosomes (Figure 7.2.2). A chromosome is one DNA molecule, from end to end, with its associated proteins.

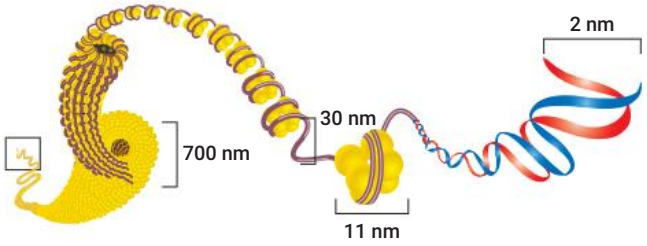


FIGURE 7.2.2 Levels of organisation in a human chromosome. Interacting proteins package loops of coiled DNA into a 'supercoil', which is organised as a cylindrical fibre.

Sister chromatids and homologous pairs

For most of the time, chromosomes are unduplicated. An unduplicated chromosome is a single, long DNA double helix molecule coiled around histone proteins. However, since chromosomes only become visible when duplicated and condensed prior to cell division, the familiar image of an X shape is actually two identical copies of the same linear chromosome (Figure 7.2.3). Each copy of the linear chromosome is not called a chromosome anymore. When they are joined by their centromeres into the X shape, each chromosome copy is now called a **sister chromatid**. It can be helpful to call the X shape a duplicated chromosome and the single shape an unduplicated chromosome to avoid this naming confusion.

sister chromatids the two identical copies of a single chromosome, formed by replication and connected by a centromere

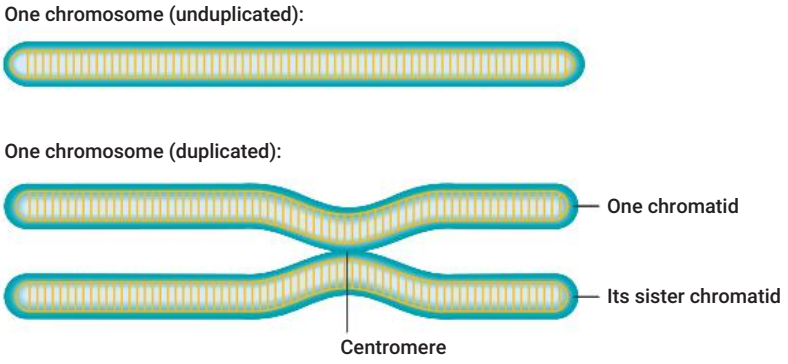


FIGURE 7.2.3 An unduplicated chromosome and a duplicated chromosome, showing the position of the centromere and the sister chromatids.

In a eukaryotic cell, each **somatic** chromosome has a pair. Together they are called **homologous pairs** and are usually denoted by different colours in diagrams. Each sister chromatid, which make up a duplicated chromosome, has an identical DNA sequence because they are direct copies of each other. But each chromosome in a homologous pair is inherited from a different parent, so their DNA sequences are similar but not identical (Figure 7.2.4). Each homologous chromosome carries the same sequence of genes along its length (i.e. both chromosomes 16s will have the *PRSS53* gene at locus 11.2 on the short arm) but the sequence of DNA bases at the locus may be different. Different base sequences at the same gene locus are called **alleles**, and they are the cornerstone of genetic variation between individuals.

somatic of the body, as distinct from the sex cells or sex chromosomes

homologous pair a pair of unduplicated chromosomes that are the same size and shape, and have the same genes at the same locations; each member of the pair may carry a different allele for any particular gene

alleles two or more alternative DNA sequences at the same gene locus on homologous chromosomes

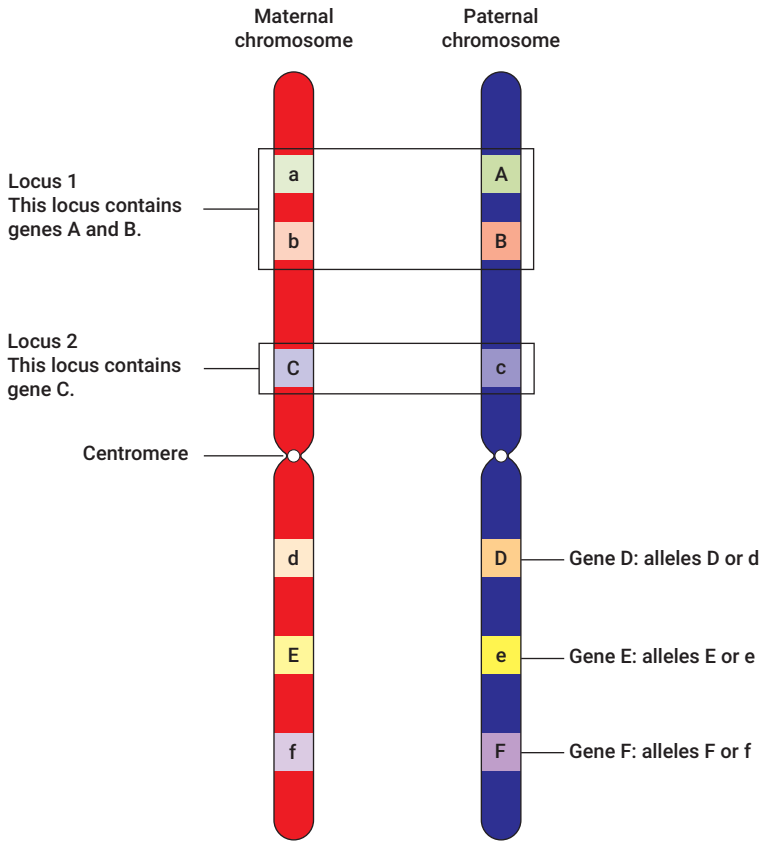
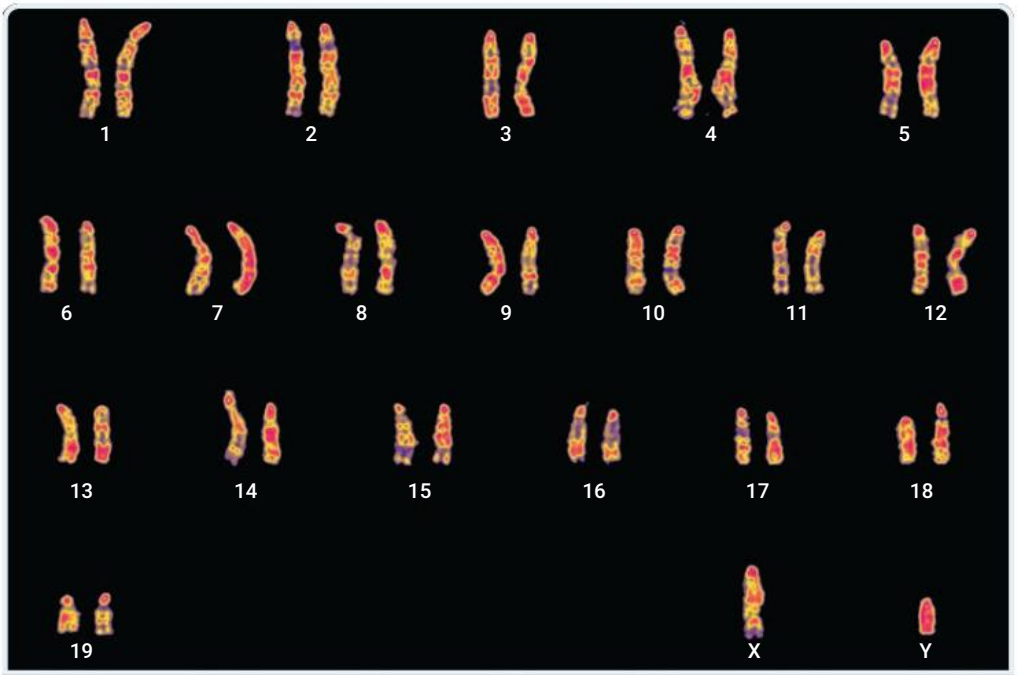


FIGURE 7.2.4 Homologous chromosomes have the same sequence of genes but may carry different DNA combinations (alleles) for those genes and result in variations of the gene.

Photographic images of the chromosomes in a dividing cell are arranged into matched and ordered pairs to create a **karyotype**, the standard way of displaying and analysing chromosomes. Somatic chromosomes are ordered by length, from longest to shortest, with members of each homologous pair sharing characteristic banding patterns that denote their matching gene loci. The exceptions are the sex chromosomes, X and Y, which do not contain a matching set of gene loci and are always placed last in a karyotype. Two X chromosomes are homologous, but X is not homologous with Y. Figure 7.2.5 shows a karyotype of a male mouse with one X and one Y chromosome. Each species has a particular number of chromosomes in its cells. Mice have 40 chromosomes (19 + 1 pairs) and humans have 46 (22 + 1 pairs).

karyotype a display of the number and appearance of the chromosomes of an organism or cell observed at metaphase



LOOK AT SCIENCES/Science Photo Library

FIGURE 7.2.5 A karyotype of a mouse. Mice have 19 pairs of somatic chromosomes and one set of sex chromosomes. This individual has one X and one Y and is genetically male.

Syllabus link
Chapter 8 discusses the use of plasmids in medical research, drug development and DNA technologies.

Circular chromosomes

Membrane-bound organelles, such as the nucleus, are not present in prokaryotes, so the DNA in prokaryotes generally forms a single circular chromosome that lies in direct contact with the cytoplasm (Figure 7.2.6). This large circular chromosome contains all the essential genes for the cell's function. Although not in a membrane-bound nucleus, it does tend to clump together in a space known as a nucleoid. Additional small rings of DNA, called **plasmids**, may also be present in the cytoplasm. These carry many non-essential, but still highly useful, genes such as those for antibiotic resistance. Plasmids can replicate independently of the main chromosome and have become important tools in genetic engineering because they can be easily transferred from one bacterium to another.

plasmid a small circular piece of DNA in bacteria that can replicate independently of the cell's chromosomes; plasmids carry antibiotic resistance markers

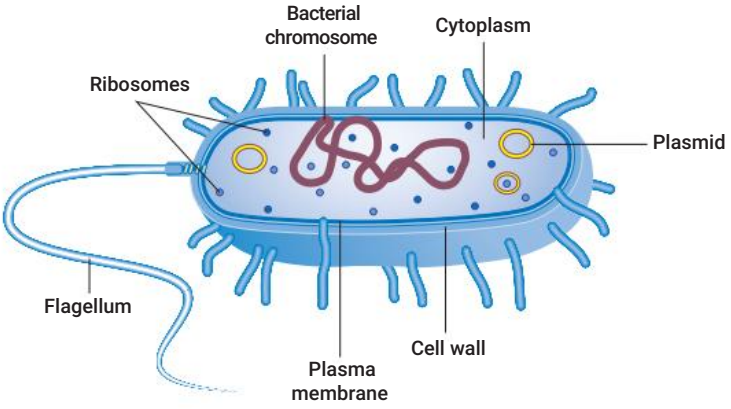


FIGURE 7.2.6 DNA in a prokaryote cell exists as circular chromosomes and plasmids.

The DNA of mitochondria and chloroplasts in eukaryotic cells is similar to the single circular chromosomes in prokaryotic cells. This feature provides strong evidence for the **endosymbiotic theory**, which proposes that eukaryotic organelles originated from prokaryotic cells that were engulfed by a host cell.

endosymbiotic theory a theory that suggests that chloroplasts and mitochondria arose from ancient prokaryotic cells that were ingested by other prokaryote host cells

LEARNING CHECK 7.2

DESCRIBING

1 **Describe** how chromosomes are ordered in a karyotype.

2 **Define**:

- **a** homologous chromosome
- **b** sister chromatid
- **c** plasmid.

APPLYING

3 **Discuss** how you would know whether two chromosomes in humans are homologous.

4 **Explain** why chromosomes are generally depicted as an X shape even though they are usually linear.

ANALYSING

5 **Distinguish** between euchromatin and heterochromatin.

6 **Compare** the DNA in mitochondria and chloroplasts with the DNA in the nucleus.

7.3 DNA replication

DNA is the master code that determines the structure and function of every body cell. It carries this information from one generation of cells to the next and from one generation of organisms to the next. Cells undergo cell division for a variety of reasons, including growth, repair and reproduction, but before they divide, cells must replicate or copy their DNA to ensure that each **daughter cell** receives the instructions for the proper functioning of that cell. Cells also replicate all their organelles, but the syllabus focuses on replication of DNA.

daughter cell either of the two cells formed when a cell undergoes cell division

DNA replication begins with the opening of a replication bubble (Figure 7.3.1) by initiator proteins. These bubbles occur at many points along the DNA strand, with replication

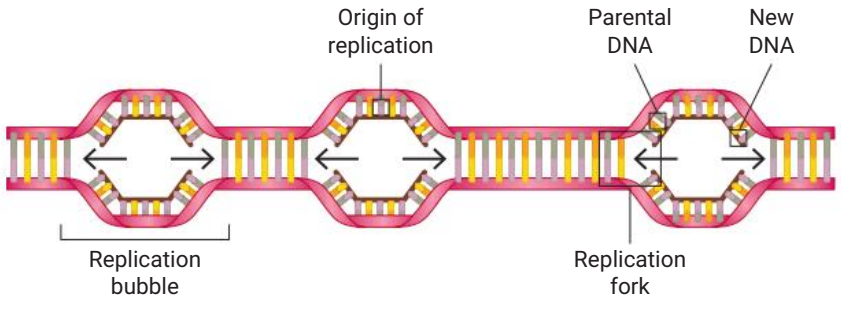


FIGURE 7.3.1 Replication bubbles form at many points along the parental DNA, with two replication forks moving outward from the origin of replication.

Weblink
Molecular visualisations of DNA

DNA helicase the enzyme that unwinds and separates the two strands of the DNA double helix in DNA replication

parental DNA the DNA of the original cell in cell division

proceeding in both directions as the replication bubble grows. To open the replication bubble, initiator proteins attract the enzyme **DNA helicase**, which unzips the helical **parental DNA** by breaking the hydrogen bonds between the nucleotide pairs. The junction between the unwound single strands of DNA and the intact double helix is called the **replication fork**. The replication fork moves along behind DNA helicase so that there is a continuous unwinding of the parental strands.

DNA polymerase forms a new complementary strand on each of the parental DNA strands **(Figure 7.3.2)**. DNA polymerase draws from a stockpile of free nucleotides to attach complementary ones to the exposed bases. It then forms the sugar–phosphate bond between the new nucleotides to finish the new complementary strand.

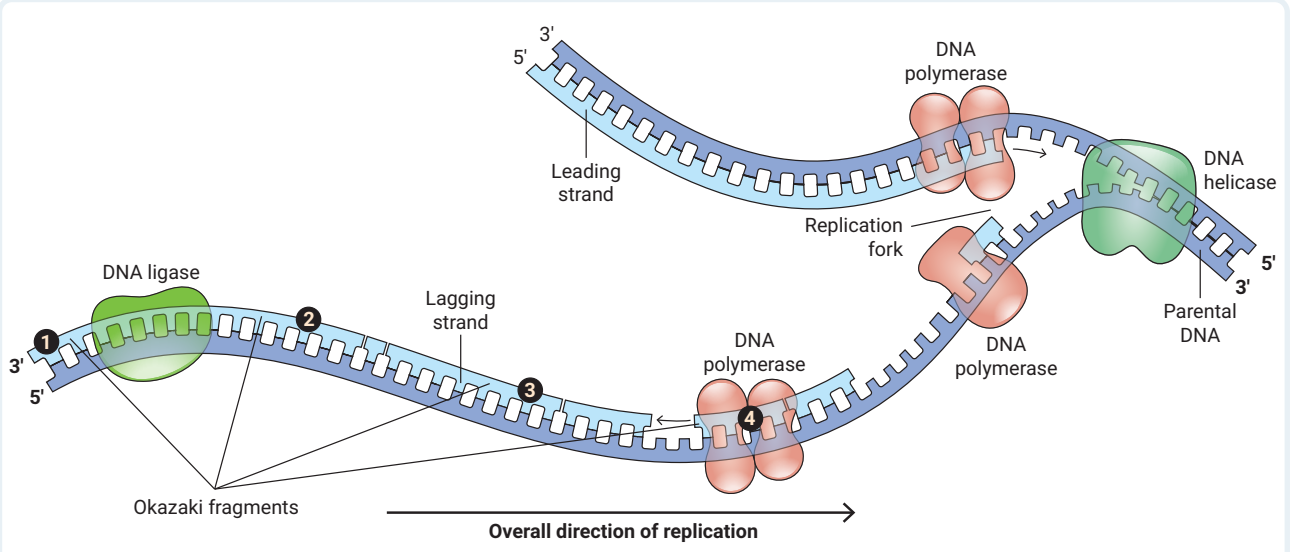


FIGURE 7.3.2 The two concurrent processes of DNA replication. DNA polymerase replicates the leading strand continuously, while it must replicate the lagging strand discontinuously. DNA ligase connects the Okazaki fragments created by discontinuous replication.

replication fork the junction between the unwound single strands of DNA and the intact double helix during replication

DNA polymerase the enzyme that forms the complementary strand in DNA replication

leading strand the DNA strand that is already in the 5′ to 3′ direction, so its complement cannot replicate continuously by DNA polymerase in the 5′ to 3′ direction because its parent strand is unzipped in the 3′ to 5′ direction

However, DNA polymerase only produces new DNA in the 5′ to 3′ direction and in double-stranded DNA the two strands run in opposite directions. This means that the two parental strands are replicated slightly differently. The strand that has DNA helicase unzipping it in the 3′ to 5′ direction will have its new strand formed to complement it (5′ to 3′). This is called the **leading strand** and can be replicated by DNA polymerase in a continuous manner; the strand is unwound by DNA helicase at the replication fork and fed almost directly into DNA polymerase.

The process becomes more complicated on the other strand, which lies in the opposite direction so must be unwound in the 5′ to 3′ direction. DNA polymerase cannot replicate in the complementary 3′ to 5′ direction, so this **lagging strand** cannot be replicated continuously. Instead, the second DNA polymerase attaches at the replication fork and moves away from the fork to produce a new strand in the 5′ to 3′ direction (Figure 7.3.2). When it reaches the end of the strand, or a previously replicated section, it falls away and must return to the replication fork. Given that the replication fork is continuously moving, by the time the DNA polymerase returns to the fork, there is a new section of lagging strand exposed. This process – replication away from the fork, return to the fork, replication away from the fork – produces a series of

disconnected fragments on the lagging strand. These are called **Okazaki fragments** after Reiji and Tsuneko Okazaki, the husband-and-wife team who discovered them in 1968.

A final enzyme, DNA ligase, travels behind the replication bubble and connects the sugar–phosphate backbone of the Okazaki fragments to form a continuous double-stranded helix on the lagging strand. This completes the process of replication, producing two double-stranded copies of the parental DNA, each consisting of one original parental strand and one newly formed daughter strand. When one of the two strands is conserved, or retained, while the other strand is new, it is referred to as **semiconservative replication**.

lagging strand the DNA strand that is already in the 5′ to 3′ direction, so its complement cannot be replicated continuously by DNA polymerase; replication forms Okazaki fragments that must be stitched together by DNA ligase

Okazaki fragments the DNA fragments caused by the discontinuous replication of DNA on the lagging strand; they are stitched together to make a continuous strand by DNA ligase

Errors in replication

While DNA polymerase is usually a highly faithful replicator, it does make approximately one mistake every 100000 nucleotides, which equates to about 120000 mistakes per replication cycle. This rate is further increased if the gene for producing DNA polymerase already carries errors, so the enzyme is not optimally built in the first place. Figure 7.3.3 shows the three most common errors in replication: insertion (adding extra nucleotides), deletion (failing to add nucleotides) and substitution (adding the wrong nucleotide).

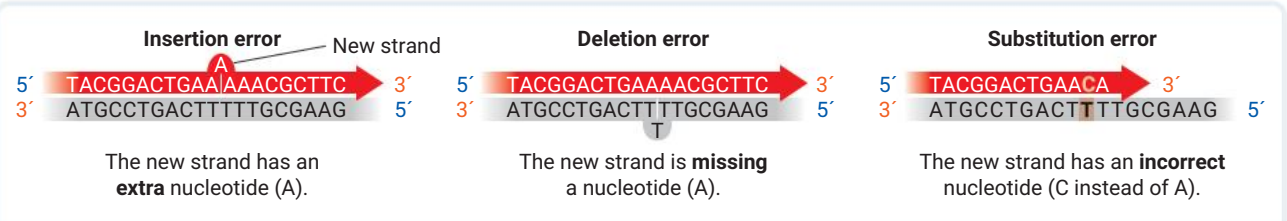


FIGURE 7.3.3 The three most common errors of DNA replication. Insertions result in too many nucleotides, deletions result in too few, and substitutions result in the wrong nucleotides.

Given how often these errors occur, DNA polymerase carries a proofreading subunit on its tail. This subunit can remove and reinsert nucleotides as necessary to correct insertion, deletion and substitution errors almost as soon as they are made. The proofreading process reduces the total number of mistakes to about 1200 per replication cycle.

DNA errors can also be due to physical or chemical factors. Ultraviolet (UV) light breaks the bonds holding nucleotides together, causing deletion errors and other issues with accurate replication. Some mutagenic chemicals, such as nitrosamines in tobacco and artificially preserved foods, directly damage stored or replicating DNA.

DNA errors that are not detected and repaired before the cell completes replication become **mutations**, permanent changes in the DNA sequence that the cell can no longer detect as abnormal. Figure 7.3.4 shows two types of mutation: point mutations and frameshift mutations. Point mutations are caused by permanent substitution errors and usually have a limited effect on the cell. The effect of point mutations is usually limited because many mutations occur in non-coding regions of DNA or lead to a change in the genetic code that still produces the same amino acid.

semiconservative replication the production of two new DNA double helix molecules, each consisting of one parental strand and one daughter strand

mutation a permanent change in a sequence of DNA

FIGURE 7.3.4 Two types of DNA mutations. Point mutations usually have small effects on cell function, whereas frameshift mutations have large effects.

Syllabus link
Chapter 11 considers the effects of DNA mutations on protein synthesis and gene expression.

Worksheets
DNA replication
Point mutations

Frameshift mutations are caused by permanent insertion or deletion errors and usually have extensive negative effects on the cell. This is because of the way DNA is read when building proteins. Frameshift mutations not only change the amino acid that the mutated section codes for, they also change how all subsequent sections of the gene are read.

LEARNING CHECK 7.3

DESCRIBING

1 **Describe** the role of the enzymes DNA helicase, DNA polymerase and DNA ligase in the process of DNA replication.

2 **Describe** what it means to say that the two strands of DNA are complementary.

3 **Describe** the four parts of DNA replication.

4 **Describe** how the cell keeps DNA replication accurate.

APPLYING

5 **Explain** the formation of Okazaki fragments.

6 DNA polymerase works at a rate that would replicate a full chromosome in about 800 h. However, DNA replication only takes about 8 h. **Explain** the mechanism that enables this.

7 Point and frameshift mutations have very different outcomes for the cell. **Identify** the types of replication error that the cell's proofreading and repair processes work hardest to prevent.

8 During DNA replication, a mistake was made and none of the DNA repair enzymes detected or repaired the damage. The section of DNA with the mistake is shown in Figure 7.3.5. **Identify** the mistake and **explain** how it occurred.

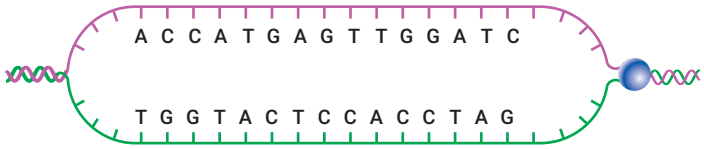
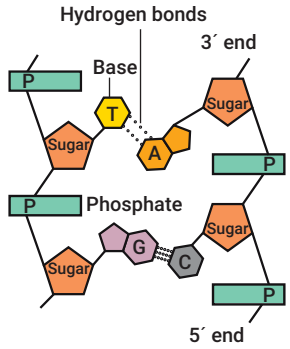


FIGURE 7.3.5 A section of DNA undergoing replication. The lettered bases represent the newly synthesised daughter strands.

CHAPTER SUMMARY

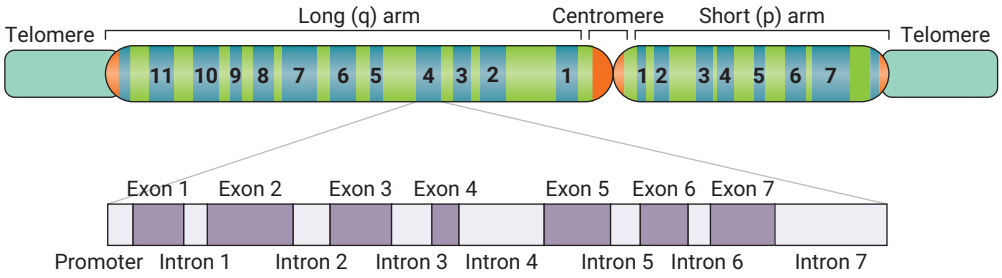
Chemical structure

- DNA contains nucleotides where each strand is held together by hydrogen bonds.
- Each nucleotide has:
  - a five-carbon sugar molecule
  - a negatively charged phosphate group
  - an organic nitrogen-containing compound called a base.



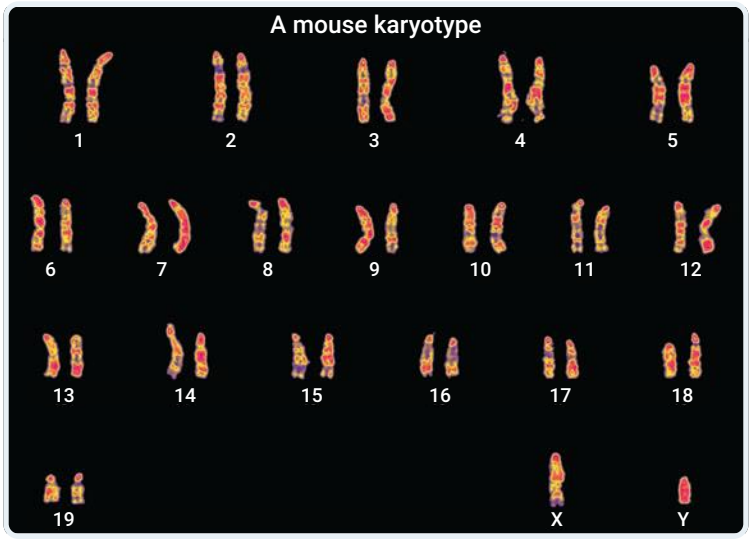
Functional structure

- Sequences of bases along a strand of DNA carry the information required for an organism to be built and function.



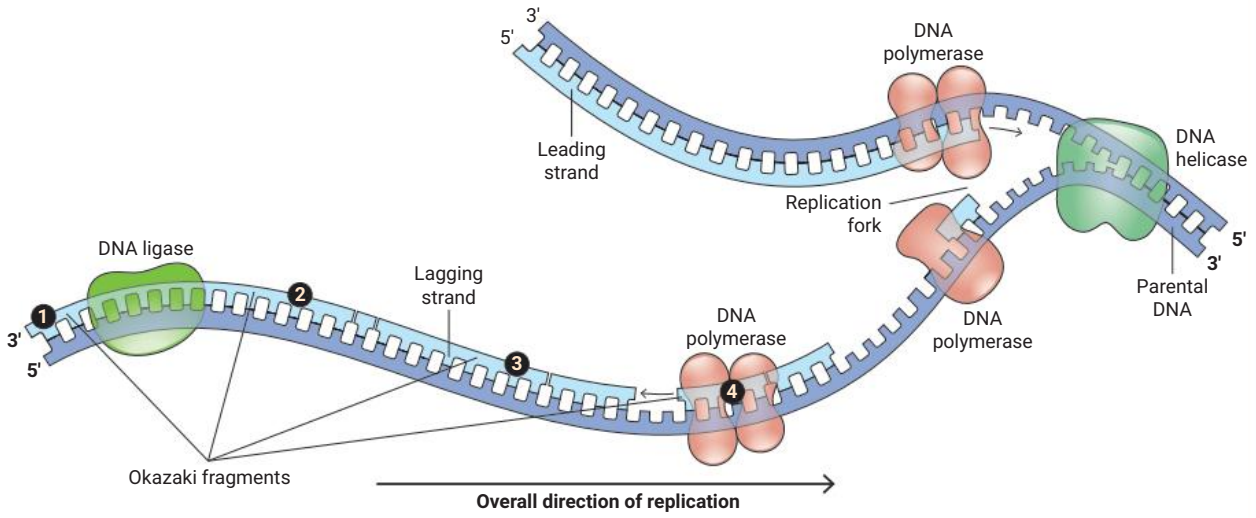
Chromosomes

- Heterochromatin is a tightly coiled region of DNA and histones with limited gene activity, whereas euchromatin is a loosely coiled region with extensive gene activity.
- Prokaryotes, along with chloroplasts and mitochondria, carry circular chromosomes.
- A karyotype shows the set of chromosomes in an organism.



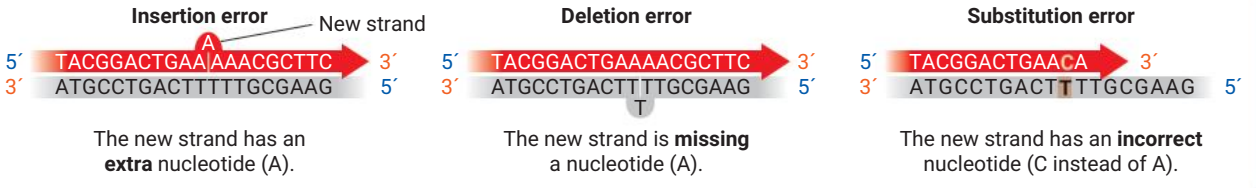
DNA replication

- Replication occurs in both directions simultaneously outwards from the origin of replication in a replication bubble.
- DNA polymerase only produces new DNA in the 5′ to 3′ direction.
- Okazaki fragments are short pieces of disconnected DNA that form on the lagging strand during replication.



Errors in replication

- Different types of errors can occur during replication.
- The three most common errors in replication are insertion, deletion and substitution.



CHAPTER EXAM

MULTIPLE CHOICE

1. In semiconservative replication of DNA:
- **A** sperm cells are produced.
- **B** genes are expressed.
- **C** one strand is new.
- **D** both strands are new.

2. If 35 per cent of the bases of a molecule of DNA are thymine, it will also contain:
- **A** 15 per cent guanine.
- **B** 25 per cent adenine.
- **C** 30 per cent uracil.
- **D** 35 per cent cytosine.

3. Which one of the following is correct?
- **A** A chromosome is composed of DNA and proteins.
- **B** Each chromosome is made up of many molecules of DNA.
- **C** One strand of DNA is maternal and one strand is paternal.
- **D** The different cell types in an organism have different DNA.

4. The statement 'All chromosomes are double-stranded and linear' is:
- **A** true for prokaryotes but not for eukaryotes.
- **B** true for eukaryotes but not for prokaryotes.
- **C** always true.
- **D** not true for eukaryotes or for prokaryotes.

5. Identify the only sections of DNA in a chromosome that directly code for a protein.
- **A** Exons
- **B** Genes
- **C** Introns
- **D** Telomeres

6. Homologous chromosomes have:
- **A** the same sequence of genes and the same sequence of DNA.
- **B** the same sequence of genes, but may have different DNA sequences.
- **C** different gene sequences, but the same sequence of DNA.
- **D** different gene sequences and different DNA sequences.

7. Which of the following do not have circular chromosomes?
- **A** Chloroplast
- **B** Mitochondrion
- **C** Nucleoid
- **D** Nucleus

8. Which of the following is not an enzyme involved in DNA replication?
- **A** DNase
- **B** DNA helicase
- **C** DNA ligase
- **D** DNA polymerase

9. Okazaki fragments are:
   - **A** errors in DNA replication.
   - **B** fragments of damaged DNA.
   - **C** synthesised on the lagging strand.
   - **D** stitched together with DNA primase.

10. Permanent substitution errors in replication are called:
   - **A** dominant mutations.
   - **B** substitution mutations.
   - **C** point mutations.
   - **D** frameshift mutations.

SHORT RESPONSE

11. **Sketch** and label a diagram of a nucleotide.

12. **Describe** the process of DNA replication.

CROSS-CHAPTER QUESTION

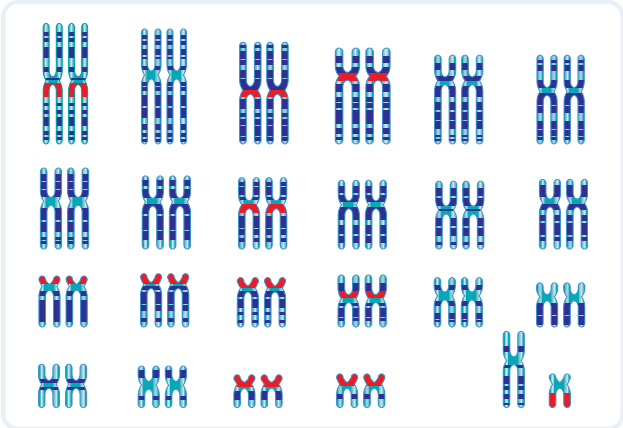
13. **Explain** how errors in DNA replication contribute to the diversity of species on Earth.

DATA ANALYSIS

14. **Apply understanding**

The image shows a human karyotype.

Identify the biological sex of the person.



15. **Interpret evidence**

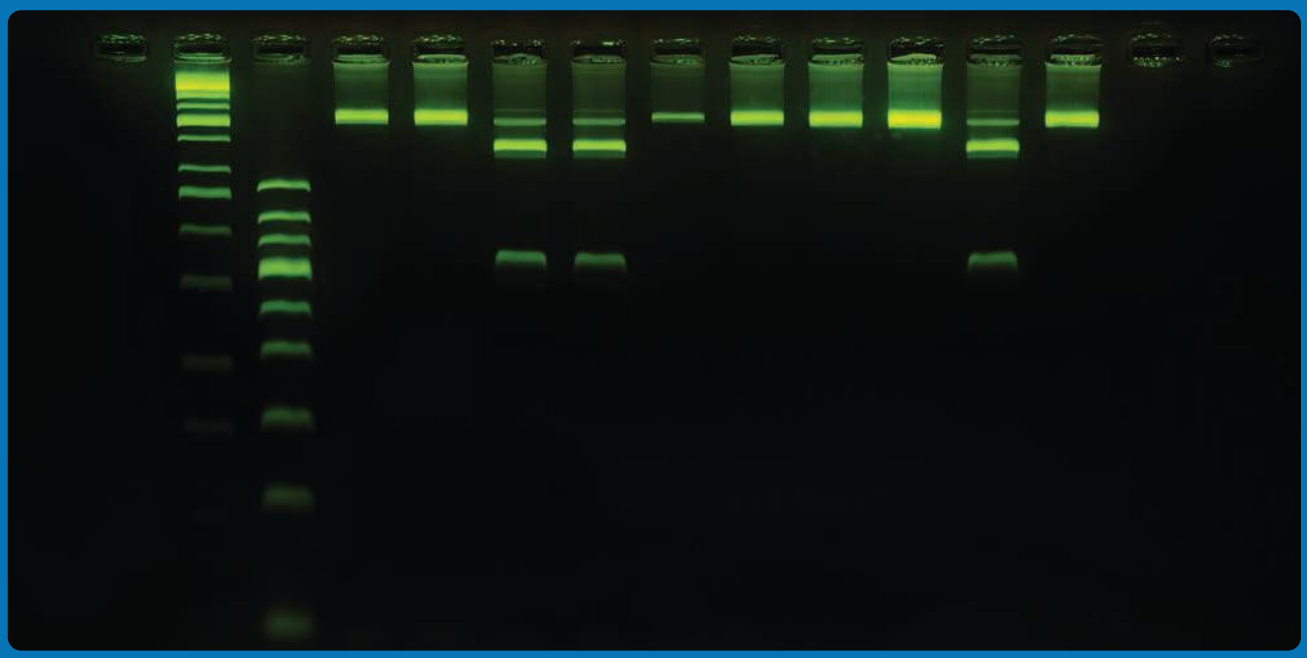
A researcher collected data from several sources on the base nucleotides in DNA and concluded that this supports the base pairing rule. Their data is shown in the following table.

Source	DNA composition (approx. %)			
	A	C	G	T
Yeast	32	17	18	33
Ox spleen	30	18	24	29
Human sperm	30	19	19	32

Deduce whether the researcher's conclusion is correct. Provide evidence from the data.

CHAPTER 8

DNA applications



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SYLLABUS DOT POINTS

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.

Introduction

The term 'biotechnology' describes the use of living things to make new products or systems. Biotechnology has been practised for thousands of years, since early Egyptian and Babylonian civilisations first used micro-organisms to make bread, beer and wine. In recent times, increased knowledge of genetics and molecular biology has revolutionised biotechnology, opening up the possibility of cloning, gene therapy, genetically modified organisms (GMOs) and the rapid diagnosis of genetic diseases. The processes of identifying and manipulating DNA, such as DNA recombination, the polymerase chain reaction (PCR) and gel electrophoresis, have evolved to the point of being considered foundational biological knowledge.

Practical

- Analysing DNA profiles

Worksheets

- Making recombinant DNA
- Gel electrophoresis
- DNA profiling

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ASSUMED KNOWLEDGE

- ✓ DNA is a polymer of nucleotides that consists of a series of genes and non-coding regions.
- ✓ DNA consists of two strands that stick together through hydrogen bonds formed between their complementary base pairs.
- ✓ Plasmids are small circular DNA strands common in bacteria.
- ✓ Enzymes are proteins with a specific functional role in the cell.
- ✓ DNA polymerase is an enzyme that synthesises the new DNA strands during DNA replication.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ describe some of the key uses for recombinant DNA
- ✓ explain how DNA is cut by restriction enzymes to form blunt or sticky ends
- ✓ describe how a gene of interest is inserted into a bacterial plasmid
- ✓ explain why bacterial plasmids are used to carry genes of interest into laboratory bacteria
- ✓ describe the roles of restriction enzymes and DNA ligase in making recombinant DNA
- ✓ describe the purpose of the polymerase chain reaction (PCR)
- ✓ explain why *Taq* polymerase is used in PCR
- ✓ explain the purpose of primers in PCR
- ✓ describe the three phases of a PCR cycle
- ✓ describe the process of gel electrophoresis
- ✓ explain how agarose gel separates DNA fragments by size
- ✓ analyse and interpret DNA profiles to determine the degree of relatedness between samples, providing reasoning.

8.1 Recombinant DNA

recombinant DNA technology the process of transferring a gene from a cell of a member of one species to the cell of a different species

genetically modified organism (GMO) an organism that has been modified by incorporating a piece of foreign DNA into its genome

vector a vehicle used to transfer DNA sequences from one organism to another

The technology that combines DNA from different sources to generate a modified DNA sequence is called **recombinant DNA technology**. The term 'recombinant' comes from the base word 'combine' and denotes that something has been recombined in a new way. A **genetically modified organism (GMO)** is a recombinant organism because its DNA has been recombined with DNA from another source. Some GMOs, such as Golden Rice, provide a more nutritious food source than native rice. Animals such as goats and cows can be genetically modified to produce medically valuable proteins in their milk. Alternatively, cultures of recombinant micro-organisms can generate pharmaceuticals such as human growth hormone and insulin. For medically valuable molecules, recombinant organisms dramatically increase the efficiency and cost-effectiveness of production.

Recombinant DNA is usually produced by using bacterial plasmids, circular pieces of DNA in bacteria that generally carry a limited number of related genes. Plasmids contain their own instructions for replication, so they reproduce independently of the bacterial chromosome (Figure 8.1.1). Because of their small size and independent reproduction, plasmids are used as **vectors** to transport a gene of interest from an unrelated organism into bacterial cells.

Weblink
Recombinant DNA technology

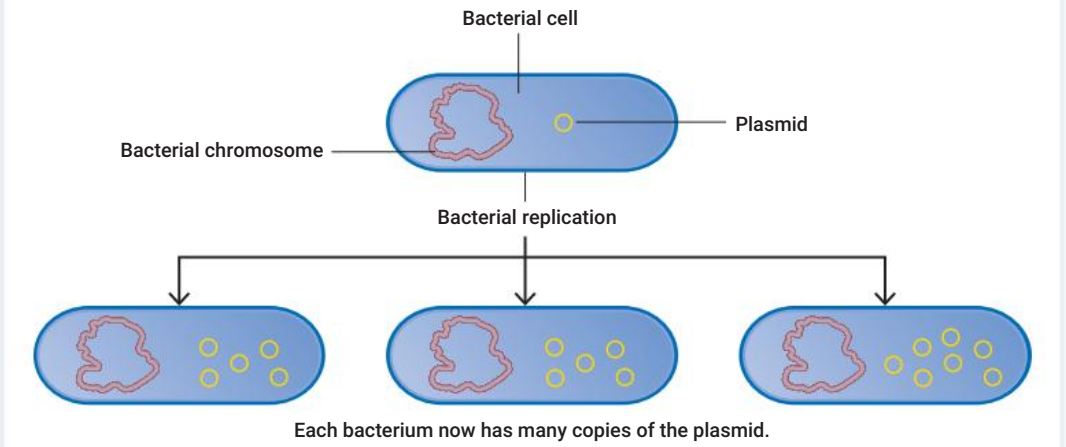


FIGURE 8.1.1 When bacteria replicate, bacterial plasmids reproduce independently of the bacterial chromosome.

Cutting DNA

To use a plasmid as a vector, the gene of interest must be inserted alongside or in place of the genes it usually carries. This requires the manipulation of the circular DNA by cutting it apart and gluing it back together. Fortunately, all cells use very similar machinery to manipulate their DNA during replication, so the enzymes that can cut DNA and those that can repair it already exist inside the cell. The key to recombinant DNA technology is harnessing those enzymes for human purposes.

Syllabus link
Chapter 7 details the enzymes that carry out DNA replication.

First, the circular plasmid must be cut to open a space for the new gene. The family of enzymes that cut DNA are called **restriction enzymes**. They occur naturally in bacteria, where they form part of the cell's immune system, cutting up foreign DNA that enters the cell from invading viruses. The cut pieces of DNA are no longer functional and the cell recycles the nucleotides for its own use.

restriction enzyme an enzyme that cuts DNA at a specific restriction site

Each restriction enzyme, named for the bacterial strain from which it was derived, cuts DNA at a specific base sequence, known as its **restriction site**. These restriction sites are between four and eight nucleotides long and are mirror sequences (Table 8.1.1). Using mirrored sequences means that the enzyme does not need to be oriented a particular way to consistently cut at the same site.

restriction site a specific nucleotide sequence (usually 4–8 base pairs) that is recognised as a cleaving site for a restriction enzyme

TABLE 8.1.1 Common restriction enzymes and their restriction sites

Enzyme	Bacterial source	Restriction site	After cutting
*Eco*RI	*Escherichia coli*	5′G↓AATTC3′ 3′CTTAA↑G5′	5′G AATTC3′ 3′CTTAA G5′
*Hind*III	*Haemophilus parainfluenzae*	5′A↓AGCTT3′ 3′TTCGA↑A5′	5′A AGCTT3′ 3′TTCGA A5′
*Alu*I	*Arthrobacter luteus*	5′AG↓CT3′ 3′TC↑GA5′	5′AG CT3′ 3′TC GA5′
*Bam*HI	*Bacillus amyloliquefaciens* H	5′G↓GATCC3′ 3′CCTAG↑G5′	5′G GATCC3′ 3′CCTAG G5′

Restriction enzymes can make one of two types of cuts to leave either sticky or blunt ends on the DNA. **Sticky ends** leave some nucleotides exposed (Figure 8.1.2a), which encourages the loose ends to find complementary sequences to re-bind. This is a useful feature if the DNA cut is only meant to be temporary, or if the re-bound DNA has a similar sequence.

sticky end the overhanging end of a DNA fragment that is produced after asymmetrical cleavage by a restriction enzyme

Blunt ends leave no exposed nucleotides **(Figure 8.1.2b)**, which is useful if the DNA cut is meant to be more permanent, or if the re-bound DNA doesn't share a similar sequence.

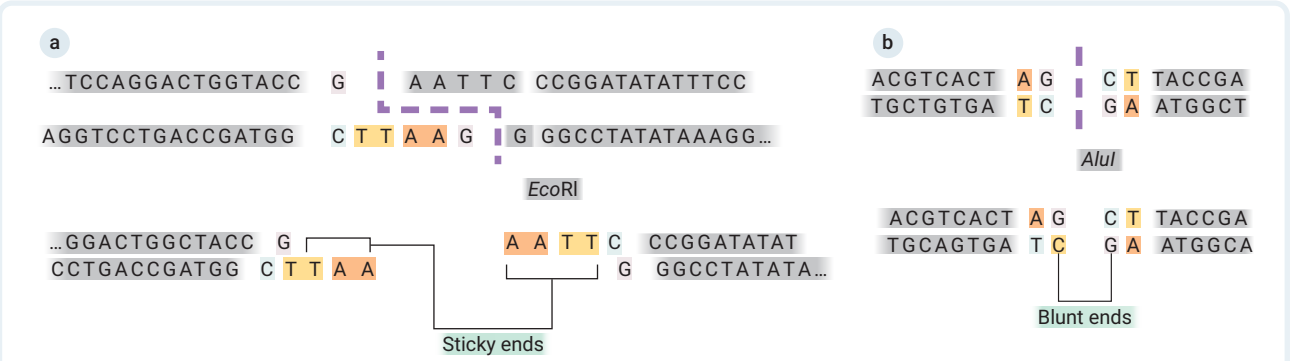


FIGURE 8.1.2 (a) Sticky ends are produced by asymmetrical cleavage, such as with the restriction enzyme *Eco*RI. (b) Blunt ends are produced by symmetrical cleavage, such as with the restriction enzyme *Alu*I.

blunt end the flat end of a DNA fragment that is produced after symmetrical cleavage by a restriction enzyme

Inserting DNA

It is simplest to make recombinant DNA when the plasmid has been cut with a sticky end restriction enzyme and the gene of interest has a matching restriction site **(Figure 8.1.3)**. Cutting both the plasmid and the gene of interest with the same restriction enzyme results in both pieces of DNA having complementary sticky ends. Combining the two DNA samples and applying the appropriate temperature and pH conditions results in a recombinant sample in which most of the DNA has formed one of three different structures: the gene of interest stuck to other genes of interest; the plasmid attached to other plasmids; or the target structure, the gene of interest stuck to a plasmid. The target structure is selected for in a process that goes beyond the scope of the syllabus.

Worksheet
Making recombinant DNA

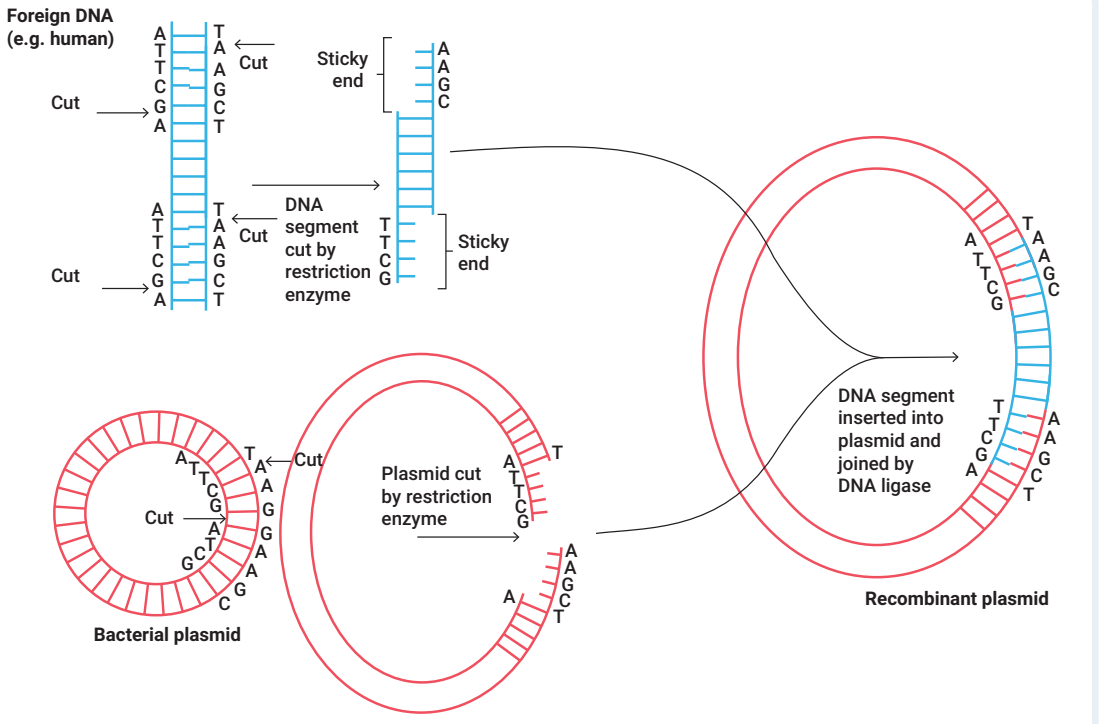


FIGURE 8.1.3 A foreign gene is inserted into plasmid DNA to produce a recombinant plasmid.

Once the nucleotides in the sticky ends are paired together, **DNA ligase** recognises and joins the breaks in the sugar–phosphate backbone. This is the same function that it provides during DNA replication, where it joins the sugar–phosphate backbones of the Okazaki fragments.

The result is a sample of **recombinant plasmids** that can be introduced to laboratory bacterial cultures, which then uptake the plasmids and begin producing the target molecule from the gene of interest.

DNA ligase an enzyme that catalyses the formation of a sugar–phosphate bond between two pieces of DNA

recombinant plasmid a plasmid with foreign DNA inserted into it

LEARNING CHECK 8.1

DESCRIBING

1 List three applications of recombinant DNA.
2 **Describe** the two types of ends created by restriction enzymes.
3 **Identify** the enzyme that repairs the sugar–phosphate backbone of recombinant plasmids.
4 **Describe** the process of making recombinant DNA.

APPLYING

5 **Explain** why plasmids are suitable for recombinant DNA.
6 **Explain** what would happen if the plasmid and the gene of interest were cut with different restriction enzymes.

ANALYSING

7 **Compare** the role of DNA ligase in DNA replication and recombinant DNA.

INTEPRETING

8 **Predict** whether the following cuts made by restriction enzymes will produce sticky or blunt ends. The arrows show where the cuts occur in the double-stranded DNA.

a TCCG↓CGGA
AGGC↑GCCT

b A↓GGGCCT
TCCCGG↑A

c GC↓GGCCGC
CGCCGG↑CG

8.2 PCR and gel electrophoresis

Biotechnology, like other areas of biology, has its own set of specialised tools for specific purposes. These include techniques for amplifying, separating and viewing sections of DNA. These techniques have a range of different uses, from isolating and amplifying genes of interest for recombinant DNA to identifying victims of crime.

Weblink
Polymerase chain reaction

Amplifying DNA: Polymerase chain reaction

DNA samples are not often taken from large volumes of biological material. At crime scenes, the sample is usually tiny and highly damaged from exposure to the environment. In antigen tests, such as those that use saliva or nasal swabs to detect respiratory viruses, the sample is miniscule – often only trace amounts. In live animal genomics, it is unethical and wasteful to use large volumes of biological material taken from the animal to analyse DNA. Even so, large amounts of DNA are required to do any useful analysis, so a tiny DNA sample needs to be amplified, copied over and over until there are millions of copies of the sample for analysis. The **polymerase chain reaction (PCR)** is a repeated series of processes that amplifies DNA samples quickly.

polymerase chain reaction (PCR) a cyclical reaction in which DNA polymerase is used to copy a DNA sample, making millions of copies of the same piece of DNA

***Taq* polymerase** DNA polymerase from the bacterium *Thermus aquaticus*; used in the polymerase chain reaction because it can withstand the high temperatures used in the process

primer a single-stranded DNA molecule that anneals to its complementary sequence on the DNA sample to act as the start of the amplification process

anneal to hydrogen bond, as when two single-stranded sections of complementary DNA align to form a double strand

The first PCRs conducted required highly trained scientists to balance a wide range of delicate equipment under strict laboratory conditions. The process had much room for error, which could ruin the entire reaction. Today, PCR is an automated process that is carried out by a machine called a thermal cycler. Each completed PCR takes a few hours and the process is very reliable.

The technique makes use of the enzyme DNA polymerase to catalyse the formation of new DNA strands by joining together free nucleotides in the PCR solution. One of the most commonly used DNA polymerases, ***Taq* polymerase**, comes from the bacteria *Thermus aquaticus*, which live in thermal springs. *Taq* polymerase is resistant to the very high temperatures used in the thermal cycler.

DNA polymerase can only extend a complementary DNA strand from an existing double-stranded section; it cannot produce a new complementary strand on single-stranded DNA. This means that PCR requires one further ingredient – primers. A **primer** is a short sequence of single-stranded DNA (about 20 nucleotides), complementary to the nucleotide sequence at either end of the DNA section that is to be copied. Primers are short enough to self-**anneal** to the single-stranded DNA, so they provide a starting point for the DNA polymerase by producing a small section of double-stranded DNA that it can work from. PCR primer design is a complex and challenging field.

Each cycle of PCR consists of three processes (Figure 8.2.1):

1. **Denaturation**: The double-stranded DNA sample is heated to 95°C, breaking the hydrogen bonds between the bases and causing the two strands to separate.

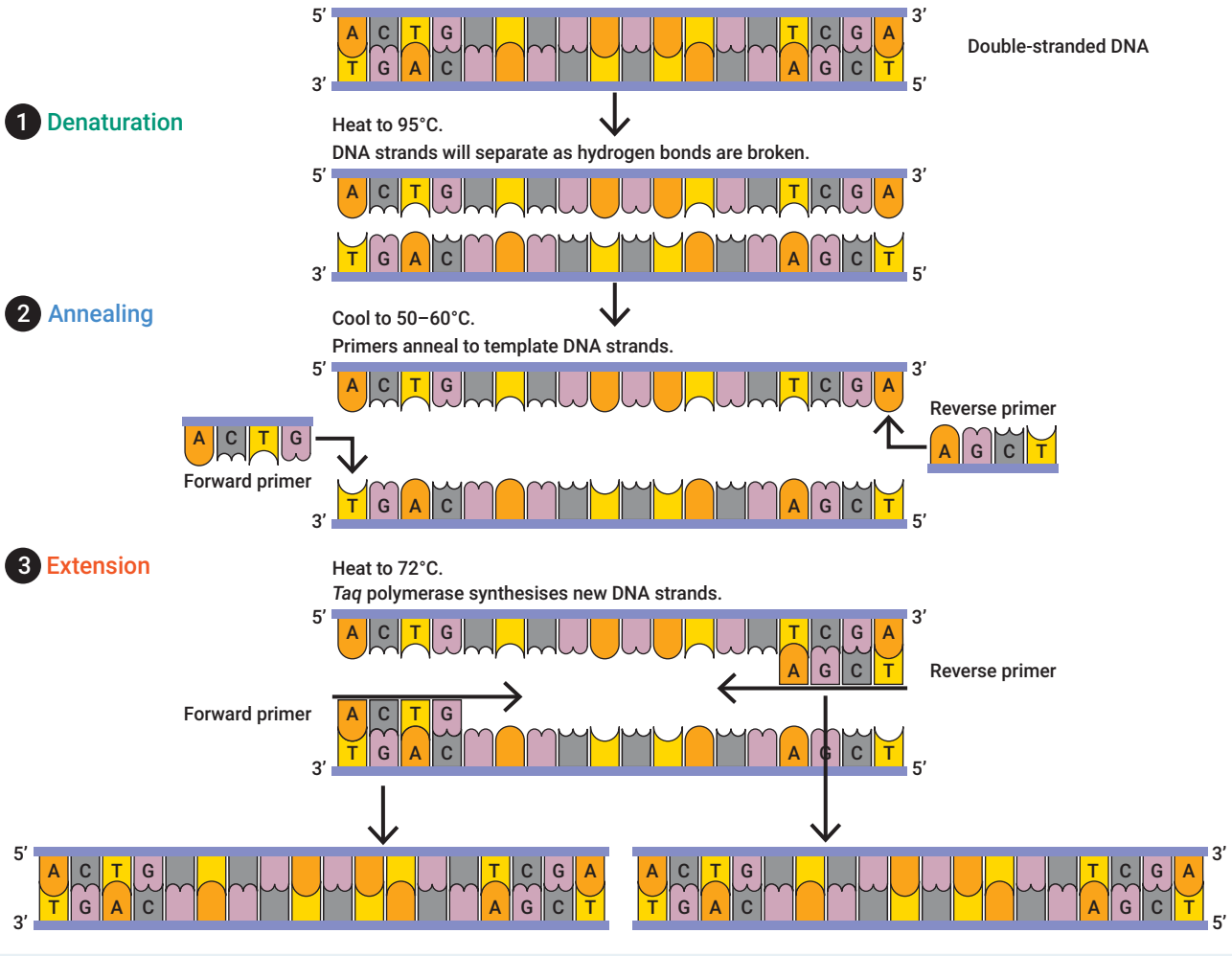


FIGURE 8.2.1 Amplifying DNA by using the polymerase chain reaction. The three major processes, denaturation, annealing and extension, are cycled through about 20 times, doubling the number of copies each cycle.

2. Annealing: The temperature is reduced to 50–60°C, allowing the primers to anneal to complementary sequences on opposite ends of each strand, either to the DNA sample or to PCR products generated during previous cycles. The reduced temperature is necessary to allow the formation of hydrogen bonds between the base pairs.
3. Extension: The temperature is raised to 72°C, the operational temperature for *Taq* polymerase. Starting from the primers, new DNA strands are synthesised from available free nucleotides. At the end of this phase, there are twice as many copies of the double-stranded DNA sequence.

The processes of denaturation, annealing and extension is a single cycle that doubles the amount of DNA present. If the thermal cycler runs 20 cycles, more than one million copies will be produced. This is more than enough for most DNA analysis techniques.

denaturation (in the polymerase chain reaction), the application of high temperatures to break the hydrogen bonds in DNA, which causes the two strands to separate

Syllabus link
Chapter 7 discusses the role of DNA polymerase in DNA replication.

Separating and viewing DNA: Gel electrophoresis

Gel electrophoresis is a technique that separates fragments of DNA or other macromolecules, such as RNA and proteins, according to their size and charge. When used with DNA, characteristic bands (Figure 8.2.2) allow individuals to be identified or genes of interest for medical diagnosis to be detected.

gel electrophoresis a technique that separates DNA fragments according to their size and charge

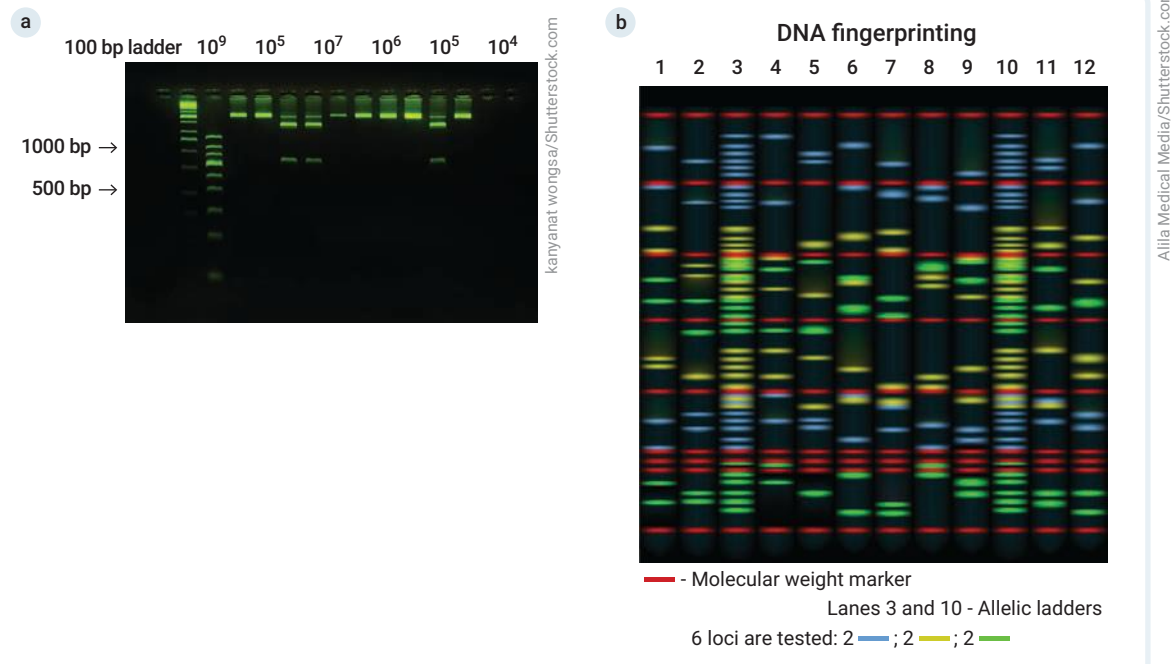


FIGURE 8.2.2 Gel electrophoresis can be used for (a) detecting a specific target sequence in DNA samples, or (b) determining the relatedness of DNA samples with a broad range of loci. (bp = base pairs)

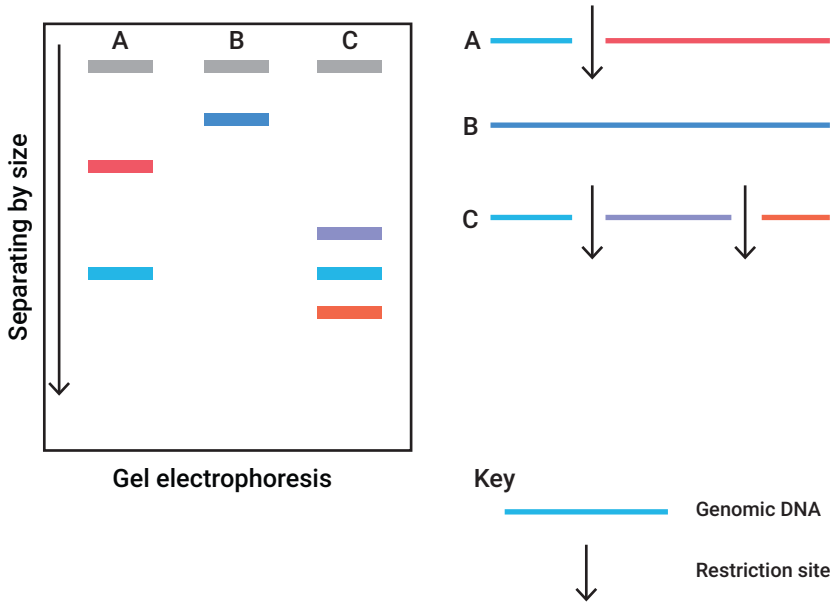
Gel electrophoresis can be conducted on a full DNA sample or a target sequence of DNA, both of which must be selected and amplified by PCR. With target sequences, the purpose of gel electrophoresis is to detect the presence or absence of a band that corresponds to the length of the target sequence (Figure 8.2.2a). PCR has amplified only the target section of DNA, of defined length, and this will appear as a single band in the gel.

For full DNA samples, gel electrophoresis is used to clarify which lengths are present and in what quantities, usually compared to another sample or control (Figure 8.2.2b). To create consistent lengths, restriction enzymes are used to cut the DNA sample wherever they find

their restriction site. Restriction sites are spaced unevenly along the DNA strand and passed on to offspring, so the lengths of DNA between cut sites will be the same in the same individual, similar in related individuals, and different in unrelated individuals (Figure 8.2.3). When the sample of cut DNA is sorted by size, it is possible to identify the degree of relatedness of individuals based on how similarly spaced their restriction sites are.

Weblink
Gel electrophoresis

Worksheet
Gel electrophoresis



Pereira, Filipe & Carneiro, João & Amorim, António. (2008). Identification of Species with DNA-Based Technology: Current Progress and Challenges. Recent patents on DNA & gene sequences. 2. 187-99. 10.2174/187221508786241738.

FIGURE 8.2.3 The number and location of restriction sites varies between individuals, so DNA samples cut with the same restriction enzyme will have different DNA lengths that appear through gel electrophoresis as different bands.

Gel electrophoresis works because DNA has an overall negative charge due to the phosphate groups in its backbone. This means DNA travels towards a positive charge and away from a negative charge. To sort by size, this technique uses a microscopic sieve made of agarose fibres in a gel. Once the **agarose gel** has set, the fibres form a dense maze for the DNA to travel through, much like a spy navigating a laser-filled hallway. Longer DNA strands, like a spy with extra baggage, take longer to navigate the gel and make forward progress. Shorter DNA strands, like a nimble mini-spy, navigate the gel more easily and make considerable forward progress in a short time.

agarose gel a gel matrix used for electrophoresis

To begin gel electrophoresis, DNA samples are loaded into well-like indentations in the gel (Figure 8.2.4). The gel is placed in a tray filled with buffer solution, and positive and negative electrodes are attached at each end of the tray. When the electrodes are turned on, electric current runs through the buffer solution and gel, moving the DNA. After a set time, the current is turned off and the gel is stained with a fluorescent DNA-binding dye. Under ultraviolet light, the dye fluoresces, showing a pattern of bands that can then be photographed. Each band on the gel contains millions of pieces of DNA of the same size.

The position of bands on an agarose gel reflects the size of DNA fragments in each band. To determine the size of a particular band, molecular biologists use **molecular size markers**. These are sets of DNA fragments with a known number of base pairs that are loaded into the first well of the gel to run alongside the samples. They are used to determine the size of the DNA fragments in different bands by comparing their location with the sample bands. Figure 8.2.4 shows four bands in the marker lane beside the three sample lanes.

molecular size marker a set of pieces of DNA of known length that is used to estimate the size of other DNA fragments in a gel

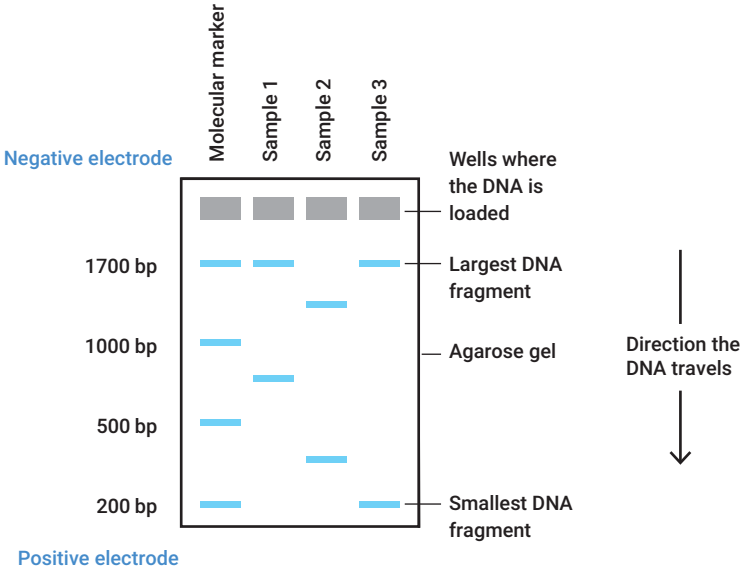


FIGURE 8.2.4 Molecular markers of known size are run alongside samples so that the size of the DNA fragments to be determined (bp = base pairs).

LEARNING CHECK 8.2

DESCRIBING

1 **Identify** the three cyclic processes in a PCR reaction.
2 **Describe** the role of primers in PCR.
3 **State** why the temperature is lowered to 50–60°C during the annealing phase of PCR.
4 **Describe** how the size of a particular fragment of DNA can be determined.

APPLYING

5 **Explain** how gel electrophoresis separates segments of DNA.
6 Agarose gels can be made with different concentrations of agarose. **Explain** the impact of increasing the concentration of agarose in a gel.
7 If a DNA sample contains five copies of a particular DNA region and the primer is appropriately designed, **calculate** how many copies would be produced by 10 cycles of PCR.
8 Using the gel in Figure 8.2.5, **identify** which lane contained each of the following sets of DNA lengths.
   a 200, 250 and 900 bp
   b 150, 400 and 600 bp
   c 50, 450 and 650 bp
   d 100, 100 and 450 bp

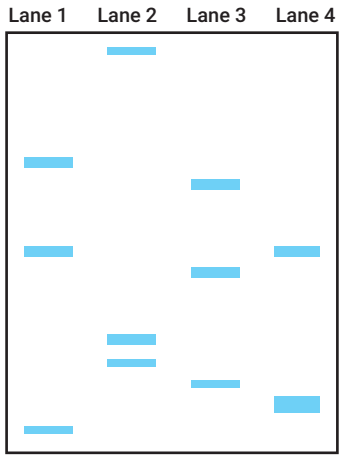


FIGURE 8.2.5 Distinct banding produced by gel electrophoresis

8.3 DNA profiling

DNA profiling a process that compares an individual's genome with another

DNA profiling is a process used to compare the DNA sequences of two or more individuals to explore the degrees of relatedness between them. It is used for paternity testing, biological confirmation for adoptees, crime victim and perpetrator identification, determining immigration eligibility and evolutionary relationships and in genealogy and medical research.

short tandem repeat (STR) a short non-coding region of DNA that is repeated many times in the genome of an organism; it is highly variable between individuals and can be used in DNA profiling to identify individuals

Rather than profiling an individual's entire genome, DNA profiling usually uses predictable sections of DNA called **short tandem repeats (STRs)**. These are sections of non-coding DNA that are repeated many times in the human genome. For example, the dinucleotide GA forms the STR, GAGAGAGA. The repeat is present in all members of the human population, but the number of repeats varies between individuals (Figure 8.3.1). DNA profiling identifies people according to differences in the length of their DNA repeats for a large number of known STRs. The more STRs included in an analysis, the more accurate the identification becomes.

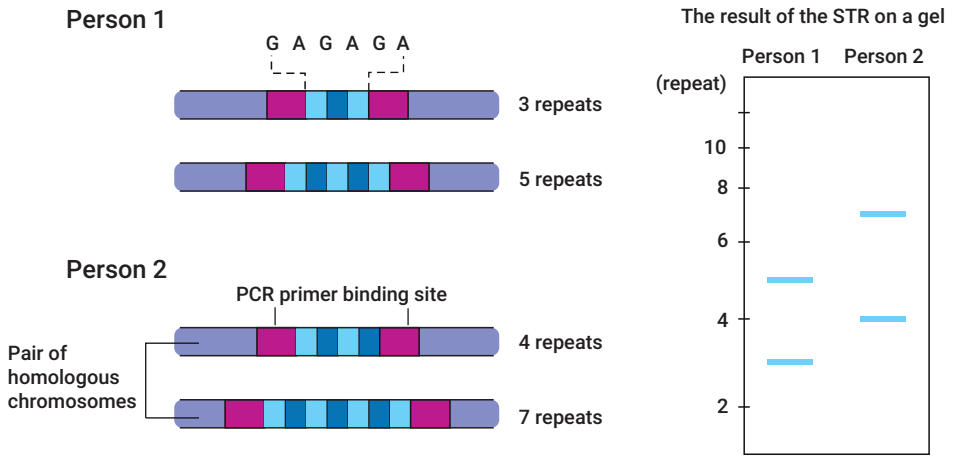


FIGURE 8.3.1 Short tandem repeats vary between individuals. More closely related individuals will share repeats of similar length.

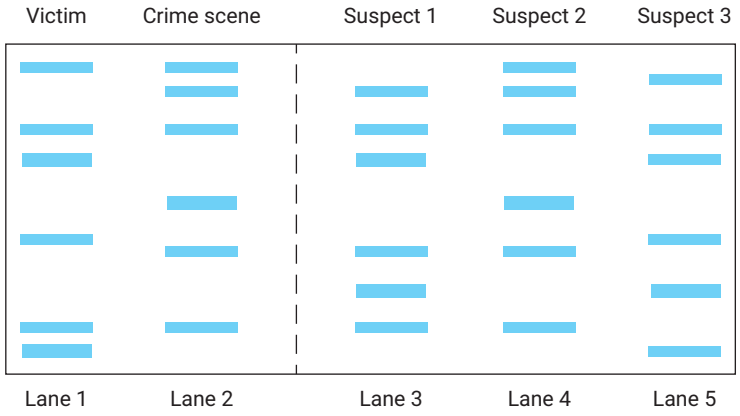
The DNA to be profiled can come from any somatic body cell that contains a nucleus, including blood or cheek cells. Primers for up to 20 different STRs are included in the PCR process so that an individual's STRs can be accurately identified. The amplified sample is then separated by gel electrophoresis, which sorts the individual's STRs according to their lengths. Smaller fragments have fewer repeats and migrate further on the gel than alleles with more repeats. A molecular marker sample is run on the same gel to identify the STR lengths.

Because an individual inherits one homologous chromosome from each parent, their DNA profile will show one band inherited from their mother and one band from their father for each STR included in the analysis. Comparing the bands in each lane allow researchers to analyse the relatedness of the individuals. More closely related individuals will share more band matches.

Worksheet
DNA profiling

WORKED EXAMPLE 8.3.1

Use Figure 8.3.2 to determine the suspect most likely to have been at the crime scene with the victim.



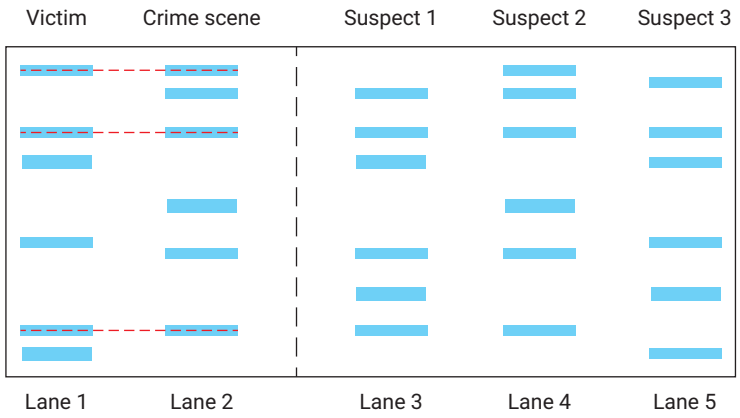
Adapted from "DNA Profiling", BioNinja. https://old-ib.bioninja.com.au/standard-level/topic-3-genetics/35-genetic-modification-and/dna-profiling.html

FIGURE 8.3.2 Gel electrophoresis of DNA samples taken from a victim, crime scene and three suspects. Three STR pairs have been used.

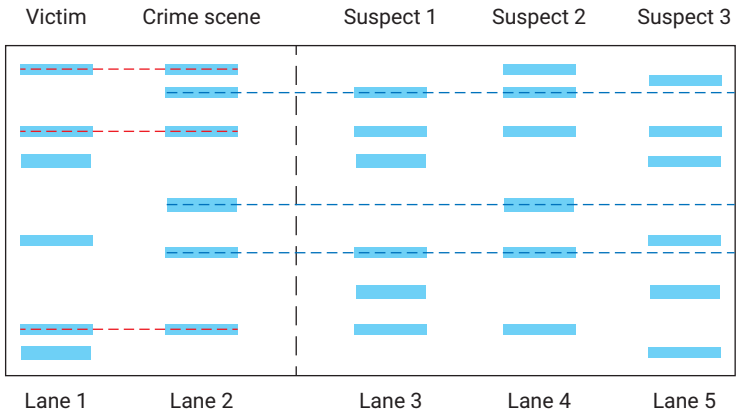
ANSWER

1 **Determine the lane that needs to be analysed.**
Lane 2 contains the sample from the crime scene, so this is the lane we need to work with.

2 **Compare the sample from the crime scene with the sample from the victim.**
The victim's profile is shown in lane 1. Any bands that the victim shares with the crime scene sample need to be crossed off lane 2. These bands cannot be used to identify a suspect because they may have come from the victim.



3 Compare the sample from the crime scene with the samples from suspects.
The remaining bands in lane 2 cannot have come from the victim and must have been left by another person at the crime scene. These bands need to be matched with bands in the three suspect lanes.



4 Identify the sample that best matches the sample from the crime scene.
Suspect 1 only shares two of the three non-victim bands at the crime scene. They may have been there, but only if another person was also. Suspect 2 shares all three of the non-victim bands at the crime scene. They may have been there alone. Suspect 3 does not share any of the non-victim bands at the crime scene. It is unlikely that they were there.

If the case evidence suggests that only one person was at the crime scene with the victim, it is most likely that they were Suspect 2 because the middle non-victim band at the crime scene is only found in Suspect 2's DNA profile.

Weblink
How is DNA profiling used to solve crimes?

LEARNING CHECK 8.3

DESCRIBING

1 **Identify** the type of DNA sequence used for DNA profiling.
2 **Describe** the role of PCR in DNA profiling.
3 **Describe** how DNA samples are separated in DNA profiling.

APPLYING

4 In the past, as few as 10 different STR regions were used in DNA profiling. **Explain** the advantage of using 20 different STRs.
5 **Explain** how DNA profiling can show that a man is not the father of a child.
6 It has been said that a match between the DNA profiles of a tissue sample at the scene of a crime and a suspect is good evidence for a conviction. **Discuss** this statement, giving reasons for your opinion.

INTERPRETING

7 Dolly the sheep is said to have three mothers: the ewe that donated the nucleus from her mammary gland for the nuclear transfer, the ewe that donated the egg, and the ewe that acted as the surrogate mother into which the egg was implanted. **Predict** which ewe's DNA profile would match Dolly's profile.

8 On 26 December 2004, a tsunami hit regions of Asia, causing a massive disaster and killing thousands of people. Many parents who had lost children laid claim to other children. In the case of disputes, DNA profiles of each individual claiming to be a child's mother were compared to that of the lost child. Figure 8.3.3 shows four possible mothers and one lost child. **Justify** which mother has the strongest claim.

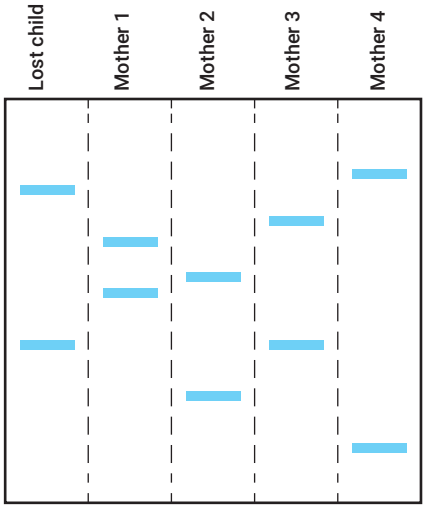


FIGURE 8.3.3 DNA profile of a 'lost child' and four potential mothers

PRACTICAL ACTIVITY 8.3.1

ANALYSING DNA PROFILES

Introduction

Family size is highly variable in black swans – between one and seven cygnets. Interestingly, family size distribution seems to be bimodal with most families having 1–3 cygnets or 5–7 cygnets. This has led many biologists to speculate that the larger families are the result of brood parasitism, the result of a female laying her eggs in the nest of a second female and leaving this second female to raise her young. This process is quite common in ducks but has not been investigated so far in black swans.

Ben Twist/Dreamstime

FIGURE 8.3.4 A black swan family

One way to determine whether a female is the biological mother of her cygnet is to create a DNA profile for both the mother and the cygnet and determine if the cygnet shares half of the female's profile.

Research question

How can DNA profiling be used to identify brood parasitism in black swans to explain the number of cygnets in some families of swans?

Aim

To determine, using DNA profiling, whether brood parasitism occurs in black swans and whether this explains the larger number of cygnets in some families

Materials

- ruler

Procedure

1 Consider the DNA profile in **Figure 8.3.5**. The necessary DNA was obtained by capturing swans, collecting a small blood sample from each, and extracting the DNA. Five STRs have been identified in black swans (Cam 1, Cam 2, Cam 3, Cam 4 and Cam 5). Using PCR, these five regions were amplified in all adults and cygnets of eight families of swans. The PCR products were then separated by agarose gel electrophoresis. Figure 8.3.5 shows the resulting gel. Each individual has two alleles for each STR, but sometimes only one band is observed because the individual has two identical alleles.

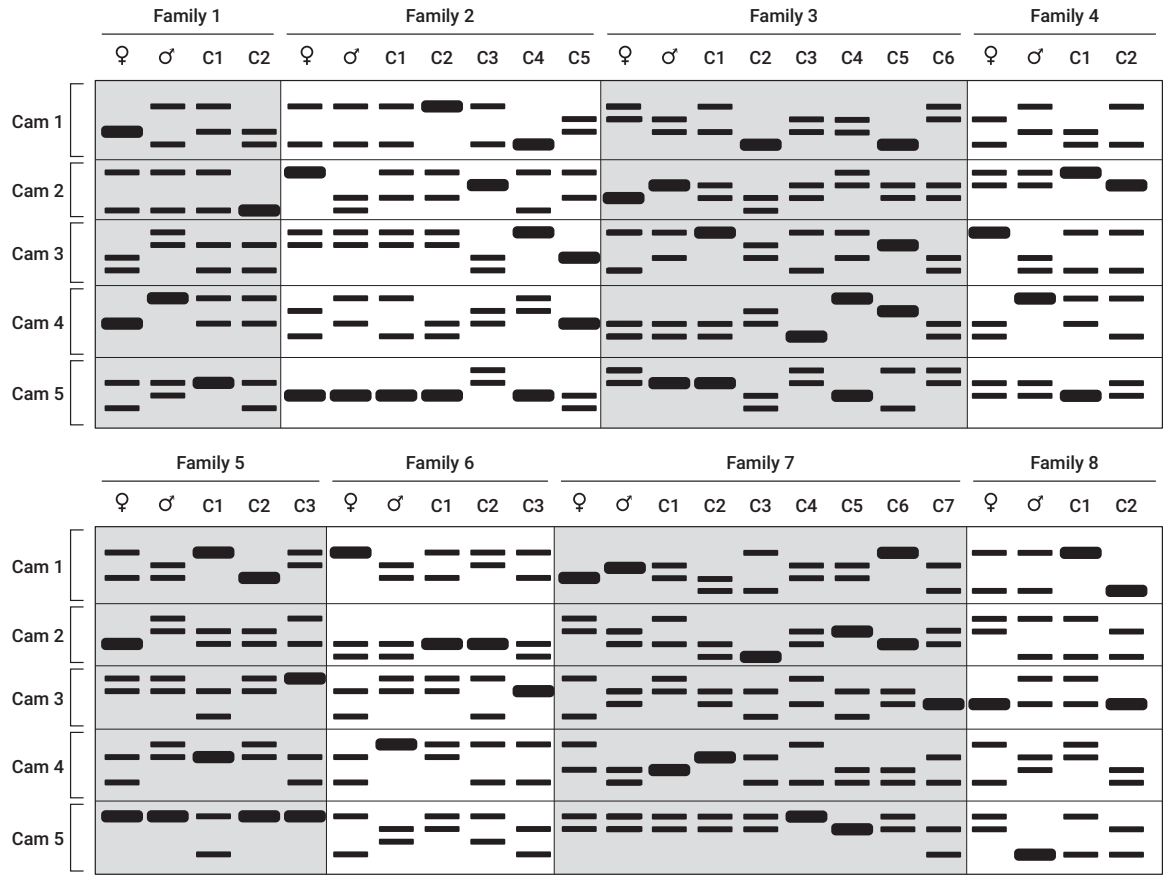


FIGURE 8.3.5 DNA profiling for the eight black swan families that include a social mother (♀), social father (♂) and cygnets (C)

2 Compare the profile of the mother of each family and the profile of each cygnet and determine if the female could have been the biological mother of the cygnet.
3 Copy the results table and record your results in the second column.
4 Calculate the proportion of parasitic cygnets in each family and include these in the third column.
5 Determine if there is any difference in proportion of parasitic cygnets between small and large families.

Results

Family	Biological cygnets	Parasitic cygnets
1		
2		
3		
4		
5		
6		
7		
8		

Analysis of results

1 Using your results, identify any evidence of brood parasitism in black swans.
2 Calculate the maximum proportion of parasitic cygnets in this sample.

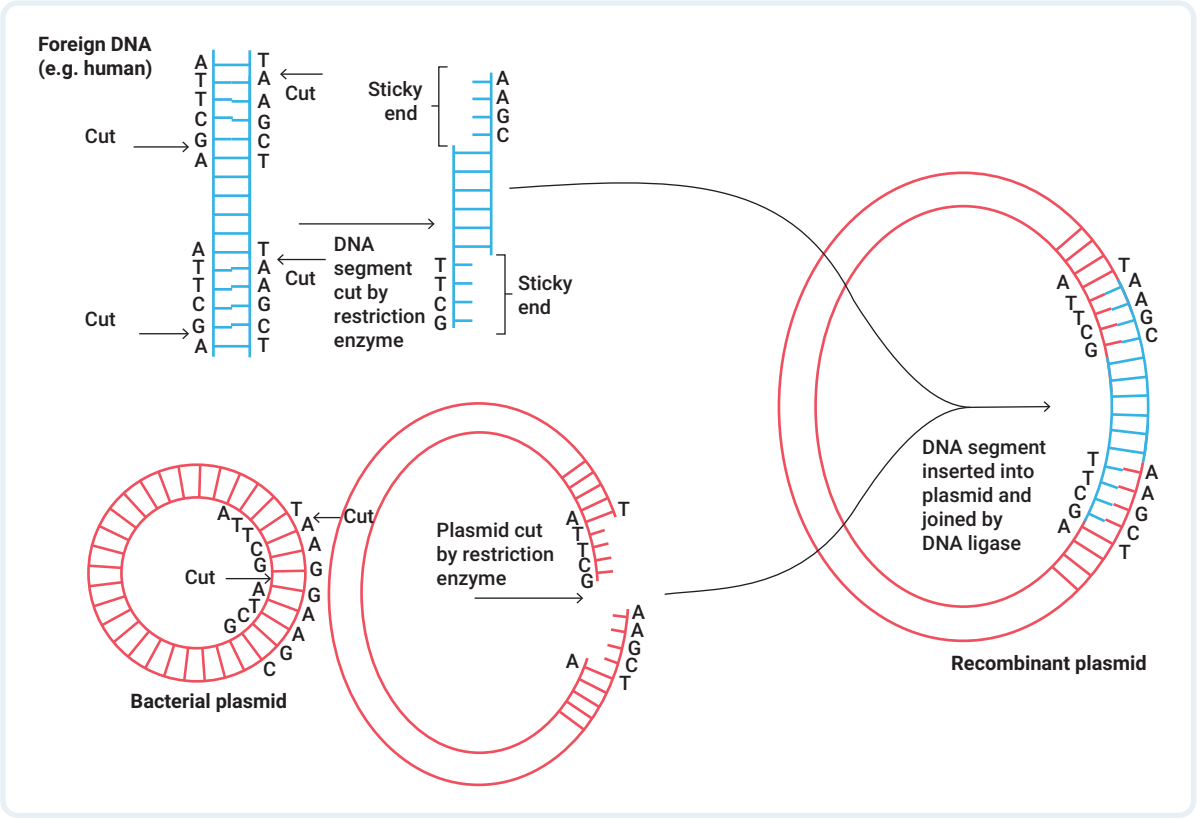
Interpretation

3 Explain whether the results confirm the belief that large black swan families are due to brood parasitism.
4 Describe how you could determine whether a cygnet has been fathered by a male other than its social father.

CHAPTER SUMMARY

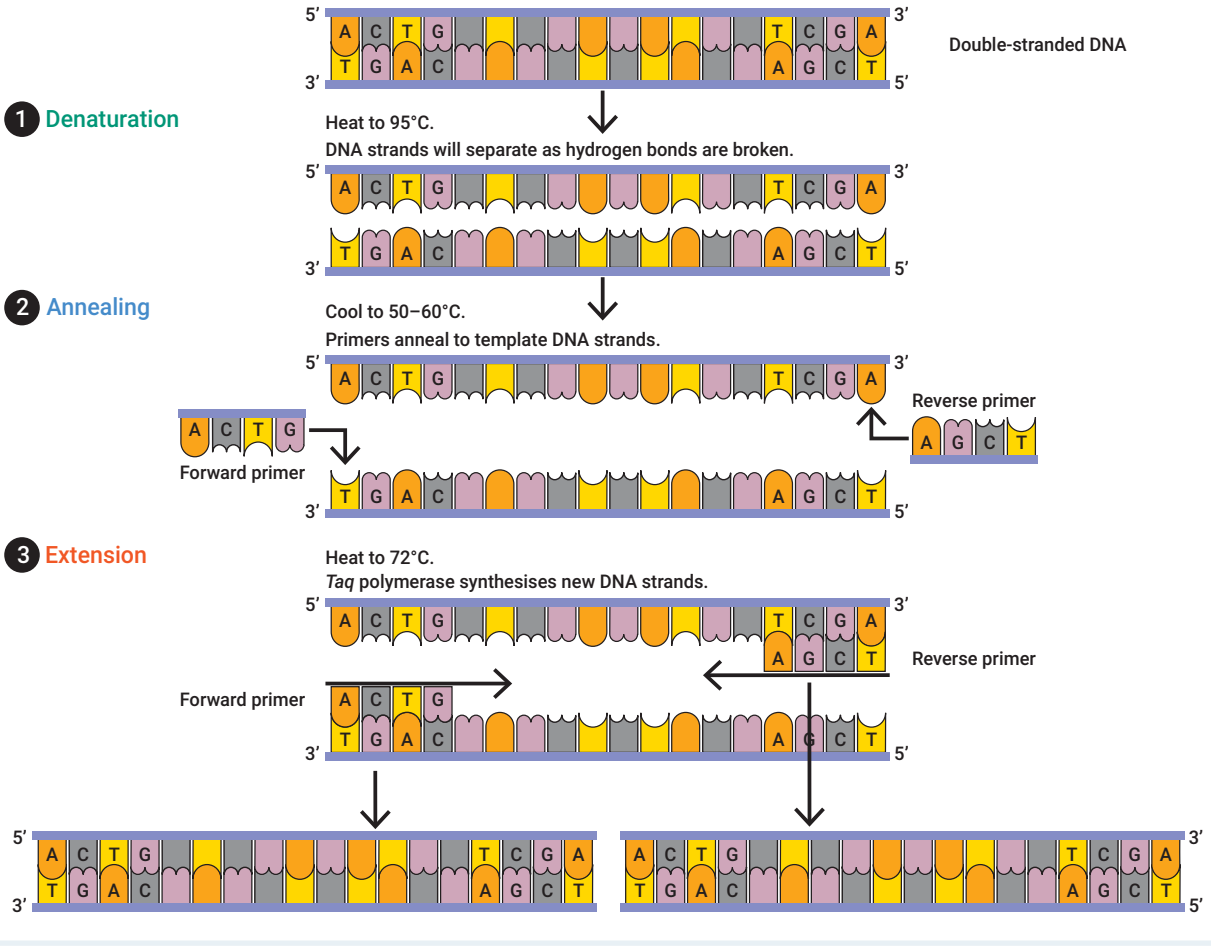
Recombinant DNA

- The steps for making recombinant DNA are as follows.
  1. Plasmids are isolated from bacteria and the gene for the target molecule is isolated from its organism.
  2. The same restriction enzyme is used to cut the plasmid and the gene of interest to ensure they have complementary sticky ends.
  3. The plasmid vector and the gene of interest are mixed and their sticky ends pair up.
  4. DNA ligase is used to join the sugar–phosphate backbone of the two segments to form recombinant plasmids.
  5. The recombinant plasmids are added to a bacterial culture, where they are taken up and the target molecule is produced from its gene of interest.



Polymerase chain reaction (PCR)

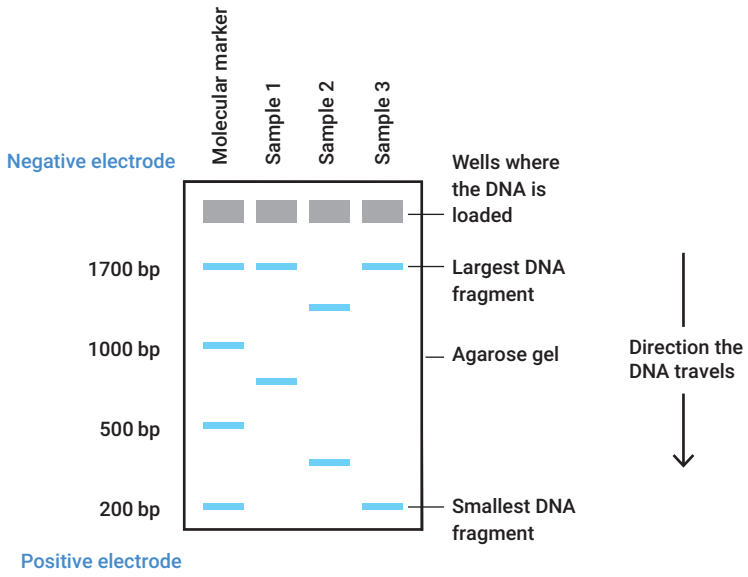
- PCR is a technique used to amplify DNA.
- The three main steps in PCR are:
  - denaturation
  - annealing
  - extension.



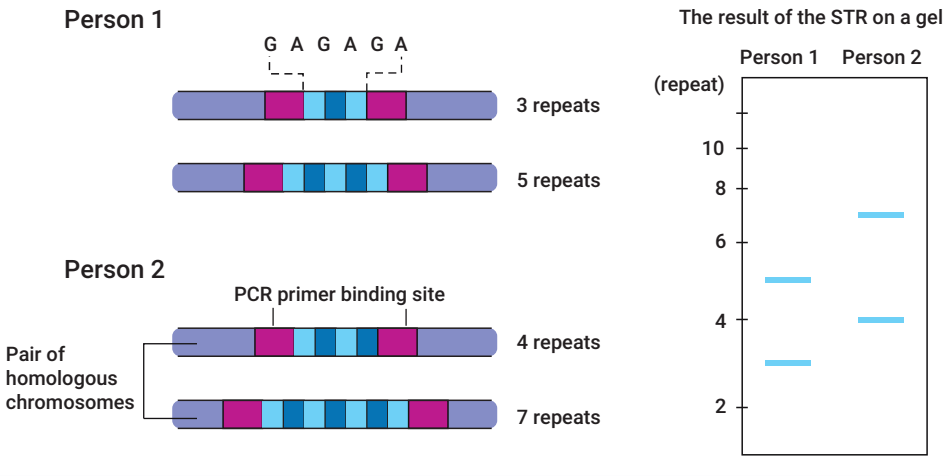
Gel electrophoresis

- Gel electrophoresis can be used to separate fragments of DNA (and other macromolecules).
- Fragments are separated based on number of base pairs (size).
- The fragments move through the gel from the negative electrode to the positive electrode.

DNA profiling



- Matching bands indicate that both processed samples contain the same length DNA fragment. This can indicate genetic relatedness, with more matches indicating closer relationships.



CHAPTER EXAM

MULTIPLE CHOICE

1. DNA profiling can be done with a very small sample. This is because:
- **A** there is 2 m of DNA in every body cell.
- **B** the polymerase chain reaction is very fast.
- **C** segments of DNA code for specific polypeptide chains.
- **D** the DNA sample can be amplified by using DNA technology.

2. Which of the following is **not** involved in making recombinant DNA?
- **A** DNA helicase
- **B** DNA ligase
- **C** Plasmids
- **D** Restriction enzymes

3. Researchers have introduced spiders' silk-spinning genes into goats, allowing them to harvest the silk protein from the goats' milk for a variety of applications. This is an example of:
- **A** DNA profiling.
- **B** gene cloning.
- **C** gel electrophoresis.
- **D** recombinant DNA.

4. Which of the following statements is correct?
- **A** Shorter DNA fragments move slower than longer ones through agarose gel.
- **B** DNA profiling can be used to determine people at risk of genetic diseases.
- **C** DNA profiling compares short tandem repeats from coding regions of the genome.
- **D** In electrophoresis, DNA moves from positive to negative, according to fragment size.

5. PCR involves all of the following except:
- **A** extending the DNA by using DNA polymerase.
- **B** cycling between the following temperatures: 95°C, 55°C and 72°C.
- **C** reducing the temperature to allow annealing of complementary bases.
- **D** increasing the temperature to 72°C to break bonds between the double-stranded DNA.

6. Which one of the following correctly describes a step in making recombinant bacteria?
- **A** Amplifying the DNA using PCR
- **B** Exposing the bacteria to PCR products
- **C** Cutting the DNA with DNA ligase
- **D** Joining the DNA with a particular restriction enzyme

7. Which of the following is **not** a phase of PCR?
- **A** Annealing
- **B** Denaturation
- **C** Extension
- **D** Replication

8. PCR requires four main inputs: DNA sample, DNA polymerase, free nucleotides and which other?
- **A** Agarose fibres
- **B** Bacterial plasmids
- **C** DNA ligase
- **D** DNA primers

9. What do the bands represent on an electrophoresis gel?
   - **A** The number of restriction sites in a sample
   - **B** The location of genes on a chromosome in a sample
   - **C** The length of DNA between restriction sites in a sample
   - **D** The number of genes that have restriction sites in a sample

10. Identical twins are likely to have:
   - **A** identical DNA profiles.
   - **B** similar DNA profiles.
   - **C** different DNA profiles.
   - **D** unusable DNA profiles.

SHORT RESPONSE

11. **Explain** why mammalian DNA polymerase is not used in PCR.

12. **Describe** how PCR and gel electrophoresis are used in DNA profiling.

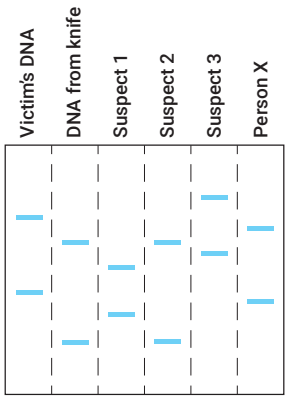
CROSS-CHAPTER QUESTION

13. Many inheritable diseases have known genes of origin, such as the mutation of the *BRCA1* and *BRCA2* genes responsible for most breast cancers. **Explain** how researchers would detect that a person was carrying a mutated gene.

DATA ANALYSIS

Questions 14 and 15 refer to the following information.

Person X has just witnessed another person being stabbed in the street and saw three individuals running from the scene. These individuals immediately became suspects. DNA profiling can provide evidence for this crime because a knife was left beside the victim. Blood and skin cells were taken from the knife, and DNA samples were collected from the three suspects. The victim's DNA and Person X's DNA were also collected. The results of the DNA profiling on one STR pair from each source is shown below.



14. **Apply understanding**

    Identify the DNA bands that match those found on the knife.

15. **Interpret evidence**

    Determine whether any of the suspects are guilty. Provide reasoning based on the DNA profile.

CHAPTER 9

Producing gametes

ChrisChrisW/iStock/Getty Images Plus/Getty Images

SYLLABUS DOT POINTS

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.
- 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.

Introduction

Some organisms use mitosis to reproduce to form two new individuals. With only one source of hereditary information, these offspring are almost identical to their parent. Other organisms inherit hereditary material from two different parents through sexual reproduction, using a form of cell division called meiosis. In this way, they gain evolutionary advantage through variation. In these organisms, each new generation resembles their parents, but the degree of variation both between generations and within generations is substantial.

Worksheets

- Meiosis
- Independent assortment
- Oogenesis and spermatogenesis

Nelson MindTap

To access resources above, visit
cengage.com.au/nelsonmindtap

ASSUMED KNOWLEDGE

- ✓ The location of a particular gene on a chromosome is referred to as its locus.
- ✓ Eukaryotic cells have two copies of every gene, called alleles, each located on one of a pair of homologous chromosomes.
- ✓ Chromosomes contain genes along their length, almost all of which are necessary for life.
- ✓ Mitosis is the division of a cell into two identical daughter cells.
- ✓ Mitosis involves four phases: prophase, metaphase, anaphase and telophase.
- ✓ Sperm are the sexually reproductive cells of human males and eggs are the sexually reproductive cells of human females.
- ✓ Children are conceived when a sperm cell and an egg cell fuse their nuclei in a process called fertilisation.
- ✓ Children are genetically similar, but not identical, to their parents, grandparents and siblings.

sexual reproduction a form of reproduction in which offspring are produced from two parents

meiosis a two-phase type of cellular division in which the chromosome number of a cell is halved to the haploid number; the basis of gamete formation in animals and spore formation in plants

gamete a cell produced in sexual reproduction, which combines at fertilisation; in humans, the gametes are ova and sperm cells; in flowering plants, pollen grains contain male gametes and ova contain a female gamete

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ describe the significance of sexual reproduction
- ✓ explain the importance of halving the chromosome number in sexual reproduction
- ✓ describe the two-division process of meiosis
- ✓ distinguish meiosis from mitosis
- ✓ explain how crossing over, independent assortment and random fertilisation produce variation in offspring
- ✓ describe spermatogenesis and distinguish it from generic meiosis
- ✓ describe oogenesis and distinguish it from generic meiosis
- ✓ compare spermatogenesis and oogenesis
- ✓ describe how chromosomal rearrangements, including deletions, inversions, duplications and translocations, affect the combination of genes in a gamete
- ✓ describe how aneuploidy occurs
- ✓ describe the impact of aneuploidy on the combination of genes in a gamete
- ✓ identify aneuploid conditions in a human karyotype and the genetic disorders they produce.

Syllabus link
Chapter 7 describes the structure and function of chromosomes.

9.1 Meiosis

Sexual reproduction occurs through **meiosis**, a special form of eukaryotic cell division. In meiosis, division results in the formation of four daughter cells, called **gametes**, each containing half the number of chromosomes of the original nucleus. At fertilisation, two of these gametes, usually from different individuals, combine to form a zygote that restores the original chromosome number.

The nucleus of each somatic cell of a human contains 46 chromosomes in 23 pairs, of which 22 are homologous. The matched pairs are called **autosomes**; the largest is numbered 1 and the smallest is numbered 22. The 23rd pair is the **sex chromosomes**, which are matched in females (XX) but unmatched in males (XY). One chromosome of each homologous pair in an individual comes from the maternal gamete, the egg or ovum, and the other from the paternal gamete, the sperm (Figure 9.1.1).

autosome a chromosome that is the same in both males and females of a species; autosomes do not include sex chromosomes

sex chromosome a chromosome that affects sexual traits; sex chromosomes are different in male and female individuals of the same species

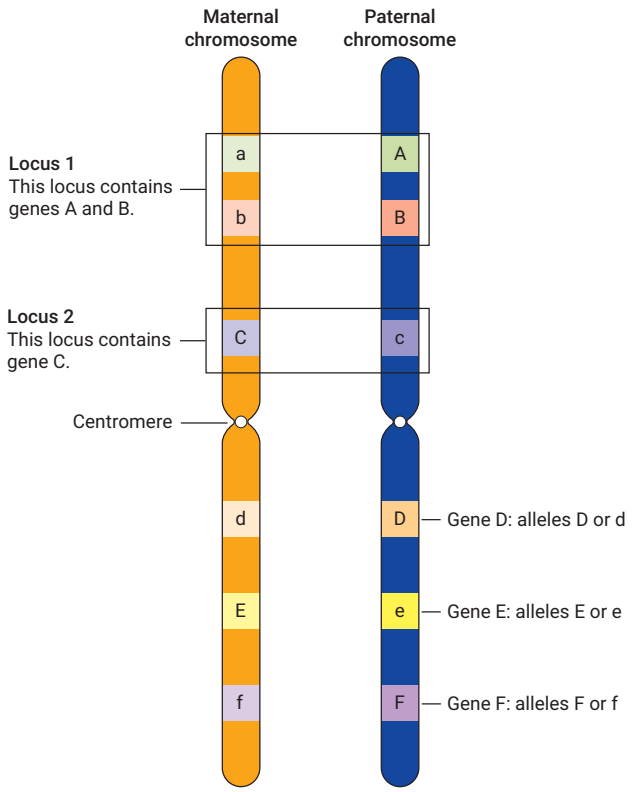


FIGURE 9.1.1 A stylised representation of one homologous pair of chromosomes from an individual. It shows one chromosome inherited from the mother and one from the father. These are homologous because the gene loci are identical, even though the alleles at each location are different.

diploid describes a cell or organism that has a genome comprising two copies of each chromosome, represented by $2n$

haploid describes a cell or organism that has a genome that contains one copy of each chromosome, represented by n

Syllabus link
Chapter 7 describes DNA replication.

When a nucleus contains all 23 pairs of chromosomes, the cell is **diploid** and the total number of chromosomes is represented as $2n$, with n representing the number of pairs in a species. After meiosis, the gametes contain only one chromosome of each homologous pair. They are **haploid**, denoted n. An egg or sperm cell contains a total of 23 chromosomes, one of each somatic chromosome and one sex chromosome. This ensures that when they combine to form a new individual, there are again two copies of each chromosome, $2n$ (Figure 9.1.2).

The process of meiosis

Prior to meiosis proper, the parent cell undergoes DNA replication, forming two identical sister chromatids for each chromosome. This produces sufficient genetic material for the efficient creation of gametes.

During meiosis, two divisions of the parent cell take place. In the first division, meiosis I, each duplicated chromosome of a pair separates to each pole of the cell. In the second division, meiosis II, the sister chromatids of each duplicated chromosome separate from each other, again moving to opposite poles. When cytokinesis occurs, four gametes are produced, each carrying a single unduplicated chromosome, half the original number of the parent cell. Figure 9.1.3 details the process of meiosis.

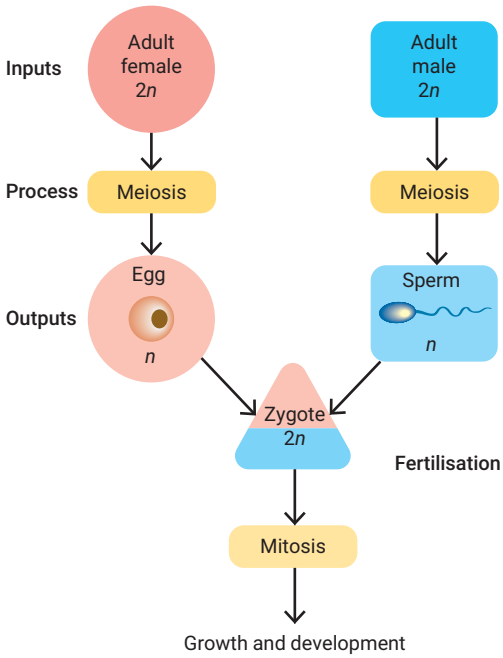


FIGURE 9.1.2 Meiosis halves the number of chromosomes in a gamete (n) so that the new offspring contains the normal number of chromosomes ($2n$).

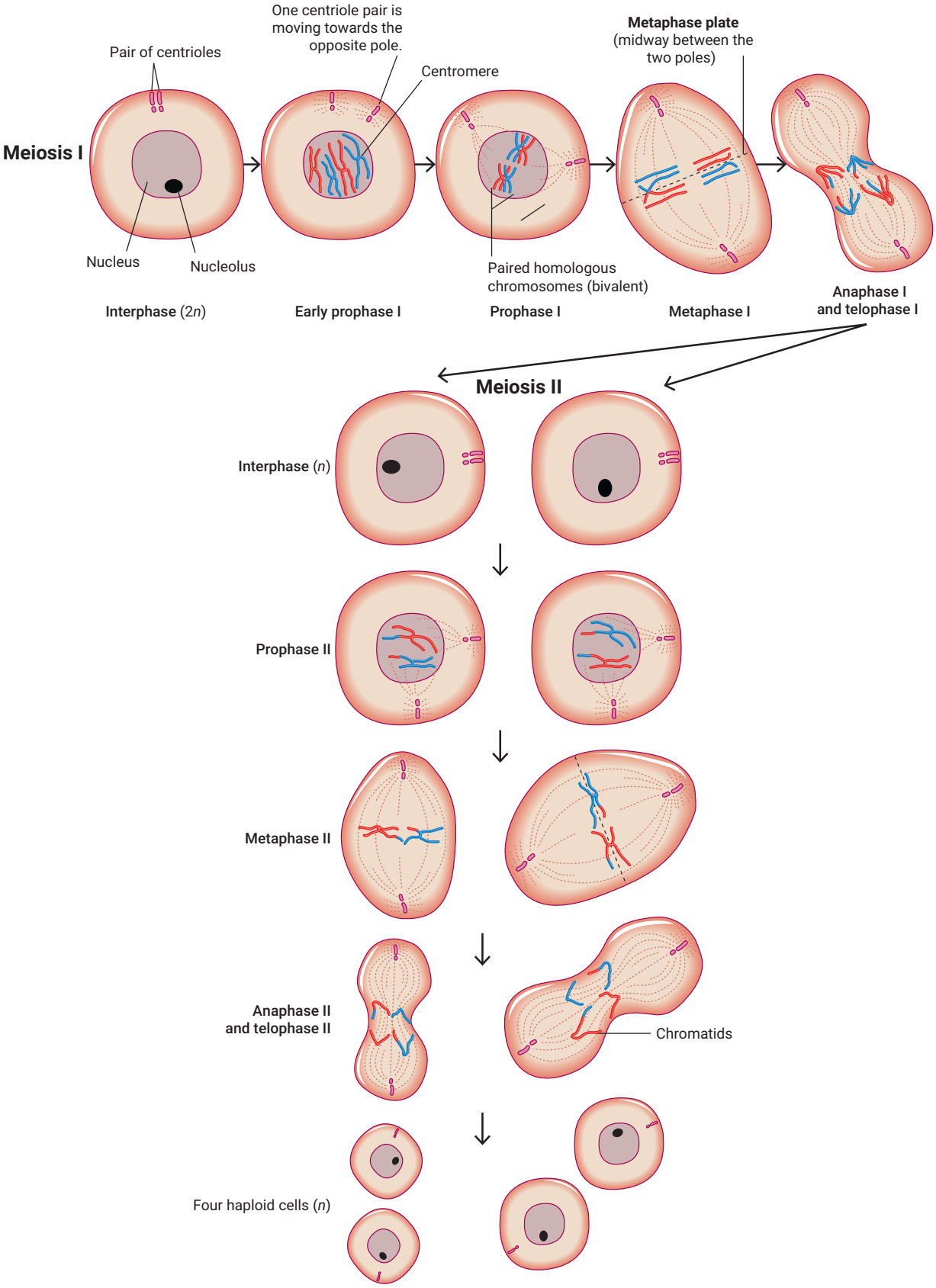


FIGURE 9.1.3 The two-stage process of meiosis

Meiosis I

The first division of meiosis is called meiosis I. It has a preliminary stage called **interphase**, and four division stages: prophase, metaphase, anaphase and telophase.

In interphase, the parent cell prepares for meiosis by duplicating its chromosomes through DNA replication and forming the centrioles that will act as the poles of the cell.

The first division stage of meiosis I is called **prophase** I. At this stage, the duplicated chromosomes condense into their classic X shape and migrate to lie side by side in a process known as **synapsis**. Spindles form from each centriole and grow towards the chromosomes in the centre of the cell. At the end of prophase I, the nuclear membrane breaks down.

In **metaphase** I, the homologous chromosomes move together to line up across the equator of the cell, equidistant from the two centrioles that represent the poles of the cell. This equator is called the **metaphase plate**. At the metaphase plate, the spindle fibres attach to the centromere of each duplicated chromosome, with spindles from opposite poles generally attaching to opposite members of a homologous pair. The orientation of the pairs along each side of the metaphase plate is random and independent of each other.

In **anaphase** I, each member of the homologous pair is pulled towards opposite poles of the cell by the spindles. Sister chromatids remain attached at their centromeres, moving together towards the same pole. The separation or **disjunction** of each pair of homologous chromosomes occurs independently of other chromosome pairs since their orientation at the metaphase plate was independent.

In **telophase** I, the spindle breaks down and nuclear envelopes form around the two groups of chromosomes. At this point, each chromosome is still duplicated, with two sister chromatids and an X shape. **Cytokinesis**, the division of the cytoplasm, completes the first stage of meiosis.

interphase the stage of the cell cycle between active divisions

prophase the first stage of meiosis where chromosomes condense and centrioles form

synapsis the physical pairing of homologous chromosomes

metaphase the second stage of meiosis where chromosomes line up at the equator of the cell

metaphase plate the equator of the cell where chromosomes line up during metaphase

anaphase the third stage of meiosis where chromosomes separate to opposite poles of the cell

disjunction the segregation of chromosomes to separate poles of the cell during anaphase

telophase the fourth stage of meiosis where membranes form around the two new nuclei

cytokinesis the division of the cytoplasm and formation of new cell membranes

Worksheet
Meiosis

Meiosis II

Between meiosis I and meiosis II, a brief interphase usually occurs. DNA does not duplicate during this interphase – only the new centrioles form in each meiosis I daughter cell. Each cell then enters the second meiotic division.

In prophase II, new spindles form and the nuclear membrane dissolves. In metaphase II, the duplicated chromosomes move to the metaphase plate and orient their sister chromatids randomly on either side. In this phase, one spindle from each centriole attaches to the single centromere of the duplicated chromosome. In anaphase II, the centromere splits in half and the sister chromatids separate, following their spindles to opposite poles of the cell. When separated, the sister chromatids are called unduplicated chromosomes again. In telophase II, the spindle apparatus dissolves, new nuclear envelopes form, and the unduplicated chromosomes de-condense to their thread-like state. One more round of cytokinesis finalises the process of meiosis.

Before meiosis, the diploid ($2n$) parent cell duplicates its DNA to form $2n$ duplicated chromosomes. In meiosis I, it splits to form two haploid daughter cells, each with n duplicated chromosomes. In meiosis II, each of these haploid daughter cells splits to form another two haploid daughter cells, each with n unduplicated chromosomes. This results in four haploid (n unduplicated) cells being formed from the original diploid ($2n$ unduplicated) parent cell.

Even though they are both types of cell division, meiosis and mitosis differ in some important ways (Table 9.1.1).

TABLE 9.1.1 The similarities and difference between mitosis and meiosis

		Mitosis	Meiosis
Similarities		Both produce new cells. They have similar basic steps. Both start with a single parent cell.	
Differences	Number of sequences	One sequence of prophase, metaphase, anaphase and telophase	Two sequences of prophase, metaphase, anaphase and telophase
	Number of stages	Four (plus interphase)	Eight (plus interphase)
	Location	Somatic cells	**Germ cells**
	Purpose	Cellular proliferation	Sexual reproduction
	Products	Two diploid daughter cells	Four haploid daughter cells
	Chromosome number	Remains the same	Halved in each daughter cell
	Change in genetic variation	Unchanged	Increased

Weblinks
Sexual versus asexual reproduction

Meiosis

germ cell a cell that produces gametes

LEARNING CHECK 9.1

DESCRIBING

1 **Describe** what *n* represents.
2 **Identify** the normal 2*n* number of chromosomes in humans.
3 **Describe** the process of meiosis.

APPLYING

4 **Explain** three differences between mitosis and meiosis.
5 **Explain** how meiosis I halves the chromosome number.

9.2 Mechanisms of variation

Crossing over

During synapsis in prophase I, homologous chromosomes pair up with each other. These chromosomes are not yet aligned at the metaphase plate, so they are able to move around each other more fluidly. Each pair coils around each other while floating in the cytoplasm of the cell. If their chromatids come into contact with each other, they are called **bivalent** and the contact points are called chiasmata (singular: **chiasma**).

bivalent visible chromosomes in a cell during prophase I of meiosis, which are made up of two homologous chromosomes joined together

chiasma the point of contact between homologous chromosomes during prophase I of meiosis

Later, during anaphase I, the chromosomes move apart but the chromatids stay attached at the chiasmata. Pulling apart can mean that segments of DNA that began on the maternal chromosome now pull away with the paternal chromosome or vice versa. This exchange of genetic material is called **crossing over**. Crossing over means that the composition of the inheritable chromosomes in the daughter cells do not stay identical to what was inherited in the parent cells. The sequence of alleles on each chromosome is now a combination of alleles from each of the homologous chromosomes (Figure 9.2.1).

crossing over an event during meiosis in which homologous chromosomes exchange segments with one another

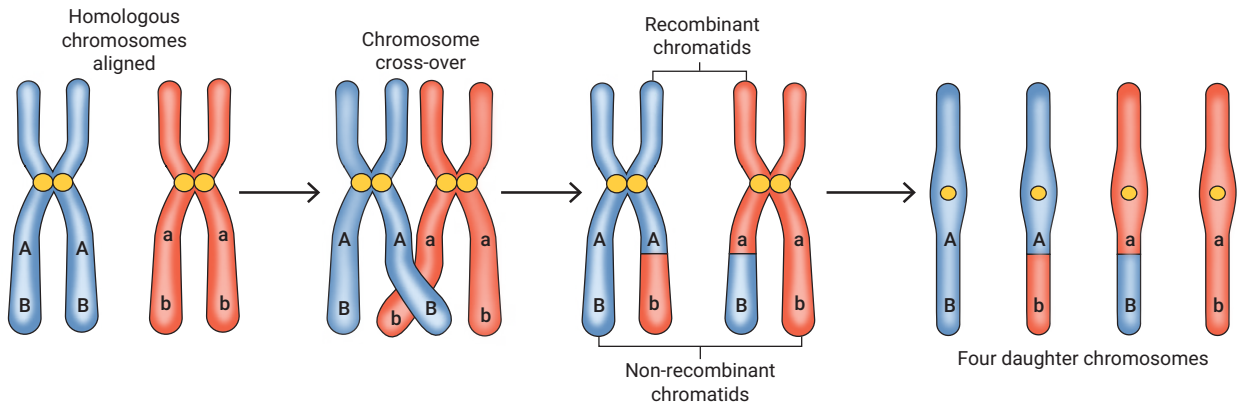


FIGURE 9.2.1 During crossing over, non-sister chromatids exchange segments with one another, which rearranges the combination of alleles on each chromosome.

Despite the final pulling apart occurring during anaphase I, the process of crossing over is cemented in prophase I, since pulling apart is inevitable after the chiasmata have formed. Therefore, crossing over is considered to be a prophase I process. Crossing over does not occur in prophase II because meiosis II is about separating the sister chromatids, not homologous chromosomes.

Independent assortment

The process of **independent assortment** is shown in Figure 9.2.2. During metaphase I, the chromosomes line up in homologous pairs at the metaphase plate. Each pair consists of one maternal and one paternal chromosome and the side of the plate that each ends up on is random and independent of the way the other pairs orient themselves. When the homologous chromosomes separate and move to opposite poles in anaphase I, the original maternal and paternal chromosomes (some of which have been recombined through crossing over) are distributed randomly to the gametes instead of as a predefined set from either parent.

independent assortment the process by which the paternal and maternal chromosomes of each homologous pair behave independently of the other homologous pairs as they separate in meiosis I

Independent assortment ensures that each resultant haploid cell contains a mixture of genes from the individual's mother and father. Because the homologous pairs carry different genetic information, independent assortment increases the number of different combinations of genes that can be carried by the gametes. The number of different combinations is 2^n, where n is the haploid number of the organism. For human gametes, with 23 pairs of chromosomes, the number of possibilities is 2^{23} or 8 388 608 possible combinations of chromosomes. Crossing over further increases the number of combinations of genes in each gamete.

Worksheet
Independent assortment

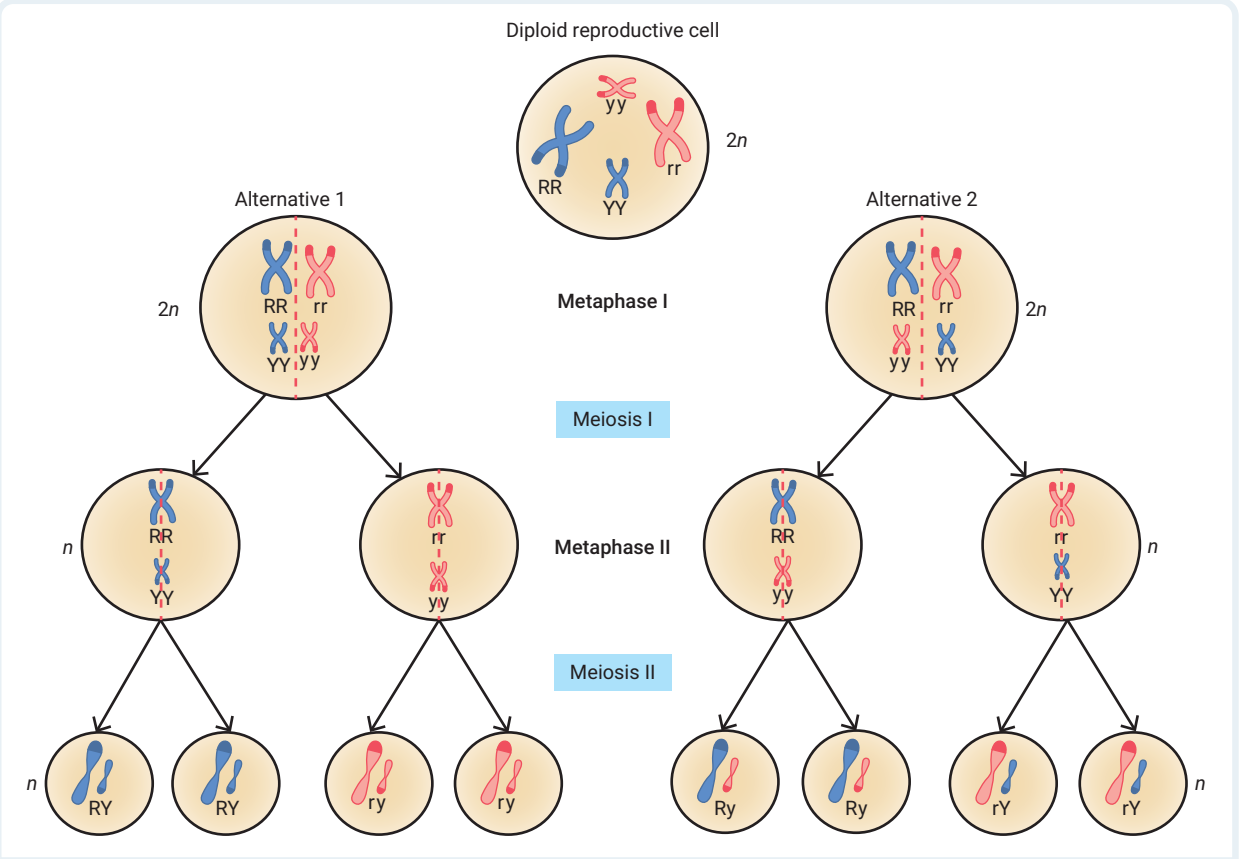


FIGURE 9.2.2 Independent assortment of chromosomes in meiosis increases the genetic variability of the offspring.

Random fertilisation

Random fertilisation also increases the possible combinations of alleles inherited by the offspring. This is because any egg, which contains just one of more than 8 million possible chromosome combinations, can be fertilised by any sperm, which also contains just one of more than 8 million possible chromosome combinations. Therefore, meiosis and fertilisation shuffle existing alleles into different combinations in each individual from one generation to the next and within the same generation. This is why one pair of reproducing parents can have dozens of children who are all only somewhat similar.

LEARNING CHECK 9.2

DESCRIBING

1 **Describe** the process of crossing over.
2 **Describe** independent assortment.

APPLYING

3 **Explain** how crossing over and independent assortment contribute to genetic variation in offspring.

9.3 Gametogenesis

In humans, females produce an **ovum** (**oogenesis**) containing 22 autosomes and one X chromosome, and males produce sperm (**spermatogenesis**) containing 22 autosomes and either an X or a Y chromosome.

The processes of oogenesis and spermatogenesis are very similar, but there are some important differences.

ovum the female haploid reproductive cell; also called an egg

oogenesis the process in the ovary that produces female gametes (ovum/egg)

spermatogenesis the continuous production of sperm cells in the testis

spermatogonia the stem cells responsible for producing cells that can create sperm

primary spermatocyte a cell that enters meiosis I in spermatogenesis

secondary spermatocyte a cell produced by meiosis I that enters meiosis II in spermatogenesis

spermatid a haploid daughter cell of spermatogenesis

Spermatogenesis

Spermatogenesis (Figure 9.3.1) is most similar to generic meiosis. Stem cells in the testes, called **spermatogonia**, undergo continuous mitosis. They produce a steady stream of **primary spermatocytes**, which are primed to undergo meiosis for spermatogenesis. During meiosis I, they form two **secondary spermatocytes**, which in turn divide in meiosis II to form four **spermatids**, which are haploid. These four spermatids are the four daughter cells of spermatogenesis. The conditions in the testis cause them to develop into four sperm cells with minimal cytoplasm (because there is no need for an extended lifetime) and a flagellum for mobility. Spermatogenesis occurs from puberty throughout a male's lifetime and can produce, in humans, at least 3 million sperm every day.

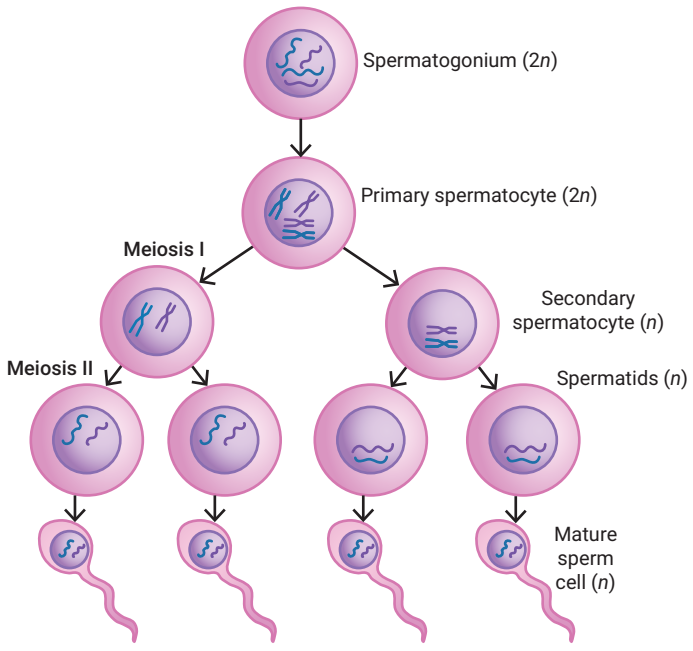


FIGURE 9.3.1 Spermatogenesis in the testis is very similar to generic meiosis, producing the haploid number of chromosomes in four sperm cells.

Oogenesis

Oogenesis (Figure 9.3.2) is not a continuous process and the requirements of the ovum (relatively long lifespan and high energy needs) require that meiosis occurs differently. It begins in the ovaries of females during embryonic development. There, **oogonia** produce **primary oocytes** through mitosis for several months before birth. At birth, the oogonia stop production and no further primary oocytes are produced in the female's lifetime. Instead, the primary oocytes remain in prophase I from birth until puberty. At that time, one primary oocyte completes meiosis I each month until the store of viable oocytes is exhausted and the woman enters menopause.

oogonia the stem cells responsible for producing cells that can create eggs

primary oocyte a cell that enters meiosis I in oogenesis

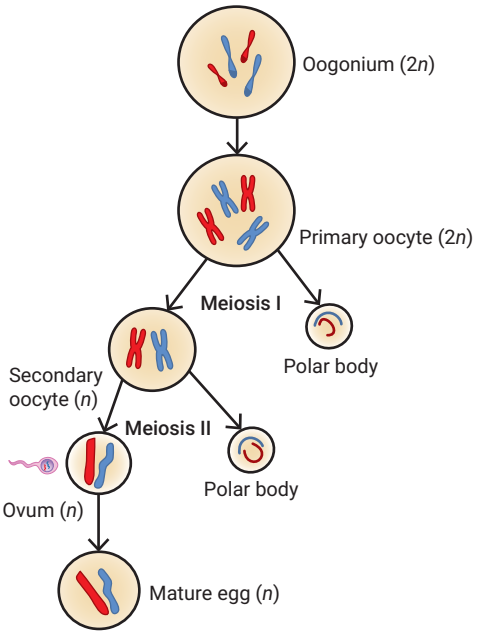


FIGURE 9.3.2 Oogenesis in the ovary is very different from generic meiosis, producing the haploid number of chromosomes in a single ovum and two polar bodies.

Meiosis I in oogenesis is also different from generic meiosis. Instead of dividing the cytoplasm equally, almost all of the cytoplasm is sequestered around one of the nuclei, the **secondary oocyte**, and the other nuclei is budded off as a structure called a **polar body**, which dies and is absorbed by the ovary. During meiosis II, progress is stopped at metaphase II. Only the entry of a sperm cell triggers the oocyte to continue with anaphase II and telophase II. At the second meiotic division, cytokinesis is again unequal. The haploid ovum nucleus retains almost all of the cytoplasm and a second polar body is formed. This produces one very large and well-supplied ovum nucleus that can absorb the sperm cell nucleus and sufficiently power the implantation, cell division and growth required for early embryonic development.

secondary oocyte a cell produced by meiosis I that enters meiosis II in oogenesis

polar body a small structure containing a nucleus and very little cytoplasm, that is produced, dies and is absorbed by the ovary during oogenesis

Although both processes involve the formation of haploid cells by meiosis, and gametes from both processes contain only half the chromosomes of a diploid cell, oogenesis and spermatogenesis differ in three main ways:

- In oogenesis, cytokinesis in both meiosis I and II is unequal and produces only a single, very large ovum and two small polar bodies that degenerate. By contrast, meiosis in spermatogenesis produces four equal sperm that are small and motile.
- At birth, an ovary contains all primary oocytes that will ever develop into ova. However, primary spermatocytes are produced throughout a male's fertile lifetime.
- Sperm are produced quickly and continuously, whereas oogenesis has long breaks between stages of division. This is because all primary oocytes are formed in the female embryo, but they will not complete meiosis unless they are fertilised, which may not occur until the woman reaches the early stages of menopause.

Worksheet
Oogenesis and spermatogenesis

LEARNING CHECK 9.3

DESCRIBING

1 **Describe** the process of spermatogenesis.
2 **Identify** the two stages at which oogenesis is paused.
3 **Describe** the end products of oogenesis.

APPLYING

4 **Explain** why oogenesis produces one ovum rather than four daughter cells.
5 It has been said that King Henry VIII of England was wrong to blame his wives who did not have sons. Comment on this statement and provide evidence to support your position.
6 In bees, females develop from fertilised eggs and are diploid, and males develop from unfertilised eggs and are haploid. In the testes of males, ordinary cell division (mitosis) produces clones of identical sperm. **Explain** the amount of variation that would be expected in eggs and sperm.
7 With reference to meiosis, **explain** why males produce more sperm in a lifetime than females produce eggs.

ANALYSING

8 **Distinguish** between autosomes and sex chromosomes.

9.4 Errors in meiosis

Unlike mitosis, which produces replacement cells for a multicellular organism, meiosis produces the foundation for an entirely new individual. This makes it all the more important that the process goes smoothly. Errors in meiosis can, and do, lead to infertility, non-viable offspring, congenital abnormalities and disease.

Syllabus link
Chapter 7 discusses small-scale mutations in DNA.

Chromosome rearrangement

Two stages of meiosis are implicated in large-scale chromosome rearrangement, where large sections of DNA can be deleted, duplicated, inverted or translocated **(Figure 9.4.1)** and even whole chromosomes can be affected. The first is the interphase prior to beginning meiosis proper. At this point, the DNA in the primary oocyte or spermatocyte is being replicated in preparation for meiosis. Breaks in a single strand of DNA are common and can easily be repaired but breaks in both strands of the DNA are both less common and less easy to repair. If several breaks occur, large sections of DNA must be reattached in the proper order to avoid passing on a large-scale mutation.

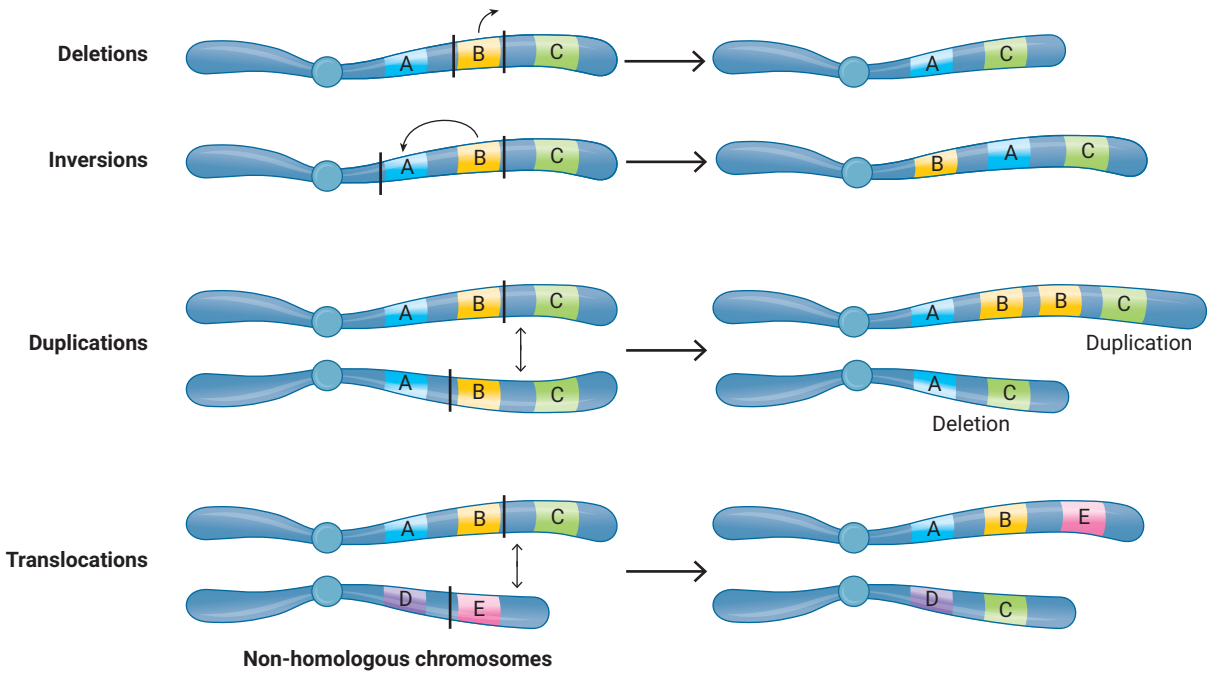


FIGURE 9.4.1 Large-scale chromosome rearrangements occur during meiosis and have significant impacts on offspring.

The second stage of meiosis that tends to produce large-scale rearrangement of genes is related to the process of crossing over that occurs during prophase I. Crossing over strictly refers to the exchange of genes between non-sister chromatids. However, the formation of chiasmata can occur between sister chromatids at non-equivalent locations, which produces duplication/deletion rearrangements, or a chromatid can fold in on itself and form a chiasma between two locations on the same strand, which produces deletion and inversion rearrangements. Both of these events rearrange the chromosome during prophase I without qualifying as crossing over.

Deletions

When the core strand of DNA is broken and reattached without the intervening section, any genes that were located on that section are effectively deleted from the chromosome and are not present in the gamete. Gene deletions are quite serious mutations and often produce non-viable offspring. Those children who do survive to birth generally battle serious disability and disorder.

Inversions

Inversions occur when the breaks are located on the same chromatid, but instead of reattaching in the correct orientation, the intervening section is reattached upside down. Since this does not usually result in the loss or deactivation of the genes on the inverted section, most inversions have only mild repercussions.

Duplications

When the breaks occur at different locations, or a chiasma forms, on both sister chromatids, the arms may be reattached to the wrong chromatid, resulting in one sister chromatid that contains a duplicated section of genes and the other with a deleted section. Gene duplications can be as serious as deletions because the duplicated gene is overactive, causing developmental and health issues.

Translocations

If the breaks occur on non-sister chromatids, the sections of DNA may be reattached to the wrong chromosome. This may have mild repercussions if both chromosomes involved in the translocation are inherited by the same gamete. Unfortunately, if this isn't the case, some genes will be missing from the gamete and the outcome will be similar to a deletion.

Aneuploidy

Errors in meiosis can also occur at the whole-chromosome scale. Gametes are usually haploid (*n*), with the normal number of chromosomes for a gamete (**euploid**). However, errors during anaphase I, when homologous chromosomes separate, and anaphase II, when sister chromatids separate, can cause significant issues. **Non-disjunction** refers to an error of meiosis where there is lack of separation at one or both of these points, so that the final gametes contain an unusual number of chromosomes, a condition called **aneuploidy**.

euploid when a cell contains the normal number of chromosomes for its species, either *n* haploid or 2*n* diploid

non-disjunction when a pair of chromosomes fails to separate during anaphase, with both members of the pair moving to the same pole of the cell

aneuploidy when a cell contains an abnormal number of chromosomes for its species, either more or fewer chromosomes than normal

Figure 9.4.2 shows the two phases at which non-disjunction can occur. During normal anaphase I, homologous pairs segregate into separate nuclei, so that the resulting cells have

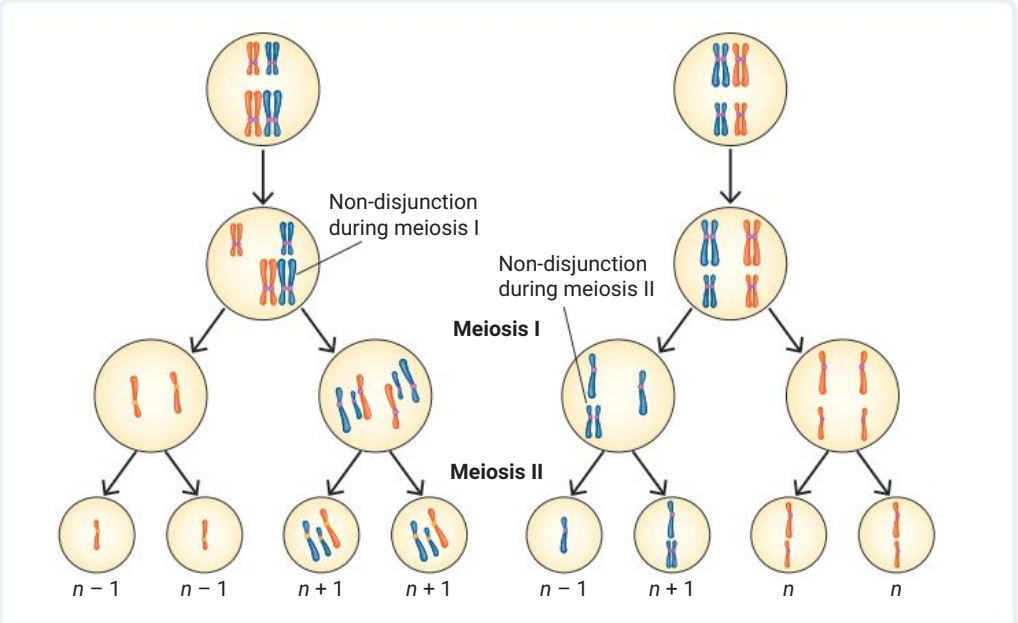


FIGURE 9.4.2 When non-disjunction occurs during anaphase I, the homologous pairs fail to segregate. When non-disjunction occurs during anaphase II, the sister chromatids fail to separate. Generally, non-disjunction only takes place with one pair of chromosomes, while the rest behave normally.

only one of each pair of chromosomes. However, occasionally both members of the homologous pair go into the same cell during anaphase I instead of separating. It results in the formation of two types of gametes in equal proportions; one type has both parents' copies of the particular chromosome and the other type has none.

Non-disjunction can also occur during anaphase II when sister chromatids fail to segregate into separate cells. Anaphase II aneuploidy generally occurs in only one of the secondary oocytes/spermatocytes; while one secondary cell divides normally, the other produces one gamete with two of the affected chromosomes and one gamete without that chromosome.

monosomy when an individual's nuclei contain only one copy of a particular chromosome

Unfortunately, children are rarely born from gametes with deleted chromosomes, since the only viable **monosomy** is Turner syndrome, where individuals have a single sex chromosome, an X.

trisomy when an individual's nuclei contain three copies of a particular chromosome

Children born from gametes with extra chromosomes are only viable when this occurs with certain chromosomes. For example, **trisomy** 21 is a viable aneuploidy, where a gamete with two copies of chromosome 21 fertilises a normal haploid gamete, resulting in three copies of chromosome 21 in the individual. This condition causes Down syndrome, characterised by issues with physical and cognitive development, as well as health and fertility problems. Trisomy 13 (Patau syndrome), trisomy 18 (Edwards syndrome), and trisomies of the sex chromosomes (XXX, XXY and XYY) are the only other aneuploidies that produce live-born children.

Aneuploidies are a significant factor in age-related infertility. With errors in meiosis considerably more common as a female's store of oocytes ages, and each month only producing one oocyte for fertilisation, the chances of the monthly egg containing an aneuploidy rises rapidly with age. For women over 35, more than 40 per cent of their eggs are aneuploid. Only five aneuploidies produce viable pregnancies (the other 41 possible aneuploidies result in spontaneous miscarriages), making it much less likely that a viable egg will be available for fertilisation each month. Figure 9.4.3 shows the probability of a pregnancy having aneuploid conditions based on maternal age, as well as the probability of pregnancy occurring at all. Although males are also affected by age-related errors in meiosis, the sheer volume of sperm produced reduces the impact of this on their overall fertility.

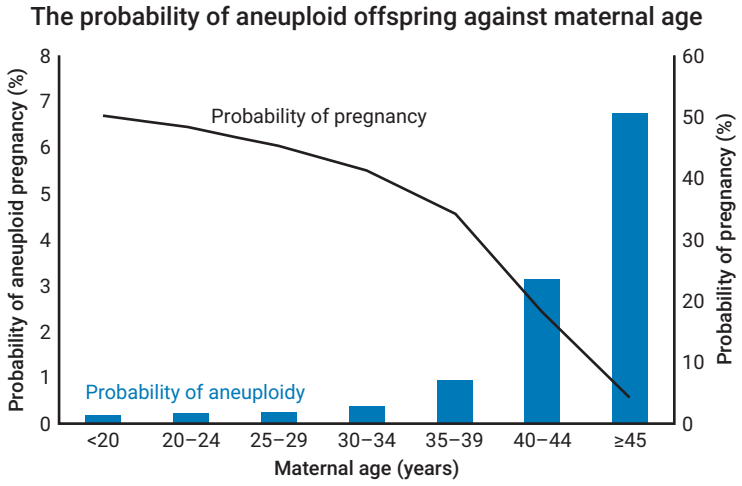
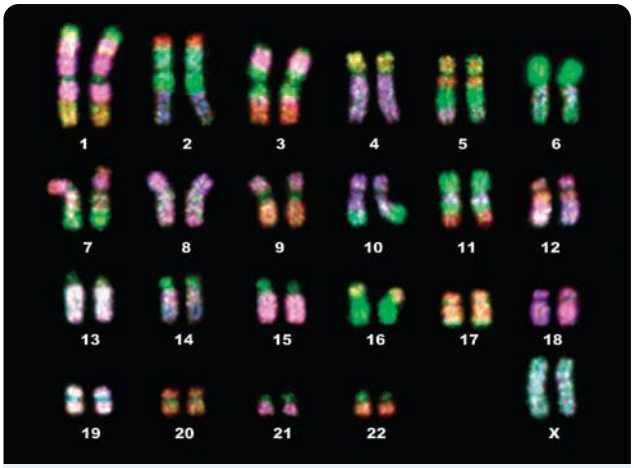


FIGURE 9.4.3 The probability of aneuploid offspring rises rapidly as women age, whereas their chance of becoming pregnant at all decreases.

Aneuploidies can be observed and analysed by examining a prepared microscope slide of stained cells that are in the process of nuclear division. This reveals a jumbled cluster of chromosomes that differ in size, shape and banding. Photographic images of chromosomes are rearranged into homologous pairs matched for size and banding pattern, and ordered from largest to smallest, to create a karyotype – the standard form used to display and analyse chromosomes. Figure 9.4.4 shows a human female karyotype.



DEPT. OF CLINICAL CYTOGENETICS, ADDENBROOKES HOSPITAL/Science Photo Library

FIGURE 9.4.4 This human female karyotype has been produced from fluorescent chromosome photographs.

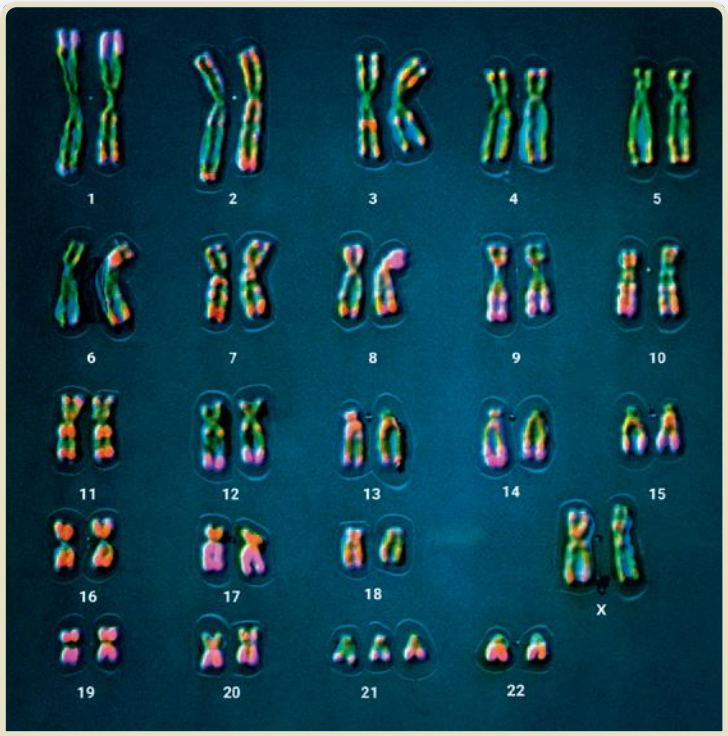
Using a karyotype

The human karyotype has 22 pairs of homologous autosomes, each pair having its own characteristic shape. The autosomal pairs also have distinctive patterns of different widths of light and dark banding relating to their particular DNA nucleotide sequences, with most of the active genes residing in the light bands.

The 23rd pair is the sex chromosomes. They may match, with banding unique to the pair, as in the case of females with XX genotype. In males, the chromosomes of the 23rd pair are unmatched. The genotype is XY, with the Y chromosome being much shorter than the X.

WORKED EXAMPLE 9.4.1

Examine Figure 9.4.4 and Figure 9.4.5. Identify any ploidy changes and predict any genetic disorders.



CNRI/Science Photo Library

FIGURE 9.4.5 A karyotype from an individual

ANSWER

1 **Determine the total number of pairs of autosomes and sex chromosome in Figure 9.4.4.**
Figure 9.4.4 has 22 pairs of autosomes and a pair of X chromosomes. The X chromosomes indicate that the individual is female.
2 **Use the answer at step 1 to predict any genetic disorders.**
No aneuploidies are present and, therefore, genetic disorders are unknown.
3 **Determine the total number of pairs of autosomes and sex chromosomes in Figure 9.4.5.**
Figure 9.4.5 has 21 pairs of autosomes, with three copies of chromosome 21 and a pair of X chromosomes. The X chromosomes indicate that the individual is female.
4 **Use the answer to step 3 to predict any genetic disorders.**
Trisomy 21 is present; therefore, this individual has Down syndrome.

LEARNING CHECK 9.4

DESCRIBING

1 **Describe** the order in which the chromosomes are arranged in a karyotype.
2 **Define** 'aneuploidy'.
3 State the cell cycle stage where errors result in aneuploidy.
4 State the cell cycle stages where errors result in chromosome rearrangements.
5 **Describe** the process of non-disjunction.
6 **Identify** a human condition that results from trisomy.

APPLYING

7 **Explain** the stage of meiosis in which chromosomes are photographed to create a karyotype.
8 Gametes produced with a missing chromosome rarely form viable offspring. **Explain** the conditions necessary for one of these gametes to produce a healthy child.

ANALYSING

9 Sequence the four categories of chromosome rearrangement by order of increasing impact.
10 **Distinguish** between monosomy and trisomy in somatic cells.

INTERPRETING

11 If diploid cells can be represented as 2*n* and haploid as *n*, predict the symbols used for aneuploid cells.
12 Examine the three human karyotypes in Figure 9.4.6 to **identify** any ploidy changes and predict any genetic disorders.

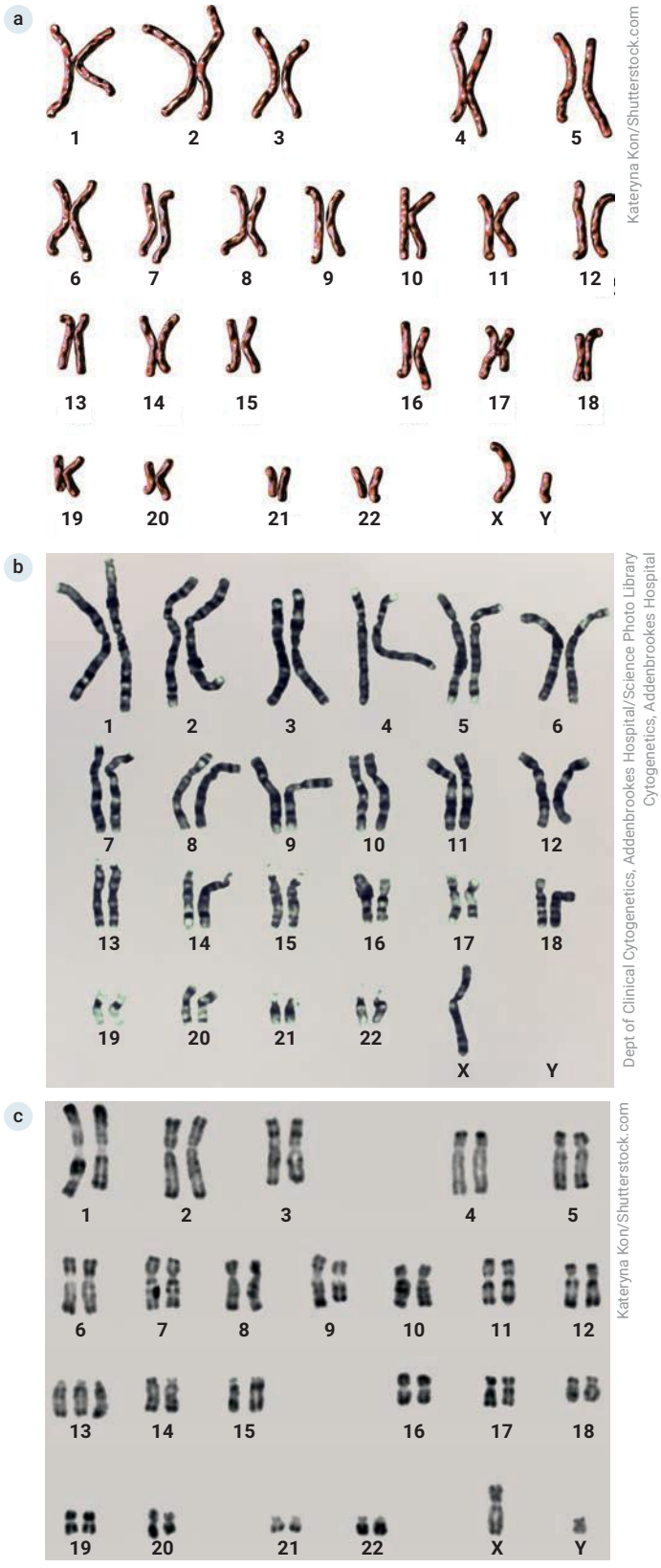
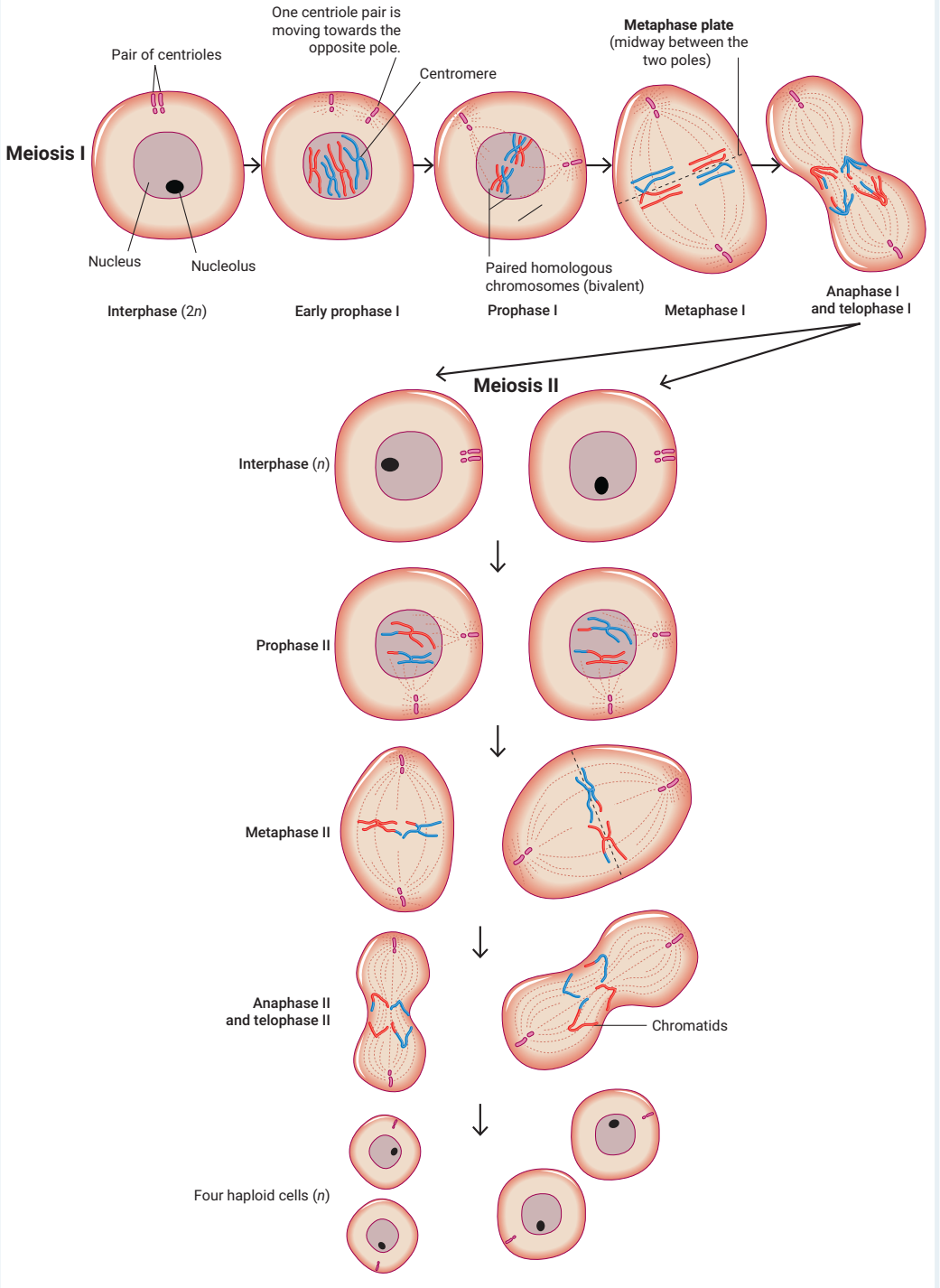


FIGURE 9.4.6 Three human karyotypes

CHAPTER SUMMARY

Meiosis

- Meiosis is a multistage process that produces four haploid cells.
- Meiosis and mitosis have similarities and differences.



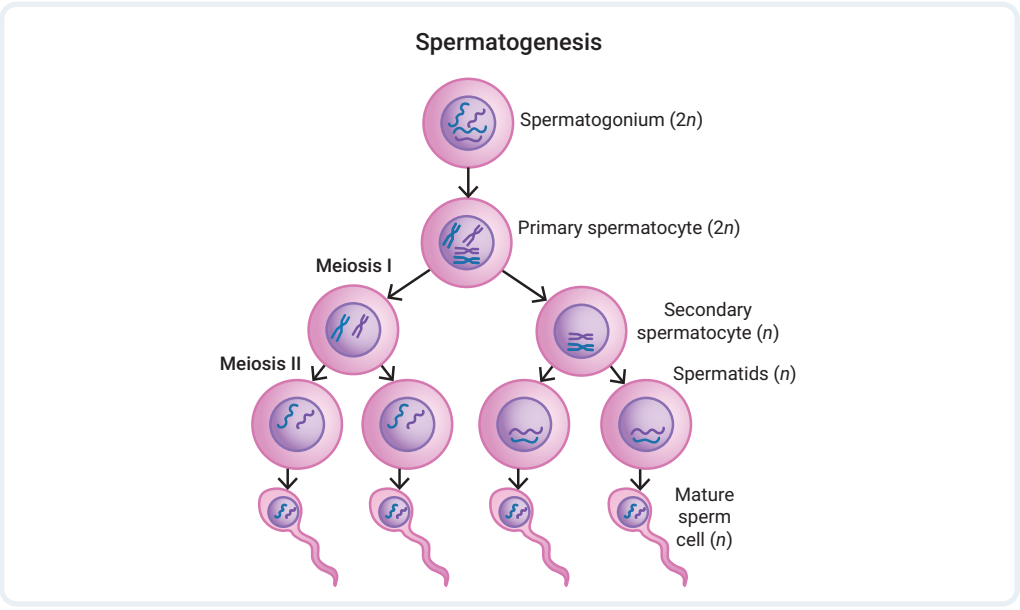
		Mitosis	Meiosis
Similarities		Both produce new cells. They have similar basic steps. Both start with a single parent cell.	
Differences	Number of sequences	One sequence of prophase, metaphase, anaphase and telophase	Two sequences of prophase, metaphase, anaphase and telophase
	Number of stages	Four (plus interphase)	Eight (plus interphase)
	Location	Somatic cells	Germ cells
	Purpose	Cellular proliferation	Sexual reproduction
	Products	Two diploid daughter cells	Four haploid daughter cells
	Chromosome number	Remains the same	Halved in each daughter cell
	Change in genetic variation	Unchanged	Increased

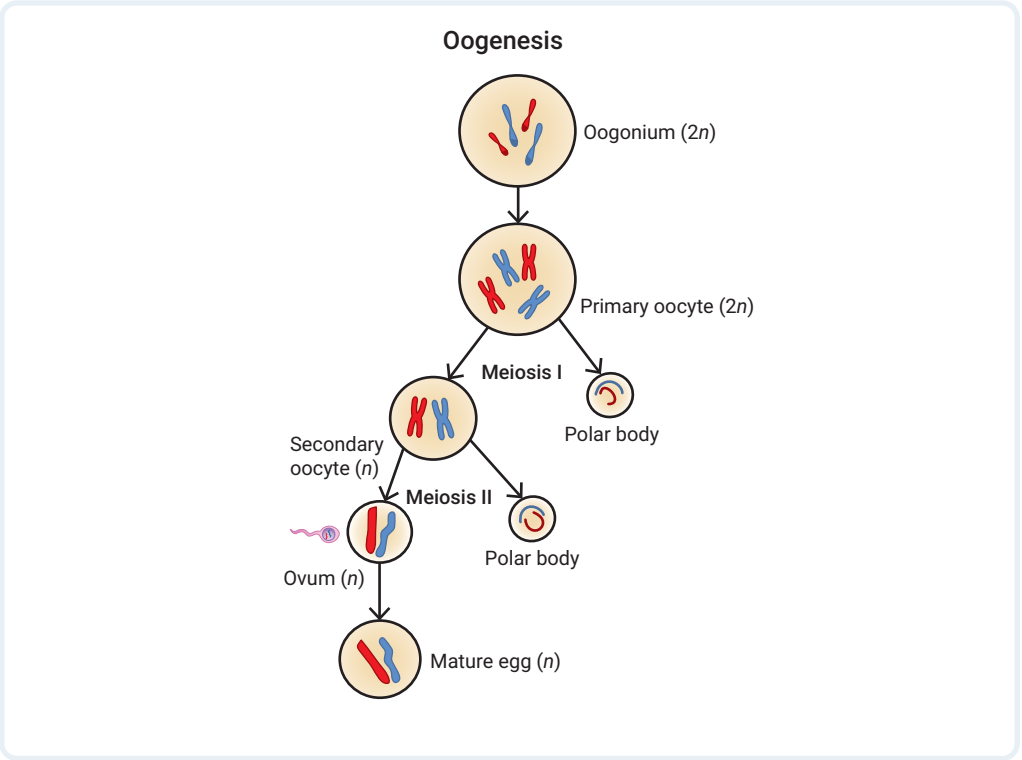
Mechanisms of variation

- Crossing over: homologous chromosomes form chiasmata and exchange segments during prophase I.
- Independent assortment: each homologous pair consists of one maternal and one paternal chromosome and the side of the metaphase plate that each ends up on is random and independent of the way the other pairs orient themselves.
- Random fertilisation: the egg that is matured and the sperm that fertilises it are randomly selected from all available gametes – no combination of genes is more likely than others.

Gametogenesis

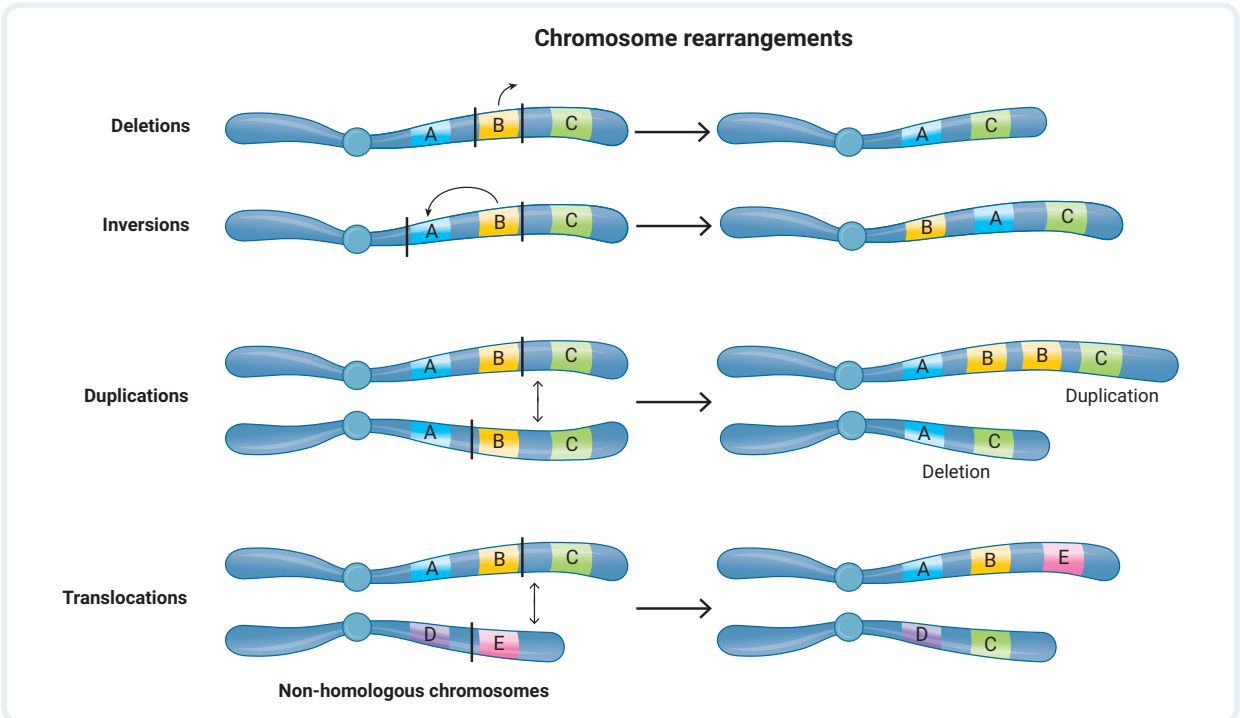
- Spermatogenesis produces sperm cells, whereas oogenesis produces a mature egg.

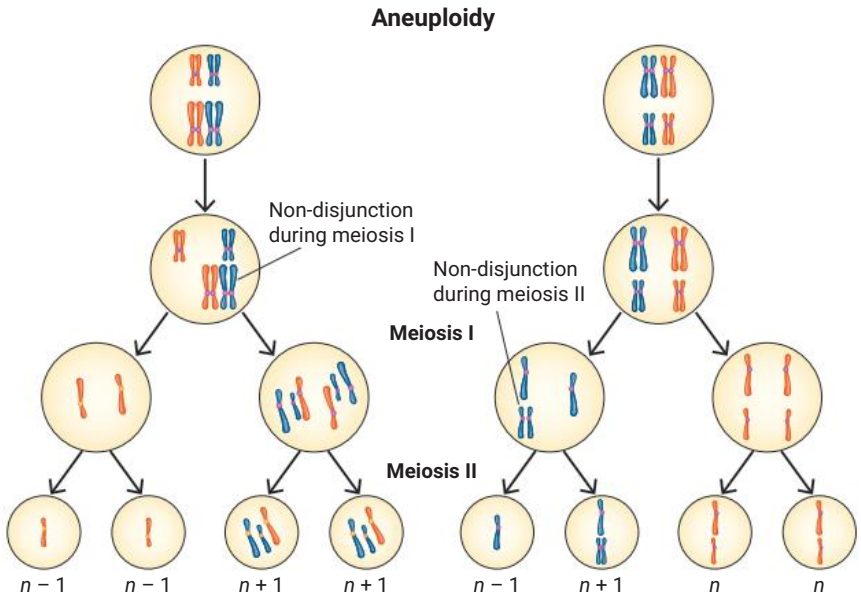




Errors in meiosis

- Errors in meiosis can result in health complications and can lead to infertility and non-viable offspring.

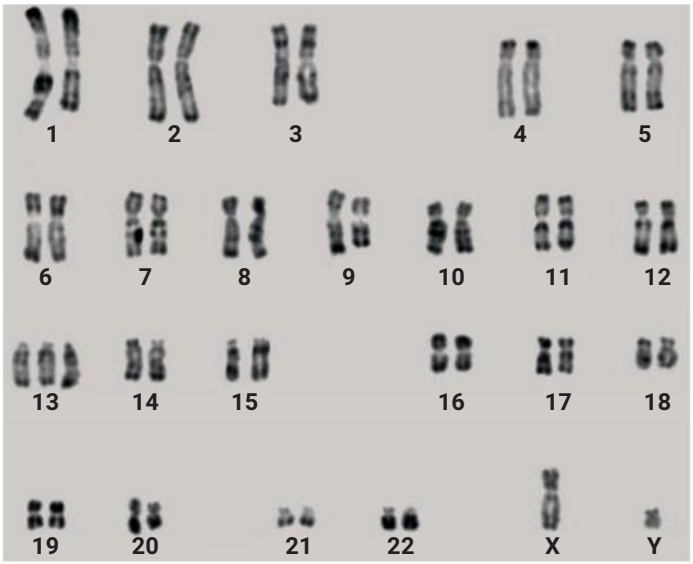




Molnar, C. & Gair, J. (2015). Concepts of Biology, 1st Canadian Edition. BCcampus. Retrieved from https://opentextbc.ca/biology.

Analysing karyotypes

- Check for sex chromosome genotype: XX is female, XY is male, aneuploidy causes various disorders.
- Check for homologous pairs: 22 autosome pairs is normal, aneuploidy causes various disorders.



Kateryna Kon/Shutterstock.com

CHAPTER EXAM

MULTIPLE CHOICE

1. State the stage of meiosis in which homologous chromosomes line up at the equator of the cell.

A Prophase I
B Metaphase I
C Prophase II
D Metaphase II

2. Crossing over contributes to genetic variation because chromosomal fragments are exchanged between:

A autosomes and sex chromosomes.
B sister chromatids of a chromosome.
C chromatids of non-homologous chromosomes.
D non-sister chromatids of homologous chromosomes.

3. What are the points of contact between homologous chromosomes in prophase I of meiosis called?

A Bivalency
B Centromeres
C Chiasmata
D Disjunctions

4. Non-disjunction occurs:

A only in mitosis.
B only in meiosis.
C in all DNA replications.
D in both mitosis and meiosis.

5. Aneuploidy in the sex chromosomes occurs:

A during DNA replication.
B in gamete cells.
C in somatic cells.
D in all cells.

6. Which of the following does not contribute to genetic variation in offspring?

A Crossing over
B Independent assortment
C Random fertilisation
D UV damage

7. Select the correct statement about gametogenesis.

A Spermatogenesis is less like generic meiosis than oogenesis is.
B Spermatogenesis and oogenesis produce four haploid daughter cells.
C Spermatogenesis occurs continuously, whereas oogenesis occurs intermittently.
D Spermatogenesis has unequal cytokinesis, whereas oogenesis has equal cytokinesis.

8. Errors in meiosis include:

A duplications where non-homologous chromosomes replicate.
B deletions where part of a chromosome transfers to a sister chromatid.
C inversions where chromosomes orient upside down at the metaphase plate.
D translocations where part of a chromosome joins a non-homologous chromosome.

9. In a human karyotype:
   - **A** only aneuploidy can be identified.
   - **B** only chromosomal rearrangement can be identified.
   - **C** aneuploidy and chromosomal rearrangement can be identified.
   - **D** neither aneuploidy nor chromosomal rearrangement can be identified.

10. Which of the following is not an aneuploid condition?
   - **A** Down syndrome
   - **B** Edwards syndrome
   - **C** Patau syndrome
   - **D** Williams syndrome

SHORT RESPONSE

11. **Compare** spermatogenesis and oogenesis.

12. **Explain** how errors in meiosis can lead to chromosomal abnormalities.

CROSS-CHAPTER QUESTION

13. **Compare** meiosis and mitosis.

DATA ANALYSIS

Questions 14 and 15 refer to the following information.
Researchers studied the rate of aneuploidy in more than 500 000 births in Denmark. Their results are summarised in the following table.

Maternal age (years)	Rate (%) of			
	Trisomy 21	Trisomy 18	Trisomy 13	Monosomy X
<20	0.09	0.04	0.02	0.02
20–29	0.10	0.02	0.01	0.04
30–34	0.19	0.05	0.02	0.04
35–39	0.62	0.16	0.05	0.04
40–44	2.14	0.69	0.10	0.05
≥45	3.22	2.34	0.02	0.02

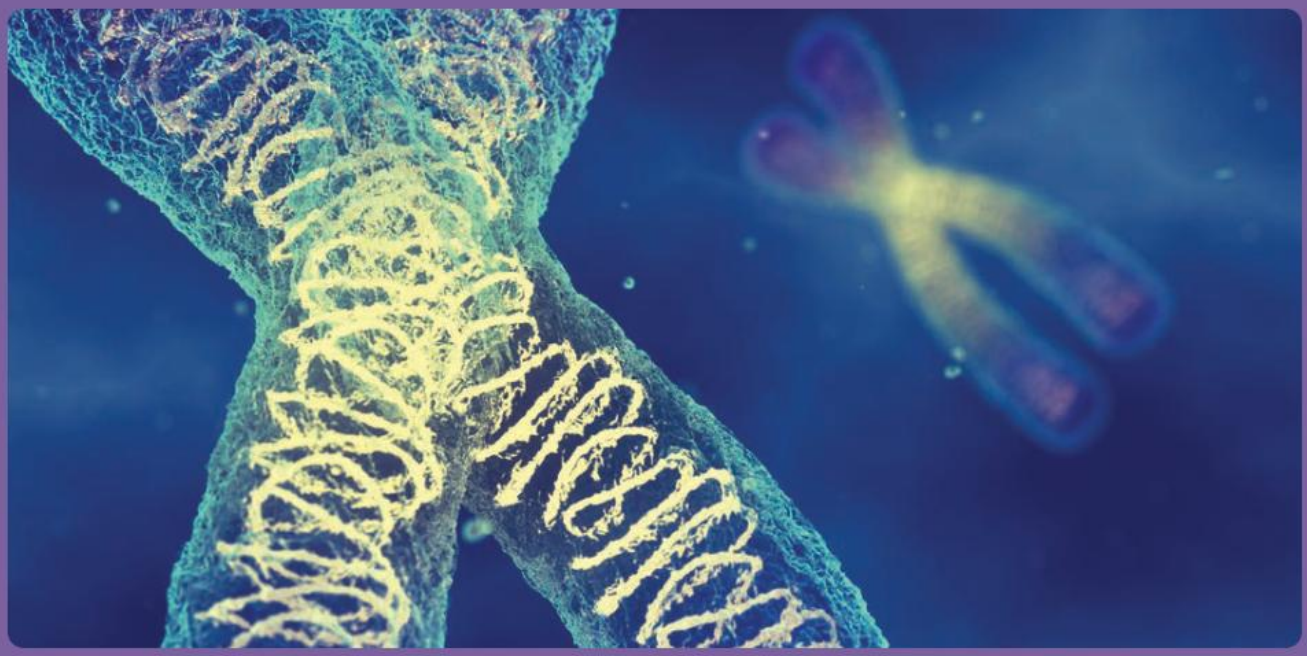
Adapted from https://obgyn.onlinelibrary.wiley.com/doi/10.1111/aogs.14713

14. **Analyse evidence**
   - **a** **Identify** a trend between maternal age and rate of trisomy 21.
   - **b** **Identify** a relationship between maternal age and aneuploidy.

15. **Interpret evidence**
   Determine the age of a mother who is least likely to give birth to a child with aneuploidy. Provide evidence for this decision.

CHAPTER 10

Inheritance



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SYLLABUS DOT POINTS

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).

Introduction

Meiosis and sexual reproduction create and maintain genetic variation in offspring, but predicting the ways that these varied traits are inherited is not an easy task. Humans, in particular, are a complex species to study because we have relatively few children from each set of parents and a long time passes between generations. Early geneticists, such as Gregor Mendel, had to study species that reproduced quickly and copiously to gather any useful data, and although genetic studies have advanced significantly since then, there is still much that we do not know about how our traits are passed on.

Worksheets

- Inheritance 1
- Inheritance 2

Nelson MindTap

To access resources above, visit
cengage.com.au/nelsonmindtap

ASSUMED KNOWLEDGE

- ✓ In meiosis, the full genome of an individual ($2n$) is divided into gametes that only contain half of the genome (n).
- ✓ Usually, each gamete contains one copy of each chromosome.
- ✓ Sexual reproduction involves the gametes of two individuals combining to form a new individual.
- ✓ Genes are sections of DNA that code for a particular trait, and alleles are variations in the sequence of this section.
- ✓ Pedigrees, also called family trees, show family relationships.
- ✓ A histogram is a bar graph that charts how often (frequency) a particular version of a trait occurs in a population.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ use the terms 'dominant' and 'recessive' to describe the alleles of a gene
- ✓ describe Mendel's study of pea plant heredity
- ✓ use conventions of inheritance to discuss Mendelian patterns of inheritance in autosomal traits
- ✓ use Punnett squares to predict the frequency of genotypes and phenotypes in monohybrid crosses between homozygous and/or heterozygous parents
- ✓ use Punnett squares to predict the frequency of genotypes and phenotypes in dihybrid crosses between homozygous and/or heterozygous parents
- ✓ analyse pedigrees to infer patterns of Mendelian inheritance
- ✓ distinguish between Mendelian and non-Mendelian patterns of inheritance
- ✓ describe sex-linked inheritance
- ✓ use Punnett squares and pedigrees to identify sex-linked inheritance and determine the genotypes and phenotypes of a range of related individuals
- ✓ describe multiple-allele inheritance
- ✓ use Punnett squares and pedigrees to identify multiple-allele inheritance and determine the genotypes and phenotypes of a range of related individuals
- ✓ describe polygenic inheritance
- ✓ analyse histograms to identify polygenic inheritance and predict the frequencies of genotypes and phenotypes in a population.

10.1 Mendelian autosomal inheritance

The first principles and patterns of inheritance were proposed in 1865 by Gregor Mendel (1822–84), an Austrian monk who carefully studied the height, colour and texture of pea plants in his garden. He discovered that genetic information is passed directly to offspring and that some genetic information is expressed in preference over others. This has formed the basis of our modern understanding of **heredity**.

heredity the study of inheritance; genetic transmission of characteristics from one generation to another

One of the traits Mendel observed was the height of the mature plant; some plants would grow tall and upright, while others appeared stunted and bushy. When he bred tall plants

with other tall plants, he would get a mixture of tall and short offspring. But when he bred short plants with other short plants, he only ever got short offspring. He concluded that the tall plants had something that they could pass to their offspring that the short plants lacked, a tall gene.

Mendel's tall gene was actually two genetic elements, called **alleles**, one that would make a plant tall (denoted with a capital T) and one that would not (denoted with a lowercase t). Each plant had two alleles, with only three possible combinations: both tall (TT), both short (tt) or one of each (Tt). Mendel did discover that if a plant received even one tall allele from its parents, TT or Tt, it would grow tall. He called the tall allele '**dominant**' because if a plant had even one of them, it would always express its tallness. He used the term '**recessive**' for the lack of a tall allele, which is now used to refer to any allele that isn't dominant.

Since Mendel's time, the study of genetics has revealed many of the mechanisms that underpinned his ideas of inheritance. For example, DNA was discovered in the late 1860s and meiosis in the 1880s, both of which confirmed that alleles occur in pairs, one on each homologous chromosome (Figure 10.1.1), and that each allele is inherited from the parent through a haploid gamete. The traits that Mendel studied were also all located on **autosomes**, which are inherited equally by male and female offspring. Mendelian inheritance is often called autosomal inheritance to highlight this fact.

alleles different versions of the same gene, determined by slightly different DNA sequences at that gene locus

dominant allele the allele that is expressed in the phenotype when at least one copy occurs in the genotype

recessive allele the allele that is expressed in the phenotype only if both copies occur in the genotype

autosome a chromosome that is not a sex chromosome

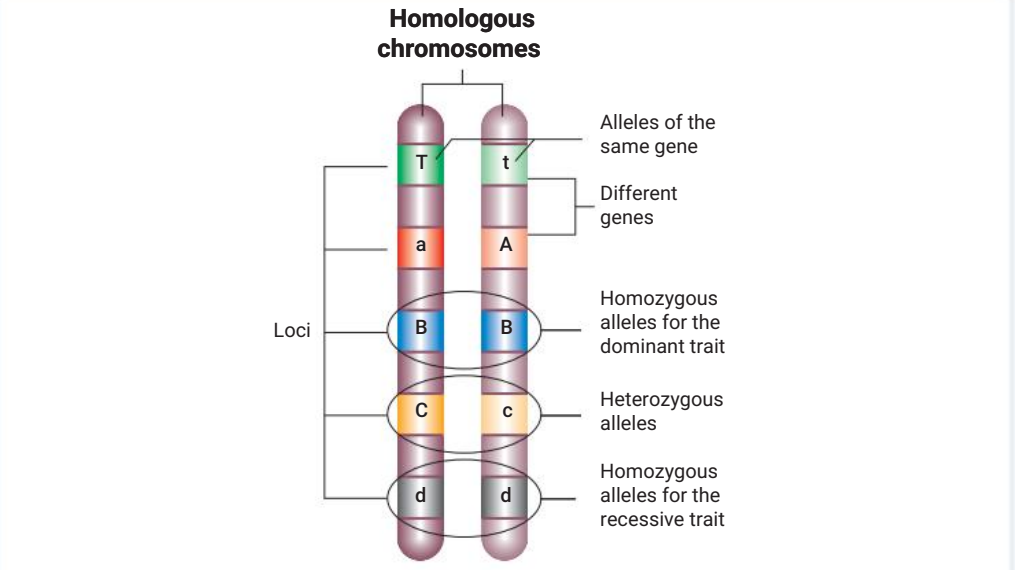


FIGURE 10.1.1 Homologous chromosomes have paired alleles. Each chromosome of each pair, with its assortment of different alleles, is inherited from either the male or female parent.

Syllabus links
Chapter 7 explains the location of alleles on homologous chromosomes.

Chapter 9 explores how alleles are distributed to gametes through meiosis.

Conventions of inheritance

As with most areas of science, there are standard conventions to use when discussing genetic inheritance. Table 10.1.1 shows the key terms and notations used in this field.

TABLE 10.1.1 Key terms related to genetic inheritance

Convention	Use
Capital letter (e.g. T, A, H, R)	Denotes the dominant member of a pair of alleles. The letter is either the first letter of the dominant trait (e.g. T for tall) or a letter whose capital is easily distinguished from the lower case (e.g. A/a, R/r rather than S/s or C/c).
Lower-case letter (e.g. t, a, h, r)	Denotes the non-dominant or recessive member of a pair of alleles.
Genotype	The combination of alleles for an individual (e.g. TT, Tt or tt).
Phenotype	The physical trait expressed in the individual (e.g. tall or short).
Homozygous	The two alleles are the same, either both dominant (e.g. TT) or both recessive (e.g. tt).
Heterozygous	The two alleles are different. The dominant allele is always written first (e.g. Tt not tT).
Carrier	An individual that is heterozygous for a recessive condition. They express the dominant phenotype but can pass the recessive allele on to their offspring.
Cross	An instance of reproduction between two individuals that produces offspring.
P generation	The biological parents of a particular set of offspring.
F_1 generation	The offspring produced from a cross in the parent generation.
F_2 generation	The offspring produced from a cross in the F_1 generation.
Monohybrid	Considering only one trait determined by the combination of two contrasting alleles (e.g. considering height, with T for tall and t for short).
Dihybrid	Considering two traits, each determined by the combination of two contrasting alleles (e.g. considering both height (T for tall and t for short) and flower colour (P for purple and p for white)).

purebred when crossed with each other, offspring all have the parent phenotype

In one of Mendel's tall plant experiments **(Figure 10.1.2)**, he began by selecting a homozygous, or **purebred**, tall plant (TT) to cross with a purebred short plant (tt). These plants were his P generation, and he collected and germinated the seeds they produced. The seeds formed the first generation of offspring, the F_1 generation. When he grew them to maturity, he discovered that all the seeds expressed the tall phenotype. Since they could only have received a T allele from their purebred tall parent, and a t allele from their short parent, all of the F_1 generation had a heterozygous genotype (Tt).

It becomes more complicated when the F_1 generation is crossed together because these are all heterozygous tall plants (Tt). Half of their gametes contain the T allele and half contain the t allele. However, this does not produce 50:50 offspring. Instead, each gamete containing a T allele may fertilise a T allele or a t allele gamete from the other parent, resulting in four equal offspring combinations: $\frac{1}{4}$ TT, $\frac{1}{4}$ Tt, $\frac{1}{4}$ tT (also written Tt by convention) and $\frac{1}{4}$ tt. Since all genotypes with at least one T allele are phenotypically tall, $\frac{3}{4}$ of the F_2 generation will be tall and $\frac{1}{4}$ will be short. This means the dominant phenotype is expressed in a ratio of 3:1 when both parents are heterozygous.

Punnett squares

Punnett square a grid used to graphically illustrate and predict the outcome of a genetic cross

In 1905, Reginald C. Punnett (1875–1967) began using a square grid system to track the production of gametes and predict offspring ratios for genetic crosses. The **Punnett square (Figure 10.1.3)** is usually a two by two grid, but can have any number of columns and rows that accommodate the P generation. There is no convention for which parent is used for the columns or rows. Instead, geneticists clearly label which parent is which.

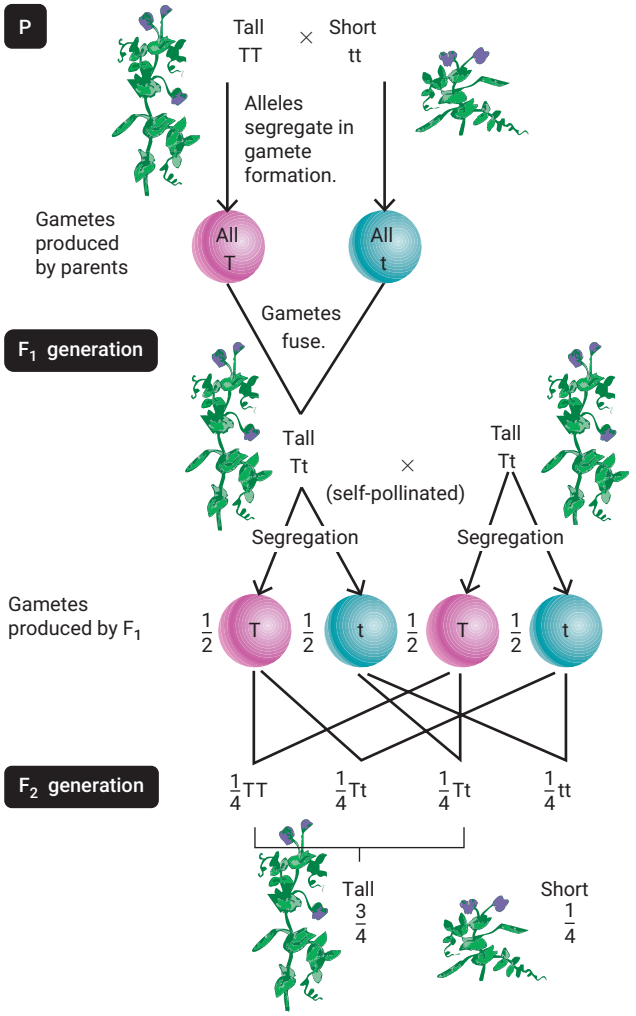


FIGURE 10.1.2 A cross between tall and short pea plants, both purebred, illustrating expected proportions of two generations of offspring

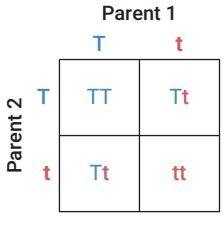


FIGURE 10.1.3 Punnett squares make predicting offspring genotypes and phenotypes relatively straightforward.

To set up a Punnett square, choose one parent for the columns. The genotype of this parent can be converted to gametes by recalling the process of meiosis (Figure 10.1.4). Write each gamete type that this parent can make as separate column headings. For homozygous parents, this may only be one column, and more complicated inheritance problems may require four or more columns.

The other parent is used for the rows. Convert the genotype of this parent into gametes and write each gamete type as a row heading. Again, for homozygous parents, this may only be one row, but more complicated inheritance problems may require more.

Once the P generation is set, all possible gamete combinations can be shown by filling in the square. Write the heading of each column in each cell down the column. Write the heading of each row in each cell along the row. A properly populated Punnett square should have each cell filled with the alleles from its corresponding column and row headings.

The completed Punnett square can then be used to calculate the expected proportion or frequency of each genotype and phenotype in the offspring.

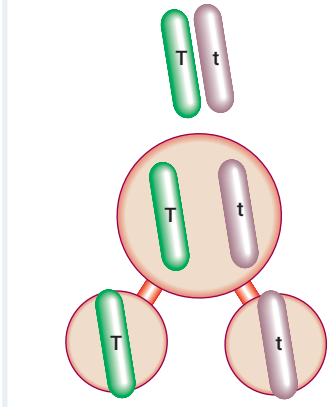


FIGURE 10.1.4 During meiosis, the parent genotype splits into separate gametes that have equal chance of being passed to offspring.

WORKED EXAMPLE 10.1.1

A purebred pea plant with green pea pods is crossed with a purebred, yellow-podded plant. All F_1 offspring produce green pods. Two of the F_1 generation plants are crossed.

Use a Punnett square to predict all possible genotypes, and thus the proportion of F_2 offspring that have green pea pods.

ANSWER

1 Identify the dominant allele and the recessive allele by assigning them a capital or lower-case letter.
All F_1 generation plants produced green pods from a green parent and a yellow parent, so green pods must be dominant to yellow. Therefore, the alleles are G = green, g = yellow.

2 State the genotypes of each parent using the allocated letters for the alleles from step 1.
The parents are both purebred, so the genotype for the green parent is GG, with only G gametes, and the genotype for the yellow parent is gg, with only g gametes.

3 Draw the Punnett square for the P generation to cross to determine the potential genotype(s) of the offspring (F_1).
The Punnett square for the P generation cross to determine the F_1 genotypes:

	Green parent G
Yellow parent g	Gg

4 State the genotype(s) and phenotype(s) of the offspring (F_1) using the results from the Punnett square in step 3.
All F_1 offspring will be genotype Gg, heterozygous green phenotype, with half G gametes and half g gametes.

5 Draw the Punnett square for two of the F_1 plants to cross, to determine the potential genotype(s) of the offspring (F_2).

		F_1 heterozygous green parent	
		G	**g**
F_1 heterozygous green parent	**G**	GG	Gg
	g	Gg	gg

6 State the genotype(s) and phenotype(s) of the offspring (F_2), using the results from the Punnett square in step 5. Then state the expected phenotypic and genotypic ratios.
The F_2 genotypes will be $\frac{1}{4}$ GG, $\frac{2}{4}$ (or $\frac{1}{2}$) Gg and $\frac{1}{4}$ gg. This means that $\frac{3}{4}$ of the F_2 generation will have green pea pods.
Genotype: 1 GG : 2 Gg : 1 gg
Phenotype: 3 green : 1 yellow

WORKED EXAMPLE 10.1.2

Consider a cross between two tall, purple-flowered pea plants, that are both heterozygous for both traits. Use a Punnett square to predict all possible genotypes and the proportion of offspring that will have each phenotype. From this, determine the Mendelian ratio for a dihybrid cross. (Note: Non-purple flowers are white.)

ANSWER

1 Identify the dominant alleles and the recessive alleles by assigning them capital or lower-case letters.
If both parent plants are heterozygous for both traits, they will express the dominant form of both traits.

Therefore, tall (T) is dominant to short (t) and purple flowers (F) is dominant to white flowers (f). (We use F/f for flower colour rather than the less distinguishable P/p.)

2 **State the genotype of each parent using the allocated letters.**
Both parents will have the genotype Tt for height and Ff for flower colour. This means each parent's genotype will be TtFf.

3 **Determine the gametes produced by each parent.**
The gametes produced by each parent plant will have one allele representing height (either T or t) and one for flower colour (F or f), so they can make four possible gametes TF, Tf, tF and tf.

4 **Draw the Punnett square for the P generation to cross, to determine the potential genotypes of the offspring (F_1).**

		Heterozygous tall, purple parent			
		TF	**Tf**	**tF**	**tf**
Heterozygous tall, purple parent	**TF**	TT FF	TT Ff	Tt FF	Tt Ff
	Tf	TT Ff	TT ff	Tt Ff	Tt ff
	tF	Tt FF	Tt Ff	tt FF	tt Ff
	tf	Tt Ff	Tt ff	tt Ff	tt ff

5 **State the phenotypes of the offspring (F_1), using the results from the Punnett square in step 4.**
All F_1 offspring with at least one T allele and at least one F allele will be tall with purple flowers. Nine of the 16 possible combinations meet this criteria.
All F_1 offspring with at least one T allele and no F allele will be tall with white flowers. Three of the 16 possible combinations meet this criteria.
All F_1 offspring with no T allele and at least one F allele will be short with purple flowers. Three of the 16 possible combinations meet this criteria.
All F_1 offspring with no T allele and no F allele will be short with white flowers. Only one of the 16 possible combinations meet this criteria.

6 **Determine the expected phenotypic ratios.**
The Mendelian ratio for a dihybrid cross is 9:3:3:1, where nine exhibit both dominant phenotypes, three exhibit one dominant phenotype, three exhibit the other dominant phenotype and one exhibits neither.

Pedigrees

Punnett squares are very useful for predicting allele inheritance between a single set of parents and their offspring. However, the grid cannot be expanded to track inheritance across multiple generations, as seen in Worked example 10.1.1, where two Punnett squares were required for a simple two-generation problem. For extended inheritance, it is easier to use a pedigree chart **(Figure 10.1.5)**.

In pedigrees, females (22XX) are represented by circles and males (22XY) by squares. The square or circle is shaded black if the individual has the phenotype and white if the phenotype is absent. Any genotype information is recorded beneath a shape, and a question mark (?) is used when an allele is unknown. Individuals are arranged so that each generation is on its own line, denoted with a Roman numeral. Individuals within a generation are numbered from left to right, so an individual in the second generation, third from the left is called II-3.

Weblinks
How to construct Punnett squares
Interactive pigeon genetics

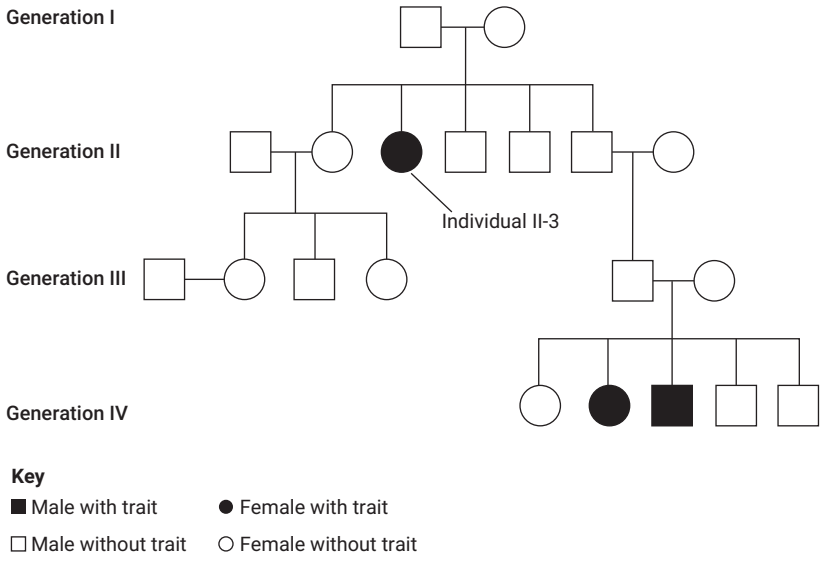


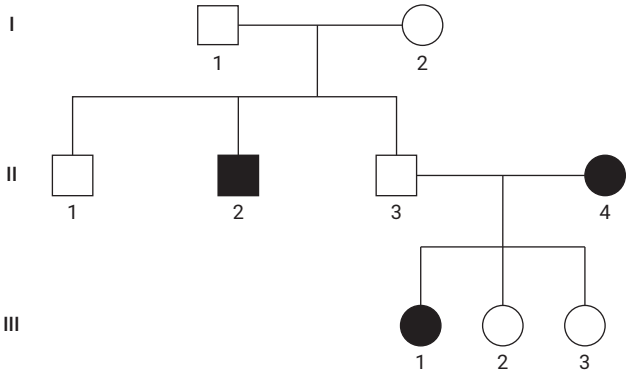
FIGURE 10.1.5 Pedigrees allow geneticists to track the flow of alleles through multiple generations.

One of the key strengths of pedigrees is their ability to show biological relationships. Reproductive pairings, where two individuals have produced children together, are connected by a horizontal line. The vertical line from this pairing represents the production of offspring. If there are multiple offspring, a horizontal bracket is used to hang them (in birth order) off their parent line.

The patterns of inheritance in a pedigree can provide clues to the phenotype being tracked. If the phenotype 'skips a generation', as it does in Figure 10.1.5, the allele that causes this phenotype must have been hidden or suppressed in the unaffected parents; therefore, the tracked phenotype is recessive. Beginning a pedigree analysis with the recessive individuals (whether they are the tracked phenotype or not) can save a lot of time.

WORKED EXAMPLE 10.1.3

Consider the following human pedigree. Explain whether the condition being tracked is dominant or recessive and determine the genotypes of all individuals.

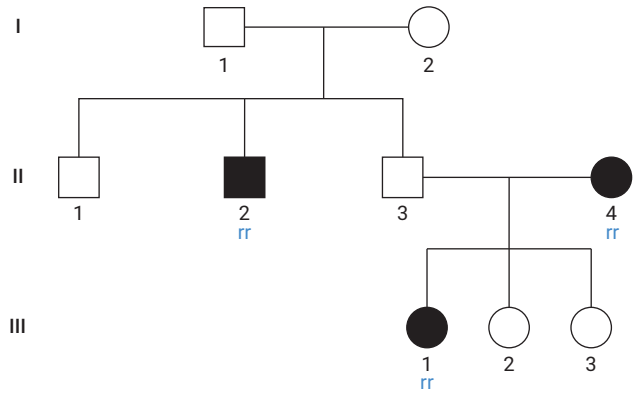


ANSWER

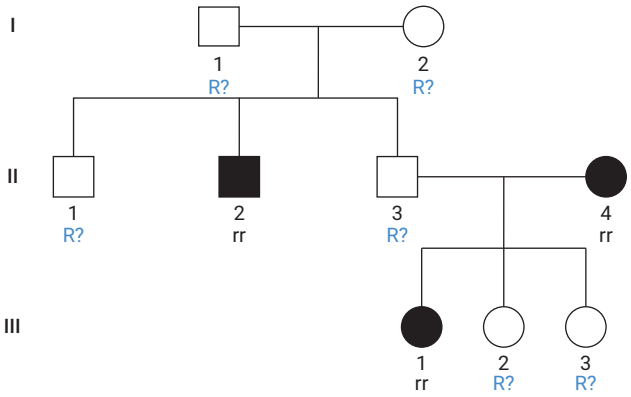
1 **Determine the first occurrence of the disease.**
The first instance of this condition is in Individual II-2. Neither of their parents is affected.

2 **Identify the possible genetic nature of the disease.**
This indicates that the condition being tracked is recessive. Let r = recessive allele and R = dominant allele.

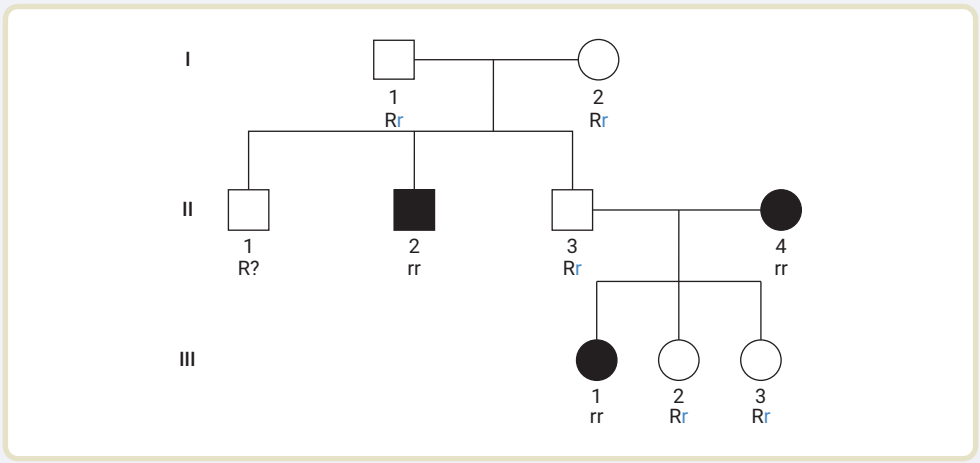
3 **Determine the genotype of affected individuals.**
Therefore, all affected individuals (II-2, II-4 and III-1) are genotype rr because a dominant allele would prevent the recessive condition from being expressed.



All other individuals are unaffected, so they have at least one dominant allele (R?).



Individuals III-2 and III-3 have one parent who can only provide r alleles; therefore, they both have an r allele (Rr).
Individuals I-1 and I-2 have produced a child with two r alleles, so they each must have an r allele to give (Rr).
Individual II-3 has produced a child with two r alleles, so they must have one to give (Rr).



There is insufficient information to determine whether Individual II-1 has received both R alleles from their parents (RR) or one R allele and one r allele (Rr). Therefore, they remain as R?.

Weblink
Pedigrees review

LEARNING CHECK 10.1

DESCRIBING

1 **Define** the P, F_1 and F_2 generations.
2 **Describe** how the genotype of an individual affects their phenotype.
3 **Describe** autosomal dominant inheritance.
4 State the Mendelian ratio of phenotypes in the offspring of a heterozygous cross.

APPLYING

5 Complete the table for the three possible genotypes of tall (T) and short (t) alleles of the height trait in Mendel's peas.

	Possible genotype	Homozygous or heterozygous	Dominant or recessive phenotype
1			
2			
3			

ANALYSING

6 In Figure 10.1.6, the phenotype being tracked is known to be dominant. This means that both homozygous dominant and heterozygous individuals will express the phenotype. **Determine** the genotypes of all individuals.

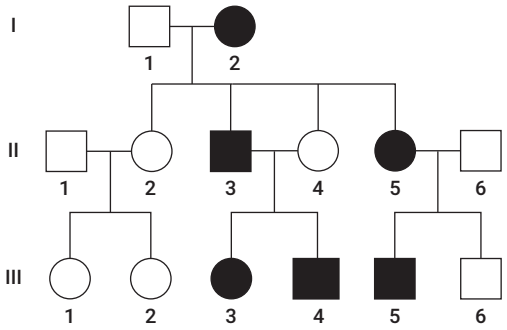


FIGURE 10.1.6 A human pedigree

INTERPRETING

7 Carnation petal colour is determined by a single gene with two alleles: one for white, one for red. Use Punnett squares and choose appropriate symbols to **determine** the genotype and phenotype ratios you would expect in the F_1 and F_2 generations of two homozygous parents – one white, one red – if white is dominant to red.

8 In some flowers, the two alleles that determine colour are equally dominant. This means that the allele for red colouring is not completely dominant over the allele for white colouring. **Predict** the colour of heterozygous flowers in species that are subject to incomplete dominance.

9 Some yeast strains can have either red or cream-coloured cells. If a purebred red yeast and a purebred cream yeast are crossed, resulting offspring are cream. Assign suitable cell colour alleles and use a Punnett square to **predict** the outcome of the cross between members of the F_1 generation.

10.2 Non-Mendelian inheritance

It turned out that Mendel was lucky. The traits that he chose to study are all single-gene-controlled autosomal traits; that is, each trait is fully determined by combining two contrasting alleles at a single gene locus on an autosomal (non-sex) chromosome pair. This is the simplest and most straightforward inheritance condition.

However, traits can also be determined by more than two alleles (multiple-allele inheritance), by more than one gene locus (polygenic inheritance) and by genes on the sex chromosomes (sex-linked inheritance). All of these conditions complicate the pattern of inheritance and Mendelian ratios no longer apply.

Sex-linked inheritance

As described in Chapter 9, in humans, females have 22 pairs of autosomes and two X chromosomes and produce gametes containing 22 single autosomes and one X chromosome. Males have 22 pairs of autosomes, one X chromosome and one Y chromosome and half of the gametes they produce contain 22 autosomes and an X chromosome and the other half contain 22 autosomes and a Y chromosome. The X and Y chromosomes are not homologous; the sequence of genes on the X chromosome is completely different from the sequence of genes

on the Y chromosome. In other species, information about sex may be carried on different chromosomes, but the key is that sex-linked inheritance requires a non-homologous pairing of whichever chromosomes designate biological sex.

Genes on these chromosomes do not show Mendelian patterns of inheritance. In humans, the X chromosome is one of the largest chromosomes and contains many genes vital for basic life processes; embryos without an X chromosome spontaneously abort. Females inherit two X chromosomes, which are homologous to each other and provide two alleles for each gene. However, males inherit only one X chromosome, so they only inherit one allele for each X-linked gene. This makes them more vulnerable to expressing recessive alleles on the X chromosome, which are called **sex-linked** because the sex of an individual makes a difference to their inheritance. The Y chromosome, in contrast, is extremely small and contains only a few genes that are only inherited by males.

sex-linked a gene located on a sex chromosome; in humans this is usually the X chromosome

Weblinks
Sex-linked inheritance
Inheritance 1

For sex-linked conditions, the notation must treat the X and Y chromosomes differently. Although the alleles are still denoted by capital (A) and lower-case (a) letters, they are written as superscripts to an X (e.g. X^A and X^a) to show that the gene is on the X chromosome. The Y chromosome, which does not carry the gene, is written with either no superscript (Y) or a superscript minus sign (Y^-).

Colour-blindness is a human sex-linked condition. The gene for colour vision is located on the X chromosome and the able allele is dominant (X^A), whereas the colour-blind allele is recessive (X^a). For females, possible combinations are X^AX^A, X^AX^a and X^aX^a in a Mendelian ratio of 1:2:1, which corresponds to a ratio of 3:1 for being able to see colour. However, for males, there are only two possible combinations, X^AY^- and X^aY^-, which is a non-Mendelian ratio of 1:1 for being able to see colour.

Punnett squares and pedigrees for sex-linked conditions are similar to those used for Mendelian conditions. However, extra care must be taken to consider the gametes produced by each parent. In sex-linked inheritance, a male cannot pass an affected X chromosome to male offspring because, to be male, they inherit his Y chromosome. However, female offspring will always receive the affected X chromosome from him.

In recessive conditions, female offspring will only show the phenotype if they inherit affected X chromosomes from both of their parents, but in dominant conditions, a single affected X chromosome is sufficient to express the phenotype. As with autosomal phenotypes, some generations may not have any members showing a recessive sex-linked phenotype, whereas dominant sex-linked phenotypes will always be expressed in each generation.

WORKED EXAMPLE 10.2.1

In fruit flies, if a white-eyed male is crossed with a red-eyed female in the P generation, all the F_1 flies have red eyes. If males and females of this F_1 generation are crossed, all of the F_2 females and half of the F_2 males have red eyes. Determine the genotypes of the F_2 generation.

ANSWER

1 **Determine the genotype of affected individuals.**
All of the F_1 flies have red eyes, which indicates that red (R) is dominant to white (r).

2 **Use the evidence to determine the genotype of individuals of the F_1 generation.**
The male and female flies of the F_2 generation inherit the trait differently, indicating that it is sex-linked (X^R, X^r and Y^-).

The male parent is white-eyed, meaning his genotype is X^rY^-. He must give X^r to his F_1 daughters, but since they are still all red eyed, they must all inherit X^R from their female parent. The male parent must give Y^- to his F_1 sons and they are also all red eyed, so they must also all inherit X^R from their female parent. This makes the F_1 female flies X^RX^r and the F_1 male flies X^RY^-.

3 Draw a Punnett square to help determine the F_2 genotypes.

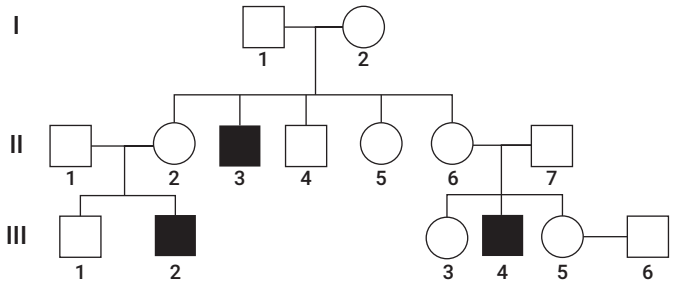
The Punnett square for the F_1 cross to determine F_2 genotypes:

F_1 male parent \ F_1 female parent	X^R	X^r
X^R	X^RX^R	X^RX^r
Y^-	X^RY^-	X^rY^-

All of the F_2 female flies are red eyed, with half homozygous (X^RX^R) and half heterozygous (X^RX^r).
Half of the F_2 male flies are red eyed (X^RY^-), and half are white eyed (X^rY^-).

WORKED EXAMPLE 10.2.2

Consider the following human pedigree. Explain whether the condition being tracked is dominant or recessive, autosomal or sex-linked, and determine the genotypes of all individuals.

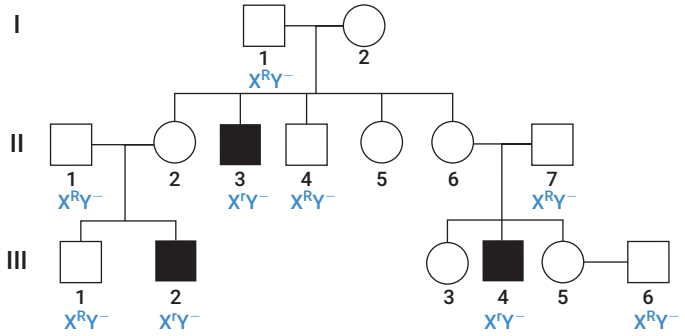


ANSWER

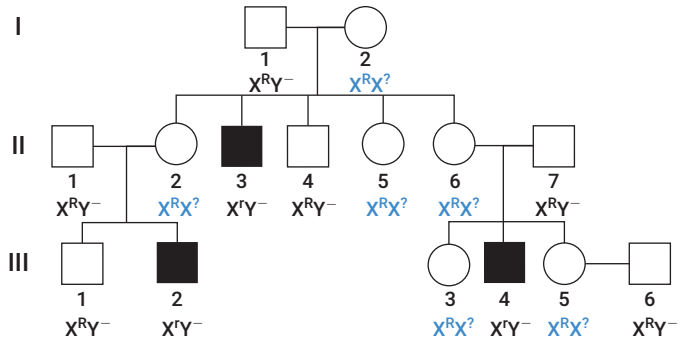
1 Determine the first occurrence of the disease.
The first instance of this condition is in Individual II-3. Neither of their parents is affected.

2 Identify the possible genetic nature of the disease.
This indicates that the condition being tracked is recessive. Let r = recessive allele and R = dominant allele.

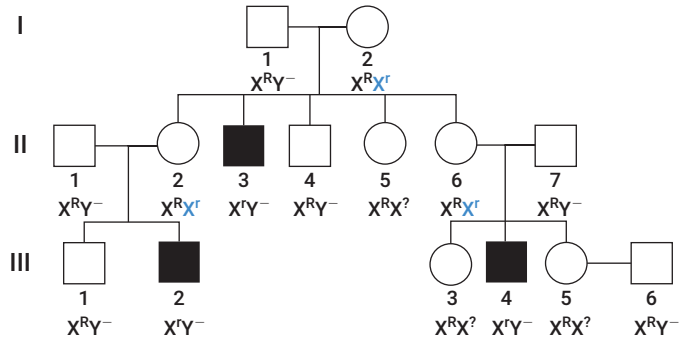
3 Determine the genotype of all individuals.
All affected individuals are male, suggesting that this trait is inherited differently in males and females. The trait is likely to be sex-linked, with alleles X^R, X^r and Y^-.
Therefore, all males in the pedigree have a Y^-.
Therefore, all affected individuals (II-3, III-2 and III-4) are genotype X^rY^- because they are males with a recessive condition. All non-affected males (I-1, II-1, II-4, II-7, III-1 and III-6) are genotype X^RY^- because they do not carry the recessive allele.



All females in the pedigree are unaffected, so they have at least one dominant allele ($X^RX^?$).



Individuals I-2, II-2 and II-6 each had a son with the condition, who must have received an X^r from them (their son's Y^- was received from their father); therefore, they are X^RX^r.



There is insufficient information to determine whether Individuals II-5, III-3 and III-5 received an X^R or X^r from their mother (they all have one X^R from their father; therefore, they remain as $X^RX^?$.

Multiple-allele inheritance

In some cases, a trait can be determined by a single gene that has more than two possible allele variants. Examples of this are coat colour in rabbits (brown, grey, black and albino) and blood type in humans. Multiple-allele inheritance produces **discontinuous variation**, a limited range of distinct phenotypes for a trait. To denote that all of the variants are of a single gene, a capital I is used as a base, with the various allele variants given in superscript, and capital and lower-case letters still used to denote dominance (e.g. I^A, I^B, i^c, i^d). Regardless of the number of allele variants, each individual can still only carry two of them.

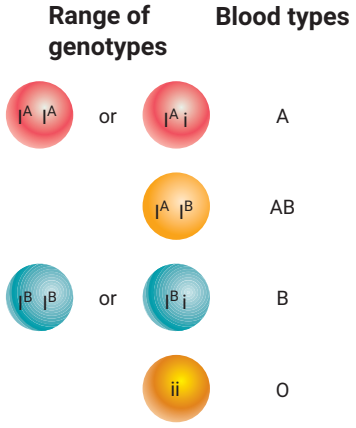


FIGURE 10.2.1 Different blood types in humans are due to different combinations of a multiple-allele gene. Blood type O does not have any markers on the red blood cells.

discontinuous variation the variation in a trait caused by two or more allele variants for a single gene; a narrow set of distinct phenotypes

Humans have three possible allele variants for the markers on the outside of red blood cells. I^A is a dominant allele that produces A-type markers. I^B is also a dominant allele that produces B-type markers. These two alleles are considered **codominant**, because if both are present, both are expressed in equal measure. The third allele is denoted by a lower-case i with no superscript and it produces no markers. This allele is recessive because an individual with genotype $I^A i$ produces A-type markers on all of their red blood cells, rather than half A-type and half with no markers. Figure 10.2.1 shows how different combinations of these alleles create the four human blood groups, A, B, AB and O.

codominant two or more alleles are equally expressed in the phenotype; produces blended phenotypes

WORKED EXAMPLE 10.2.3

Parents, both of whom have A-type blood, had a baby with O-type blood. Explain, using a Punnett square, how this could happen, and what the expected frequency of O-type offspring would be.

ANSWER

1 **Determine the potential genotype(s) of both parents.**
Since both parents are A-type, they must have at least one A allele and no B allele (I^A?). The unknown allele could be another I^A or the recessive i.

2 **Use the baby's blood type to determine the genotype of both parents.**
The baby is O-type so must have two recessive alleles (ii), receiving one from each parent. If the baby received an i allele from each parent, the parents must both be genotype $I^A i$.

3 **Draw a Punnett square to determine the expected frequency.**
The Punnett square for the cross of two heterozygous A-type ($I^A i$) parents to determine the expected frequency of O-type offspring:

		Parent 1	
		I^A	i
Parent 2	I^A	$I^A I^A$	$I^A i$
	i	$I^A i$	ii

The probability of O-type (ii) offspring is $\frac{1}{4}$.

polygenic inheritance the transmission of characteristics controlled by two or more genes

continuous variation the variation in a trait caused by two or more genes; the range of different phenotypes is wide with small, smooth gradations between differences

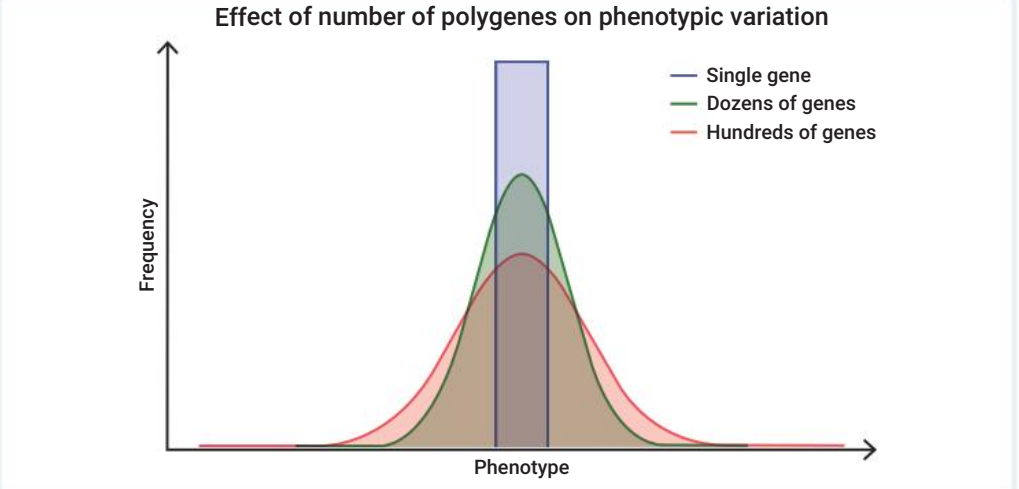
polygenes genes for which different alleles have a small additive effect on a phenotype; contribute to continuous variation in polygenic phenotypes

Polygenic inheritance

Genetics is simplest to understand when a trait is controlled by the alleles of one gene. However, most human physical characteristics, such as eye, skin and hair colour, are controlled by the alleles of two or more genes that interact with one another but are inherited independently. A trait controlled by more than one gene is known as polygenic, and its transmission is called **polygenic inheritance**.

One example of polygenic inheritance in humans is height. Unlike pea plants, which are either tall or short, humans show a broad range of heights, although a larger number of people have heights clustered around the mid-height, with fewer at the low and high height extremes.

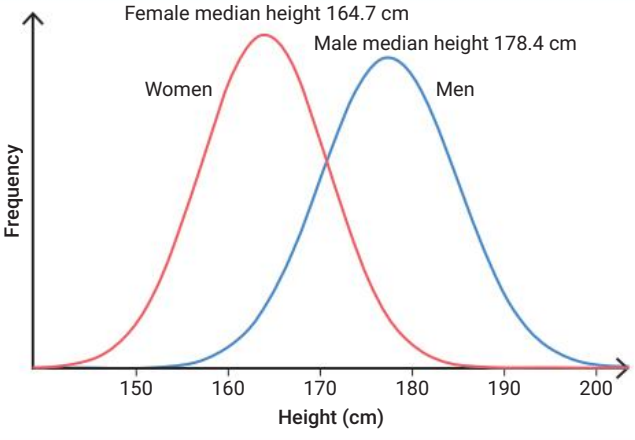
The smooth gradation across the range of heights in a population is called **continuous variation**. The more genes involved in the expression of a trait, the more continuous the variation is (Figure 10.2.2). Human height is controlled by at least 400 **polygenes** and is affected further by environmental factors such as nutrition, so the expression of height in a population is essentially a smooth curve (Figure 10.2.3).



Bioninja. https://old-ib.bioninja.com.au/higher-level/topic-10-genetics-and-evolu/102-inheritance/polygenic-traits.html

FIGURE 10.2.2 The number of polygenes involved in a trait influence the range of phenotypes expressed. The more genes involved, the more continuous the variation and the smoother the curve.

Worksheet
Inheritance 2



Max Roser, Cameron Appel and Hannah Ritchie (2021) - "Human Height" Published online at OurWorldinData.org. Retrieved from: 'https://ourworldindata.org/human-height' [Online Resource]

FIGURE 10.2.3 Global distribution of human heights

LEARNING CHECK 10.2

DESCRIBING

1 **Describe** the inheritance patterns that indicate a sex-linked trait.

2 **Describe** the inheritance patterns that indicate a multiple-allele trait.

3 **Describe** the inheritance patterns that indicate a polygenic trait.

APPLYING

4 **Explain** why superscripts are used in non-Mendelian inheritance.

5 **Distinguish** between the inheritance conditions that lead to continuous and discontinuous variation.

6 **Identify** the inheritance pattern in the pedigree in Figure 10.2.4 and determine the genotypes of all individuals.

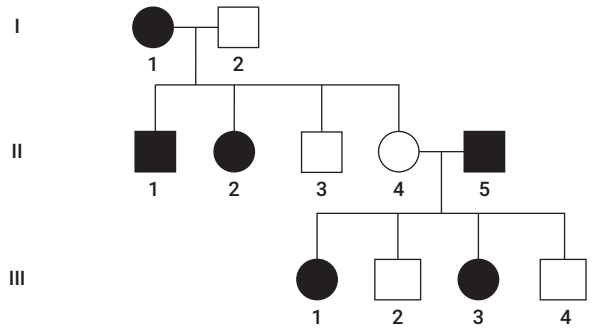


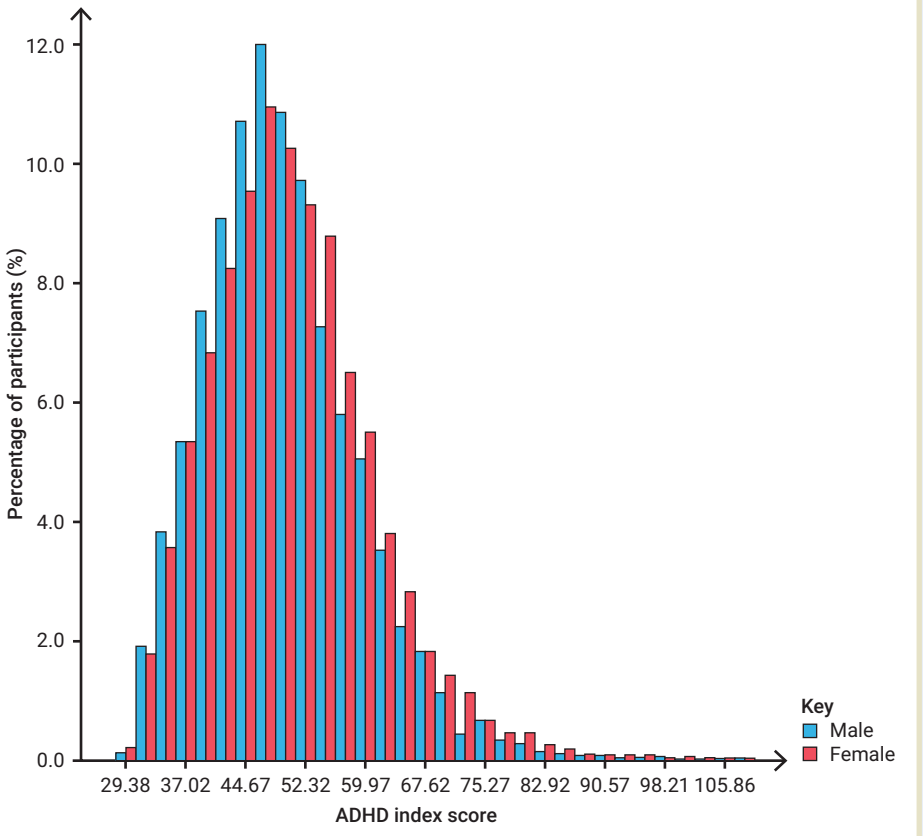
FIGURE 10.2.4 A human pedigree

7 Figure 10.2.5 shows the index scores for attention deficit hyperactivity disorder (ADHD) for more than 12 000 individuals.

a **Explain** why polygenic inheritance is most likely for ADHD traits.

b Suggest why there is a long tail of scores at the top end, but not near the bottom end.

Weblink
Non-Mendelian inheritance



Boomsma DI, Saviouk V, Hottenga J-J, Distel MA, de Moor MHM, Vink JM, et al. (2010) 'Genetic Epidemiology of Attention Deficit Hyperactivity Disorder (ADHD Index) in Adults'. *PLoS ONE* 5(5): e10621. https://doi.org/10.1371/journal.pone.0010621.

FIGURE 10.2.5 The distribution of ADHD index scores for a large sample of individuals

8 Ichthyosis is an inherited condition characterised by scaly skin. The condition affects about one in 6000 males, but female cases are almost unknown.

- **a** **Determine** how ichthyosis is inherited.
- **b** **Identify** the parent from which an affected person would inherit their affected allele(s).
- **c** **Calculate** the probability of an affected male passing the condition to his son.

ANALYSING

9 The capacity to tolerate high salt concentrations varies between different individuals of a population of salmonid fish.

Sketch a curve to approximate the shape of a graph of salinity tolerance versus number of fish in the population.

INTERPRETING

10 An individual with heterozygous A-type blood and an individual with heterozygous B-type blood had offspring. **Determine** the genotypes and phenotypes of the offspring.

11 **Determine** the probability that a person with AB-type blood will have an O-type child.

12 Figure 10.2.6 shows a sample of corn (*Zea mays*). The colours are produced by yellow carotenoid pigments, and red and purple anthocyanine pigments. **Justify** whether corn colour is subject to multiple-allele or polygenic inheritance.

Christian Vinces/Shutterstock.com

FIGURE 10.2.6 Corn cobs display a large range of colour phenotypes.

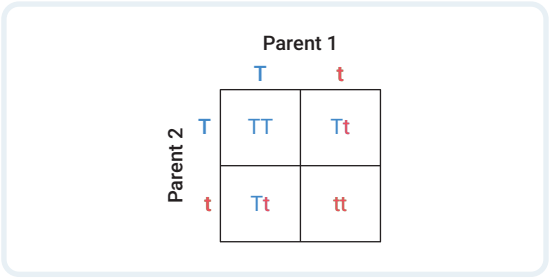
CHAPTER SUMMARY

Genetic inheritance

- Mendelian inheritance involves traits controlled by a single gene on a non-sex chromosome, with two contrasting alleles.
- In sex-linked inheritance, traits are controlled by a single gene on a sex chromosome (usually the X chromosome) with two contrasting alleles.
- Multiple-allele inheritance occurs when traits are controlled by a single gene on a non-sex chromosome that has more than two possible alleles.
- Polygenic inheritance involves traits controlled by multiple genes on different chromosomes, each with two or more alleles.
- An individual's genotype is the specific combination of alleles they have (e.g. TT, Tt or tt).
- The phenotype is the physical expression of a trait in an individual (e.g. tall or short).
- An individual is homozygous when both alleles are the same, either both dominant (TT) or both recessive (tt).
- An individual is heterozygous when they have two different alleles; the dominant allele is written first (e.g. Tt).
- The P generation refers to the biological parents of a particular set of offspring.
- The F_1 generation is the first generation of offspring produced from a cross of the P (parent) generation.
- The F_2 generation is the offspring produced from a cross within the F_1 generation.

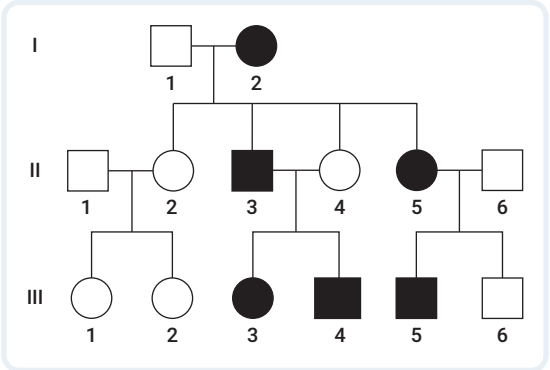
Punnett squares

- Punnett squares are a tool to help predict the genotypes (and phenotypes) of offspring.



Pedigrees

- Pedigrees help track the inheritance of phenotypes.
- Females are represented by circles and males by squares.
- Individuals with the phenotype have their circles/squares shaded in black, while those who do not have the phenotype are white.



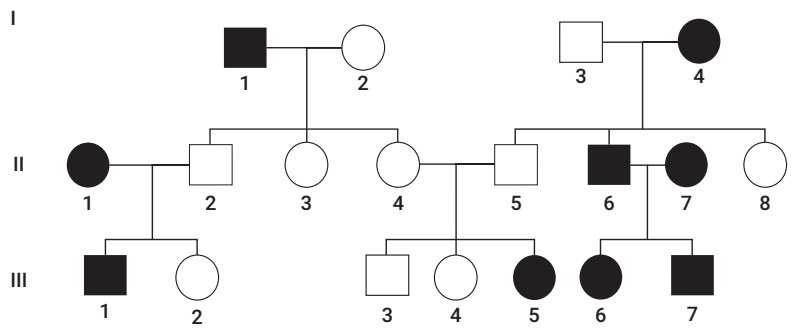
CHAPTER EXAM

MULTIPLE CHOICE

1. In the case of a recessive allele:
- **A** two copies of the allele are required for the phenotype to be observed.
- **B** if two copies of the allele are present, the offspring will never survive.
- **C** only one copy of the allele is required for the phenotype to be observed.
- **D** only the recessive phenotype is ever observed if it is present in the genotype.

2. What is the Mendelian inheritance ratio for the phenotypes in a monohybrid cross with heterozygous parents?
- **A** 2:1
- **B** 3:1
- **C** 1:2:1
- **D** 1:3:1

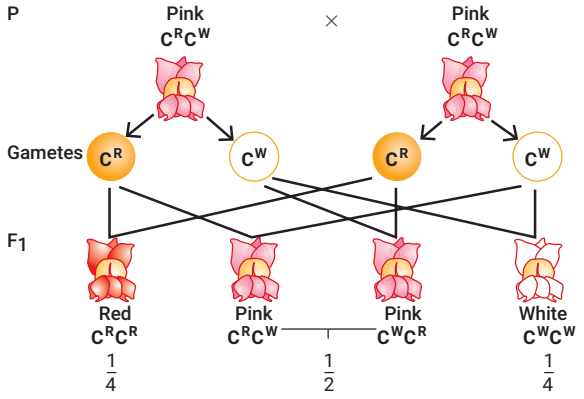
3. What is the genotype of individual II-4 in the following human pedigree?
- **A** AA
- **B** Aa
- **C** X^AX^A
- **D** X^AX^a



4. In sex-linked inheritance, the gene concerned:
- **A** is on the X chromosome.
- **B** is on the Y chromosome.
- **C** only occurs in the female.
- **D** is on one of the sex chromosomes.

5. The following pattern of inheritance in snapdragons is called:

A incomplete dominance inheritance.
B multiple-allele inheritance.
C polygenic inheritance.
D sex-linked inheritance.



6. The type of inheritance that causes continuous variation of a trait across a population is:

A incomplete dominance.
B multiple-allele inheritance.
C polygenic inheritance.
D sex-linked inheritance.

7. The type of inheritance involved in human blood groups is:

A incomplete dominance.
B multiple-allele inheritance.
C polygenic inheritance.
D sex-linked inheritance.

8. A parent (P) generation cross between a homozygous dominant male and a homozygous recessive female produced many first generation (F_1) offspring. A self-cross was conducted between F_1 offspring. What is the probability that the second generation (F_2) offspring will show the dominant trait?

A $\frac{1}{4}$
B $\frac{1}{2}$
C $\frac{3}{4}$
D 100%

9. For a sex-linked condition, a pairing occurs between a dominant male and a homozygous recessive female. What is the probability that their son would show the recessive trait?

A $\frac{1}{4}$
B $\frac{1}{2}$
C $\frac{3}{4}$
D 100%

10. Considering the general human population, which of the following traits is unlikely to be polygenic?

A Height
B Skin tone
C Hair curl
D Blood type

SHORT RESPONSE

11. **Compare** Mendelian inheritance with sex-linked, multiple-allele and polygenic inheritance.

12. Two black guinea pigs produced 29 black and nine white offspring. Assuming this is a form of autosomal inheritance, assign appropriate allele symbols and **justify** the genotypes of the two black guinea pig parents.

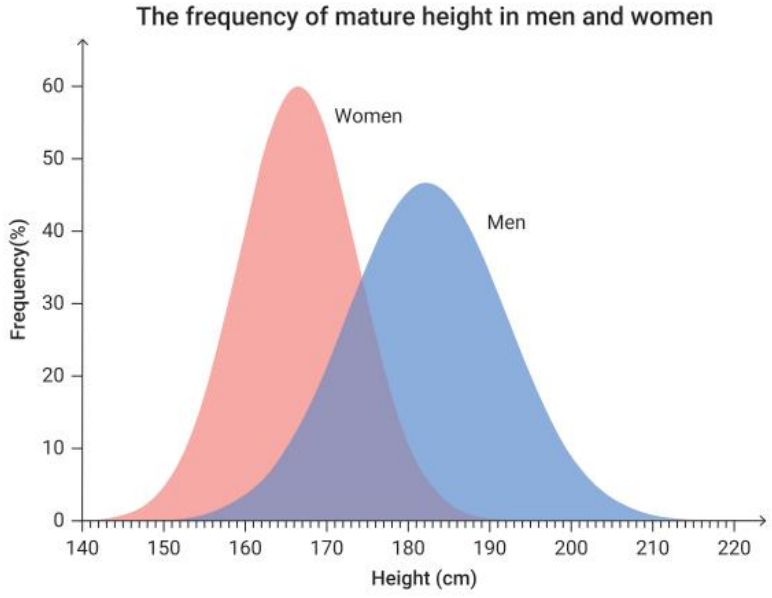
CROSS-CHAPTER QUESTION

13. An error in meiosis caused non-disjunction in one of the parents. **Demonstrate** the effect of this on the genotypes of their potential offspring.

DATA ANALYSIS

Questions 14 and 15 refer to the following information.

The following graph displays the general frequency of height among men and women.



14. **Analyse data**

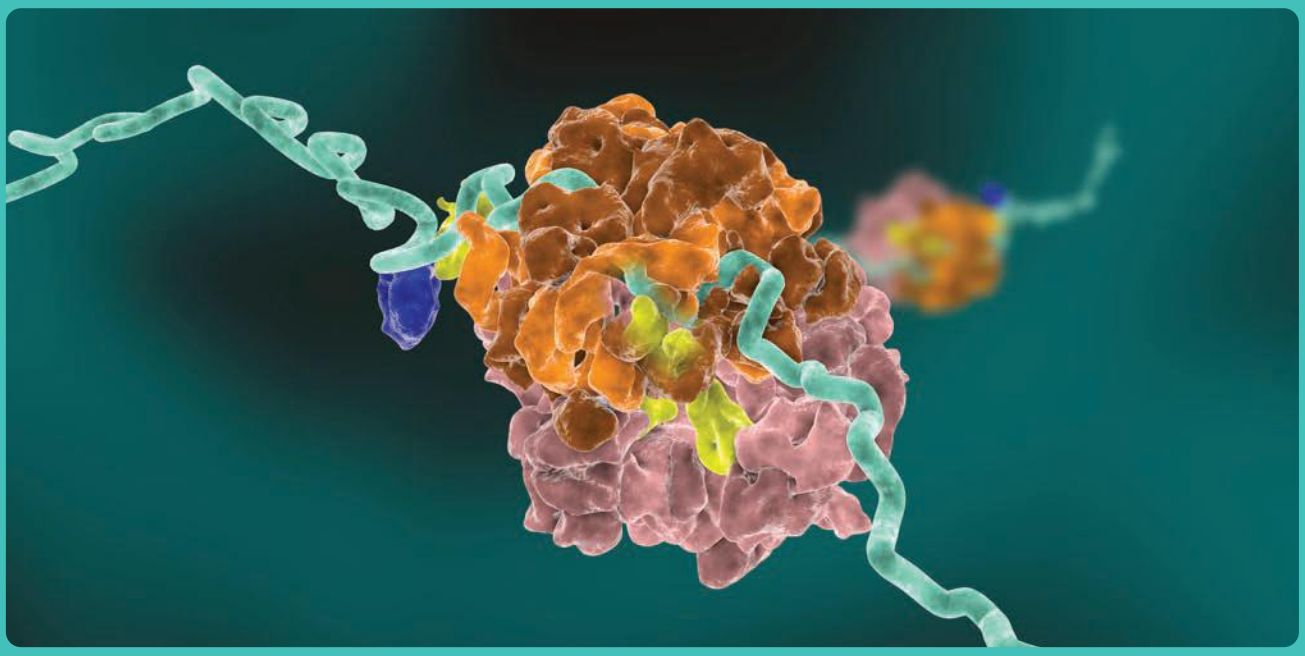
State the median heights of women and men.

15. **Interpret data**

Almost 400 polygenes are involved in the expression of human height. Using information from the graph, **justify** whether all of those polygenes are autosomal.

CHAPTER 11

Protein synthesis and gene expression



Ramon Andrade 3DCIENCIA/Science Photo Library

SYLLABUS DOT POINTS

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.
- Determine the effect of point and frameshift mutations on polypeptides using the genetic code.
- 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.

Introduction

The genes inherited by organisms control the way they grow and develop. Genes are segments of DNA, scattered along chromosomes. Early geneticists did not understand how genetic material affected development without leaving the nucleus. In 1941, genes were shown to trigger the production of proteins (protein synthesis), but it wasn't until 1952 that genes were shown to be made of DNA, which put them right back where they started – how does inherited DNA, in the nucleus, affect protein production in the cytoplasm? In an avalanche of scientific discoveries between 1953 and 1964, the two-phase process of protein synthesis, transcription and translation, was discovered and described, laying the foundation for the boom of genetic understanding that was to follow.

Worksheets

- Transcription
- Translation
- Regulation of gene expression

Nelson MindTap

To access resources above, visit
cengage.com.au/nelsonmindtap

ASSUMED KNOWLEDGE

- ✓ Proteins are biological macromolecules consisting of long strands of amino acids.
- ✓ Cells require many kinds of proteins to function, including enzymes.
- ✓ Sections of DNA, called genes, carry the instructions for producing proteins of all kinds.
- ✓ When DNA is stored for a long time, it is tightly wrapped around nucleosomes, each made of eight histone proteins.
- ✓ Ribosomes are the cell structures that produce proteins and are located either in the cytoplasm or embedded in the rough endoplasmic reticulum.
- ✓ Complementary base pairing occurs between nucleotides on separate strands, both in DNA (C–G and A–T) and RNA (C–G and A–U).
- ✓ Mutations in DNA can be caused by DNA replication errors, mutagenic chemicals in the environment, mutagenic radiation and errors in meiosis.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ identify the two major phases of protein synthesis
- ✓ distinguish between DNA and RNA
- ✓ describe the process of transcription
- ✓ explain the role of transcription in protein synthesis
- ✓ describe the three processes in RNA processing
- ✓ explain the role of the 5′ cap, RNA splicing and poly-A tail in efficient protein synthesis
- ✓ describe the structure and function of the ribosome
- ✓ describe the structure and function of tRNA
- ✓ describe the process of translation
- ✓ explain the role of translation in effective protein synthesis
- ✓ use a codon table to deduce the amino acid sequence produced by a given mRNA sequence
- ✓ explain how substitution errors produce point mutations
- ✓ determine the effects of silent, missense and nonsense point mutations
- ✓ explain how insertion and deletion errors produce frameshift mutations
- ✓ determine the effects of frameshift mutations
- ✓ explain how gene expression is regulated in the long term by heterochromatin and euchromatin
- ✓ explain how gene expression is regulated in the short term by transcription factors
- ✓ explain how the HOX family of transcription factors determines the body plan of bilateral animals.

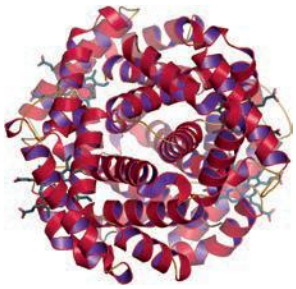
11.1 Protein synthesis

Syllabus link
Protein structure is detailed in Chapter 4 of *Nelson QCE Biology Units 1 & 2*.

Proteins are the essential workers of the cell. Their effectiveness is strongly determined by their structure, but their structure is vulnerable to small changes in the cell's environment (Figure 11.1.1). This means that cells need to be able to synthesise (produce) proteins quickly and easily, to respond to changing conditions in the cell and replace damaged or ineffective proteins as required. Therefore, the process of protein synthesis must be one of the most efficient and well-controlled processes in the cell.

Protein synthesis has two major phases: **transcription** and **translation**. In brief, transcription (from the Latin *script*, meaning 'writing') is where the nuclear DNA sequence is copied into temporary **messenger RNA (mRNA)**, like a student carefully making exact notes from a reference text so they can take the notes out of the library. Both DNA and RNA are the same 'language', written in nucleic acid bases. Translation (from *translate*, meaning 'to change from one language to another') is where the sequence of the mRNA is converted into an equivalent sequence of amino acids, which folds into a protein.

Messenger RNA has specific qualities that make it ideal for its purpose. Compared to DNA, RNA is formed with a less stable ribose-based sugar–phosphate backbone and has the base uracil (U) instead of thymine (T) (Table 11.1.1). By using a less stable messenger, the cell can ensure that each instruction it sends out will be used only for a limited time before it is broken down. This gives the cell strong control over when, where and how much a protein is produced.



Johannes Kaestner/Dreamstime.com

FIGURE 11.1.1 A computer-generated representation of a haemoglobin protein. Without this specific structure, haemoglobin would be unable to take up oxygen, its most important function.

TABLE 11.1.1 Comparison of DNA and RNA molecules

Feature	DNA	RNA
Sugar	Deoxyribose sugar	Ribose sugar
Number of strands	Double-stranded	Single-stranded
Nitrogen bases	Cytosine bonds with guanine. Adenine bonds with thymine.	Cytosine bonds with guanine. Adenine bonds with uracil.
Comparative length	Much longer than RNA	Much shorter than DNA

Transcription

Transcription is the first phase of protein synthesis and occurs in the nucleus. As cells need a constant supply of proteins, transcription is active at all stages of the cell cycle, including during DNA replication.

The first step of transcription (Figure 11.1.2), occurs when DNA in the target gene location is prompted to unwind and unzip, exposing the nucleotide bases of both DNA strands. Despite both strands being available, only the **template strand** is used to synthesise mRNA. The other strand of DNA is called the **non-template strand**, or complementary strand. The template strand varies between genes.

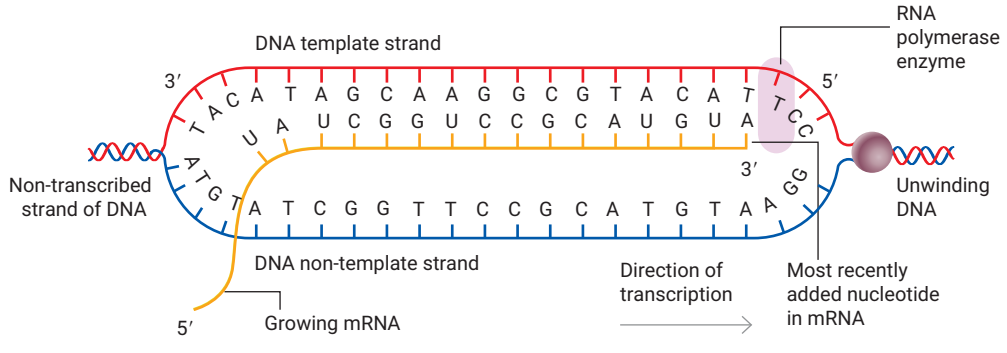


FIGURE 11.1.2 Transcription of mRNA from a DNA template. The double-stranded DNA molecule unwound on the left-hand side of the diagram and RNA polymerase has paired RNA nucleotides with the exposed bases on the template strand, moving across the diagram to the right.

transcription the formation of an mRNA molecule against the template strand of a DNA molecule in the nucleus by complementary nucleotide base pairing

translation the joining of amino acids in a specific order to form a polypeptide, according to the mRNA sequence read by ribosomes

messenger RNA (mRNA) a ribonucleic acid molecule formed in the nucleus during transcription; its nitrogen base sequence is complementary to the DNA template segment; travels to cytoplasm for translation

template strand the DNA strand that serves as a pattern for making complementary polynucleotide

non-template strand the DNA strand complementary to the template strand; does not form the pattern for the synthesis of complementary polynucleotide

Weblink
Translation: DNA to mRNA to protein

promoter region a non-coding section of DNA upstream of a gene that initiates transcription

RNA polymerase the enzyme that produces mRNA from the DNA template strand; major enzyme in transcription

exon a section of DNA or mRNA that codes for a polypeptide

intron a section of DNA or mRNA that does not code for a polypeptide

RNA splicing the process of removing parts of an mRNA strand, particularly any unnecessary introns, to produce mature mRNA

Worksheet
Transcription

Once unzipped, the beginning nucleotides of a gene, called the **promoter region**, are recognised by the enzyme **RNA polymerase**. This enzyme assembles RNA nucleotides by matching complementary bases to the DNA template strand and joining them together as it moves along the length of DNA. Unlike in DNA replication, the use of uracil (U) as a base means that the mRNA strand does not stay bound to the template and the two DNA strands zip up again behind the RNA polymerase. A termination sequence at the end of the gene serves as a stop signal, where RNA polymerase detaches from the template strand and the mRNA is released.

mRNA processing

The mRNA strand at this stage is a direct copy of the DNA template (therefore, its sequence is identical to the non-template strand). However, it is not ready for the second phase of protein synthesis. Genes contain several sections of coding DNA, called **exons**, scattered throughout sections of non-coding DNA, called **introns**. There is also the matter of the promoter region, which was recognised and transcribed by the RNA polymerase at the beginning of the gene. Although introns and promoter regions contain necessary instructions for regulating how, where and when a protein is produced, they do not describe the sequence of amino acids required for the protein. That is reserved for the exons.

RNA splicing is the process of snipping out parts of the mRNA sequence and reattaching only the required exons (Figure 11.1.3). Recent advances in protein biochemistry have revealed that a single gene may actually produce an entire family of proteins through alternative splicing where some proteins require all of the exons of a gene, some only a few. The instructions for which exons are spliced together are contained in the intervening introns and the process is affected by the type of tissue a cell belongs to.

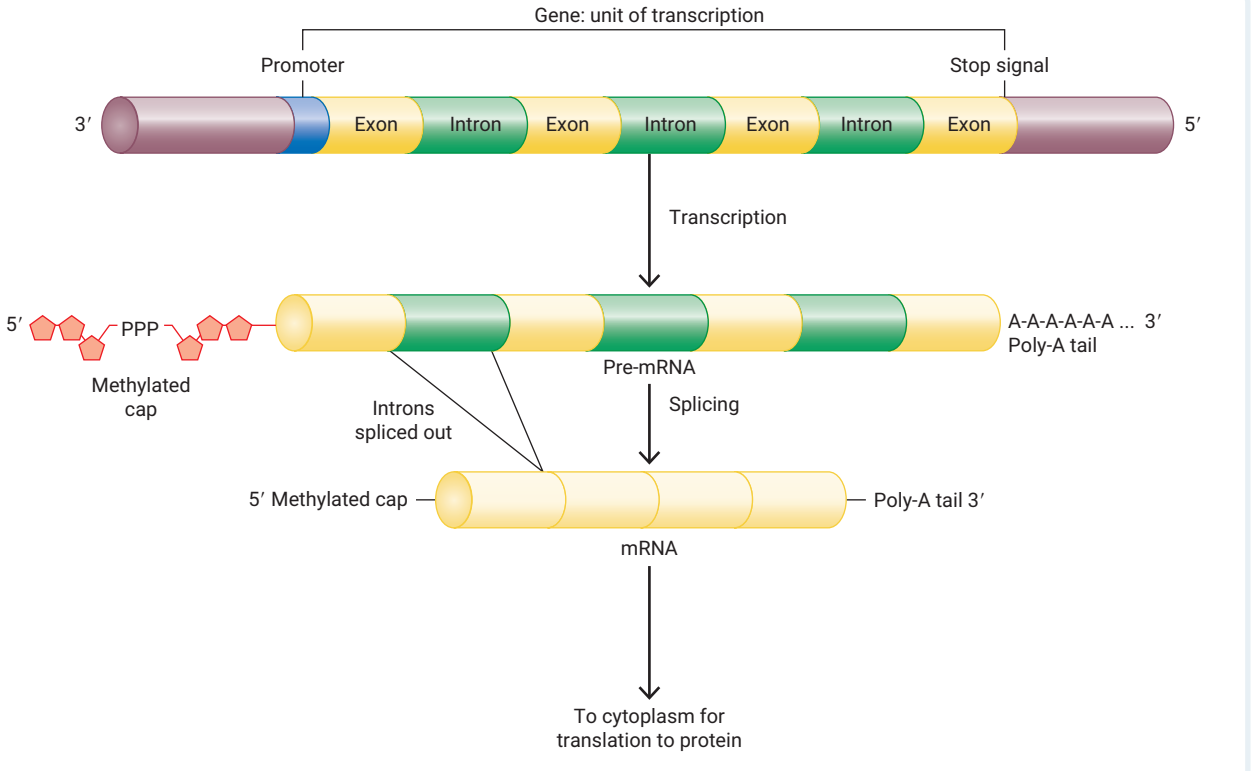


FIGURE 11.1.3 Modification of mRNA molecules occurs in the nucleus of a cell before they are exported to the cytoplasm for translation into polypeptides.

Before it leaves the nucleus, spliced mRNA is modified by the addition of a **5′ cap** and a **poly-A tail** to protect the ends of the mRNA molecule as it moves out of the nucleus. The 5′ cap is a guanine nucleotide attached by three phosphates in an unusual manner. This protects the 5′ end of the mRNA, but also serves to direct the strand out of the nucleus and attract the enzymes required for the next phase. The poly-A tail is a series of adenosine molecules that protect the end of the mRNA strand from degradation. The length of the poly-A tail is determined by the introns of the gene. Longer tails take longer to degrade; therefore, they protect the mature mRNA sequence for a longer period of time.

5′ cap a molecule added to the 5′ end of an mRNA strand to protect it from degradation and direct it out of the nucleus

poly-A tail a section of repeated adenosine bases added to end of an mRNA strand to protect it from degradation

Translation

When mature mRNA moves from the nucleus into the cytoplasm, the 5′ cap attracts a large multi-unit enzyme called a **ribosome**. Ribosomes are protein–RNA hybrid enzymes that are formed in the nucleolus and consist of two subunits: the smaller one has embedded RNA to read the mRNA strand; the larger one has an internal channel for facilitating the production of the **polypeptide** (Figure 11.1.4). The mature mRNA strand enters the small subunit and is held in place for the translation to begin. The ribosome locks onto the mRNA molecule and moves along it to translate its code and link amino acids.

ribosome the organelle where polypeptide synthesis occurs in all cells

polypeptide a polymer of many amino acids linked by peptide bonds; forms a protein or part of a protein

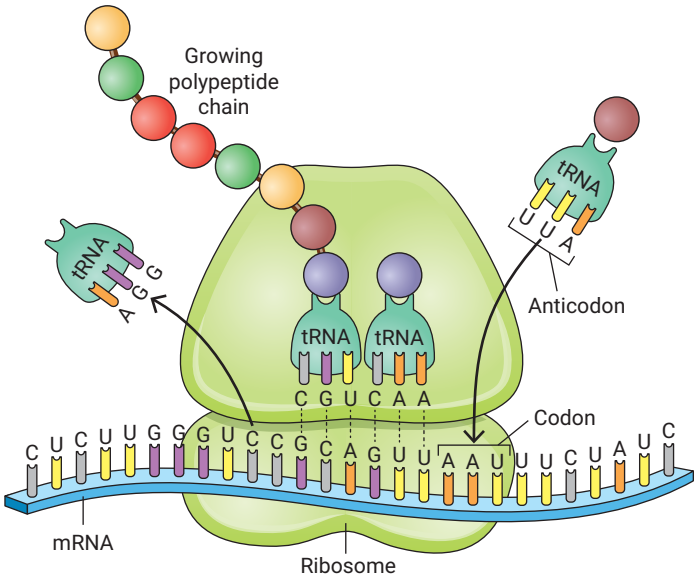


FIGURE 11.1.4 Translation occurs within a ribosome. One subunit of the ribosome reads mRNA codons, and the other handles the tRNA to synthesise the polypeptide chain.

Any process of translation must consider the two 'languages' that are involved. There are four nucleotides (A, G, C, T (U in RNA)), but 20 amino acids. Therefore, more than one nucleotide must be used to code for an amino acid. If two bases are used, 4^2 or 16 amino acids can be coded for, which is still insufficient. Three bases provides 4^3 or 64 combination options. This allows for multiple redundancies in case of minor mutations and for specific combinations that signal the start and stop of a translation sequence. Each combination of three bases is known as a **codon**.

codon a series of three adjacent nucleotide bases in DNA and mRNA that codes for a particular amino acid to be added to a polypeptide or signals start or stop

Translation also requires something that 'speaks both languages'. In this case, the actual translating molecule is **transfer RNA (tRNA)**, another protein–RNA hybrid. A tRNA molecule is a specific RNA strand that has folded back on itself to form a compact three-dimensional structure rather like a T (Figure 11.1.5). At the central bend, three RNA bases are turned

transfer RNA (tRNA) a ribonucleic acid molecule with a specific RNA codon, paired with a particular amino acid from the cytoplasm, to deliver the amino acid to a growing polypeptide chain inside a ribosome

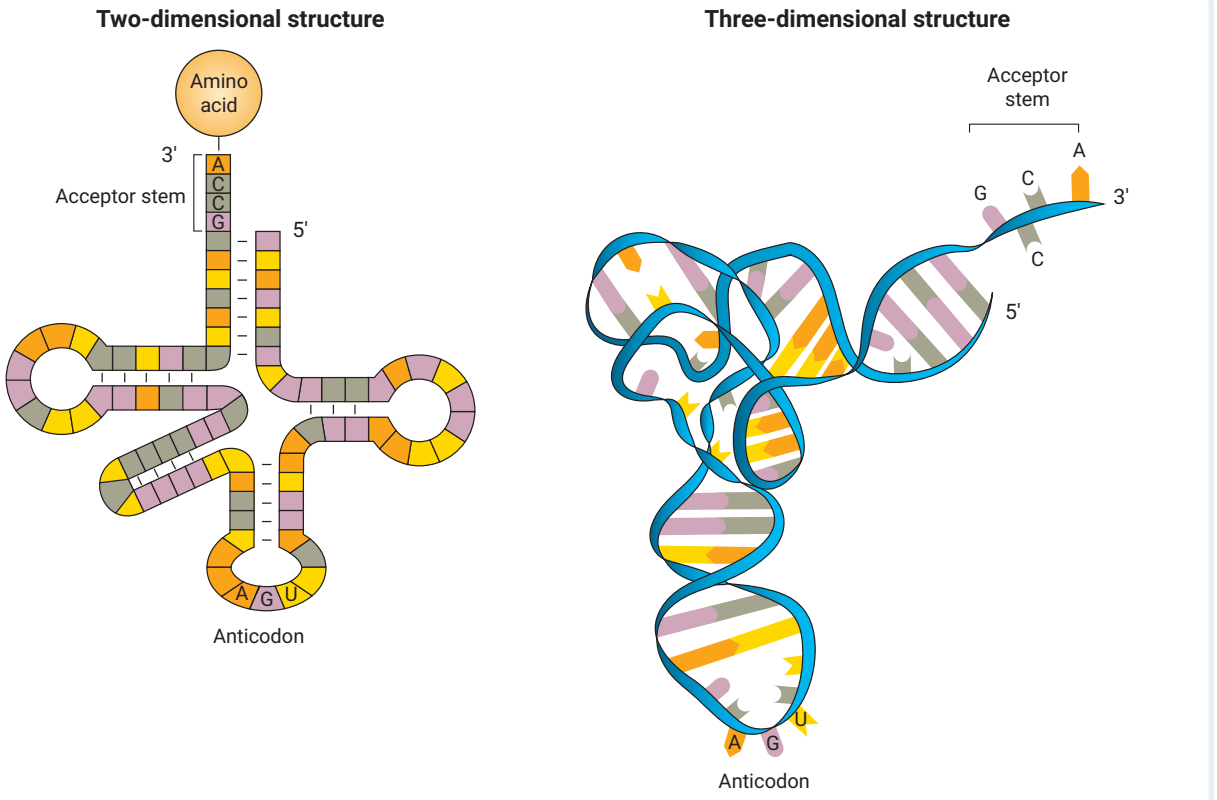


FIGURE 11.1.5 The structure of tRNA. The amino acid that binds to the 3′ end is specific to the anticodon at the central bend.

anticodon a sequence of three nucleotide bases on a tRNA molecule that pairs with complementary bases on an mRNA strand during translation at a ribosome

start codon the first codon of an mRNA strand translated by a ribosome

outwards. These are called the **anticodon** because they are the complementary sequence to the codons on the mRNA. There are 64 different tRNAs, one for each possible codon. At the 3′ end of each tRNA molecule, a short single-stranded region allows its specific amino acid to bind. Some amino acids bind to several tRNAs and some bind to only one.

The small subunit of the ribosome moves the mRNA strand along until it comes to a specific three-base sequence, AUG, which signals the start of translation. Figure 11.1.6 features a codon table, which displays the 64 different mRNA codons and the amino acids that they code for. AUG codes for methionine (Met) and is also the **start codon** for almost all translations.

The large subunit of the ribosome takes tRNA molecules from the cytoplasm and tests their match with the mRNA strand. When the correct tRNA is found, whose anticodon is complementary to the codon on the mRNA strand, the amino acid at the 3′ end of that tRNA is joined to the growing chain of amino acids. Stop codons – UAA, UAG and UGA – do not have an amino acid on their tRNA. This triggers the ribosome to stop translating and release both the polypeptide and the mRNA strand.

All molecules used in protein synthesis are recycled. tRNA molecules that have donated their amino acid to a polypeptide can pick up another one in the cytoplasm. mRNA strands that have been translated are degraded into their component nucleotides to be used for new transcriptions. Proteins that have served their purpose in the cell are digested into their component amino acids for tRNA to pick up.

Weblink
From DNA to protein

Worksheet
Translation

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	phenylalanine
Pro	proline
Ser	serine
Thr	threonine
Trp	tryptophan
Tyr	tyrosine
Val	valine

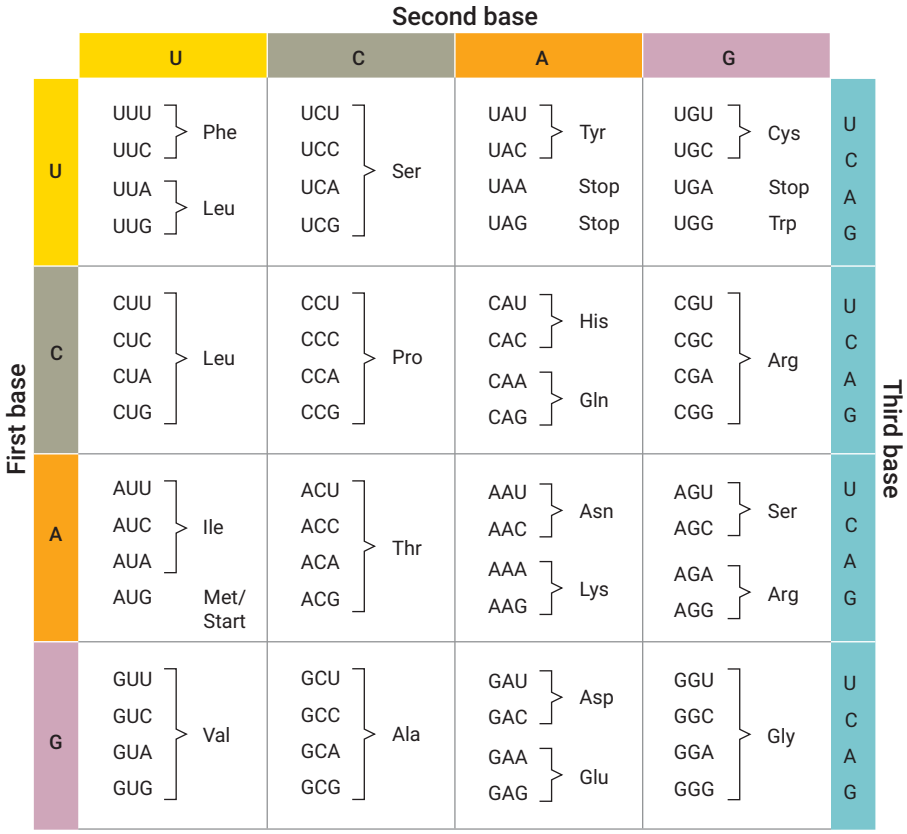


FIGURE 11.1.6 A codon table. The codons correspond to the 20 amino acids (whose abbreviations are shown on the left). The first base of the codon gives the row that it will be located in, the second base gives the column and the third base gives the order of the codons within the cell.

LEARNING CHECK 11.1

DESCRIBING

1 **Describe** mRNA.
2 **Describe** tRNA.
3 State the cell locations for transcription and translation.
4 State the three parts of RNA processing.
5 **Describe** the outcome of alternative splicing in mRNA.

APPLYING

6 **Explain** why transcription and translation are appropriate words for these processes.
7 Referring to the codon table in Figure 11.1.6, **identify** the start and stop codons.
8 A DNA template strand has the base sequence AGC TAT CGA GTC AAA.
   a Write the complementary mRNA sequence.
   b **Identify** the five amino acids that this sequence would code for.
9 **Identify** two advantages that RNA processing gives an organism compared to organisms without it.

ANALYSING

10 Distinguish between:

- **a** transcription and translation
- **b** immature and mature mRNA
- **c** codons and anticodons.

11.2 Errors in protein synthesis

Syllabus link
Chapter 7 introduces different types of mutations in DNA replication

Errors can occur when DNA is copied. Transcription occurs almost continuously and RNA polymerase has very limited error correction mechanisms, making this a frequent source of both point and frameshift errors. Errors that occur during DNA replication are made permanent through cell division, transforming them from an error, which can be corrected, to a mutation, which cannot. Although errors made during protein synthesis are not permanent, generally they cannot be corrected before they are translated into a protein that may or may not function well.

Point mutations

point mutation a mutation that affects a single base-pair position within a gene

substitution when a single nucleotide is swapped for another

Weblink
Point mutations

Point mutations are errors that involve a single nucleotide. They are created by **substitution**, where the correct nucleotide is replaced by a different one. Point mutations can have a range of effects, from no effect at all (silent mutations) to destabilising the protein structure (missense mutations) to completely disabling the gene product (nonsense mutations). The effect of a point mutation depends on which nucleotides are substituted.

For example, an mRNA sequence for a particular protein may include UGG GCU AGA GAG UAU, which, from Figure 11.1.6, would code for Trp–Ala–Arg–Glu–Tyr. These amino acids have a role in maintaining the structure and function of the protein. The second amino acid in this sequence, Ala, has four codons that code for it. This means that the final nucleotide in this codon can be substituted for any other nucleotide and Ala would still be incorporated into the protein as though nothing had happened. This is a silent mutation **(Figure 11.2.1)**.

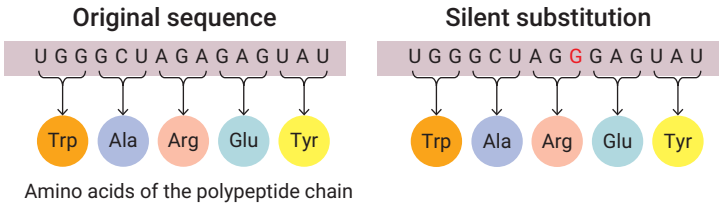


FIGURE 11.2.1 A silent point mutation after a substitution, as shown by the red G. The amino acid sequence in the mutated polypeptide chain is identical to what was originally coded for.

However, UGG is the only codon on RNA that codes for Trp. If a point mutation occurred substituting any of the nucleotides in that codon, the first amino acid in the sequence would not be Trp (e.g. UCG: Ser) and the structure and function of the protein would be compromised **(Figure 11.2.2)**. If the point mutation in that codon created a stop codon (e.g. UGA: stop), the ribosome would cease to translate the rest of the protein and the stunted, partial polypeptide would be useless **(Figure 11.2.3)**.

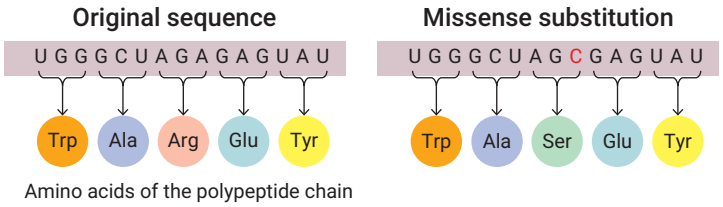


FIGURE 11.2.2 A missense point mutation after a substitution, as shown by the red C. The amino acid sequence in the mutated polypeptide chain is different to what was originally coded for and its function would be compromised.

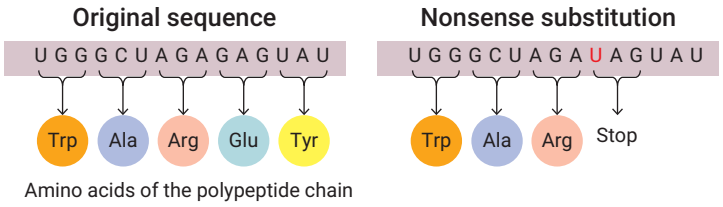


FIGURE 11.2.3 A nonsense point mutation after a substitution, as shown by the red U. The amino acid sequence in the mutated polypeptide chain is very different to what was originally coded for and function would be severely compromised.

Frameshift mutations

Frameshift mutations are those that produce a shift in the **reading frame** of a strand of mRNA. Since mRNA does not have convenient spaces between codons, ribosomes read the sequence of nucleotides in triplets from the beginning to the end. The reading frame is then represented in print by adding spaces between the codons: UGG GCU AGA GAG UAU. However, if the first nucleotide is missing, the reading frame shifts, with the new triplets looking like this: GGG CUA GAG AGU AU.

Frameshift mutations occur whenever an **insertion** or **deletion** error occurs during transcription (e.g. UGG**A** GCU AGA GAG UAU). The ribosome does not have the benefit of spaces between codons, so it cannot tell that a nucleotide has been added. Instead, it translates the nucleotides in triplets from the beginning: UGG AGC UAG AGA GUA U. Since the nucleotides are shifted into different codons, all codons downstream of the error are affected, thus frameshift mutations cause extensive issues with the new protein **(Figure 11.2.4)**.

frameshift mutation a mutation that dislocates the translational reading frame

reading frame the ribosome's division of nucleotides into triplets for translation; shifted by insertion or deletion mutations

insertion the addition of a single nucleotide within a sequence

deletion the removal of a single nucleotide from a sequence

Weblink
Frameshift mutations

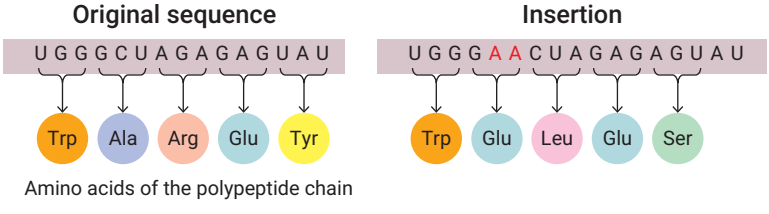


FIGURE 11.2.4 A frameshift mutation after an insertion, as shown by the red AA. The amino acid sequence in the mutated polypeptide chain is very different from what was originally coded for.

WORKED EXAMPLE 11.2.1

Consider an original nucleotide sequence: AUG GGA CUA CCC CGC AAA.

1 Determine the amino acid sequence:
- **a** of the original polypeptide
- **b** after a point mutation of the first C to a U
- **c** after a frameshift mutation where the first C is deleted.

2 Justify whether the change in part b or part c has a greater effect on the polypeptide's function.

ANSWERS

1 a **Use Figure 11.1.6 to translate the nucleotide sequence to the amino acid sequence.**

AUG	GGA	CUA	CCC	CGC	AAA
Met	Gly	Leu	Pro	Arg	Lys

b **Determine the nucleotide sequence after the point mutation.**

AUG GGA **U**UA CCC CGC AAA.

Determine the new amino acid sequence.
Using the codon table in Figure 11.1.6, the amino acid sequence for the point mutation is:

AUG	GGA	**UUA**	CCC	CGC	AAA
Met	Gly	**Leu**	Pro	Arg	Lys

c **Determine the nucleotide sequence after the deletion.**

AUG GGA UAC CCC GCA AA

Determine the new amino acid sequence.
Using the codon table in Figure 11.1.6, the amino acid sequence for the frameshift mutation is:

AUG	GGA	**UAC**	CCC	**GCA**	**AA**
Met	Gly	**Tyr**	Pro	**Ala**	**–**

2 **Compare the impact of both mutations.**
In the point mutation, CUA and UUA both code for leucine (Leu), so this is a silent mutation that has no effect on the polypeptide produced. In the frameshift mutation, the frameshift occurs in the third codon, and the first two are unchanged. The remainder of the polypeptide now codes for only three amino acids (Tyr–Pro–Ala) rather four (Leu–Pro–Arg–Lys). This is a significant change that would have a considerable effect on the function of the polypeptide. Therefore, the frameshift mutation would have a greater effect on the polypeptide's function because it changes the sequence of the remainder of the amino acids and shortens the polypeptide by one amino acid.

LEARNING CHECK 11.2

DESCRIBING

1 **Define**:
- **a** point mutation
- **b** frameshift mutation.

APPLYING

2 **Explain** why a frameshift mutation can have much greater effects than a point mutation.

3 For the mRNA sequence AAC UAC GGA UCA GCG GAU:

- **a** **determine** the amino acid sequence
- **b** suggest a mutation that would produce a stop codon in the sequence
- **c** suggest a mutation that would include a glutamic acid (Glu) in the sequence
- **d** suggest a mutation that would be a silent mutation (i.e. it would not change the amino acid sequence).

11.3 Regulation of gene expression

Gene expression refers to a gene being actively used or 'on'. Genes that are being transcribed into mRNA and translated into a polypeptide, or transcribed into another functional RNA, are being 'expressed'. **Gene regulation** refers to the processes within cells that control when and where a gene is expressed. For example, all cells contain all genes, but some genes are only expressed in particular cells or at certain times or at different rates in different places in the body.

gene expression the process of a gene being transcribed and translated into products (proteins or functional RNA)

gene regulation various processes that enable a gene to be expressed (or not) in specific cells at specific times and allow the proteins to be produced at required rates

Long-term gene regulation

In eukaryotic cells, the default state of expression for most genes is 'off'. This allows an individual tissue to turn 'on' the genes it requires, such as the genes for colour vision in the retinas of the eyes or the genes for creating insulin in the β cells of the pancreas; colour vision is not necessary in the pancreas, nor is insulin secretion necessary in the retinas. Gene regulation allows the body to conserve resources by only expressing the genes required for that tissue.

The process of cell differentiation in the embryo is most accurately considered a process of regulating the genes to be expressed by those cells in the future. If the difference between a retinal cell and a pancreatic β cell is in their function, and their function is carried out by the enzymes they produce, and the enzymes they produce are determined by the genes that are turned 'on' and 'off' in their nucleus, it should be theoretically possible to change one type of cell into any other type of cell simply by changing their patterns of gene expression.

This is true to an extent. Totipotent stem cells that can be transformed into any type of cell are those whose genes have not yet been regulated. For humans, these only occur in the undifferentiated embryo. Generally, once the embryo begins the process of differentiation, each successive phase of gene regulation restricts the type of cells that a cell can transform into. Some gene regulation processes are temporary, but many that occur during cell differentiation are essentially permanent.

Syllabus links
Stem cells and differentiation are detailed in Chapter 1 of *Nelson QCE Biology Units 1 & 2*.
Chapter 7 of this textbook describes the structure of chromosomes.

One of the mechanisms for permanent gene regulation is through embedding that section of the DNA strand deeply into the **nucleosomes**, forming **heterochromatin (Figure 11.3.1)**. Genes that reside on a deeply embedded section of DNA cannot be unwound for transcription. These are considered to be 'switched off'.

nucleosome the basic structural unit of chromatin, comprising a DNA strand wrapped tightly around a group of eight histone proteins

heterochromatin a tightly coiled complex of proteins and DNA that is characterised by few genes and limited transcription activity

Genes that are carried on loosely-bound nucleosomes, called **euchromatin**, are generally considered to be available for expression. Chemical tags can be applied to the histone tails to make the DNA–nucleosome bond stronger (making expression more difficult) or weaker (making expression easier). Different types of cells have different sections of their DNA bound into heterochromatin and euchromatin, so that different genes are switched 'on' and 'off'. The genes for colour vision are likely to be bound in euchromatin in the retinal cells, and heterochromatin everywhere else.

euchromatin a loosely coiled complex of proteins and DNA that is characterised by many genes and high transcription

However, not all genes are switched 'off' by default. Some genes code for proteins that maintain basic cellular processes and must be continually expressed at some level to support basic life. These are called **housekeeping genes**. For example, genes that express enzymes

housekeeping gene a gene that encodes a polypeptide essential for basic cellular processes

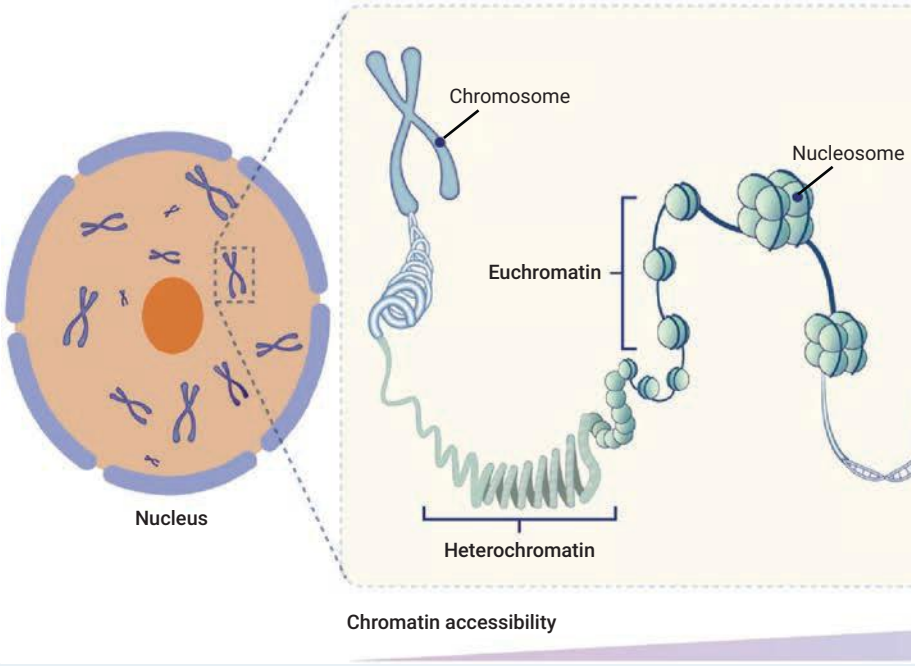


FIGURE 11.3.1 Long-term gene regulation. The process of switching genes on and off by chemical modification of chromatin.

used in glycolysis must be 'on' by default. These are always found in euchromatin with the chemical tags that make those bonds especially weak.

Short-term gene regulation

Even when genes are carried in euchromatin and are required by the cell type, there are controls over how fast and how often specific genes are transcribed and translated. Short-term regulation of genes occurs at several levels. The major regulatory effects occur before transcription, where genes are actually switched 'on' so that mRNA is produced.

transcription factor a regulatory protein whose function is to activate or inhibit transcription of coding DNA by binding to specific non-coding segments near the gene to be expressed or inhibited

Transcription factors are regulatory proteins that are expressed in response to environmental signals, such as hormones. These transcription factors bind to DNA and most of them activate gene expression. Activating transcription factors bind to a section of non-coding DNA near or within the gene and enable it to unwind from histone proteins to be transcribed. Some transcription factors switch 'on' multiple genes in the same region, while others are highly specific. Transcription factors that bind to the promoter region upstream of a gene attract RNA polymerase to begin transcription, or block RNA polymerase from access to inhibit gene expression **(Figure 11.3.2)**.

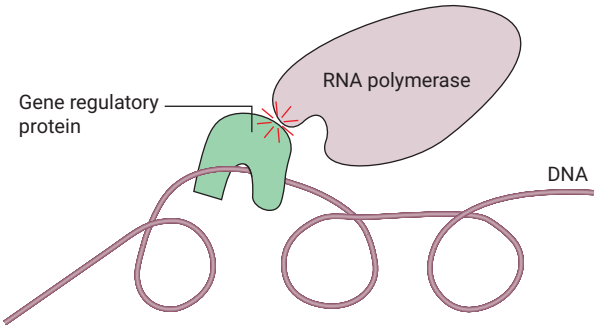


FIGURE 11.3.2 Regulatory proteins like transcription factors can attract or repel RNA polymerase.

Additional regulatory mechanisms occur during RNA processing, translation and even post-translation, where proteins can be temporarily deactivated by inhibitors. These additional mechanisms provide extremely precise control over the function of enzymes in the cell, allowing cells to respond within fractions of a second to changes in environmental conditions.

Syllabus link
Enzyme inhibition is detailed in Chapter 4 of *Nelson QCE Biology Units 1 & 2*.

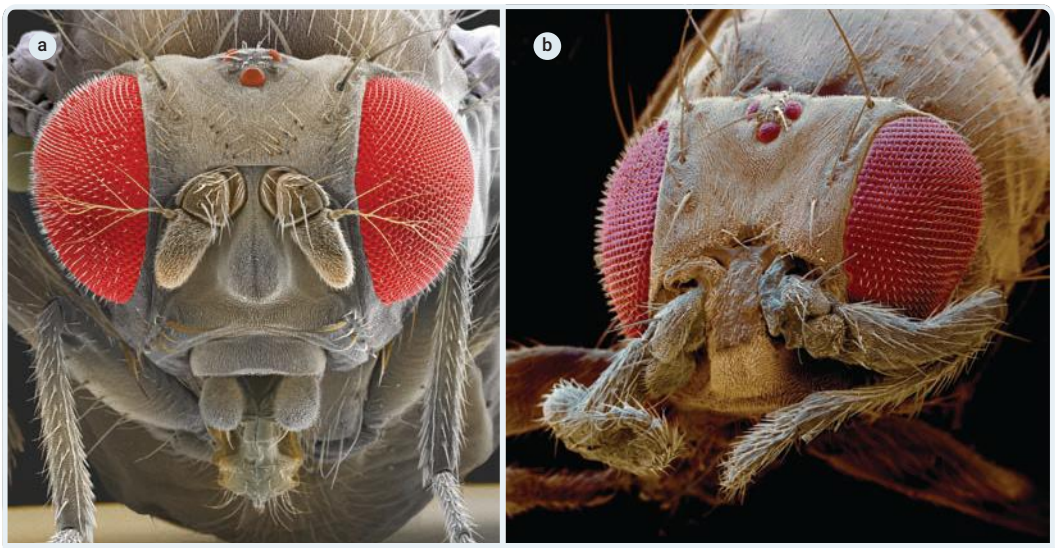
Homeobox genes

The homeobox family of genes is subject to both long-term and short-term regulation. This set of genes is responsible for the growth and development of an organism, producing its particular **morphology** – its structural form and shape.

morphology the shape and form of an organism or its parts

Early clues to the influence of individual genes in this process came from studies that demonstrated how a single nucleotide error can dramatically alter the structural development of an organism; for example, mutant fruit flies developed well-formed legs in place of their antennae (Figure 11.3.3). By altering the DNA to remove certain genes, the effect of that gene can be isolated.

Power and Syred/Science Photo Library



Eye of Science/Science Photo Library

FIGURE 11.3.3 (a) A normal fruit fly (*Drosophila melanogaster*) and (b) a fruit fly showing abnormal development of legs at the sites where antennae should be

For example, as few as eight **HOX genes**, a subset of homeobox genes, lay out the body plan in all animals with bilateral symmetry. Each HOX gene is expressed precisely in specific parts of the animal embryo during development (Figure 11.3.4). Errors in these genes cause significant body plan abnormalities, including missing limbs, extra digits and misplaced internal organs.

HOX genes a gene family that codes for proteins that regulate the body plan in the developing embryo

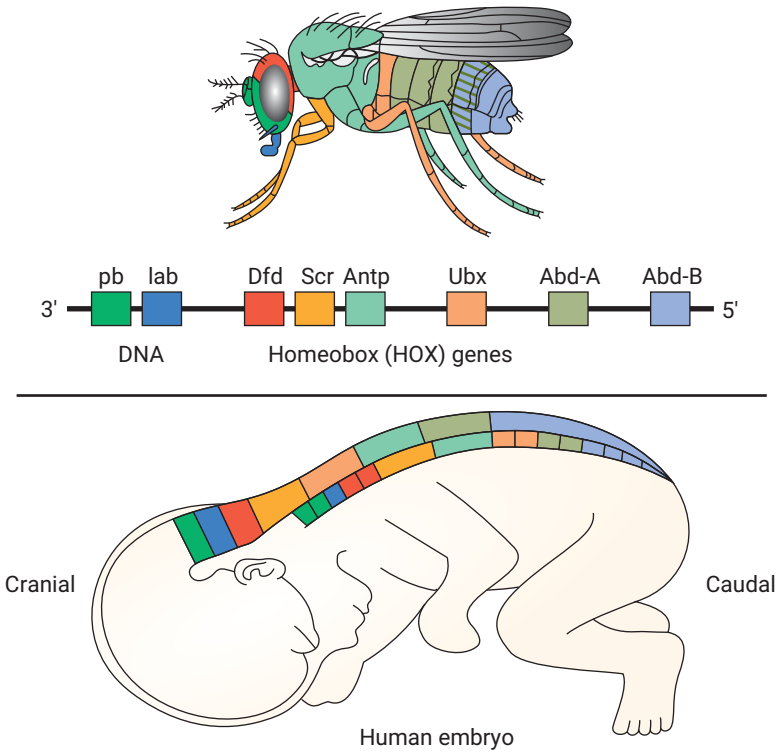


FIGURE 11.3.4 Eight HOX genes regulate the formation of the fruit fly body, whereas 39 HOX genes control the development of the human body plan. Each is expressed in a precise location within the individual during development.

Syllabus link
Chapter 7 details how errors manifest in genes and Chapter 10 discusses inherited genetic conditions.

HOX genes direct body plan development through a combination of short- and long-term regulation of gene expression. It is accomplished through specific proteins produced in the egg before fertilisation that diffuse across the egg, forming concentration gradients that convey positional information in the egg **(Figure 11.3.5a)**. For example, the zone of highest concentration of one of these proteins, called Bicoid protein, identifies the future embryo's anterior (front) end. The lowest concentration of Bicoid protein will become the embryo's posterior (rear) end. Other proteins create concentration gradients that mark other important positions within the egg **(Figure 11.3.5b)**.

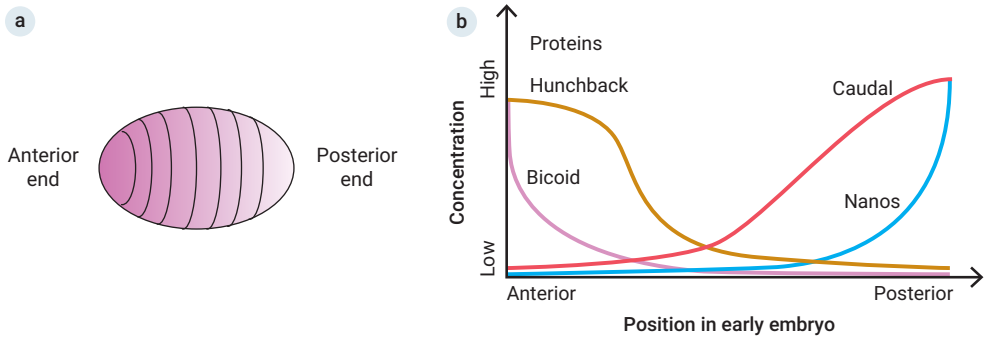


FIGURE 11.3.5 (a) Bicoid protein in an egg diffuses to create a concentration gradient. The highest concentration marks the future embryo's anterior end. (b) The relative concentrations of four different proteins conveying positional information in the developing embryo.

When the zygote divides, these protein concentrations are preserved, so that daughter cells formed from the high Bicoid concentration cytoplasm continue to have high Bicoid concentration that marks the anterior end of the embryo. Daughter cells formed from the low Bicoid concentration section of the egg cytoplasm continue to have low Bicoid concentration, indicating the posterior end of the embryo. This positional information is retained by all later generations of daughter cells in the developing embryo.

These positional proteins are transcription factors that interact with non-coding DNA regions immediately adjacent to the HOX genes to either activate or repress gene expression. For example, high concentrations of Bicoid activate HOX genes that code for the development of the anterior of the individual, the skull and head organs, but repress those genes that are not required for this development, such as the limbs and digestive organs.

Each HOX gene is activated by specific combinations of positional proteins. The pattern of expression of these genes ultimately reflects the concentrations of the positional transcription proteins within the developing embryo as it undergoes cell division.

HOX genes tend to be active throughout embryonic development and continue at different rates through childhood. In adults, HOX genes are generally deactivated with the more long-term regulation of heterochromatin.

Worksheet
Regulation of gene expression

LEARNING CHECK 11.3

DESCRIBING

1 **Define**:
   - **a** gene expression
   - **b** gene regulation.
2 **Identify** the stage of protein synthesis where most gene regulation occurs.
3 **Describe** the two forms of chromatin.
4 **Describe** the role of HOX genes in animals.

APPLYING

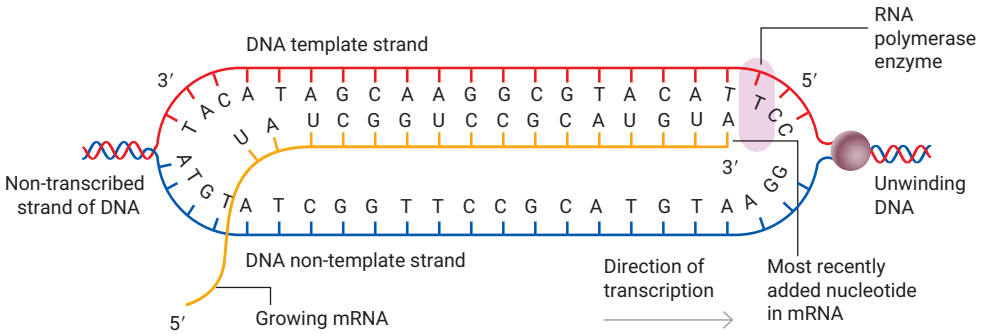
5 **Explain** why cells do not express all genes all the time.
6 **Explain** the role of housekeeping genes.
7 **Explain** how genes are regulated in the long term.
8 **Explain** how genes are regulated in the short term.
9 **Explain** why the default state of expression of many genes in eukaryotic cells is 'off'.
10 **Explain** how environmental signals, such as hormones, can affect gene expression in a cell.
11 **Explain** how positional proteins affect body plan development.

CHAPTER SUMMARY

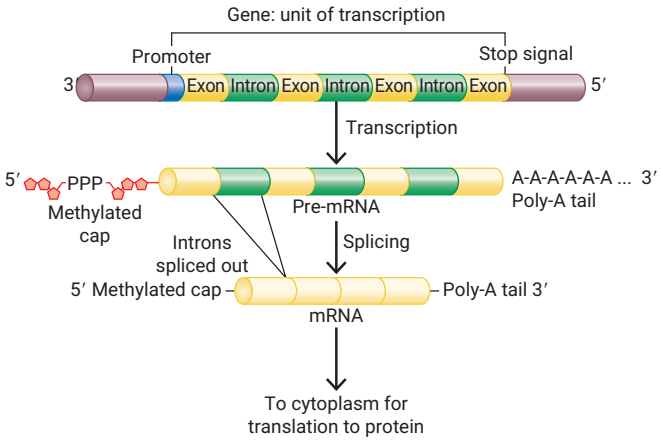
Protein synthesis

- Proteins are made in two major phases:
  - transcription – copying of DNA into mRNA
  - translation – mRNA is translated into an amino acid sequence.

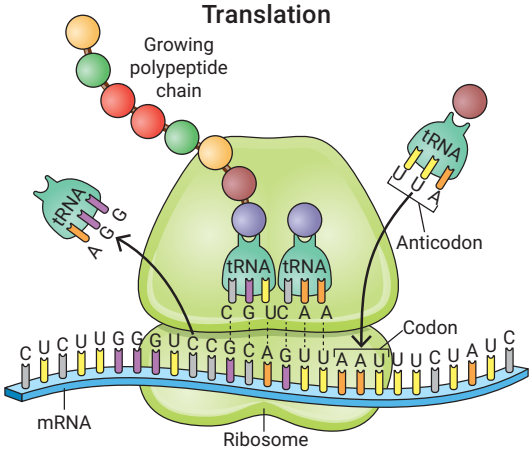
Transcription



RNA processing

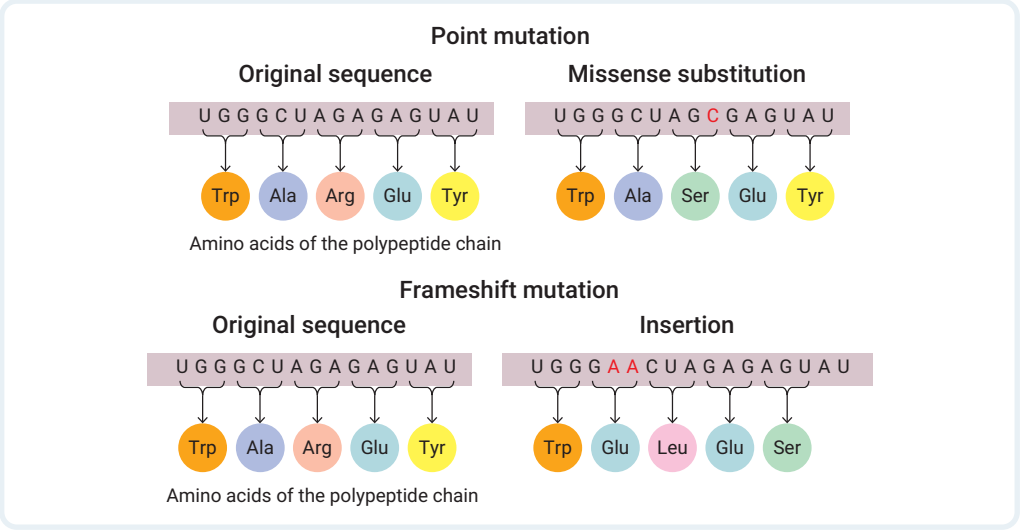


Translation



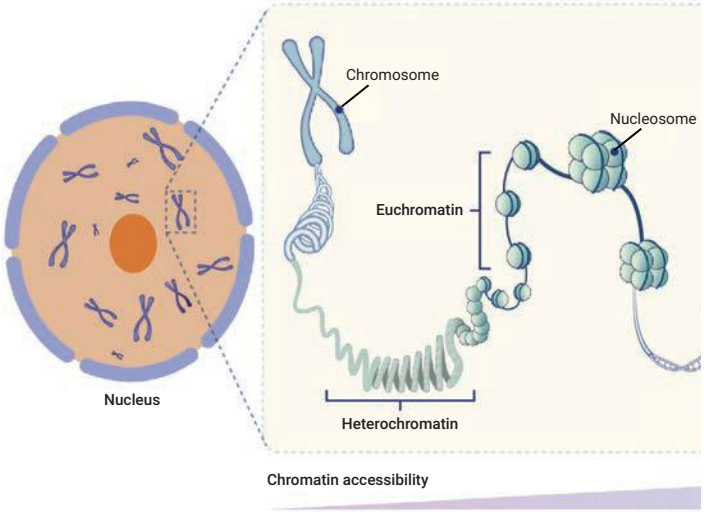
Errors in protein synthesis

- Errors that occur when DNA is being transcribed can have different effects – from producing non-functional proteins to having no obvious impact.
- Errors include point mutations and frameshift mutations.

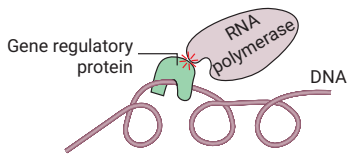


Regulation of gene expression

- Gene expression helps to control which genes are expressed at any point in time.
- The regulation of gene expression can be described as being short term or long term.



Short-term regulation: Transcription factor



CHAPTER EXAM

MULTIPLE CHOICE

1. The correct sequence of processes in protein synthesis is:
   - **A** translation of mature mRNA, modification of mRNA, transcription.
   - **B** modification of mRNA, translation of mature mRNA, transcription.
   - **C** transcription, modification of mRNA, translation of mature mRNA.
   - **D** transcription of mature mRNA, modification of mRNA, translation.

2. The process of creating mRNA from a DNA template is most accurately called:
   - **A** gene expression.
   - **B** RNA processing.
   - **C** transcription.
   - **D** translation.

3. Introns are:
   - **A** non-coding sections in mRNA that remain in mRNA.
   - **B** coding sections in mRNA that remain in mature mRNA.
   - **C** non-coding sections in mRNA that are removed in mature RNA.
   - **D** coding sections in mRNA that are removed in mature mRNA.

4. The 5′ cap and poly-A tail are:
   - **A** removed by the ribosome.
   - **B** transcribed by RNA polymerase.
   - **C** protecting the ends of mature mRNA.
   - **D** spliced out of mRNA to produce mature mRNA.

5. Choose the correct statement.
   - **A** Codons occur in DNA, mRNA and tRNA.
   - **B** Codons occur in DNA; anticodons occur in RNA.
   - **C** Codons occur in DNA and mRNA; anticodons occur in tRNA.
   - **D** Codons specify amino acids; anticodons specify stop and start signals.

6. A ribosome has two subunits:
   - **A** a large subunit to read mRNA and a small subunit to handle tRNA.
   - **B** a small subunit to read mRNA and a large subunit to handle tRNA.
   - **C** a large subunit to produce a protein and a small subunit to modify it.
   - **D** a small subunit to produce a protein and a large subunit to modify it.

7. Choose the correct statement.
   - **A** An insertion error causes a point mutation.
   - **B** Aneuploidy is an example of a point mutation.
   - **C** A substitution error causes a frameshift mutation.
   - **D** A point mutation is caused by a substitution error.

8. A silent mutation produces a protein that:
   - **A** is identical to the original.
   - **B** has less useful properties than the original.
   - **C** works better compared to the original.
   - **D** has improved properties compared to the original.

9. Gene expression is regulated by all of the following, except:
   - **A** euchromatin.
   - **B** DNA polymerase.
   - **C** heterochromatin.
   - **D** transcription factors.

10. The family of genes that regulate body plan in bilaterial animals is called:
   - **A** BOX genes.
   - **B** HOX genes.
   - **C** POX genes.
   - **D** SOX genes.

SHORT RESPONSE

11. **Explain** the process of RNA splicing and its role in protein synthesis.

12. **Explain** the role of transcription factors in gene regulation.

CROSS-CHAPTER QUESTION

13. Inheriting trisomy 21 causes Down syndrome, a condition with characteristic morphology, including a flattened face, wideset eyes, a short neck and wide tongue, but none of the 39 human HOX genes are located on chromosome 21. **Explain** how HOX genes can still be affected by this condition.

DATA ANALYSIS

Questions 14 and 15 refer to the following information.

Consider the mutations:

(i) CC* CCC ACC CAC C, where A is inserted at *

(ii) CCC CCA CCC ACC, where the second C is deleted.

14. **Apply understanding**

    Determine the resulting amino acid sequence for each mutation. Refer to the codon table in Figure 11.1.6.

15. **Interpret evidence**

    Determine which mutation would cause the greatest difference to a polypeptide that is normally produced by the unmutated nucleotide sequence CCC CCA CCC ACC.

SCIENCE AS A HUMAN ENDEAVOUR

Syllabus dot point

- Full genome sequencing enables people to identify whether they have certain gene variants, which may enable doctors to structure individualised healthcare programs that will lead to better health; however, there is concern about the risks of making this data available, and the privacy issues regarding ownership and availability of the information

The promise and perils of whole genome sequencing

Whole genome sequencing has revolutionised the field of personalised medicine by helping medical professionals tailor treatments and healthcare strategies to an individual's genetic makeup.

The process involves taking a DNA sample – from blood, saliva or cheek scrapings – and subjecting it to a series of procedures that fragment the DNA and detect the sequence of bases in each fragment. By overlapping fragments with matching sequences, the full genome can be successfully pieced together (Figure 1). However, knowing the sequence of a single person does not provide much information for health care. The key to many of the applications of whole genome sequencing is the preparation of a library of existing samples, which are compared to the individual's DNA sequence. By comparison to thousands of other human genomes, this technique identifies genetic mutations that influence disease risk, drug response and treatment outcomes.

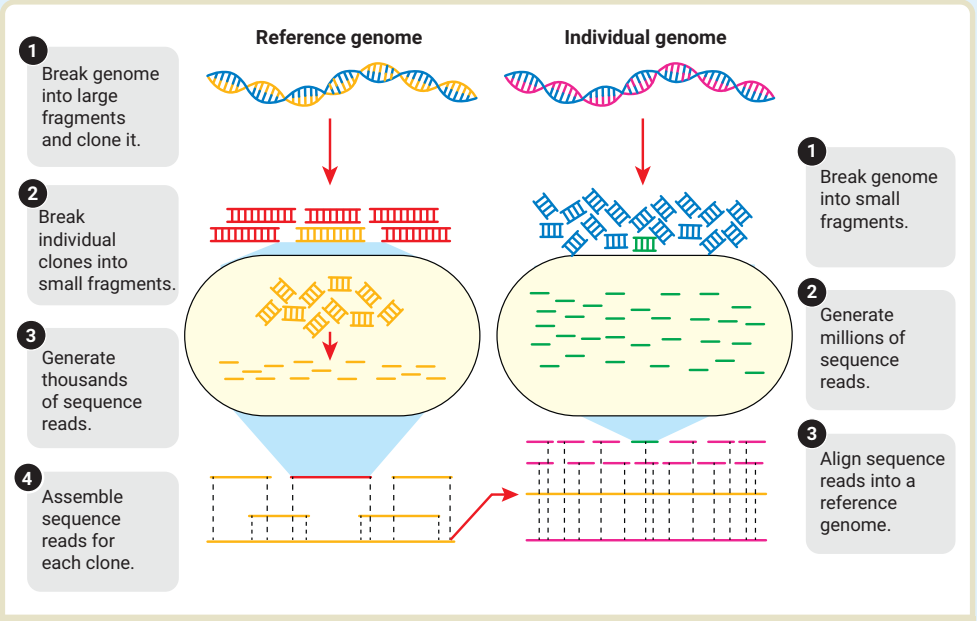


FIGURE 1 The overall processes involved in whole genome sequencing

The promise of whole genome sequencing lies in detecting a genetic predisposition to disease. For example, mutations in genes such as *BRCA1* and *BRCA2* are linked to a higher risk of breast and ovarian cancers. If medical professionals know that an individual carries these mutations, they can advise preventative measures, such as lifestyle changes or enhanced screening protocols.

At a larger scale, whole genome sequencing can also help us to better understand the common causes of diseases and help to identify people who are high and low risk. Figure 2 outlines some of the key applications of whole genome sequencing.

Despite its promise, whole genome sequencing faces several challenges in personalised medicine, such as the misinterpretation of data and multiple ethical concerns. One critical issue in the interpretation of data is distinguishing between harmless variants and those that affect health. A human genome has more than 3 billion base pairs, with millions of genetic variants, including many silent mutations with no effect on the individual at all. Distinguishing between those that do and do not affect health is highly complex and requires advanced computational tools, considerable field expertise and an enormous comparison library. The understanding of how genetic variants interact with environmental factors and lifestyle choices is also incomplete, further limiting the predictive power of whole genome sequencing.

Whole genome sequencing also has ethical concerns. For example, it can reveal sensitive information, such as an individual's risk for untreatable or late-onset diseases such as Alzheimer's. This raises questions about psychological impacts and the individual's right to not know their genetic information. Privacy is another concern, as genomic data is very sensitive, and misuse of this data by insurers, employers or hackers could lead to discrimination or breaches of confidentiality.

Addressing these ethical and technical challenges is crucial to ensure the responsible use of whole genome sequencing in personalised medicine, so that it can continue to deliver a more efficient and effective healthcare system.

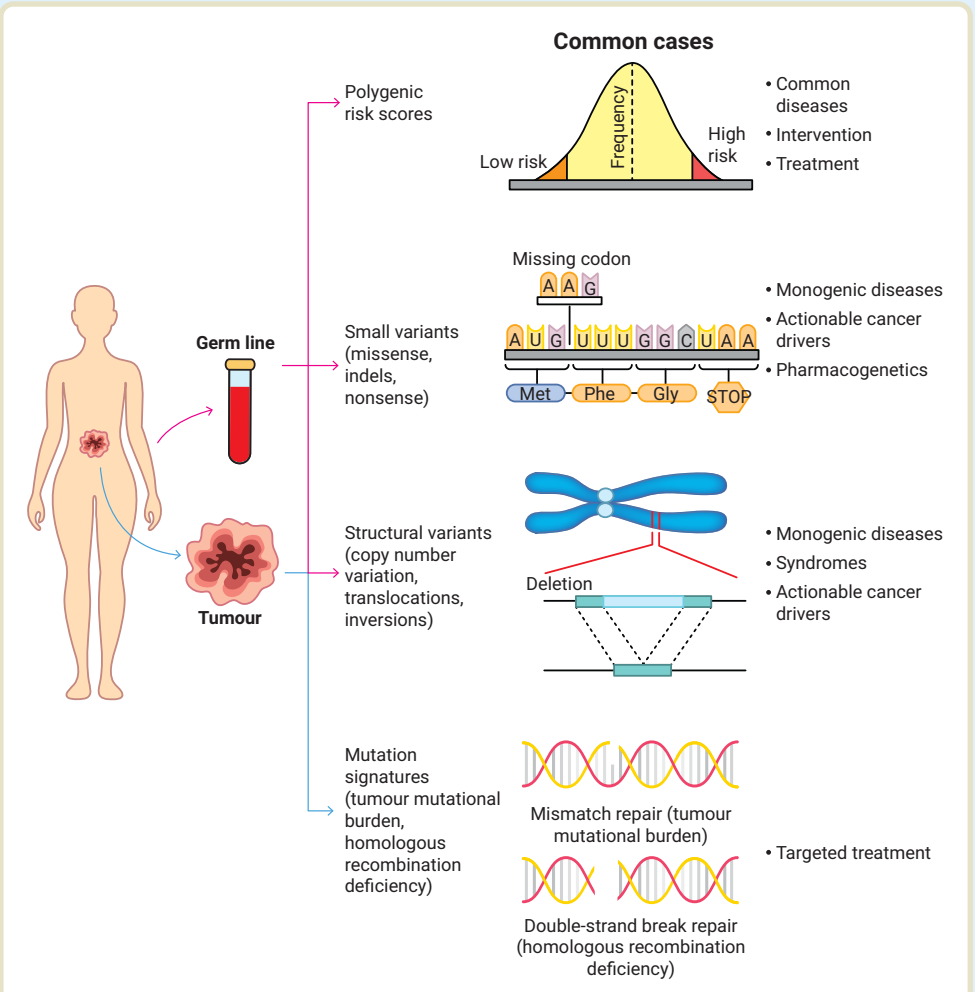


FIGURE 2 Clinical applications of whole genome sequencing

Weblinks

Research ethics and the challenge of whole genome sequencing

National Human Genome Research Institute (NHGRI)

What are whole exome sequencing and whole genome sequencing?

Privacy and ethical challenges in next-generation sequencing

Whole genome sequencing

CHAPTER 12

Evolution: Natural selection and microevolution

Pascal Kobeh/naturepl.com

SYLLABUS DOT POINTS

SCIENCE UNDERSTANDING

- Distinguish between microevolution and macroevolution.
- Explain microevolutionary change through the main processes of mutation, gene flow and genetic drift.
- 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.

SCIENCE INQUIRY

- Analyse genotypic changes for a selective pressure in a gene pool (laboratory work or computer simulation).

Introduction

Industrial melanism occurs when darker pigmented organisms containing more melanin become more common in polluted environments. The most common example given is the peppered moth (*Biston betularia*), which is widespread in the UK. The moth's wing pigmentation changed from white speckled with black spots to predominantly black in response to an increase in environmental soot. Once the pollution levels decreased, the lighter wing phenotype became more common again.

Recent studies provide evidence of a similar process occurring in the turtleheaded sea snake (*Emydocephalus annulatus*) in waters off Australia. The melanin pigment in the snakes' scales binds to many trace element pollutants. Snakes with more melanin in their scales can trap pollutants in their skin, which is then shed, removing the pollutants from their body. Sea snakes living in less polluted environments retain the original banding patterns of black and white, whereas snakes in more polluted areas are losing the banding pattern and turning entirely black. This research provides evidence for a relationship between an organism's phenotype and changes in its environment.

ASSUMED KNOWLEDGE

- ✓ Genes are sections of DNA that an offspring inherits from its parents.
- ✓ There are different forms of genes called alleles.
- ✓ Alleles interact to produce particular phenotypes.
- ✓ Sexual reproduction results in offspring with different combinations of alleles.
- ✓ Different forms of alleles arise through mutations.
- ✓ Organisms have specific features that allow them to survive in their particular habitat.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ identify differences between microevolution and macroevolution
- ✓ explain how mutation contributes to microevolutionary change
- ✓ explain how gene flow contributes to microevolutionary change
- ✓ explain how genetic drift contributes to microevolutionary change
- ✓ explain how natural selection results in the differential survival of organisms
- ✓ identify the selection of phenotypes as stabilising, directional or disruptive
- ✓ use genotype data to calculate allele frequencies
- ✓ analyse data to identify whether a selection pressure has had an effect on alleles in a population
- ✓ analyse data to decide if the selection for an allele has been positive (increase in frequency) or negative (decrease in frequency).

evolution the change in the genetic composition of a population during successive generations, which may result in the development of new species

microevolution small-scale variation of allele frequencies within a species or population, in which the descendant is of the same taxonomic group as the ancestor

macroevolution the variation of allele frequencies at or above the species level, over geological time, resulting in the divergence of taxonomic groups, in which the descendant is in a different taxonomic group from the ancestor

heritable capable of being passed on to the next generation

Syllabus link
Chapter 1 discusses taxonomic classification of species.

12.1 Microevolution

Evolution refers to change over time, specifically the process of living organisms accumulating changes to their genomes over varying timeframes. On a small scale over a short timeframe, this process is called **microevolution** and refers to any change in the range of genes an organism can inherit in a population. For example, some lizards such as the Australian sand goanna (*Varanus panoptes rubidus*) **(Figure 12.1.1)** have evolved resistance to particular types of neurotoxic snake venom, allowing them to prey on venomous snakes (such as brown snakes or death adders) and remain unaffected by any bites. Another example is the acquisition of antibiotic resistance in a population of bacteria, after exposure to antibiotics.

In microevolution, the descendant is classified in the same taxonomic group as the ancestor even though there may be small variations in allele frequencies within the species or population.

In contrast, **macroevolution** is defined as the large-scale **heritable** changes that result in the formation of new taxonomic groups, in which the descendant is a different species from the ancestor. In macroevolution, a single species with genetic variations that allow it to exploit new ecological roles diverges to form new groups of organisms comprising many new species. For example, in many African freshwater lakes, such as Lake Victoria, hundreds of different species of cichlid fish have evolved within the last 15 000 years from a single ancestor.

Macroevolution and microevolution involve the same processes acting over different time scales. Macroevolution can be thought of as the compounded effects of microevolution, the accumulation of microevolutionary changes over a long period of time to the point that the population is unique from other populations and is considered a distinct species.

BIOSPHOTO/Alamy Stock Photo

FIGURE 12.1.1 Australian sand goannas can feed on snakes while remaining unaffected by venom from bites.

LEARNING CHECK 12.1

DESCRIBING

1 **Define**:
   - **a** evolution
   - **b** microevolution
   - **c** macroevolution.

2 State the major difference between microevolution and macroevolution.

INTERPRETING

3 The polar bear is a member of the Ursidae family and has a common ancestor with the black and brown bears. **Justify** whether this information demonstrates microevolution or macroevolution.

12.2 Microevolutionary changes

If microevolution is a change in the alleles that can be inherited, then mutations that change gamete DNA will cause microevolutionary changes. The mechanisms that affect how these mutations are passed on to offspring will also result in microevolutionary changes, including the role of gene pools, gene flow and genetic drift.

Mutation

New alleles generally come from old alleles through mutation. Mutations in gamete DNA that result in live offspring are rare and are mostly noticed when there are harmful effects that result from the changes to the DNA sequence. When mutations result in recessive alleles, the change can be masked by the effects of the original allele, which remains the dominant allele. In a large population, individual mutations are barely noticeable. However, they are essential because they are the ultimate source of variation within populations.

Ikonya/Shutterstock.com

FIGURE 12.2.1 The koala (*Phascolarctos cinereus*) is one of the few animals that can eat eucalypt leaves. This is probably a result of a mutation that means its digestive system can remove toxic eucalyptus oil.

Individuals in any population express a range of different phenotypes, caused by variation in their genotypes. This genetic variation is heritable – it can be passed to the next generation.

Under certain circumstances, a mutation may give an individual an advantage in survival and reproduction compared to the rest of the population. For example, most animals cannot eat eucalypt leaves because of their toxicity. Dr Rebecca Johnson, co-chief investigator of the Koala Genome Consortium, and her team showed that the part of the genome that codes for detoxifying proteins is approximately twice the size in koalas **(Figure 12.2.1)** than in other mammals. This is probably the result of a duplication mutation. This means the koala digestive system can remove toxic molecules in the eucalyptus leaves, providing a survival advantage over other mammals that cannot eat this food source.

In other cases, genotypic variation may lead to a disadvantage, meaning the organism is less likely to survive and reproduce, or it may have no evolutionary effect. Either way, genetic mutation in gamete DNA introduces new alleles and, therefore, new genetic variation into populations. Variations in populations can be very small, but they are the basis of evolution.

Gene pools

The total collection of alleles within a population is referred to as a **gene pool (Figure 12.2.2)**. In biological terms, a population is a group of individuals of the same species that live in the same geographic area and readily interbreed to produce fertile offspring. All individuals in a population belong to the same gene pool.

gene pool the range of genes and all their alleles present in a population

Weblinks
Koala Genome Consortium
Genetic variation

The range of variation possible in a population is restricted by the alleles available in its gene pool. For example, bearded dragons (genus *Pogona*, eight species) do not carry genes for wings or hard-shelled eggs or the enzymes required to synthesise chlorophyll. However, all bearded dragons carry genes for a tail, rudimentary teeth, scales and four legs **(Figure 12.2.3)**.

Genes that have only one possible allele in a gene pool are considered 'fixed' in the population. They do not contribute to any variation. Scientists suggest that approximately 80–85 per cent of genes are fixed in this way. These genes do not make a significant contribution to evolution because there is no variety to draw on. It is the other 15–20 per cent that can be drawn upon during evolutionary change.

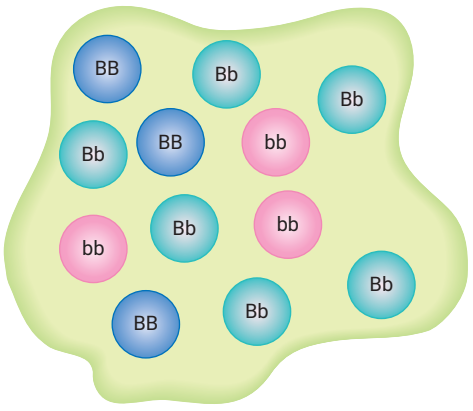


FIGURE 12.2.2 The sum of all alleles found in a population is called the gene pool.

Juniors Bildarchiv GmbH/Alamy Stock Photo

FIGURE 12.2.3 Bearded dragons have genes for a tail, scales and rudimentary teeth, but do not have genes for wings.

The gene pool of a population is subject to many external influences, shaped by the migration of individuals and by environmental events that can sometimes rapidly and considerably change the composition of populations.

For variation to occur in a population, more than one allele of a gene must exist. When there are different phenotypes due to different alleles of a gene, they are termed 'genetic polymorphisms' (from the Greek *poly* meaning 'multiple' and *morph* meaning 'form'). The frequency of polymorphic alleles is not usually constant and can be affected by:

- the mutation of an allele
- gene flow (immigration of individuals into the population or emigration of individuals out of the population)
- the reproduction rate of various individuals in the population; that is, the number of offspring born per year to an individual
- genetic drift, including a bottleneck effect or a founder effect.

Weblinks
Allele frequencies and gene variation

Allele frequencies in worldwide populations

Syllabus links
Chapter 9 discusses the possible causes and effects of mutations on alleles.

Chapter 10 discusses the inheritance of ABO blood groups.

Gene flow

Populations, and their gene pools, become isolated from one another when migration between populations no longer occurs. **Gene flow** may occur if the migrants join the local gene pool by breeding with their new population. For example, immigrants may add new alleles to the gene pool and emigrants may completely remove some alleles or significantly change the frequency of others **(Figure 12.2.4)**.

gene flow the transfer of alleles that results from emigration and immigration of individuals between populations

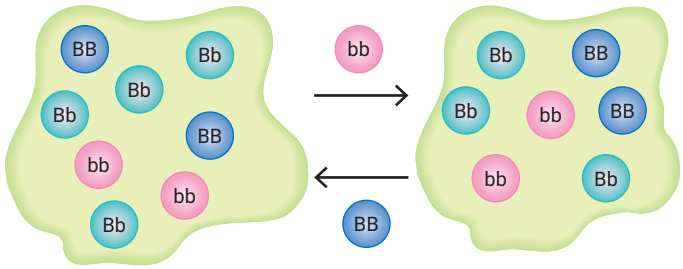


FIGURE 12.2.4 Gene flow is the transfer of alleles that results from emigration and immigration of individuals between populations.

Humans are polymorphic for a range of blood groups, including the ABO blood group. Among Indigenous Australians, some alleles are present at frequencies different from other populations in the world. A 2022 study that focused on the relatively isolated population of Tiwi Islanders (located approximately 80 km north of the Australian mainland) showed the distribution of ABO antigens in Tiwi Islanders was distinct from that in other populations. The distribution of the O phenotype was very high, about 81 per cent, compared with the other populations (Caucasian 44 per cent, African 49 per cent and Asian 43 per cent), indicating limited gene flow with the population on the Tiwi Islands.

Genetic drift

The term **genetic drift** applies to random changes in small populations. In all sexually reproducing animals, every reproductive event involves chance. Each organism inherits half their alleles from their mother and half from their father. The combination of alleles passed on is a matter of chance, resulting from meiosis, gamete production and fertilisation. In large

genetic drift a change in the gene pool of a population as a result of chance; usually occurs in small populations

populations, this randomness in inheritance of alleles is not usually noticeable. However, if a population is small, there is a chance that some alleles present in a parental group will not be passed on at all (Figure 12.2.5). These alleles may be permanently lost from the gene pool. It is very difficult to replace these alleles once lost.

Syllabus link
Chapter 9 discusses meiosis, gamete production and fertilisation.

Weblink
Genetic drift

Worksheet
Microevolution

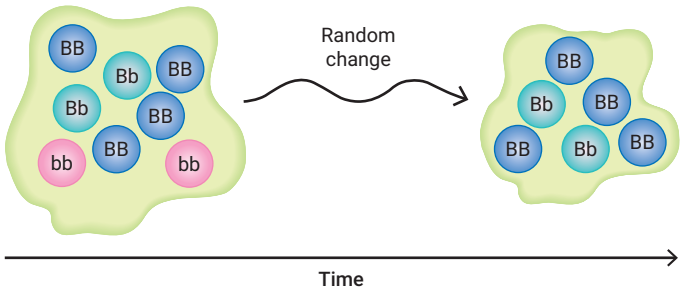


FIGURE 12.2.5 Chance events can cause the allele frequency in a population to change. This is known as genetic drift.

Genetic drift can occur in a small population or when a large population is reduced suddenly (Figure 12.2.5), and there is a loss of genetic diversity. The two main types of genetic drift are the bottleneck effect and the founder effect.

Bottleneck effect

bottleneck effect when a catastrophic event or a period of adverse conditions drastically reduces the size of a population, reducing genetic variation within the population

The **bottleneck effect** is caused when a catastrophic event, such as a cyclone or bushfire, or a period of adverse conditions, such as a drought, drastically reduces the size of a population. Some alleles may be lost through chance depending on which individuals survive. The remaining portion of the population is unlikely to have the same allele frequencies as the original gene pool. Individuals of the population continue to reproduce. However, they can only pass on the alleles that remain in the individuals that survived the event. Even after the population recovers, the diversity of genetic variation is lost (Figure 12.2.6).

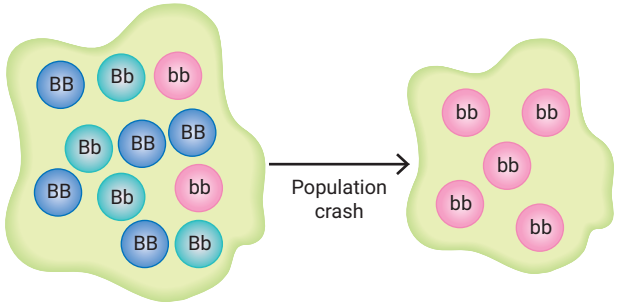


FIGURE 12.2.6 A catastrophic decrease in population size can result in a loss of some alleles from the gene pool. This is the bottleneck effect. Deleterious genes can be preserved by chance.

Around 45 years ago, the northern hairy-nosed wombat (*Lasiorhinus krefftii*) population in Queensland was listed as only 35 individuals. This significant reduction in population size is an example of a population bottleneck due to a combination of habitat clearing and destruction, along with increased competition for food from introduced species.

David Dennis/Shutterstock.com

FIGURE 12.2.7 A northern hairy-nosed wombat

Founder effect

When a few individuals move to a new area and become isolated from a larger population, they might not carry all the alleles that were present in the original population **(Figure 12.2.8)**. This means that the isolated population has less genetic diversity than the original population and deleterious recessive alleles may have a higher chance of coming together than they did in the original population. A key difference between the **founder effect** and the bottleneck effect is that, in the founder effect, the original population survives and can potentially reintroduce missing alleles through gene flow, whereas in the bottleneck effect, the original population is lost to disaster.

founder effect a type of gene flow that occurs when a few individuals that have become isolated from a larger population do not carry all the alleles that were present in the original population

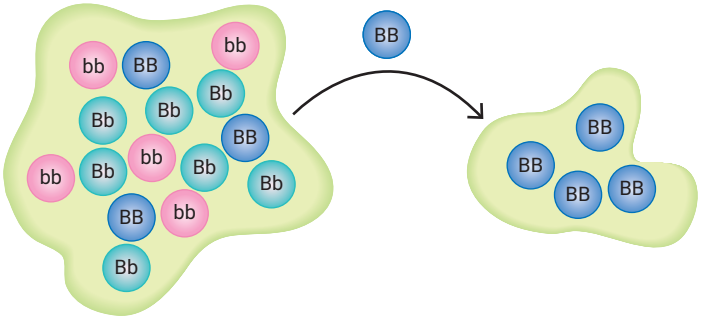


FIGURE 12.2.8 The founder effect occurs when a few individuals carry alleles to a new, isolated area and a new population is formed with different allele frequencies from the original population.

Littlejohn's treefrog (*Litoria littlejohni*) **(Figure 12.2.9)**, has a fragmented distribution in south-east New South Wales from near Wollongong in the south to the central coast. Researchers suggest that a series of founder effects due to events such as habitat fragmentation have resulted in restricted gene flow between populations. Evidence of recent loss of individuals was shown in three populations that had very small effective population sizes, reduced genetic diversity and high inbreeding. The risk of extinction increases significantly when populations have high inbreeding rates along with small population sizes.

Robert Valentic/Nature Picture Library

FIGURE 12.2.9 Littlejohn's treefrog occurs in different areas in south-east New South Wales.

LEARNING CHECK 12.2

DESCRIBING

1 **Define**:
   - **a** gene flow
   - **b** genetic drift.

2 **Recall** the relationship between genotype and phenotype.

APPLYING

3 Outline why variations must be heritable for them to be relevant to evolutionary change.

4 **Explain** the mechanisms that can lead to changes in the gene pool of a population.

5 Outline how gene flow can affect allele frequency.

6 Mutations are barely noticeable in large populations. **Explain** how mutations are still essential to evolutionary change.

ANALYSING

7 **Distinguish** between a gene and an allele.

8 **Distinguish** between the bottleneck and founder effects.

12.3 Natural selection

In 1858, a joint paper was presented to the Linnean Society based on the ideas of Charles Darwin (1809–82) (Figure 12.3.1) and Alfred Russel Wallace (1823–1913) (Figure 12.3.2). Darwin and Wallace outlined their understanding of species forming varieties (Wallace) and species by natural means of selection (Darwin). Together these observations formed the basis for the evolution of life, what they referred to as 'descent with modification'; life that exists today has descended from shared ancestors. Natural selection was the proposed mechanism, where favourable traits are selected for as the individuals survive and inherited as they reproduce. These traits become more common in subsequent generations. Individuals with unfavourable traits are less likely to survive and reproduce so these traits become less common in subsequent generations.

Weblink
The original papers by Charles Darwin and Alfred Wallace
Charles Darwin
Alfred Russel Wallace

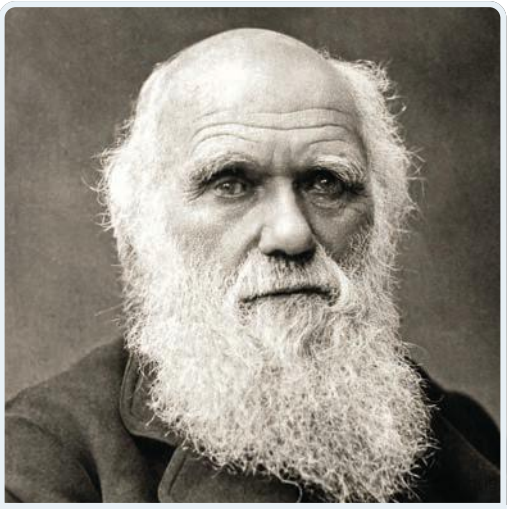


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FIGURE 12.3.1 Charles Darwin

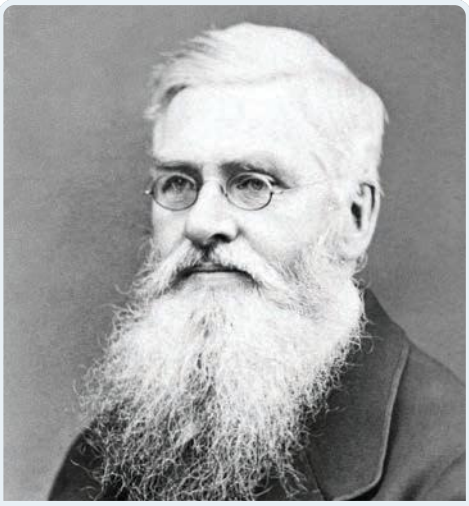

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FIGURE 12.3.2 Alfred Russel Wallace

The principle of natural selection leading to evolutionary change rests on four key propositions:

- Individuals differ from one another through genetic variation.
- These variations are caused by mutations in alleles and are heritable.
- In general, more offspring are born than can survive to maturity and reproduce. This leads to a struggle for existence and only some organisms can survive long enough to reproduce.
- Some individuals have traits that make them more suited than other individuals to their environment (**viability**), so they are better able to reproduce and pass on their alleles to the next generation (**fecundity**).

Natural selection results in changes to populations over time (Figure 12.3.3). Natural selection acts on the phenotypes of individuals, not on the genotypes. This means some organisms survive and reproduce, passing on their alleles. Some recessive alleles can remain in a population through the natural selection process when they are masked by a dominant allele (and phenotype). An adaptation is a heritable behavioural, morphological or physiological trait that has evolved through this process of natural selection. The capacity of an individual to survive and reproduce viable offspring is referred to as its **fitness**, a combination of its viability and fecundity. Since environments vary from time to time and from place to place, a phenotype that is favourable in one place and time may not be favourable or may even be disadvantageous in another place or time.

viability the capacity of an organism to stay alive

fecundity a measure of fertility; the capacity to reproduce

fitness the capacity of an individual to survive and pass on alleles to viable offspring

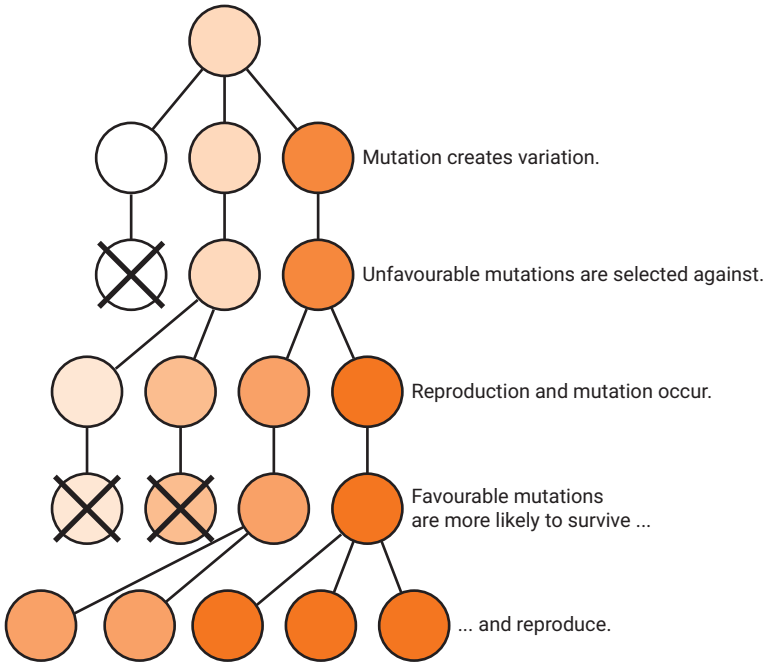


FIGURE 12.3.3 A diagrammatic representation of natural selection. In this example, the darker alleles confer an advantage over lighter alleles.

It is important to understand that individuals do not evolve, even though natural selection acts on individuals. It is the population that evolves over time as the alleles present in the gene pool change.

Selection pressures

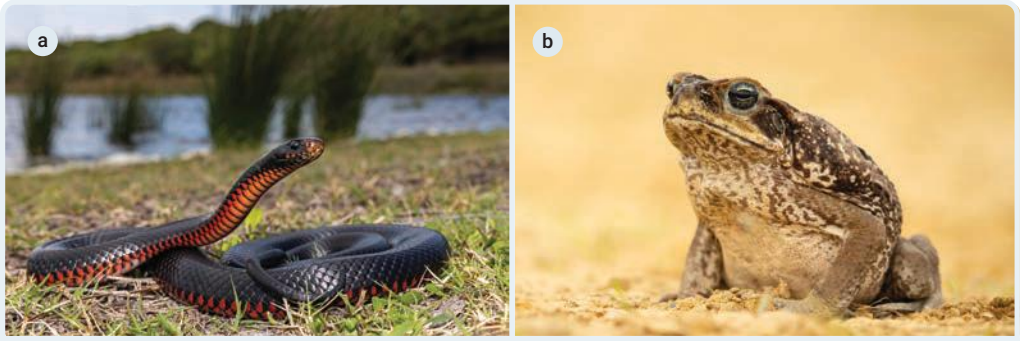
selection pressure a factor that influences the survival of an individual within a population

Darwin believed that the rapid changes produced by selectively breeding dogs, or pigeons, could also occur naturally in the wild. Naturally occurring **selection pressures** would act on traits in the population, resulting in some traits becoming more common as others became less common. Selection pressures are factors that influence the viability and fecundity of an individual, a population or a species. Some examples are:

- competition between species for food and territories
- predator–prey relationships
- competition within species for food or water
- competition within species for territories or nesting places
- sexual selection; that is, selection of traits that successfully attract mates.

Invasive species in Australia provide examples of recent evolution due to changing selection pressures. Australian black snakes (*Pseudechis porphyriacus*) are opportunistic carnivorous snakes that feed on reptiles, amphibians and fish. In 2006, University of Sydney researchers showed that this species of snake has undergone a rapid adaptive response in feeding behaviour and physiological resistance to the lethal cardiotoxin released by the cane toad (formerly *Bufo marinus* now *Rhinella marina*). In areas where cane toads occurred, snakes showed less interest in toads as food and increased resistance to toad toxin. These observations were supported with laboratory experiments that showed changes in snake behaviour were not learnt nor was the cardiotoxin resistance an acquired immune response.

Since cane toads were only introduced in 1935, this supports the conclusion that black snake behaviour and physiology have evolved rapidly (in about 23 generations) in response to the selection pressure of toxic prey provided by the presence of toads.



Ken Griffiths/Shutterstock.com

Milan Zygmunt/Shutterstock.com

FIGURE 12.3.4 An Australian black snake and the invasive cane toad

Types of phenotypic selection: stabilising, directional or disruptive

Natural selection is most obvious when it is leading to changes in the gene pool of a population, causing some observable change in phenotype. The population may be gradually changing colour or individuals may be getting larger or smaller due to selective pressures in a changing environment. **Figure 12.3.5** shows the three types of selection that can affect the distribution of phenotypes:

- stabilising selection
- directional selection
- disruptive selection.

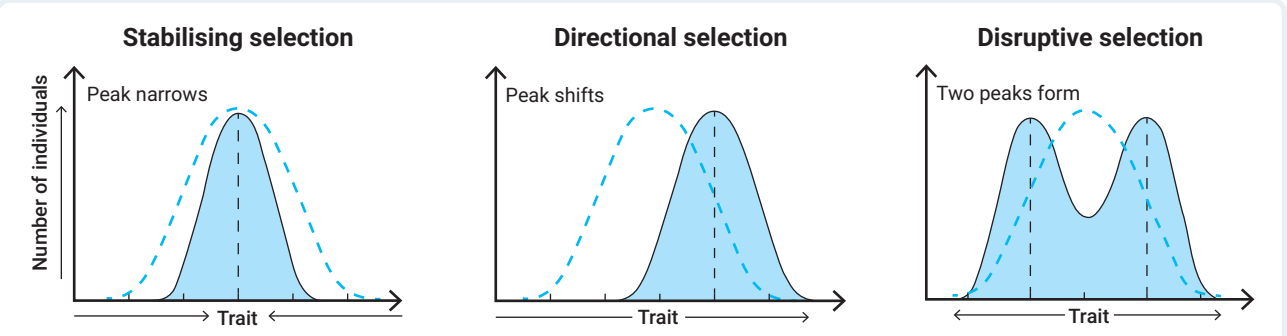


FIGURE 12.3.5 Selection can change the distribution of phenotypes (and therefore genotypes) in three ways: stabilising selection (moderate traits are favoured), directional selection (one extreme is favoured) and disruptive selection (both extremes are favoured). The original distribution of traits is shown with dotted lines in each graph.

Stabilising selection

As long as the environment of an organism is stable, the selective pressures in an environment will favour the intermediate phenotype that has the highest fitness. Selection acts against the extreme phenotypes. This is referred to as **stabilising selection**.

stabilising selection a form of selection that tends to favour organisms with a phenotype similar to their parents; usually occurs when the environment is very stable and unchanging and selects against extremes of phenotype

An example of stabilising selection is shown in hooded warblers (*Setophaga citrina*) **(Figure 12.3.6)**, insectivorous birds that live in shrubby understoreys in forests of eastern areas of northern and central America. *S. citrina* flicks the white patches on its tail to startle insects into flight to make them easier to feed on. Data collected over a 14-year study and published in 2023 showed that warblers with average-sized white dots survived longer than birds with smaller or larger white dots. Over time, the frequency of warblers born with very small or very large white dots will decrease, leading to a narrower range of dot sizes in the population.

Worksheet
Natural selection

Agami Photo Agency/Shutterstock.com

FIGURE 12.3.6 The male hooded warbler. The size of the white parts on the tail affects the bird's survival and is an example of stabilising selection.

Directional selection

directional selection
a form of selection where one phenotype is favoured, causing the allele frequency to shift in one direction

Directional selection results in a change in the most common phenotype over time. Gradual or sustained changes in the environment lead to selective pressures favouring more extreme phenotypes, thereby shifting a population's allele frequency distribution in one direction or the other.

An example of directional selection is shown in the lamina length (leaf blade) of the seedling of the Australian snow gum (*Eucalyptus pauciflora*) **(Figure 12.3.7)**. Research shows that under drier conditions, lamina length in seedlings decreases. This is evidence of directional

iPlantsman/Shutterstock.com

Kevin Wells Photography/Shutterstock.com

FIGURE 12.3.7 The leaves of seedlings of the Australian snow gum become shorter under drier conditions.

selection consistent with a past adaptation to reduce seedling susceptibility to acute drought. Over time, as short-leaved seedlings survive drought to mature and reproduce, the frequency of new seedlings with longer leaves will decrease, leading to a shorter-leaved population.

Disruptive selection

A third mode of selection, **disruptive selection**, operates in favour of extremes in phenotype. The individuals with the lowest fitness are those with an intermediate phenotype. This type of selection is seen in organisms with multiple mating strategies or when there are fluctuating environmental conditions. It results in a bimodal distribution of phenotypes and can lead to speciation.

disruptive selection a form of selection that operates in favour of extremes and against intermediate forms

For example, *Abdopus aculeatus* is a small species of octopus that lives throughout intertidal zones along the Indonesian, Philippine and northern Australian coastlines **(Figure 12.3.8)**. Many larger males of this species guard the den of a specific female for days, to prevent other males from mating with her. A different approach is used by smaller males, who swim low to the ocean floor, disguising themselves as females in order to sneak past larger, stronger males. Thus, the males who successfully reproduce represent the extremes of size – small or large. Average-sized males are not large or strong enough to guard females nor are they small enough to masquerade as females to sneak into a den. Over time, the frequency of moderate-sized males being born will decrease due to moderate-sized males failing to reproduce, leading to a population with only very small or very large males.

Nature Picture Library/Alamy Stock Photo

FIGURE 12.3.8 *Abdopus aculeatus* is an octopus about 30 cm long, also known as the algae octopus.

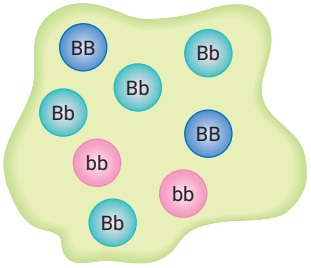
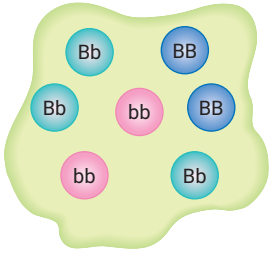
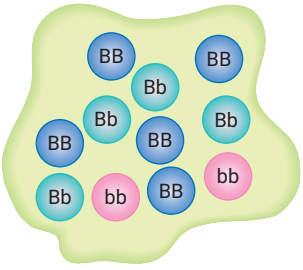
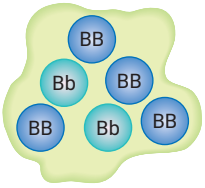
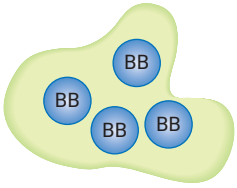
Regardless of phenotypic selection type, the amount of variation in the trait will change in the population as the selection process occurs. While stabilising selection typically maintains the existing predominant phenotype, directional selection and disruptive selection have the biggest effect on changing phenotypes and gene pools and are therefore more likely to lead to speciation.

Calculating allele frequencies

Determining phenotypic selection in a population requires scientists to calculate the frequency of alleles in that population. Allele frequency can be presented as a decimal, percentage or fraction. It is calculated by dividing the number of times the allele of interest is observed in a population by the total number of all the alleles at that particular gene locus in the population **(Table 12.3.1)**. Monitoring allele frequencies over time can indicate whether genetic drift, gene flow or mutations have occurred.

Weblink
Natural selection simulation

TABLE 12.3.1 Example calculations of allele frequencies as a result of different changes

Scenario	Gene pool	Total count	Allele frequency
Original population: Three genotypes.		B = 8	$\frac{8}{16}$ = 0.5 or 50%
		b = 8	$\frac{8}{16}$ = 0.5 or 50%
		Total alleles = 16	
Population after gene flow (emigration) – no change to the allele frequencies: Three genotypes		B = 7	$\frac{7}{14}$ = 0.5 or 50%
		b = 7	$\frac{7}{14}$ = 0.5 or 50%
		Total alleles = 14	
Population after gene flow (immigration) – increase in frequency of B allele, decrease in frequency of b allele: Three genotypes		B = 14	$\frac{14}{22}$ = 0.64 or 64%
		b = 8	$\frac{8}{22}$ = 0.36 or 36%
		Total alleles = 22	
Population after a bottleneck – decrease in frequency of b allele, increase in the frequency of B allele: Two genotypes		B = 10	$\frac{10}{12}$ = 0.83 or 83%
		b = 2	$\frac{2}{12}$ = 0.17 or 17%
		Total alleles = 12	
Population after a founder effect – loss of b allele, so now only one form of allele at this locus for this this population: One genotype		B = 8	$\frac{8}{8}$ = 1.0 or 100%
		b = 0	$\frac{0}{8}$ = 0 or 0%
		Total alleles = 8	

CASE STUDY 12.3.1

ROCK POCKET MICE

Analysis of data

The graphs in Figure 12.3.9 show the changing populations of the two phenotypes of rock pocket mice in two US states: New Mexico and Arizona. The rock pocket mouse (*Chaetodipus intermedius*) has two colours in order to better survive in changing habitats. Dark-coloured mice live in habitats where black lava rock dominates the landscape. Light-coloured mice live in habitats with light-coloured rocks and sandy soils.

Adapted from by Laura Helft, *The Making of the Fittest: Natural Selection and Adaptation*, Howard Hughes Medical Institute, 2011

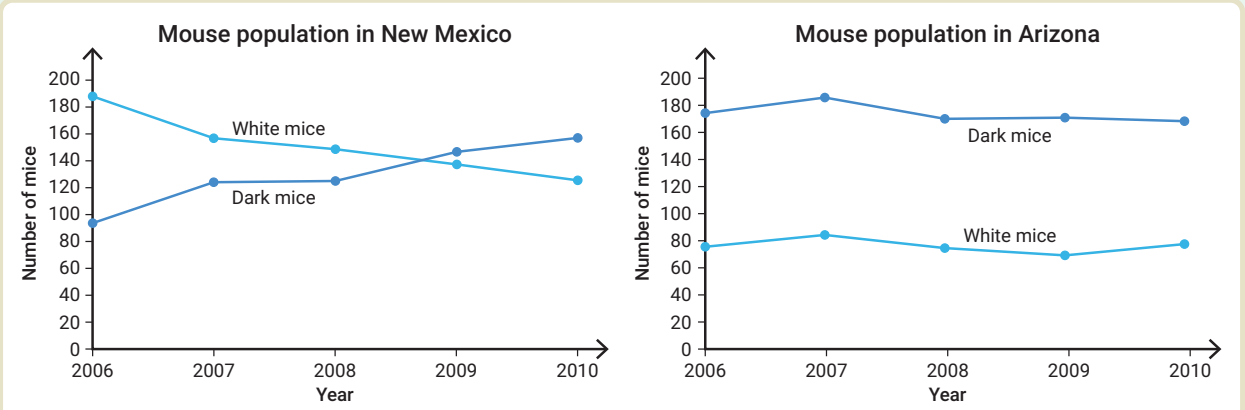


FIGURE 12.3.9 The rock pocket mouse populations in New Mexico and Arizona

Rick & Nora Bowers/Alamy Stock Photo

Michael/Adobe Stock Photos

FIGURE 12.3.10 (a) The light-coloured and (b) the dark-coloured rock pocket mouse

Interpretation

1 Identify any trends, patterns or relationships shown in the graphs.

New Mexico

Trend: Over time, the number of dark mice increases and the number of light mice decreases.
Pattern: The total number of mice present each year remains approximately constant at about 250 mice.

Arizona

Pattern: The number of dark mice is always higher than the number of light mice, by about 100 individuals each year.
Pattern: The total number of mice present each year remains approximately constant at 250–270.

2 Complete an interpretation by providing an explanation for the observed trends and patterns.

New Mexico

The changing proportions of mouse colour suggests that there is a new selection pressure – the environment has become a darker colour. Consequently, the lighter coloured mice are more visible to predators and are eaten before reproducing successfully, so their alleles are removed from the population. The darker coloured mice are better camouflaged; therefore, they are more likely to survive long enough to reproduce and pass on the alleles for the darker fur colour. Over 3 years (2006–2009), the alleles controlling light-coloured fur are reduced (selected against) in the population and the alleles for dark-coloured fur become more common (selected for).

This change is unlikely to be due to gene flow (immigration or emigration) because there is no overall change in population size.

This change is unlikely to be due to genetic drift because the overall population size is unchanged, and genetic drift occurs when there is a dramatic drop in population size due to the bottleneck or founder effects.

This change is unlikely to be due to a new mutation because there are still only two phenotypes present in the population.

Arizona

During the same timeframe, there has been no change in selection pressure because the number and proportion of each colour of mouse has remained relatively constant. This suggests that there has been no change in allele frequency either.

PRACTICAL ACTIVITY 12.3.1

ANALYSING GENOTYPIC CHANGES FOR A SELECTIVE PRESSURE IN A GENE POOL

Introduction

Natural selection can alter the frequency of genotypes in a gene pool. Selective pressures can have a positive or a negative effect on alleles. Those individuals with alleles that give them an advantage of survival and reproduction will contribute those alleles to future generations. Individuals with alleles that put them at a disadvantage contribute fewer of those alleles to future generations. Different phenotypes in a population are favoured by three main types of phenotypic selection – stabilising, directional and disruptive.

In this scenario, an artificial population consisting of paper squares will represent bugs. The bug population has an inherited variation in colour – black, grey and white. Students will represent bird predators of the bug.

Selection pressure will be determined by the background (environment):

- A snow-covered area (white background)
- An area exposed to a local coal mine (black background)
- An area where the snow-covered and coal-exposed areas are next to each other (black and white background)
- A natural area with no covering (grey background)

Bug colour is determined by a pair of alleles showing incomplete dominance:

- Black = C^BC^B
- Grey = C^BC^W
- White = C^WC^W

Research question

Does the allele frequency within a gene pool change because of the selective pressure of environment colour?

Aim

To analyse changes in genotypes in a gene pool when a hypothetical population of bugs is exposed to stabilising, directional and disruptive selection pressures

Materials (per group)

- 3 cm × 3 cm squares of paper or cardboard – 50 black, 50 grey, 50 white
- 3 × A3 or poster-size pieces of cardboard – 1 black, 1 grey, 1 white
- paper bag or cup

Preparation

The bug population at the beginning of this scenario consists of 10 black, 10 grey and 10 white. The initial genotypes can be shown in the table.

Black bug	Grey bug	White bug
C^BC^B	C^BC^W	C^WC^W

1 Record the initial allele frequency in a table like the one below:

C^B	C^W

Breeding of a pair of bugs results in one offspring.

2 Determine the ratio of expected offspring by completing Punnett squares of the possible matings: black × black, black × grey, grey × grey, grey × white, white × white, white × black.

Procedure

Your teacher may choose for each group to complete one scenario and then share the data for the other scenarios.

1 To represent random mating, mix the 30 black, grey and white squares together in a paper bag or cup, then draw out four pairs. Add four offspring based on the Punnett square for the randomly selected parent pairs. The population now consists of 46 individuals.

2 In the first scenario, snow falls. Place the 46 squares randomly on the white cardboard. A predator (a student in the group) looks away from the cardboard then looks back to the cardboard and takes the first square they see. Other members of the group follow the same procedure until 15 squares have been taken.

3 Count the number of squares of each colour remaining and enter the phenotypes in Table 12.3.2 and genotypes in another table for Generation 2. The remaining squares make up the breeding population for the next generation.

4 Repeat steps 1–3, recording the genotypes for five generations.

5 In the second scenario, a coal station is established in the area and a layer of coal dust spreads over the ground. Repeat steps 1–4, using the black cardboard as the background.

6 In the third scenario, snow covers part of the coal dust area. Repeat steps 1–4, using white and black cardboard placed next to each other.

7 In the fourth scenario, the ground is not covered with either snow or coal dust. Repeat steps 1–4, using grey cardboard as the background.

Results

Draw up eight tables similar to Table 12.3.2, showing the phenotypes, genotypes and allele frequencies of bugs in each generation for the four scenarios.

TABLE 12.3.2 Phenotype frequencies in a bug population

Scenario:				Allele frequency	
Generation	**Black bugs**	**Grey bugs**	**White bugs**	**C^B**	**C^W**
Parents					
1					
2					
3					
4					
5					

Analysis of results

1 Calculate the percentage of C^B and C^W alleles in each generation for each scenario.

2 Identify trends relating to phenotypes and allele frequencies in each scenario.

3 Identify the alleles that are selected for and the alleles that are selected against in each scenario.

Interpretation

4 Explain the factor in each scenario that has brought about the genotypic changes.

5 Explain how a situation could arise where the percentages of C^B and C^W alleles are equal but only one phenotype is selected for. Identify in which scenario this happened.

6 Identify and explain which scenario is typical of:

- **a** stabilising selection
- **b** directional selection
- **c** disruptive selection.

7 Explain how different selective pressures affect the survival and reproduction of specific genotypes and phenotypes in a population to provide an answer to the research question.

Evaluation

8 Compare the assumptions made in this activity to the real-life situation faced by a bug population.

LEARNING CHECK 12.3

DESCRIBING

1 **Describe** how natural selection contributes to evolutionary change.

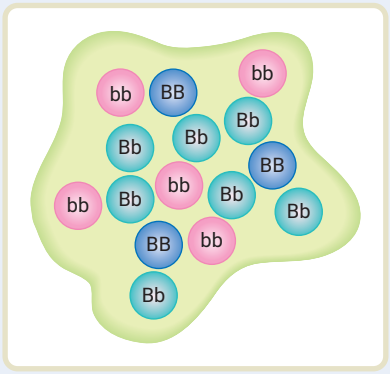
2 State the three types of phenotypic selection and provide an example of each.

APPLYING

3 A population of parrots in tropical Queensland has darker feathers than parrots in other parts of Queensland. These parrots are more suited to the low light intensities of tropical rain forests.

Explain the type of phenotypic selection this represents.

4 **Calculate** the frequency of each allele represented in the following population.



INTERPRETING

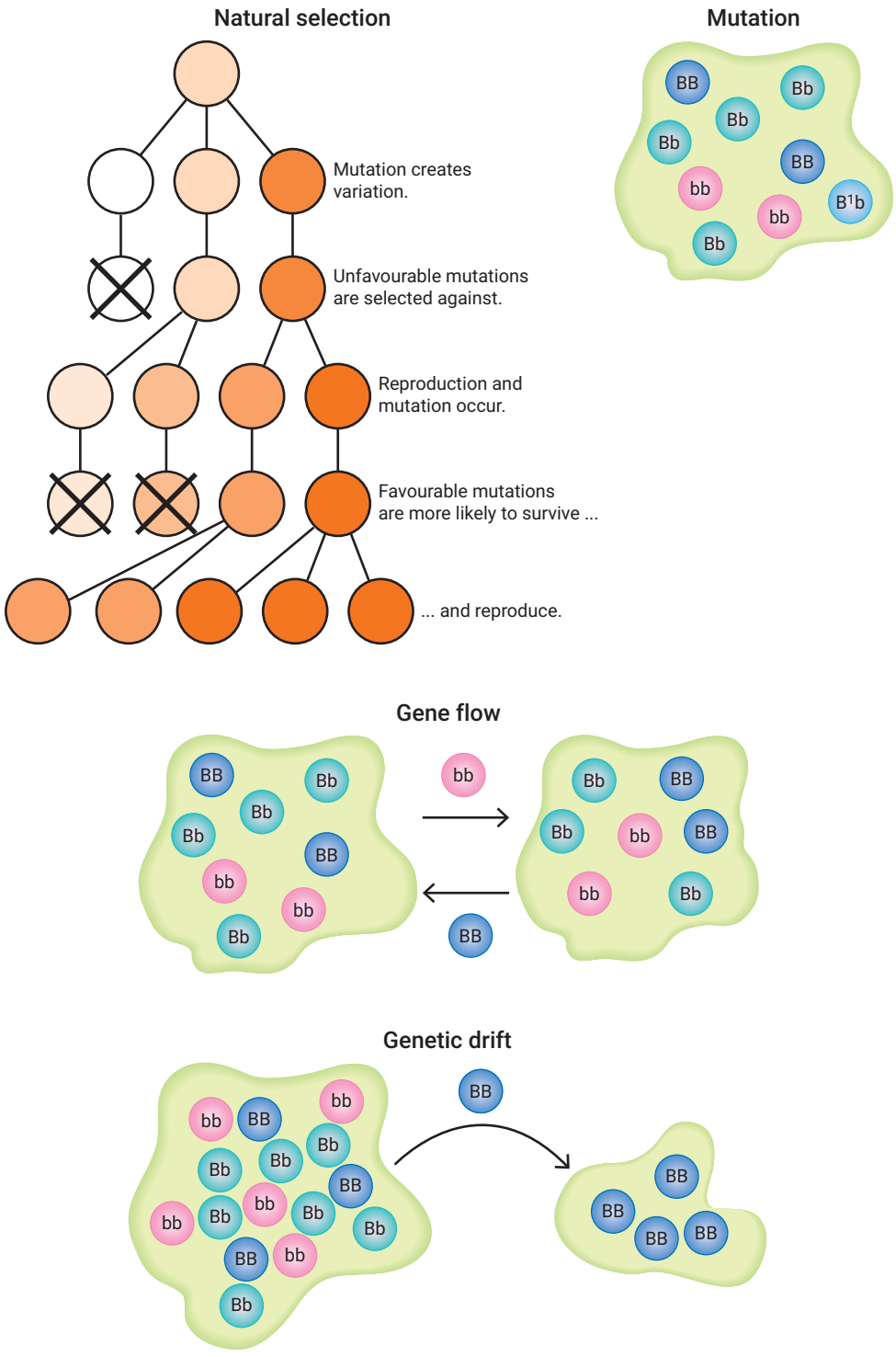
5 *Abdopus aculeatus* is a small species of octopus. The male octopus generally chooses the biggest female octopus to mate with, regardless of his own size, because the larger females lay more eggs.

Determine whether males of the species are providing a selection pressure on females. Provide reasons.

CHAPTER SUMMARY

Microevolution

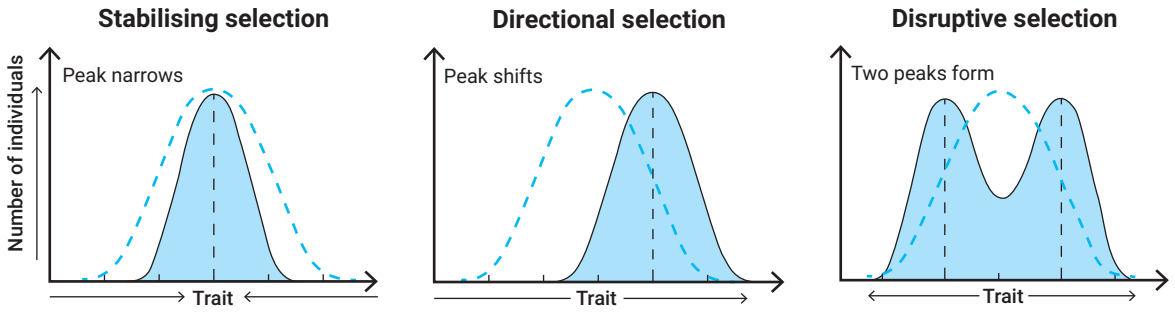
- Microevolution involves a change in allele frequency of a population over a short time. Individuals are still considered the same species.



Selection

- Selection pressures cause some traits in a population to become more common and others to become less common.

Types of phenotypic selection



CHAPTER EXAM

MULTIPLE CHOICE

1. Which of the following is true of gene pools?
- **A** Alleles within a gene pool are all favourable.
- **B** New alleles can be introduced into a gene pool via mutations.
- **C** Small gene pools are an advantage in a particular population.
- **D** A gene pool includes half of the alleles for a trait within a population.

2. A new road was constructed that isolated a small percentage of a cricket population. After several generations, the isolated population showed very different genetic make-ups compared to the original population. This is an example of:
- **A** emigration.
- **B** gene flow.
- **C** genetic drift.
- **D** migration.

3. Natural selection is based on the idea that some individuals will survive and reproduce at the expense of others. This is known as survival of the fittest. The fittest individuals are those who:
- **A** live the longest due to being fit throughout their lives.
- **B** can out-run any competitors because they are physically healthy.
- **C** are the most successful fighters, who regularly kill their opponents.
- **D** produce the largest number of viable offspring and therefore have the greatest influence on the next generation's phenotype.

4. A scientist measured the circumference of gumnuts in a population of snow gums and found that the average circumference was 2.5 cm. After 10 generations of stabilising selection, it is expected that the average circumference would be:
- **A** 2.5 cm.
- **B** less than 2.5 cm.
- **C** greater than 2.5 cm.
- **D** greater than 2.5 cm or less than 2.5 cm.

Questions 5 and 6 relate to the following information.
Sockeye salmon migrate to reproduce in the same river in which they were born. In the Bristol Bay in Alaska, USA, the timing of migration has shifted to 4 days earlier than usual, which is a significant change. The shift is thought to be due to changes in water temperature and later periods overlapping with heavier fishing by local people.

5. This change in the salmon's behaviour is an example of:
- **A** artificial selection.
- **B** directional selection.
- **C** disruptive selection.
- **D** stabilising selection.

6. The selection pressure is:
- **A** changing pH.
- **B** changing salinity.
- **C** changing air pressure.
- **D** changing temperature.

7. A population had 10 individuals with AA genotype, 10 individuals with Aa genotype and five individuals with aa genotype. The allele frequencies are:
   - **A** A = 0.5, a = 0.5
   - **B** A = 1.0, a = 0.0
   - **C** A = 0.6, a = 0.4
   - **D** A = 0.75, a = 0.25

8. Microevolutionary changes result in different allele frequencies that mean individuals from the population are:
   - **A** a new species.
   - **B** unable to be classified.
   - **C** now part of multiple species.
   - **D** still part of the same species.

9. For evolution to occur, any mutation must be:
   - **A** advantageous.
   - **B** deleterious.
   - **C** harmful.
   - **D** heritable.

10. From a population of 100 individuals, six breeding pairs moved to a different area, forming a new population. This is an example of:
   - **A** genetic drift.
   - **B** gene flow.
   - **C** immigration.
   - **D** mutation.

SHORT RESPONSE

11. **Compare** gene flow and genetic drift.

12. A population of rabbits has a range of colours from black to white. In their normal habitat of open grassland, grey rabbits are the most common; black and white rabbits are rare. The rabbits moved to an area that had very dark black rocks as well as white rocks.
   - **a** **Describe** the expected changes in population phenotypes over time.
   - **b** Name the type of phenotypic selection this represents.
   - **c** Outline how the expected changes in population phenotypes came about.

CROSS-CHAPTER QUESTION

13. **Explain** how mutation and meiosis lead to genetic variation that can be acted on by microevolutionary processes.

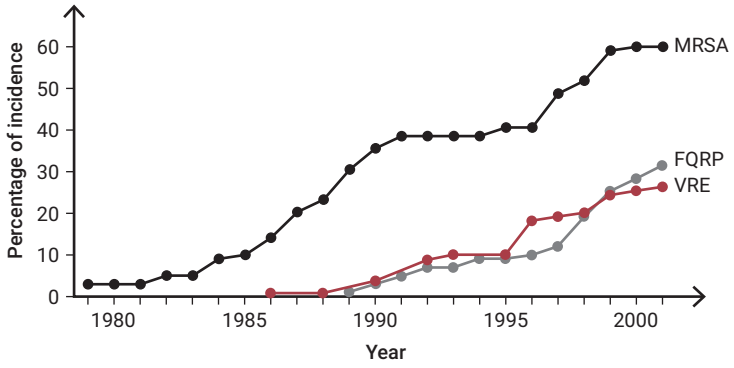
DATA ANALYSIS

Questions 14 and 15 refer to the following information.

There is a natural variation in the resistance of bacteria to antibiotic drugs. Before the development of antibiotics in the 1940s, there was no advantage for bacteria to be antibiotic resistant. After antibiotics were developed and used, the range of bacterial drug resistance changed. The following graph shows the increase in resistance rates for three bacteria that are of concern to public health officials: methicillin-resistant *Staphylococcus aureus* (MRSA),

vancomycin-resistant enterococci (VRE) and fluoroquinolone-resistant *Pseudomonas aeruginosa* (FQRP). The data was collected from hospital intensive care units that participate in the National Nosocomial Infections Surveillance System, a component of the Centers for Disease Control and Prevention in the USA.

Antibiotic resistance of methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci (VRE), and fluoroquinolone-resistant *Pseudomonas aeruginosa* (FQRP)



14. Analysing data

a **Identify** a trend in the antibiotic resistance of MRSA.

b **Identify** a pattern shown by the three types of bacteria.

15. Interpreting evidence

Determine whether this data provides evidence for natural selection. Provide reasoning that includes data from the graph.

CHAPTER 13

Evolutionary processes

Avalon.red/Alamy Stock Photo

SYLLABUS DOT POINTS

SCIENCE UNDERSTANDING

- 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.
- Explain why populations with reduced genetic diversity face increased risk of extinction.
- Explain how comparative genomics provides evidence for the theory of evolution and how conserved sequences can be used to date divergence.
- Infer species relatedness from cladograms, phylograms and molecular sequence data.
- Determine episodes of evolutionary radiation and mass extinctions from an evolutionary timescale of life on Earth (approximately 3.5 billion years).

Introduction

Australia is the only continent that is home to all three lineages of mammals: monotremes, marsupials and placentals. They all share these mammalian characteristics: mammary glands to produce milk, a single bone on each side of the lower jaw and some body hair. Australian mammals range in size from a few grams – the smallest marsupial being the long-tailed planigale (*Planigale ingrami*) (2.6–6.6 g) – to more than 90 kg for marsupials such as the red kangaroo (*Osphranter rufus*).

About 87 per cent of Australia's mammals only live in Australia. This is also true for 93 per cent of Australia's flowering plants, more than 80 per cent of its invertebrates, 93 per cent of its reptiles, 94 per cent of its frogs, 74 per cent of its freshwater fishes and 50 per cent of its temperate marine fishes. What processes have occurred to mean that Australia has so many species of unique flora and fauna? The answer is isolation.

ASSUMED KNOWLEDGE

- ✓ Gene flow, genetic drift, mutation and natural selection are microevolutionary processes.
- ✓ A population is a group of organisms of the same species living in the same area.
- ✓ A genome is the complete set of genetic information (DNA) in an organism.
- ✓ A gene pool is all the alleles in a reproducing population.
- ✓ Species concepts include the biological, morphological and ecological species concepts.
- ✓ A molecular sequence is a single continuous sequence of DNA or amino acids.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ describe types of evolution with examples, including divergent, convergent, parallel and coevolution
- ✓ describe how microevolutionary changes of gene flow, genetic drift, mutation and natural selection lead to each type of evolution
- ✓ explain how temporal isolation affects gene flow, leading to the formation of a new species
- ✓ explain how geographic isolation affects gene flow, leading to the formation of a new species
- ✓ explain how spatial isolation affects gene flow, leading to the formation of a new species
- ✓ explain whether the type of isolation affecting gene flow results in allopatric, sympatric or parapatric speciation
- ✓ explain why a population is at a higher risk of extinction when there are fewer alleles for genes
- ✓ explain the evidence for evolution that is provided by comparing the genomes of different species
- ✓ explain how differences in genetic sequences conserved between species are an indication of the length of time since those species diverged
- ✓ use data presented as cladograms, phylograms and molecular sequences to draw conclusions about how related particular species are
- ✓ use information presented over a large time scale (approximately 3.5 billion years) to identify periods of increasing species (evolutionary radiations) and periods of decreasing species (mass extinctions).

13.1 Speciation

Before Darwin's theory of evolution by natural selection, the general belief was that species were unchanging because each species had been put on Earth in its current form and could not change over time. In general, the fossil record shows that not only do species change, but that these changes can be dramatic. It also shows that a single species can diverge to produce several new species. After observing giant tortoises on mainland South America and the geologically young Galapagos Islands 1000 km off the coast of Ecuador, Darwin proposed that the ancestral type of tortoise that still exists on the South American mainland had somehow split to create new species of giant tortoise on the Galapagos Islands, more suited to the island environment. Darwin represented this process using a series of branching diagrams that show diverging lineages over multiple generations forming new species with populations that can no longer interbreed (Figure 13.1.1). The formation of one or more descendant species from an ancestor species is known as **speciation**.

speciation the evolution of one or more new species from an ancestral species

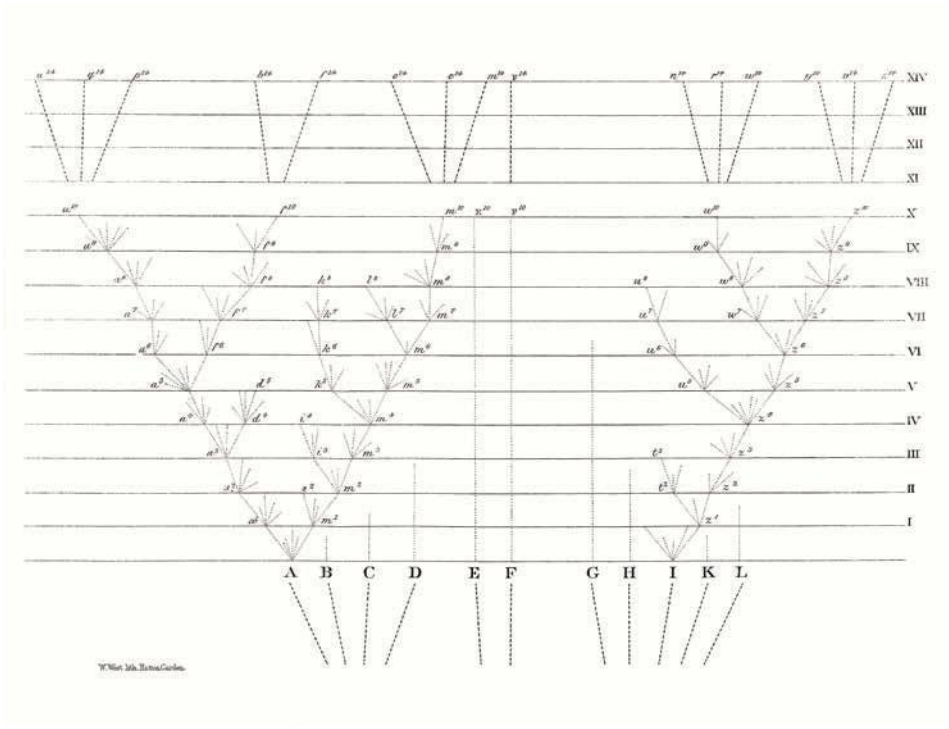


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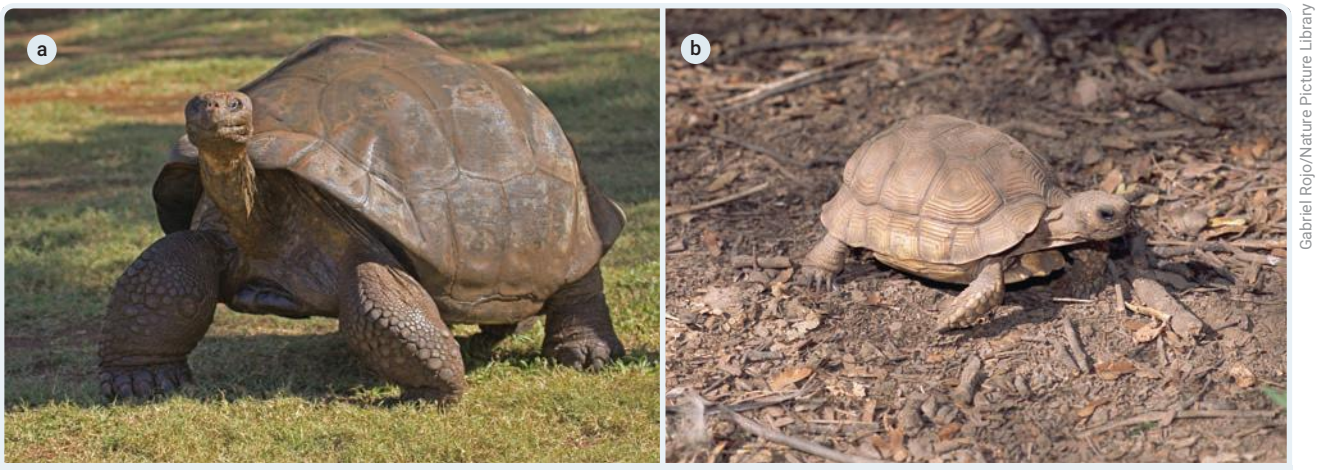
FIGURE 13.1.1 Darwin's speciation diagram

Weblinks
Speciation
Defining speciation

Worksheet
Macroevolution

macroevolution the variation of allele frequencies at or above the species level, over geological time, resulting in the divergence of taxonomic groups, in which the descendant is in a different taxonomic group from the ancestor

microevolution small-scale variation of allele frequencies within a species or population, in which the descendant is of the same taxonomic group as the ancestor



Rico Leffanta/Dreamstime LLC

Gabriel Rojo/Nature Picture Library

FIGURE 13.1.2 (a) The famous Galapagos tortoise (*Chelonoidis nigra*). Nothing like it exists anywhere else in the world, although it is similar to (b) the much smaller Chaco tortoise (*Geochelone chilensis*) from South America.

The emergence of new species through **macroevolution** results from an accumulation of **microevolutionary** changes (due to genetic drift, mutation, natural selection and gene flow) over a long time scale.

Scientists have hypothesised that there may be more than be 8 million different species on Earth, but this is difficult to estimate accurately because only about 1.2 million species have been identified and classified. How new species have evolved in such large numbers is a key part of the theory of evolution.

Weblinks
Natural selection
What is macroevolution?
Reproductive isolation

Three broad processes work together in the evolution of this great diversity:

- Natural selection favours phenotypes that makes individuals in a population better suited to their environment. Populations change over time as their gene pools accumulate small changes in response to natural selection, genetic drift, gene flow and mutations.
- Eventually a population accumulates so many changes that a new species can be identified. This process can lead to speciation – the multiplication of species.
- Sometimes a rapid series of speciation events leads to new species, or even genera, families and higher classification groups.

Syllabus link
Chapter 12 discusses microevolutionary changes such as gene flow, genetic drift and natural selection.

LEARNING CHECK 13.1

APPLYING

1 **Explain** how microevolutionary changes can lead to speciation.

13.2 Isolation

Isolation processes explain how a single population can be split into two populations, with gene flow between them blocked by the isolating mechanism (Figure 13.2.1). When the two populations experience different selection pressures, caused by geographic, temporal or spatial differences in their respective environments, different microevolutionary changes accumulate in each population. Without gene flow between them, these genetic changes cannot be shared and, over time, the populations diverge to the point where they cannot reproduce successfully if reunited.

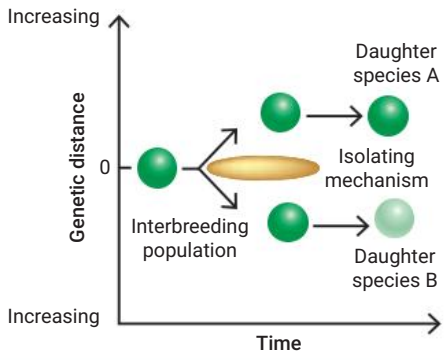


FIGURE 13.2.1 An isolating mechanism can prevent two subgroups of a species from breeding, until they are so genetically diverse that they form two new species. After a period of time they are no longer able to interbreed, even if the populations come back together.

reproductive isolation processes that prevent individuals of separated populations from mating and producing fertile offspring

Isolation occurs over different time scales and in different ways. Some researchers describe **reproductive isolation**, the inability to successfully interbreed, as an outcome, while others describe it as a process. Reproductive isolation can be prezygotic and occur before gametes form a zygote, or it can be postzygotic, affecting the viability and fertility of offspring. Prezygotic isolation can result from geographic, temporal, spatial or behavioural barriers. Most evidence suggests that separation of populations is not sudden and that the rate of change is highly variable across species.

Geographic isolation

Geographic isolation occurs when individuals are separated by geographic features, such as seas, mountains, rivers, roads and urban development. The isolation may happen on a small scale, such as when a river or stream changes course and divides a population of small animals that cannot cross it or on a larger scale, such as deserts expanding and cutting off populations that cannot live in desert conditions. Environmental disasters such as fire and earthquakes can also separate populations.

geographic isolation when populations of the same species are separated by a type of physical barrier

The effectiveness of a geographic feature as an isolating mechanism depends on its ability to reduce or prevent gene flow, which is closely linked to the size and mobility of the individuals in the population. For example, small organisms may be easily carried across ocean barriers by other animals. Parts of plants, such as seeds and stems, can float; small rodents can cling to floating vegetation carried by tides; and winds may carry insects over bodies of water.

Over different timeframes, populations can be separated by water (for terrestrial organisms), land (for aquatic organisms), mountains, continental drift, rising sea levels or climate change.

If gene flow between populations is no longer possible after the environmental change and environmental conditions exert different selection pressures, new species may form.

Spatial isolation

Spatial isolation (sometimes considered habitat isolation) occurs when populations that could interbreed do not because the species live in different areas and are separated by spaces in which they do not travel. The space or distance creates an impracticality rather than a geographical or physical barrier. Just like geographic isolation, the effectiveness of space as a barrier depends on the mobility of the species.

An example is a population of sea cucumbers (*Pearsonothuria graeffei*) **(Figure 13.2.2)** with a continuous distribution along the coastlines of Queensland, Northern Territory and Western Australia. This coastline is many kilometres long and sea cucumbers at their most mobile cannot move from Queensland to Western Australia. Research published in 2023 shows that *P. graeffei* movement rates average 9 m year^{-1}. They have no need to move long distances because they find plenty of food and potential mates in the metres either side of them.

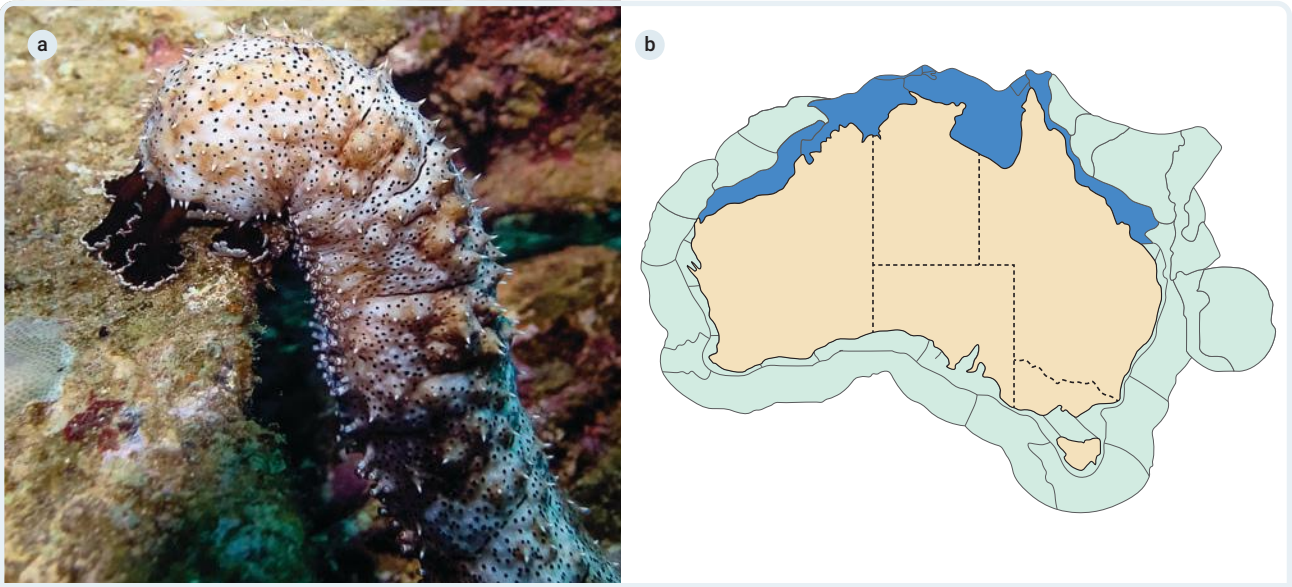


FIGURE 13.2.2 (a) *Pearsonothuria graeffei* and (b) a map showing the distribution of *Pearsonothuria graeffei* around Australia

Over time, despite a continually reproducing population that is not geographically separated, there may be gene flow only between small pockets not through the whole habitat. Eventually, this could lead to reproductive isolation, then speciation, where the Western Australian individuals can no longer successfully interbreed with the Queensland individuals.

Temporal isolation

Temporal (time) isolation occurs when the timing of mating varies and individuals breed at different times of the day, season or year.

Temporal isolation is a common feature of the coral genus *Acropora* populations at Scott Reef off the coast of north-west Western Australia **(Figure 13.2.3)**. Six of the species sampled in research published in 2016 showed that one species (*A. millepora*) spawned only in spring, whereas five species spawned only in autumn. Even though these species occur in similar locations, gene flow is prevented between *A. millepora* and the species that spawn only in autumn because of the different timings of their spawning.

Kornniphab84/Shutterstock.com

FIGURE 13.2.3 An example of an *Acropora* species of coral

Some isolating processes prevent organisms from interacting to reproduce, preventing the zygote from forming and are considered prezygotic. Other forms of prezygotic isolation described in research (not stated in the syllabus) are:

- behavioural isolation: individuals have different courtship patterns or mating rituals, which are necessary for organisms to recognise potential reproductive partners (e.g. movements, dances or sounds)
- morphological/mechanical isolation: individuals have different reproductive structures so that mating is physically impossible (e.g. genitalia of different size, shape or location)
- gamete mortality: the gametes do not survive; therefore, fertilisation cannot occur
- chemical isolation (e.g. pollinators do not recognise a particular scent released by flowers).

Reproductive isolation can also occur due to postzygotic processes, where the lack of successful breeding only occurs after a mating has happened and produced a zygote. This prevents offspring viability, including:

- zygote mortality: the zygote forms but does not survive
- hybrid viability or sterility: adult offspring are formed but are infertile because they are unable to produce viable gametes, usually because each species has a different number or structure of chromosomes. Hybrids may not develop to reproductive maturity or F_1 hybrids may be fertile, but not F_2 hybrids.

Note that identifying prezygotic or postzygotic mechanisms is not stated in the 2025 syllabus.

LEARNING CHECK 13.2

DESCRIBING

1 **Identify** three types of barriers that separate populations, leading to speciation.
2 **Describe** how reproductive isolation results in speciation.

APPLYING

3 **Explain** a key difference between geographic and spatial isolation.
4 **Explain** why temporal isolation can lead to reproductive isolation.

13.3 Modes of speciation

Speciation is the accumulation of genetic differences that build up over time due to reproductive isolation resulting from barriers that mean gene flow is rare or ineffective. Each type of isolation – geographic, spatial or temporal – is associated with a different mode of speciation.

Syllabus link
Chapter 5 also discusses habitat fragmentation.

Allopatric speciation

In **allopatric speciation**, gene flow is disrupted as populations become physically separated through geographic isolation (Figure 13.3.1). The populations diverge because of mutations arising, genetic drift and/or the action of selection pressures occurring differently on either side of the barrier. Allopatric speciation is the most commonly observed form of speciation, and is becoming more common due to urban development fragmenting natural habitats. One way to encourage gene flow between artificially fragmented habitats is by providing wildlife corridors that link separated populations.

allopatric speciation the speciation that is due to geographic isolation

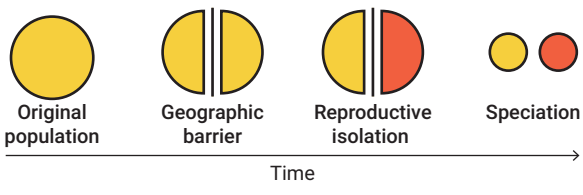


FIGURE 13.3.1 Allopatric speciation results from geographic isolation.

Weblinks
Natural selection
Allopatric speciation
Parapatric speciation

The common Sydney octopus (*Octopus tetricus*) (Figure 13.3.2) lives throughout waters of subtropical eastern Australia. A closely related species (*O.* cf. *tetricus,* now know as *O. djinda*) lives at similar latitudes in waters off Western Australia. Research published in 2014 suggests that speciation between *O. tetricus* and *O. djinda* is probably due to allopatric speciation as the eastern and western populations became reproductively isolated. Divergence of *O. tetricus* (east Australian population) and *O. djinda* (Western Australia) was estimated to have occurred somewhere within the last 3.2–6.9 million years.

Dirk van der Heide/Shutterstock.com

FIGURE 13.3.2 *Octopus tetricus*, also known as the common Sydney octopus or peachy octopus

Parapatric speciation

parapatric speciation the speciation that occurs when populations are separated by an extreme change in habitat; populations may interbreed in bordering areas

Sometimes, even though gene flow within a population is not prevented by a physical barrier, reproductive isolation still arises. **Parapatric speciation** results from spatial isolation, where individuals are more likely to mate with individuals in their immediate habitat or niche than with individuals in a different area of the same environment (Figure 13.3.3). Populations undergoing parapatric speciation may also have a hybrid zone where individuals have reduced genetic fitness.

This could arise if members of a population expanded into areas surrounding the original population. Individuals at each edge of the larger area are unlikely to breed with each other and they may be subject to different selection pressures (like the sea cucumbers mentioned earlier). Gene flow would still continue in a hybrid zone where two populations meet, but over time different areas of the original population diverge to become better adapted to the different conditions in different areas of the environment. If the hybrids are 'unfit', it reinforces reproductive barriers.

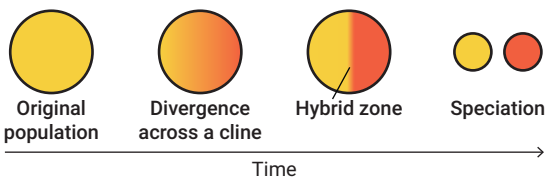


FIGURE 13.3.3 Parapatric speciation results from spatial isolation over time.

Sympatric speciation

Sometimes species diverge without any obvious spatial or geographic isolation. **Sympatric speciation** refers to the evolution of two or more new species from a single population within the same place. Sympatric speciation still requires reproductive isolation. It might be that groups within a single population feed on different things, or choose mates based on different characteristics (behavioural isolation). They may also choose to mate at different times (temporal isolation), or they may experience morphological/mechanical or chemical isolation. If gene flow between the isolated population and main population is prevented, and different selection pressures act on the populations, allele frequencies may become so different that individuals may be unable to interbreed, resulting in evolution of new species from a single population within the same place.

sympatric speciation the speciation that occurs without spatial or geographic isolation

Weblink
Sympatric speciation

Worksheet
Speciation

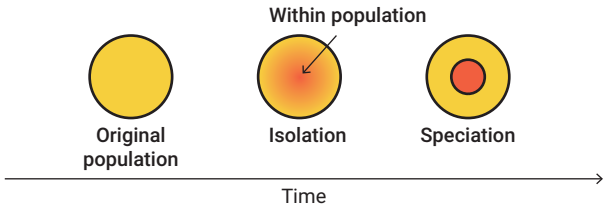


FIGURE 13.3.4 Sympatric speciation results from mainly behavioural or temporal isolation.

There are not as many clear examples of this type of speciation, but two species of palm that originated on the relatively small Lord Howe Island, *Howea bemoreana* and *Howea forsteriana*, grow in the same area but are different species (Figure 13.3.5). *H. forsteriana* flowers approximately

FIGURE 13.3.5 (a) Lord Howe Island, (b) the palm species *Howea belmoreana* and (c) the palm species *Howea forsteriana*

6 weeks before *H. bemoreana*, meaning cross-pollination and fertilisation cannot occur. The difference in timing seems to have resulted from the physiological stress caused by the alkaline, nutrient-poor soil *H. forsteriana* grows in, triggering earlier flowering than *H. bemoreana*, which grows in neutral to acidic soils.

LEARNING CHECK 13.3

DESCRIBING

1 **Describe** the process of sympatric speciation and provide an example.
2 **Identify** at least four factors that can act as geographic barriers.
3 **Describe** how forest fragmentation can contribute to speciation.

APPLYING

4 **Explain** the process of allopatric speciation and provide an example.
5 **Explain** the process of parapatric speciation and provide an example.

13.4 Patterns of evolution

The process of speciation can lead to different patterns of species diversification. Since selection pressures affect the evolutionary pathway of each species, evolution gives rise to groups of organisms that become very different from each other as well as groups of organisms that are similar yet not closely related. Four patterns of evolution are identified: divergent, convergent, parallel and coevolution, shown in **Figure 13.4.1**.

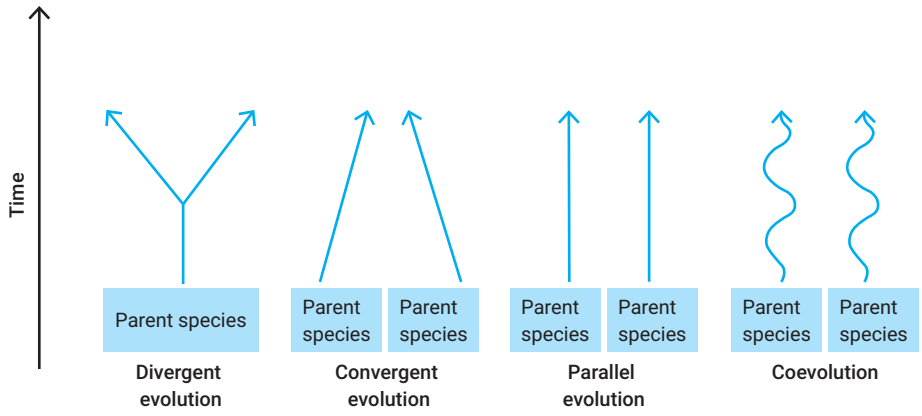


FIGURE 13.4.1 The four types of evolution: divergent, convergent, parallel and coevolution

Divergent evolution

Divergence is the pattern of evolution that arises from reproductive isolation. A population of a species, known as the common ancestor begins to accumulate genetic differences. Over time, organisms from the same species become reproductively isolated from each other. Different selection pressures, mutations and genetic drift, along with reduced gene flow, mean there are increasing differences, until speciation occurs. The more recent the common ancestor, the more closely related the species are.

For example, koalas (tree-dwelling herbivores), Tasmanian devils (ground-dwelling carnivores) and marsupial moles (dune-burrowing insectivores) have a common marsupial ancestor (Figure 13.4.2). However, they have quite different feeding structures that suit their different diets. These animals are an example of **divergent evolution** because they have evolved into separate species from a common ancestor.

divergent evolution a process whereby related organisms acquire new traits over time, away from the common ancestor, to give rise to new species

Martin Valigursky/Shutterstock.com; james_stone76/Shutterstock.com Tom McHugh/Science Source

FIGURE 13.4.2 (a) Koalas, (b) Tasmanian devils and (c) marsupial moles evolved from a common ancestor. They are examples of the divergent evolution of marsupials.

Convergent evolution

Convergent evolution is a pattern that occurs when unrelated organisms have similar adaptations in response to similar selection pressures. The similar adaptations are not inherited from a recent common ancestor and they did not speciate from each other.

convergent evolution a process whereby unrelated organisms evolve similar adaptations in response to similar environmental pressures

An example of convergent evolution is provided by two marine species in Australian waters. Sharks, such as the great white shark (*Carcharodon carcharias*), are classified as chondrichthyes or cartilaginous fish, that complete gas exchange via gills. Dolphins, such as the bottlenose dolphin (*Tursiops truncatus*), are classified as mammals, exchanging gas through lungs. These two species do not have a recent common ancestor. However, dolphins and sharks both have streamlined body shapes that minimise drag, dorsal fins and powerful tails that allow them to move effectively through water. Sharks and dolphins have developed similar shapes independently, rather than inheriting them from a common ancestor. The results of convergent evolution often show up as adpatations of different structures that solve a problem in a similar way.

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FIGURE 13.4.3 (a) Sharks and (b) dolphins both have streamlined shapes, showing convergent evolution.

Parallel evolution

parallel evolution a process whereby related organisms are reproductively isolated but evolve similar adaptations in response to the same environmental pressures

Parallel evolution describes the pattern where two species initially diverge from a common ancestor. However, they develop similar characteristics, despite not living in the same location. This pattern of evolution occurs where several species respond to similar selection pressures in a similar way. The independent development of similar features in marsupial mammals in Australia to placental mammals on other continents that occupy different but equivalent habitats is an example of parallel evolution **(Figure 13.4.4)**.

FIGURE 13.4.4 Parallel evolution of the (a) Australian sugar glider (*Petaurus breviceps*) and (b) North American flying squirrel (*Glaucomys volans*). Both have a membrane along either flank, attached to the forelegs and hind legs, allowing them to glide through the air.

Coevolution

coevolution a process whereby an evolutionary change in one species influences the evolution of another species

Where there is a close relationship in species that interact with each other, such as predator–prey, parasite–host, competitive and mutualistic species, evolutionary changes are closely connected. This pattern of evolution is called **coevolution**.

Research published in 2004 compared the responses of Australian native bees (*Austroplebia australis*) and introduced honeybees (*Apis mellifera*) when choosing to land on daisies. Some flowers were occupied by the Australian crab spider (*Thomisus spectabilis*), a species that manipulates visual flower signals to lure bees **(Figure 13.4.5)**. Although native bees made more approaches to spider-occupied flowers, they landed on vacant flowers more frequently. This bee, which coevolved with *T. spectabilis* showed an anti-predatory response to avoid flowers occupied by this predator. The Australian native bees perceive and avoid their spider predators, unlike introduced European honeybees.

In a predator–prey relationship, the activities of both predator and prey apply selection pressures. In the previous example, the prey species has become effective at avoiding flowers hosting predators; therefore, predators will need to develop new strategies to attract prey (e.g. by making themselves less conspicuous).

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FIGURE 13.4.5 (a) Predators, such as this crab spider, have evolved abilities to catch their prey (bees). (b) European honeybees have not evolved ways to protect themselves from the crab spider but (c) native bees have. This is an example of coevolution between native crab spiders and native bees.

LEARNING CHECK 13.4

DESCRIBING

1 **Describe** the four patterns of evolution: divergent, convergent, parallel and coevolution.

APPLYING

2 During his famous voyage to the Galapagos Islands, Charles Darwin noticed different species of giant tortoises on different islands. The ancestral species lives on mainland Ecuador. Suggest the pattern of evolution involved and **explain** how new species of giant tortoises formed.

3 In a parasite–host relationship, the parasite's harmful effects and the host's resistance act as selective agents. **Explain** why this is an example of coevolution.

INTERPRETING

4 Many animals eat ants and termites and have developed similar structures even though they are not closely related. Modern anteaters include monotreme echidnas, marsupial numbats, placental aardvarks and pangolins (Figure 13.4.6). These species have the following similar features:

- An elongated snout that functions as a smelling and digging device
- A long extendable tongue that can extract ants from crevices
- Powerful claws that are used for digging up ant and termite nests

Determine whether ant-eating mammals provide evidence of convergent evolution or parallel evolution. Provide reasoning for your argument.

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FIGURE 13.4.6 Ant-eating mammals include (a) echidnas (monotremes), (b) numbats (marsupials) and (c) pangolins (placentals), which show convergent evolution with ant-eating structures.

13.5 Evolution and extinction

Earth was formed about 4.5 billion (4500 million) years ago and life has existed on Earth for approximately 3.5 billion (3500 million) years. Time scales such as periods, eras, epochs and eons have been devised to measure enormous lengths of time. These measurements are known as geologic time and are expressed as millions of years ago (mya). Over the course of its history, Earth's climate has oscillated between hot and humid and cold and dry. Some of these changes were rapid and dramatic, causing major changes to sea levels and temperatures; others occurred more slowly. Earth has been much warmer than it is today and the temperature difference between the equator and the poles was not as large. At other times, snow, glaciers and sheets of ice covered much of Earth and sea levels were lower.

Weblinks
Mass extinction

The origin of life on Earth, explained

These environmental changes contribute to another powerful process: extinction. The logical extension of the theory of evolution and the process of natural selection is that changes in the environment of an organism may make the habitat so unsuitable that all members of the species die, and the species becomes extinct.

Naturally occurring extinctions are primarily the result of two interacting processes: competition between species and environmental change. As environments change, they impose pressures on species to adapt to such changes. Species that are unable to survive in the changing environment are replaced by species that can. For example, the Nullarbor Plain, which extends across southern Western Australia and South Australia, once formed part of an inland sea and swamp area. As the water dried up, only the hardiest of plants and animals – those who could survive for long periods with little or no water – were able to inhabit the area.

The fossil record shows that nearly all species that ever lived are now extinct. In most cases, they represented the end of an evolutionary lineage and left no descendants. Although extinction occurs quite regularly, there have been periods when the rate of extinction has been very high. These are referred to as **mass extinctions**.

mass extinction a short period of geological time during which a high percentage of species die out

Table 13.5.1 shows that the rate of extinction has not been uniform, with five major extinction events in the history of life on Earth. In the biggest such event, at the end of the Permian period (250 mya), 96 per cent of species were wiped out in mass extinctions. With the destruction of so many species, major competitors were removed, and survivors had unprecedented access to new habitats and no longer had to compete for food and water. The fossil record shows that periods of **evolutionary radiation**, where many new species evolved from a single ancestral form, always followed mass extinctions.

evolutionary radiation an increase in taxonomic diversity or morphological disparity

All the species existing at a particular time are direct descendants of ancestral species. These ancestral species may not be currently living in their ancestral form, but instead have developed into different species over a long period of time. However, in other instances, groups of organisms became extinct without leaving descendants. The high rate of current species loss, caused by human activities, are considered extinctions rather than evolutions because they do not involve existing species being transformed into new ones.

Time scales of geological and biological events on Earth

Key events that have occurred so far in Earth's timeline are summarised in Table 13.5.1.

TABLE 13.5.1 Geologic timeline and key events

Era and eon	Period (and epochs)	Time scale (mya)	Continental associations	Animals and plants
Precambrian eon		4560–570		• First archaea • First bacteria • First eukaryotes • First multicellular organisms
Palaeozoic	Cambrian	570–510	• Landmasses aggregate at equatorial zone • Australia part of Gondwana • North America and Greenland part of Laurentia • Europe part of Baltica	• First invertebrates • Arthropods, including trilobites, brachiopods dominate
	Ordovician	510–439	• Northern landmasses form supercontinent Laurasia	• Diverse marine communities, reef-forming organisms • Brachiopods and cephalopods • Jawless fish • **First mass extinction**
	Silurian	439–408		• First land plants and arthropods • Jawed fish
	Devonian	408–362	• Gondwana moves south	• First trees • Land plants and fish spread • First land vertebrates (tetrapods) descend from lobe-finned fish • **Second mass extinction**
	Carboniferous	362–290		• Ferns dominate • Swamp forests • Insects dominate as the first winged animals • First reptiles and amphibious tetrapods abundant
	Permian	290–245	• Laurasia and Gondwana unite to form Pangaea	• Reptiles dominate, rise of reptilian ancestors of mammals • **Third mass extinction: 96% of all species eliminated**

Era and eon	Period (and epochs)	Time scale (mya)	Continental associations	Animals and plants
Mesozoic	Triassic	245–208		• Diversification of dinosaurs and marine reptiles • First mammals • **Fourth mass extinction**
	Jurassic	208–146	• 200 mya: Pangaea begins to break up • 180 mya: Africa breaks from Gondwana	• Dinosaurs dominate • Cycads and conifers • Flying reptiles (pterosaurs) • *Archaeopteryx* (first dinosaur–bird fossil) dies and fossilises in Bavaria
	Cretaceous	146–65	• 120 mya: India breaks from Gondwana and moves north • Gondwana breaks from Laurasia and drifts south • Gondwana breaks up • Late Cretaceous: Australia and Antarctica still attached	• First flowering plants • Arrival of marsupials in Australia via Antarctica • Dinosaurs populate huge rift valley between southern Australia and Antarctica • Cool temperate forest of podocarps, celery pines, proteas • Southern beech (*Nothofagus*) established • **Fifth mass extinction**
Cenozoic	**Paleogene** – Palaeocene	65–54		• Dinosaurs now extinct • Flowering plants, birds and mammals radiate into newly vacant niches left by dinosaurs
	– Eocene	54–40	• 50 mya: Australia begins to break from Antarctica and drifts north • Inland seas form as eastern highlands lift • Antarctic ice cap begins to form	
	– Oligocene	40–23	• 30 mya: separation of Australia and Antarctica complete	• First *Eucalyptus* species
	Neogene – Miocene	23–5	• Slow drying of southern parts of the Australian continent	• Rainforests contract to the equator • First *Acacia* species • Large marsupials are well established

Era and eon	Period (and epochs)	Time scale (mya)	Continental associations	Animals and plants
	– Pliocene	5–2.6		• Australia close enough to Asia to allow exchange of plants and animals (e.g. bats, rodents)
	Quaternary – Pleistocene	2.6		• Major ice ages • First humans arrive and increase in range
	– Recent (Holocene)	(10 000 years)		• 8000 years before present: Great Barrier Reef begins to form

Low genetic diversity

Certain species are more prone to extinction than others. Large populations can be more resilient than small populations, because they usually have a more diverse gene pool and hold a greater reserve of different alleles to draw on as the pressures from natural selection change.

When only a small number of individuals survive a major catastrophic event or quickly changing adverse environmental conditions such as in a population bottleneck, the surviving population is unlikely to carry all the alleles that were present in the original population. This results in low genetic diversity. Inbreeding within a small population further reduces the gene pool.

If this population is then exposed to a changed selection pressure, natural selection will act on 'fit' individuals with the best-suited alleles for survival and reproduction. When genetic variation is low, there is less chance of there being alleles that suit the selection pressure. If no individuals in the species have the right genetic variation, the species becomes extinct.

The genetic diversity of the Tasmanian devil (*Sarcophilus harrisii*) **(Figure 13.5.1)** was drastically reduced when population numbers fell during an ice age about 20000 years ago and again during a prolonged drought 5000 years ago. This led to inbreeding, further reducing genetic diversity. The species has survived but is now at serious threat of extinction. A new selection pressure, the fatal devil facial tumour disease, has spread throughout the species, infecting 80 per cent of the population. Having a low genetic diversity means members of the species are all genetically very similar and so respond in a similar way to this disease.

Syllabus links
Chapter 12 describes the mechanism and consequences of a population bottleneck.

Chapter 5 explores the impact of reduced biodiversity on ecosystems.

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FIGURE 13.5.1 The Tasmanian devil (*Sarcophilus harrisii*) is facing extinction because of its low genetic diversity and a new selection pressure (facial tumour disease).

CASE STUDY 13.5.1

EASTERN BARRED BANDICOOT

The eastern barred bandicoot (*Perameles gunnii*) (Figure 13.5.2) was once common over a wide area of southwestern Victoria. Numbers reduced dramatically in the 1900s. This resulted from a change in environmental conditions (in particular, the loss of native grasslands and the introduction of foxes), which severely reduced its available habitat in Victoria and increased predation. In 1989, the total population of eastern barred bandicoots was fewer than 150. In 2013, the species was declared extinct in the wild on mainland Australia, until 2021 when they were reclassified as endangered.

Ingo Oeland/Alamy Stock Photo

FIGURE 13.5.2 The eastern barred bandicoot (*Perameles gunnii*) has become endangered because of changing environmental conditions.

Eastern barred bandicoots live for 2–3 years in the wild, and have a 12.5-day gestation period, the shortest of any mammal. This allows for quick reproduction with litters of 1–3 young. In 1988, 42 eastern barred bandicoots were taken into captivity with Zoos Victoria from their last known wild site at Hamilton, Victoria, by the Eastern Barred Bandicoot Recovery Team. This captive breeding program has had varying success, with many reintroductions failing because of introduced predators, such as feral cats.

In late 2015, 20 bandicoots were released onto Churchill Island (*Moonah'mia*). Because this island was predator free, the bandicoot populations reached a carrying capacity of 120–150 individuals. Some bandicoots crossed the bridge from Churchill Island to Phillip Island.

A fox eradication program, that began in 2007 of Phillip Island (*Millowl*), was declared successful in 2017, although feral cats are still present.

Conservation plans for the eastern barred bandicoot depend heavily on how populations are classified. The Tasmanian bandicoot population is not regarded as endangered, due to relatively healthy population sizes. A number of studies were conducted on the Victorian and Tasmanian populations in an attempt to protect the Victorian population. The bandicoots were trapped, had small blood samples taken and then immediately released into the same areas. The blood was snap frozen and later a DNA fingerprint was taken by analysing genomic variable nucleotide tandem repeats. The average percentage difference in variable nucleotide tandem repeats within the populations around Hamilton, Victoria, was about 23 per cent, and for those in Tasmania it was 21.8 per cent (Figure 13.5.3). The average percentage difference between the Victorian and Tasmanian populations was 44.8 per cent.

Further testing was done by mitochondrial DNA (mtDNA) restriction fragment length polymorphism analysis. This revealed a 0 per cent nucleotide variation within the Tasmanian populations and a 1.1–1.7 per cent variation for the Victorian populations. The percentage variation between the Victorian and Tasmanian populations was 2.3 per cent. A variation of 2 per cent is the average difference between subspecies of mammals, with subspecies being groups of geographically isolated individuals of one species that may diverge to become two different species.

Variation in mtDNA within species can be as low as 0.1 per cent, but usually falls between 2 and 5 per cent. Variations greater than 5 per cent are more commonly seen between species. However, it is important to note that mutation rates, generation times and selection pressures can affect the mtDNA differences.

There is no doubt that the two populations have diverged to some extent because of geographical isolation. But knowing whether the two populations are separate subspecies is vital to how the conservation of these two populations of eastern barred bandicoots is managed.

FIGURE 13.5.3 DNA variability in different populations of eastern barred bandicoots

INQUIRY ACTIVITY 13.5.1

THE BANDICOOT

Introduction

The Australian Government, through the Department of Sustainability, Environment, Water, Population and Communities, lists two subspecies of *Perameles gunnii*. The following is an excerpt from the listing.

> Scientific name: *Perameles gunnii* unnamed subspecies
>
> Common name: Eastern barred bandicoot (mainland)
>
> The genetic diversity, as measured by the variable number of tandem repeat markers and mitochondrial DNA restriction fragment length polymorphisms, among specimens from Hamilton, Victoria, was greater than that found in widespread populations of the Tasmanian subspecies (*Perameles gunnii gunnii*). The justification for considering the mainland form to be distinct is based in part on morphological comparisons of island and mainland forms, and that mtDNA data indicated separation of 270 000–620 000 years ago.

Aim

To investigate speciation in the eastern barred bandicoot and relate this to conservation approaches

Interpretation

1. What species definition could be used to justify classifying the two populations as separate subspecies?
2. What does the DNA evidence suggest about how the populations became separated? To what extent does this example illustrate the concept of allopatric speciation?
3. Would the small genetic variability found in the eastern barred bandicoot populations affect their survival? Explain.
4. What advantages does the eastern barred bandicoot have to improve the likelihood of its long-term survival as a species?
5. Predict the most likely outcome for the eastern barred bandicoot: speciation to form two species or extinction of the mainland subspecies. Explain why the identification of the two possible subspecies of bandicoot is important for their conservation.

Syllabus link
Chapter 8 describes processes and applications of genetic technology.

LEARNING CHECK 13.5

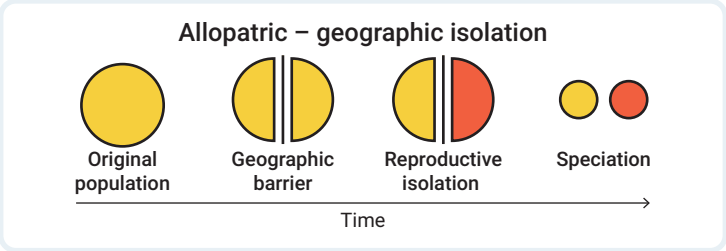
APPLYING

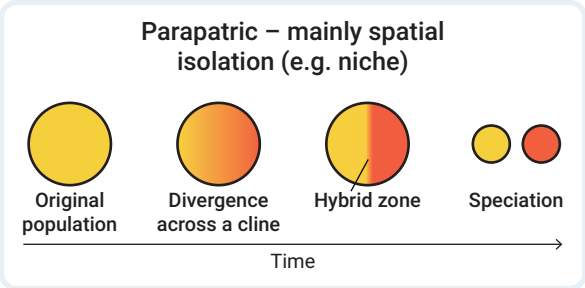
1 **Explain** how a population bottleneck can cause a species to become extinct.
2 **Explain** why small populations are more likely than larger populations to become extinct.
3 **Explain** the effect of a changed selection pressure on natural selection in a small population with low genetic diversity and inbreeding.
4 **Explain** why a mass extinction is often followed by an evolutionary radiation.

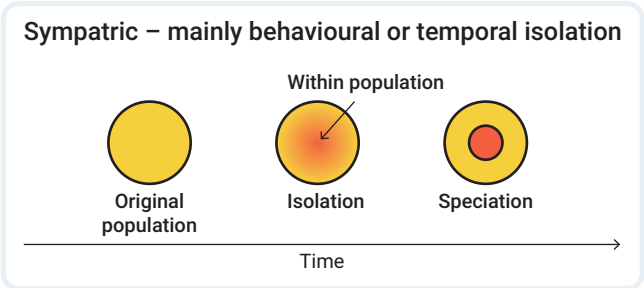
CHAPTER SUMMARY

Speciation

- Speciation is the process of evolution of species from an ancestor

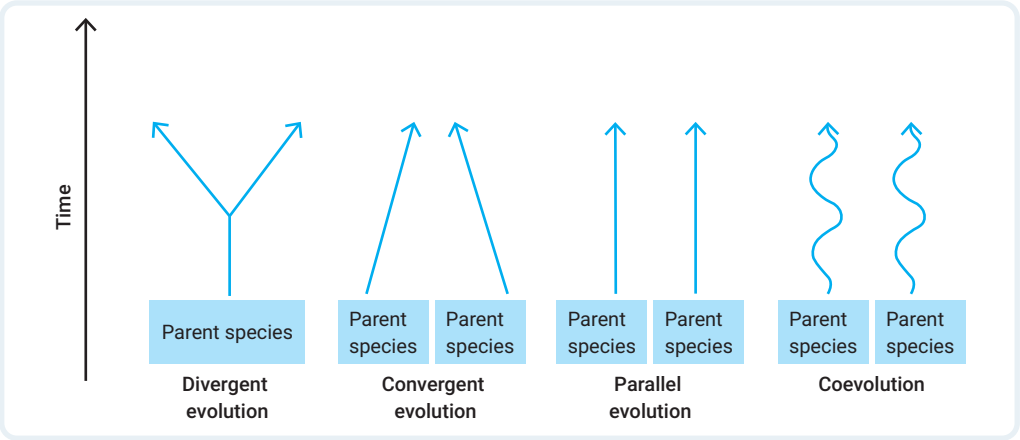






Evolution patterns

- There are four types of evolution: divergent, convergent, parallel and coevolution.



Extinction patterns

- Mass extinctions occur over a short period of time where a large percentage of species die out.
- Evolutionary radiation increases taxonomic diversity or morphologic disparity.

CHAPTER EXAM

MULTIPLE CHOICE

1. Darwin's finches are a group of 15 species of birds that have very different beak form and function. The different species are thought to have evolved from a common ancestor that reached the Galapagos Islands from Central or South America millions of years ago. The evolution of these finches **cannot** be described as:

A descent with modification.
B divergent evolution.
C evolutionary radiation.
D microevolution.

2. Which of the following statements best defines macroevolution?

A The difference between individuals in terms of alleles
B The close resemblance between parents and their offspring
C Individuals in the two populations having different appearances
D Accumulation of changes in genetic composition of a population over time

3. Two species of wild daisy grow in the same area, but they do not interbreed because one flowers in early spring and the other flowers in summer. This is an example of:

A geographic isolation.
B mechanical isolation.
C post-reproductive isolation.
D temporal isolation.

4. Speciation occurs when a single population becomes two separate populations that do not interbreed. Which of the following occurs in allopatric speciation?

A Behavioural isolation
B Geographical isolation
C Morphological differences
D Temporal isolation

5. Wildlife corridors are intended to:

A increase the likelihood of inbreeding.
B allow animals to escape a wildfire in their normal habitat.
C concentrate animals in smaller areas, minimising their impact on human activities, especially agriculture.
D link conservation areas that have been isolated by human activities, allowing for gene flow.

6. When large-scale extinctions occur, some species seem to be at more risk than others. Extinction is more likely when:

A individuals are small.
B there is minimal immigration.
C the population is large and has high density.
D the population is small and individuals are dispersed.

7. Two species of plants grow in desert areas of Peru and northern Africa. They are very similar in appearance. This is most likely an example of:

A coevolution.
B convergent evolution.
C divergent evolution.
D parallel evolution.

8. A population of fish formed separate colonies after a river system dried up during a prolonged drought, leaving isolated bodies of water. This could lead to speciation if conditions remain the same for a long period of time. This is most likely an example of:
   - **A** allopatric speciation.
   - **B** parapatric speciation.
   - **C** peripatric speciation.
   - **D** sympatric speciation.

9. Isolating mechanisms affect populations by:
   - **A** facilitating gene flow.
   - **B** increasing genetic diversity.
   - **C** reducing gene flow.
   - **D** triggering a high rate of mutations.

10. The red-necked wallaby is distributed throughout eastern parts of Australia from Queensland through New South Wales, South Australia and to Tasmania. Even though the Tasmanian population is separated by Bass Strait, separate species have not evolved. A possible reason for this is:
   - **A** a population bottleneck has occurred.
   - **B** mutation rates in all populations are very high.
   - **C** populations are very small with low genetic diversity.
   - **D** selection pressures in Tasmania and mainland Australia are similar.

SHORT RESPONSE

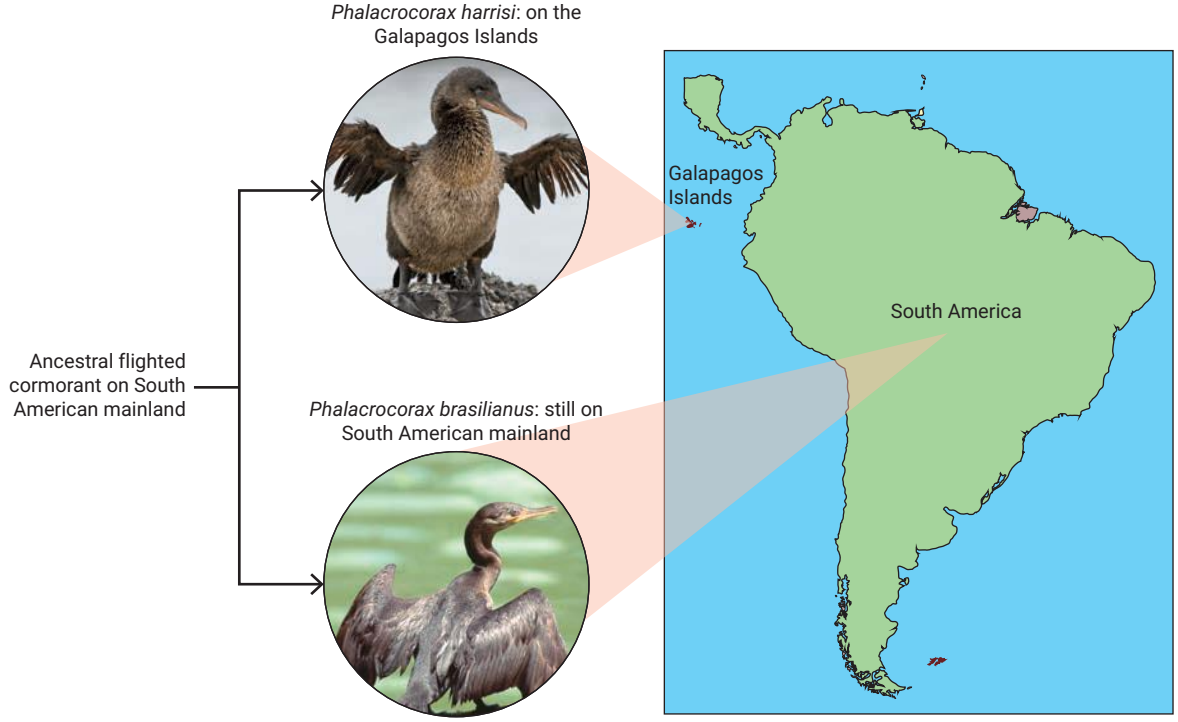
11. The last known Tasmanian tiger (*Thylacinus cynocephalus*) died in Hobart in 1936.
   - **a** **Describe** the amount of genetic diversity expected in a species facing extinction.
   - **b** Provide a possible reason for the Tasmanian tiger becoming extinct.
   - **c** **Explain** why small populations are more prone than large populations to extinction.

12. Species of insects have evolved a long tongue-like proboscis to reach the nectar in long floral tubes of flowers. Pollen is picked up on the insect's body, resulting in flower pollination. **Explain** how this is an example of coevolution.

CROSS-CHAPTER QUESTION

13. On the Galapagos Islands, Charles Darwin noticed a flightless cormorant (*Phalacrocorax harrisi*). This species most likely originated from a small population of ancestral flying species that reached the islands from the South American mainland, 1000 km away. The islands were totally free from predators. This cormorant's wings reduced in size and changed shape to be well suited to movement under water but which no longer allowed flight. The more recent arrival of feral dogs and cats to the islands has once again led to a change in selection pressures on this animal. This has resulted in dramatic reductions in the cormorant population. The flightless cormorant is now recognised as an endangered species.

***Phalacrocorax harrisi* is most closely related to cormorants such as the neotropic cormorant (*P. brasilianus*), which is widespread throughout tropical regions of South and North America.**



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a **Explain** examples of each microevolutionary process, mutation, genetic drift and gene flow, in the scenario observed by Darwin.

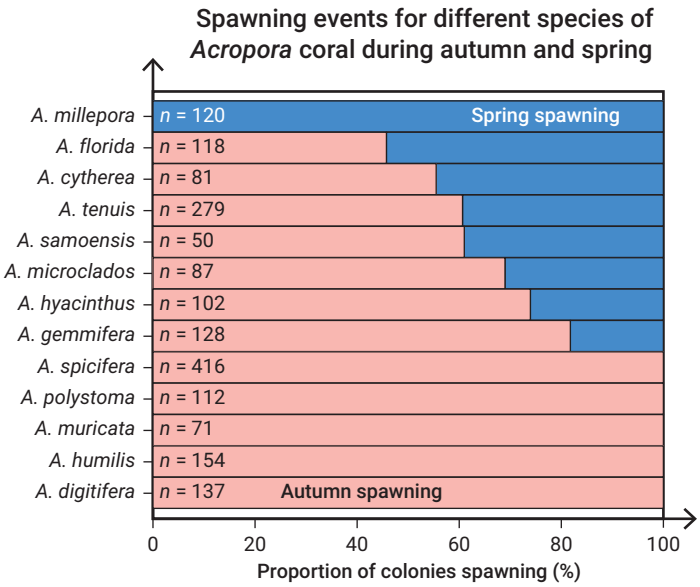
b **Explain** whether the Galapagos Island cormorants underwent stabilising, disruptive or directional selection.

c **Explain** how this cormorant population provides an example of allopatric speciation.

DATA ANALYSIS

Questions 14 and 15 refer to the following information.

Coral spawning was observed in north-western Australia reef systems during autumn and spring. Results of a 13-year survey of spawning time for different *Acropora* species of coral are summarised in the following graph. Spawning occurs when corals synchronise the release of egg and sperm bundles into the water to allow for fertilisation and zygote formation.



Gilmour JP, Underwood JN, Howells EJ, Gates E, Heyward AJ. Biannual Spawning and Temporal Reproductive Isolation in Acropora Corals. PLoS One. 2016 Mar 10;11(3):e0150916. doi: 10.1371/journal.pone.0150916.

14. Apply understanding

Identify the two species that would most likely be able to breed with *A. millepora*.

15. Interpret evidence

Deduce the most likely isolation process evident in the data that allows for different species of coral to develop.

CHAPTER 14

Evolutionary relationships

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SYLLABUS DOT POINTS

SCIENCE UNDERSTANDING

- Explain how comparative genomics provides evidence for the theory of evolution and how conserved sequences can be used to date divergence.
- Infer species relatedness from cladograms, phylograms and molecular sequence data.

Introduction

Phylogenies are used to organise information about biological diversity and the evolutionary relationships between species. The information is used as the basis for classification, to interpret evolutionary events, and assumes all species arise from a common ancestor with the branches of the tree representing transmission of genetic material. Originally phylogenies were based on morphology. The first gene sequence-based quantitative assessment of phylogenetic relationships was published in 1977 (Woese and Fox) and showed three groups of life: eukaryotes, eubacteria and archaebacteria.

Worksheets

- Species relatedness
- Phylogenetic relationships

Nelson MindTap

To access resources above, visit
cengage.com.au/nelsonmindtap

ASSUMED KNOWLEDGE

- ✓ Species have common ancestors that may be recent or distant.
- ✓ Speciation results from reproductive isolation and changes in alleles.
- ✓ Molecular sequence data includes sequences of DNA or amino acids.

LEARNING OUTCOMES

By the end of this chapter, you should be able to:

- ✓ explain the evidence for evolution that is provided by comparing the genomes of different species
- ✓ explain how differences in genetic sequences conserved between species are an indication of the time since those species diverged
- ✓ use data presented as cladograms, phylograms and molecular sequences to draw conclusions about how related particular species are.

14.1 Species' evolutionary relatedness

common ancestor a species or organism whose offspring diverged over time

homology a similarity due to a common origin

molecular homology the identification of shared biomolecular elements – generally genes – used to test the relationships between organisms, which can demonstrate common ancestry

comparative genomics the study of DNA similarities across species

conserved sequence a DNA or protein sequence that is preserved across species because it is necessary for optimal function

It is reasonable to expect that species that have a **common ancestor** also share traits inherited from that ancestor. The shared features are known as **homologies** and are identified by comparing anatomy (morphology), embryological development and cellular processes. Different organisms also share **molecular homologies** as well as structural ones; however, the homologies are more complex, and profound, at a genetic level. **Comparative genomics** studies the similarities and differences between the genes of organisms to further our understanding of their relatedness.

Molecular conservation

Proteins, and the alleles that encode them, are subject to the same process of evolution by natural selection as the observable traits that individuals possess. A protein that is well suited to its function will be a **conserved sequence** through time, while other traits around it may evolve. This is because mutations in this well-suited protein are more likely to reduce its function than improve it, and individuals with the altered protein will not survive as well as those with the better version. Natural selection is likely to act on mutations in proteins that are vital to successful survival.

Protein sequences that are efficient and effective are generally conserved through time. Therefore, two distantly related species who require the same protein function may have very similar sequences for the protein. Some small differences that do not negatively affect function will accumulate, but the general functional sequence is often the same. This is the case with the histone proteins.

In eukaryotes, DNA is stored around histones to prevent all genes from being expressed continuously. A particular section of DNA must be unwrapped from its histone for the enzymes involved in replication and expression to gain access to it. Mutations in the histone proteins can cause the DNA to bind only loosely, or not at all, or to bind so tightly that the mechanisms in place for unwrapping the DNA are not effective. All of these would result in genetic damage so severe as to be entirely incompatible with life.

Given the importance of fully functioning histones to life, it is no surprise that the optimal sequence is present in most eukaryotic organisms. Figure 14.1.1 shows part of the sequence

Weblink
Histone

Syllabus link
Chapter 7 details the relationship between DNA and histones.

for histone H1 in five mammals. The level of conservation is extremely high; only a few amino acid **residues** are different, as denoted by the light blue colour. The human and chimpanzee sequences are identical, indicating that they are more closely related to each other than to the other three mammals. The mouse and rat are closely related to each other, but the two differences show that they are not as close as the human and chimpanzee are. The mouse and cow differ by five residues, indicating that they are more distantly related.

residue a single unit that makes up a polymer; e.g. a single amino acid in a protein sequence

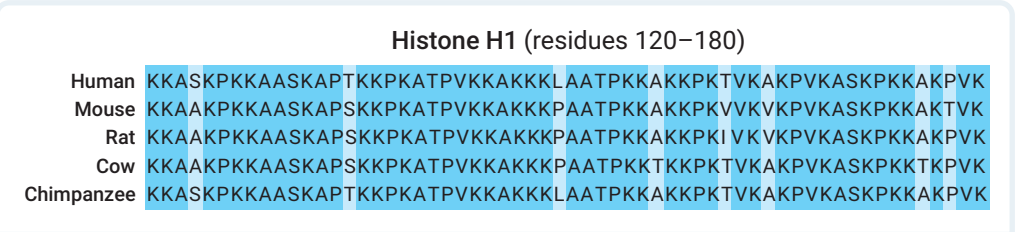

FIGURE 14.1.1 Histone H1 is a common example of protein conservation, given its vital role in the storage and access of DNA. Residues 120–180 are shown here. One-letter amino acid codes have been used.

Comparative genomics

Comparative genomics looks at genome sequences of different species to identify similarities and differences. The molecular level comparison allows researchers to distinguish what makes organisms different at a molecular level. It is possible to identify genes that are conserved (found in all or many organisms) as well as genes that give each organism unique characteristics.

comparative genomics the study of DNA similarities across species

The mapping of the human genome in the Human Genome Project took 13 years and cost billions of dollars. The technological developments made during this project made it possible to sequence many more genomes. They have also enabled large-scale studies of genome evolution, as well as comparative and human medicine. Since 2005, more powerful and less expensive next-generation sequencing methods provide complete DNA sequences of many species of animals, plants and micro-organisms. This process produces a detailed picture of DNA sequences and sequence conservation, making it possible to trace evolutionary processes responsible for the divergence of two genomes.

Using molecular data for analysis has some advantages over morphological data:

- Bases A, C, G and T are recognisable and cannot be mistaken for each other (unlike some morphologies; e.g. shape due to convergent evolution).
- Large datasets can be generated quickly.
- Data can easily be converted to a numerical form for analysis.

The core process in comparative genomics is the use of sequence alignment techniques to identify similarities and differences in DNA from different sources. Several powerful alignment algorithms have been developed for this. Only recently has it become possible to undertake these analyses rapidly, due to advancements in computer science, engineering and mathematics.

A simple comparison may focus on genome size, number of genes or chromosome number. For example, the tiny flowering plant *Arabidopsis thaliana* has approximately the same number of genes as humans (about 25000) even though it has only 157 million base pairs compared to 3 billion in a human. This comparison shows that the number of genes is not necessarily proportionate to genome size. Direct DNA sequence comparisons between species allows for more detail in the comparison, especially when aligning homologous DNA from different species.

When contrasting the base-pair composition of genes of seemingly unrelated organisms that code for comparable structures, the composition of each gene is remarkably similar. For example, the genes that code for 'building eyes' on vertebrates such as humans, called *PAX6*, are more than 78 per cent similar to those responsible for building the eyes of the invertebrate octopus **(Figure 14.1.2)**.

Weblink
All about the Human Genome Project

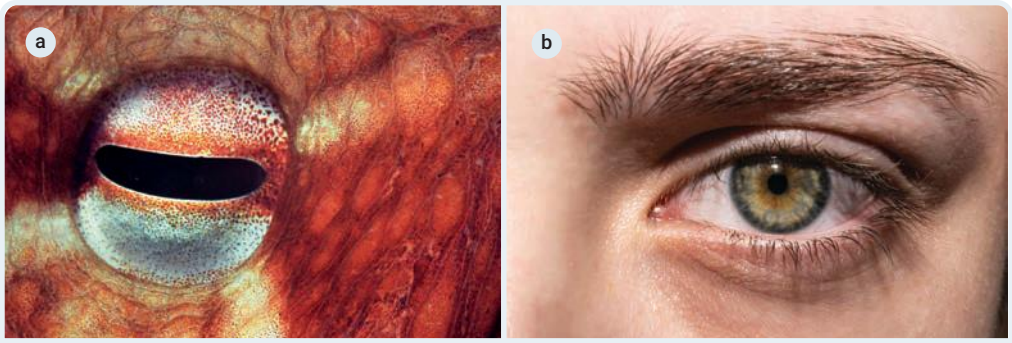

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FIGURE 14.1.2 (a) Octopus eyes and (b) human eyes appear different but *PAX6* genes that code for 'building eyes' are more than 78 per cent similar in the two groups.

Syllabus links
Chapter 7 details the different types of DNA mutations.
Chapter 11 explores the effects of mutations on protein production.

Dating divergence

In the absence of external influences such as ionising radiation and chemical mutagens, there is a natural baseline rate of mutation in DNA, including mitochondrial DNA. If mutations change the structure or function of the proteins that are encoded, they will change the way those proteins are passed to the next generation, making them either more or less common in subsequent generations. In many cases, mutations may arise in non-coding regions or may change a sequence to one that encodes the same amino acid as before, resulting in a neutral mutation of little consequence to survival and reproduction. The frequency of neutral mutations within a species is called the **mutation rate**. When comparing the genomes of two species, the mutation rate can be used as a molecular clock to estimate when those species diverged from a common ancestor. For humans, the mutation rate is estimated to be approximately 10^{-8} mutations per nucleotide site per generation.

mutation rate the estimated number of base pair changes per nucleotide site per generation of a population

The molecular clock hypothesis assumes that there is a relatively constant rate of DNA and protein sequence evolution over time and among different organisms. Therefore, the genetic difference between any two species is proportional to the time since those species last shared a common ancestor. Researchers acknowledge that this assumption is simplistic and that mutation rate is likely to vary with lineages, so appropriate adjustments are made depending on how the molecular clock is being used.

INQUIRY ACTIVITY 14.1.1

THE MOLECULAR CLOCK AND SPECIES RELATEDNESS

Introduction

The molecular clock hypothesis is an underlying assumption for many areas of evolutionary biology. It hypothesises that the base rate of neutral mutation in molecular sequences, including DNA and proteins, is stable between generations of a single species. It also hypothesises that this rate may differ between different species because of influences such as lifespan and metabolic rate.

The base rate of mutation is determined by analysing the sequence differences between two species whose divergence is already well dated. This could be through fossil records or by dating geographic events such as volcanic eruptions and the filling of inland seas, which would have split a single population of organisms and initiated their speciation. The base rate of mutation is then calculated by dividing the number of point differences by the number of residues analysed and then dividing this number by the time since divergence.

For species whose divergence is not well dated, molecular clock data can be used to make estimates. By dividing the number of point differences by the number of residues analysed, and then multiplying this by the sum

of the base rates of mutation for two similar species, researchers can estimate when the two species last shared a common ancestor. These estimates are fraught with error, but are often the best guesses we have available when palaeontological data is scarce.

Analysis of results

1 Construct a formula for calculating the base rate of mutation, based on the second paragraph of the introduction.

2 Calculate the base rate of mutation for the two species in Table 14.1.1.

TABLE 14.1.1 Protein sequences for cytochrome c (residues 5–25) for yeast and primates, which diverged 1.5 billion years ago. One-letter amino acid codes have been used

Species	Molecular sequence
Yeast	G D V E K G K K I F I M K C S Q C H T V
Primates	G S A K K G A T L F K T R C L Q C H T V

3 Estimate the date of divergence for humans and chimpanzees, using the base rates in Table 14.1.2 and the sequences in Table 14.1.3.

TABLE 14.1.2 Base rate of mutation of DNA for several species

Organism	Approximate base rate of mutation in DNA (mutations/base pairs/year)
Yeast	1×10^{-8}
Primates	1.2×10^{-8}
DNA viruses	3×10^{-6}

TABLE 14.1.3 DNA sequences for human and chimpanzee in non-coding area. One-letter amino acid codes have been used.

Species	DNA sequence
Human	A T G T A T C C A G G T A G T G G A C G T T A C A C C T A C A A C A A C G C T G G T G G T A A T G G
Chimpanzee	A T G T T T C G A G G T A G T G G T C G T T A G A A C T A C T A C A A G G C T G G T G G T A A T T G

Interpretation

4 Comment on differences between the base rate of mutation for cytochrome c and the approximate base rates of mutation for DNA.

5 Explain whether the estimate of the date of divergence for humans and chimpanzees is reasonable, in light of the date of divergence for primates and yeast and your own knowledge.

6 Modern estimates for the divergence of humans and chimpanzees, using the molecular clock method, range between 6 and 15 million years ago. Given that this is an error rate of nearly 50 per cent, outline three limitations of the method that contribute to such enormous uncertainty.

LEARNING CHECK 14.1

DESCRIBING

1 **Define** 'comparative genomics'.
2 **Describe** what a conserved sequence is.
3 State what 'divergence' means.

APPLYING

4 **Explain** the process of comparative genomics and the value of this procedure.
5 **Explain** how a comparison of the degree of similarity of DNA in two species, expressed as a percentage, can be used to clarify evolutionary relationships of a group of different species.
6 **Explain** how it is possible to determine when divergence has occurred, with reference to neutral mutations.

14.2 Cladistics – inferring relatedness

All organisms on Earth are related to one another, meaning that at one time they had a common ancestor. Over generations, populations change as organisms adapt to their environments. The more recently that two species had a common ancestor, the more closely related they are and the more features they will have in common.

In 1966, German scientist Willi Hennig published the evidence-based methodology he developed for constructing **phylogenetic trees**, basing classifications on the branching patterns from a common ancestor, called **cladistics**. Taxonomists use this methodology to identify the descendants of a particular ancestral species, referred to as a **clade**. Thus, a clade is a grouping of species that includes a single common ancestor and *all* descendant species (Figure 14.2.1). Cladistics has a number of assumptions associated with the required presence of shared characteristics derived from a common ancestor:

- Groups of organisms are related because of descent from a common ancestor.
- The offspring of an ancestral species diverge dichotomously (bifurcation). It suggests that all speciation events (where a new species develops) are singular splits, that the new generation of a particular organism will be either the same as their parent generation or different in only one way.
- Change in characteristics occurs in lineages over time and organisms become increasingly different. This allows for organisms that share a characteristic to be grouped separately from organisms that don't share that characteristic.
- When there are multiple ways that organisms can be related, the simplest explanation is the most likely to be correct. It is usually more likely that a feature evolved once in a common ancestor rather than evolving independently for each organism.

phylogenetic tree a branching diagram showing evolutionary relationships

cladistics a taxonomic technique that arranges organisms by clade

clade a group consisting of all the descendants of a particular ancestor organism

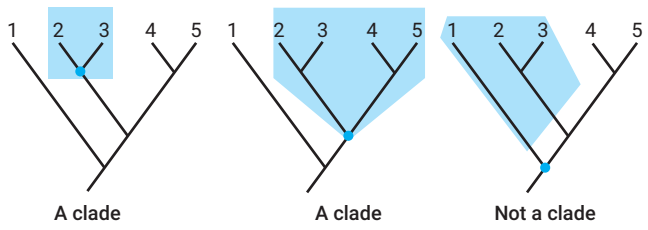


FIGURE 14.2.1 Groupings must include all descendants of a single ancestor to be considered a clade.

Using cladistics, taxonomists produce phylogenetic trees referred to as **cladograms** or **phylograms**. Like trees, these diagrams follow a branching pattern. Unlike trees, they are always **dichotomous**, each split having only two branches. Each **extant** organism is a 'leaf' on the tree and each point of divergence (**node**) represents the most recent common ancestor, who is likely to be but is not always extinct.

Phylogenetic relationships can be determined by using data derived from several sources. Historically, sources included body structures, comparative anatomy and fossilised structures, such as bones and teeth. More recently, in what is termed 'molecular phylogeny', molecular sequencing has become an important source of data, even for organisms from the past. The assumption underlying molecular phylogeny is that the closer the relationship between two organisms, the greater the similarities in their DNA. Molecular investigations often confirm accepted evolutionary relationships based on morphology. In other instances, molecular investigations have successfully established phylogeny in groups that had not previously reached a consensus. In all cases, the comparison of genomic features, such as the degree of similarity of DNA, provides strong evidence for the theory of evolution.

Phylogenetic trees are often organised vertically, such as in Figure 14.2.2a,b. These trees are generally oriented with the bottom of the tree representing a time far in the past and the top representing species that exist today. They can also represent higher taxonomic levels, such as phylum or class towards the bottom of the tree and lower levels, such as genus and species, towards the top. Figure 14.2.2c shows the same tree in a circular arrangement. This style is often used for very large and complicated phylogenetic trees because it uses the space on a page more effectively.

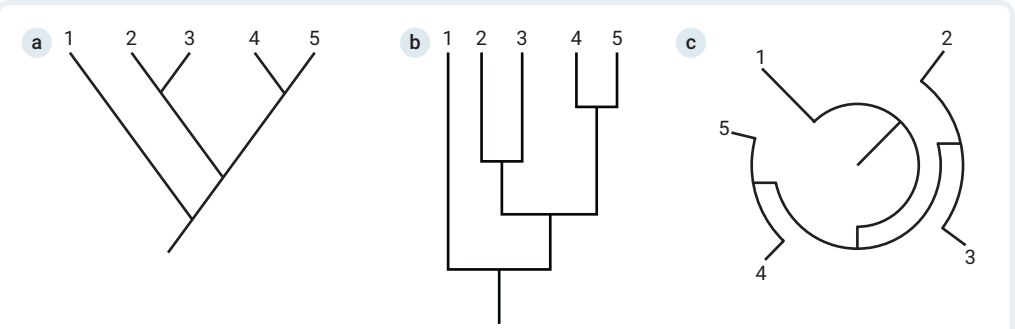


FIGURE 14.2.2 Phylogenetic trees are used to show the relatedness of extant species. This tree is drawn in three ways, showing that species 2 and 3 are closely related and that both of these are more closely related to species 4 and 5 than to species 1.

A cladogram is generally considered to be an unscaled representation of a phylogeny without a time axis or indication of genetic difference. Therefore, branch lengths are not proportional to time or the number of evolutionary changes. A cladogram shows relative statements of relationship – it is a hypothesis.

A phylogram, on the other hand, is considered to represent accurate evolutionary relatedness between different species or groups of organisms where the length or width of branches represents the distance of the relationship through either time (also called a chronogram) or genetic difference.

Constructing phylogenetic trees

Since a phylogenetic tree shows evolutionary relationships and the points at which lineages diverge, the root of the tree represents the ancestral lineage and is the initial common ancestor of all the organisms in that clade. The branching points are called nodes and represent the hypothetical ancestor that gave rise to the daughter taxa. The tips of the branches represent the

cladogram a phylogenetic tree in which all organisms are grouped according to their most likely evolutionary relationships

phylogram a phylogenetic tree in which branch length or width represents genetic differences or time since divergence

dichotomous having two branches, two opposing aspects

extant currently in existence, not extinct

node a point in a diagram where lines branch or intersect

phylogenetic relationship an evolutionary relationship that exists between a group of species, often expressed as a tree-like diagram

Worksheet
Phylogenetic relationships

descendants of that ancestor. The branch length can represent the extent of divergence or the extent of the relationship among different taxa.

Moving from the root to the tips means moving forward in time. Each fork on a branch marks a point at which new species arise. This means that each node represents an ancestor common to all the species after that node. Phylogenetic trees often have a reference point for comparison with the rest of the tree, known as an outgroup, which shows the most distantly related group of organisms that is not part of a clade.

The first step in constructing a phylogenetic tree is to acquire the data (morphological or molecular sequences). The second step is to create a table of the characteristics, known as a **character matrix**, to be used for classification. Within the character matrix, each characteristic is assessed as present or absent in the organism or group of organisms. Molecular sequences are aligned to identify similarities or differences. It is possible to use molecular data to calculate how similar any two sequences are, providing a value to the length/width of the branch.

Table 14.2.1 shows a completed character matrix for the four major plant groups.

Syllabus link
Chapter 13 discusses the natural mechanisms for formation of new species.

character matrix a table of characteristics used for classification

TABLE 14.2.1 A character matrix of major plant groups

Characteristic	Bryophytes (mosses)	Pteridophytes (ferns)	Gymnosperms (conifers)	Angiosperms (flowers)
Perform photosynthesis	Present	Present	Present	Present
Have vascular tissues	Absent	Present	Present	Present
Make seeds	Absent	Absent	Present	Present
Enclose seeds in an ovary	Absent	Absent	Absent	Present

The next step is to take the character matrix and determine how the organisms or groups of organisms can be assembled into clades. Remember, clades must have a common ancestor and must include all descendants of that ancestor. For example, the first clade that can be made with Table 14.2.1 contains all of the plants that can perform photosynthesis (all groups). Another clade can be made with all the groups that have vascular tissues (all except bryophytes). These two clades give us the first point of cladogenesis, when bryophytes were first excluded. The other two clades include plants that make seeds (gymnosperms and angiosperms) and those that enclose their seeds in an ovary (angiosperms only). The split between clades will be represented with a V shape in the cladogram, with the point of the V (called a **node**) representing the last ancestor the clade had in common.

Figure 14.2.3 shows how each organism is included in a cladogram, beginning with the first branch point excluding bryophytes (the only ones without vascular tissue) and continuing through the subsequent branches excluding pteridophytes (do not make seeds), and then gymnosperms (do not have ovaries). Note that the feature used for each exclusion is written on the diagram alongside its associated branch.

Weblink
How to make a cladogram

Worksheet
Species relatedness

node a point in a diagram where lines branch or intersect

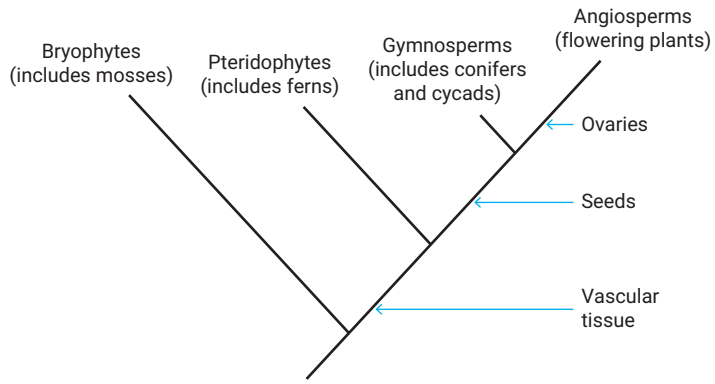
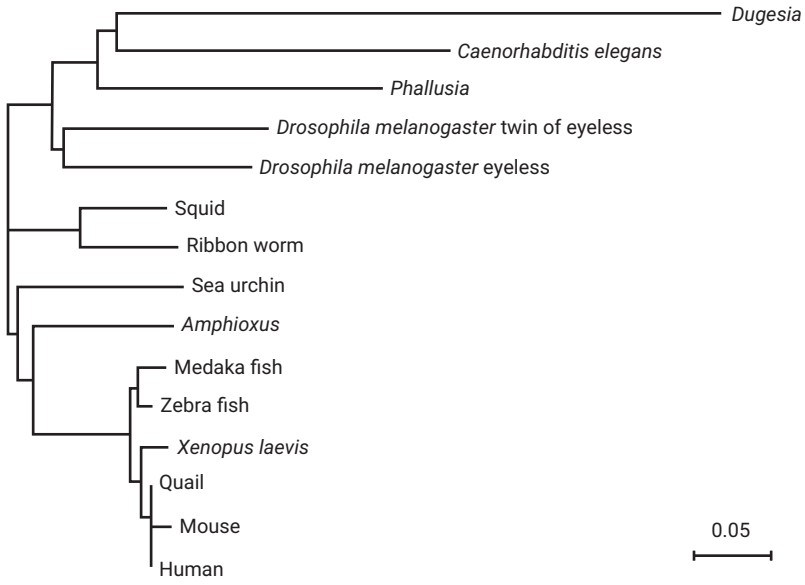


FIGURE 14.2.3 Cladograms are constructed by arranging the clades in order from most organisms in the clade to fewest organisms in the clade.

Figure 14.2.4 shows a phylogram built by using the molecular homologies of the eye-building *PAX* gene. The scale shows the number of amino acid substitutions per site.



Adapted from Walter J. Gehring (2011). *Chance and Necessity in Eye Evolution, Genome Biology and Evolution*, volume 3, pages 1053–1066.

FIGURE 14.2.4 Comparative genomics has found shared 'eye-building' genes across a range of animals with eyes.

WORKED EXAMPLE 14.2.1

Lactate dehydrogenase (LDH) is a key enzyme in the glycolysis pathway, which provides energy to almost all living cells. Its importance makes it a good candidate for comparative genomics. The amino acids of residues 195–211 of LDH from several organisms have been sequenced, as shown in **Table 14.2.2**. Use this data to infer the evolutionary relationships of the organisms. Summarise your findings in a phylogenetic tree as a cladogram.

TABLE 14.2.2 LDH sequences (residues 195–211) from seven organisms. One-letter amino acid codes have been used (grouped for ease of reading)

Organism	LDH sequence (residues 195–211)
1	GDQVQ CFCCG GKLKN WE
2	GDQVQ CFCCG GKLKN WE
3	DDQVQ CFCCG GKLKN WE
4	RDHVK CFHCD GGLRN WE
5	LDHVK CVWCN GVIAK WE
6	DDQVQ AFCCG GKLKN WE
7	DDNVQ CFCCG GGLSG WE

ANSWER

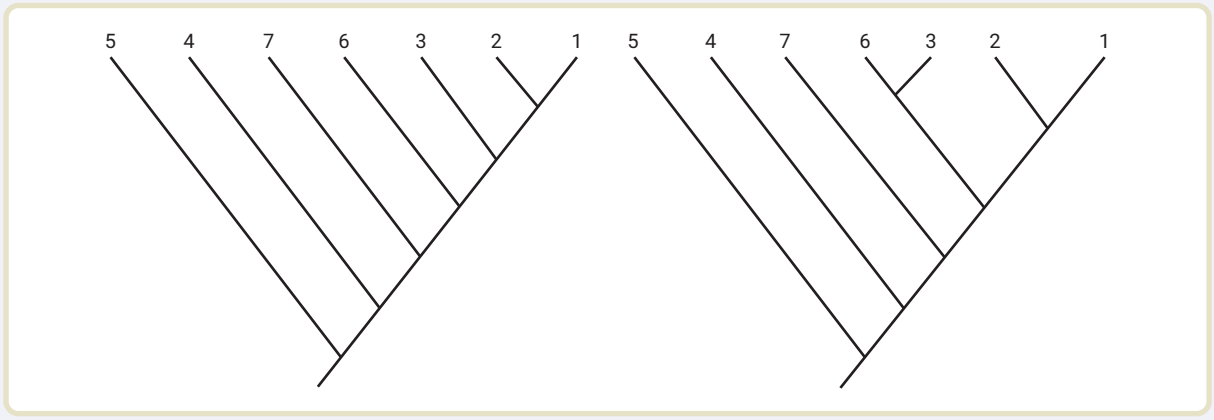
1 **Review the amino acid sequences and highlight the *similarities* between species.**
The sequence for organisms 1 and 2 are the same; therefore, they are the most closely related species in this table. Use this to generate a matrix.

2 **Create a matrix.**
The matrix shows the number of amino acids that are the same and in the same location in the sequence. A higher number of similarities means that the organisms are more closely related. Note: The matrix may also be constructed using differences, with high numbers meaning organisms are less closely related.

	1	2	3	4	5	6	7
1		17	15	10	7	15	12
2			15	10	7	15	12
3				10	7	16	13
4					9	9	10
5						6	7
6							12
7							

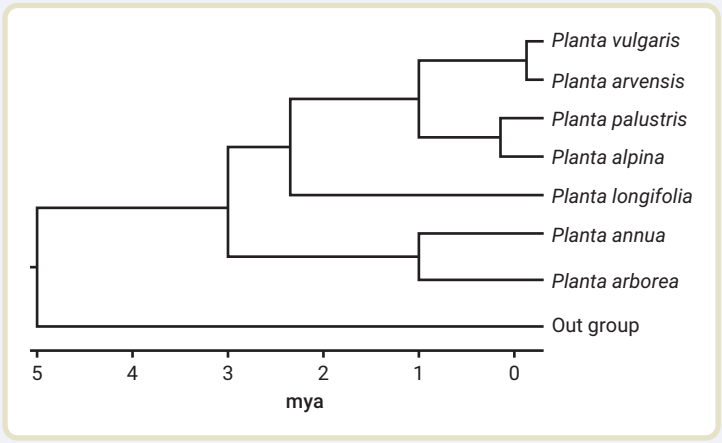
3 **Identify the similarities.**
The more amino acids in common, the more closely related the organisms are.
1 and 2 are most closely related.
3 and 6 are the next most closely related.
Then 1 and 3, 2 and 3 along with 1 and 6, 2 and 6.
7 is the next most closely related to 3, 1, 2 and 6.
5 is least closely related to any other organism, and then 4 is the second-least.

4 **Construct a cladogram.**
Remember, a cladogram is essentially a hypothesis, so the data can support multiple structures. Begin with the least closely related organism (5) as the first to be excluded, then move up the range of relatedness (4, then 7). When we reach 3 and 6, 3 is slightly more closely related to 6 (16 similarities) than to 1 and 2 (15 similarities), so these are likely to be on their own branch together (see option on the right), but could be excluded very shortly after each other (option on the left). Species 1 and 2 are identical, so they belong on their own branch together as well.



WORKED EXAMPLE 14.2.2

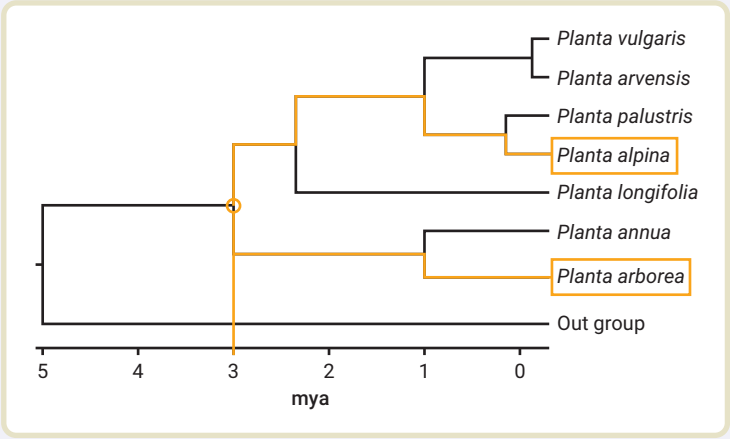
Planta alpina and Planta arborea have a common ancestor. Based on the chronogram shown, how long ago did these two species diverge from their common ancestor?



ANSWER

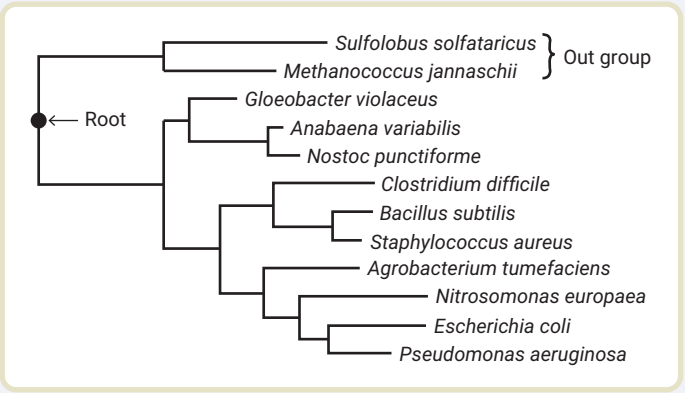
1 **Determine the node that represents the common ancestor.**
Their most recent common ancestor occurred at the node identified in orange.

2 **Identify the time relationship between the two species.**
A time-based chronogram usually contains a time scale along the base of the diagram. Based on the common ancestor, this lines up at approximately 3 mya.



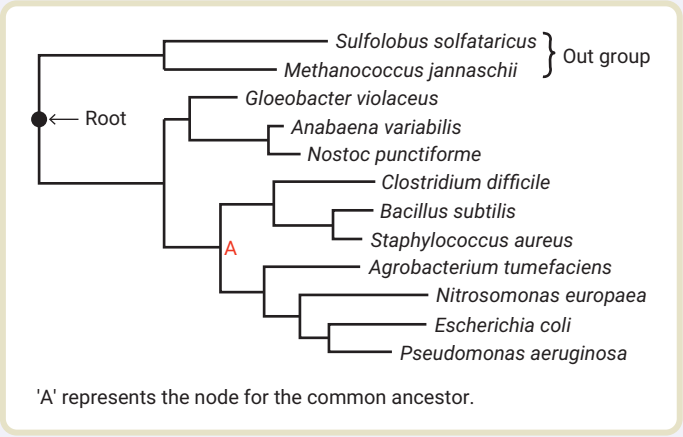
WORKED EXAMPLE 14.2.3

Using the phylogenetic tree, describe the relatedness of *Clostridium difficile* and *Escherichia coli*.



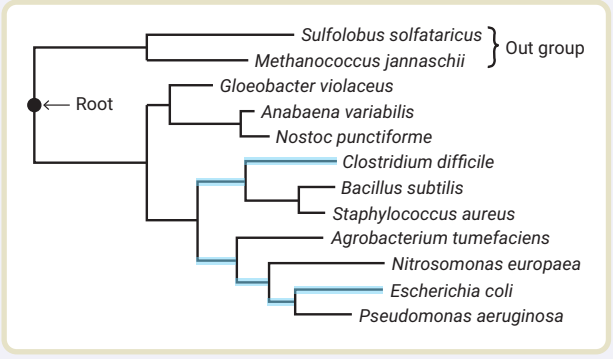
ANSWER

1 Identify the common ancestor for the two species.



'A' represents the node for the common ancestor.

2 Analyse the length of the branches from the common ancestor.



To identify how closely related the species are, add together the length of the branch from one species to the other; for example, *E. coli* to *C. difficile*. The total length of the branches (highlighted in blue) is proportional to the genetic differences between them.

3 **Determine the genetic difference.**
Considering the lengths of both species, there is a relatively large genetic difference between the two species and, therefore, the two are not closely related.

The differences between a cladogram and a phylogram are summarised in **Table 14.2.3**.

TABLE 14.2.3 A summary of the differences between a cladogram and a phylogram

Characteristic	Cladogram	Phylogram
Use	Simple and used for general classification.	More complex and mostly used to determine the evolutionary relationships.
Focus	Shared traits among organisms.	Genetic differences and time of evolutionary divergence.
Purpose	Provides a hypothetical picture of evolutionary relationships.	Provides an actual representation of the evolutionary relationships.
Length of branches	Branches do not represent any evolutionary distance so are equal in length.	Branches represent evolutionary distance so are different lengths. • Representing time – finish at the same point (sometimes called a chronogram). • Representing molecular difference – finish at different points.
Evolutionary time	Separates the organism solely by the defined charactersistics.	Indicates relative divergence and duration of evolution.

LEARNING CHECK 14.2

DESCRIBING

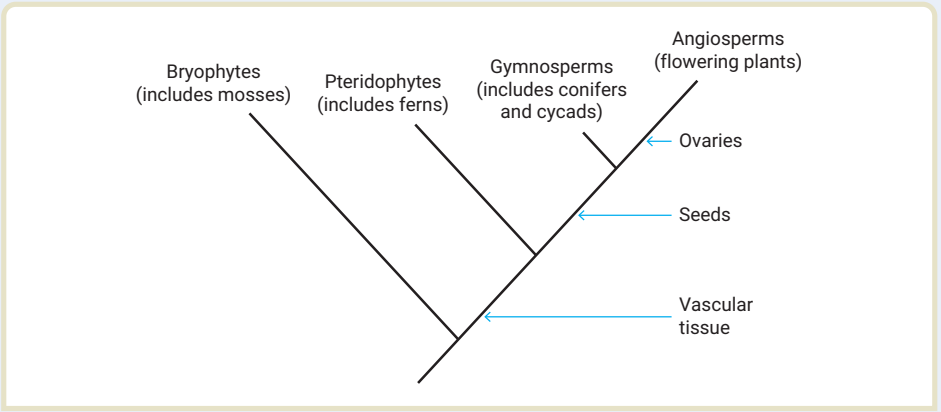
1 **Define**:
   a clade
   b common ancestor.
2 State three assumptions of cladistics.
3 **Recall** what it means in terms of time to move from the root to the tips of a phylogenetic tree.
4 **Describe** what is meant by 'phylogenetic relationships'.
5 **Describe** what the evolutionary history of a given group of organisms can tell about that group.

Weblink
Reading trees

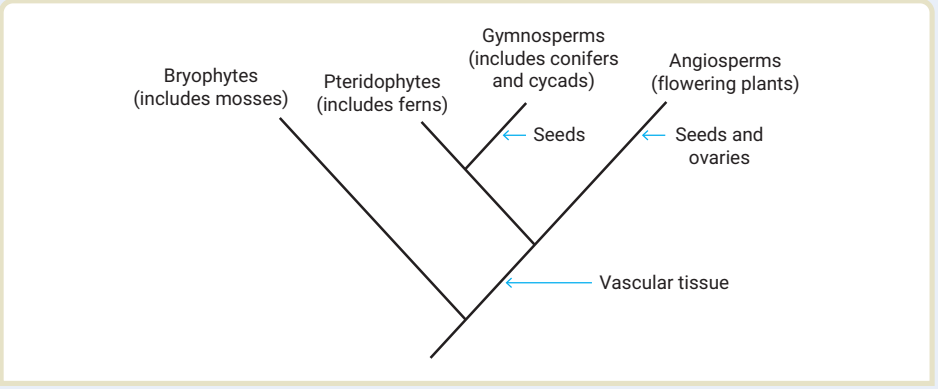
APPLYING

6 **Explain** the meaning of a fork on the branch of a phylogenetic tree.

7 Consider the following diagram. At each branching point, some of the offspring of the ancestor developed a new feature, whereas others did not. This evolution of features has created a wide, but interrelated, variety of life on Earth. Using this diagram, **explain** why there is only one possible clade that includes the bryophytes and yet every possible clade includes the angiosperms.



8 Alternative cladograms such as the one shown below are possible, but are often unlikely. Explain why the relationships between the major plant groups shown in Question 7 is not a likely option compared to the following diagram.



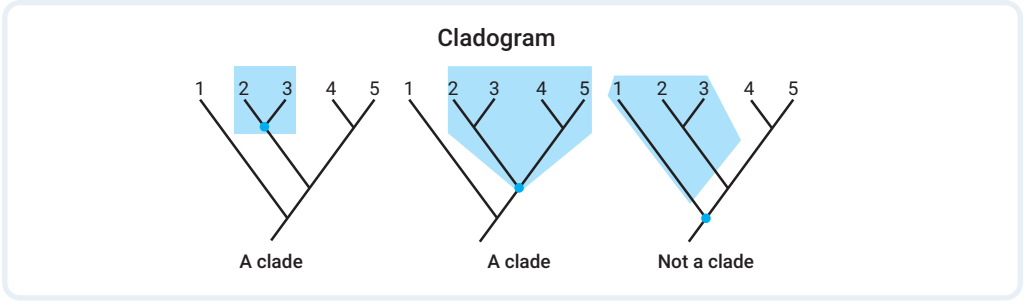
CHAPTER SUMMARY

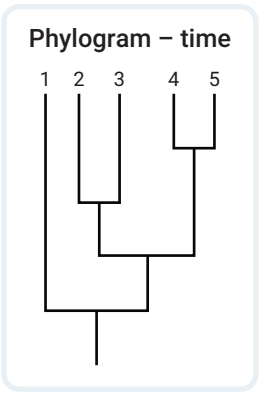
Genes and relatedness

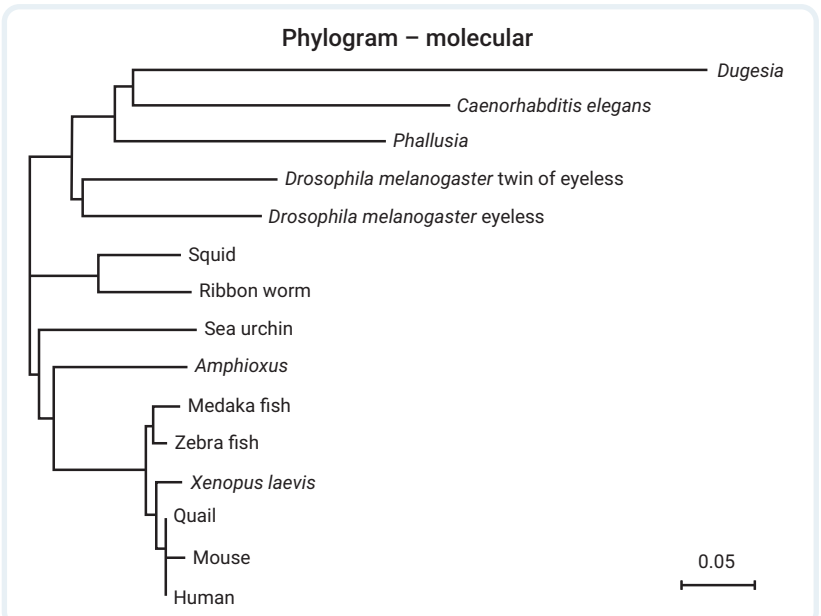
- A conserved sequence is a sequence of nucleotides in DNA or amino acids in proteins that is present across multiple species and that has remained unchanged for multiple generations.
- In comparative genomics, complete genome sequences of different species are compared to identify similarities and differences.

Phylogenetic trees

- Phylogenetic tree assumptions:
  - Groups of organisms are related because of descent from a common ancestor.
  - The offspring of an ancestral species diverge dichotomously (bifurcation).
  - Changes in characteristics occur in lineages over time and organisms become increasingly different.
- Constructing phylogenetic trees:
  1. Acquire the data (morphological or molecular sequences).
  2. Create a table of the characteristics, known as a character matrix, to be used for classification.
  3. From the character matrix, determine how the organisms or groups of organisms can be assembled into clades.







CHAPTER EXAM

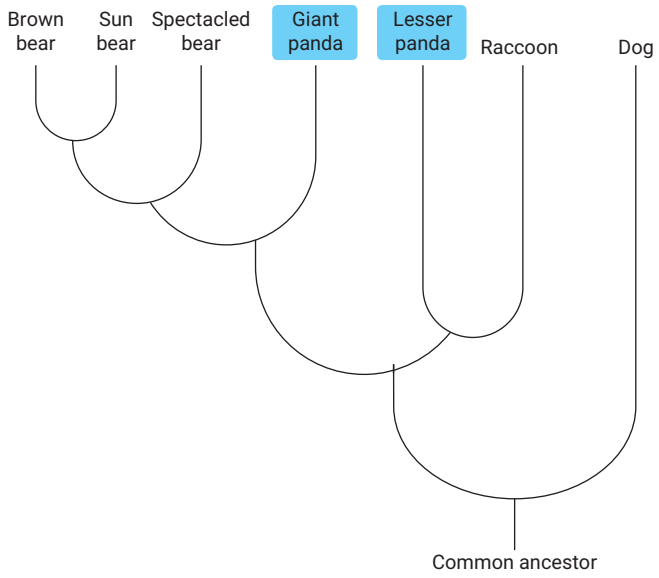
MULTIPLE CHOICE

1. Nodes in a cladogram represent:
   - **A** convergent points.
   - **B** divergent points.
   - **C** sequences of DNA.
   - **D** sequences of RNA.

2. Comparative genomics relates to:
   - **A** differences in animal structures.
   - **B** differences in animal behaviours.
   - **C** similarities of DNA sequences.
   - **D** similarities in animal structures.

3. Histones are a good candidate for molecular sequence conservation because the histone:
   - **A** DNA is very stable.
   - **B** RNA is very stable.
   - **C** plays a crucial role in genome compaction.
   - **D** plays a crucial role in genome destruction.

Questions 4–6 relate to the following information.
Analysis of the degree of similarity of DNA has been used to resolve the debate about the relationship between giant pandas, lesser pandas, bears and American raccoons. Data derived from body structures was inconclusive, but data from DNA analysis was used to produce the following phylogenetic tree.

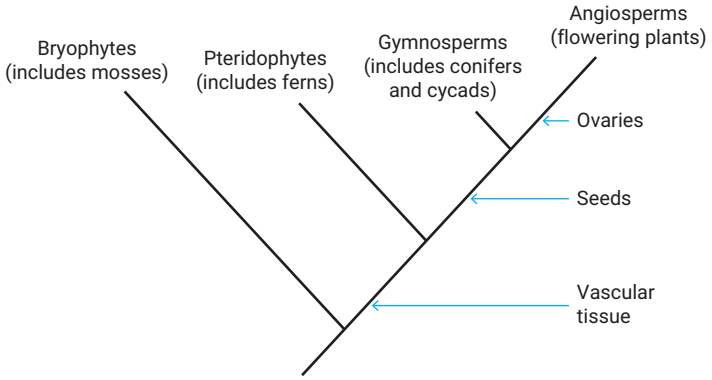


4. Identify the most closely related organisms.
   - **A** Brown bear and dog
   - **B** Brown bear and raccoon
   - **C** Brown bear and giant panda
   - **D** Brown bear and sun bear

5. Identify the least closely related organisms.
   - **A** Brown bear and dog
   - **B** Brown bear and raccoon
   - **C** Brown bear and giant panda
   - **D** Brown bear and sun bear

6. Researchers would expect to find more DNA similarities between the giant panda and the lesser panda compared to the:
   - **A** lesser panda and the raccoon.
   - **B** lesser panda and the dog.
   - **C** dog and the raccoon.
   - **D** brown bear and the raccoon.

Questions 7–9 relate to the following clade, which shows the relationship between photosynthetic organisms.



7. The clade shows that the first characteristic to arise after photosynthetic tissue is:
   - **A** bryophytes.
   - **B** ovaries.
   - **C** seeds.
   - **D** vascular tissue.

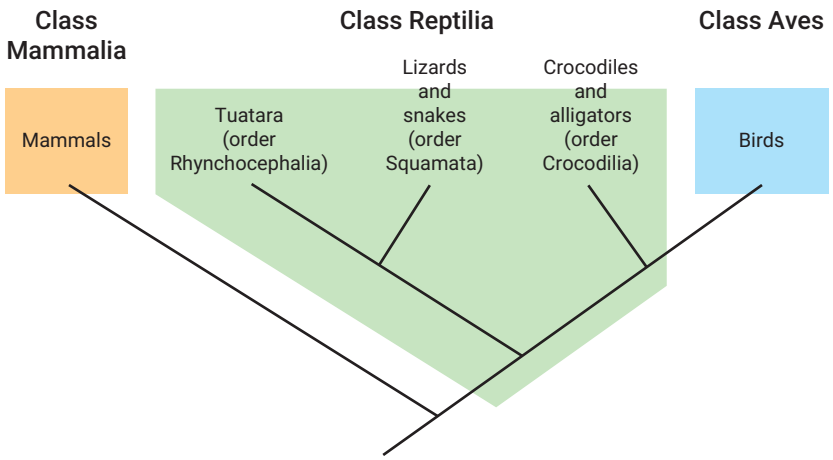
8. The clade shows that gymnosperms have:
   - **A** no ovaries, seeds or vascular tissue.
   - **B** ovaries, seed and vascular tissue.
   - **C** ovaries and seeds, but not vascular tissue.
   - **D** seeds and vascular tissue, but not ovaries.

9. If an organism was found to have seeds, it could be:
   - **A** an angiosperm or a bryophyte.
   - **B** an angiosperm or a gymnosperm.
   - **C** a gymnosperm or a bryophyte.
   - **D** a gymnosperm or a pteridophyte.

10. The correct definition for phylogenetic tree is:
    - **A** a branching diagram showing evolutionary relationships.
    - **B** a point in a diagram where lines branch or intersect.
    - **C** currently in existence, not extinct.
    - **D** having two branches, two opposing aspects.

SHORT RESPONSE

11. The following diagram shows the currently accepted cladogram for the major classes of amniotes (animals whose offspring develop in amniotic fluid).



Scientists have used this cladogram to argue that class Reptilia and class Aves should be completely reclassified. State whether you agree or disagree and **justify** your opinion.

12. Outline how mutation rate could be used to determine how long ago two species diverged.

CROSS-CHAPTER QUESTION

13. **Explain** how multiple organisms could have the same amino acid sequences in a genomic analysis but different bases sequences if the molecular comparison was run using DNA.

DATA ANALYSIS

Questions 14 and 15 refer to the following.

A comparison of the degree of similarity of DNA between two species can also be expressed as a percentage. The following table shows a comparison of human DNA with DNA from other primates.

Primate	Similarity with human DNA (%)
Human	100
Chimpanzee	97.6
Gibbon	94.7
Rhesus monkey	91.1
Capuchin	84.2

14. Analyse data

Identify an evolutionary relationship between the organisms listed in the table by constructing a cladogram.

15. Interpret evidence

Deduce whether the protein synthesised from this DNA sequence in the human and the rhesus monkey would consist of the same amino acids in the same sequence.

SCIENCE AS A HUMAN ENDEAVOUR

Syllabus dot point

- ICTs such as genetic databases and The Basic Local Alignment Search Tool (BLAST) have allowed large-scale mapping and analysis of DNA and protein sequences. Technological developments in the fields of comparative genomics, comparative biochemistry and bioinformatics have enabled identification of further evidence for evolutionary relationships.

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The collision of technology and biology

The merging of technology and traditional biology allowed two new fields to develop: bioinformatics and genomics. Bioinformatics uses mathematics, statistics and computer science to analyse complex biological systems, whereas genomics investigates the complete genomes of organisms, including the way genes interact with each other and the environment. Although both fields have their roots in the 1960s and 1970s, they began to accelerate in the late 1900s thanks to the development of technologies such as automated DNA sequencing. The advancements in DNA sequencing allowed researchers to complete one of the greatest projects in science – mapping the human genome (Figure 1).

WANTED

20 Volunteers

to participate in the

Human Genome Project

a very large international scientific research effort.

The goal is to decode the human hereditary information (*human blueprint*) that determines all individual traits inherited from parents. The outcome of the project will have tremendous impact on future progress of medical science and lead to improved diagnosis and treatment of hereditary diseases.

Volunteers will receive information about the project from the Clinical Genetics Service at Roswell Park, and sign a consent form before participating.

No personal information will be maintained or transferred.

Volunteers will provide a one-time donation of a small blood specimen. A small monetary reimbursement will be provided to the participants for their time and effort.

Individuals must be at least 18 years of age.
Persons who have undergone chemotherapy are not eligible.

ROSWELL PARK CANCER INSTITUTE

For more information please contact the Clinical Genetics Service 845-5720 (9:00 am - 3:00 pm) March 24 - 26, 1997

FIGURE 1 A newspaper advertisement from 1997 asking for volunteers to provide blood samples and DNA for the Human Genome Project

National Human Genome Research Institute; Link: https://www.genome.gov/about-genomics/educational-resources/fact-sheets/human-genome-project

Both fields have contributed significantly to comparative biology, a multidisciplinary approach that analyses natural variation, then correlates differences among species to understand phylogenetic histories This helps biologists use the features of one species to learn about an aspect of a second species. Scientists are now able to use detailed protein structures and gene interactions to uncover complex evolutionary connections between species. These interactions enable large-scale sequencing, analysis and comparison of genetic data, so scientists can track the evolutionary history of genes, proteins and species across time. Below are several examples of publicly available databases and specific tools that have facilitated large-scale mapping and analysis of DNA and protein sequences, which are now central to evolutionary studies.

Basic Local Alignment Search Tool

The Basic Local Alignment Search Tool (BLAST) compares protein or nucleotide sequences to find regions of similarity between a sequence of interest ('query') and a database ('subject') sequence.

Sequence similarities can be used to infer evolutionary relationships and gene function, which supports the development of phylogenetic trees and the identification of conserved genetic regions as well as the prediction of gene function, all based on similarities to known sequences in the database.

Alphafold Protein Structure Database

Understanding the structure of proteins, particularly enzymes, helps to better understand their function. AlphaFold uses AI technology developed by DeepMind to predict protein structures (Figure 2). More than 200 million protein structure predictions are

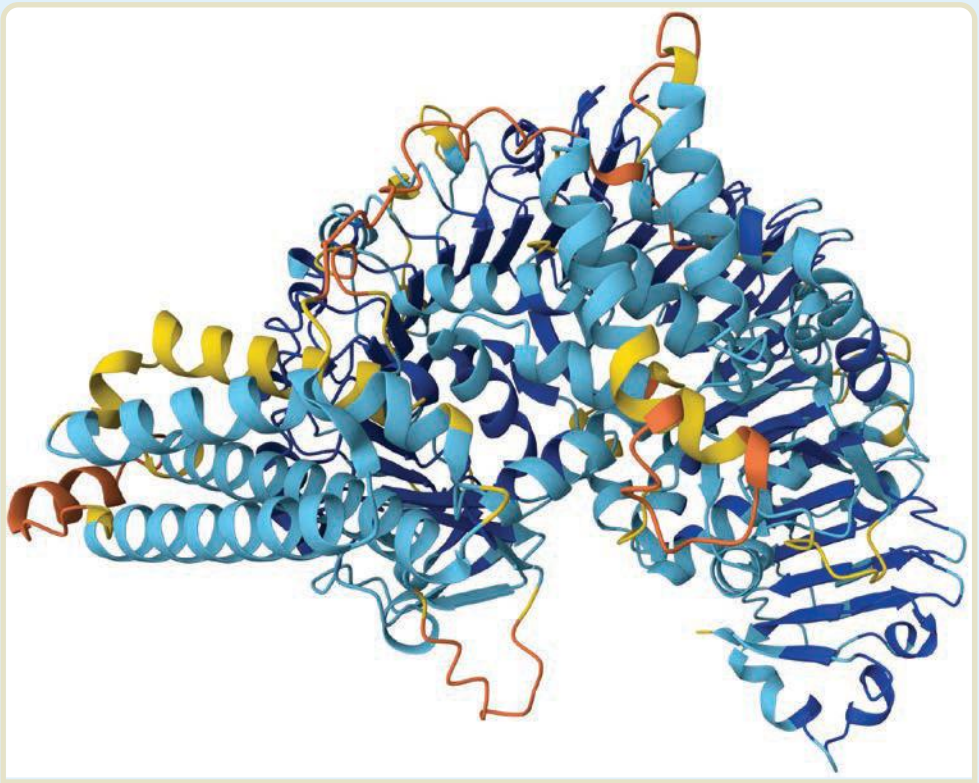
Weblinks

Steps involved in BLAST searches

BLAST online database

AlphaFold Protein Structure Database

GenBank



AlphaFold DB version 2022-11-01. Jumper, J et al. Highly accurate protein structure prediction with AlphaFold. Nature (2021). Varadi, M et al. AlphaFold Protein Structure Database in 2024: providing structure coverage for over 214 million protein sequences. Nucleic Acids Research (2024).

FIGURE 2 As of January 2025, it is believed that AlphaFold has predicted more than 214 million protein structures.

available, through a partnership with European Molecular Biology Laboratory's European Bioinformatics Institute.

Different organisms have similar amino acid sequences in key proteins. Amino acid substitutions are prevented in particular positions by strong selective pressures to ensure the correct three-dimensional shape in the final structure. Predicting the three-dimensional protein shape can allow for the analysis and comparison proteins that are not easily available, such as very rare, scarce or ancient proteins.

GenBank

GenBank is a genetic sequence database that allows the public to access DNA sequence information that is comprehensive and recent. It is maintained by the National Center for Biotechnology Information in the United States.

Researchers can access millions of DNA sequences for comparative genomics to better understand evolutionary relationships and gene families.

Phylogenetic analysis tools

With such large databases now available, phylogenetic tools can use algorithms to align DNA, RNA or protein sequences. This is used to build and analyse phylogenetic trees to reflect the evolutionary history of species or of particular genes.

Bioinformatics and genomics have improved and accelerated our understanding of biology. As technology improves, we will be able to unlock even more insights about many different fields including disease, drug development and even personalised medicine.

Weblinks

Phylogeny

Constructing phylogenetic trees

MrBayes

PhyML

PAUP*

BEAST

Cytoscape

GROMACS

KEGG

MEGA

RAxML

RefSeq

The 1000 Genomes Project

ANSWERS

CHAPTER 1 CLASSIFYING SPECIES

LEARNING CHECK 1.1

DESCRIBING

1 The biological species concept defines a species as organisms that can reproduce offspring that are both viable and fertile.

2 The morphological species concept

3 The biological species concept does not allow for classification of fossils or asexually reproducing organisms.

APPLYING

4 The morphological species concept is based on anatomical or other easily observable structures, whereas the biological species concept is based on reproduction of viable and fertile offspring.

LEARNING CHECK 1.2

DESCRIBING

1 Taxonomy is the naming, describing and classifying of organisms.

2 Benefits: allows organisms to be easily identified; helps to explain the evolutionary history of organisms

3 allows for understanding of relationships between organisms.

APPLYING

4 Limitations: relies on observable characteristics; is hierarchical and does not allow for organisms that have characteristics that fit into more than one category; relies on human interpretation, therefore has some bias (some limitations of morphological classification system have been overcome with molecular sequencing)

LEARNING CHECK 1.3

DESCRIBING

1 Domain, kingdom, phylum, class, order, family, genus, species

2 Fungi – multicellular, with organelles, chitin cell walls, saprophytic nutrition

Protista – single-celled, organelles, autotrophic or heterotrophic nutrition

Plant – multicellular, with organelles, autotrophic, chlorophyll.

Animal – multicellular, with organelles, heterotrophic

3 *L. confertus*

APPLYING

4 Woylie and Boodie. These two species belong to the same genus. All four animals are part of the same phylum. Although the wren and the parrot are in the same class, being in the same genus means the Woylie and the Boodie have more characteristics in common and are the most closely related.

5 DNA evidence is based on DNA sequences that are objectively determined by DNA base sequencing processes and are A, T, C or G. Physical appearance (morphology) is based on human observations, which are open to interpretation. Physiological traits may be similar as a survival requirement, rather than being due to common ancestry.

LEARNING CHECK 1.4

APPLYING

1 Dark green upper surface and pale lower surface

2 *Eucalyptus planchoniana* and *Eucalyptus carnea*

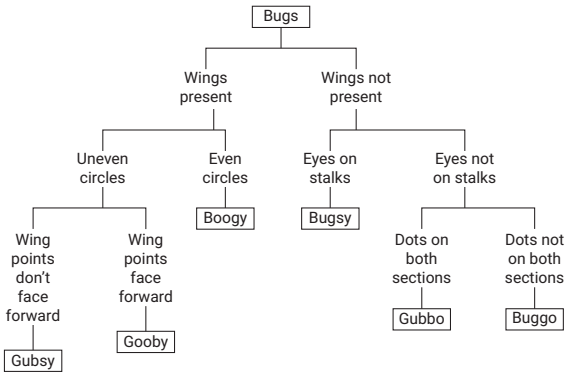
ANALYSING

3 Differences: *E. microcorys* has reddish brown outer bark whereas *E. acmenoides* has yellow or grey outer bark. *E. microcorys* has rounded buds on long, slender stalks whereas *E. acmenoides* oval, pointed buds. *E. microcorys* has gumnuts with a tapered base whereas *E. acmenoides* has gumnuts that are hemispherical.

4 Example similarities: body spots, three pairs of legs – Bugsy, Buggo, Gubbo; two wings with spots – Gubsy, Boogy, Gooby

Example differences: eyes on stalks – Bugsy, not on stalks – Buggo, Gubbo; dots on both sections – Gubbo, not on both sections section – Buggo; evenly sized circles – Gubsy, Gooby, unevenly sized circles – Boogy; wing points face forward – Gooby, wing points don't face forward – Gubsy

5



INTERPRETING

6 Debug would end up at Boogy. This bug is not the same as Boogy; therefore, this bizarre bug would not be classified using the key designed because Debug is more similar to Gooby. Note: this response depends on the structure of the key designed by the student.

CHAPTER EXAM

MULTIPLE CHOICE

1 A
2 A
3 A
4 C
5 D
6 B
7 A
8 D
9 D
10 C

SHORT RESPONSE

11 Each species concept has limitations that mean organisms that have existed or currently exist are not included within the descriptors. For example, asexually reproducing organisms do not produce genetically different offspring from two different parents. The reproductive strategies of fossilised organisms cannot be determined from their fossilised remains. Therefore, these organisms are not included in the biological species concept definition.

12 'Big' or 'small' are subjective descriptions. For example, an apple is big compared to a strawberry but small compared to a watermelon. A dichotomous key requires clearly defined attributes that are not open to interpretation.

CROSS-CHAPTER QUESTION

13 Currently, archaebacteria are a separate domain based on the absence of organelles and the way DNA is stored. If mitochondria were discovered in one species, this would mean that this species includes a membrane-bound organelle. If only one species of archaebacteria contained mitochondria, the domain structure would need to be reviewed. If all species of archaebacteria have mitochondria, then no change to domains is needed.

DATA ANALYSIS

14 Similarities: two pairs of wings, feeding on flowers, same kingdom, phylum, class, order, family. Differences: genus and species, wing shape and colour.

15 These two butterflies would not be able to produce fertile offspring because, even though they have morphological similarities and belong to the same family, they belong to different species.

CHAPTER 2 ECOSYSTEM DIVERSITY

LEARNING CHECK 2.1

DESCRIBING

1 **a** A species is a group of organisms that interbreed to produce viable and fertile offspring.

b An ecosystem is a community of organisms that are interacting with each other and their physical environment.

2 Genetic diversity: the range of different genes within a species.

Species diversity: the range of different species in an ecosystem.

Ecosystem diversity: the range of different living organisms, their interactions and physical environments in a particular location.

APPLYING

3 All types of diversity are important to maintain long-term stability of species, communities and ecosystems through maintaining biodiversity. If diversity is not maintained, it may result in inbreeding, vulnerability to disease, over-predation and ecosystem breakdown.

LEARNING CHECK 2.2

DESCRIBING

1 Species richness, species evenness, percentage cover, percentage frequency and Simpson's diversity index (SDI)

APPLYING

2 Species richness refers only to the number of species present in an ecosystem, as a whole number, whereas species evenness refers to how many of each species are present.

3 Percentage cover can be a better indicator for plants, such as grass, than species evenness because these organisms can be difficult to count individually; therefore, the area they cover is a better indication of abundance.

4

Species	n	$n(n-1)$
Flathead	36	$36(35) = 1260$
Australian bass	720	$720(719) = 517\,680$
Garfish	934	$934(933) = 871\,422$
Pearl perch	60	$60(59) = 3540$
Tailor	14	$14(13) = 182$
	$N = 1764$	$\sum n(n-1) = 1\,394\,084$

$$SDI = 1 - \left(\frac{\sum n(n-1)}{N(N-1)} \right)$$
$$= 1 - \frac{1394\,084}{1764 \times 1763}$$
$$= 1 - 0.45$$
$$= 0.55$$

LEARNING CHECK 2.3

DESCRIBING

1 Organisms can be distributed uniformly, in a predictable pattern; randomly, without a predictable pattern; or clumped, with organisms together in small groups.

2 Temperature, light intensity, salinity, pH, space, shelter

APPLYING

3 Diseases can affect the distribution of organisms as close contact generally increases the transmission of infectious disease. If the disease is fatal, population size is reduced, meaning there are fewer organisms using the available space.

ANALYSING

4 Similarity: Both have all the conditions required for an organism's survival.

Differences: Microhabitats occur on a small scale, whereas habitats are on a larger scale.

LEARNING CHECK 2.4

DESCRIBING

1 Stratified sampling is a method where a proportionate number of observations is taken from each different environment, or stratum, the sample area.

2 The quadrat method involves placing flat squares randomly around an area to count individuals within the square. Quadrat sampling allows for data about species richness, evenness, % cover, % frequency to be collected and allows for SDI to be calculated. The transect method involves laying a straight line through the area and counting individuals along the line. Transect sampling gathers information about the presence or absence of species and is used to determine the distribution of species against an environmental gradient (zonation); can give an indication of species richness.

3 Appropriate size and number of samples; consistent counting criteria; random generation of numbers to decide placement of quadrat/transect; calibrating equipment, ensuring precision is noted

APPLYING

4 Animals are mobile, whereas quadrats and transects are placed in fixed locations. Mobile animals will not stay within the sampling area to be counted effectively. Also, many animals are too large to be accurately sampled with quadrats or transects.

5 Consideration should be given to the time (available for sampling), space (sampling size and area) and equipment resources available (transects, quadrats or traps). Answer should explain how the differences in these factors results in a difference in the types of species identified and the number of each species identified.

6 At different times of day or season, different numbers and types of species will be active and able to be counted. This means that the species diversity may vary depending on when sampling occurs.

7 Stratified sampling considers the size of the habitat when allocating quadrats, so the data that is returned is representative of the actual area that the species inhabits. Random sampling may also produce quadrats that are along the boundaries of two habitats and would return data that does not reflect the true combination of species and ground coverage.

LEARNING CHECK 2.5

DESCRIBING

1 Potential evapotranspiration ratio, annual precipitation (mm), biotemperature

2 Percentage cover of the dominant layer, height of the dominant layer

INTERPRETING

3 **a** Holdridge life zones: moist forest

b Specht's classification: eucalypt tall open forest

CHAPTER EXAM

MULTIPLE CHOICE

1 C
2 C
3 B
4 B
5 B
6 B
7 D
8 C
9 C
10 A

SHORT RESPONSE

11 The inclusion of a species or common name makes it easier to communicate and identify vegetation types, especially for non-specialists. It also provides ecological context by highlighting the dominant species that shape the structure and function of the ecosystem.

12 a Eucalypt species A

b Approximately 30%

c An image of the transect along line X:

d Closed scrub

CROSS-CHAPTER QUESTION

13 Ecologists would use a key to identify the species present, which would then allow them to determine species richness (number of different types of species present) or calculate SDI (using abundance as well as richness).

DATA ANALYSIS

14 a Frog species are found in their highest numbers in areas that are humid. Species numbers range from 20-40 across northern Australia and down the east coast. (Humidity is seems to have more effect that temperature as there are warm to hot areas of Australia that are not humid and these have few frog species.)

b Quolls are distributed through humid zones of Australia. Mainly in hot humid areas, but also warm humid areas.

15 The Australian climate zones are relatively consistent over this time period (1940–2022) yet the quoll distribution has changed. The current distribution of quolls still includes hot, humid areas in Northern and Eastern Australia. However, quolls are now occupying an area of Western Australia that while hot, is not humid. this means quolls have moved out of their preferred humid environment, even though it still exists. Therefore, a biotic factor is likely to have been the cause of this change.

CHAPTER 3 POPULATIONS

LEARNING CHECK 3.1

APPLYING

1 a Large pond: $M = 20$, $n = 20$, $m = 2$

$$N = \frac{20 \times 20}{2} = 200$$

b Small pond: $M = 20$, $n = 20$, $m = 8$

$$N = \frac{20 \times 20}{8} = 50$$

LEARNING CHECK 3.2

DESCRIBING

1 Initially, growth is slow, then there is a rapid exponential growth, followed by levelling out at a stable number (carrying capacity).

APPLYING

2 Exponential growth cannot be sustained because eventually one (or more) resources becomes limiting and there isn't enough to support the population's continued growth and the population crashes to low numbers or dies out.

ANALYSING

3 Similarity: Both have initial exponential growth.

Difference: In logistic growth, the population levels out at a carrying capacity, whereas exponential growth crashes after reaching a peak.

INTERPRETING

4 The recently logged forest is likely to experience exponential growth because there are many resources required by plants (e.g. light, space, water) that are available because logging removes the trees. The old growth forest is likely to experience logistic growth as the forest is already at carrying capacity and there is already competition for the required resources.

LEARNING CHECK 3.3

1 a Population: total number of individuals of one species in an area

b Carrying capacity: the maximum population size of a species that can be supported in a given environment.

APPLYING

2 Biotic – four possible answers

Factor being changed	Increasing this factor decreases carrying capacity	Decreasing this factor increases carrying capacity
Competitors	More competition for food, shelter or resources	More food, shelter or resources are available with less competition for them.
Reproductive mates	More offspring, which ultimately increases competition for resources	Fewer offspring, which ultimately reduces competition for resources.
Predators	Fewer individuals can survive as more are eaten	More individuals can survive as fewer are eaten
Disease-causing organisms	More pathogens, fewer individuals can survive	Fewer pathogens, more individuals can survive

3 Abiotic – four possible answers

Factor being changed	Increasing this factor decreases carrying capacity	Increasing this factor decreases carrying capacity
Shelter availability	More available locations results in fewer individuals exposed to changes in environmental conditions, increasing survival	Fewer available locations leads to individuals being more exposed to changes in environmental conditions, reducing survival
Nesting sites	More suitable locations leads to more offspring	Fewer suitable locations leads to fewer offspring
Environmental factor (e.g. light)	More photosynthetic organisms survive, increasing producers, supporting food webs	Fewer photosynthetic organisms survive, reducing producers impacting food webs
Environmental factor (e.g. water)	More organisms have access to sufficient water (e.g. plants – more photosynthesis; animals – more hydration), so more survive.	Fewer organisms have access to sufficient water (e.g. plants – less photosynthesis; animals – less hydration), so fewer survive.

INTERPRETING

4 a Flood – increase in water leads to increased growth of plants, thus increase in animals with increased shelter and availability of food. Also, increased aquatic habitats for fish, birds and insects. Increased carrying capacity.

or

Increase in water washes away soil, vegetation and organisms that are unable to swim or find higher ground, reducing carrying capacity.

b Fire – removal of vegetation and fauna that are unable to escape. Fewer nesting sites, less food and less shelter. Decreased carrying capacity.

LEARNING CHECK 3.4

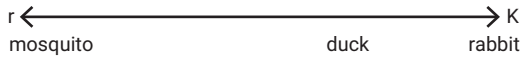
DESCRIBING

1 High parental input, few offspring, low reproductive rate, late reproductive maturity, low growth rate, specific niche and diet

2 Many offspring, low parental input, short lifespan, early reproductive maturity, high growth rate, generalist niche and diet

ANALYSING

3



INTERPRETING

4 Mosquito has no parental input – eggs laid into water, many offspring – up to 200 eggs, therefore close to 'r'.

Rabbit and duck have similar parental time input of 2 months. Duck lays up to 12 eggs, but rabbit gives birth to fewer young (7). Therefore both at the 'K' end of the spectrum, but with rabbit closer due to fewer offspring.

LEARNING CHECK 3.5

DESCRIBING

1 Births, deaths, immigration and emigration

2 An increase in predation, disease or competition will decrease a population. An increase in reproductive mates should increase a population.

3 An increase in shelter, water, light should increase a population.

APPLYING

4 $B + I - D - E = 1000 + 72 - 108 - 345 = 619$. The population has increased by 619 individuals in the year.

5 $BR = \frac{59}{1000}$

$IR = \frac{105}{1000}$

$DR = \frac{86}{1000}$

$ER = \frac{40}{1000}$

Growth rate $= (BR + IR) - (DR + ER)$

$= \frac{164}{1000} - \frac{126}{1000} = \frac{38}{1000}$

or 38 individuals per 1000 growth per year

Expressed as a % $= \frac{38}{1000} \times 100 = 3.8\%$ per year increase

6 $BR = \frac{150}{1000}$

$IR = \frac{59}{1000}$

9780170483384

$$DR = \frac{290}{1000}$$

$$ER = \frac{30}{1000}$$

Growth rate = (BR + IR) − (DR + ER)

$$= \frac{209}{1000} - \frac{320}{1000} = -\frac{111}{1000}$$

or 111 individuals per 1000 decrease per year

Expressed as a % $= \frac{111}{1000} \times 100 = 11.1\%$ per year decrease

INTEPRETING

7 Population size is increasing because more individuals are added to the population than are removed.

CHAPTER EXAM

MULTIPLE CHOICE

1 C

2 C

3 B

4 C

5 D

6 D

7 D

8 D

9 B

10 B

SHORT RESPONSE

11 a Biotic – low levels of competition, high food availability, absence of disease. Abiotic – high rainfall

b Exponential growth – J curve

c Plague numbers are not sustainable because the population grows at a faster rate than the food source. Once the food is insufficient for the population, the locusts die before reproducing and the population crashes.

12 Individuals marked in the first capture could either die or emigrate before recapture. There may also be individuals that immigrate or are born, changing the ratio of individuals in the population that is used to calculate the Lincoln index.

CROSS-CHAPTER QUESTION

13 a Soil nutrients and water

b Breeding sites and other penguins

c Water, sunlight, climatic conditions

DATA ANALYSIS

14 Population A: $M = 30$, $m = 10$, $n = 50$

$$N = \frac{30 \times 50}{10} = 150$$

Population B: $M = 100$, $m = 50$, $n = 200$

$$N = \frac{100 \times 200}{50} = 400$$

15 Similarity: both populations had individuals in the recapture that were marked.

Difference: Population B had a higher number of initially marked turtles at 100 than Population A at 30. Population B also had a higher number of marked turtles in the recapture at 50 than Population A at 10.

CHAPTER 4 TRANSFER AND TRANSFORMATION

LEARNING CHECK 4.1

DESCRIBING

1 Water cycle, carbon cycle, nitrogen cycle

2 Photosynthesis takes CO_2 out of the atmosphere and combines it with water to produce glucose. Respiration converts energy stored in glucose to ATP. This releases carbon in the form of CO_2 into the atmosphere as well as water.

3 Condensation, evaporation, precipitation, percolation

APPLYING

4 Nitrogen-fixing bacteria convert N_2 gas into NH_3. The NH_3 is converted by other bacteria into nitrites and nitrates, which can be used by plants to make amino acids, then proteins. As the denitrifiers continue to release nitrogen gas into the atmosphere again, the stores of nitrogen in the soil would run out, amino acids and proteins would not be made, plants would die off. Without nitrogen-fixing bacteria, nitrogen cannot be used by living things directly; therefore, this would limit growth and survival of plants and all consumers dependent on plants.

5 Burning fossil fuels releases CO_2 into the atmosphere at a faster rate than it would be released by respiration or decomposition. Removal of forests means there are fewer trees to complete the process of photosynthesis, which removes CO_2 from the atmosphere. Overall, there is a net increase in CO_2 in the atmosphere.

LEARNING CHECK 4.2

DESCRIBING

1 About 70 per cent of the incoming energy from the Sun is absorbed by the atmosphere and Earth's surface. The remaining 30 per cent is reflected back into space. Leaves absorb, reflect and transmit most of the visible light energy reaching Earth's surface.

2 Consumption – chemical energy is transferred from one organism to another by eating.

Respiration – chemical energy is transferred from glucose to ATP and transformed into heat energy.

Decay – some chemical energy is transferred in nutrients and ultimately transformed into heat energy.

Fire – burning transforms chemical energy into heat and light energy.

APPLYING

3 Chemical energy is transferred from wastes and dead organisms to detritovores and decomposers when these organisms feed. This chemical energy is either used by the decomposers and detritovores to survive or released to the environment as heat energy resulting from their metabolism.

4 During the transfer of chemical energy, some is also transformed into heat energy. As animals produce ATP, then complete other metabolic reactions, heat energy is also released. In endotherms, this heat energy helps to maintain a constant internal temperature.

LEARNING CHECK 4.3

APPLYING

1 GPP is the total organic matter produced annually in an area by photosynthesis, whereas NPP is the amount of organic matter made available to herbivores annually and equals GPP minus the energy required by the producers themselves.

2 Biomass pyramids show the mass of different organisms feeding at different trophic levels in different ecosystems. This allows for the condition of the ecosystem to be monitored and potentially reduce further damage due to loss of organisms, e.g. producers. Limitations are that species may occupy multiple trophic levels, but their biomass cannot be located in two levels at the same time; therefore biomass pyramids are suited to food chains, not food webs. Pyramids don't necessarily account for seasonal variations. Nor do biomass pyramids generally include saprophytes (fungi).

3 Energy lost = NPP TL1 – NPP TL2 = 6300 – 1250 = 5050 kJ m^{-2} $year^{-1}$.

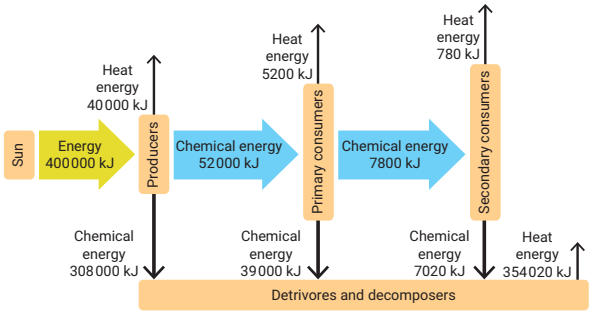
4 $$\%\ \text{efficiency} = \frac{\text{NPP TL3}}{\text{NPP TL2}} \times 100 = \frac{250}{1250} \times 100 = 20\%$$

5 $$\%\ \text{efficiency} = \frac{\text{NPP TL4}}{\text{light energy}} \times 100 = \frac{50}{42\,000} \times 100 = 0.12\%$$

ANALYSING

6 The producers level should be 20 cm wide, primary consumers should be 6.75 cm wide, secondary consumers should be 1.5 cm wide and tertiary consumers should be 0.75 cm wide.

7



CHAPTER EXAM

MULTIPLE CHOICE

1 A
2 A
3 C
4 D
5 A
6 C
7 D
8 B
9 C
10 D

SHORT RESPONSE

11 A food web shows feeding relationships. Organic molecules in food contain carbon. When food is digested after consumption, CO_2 is released after glucose is used in respiration. Plants take CO_2 out of the atmosphere through the process of photosynthesis, and it is once again stored in food molecules. For example, grass completes photosynthesis and removes CO_2, converting it to glucose. The purple swamp hen feeds on the grass, consuming the carbon in the glucose, releasing it back to the atmosphere as CO_2 through respiration.

12 Each transfer in a food chain is approximately 10 per cent of the previous trophic level. Carnivores are at least TL3. Therefore, if humans eat a carnivore, the human is TL4 and receiving a smaller percentage of the energy. For example, if the plant has 100 units of energy, the herbivore receives 10 units, the carnivore receives 1 unit, leaving the human with 0.1 unit of energy.

CROSS-CHAPTER QUESTION

13 Initially, there would be greater competition with the coot, swamphen and water flea for the bulrush. This would result in a reduction in the bulrush population, as there is an increase in bulrush consumers. This would reduce the biomass of TL1. Because the bulrush is a producer, less CO_2 would be taken from the atmosphere through photosynthesis. Species diversity would initially increase because of the new species present. Over time, the species would compete for the bulrushes. This may lead to reduced species diversity if one species outcompetes others (competitive exclusion). Depending on which species survive the competition, other feeding relationships at higher trophic levels may also change if the existing species of water flea, coot or swamp hen are lost to the system.

DATA ANALYSIS

14 $\%\ \text{efficiency} = \frac{1609}{14\,146} \times 100 = 11.4\%$

15 Heat losses = 50 303 + 7938 + 1328 + 55 + 19 210 = 78 834. This does not equal energy brought into the system by producers (87 403). The difference of 8569 may be attributed mostly to emigration (10 500) minus the immigrants who died without respiring (2031).

CHAPTER 5 INTERACTIONS

LEARNING CHECK 5.1

DESCRIBING

1 Competition within a species: for a reproductive mate, nesting site, space or territories, light

Competition between two species: food (e.g. carnivores eating the same species), space, nesting sites.

2 Keystone species fill an important ecological role, and the removal of this species would have a damaging effect on the ecosystem, e.g. population regulation, nutrient cycling or ecosystem engineers.

3 The purple sea star (*Pisaster ochraceus*) is a natural predator of mussels in the intertidal zones and act as population controllers. If the purple sea stars were removed from this environment, the mussels would no longer be affected by predation and their population would expand and displace species such as barnacles and limpets.

APPLYING

4 When predators are scarce, prey increase in abundance. As their food source increases, predators reproduce more and their population increases, decreasing prey abundance. Once the prey population decreases again, the predator abundance decreases due to lack of food and the cycle begins again. This is driven by density-dependent interactions between the populations.

5 Commensalism is an association between two organisms where one benefits and the other is unaffected, neither benefiting nor being harmed.

Mutualism occurs when two species benefit from any interactions that may occur. This could include 'goods' or 'services' that they cannot produce themselves, such as nesting space, nutrition or defence from predators.

Parasitism occurs when an organism, the parasite, lives in (endoparasite) or on (ectoparasite) another organism, the host, to consume nutrients. Unlike predation, parasites leave their host alive, if unwell. The parasite benefits from the interaction because they gain nutrition and a habitat. Hosts are harmed.

Predation occurs when one organism, the predator, hunts and kills another organism, the prey, then consumes part or all of it for its food.

ANALYSING

6 The relationship between the elephant and acacia tree is mutualism (the elephant gets food and the acacia ends up with beetle-free seeds that are dispersed). The relationship between the beetle and acacia is a feeding relationship, with the beetle being a consumer of the seeds. The relationship between the elephant and the beetle is competition (they compete for the seeds).

LEARNING CHECK 5.2

DESCRIBING

1 A fundamental niche describes the habitat and role the organism could survive in. A realised niche is the actual habitat and role the organism occupies. It is usually smaller than the fundamental niche.

2 **a** Any animal that is more effective at eating lizards, insects, small birds and cockatoos

b Dingo – competes for the cockatoo. Small birds or lizards – compete for the insects.

APPLYING

3 Feral cats do not have a natural predator. They are effective predators. They eat native animals and birds and also out-compete native animals for their food sources. See Figure 5.2.4 as an example.

4 Resource partitioning ensures that species are not in direct competition with each other for resources such as food or space.

INTERPRETING

5 The channel-billed cuckoo area would have a lower magpie population because fewer magpie eggs would survive in the nests because the magpie eggs would be displaced by cuckoo eggs. In the non-cuckoo area, the magpie population would be higher because magpie eggs would be more likely to survive to maturity because there are only magpie eggs in the nest.

LEARNING CHECK 5.3

APPLYING

1 Narrow niches allow for a greater variety of species to survive in one area, thus increasing biodiversity.

2 The dominant species is the most commonly occurring species in an environment. This species may not be essential to the survival of the ecosystem. If its population was reduced, the environment would be affected but survive. A keystone species is essential to the survival of the ecosystem, both directly and indirectly managing the biodiversity of the community.

INTERPRETING

3 Arguments for: Allows for organisms in the same environment as the keystone species to be conserved as well; can draw public attention to habitats that need to be conserved

Arguments against: Could ignore organisms that are important indicators of biodiversity; overlook the importance of other species to a habitat or ecosystem and result in misdirected resources

4 This data does not continue to support predation or competition. Figure 5.3.3 shows that the cassowary sightings remain relatively low for the year. Small fluctuations occur independently of the feral pig population. The large increase in feral pig sightings in Jul–Aug does not correspond with a large drop in cassowary sightings, as would be expected if predation and/or competition were occurring. In Figure 5.3.2, cassowary sighting lows tend to occur at or after peaks in feral pig sightings, e.g. Nov–Dec 2020 and Aug–Oct 2023.

LEARNING CHECK 5.4

DESCRIBING

1 Air pollution: respiratory issues. Water pollution: aquatic toxicity, contributing to bioaccumulation. Land pollution: loss of fertile land.

2 Habitat destruction has a negative effect on populations by removing plant species, which reduces food sources, space, shelter and other resources from consumers. This reduces the populations of both producers and consumers.

APPLYING

3 Monocultures affect community structure because they reduce plant biodiversity (including crops), result in soil degradation, increase the use of fertilisers, which can also affect aquatic systems (due to fertiliser run-off), and have an effect on pollinators. These affect community structure by changing the number and type organisms present in an environment and, therefore, how organisms can interact.

4 Overexploitation threatens biodiversity and can degrade ecosystem services by reducing species populations below natural self-sustaining levels and disrupting ecosystem functions and species interactions. This can lead to irreversible loss of species and populations. In turn, ecosystem services are affected, such as loss of food, water, timber, and functions such as pollination, decomposition, water purification, erosion and flood control, and carbon storage (matter cycling) and climate regulation are disrupted.

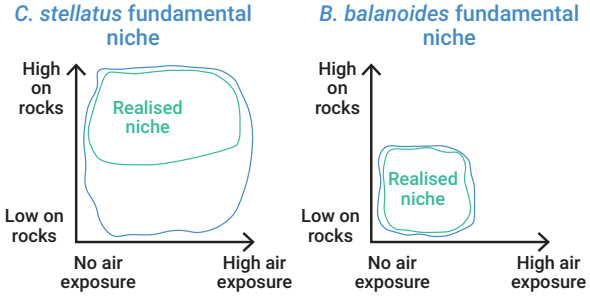
CHAPTER EXAM

MULTIPLE CHOICE

1 C
2 B
3 C
4 A
5 D
6 A
7 C
8 D
9 B
10 C

SHORT RESPONSE

11 *Chthamalus stellatus* has a larger fundamental niche because it is able to survive in both low and high tides, regardless of exposure to air. However, *Balanus balanoides* has a smaller fundamental niche because it is unable to survive exposed to air on the higher rocks. Therefore, when both barnacles are present, *B. balanoides* can effectively out-compete *C. stallatus*, meaning that the realised niche of *C. stallatus* is smaller than its fundamental niche.



12 When the two species are grown independently, both populations increase and reach a carrying capacity where the populations become stable. When the two species are grown together, the population of *P. aurelia* increases and reaches a carrying capacity; whereas the population of *P. caudatum*, initially increases then collapses as *P. aurelia* successfully competes for the resources, excluding *P. caudatum*.

CROSS-CHAPTER QUESTION

13 The northern hairy-nosed wombat is restricted to two locations in Queensland. This means that these two populations are separated because their habitat has been fragmented. Individuals are only able to breed within their populations. If a new mutation arises or if individuals in the isolated population are lost to breeding due to genetic drift or differing selection pressures, allele frequencies and genetic diversity change because there is no longer any gene flow between these populations due to their spatial isolation.

Key points to include for any example: inbreeding due to isolation, genetic drift, different selection pressures, changes to allele frequencies, reducded gene flow.

DATA ANALYSIS

14 When the sea urchin population is high (>300 g per 0.25 m^2), kelp population is low (<2 per 0.25 m^2). However, when the sea urchin population is low (<100 g per 0.25 m^2), the kelp population is high (>8 per 0.25 m^2). The sea urchin is a consumer of the kelp.

15 Sea otter – when sea otters are eaten by orcas, the population of urchins increases dramatically and reduces the kelp significantly from >8 to <2 per 0.25 m^2. If the kelp is lost, then there would be no producer for the system. When the sea otter is present, the urchin population is kept under control and the kelp can survive.

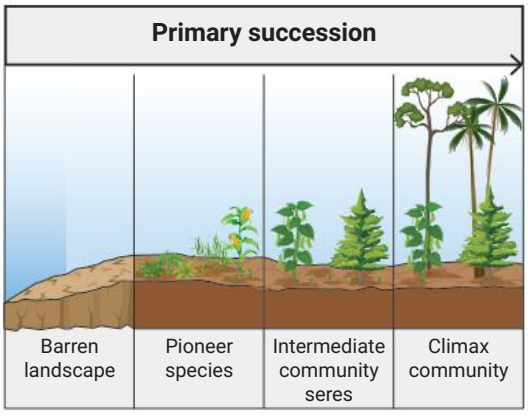
CHAPTER 6 SUCCESSION

LEARNING CHECK 6.1

DESCRIBING

1 Fire, extreme weather, selective grazing by herbivores, human intervention by logging and land clearing for agriculture

2



APPLYING

3 Primary succession begins with bare rock and no autotrophs due to the formation of new rock. This means that the succession goes through multiple stages before reaching a climax community. A secondary succession begins with soil, nutrients and sometimes some plants, and as a community is disrupted rather than returned to bare rock. There are fewer stages and a shorter time frame before the climax community is reached.

4 Pioneer species have to survive extreme conditions of high light intensity, variable temperatures, low water and low nutrients. Therefore, they have to be able to fix nitrogen, photosynthesise and withstand environmental extremes and have a high reproductive rate.

LEARNING CHECK 6.2

APPLYING

1 r-selected species: small organisms, fast growing. Because of the unstable environmental conditions, organisms need to be able to reproduce rapidly. Competitive adaptations offer little advantage because the environment is likely to change suddenly. Found in stages close to colonisers.

K-selected species organisms larger in size; slow growing. Because of the stable environmental conditions, species can have long gestation periods, high parental investment and few offspring. Found in stages closer to climax community.

INTEPRETING

2 Ongoing small-scale disturbances after reaching a climax community would lead to a cycle of increased then decreased species diversity as new habitats are made available, species arrive, compete for the available resources, then alter the habitat, and species are out-competed, reducing richness again.

LEARNING CHECK 6.3

DESCRIBING

1 Temporal scale change in an ecosystem – time of day (e.g. morning or evening), season of the year (e.g. summer or winter).

2 Spatial scale change in an ecosystem – large (e.g. clearing a forest) or small (e.g. turning over a rock).

APPLYING

3 Sampling ice cores can give evidence of climatic change as trapped gas bubbles and the presence or absence of traces of organisms reveal information about changes in temperature and relative concentrations of atmospheric gases from thousands of years ago.

INTERPRETING

4 Initially, smaller plants were able to grow in the existing soil (secondary succession). This changed the environment, allowing for shrubs to become established at around 50 years. Between 50 and 100 years, there was a disturbance and shrubs were cleared, leaving soil. This would have increased temperatures and pioneer species increased in number as the environmental factors were more extreme after the removal of many of the shrubs, shown by the percentage at 100 years.

CHAPTER EXAM

MULTIPLE CHOICE

1 C
2 D
3 B
4 D
5 A
6 B
7 A
8 C
9 D
10 C

SHORT RESPONSE

11 High growth and reproduction rate, tolerant of a wide range of environmental conditions and low nutrients, autotrophs/photosynthetic, nitrogen-fixing

12 Comparing present biota with those in the fossil record helps us to understand changes in living components of ecosystems over time. Different species found in fossils give evidence of the climatic and other abiotic components of ecosystems that supported their existence at that time. Differences can then be documented and compared to current biotic and abiotic factors.

CROSS-CHAPTER QUESTION

13 The complexity would increase when moving away from the shoreline. Initially, there would only be a few autotroph pioneer species. Because these species alter the environment by providing shade, trapping sand and increasing nutrients, more consumer species can survive, increasing the number of species in the environment and therefore, the diversity of number and variety organisms in the food web would increase. Thus the food web becomes more complex due to increasing numbers of interactions.

DATA ANALYSIS

14 Parts of the mountain now covered in scoria, lava or ash would experience a primary succession because there is no soil available. The western section that has some plants remaining would most probably undergo a secondary succession. Therefore, the northern, eastern and southern parts would probably undergo a different succession from the western section.

15 The predicted succession has not returned to a climax community. Although the colonising lichen species are no longer present, the dominant species are shrubs at 12% cover, along with some grass (1%) and small trees (5%). There is no evidence of large tree species as would be expected in a climax community. This suggests that the predicted succession is in a seral stage.

CHAPTER 7 DNA STRUCTURE AND FUNCTION

LEARNING CHECK 7.1

DESCRIBING

1 James Watson, Francis Crick and Rosalind Franklin.

2 DNA has a sugar–phosphate backbone with 5′ to 3′ directionality, two antiparallel strands held together by hydrogen bonds between complementary bases – adenine pairs with thymine (A–T) and cytosine pairs with guanine (C–G).

3 A phosphate group, a deoxyribose sugar and a nitrogenous base (A, T, C or G).

4 Telomeres protect the ends of chromosomes from degradation and prevent them from fusing with other chromosomes.

5 Hydrogen bonds between complementary bases

6 **a** A coding region of a gene that is expressed in the final mRNA

b The region of a chromosome where sister chromatids are joined and spindle fibres attach during cell division

APPLYING

7 CGGATAACGT

LEARNING CHECK 7.2

DESCRIBING

1 Chromosomes are arranged in pairs by size, banding pattern and centromere position, from largest to smallest, with sex chromosomes shown last.

2 **a** One of a pair of chromosomes that have the same genes in the same order but may carry different alleles

b Identical copies of a single chromosome, joined at the centromere, formed during DNA replication

c A small, circular DNA molecule in bacteria and some eukaryotes that can replicate independently of chromosomal DNA

APPLYING

3 They will be the same size, have the same centromere position and carry the same genes in the same order, although they may differ in alleles.

4 Chromosomes appear X shaped only during cell division (metaphase), when each consists of two sister chromatids joined at a centromere; otherwise, they exist as uncondensed linear strands.

ANALYSING

5 Euchromatin is loosely packed and transcriptionally active, whereas heterochromatin is tightly packed and usually transcriptionally silent.

6 Mitochondria and chloroplasts contain circular DNA, inherited maternally (mitochondria) or biparentally (chloroplasts in plants), and encode some of their own proteins, whereas nuclear DNA is linear, organised into chromosomes, and encodes most of the organism's genome.

LEARNING CHECK 7.3

DESCRIBING

1 DNA helicase unwinds the double helix by breaking hydrogen bonds between bases. DNA polymerase adds complementary nucleotides to the growing DNA strand. DNA ligase seals the gaps between Okazaki fragments on the lagging strand to create a continuous strand.

2 Each base on one DNA strand pairs specifically with its partner on the opposite strand – A with T, and C with G – ensuring accurate replication.

3 Initiation where DNA is unwound by helicase, elongation where DNA polymerase synthesises new strands, primer removal and replacement where RNA primers are removed and replaced with DNA, and ligation where DNA ligase joins fragments to complete the strand.

4 DNA polymerase has proofreading ability to correct errors, and mismatch repair systems fix any remaining mistakes.

APPLYING

5 On the lagging strand, DNA is synthesised in short segments called Okazaki fragments because DNA polymerase can only build in the 5′ to 3′ direction.

6 Multiple replication forks are formed at many origins of replication along the chromosome, allowing simultaneous replication of different sections.

7 Proofreading and repair mechanisms are especially focused on preventing frameshift mutations, such as insertions or deletions, because these can drastically alter protein coding and are more harmful than point mutations.

8 A base substitution has occurred where a T is paired with a C. This has occurred because DNA polymerase made a mistake that wasn't corrected.

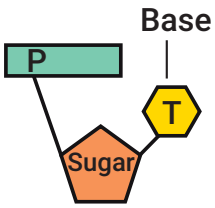
CHAPTER EXAM

MULTIPLE CHOICE

1 C
2 A
3 A
4 B
5 A
6 B
7 D
8 A
9 C
10 C

SHORT RESPONSE

11



12 First, DNA helicase unwinds the double helix and separates the strands. Then, DNA polymerase adds complementary nucleotides to the template strand. The leading strand is synthesised continuously, while the lagging strand is synthesised discontinuously and forms Okazaki fragments. Finally, DNA ligase joins the fragments on the lagging strand.

CROSS-CHAPTER QUESTION

13 Errors in replication can lead to mutations (e.g. point or frameshift mutations) and some of these mutations alter traits, potentially affecting survival or reproduction. Over generations, these mutations contribute to genetic variation, which drives evolution and species diversity through natural selection.

DATA ANALYSIS

14 The person is biologically male because the 23rd pair is an X and Y chromosome.

15 In all three sources, the percentage of A and T nucleotides are very similar $\left(\frac{32}{33}, \frac{30}{29} \text{ and } \frac{30}{32}\right)$. All three sources also have a similar percentage of C and G $\left(\frac{17}{18}, \frac{18}{24}, \frac{19}{19}\right)$. Despite the ox spleen having more G than C, the C–G pairing is still quite dissimilar from the 30% A, 29% T pairing. Therefore, this data supports the researcher's conclusion.

CHAPTER 8 DNA APPLICATIONS

LEARNING CHECK 8.1

DESCRIBING

1 Producing insulin and other therapeutic proteins, creating genetically modified crops and developing gene therapies for genetic disorders

2 Sticky ends are overhanging sequences that can base-pair with complementary sequences; blunt ends are straight cuts with no overhangs.

3 DNA ligase

4 A gene of interest is cut with a restriction enzyme and inserted into a plasmid vector, then sealed with DNA ligase.

APPLYING

5 Plasmids are small, easily manipulated, replicate independently in bacteria, and can carry inserted genes.

6 The ends of the plasmid and gene will not match, preventing the gene from being inserted properly.

ANALYSING

7 In DNA replication, ligase joins Okazaki fragments on the lagging strand, whereas in recombinant DNA, it joins DNA fragments (e.g. plasmid and gene insert) by sealing the sugar–phosphate backbone.

8 **a** Blunt
b Sticky
c Sticky

LEARNING CHECK 8.2

DESCRIBING

1 Denaturation (usually ~95°C) where DNA strands separate, annealing (~50–60°C) where primers bind to target sequences and extension (~72°C) where DNA polymerase synthesises new DNA strands.

2 Primers bind to specific sequences on the template DNA to provide a starting point for DNA polymerase.

3 To allow primers to bind (anneal) to the complementary DNA strands without denaturing.

4 Use gel electrophoresis to compare the fragment's movement to a DNA ladder with known sizes.

APPLYING

5 DNA fragments are pulled through a gel by an electric current; smaller fragments move faster and farther than larger ones.

6 A higher agarose concentration results in a denser gel, which better separates smaller DNA fragments but slows the movement of larger ones.

7 After 10 cycles, the number of copies is $5 \times 2^{10} = 5 \times 1024 = 5120$ copies.

8 **a** Lane 2
b Lane 3
c Lane 1
d Lane 4

LEARNING CHECK 8.3

DESCRIBING

1 DNA profiling uses short tandem repeats (STRs), which are repeating sequences of 2–6 base pairs in non-coding regions of DNA.

2 PCR amplifies specific STR regions from very small or degraded DNA samples to generate enough DNA for analysis.

3 By gel electrophoresis or capillary electrophoresis, which separates DNA fragments based on their length.

APPLYING

4 Increases the accuracy and discriminatory power of the profile, making it extremely unlikely for two individuals (except identical twins) to have the same pattern.

5 If the child has STR alleles that are not present in the alleged father but present in the mother, then the man is not the biological father.

6 Yes, a DNA match can be good evidence because a strong DNA match provides statistically powerful evidence that the suspect was at the scene. However, DNA profiles only use a small number of STRs rather than the whole genome, so they cannot definitively prove that the suspect was the person who left that sample.

INTERPRETING

7 The ewe that donated the nucleus from her mammary gland, as Dolly's DNA came entirely from that somatic cell.

8 Mother 3 has the strongest claim. None of the mothers match the first band in the child's DNA profile, indicating that this band may have come from the child's father. But the child's second band matches one of the bands from Mother 3, which indicates that the child may be hers. Neither of the child's bands match any of the other mothers, which is stronger evidence that they are not this child's mother.

CHAPTER EXAM

MULTIPLE CHOICE

1 D
2 A
3 D
4 B
5 D
6 A
7 D
8 D
9 C
10 A

SHORT RESPONSE

11 Mammalian DNA polymerase cannot withstand the high temperatures (~95°C) required for denaturation during PCR, whereas heat-stable enzymes like Taq polymerase from *Thermus aquaticus* are used because they remain active at high temperatures.

12 PCR amplifies specific regions of DNA from a small sample. Gel electrophoresis then separates these DNA fragments by size, producing a banding pattern that is unique to the individual.

CROSS-CHAPTER QUESTION

13 Researchers extract a person's DNA and use PCR to amplify the gene of interest. They then use gel electrophoresis to detect specific mutations by comparing the sample to a normal gene sequence.

DATA ANALYSIS

14 Both bands from Suspect 2 match the two DNA bands on the knife. There are no other bands that match.

15 Although Suspect 2 can be reasonably assumed to be at the scene because their DNA matches the DNA on the knife, it is not clear whether this suspect is guilty because neither of the victim's DNA bands match the DNA on the knife. Either this knife did not stab the victim, or the lab has made an error; therefore, guilt cannot be confirmed.

CHAPTER 9 PRODUCING GAMETES

LEARNING CHECK 9.1

DESCRIBING

1 *n* represents the number of chromosomes in a haploid cell.

2 The normal diploid ($2n$) number in humans is 46 chromosomes.

3 Meiosis is a two-stage cell division process that reduces the chromosome number by half, producing four genetically distinct haploid gametes from one diploid cell. It includes meiosis I, in which homologous chromosomes separate, and meiosis II, in which sister chromatids separate.

APPLYING

4 Mitosis involves one cell division to produce two identical diploid cells, whereas meiosis involves two divisions to produce four non-identical haploid cells. They also have different purposes: mitosis is for growth and repair, whereas meiosis is for gamete formation.

5 During meiosis I, homologous chromosomes (each consisting of two sister chromatids) separate into different cells. This reduces the chromosome number from diploid ($2n$) to haploid (n), as each resulting cell receives only one chromosome from each homologous pair.

LEARNING CHECK 9.2

DESCRIBING

1 Crossing over occurs during prophase I of meiosis, when homologous chromosomes pair up and exchange segments of genetic material, creating new combinations of alleles.

2 Independent assortment occurs during metaphase I, when homologous chromosome pairs align randomly at the metaphase plate, leading to a random distribution of maternal and paternal chromosomes to gametes.

APPLYING

3 Crossing over moves genes between homologous chromosomes, and independent assortment randomises which chromosomes are passed to gametes. Together, they increase the genetic diversity of offspring by producing many possible combinations of alleles.

LEARNING CHECK 9.3

DESCRIBING

1 Spermatogenesis occurs in the testes and involves the continuous division of diploid germ cells by meiosis to produce four haploid sperm cells.

2 Oogenesis is paused at prophase I (before birth) and again at metaphase II (until fertilisation).

3 Oogenesis produces one viable ovum and three polar bodies, which are reabsorbed by the body.

APPLYING

4 Oogenesis produces one large ovum to ensure it has sufficient cytoplasm and nutrients to support early embryonic development.

5 The sex of a child is determined by the sperm, which can carry either an X or a Y chromosome. Eggs always carry an X. Therefore, the child's sex was determined by the king's sperm, not by his wives.

6 Bee eggs would show normal genetic variation due to meiosis from diploid females. However, sperm from haploid males are produced by mitosis, so they are genetically identical to the male, with no variation.

7 Each round of meiosis in males produces four sperm, whereas each round of meiosis in females produces one egg. Even if males did not continuously undergo spermatogenesis, they would produce four times more sperm than females produce eggs. Since males do continuously produce sperm, while females only undergo oogenesis once per fertile month, the actual variation is many millions of times more.

ANALYSING

8 Autosomes are chromosomes that carry genes unrelated to sex determination, while sex chromosomes (X and Y) determine biological sex and carry sex-linked traits.

LEARNING CHECK 9.4

DESCRIBING

1 Chromosomes are arranged in a karyotype in decreasing order of size.

2 Aneuploidy is the state of having an abnormal number of chromosomes.

3 Anaphase I and II

4 Interphase and prophase I

5 During meiosis, homologous chromosomes at the metaphase plate are meant to separate to opposite poles of the cell. During anaphase I, non-disjunction occurs when both are pulled to the same pole. This can also occur with sister chromatids at anaphase II.

6 Down syndrome, Patau syndrome, Edwards syndrome and trisomies of the sex chromosomes (XXX, XXY and XYY)

APPLYING

7 Chromosomes are photographed in metaphase when they are most condensed and often already paired.

8 Gametes with missing chromosomes need to pair with a gamete that contains the genes it is missing to produce a healthy child.

ANALYSING

9 The rearrangements with the least impact are inversions because they don't cause loss of genes or moving genes between chromosomes. Duplications have more impact because they can cause overactive genes, but don't result in loss of any. Translocations can have mild repercussions if both chromosomes involved are inherited by the same gamete and major repercussions if they aren't. Deletions have the most impact because they always cause loss of genes.

10 Monosomy is where a member of a chromosome pair is missing. This causes the body to rely on the single chromosome and any mutations or issues with that chromosome have major impacts. Trisomy, on the other hand, is when there is an extra chromosome, which causes overactive genes, which has its own consequences.

INTERPRETING

11 $2n - 1$ or $2n + 1$

12 **a** 23 pairs, one X, one Y – biological male, no ploidy changes

b 23 pairs, one X, no second sex chromosome – monosomy X, Turner syndrome

c 22 pairs, three chromosome 13s, one X, one Y – biological male, trisomy 13, Patau syndrome

CHAPTER EXAM

MULTIPLE CHOICE

1 B

2 D

3 C

4 D

5 B

6 D

7 C

8 D

9 C

10 D

SHORT RESPONSE

11 Spermatogenesis occurs continuously in males and produces four equal-sized sperm cells from each germ cell, whereas oogenesis occurs intermittently in females, producing one large ovum and three polar bodies due to unequal cytokinesis.

12 Errors such as non-disjunction during meiosis can result in gametes with an extra or a missing chromosome, leading to conditions such as Down syndrome (trisomy 21) or Turner syndrome (monosomy X).

CROSS-CHAPTER QUESTION

13 Meiosis produces four genetically unique haploid cells for sexual reproduction, involving two divisions and processes like crossing over. Mitosis, on the other hand, produces two genetically identical diploid cells for growth and repair, involving a single cell division without recombination.

DATA ANALYSIS

14 a As maternal age increases, rate of trisomy 21 increases.

b Increasing maternal age appears to increase the rate of some aneuploidies, such as trisomies 21 and 18, while not increasing the rate of other aneuploidies, such as trisomy 13 and monosomy X.

15 A mother who is least likely to give birth to a child with aneuploidy would be less than 30 years old. The data shows that mothers under 20 and those between 20 and 29 both have a total rate of 0.17%, while mothers older than 30 have a total rate that begins at 0.30% and increases from there.

CHAPTER 10 INHERITANCE

LEARNING CHECK 10.1

DESCRIBING

1 The P generation refers to the original parents, the F_1 generation is the direct offspring of those parents and the F_2 generation is the offspring of the F_1 generation.

2 The genotype of an individual refers to the two alleles they carry for a particular trait. Different combinations of alleles produce different phenotypes.

3 Autosomal dominant inheritance is where a trait is expressed when only one of the two contrasting alleles appears at a single gene locus on an autosomal (non-sex) chromosome pair.

4 3:1

APPLYING

5

	Possible genotype	Homozygous or heterozygous	Dominant or recessive phenotype
1	HH	Homozygous	Dominant
2	Hh	Heterozygous	Dominant
3	hh	Homozygous	Recessive

ANALYSING

6 All unaffected individuals are homozygous recessive (aa) and all affected individuals are heterozygous (Aa).

INTERPRETING

7 White is dominant so appropriate symbols: W = white and w = red. F_1 generation genotype all Ww, phenotype all white. F_2 generation genotypes 1WW : 2Ww : 1ww, phenotypes 3 white : 1 red.

8 If red and white are not completely dominant, both will be expressed together, resulting in a mixed pink colour.

9 Cream is dominant so appropriate symbols: C = cream and c = red. If the F_1 generation is heterozygous, the F_2 generation will have genotypes 1CC : 2Cc : 1cc, phenotypes 3 cream : 1 red.

LEARNING CHECK 10.2

DESCRIBING

1 Sex-linked traits are indicated by a disparity in the number of males and females affected.

2 Multiple-allele traits are indicated by discrete or discontinuous variation, where there are more than two variants, but each forms a separate group in the population (e.g. blood types).

3 Polygenic traits are indicated by continuous variation, a smooth distribution of variation within a population (e.g. height).

APPLYING

4 Superscripts are used in non-Mendelian inheritance because the alleles either are held on a non-homologous pair (XY) or have more variants than can be denoted by a single capital–lower case pair.

5 Continuous variation is caused by polygenic inheritance where the trait is determined by more than one separately inherited gene, while discontinuous variation is caused by multiple-allele inheritance where the trait is determined by a single gene with more than two possible allele variants.

6 Sex-linked dominant inheritance: all unaffected males X^hY, all affected males X^HY, all unaffected females X^hX^h, all affected females X^HX^h.

7 a The graph shows continuous variation, suggesting that ADHD follows polygenic inheritance.

b Individuals who would score quite low on the scale are not likely to be assessed for an ADHD index in the first place.

8 a Sex-linked inheritance due to the disparity in male vs female inheritance. It is recessive due to the rarity of females inheriting the condition.

b An affected male (X^aY) would need to inherit their affected allele from their mother. An affected female (X^aX^a) would need to inherit an affected allele from both their mother and father.

c No chance. An affected male (X^aY) would only pass his Y chromosome to his son. A son can only inherit sex-linked conditions from their mother.

ANALYSING

9 The sketched graph should show a normal distribution curve, with salinity tolerance on the *x*-axis and number of fish on the *y*-axis.

INTERPRETING

10 $\frac{1}{4}$ I^AI^B type AB, $\frac{1}{4}$ I^Ai type A, $\frac{1}{4}$ I^Bi type B, $\frac{1}{4}$ ii type O

11 No chance. Type AB can only produce I^A and I^B alleles, so a type O (ii) child cannot be produced.

12 This trait is polygenic. There are a number of clues, including the wide colour range in the corn in Figure 10.2.6, the presence of smooth variations in the colour of kernels within a single cob of corn, and the information that two different pigment families (which would be produced by at least two different genes) are responsible.

CHAPTER EXAM

MULTIPLE CHOICE

1 A
2 B
3 B
4 D
5 A
6 C
7 B
8 C
9 D
10 D

SHORT RESPONSE

11 Mendelian inheritance is similar to other forms of inheritance in that one allele for each gene is inherited from each parent. It is different from other forms of inheritance because it only applies to autosomal single-gene traits that have only two allele variants. Relatively few human traits are Mendelian.

12 Since black colouring was dominant in the offspring, appropriate allele symbols are black (B) and white (b). The two black parents must have at least one black allele (B?), but for them to produce any white offspring, they must each have a white allele to pass on (Bb). Two heterozygous parents can be confirmed by the approximately 3:1 Mendelian ratio of black to white offspring.

CROSS-CHAPTER QUESTION

13 If one parent experienced non-disjunction, half of their gametes would have one extra chromosome and the other half would be missing this chromosome. If a targeted gene was on this chromosome, the parent would produce some offspring with only one allele from their other parent (e.g. genotypes A_ or a_) and some offspring with two alleles from this parent and one from their other parent (e.g. genotypes AAa, Aaa, aAA).

DATA ANALYSIS

14 Women: 166–167 cm. Men: 182–183 cm

15 Across the entire human population, gender differences, such as a 16 cm disparity in median height should not occur if the trait was inherited only on autosomes. While the shortest males are of similar stature to the shortest females, the tallest males are 210 cm while the tallest females are only 190 cm. A 20 cm disparity between the upper height limits, and a 16 cm disparity between the median heights, indicate that at least some of the genes that produce height in humans are on the sex chromosomes.

CHAPTER 11 PROTEIN SYNTHESIS AND GENE EXPRESSION

LEARNING CHECK 11.1

DESCRIBING

1 mRNA is a single-stranded molecule made of ribonucleic bases that carries genetic information from DNA in the nucleus to the ribosomes for protein synthesis.

2 tRNA is a small RNA molecule that is folded into a t-shape and carries a specific amino acid into the ribosome during translation.

3 Transcription occurs in the nucleus; translation occurs in the cytoplasm at ribosomes.

4 The three parts of RNA processing are adding a 5′ cap, adding a poly-A tail to the 3′ end, and splicing out introns to form a mature mRNA transcript.

5 Alternative splicing allows a single gene to produce multiple protein variants by including or excluding different combinations of exons in the final mRNA transcript.

APPLYING

6 Transcription (from script writing) involves copying genetic information from DNA to RNA. Translation involves switching the information from RNA nucleic acids into protein amino acids.

7 Start: AUG. Stop: UAA, UAG or UGA

8 **a** UCG AUA GCU CAG UUU

b Ser–Ile–Ala–Gln–Phe

9 RNA processing increases the organism's ability to make multiple proteins from the same gene through removing different patterns of introns and exons. It also stabilises the mRNA with a 5′ cap and poly-A tail, which improves its lifespan and the efficiency of translation. Organisms without RNA processing would have bulkier DNA to produce the same range of proteins, and translation would be slower and more prone to errors.

ANALYSING

10 **a** Transcription is the process of synthesising mRNA from a DNA template, while translation is the process of assembling proteins based on the mRNA sequence.

b Immature mRNA contains introns and has not undergone RNA processing, whereas mature mRNA has a 5′ cap, a poly-A tail, and has had the introns removed.

c Codons are three-base sequences on mRNA that specify amino acids, while anticodons are complementary three-base sequences on tRNA that pair with codons during translation.

LEARNING CHECK 11.2

DESCRIBING

1 **a** In a point mutation, a single nucleotide is changed, inserted or deleted.

b In a frameshift mutation, a nucleotide is inserted or deleted, shifting the reading frame of the genetic sequence, altering downstream codons.

APPLYING

2 Frameshift mutations change the reading frame, potentially altering all downstream amino acids, whereas point mutations typically affect only one codon.

3 **a** Asn–Tyr–Gly–Ser–Ala–Asp

b Change the codon UAC to UAG (stop codon)

c Change GGA to GAA (Glu)

d Change AAC to AAU (both code for Asn)

LEARNING CHECK 11.3

DESCRIBING

1 **a** Gene expression is the process by which a gene's information is used to produce a functional product, such as a protein.

b Gene regulation is the control of when, where and how much a gene is expressed.

2 Transcription

3 Euchromatin is loosely packed and transcriptionally active whereas heterochromatin is tightly packed and transcriptionally inactive.

4 HOX genes regulate body plan development by determining the identity and arrangement of body structures.

APPLYING

5 Cells only express the genes needed for their specific functions and environmental conditions to conserve energy and resources.

6 Housekeeping genes are continually expressed to maintain basic cellular functions, such as metabolism and repair.

7 Genes are regulated in the long term through epigenetic modifications such as DNA methylation and histone modifications, which can silence or activate genes.

8 Genes are regulated in the short term by transcription factors, activators or repressors responding to immediate environmental or cellular signals.

9 Human DNA carries thousands of genes, most of which are only relevant to one particular type of cell, and often, only for limited periods of time. Each cell is only likely to be using a small portion of these genes at any one time, so it is more efficient to turn on the genes it currently needs than to turn off all of the genes it doesn't.

10 Hormones bind to receptors, triggering intracellular signalling pathways or acting directly as transcription factors to activate or repress specific genes.

11 Positional proteins, such as Bicoid protein, create gradients that provide spatial information to cells, guiding the differentiation and arrangement of tissues and organs during development.

CHAPTER EXAM

MULTIPLE CHOICE

1 C
2 C
3 C
4 C
5 C
6 B
7 D
8 A
9 B
10 B

SHORT RESPONSE

11 RNA splicing involves introns (non-coding regions) being removed from an mRNA transcript, and the exons (coding regions) being joined together to form a mature mRNA molecule. This process ensures that only the necessary coding sequences are translated into proteins during protein synthesis, and it allows a single gene to produce multiple protein variants, increasing the functional capacity of cells.

12 Transcription factors are proteins that regulate gene expression by binding to specific DNA sequences near gene promoters to activate or repress transcription. They help control when and how much a gene is expressed in response to cellular signals and environmental factors. Some transcription factors recruit RNA polymerase to initiate transcription, while others block its access to prevent gene expression, ensuring precise control over cellular function and development.

CROSS-CHAPTER QUESTION

13 Although no HOX genes are located on chromosome 21, Down syndrome can still affect their function through indirect mechanisms. The extra chromosome can disrupt the balance of gene regulation within the cell, such as altering the expression of transcription factors or other proteins that interact with HOX genes, affecting these genes' ability to properly guide body plan development.

DATA ANALYSIS

14 (i) Mutated sequence (CCA CCC ACC CAC C)→Pro–Pro–Thr–His

(ii) Mutated sequence (CCC CAC CCA CC)→Pro–His–Pro

15 The deletion mutation (ii) causes the greatest difference because it results in a frameshift mutation that affects several downstream codons and cuts the peptide down to three amino acids. The insertion mutation (i), while still causing a frameshift mutation, leaves the first two amino acids and the number of animo acids unchanged, making it less disruptive overall.

CHAPTER 12 EVOLUTION: NATURAL SELECTION AND MICROEVOLUTION

LEARNING CHECK 12.1

DESCRIBING

1 **a** Evolution is the change in the genetic composition of a population during successive generations, which may result in the development of new species.

b Microevolution is the small-scale variation of allele frequencies within a species or population, in which the descendant is of the same taxonomic group as the ancestor.

c Macroevolution is the variation of allele frequencies at or above the level of species, over geological time, resulting in the divergence of taxonomic groups, in which the descendant is in a different taxonomic group from the ancestor.

2 Microevolution occurs over a short time scale and individuals still belong to the same species, whereas macroevolution occurs over a long time scale and individuals end up belonging to different species.

INTERPRETING

3 This demonstrates macroevolution because polar bears, black bears and brown bears are now classified as different species. This means each species has acquired different allele combinations over time, so they are different to each other and the common ancestor.

LEARNING CHECK 12.2

DESCRIBING

1 **a** Gene flow is the transfer of alleles that results from emigration and immigration of individuals between populations.

b Genetic drift is a change in the gene pool of a population as a result of chance; usually occurs in small populations.

2 A phenotype is the observable expression of an individual's genotype.

APPLYING

3 When a change happens to a gene producing a new allele that can be acted on by a selection pressure. For it to affect future populations, it must occur in a gamete that is part of fertilisation. If the change happens in body cells, it cannot be passed on to the next generation.

4 Changes in the gene pool of a population can occur due to:

- gene flow – some individuals emigrate, taking their alleles with them, while others immigrate, bringing other alleles with them
- genetic drift - a change in the gene pool of a population as a result of chance. Examples of genetic drift are the bottleneck effect, which occurs when a catastrophic event or a period of adverse conditions drastically reduces the size of a population, and the founder effect, which occurs when a few individuals that have become isolated from a larger population do not carry all the alleles that were present in the original population.

5 Gene flow can affect allele frequency by reducing or removing an allele from a population when the individuals with this allele leave (emigrate). Gene flow can also increase the frequency of an allele or introduce a new allele to a population when individuals move into the population (immigrate).

6 Mutations generate different forms of alleles that may respond differently to selection pressures, conferring an increased or decreased likelihood of survival. As evolution is defined as change over time, these changes are an important part of evolution.

ANALYSING

7 A gene is a sequence of DNA that controls a particular trait, whereas an allele is a version of the gene that codes for the same trait, but produces a different form/results in a different phenotype.

8 A bottleneck results from the drastic reduction in the size of a population leaving few individuals remaining after the loss of most of the population, whereas a founder effect results from a few individuals becoming isolated from the original population and the original population survives.

LEARNING CHECK 12.3

DESCRIBING

1 Natural selection contributes to evolutionary change through changing allele frequencies. When populations of the same species experience different selection pressures, the organisms that survive long enough to reproduce may pass on different combinations of alleles.

2 Directional selection – favours an extreme of the phenotype (e.g. the Australian snow gum has a shorter leaf blade length in drier conditions).

Stabilising selection – favours the intermediate phenotype (e.g. hooded warblers with medium dots are more likely to survive than those with small or large dots).

Disruptive selection – favours both extremes of the phenotype (e.g. when a male octopus is more successful at mating if he is small or large).

APPLYING

3 This represents directional selection as all parrots are more likely to survive with darker feathers than medium or light coloured feathers, showing that an extreme of the phenotype has the highest reproductive success.

4 $B = 3 \times BB + 7 \times B = 13\ B$

$b = 5 \times bb + 7 \times b = 17\ b$

Total allele number $= 30$

Therefore, frequency of $B = \frac{13}{30} = 0.43$

and frequency of $b = \frac{17}{30} = 0.57$

INTERPRETING

5 Yes. Larger females are more likely to successfully reproduce as they are selected for by males over smaller females. Therefore, alleles for larger females are more likely to be passed on to the next generation.

CHAPTER EXAM

MULTIPLE CHOICE

1 B

2 C

3 D

4 A

5 B

6 D

7 C

8 D

9 D

10 A

not immigration as the breeding pairs are not joining a population, they are starting a population.

SHORT RESPONSE

11 Similarity: Both involve a potential change in allele frequencies in a population.

Difference: Gene flow results from the movement of organisms (and their alleles) into and out of populations, whereas genetic drift results from random changes to allele frequencies in a population that are the result of chance.

12 a It is expected that grey rabbits would decrease in number as they would no longer blend in with the environment and be killed by predators. White rabbits and black rabbits would increase in number as they are better suited to the environment's colours therefore more likely to survive and reproduce.

b Disruptive selection.

c The environment changed and rabbits with the 'average' colour phenotype became more visible to predators. Rabbits that were black or white were more likely to survive long enough to reproduce, passing their alleles on to the offspring. This means that over time the population phenotype shifted towards the two extremes.

CROSS-CHAPTER QUESTION

13 Mutations produce different variations of alleles for particular traits as they result from a change to the DNA sequence at a locus. Alleles for a trait can experience selection pressures – conferring an advantage means they are more likely to persist in a population; move with individuals that immigrate or emigrate; or be retained after genetic drift.

Meiosis can lead to different combinations of alleles in offspring compared to what was present in the parent generation. During prophase I, homologous chromosomes can cross over, recombining maternal and paternal DNA (therefore alleles) on the one chromosome. At metaphase, independent assortment of chromosomes occurs so that there is any one of 2^{23} combinations of chromosomes present in each gamete. The new combination of alleles may confer an advantage in offspring when exposed to particular selection pressures.

DATA ANALYSIS

14 a As the years of use increases, the percentage incidence of resistance also increases. In 1908, percentage incidence was close to zero, rising to 60 per cent after the year 2000.

b All three bacterial types show an increased antibiotic resistance, going from 0 to 28, 32 and 60 per cent after 2003.

15 Yes. Bacteria have been exposed to the selection pressure of antibiotics. Initially, most bacteria exposed to antibiotics died (e.g. MRSA in 1980–85 or VRE in 1987–90 as percentage of resistant bacteria close to 0 per cent). However, some with a variation that conferred resistance survived long enough to reproduce and pass this trait of resistance on to their offspring. The population increasingly consisted of bacteria with a resistance to antibiotics (e.g. MRSA up to 60 per cent resistance by 2000 or VRE 26 per cent resistance in 2003).

CHAPTER 13 EVOLUTIONARY PROCESSES

LEARNING CHECK 13.1

APPLYING

1 An accumulation of microevolutionary changes (due to genetic drift, mutation, natural selection and gene flow) over a long time can lead to a population acquiring enough differences that they can no longer breed with other populations from the same original species.

LEARNING CHECK 13.2

DESCRIBING

1 Geographic barriers, temporal barriers, spatial barriers.

2 Reproductive isolation results from a lack of gene flow between populations, causing the allele frequencies of specific genes to become so different that the populations are regarded as two separate species. They can no longer interbreed.

APPLYING

3 Geographic isolation results when a physical barrier prevents individuals from mating (e.g. a mountain or an ocean), whereas spatial isolation has no physical barrier, but the distance is too great for individuals to meet and breed.

4 When organisms are not present in the environment at the same time, they are unable to breed with each other (e.g. plants flowering in different months or insects being active at different times of day), stopping gene flow.

LEARNING CHECK 13.3

DESCRIBING

1 Sympatric speciation refers to the evolution of two or more new species from a single population at the same location. It requires a barrier (temporal or behavioural) that isolates members of a population from the rest of the population in the same area. If gene flow between the isolated population and main population is prevented and different selection pressures act on the population, allele frequencies may become so different that individuals cannot interbreed, resulting in the evolution of new species from a single population within the same place. An example occurs on Lord Howe Island with two species of palm that are in the same location but one flowers 6 weeks earlier than the other. Another example may include subterranean diving beetle found in aquifiers in arid Australia occupying slightly different niches.

2 Large bodies of water such as seas or oceans, rivers, mountain ranges, deserts.

3 Forest fragmentation isolates small groups of organisms of a particular species. This reduces gene flow throughout the whole population. Separated populations exposed to different selection pressures may lead to changing allele frequencies, a component of speciation.

APPLYING

4 In allopatric speciation, gene flow is disrupted or prevented as populations become physically separated through geographic isolation.

5 In parapatric speciation individuals are more likely to mate with individuals in their geographic area rather than individuals in a different area. Gene flow still continues in the bordering areas, but over time the populations diverge to become better adapted to the different conditions in different areas of the environment. Examples include grasses growing in contaminated soil.

LEARNING CHECK 13.4

DESCRIBING

1 Divergent evolution is a process in which related species acquire new traits over time, away from the common ancestor, to give rise to new species. Convergent evolution is a process in which unrelated organisms evolve similar adaptations in response to similar environmental pressures. Parallel evolution is a process in which related organisms are reproductively isolated but evolve similar adaptations in response to the same environmental pressures. Coevolution is a process in which an evolutionary change in one species influences the evolution of another species

APPLYING

2 The giant tortoises showed divergent evolution. As time passed, each population adapted to its own unique island habitat. Gene flow between islands was prevented and, because of the reproductive isolation, new species formed.

3 A parasite population imposes a selective pressure on a host population, which responds to the selection pressure, in turn imposing a selective pressure on the parasite population. If the parasite species becomes more harmful and kills the host, this may select for individuals in the host species who can resist parasite infection. In this case, more resistant individuals will pass their genes to the next generation. If parasites respond to the host's selective pressure and become less harmful, more hosts will survive, allowing parasites to infect hosts without killing them.

INTERPRETING

4 Ant-eating mammals have been subject to similar selection pressures that resulted in them developing three similar characteristics. All the animals are mammals, suggesting that they have diverged from a more recent common ancestor. Although these mammals do not live in the same location, the similarity of their selection pressures has led to parallel evolution of these three characteristics. Convergent evolution arises when organisms are unrelated and any common ancestor was not recent.

LEARNING CHECK 13.5

APPLYING

1 After a population bottleneck, the surviving population is unlikely to carry all the alleles that were present in the original population. This reduction in genetic diversity makes the species vulnerable to changes in selection pressures.

2 Large populations generally have a diverse gene pool and a greater reserve of different alleles to draw on as the pressures from natural selection change. Small populations are unlikely to carry a large range of alleles. This results in low genetic diversity.

3 Natural selection will act on 'fit' individuals with the best-suited alleles for survival and reproduction. When genetic variation is low, there is less chance of the presence of alleles suiting the selective pressure. If no individuals in the species have the right genetic variation, the species will become extinct.

4 The mass extinction removes many species from the environment. This leads to an increase in available niches that the surviving populations of organisms can occupy. If these populations experience different selection pressures and/or changes to gene flow and/or genetic drift, speciation may occur in a relatively short period of time.

CHAPTER EXAM

MULTIPLE CHOICE

1 D
2 D
3 D
4 B
5 D
6 D
7 B
8 A
9 C
10 D

SHORT RESPONSE

11 a Genetic diversity expected in a species facing extinction is usually low.

b Selection pressures changed, most likely hunting by humans, and the Tasmanian tigers were not able to reproduce enough viable offspring to survive.

c Small populations are more prone to extinction than large populations because there are fewer individuals, gene flow is reduced, genetic drift can change allele frequencies dramatically and inbreeding reduces genetic diversity meaning any changes to selection pressures are likely to affect the whole population.

12 The length of the tongue-like proboscis has evolved in response to the shape of the flowers, allowing the insects to reach the nectar. Collecting nectar requires the insect to contact the flower, collecting pollen that is transferred to the next flower. This is coevolution as the flowers depend on the insects for pollination and the insects depend on these flowers for food.

CROSS-CHAPTER QUESTION

13 a Mutation: A reduction in the size and shape of the wings to be well suited to movement under water, but which no longer allowed flight resulted from a mutation(s) that conferred an advantage to cormorants that could swim more effectively (the selection pressure).

Genetic drift: The original population that left the mainland may not have had the same allele frequencies as the mainland population.

Gene flow: Gene flow was prevented as wing size decreased and the ability to fly was lost, so cormorants could no longer return to the mainland to breed.

b This is an example of directional selection because the wings only decreased in size. If it was stabilising, an average wing size would be expected. If it was disruptive, both large and small would be expected.

c This cormorant population provides an example of allopatric speciation because there was a geographic barrier of a large body of water that meant populations were kept separate because cormorants ultimately could not fly or swim to the mainland.

DATA ANALYSIS

14 *A. florida* and *A. cytherea*

15 Temporal isolation – in the data, there are five species of coral that spawn in autumn only and one (*A. millepora*) that spawns in spring only. The further apart spawning times are, the less likely it is for populations to interbreed, resulting in isolation.

CHAPTER 14 EVOLUTIONARY RELATIONSHIPS

LEARNING CHECK 14.1

DESCRIBING

1 Comparative genomics is the study of DNA similarities across species.

2 A conserved sequence is a DNA or protein sequence that is kept the same, or very similar, across species due to its necessity for optimal function.

3 Divergence occurs when species that have a common ancestor become more dissimilar over time due to different selection pressures, which gradually leads to speciation over an evolutionary time.

APPLYING

4 Comparative genomics analyses the hereditary information of organisms as encoded in their DNA. This process produces a detailed picture of DNA sequence conservation, making it possible to trace evolutionary processes responsible for the divergence of two genomes.

The main process in comparative genomics is the use of sequence alignment techniques to identify similarities and differences in DNA from different sources. The value of this procedure is that it allows for genome size, number of genes or chromosome number to be compared, which allows the evolutionary relationships between organisms to be identified, along with differences and similarities within and between species.

5 First, a sequence is chosen and sequenced in both organisms. The number of point differences is divided by the number of residues analysed. This ratio can be compared to other species to determine relatedness. Species with greater similarity in their sequences will be more closely related. The more time two species have been reproductively separated, the more differences they will have accumulated in their DNA. Therefore, as the percentage similarity in their DNA increases, the closeness of the relationship between those species increases.

6 Divergent evolution assumes that two species will become increasingly different as they get further from their point of divergence. The mutation rate estimates the number of differences accumulated per generation by looking at neutral mutations (changes that are not influenced by selection pressures). By counting the total number of differences and comparing it to the estimated number of differences per generation, scientists can estimate the number of generations that occurred between their point of divergence and now.

LEARNING CHECK 14.2

DESCRIBING

1 **a** Clade: a group comprising all the descendants of a particular ancestor organism

b Common ancestor: a species of organism whose offspring diverged over time

2 Cladistics assumes common ancestry (any two species will have a common ancestor somewhere), dichotomous cladogenesis (each point of cladogenesis results in only two outcomes, similar to the parent species and different from the parent species) and ever-widening difference (species become increasingly dissimilar the further they get from their common ancestor).

3 Moving forward in time

4 Phylogenetic relationships are evolutionary relationships that show links between groups of organisms. A study of phylogeny tries to reconstruct the evolutionary history of any given group of organisms.

5 The evolutionary history of a group of organisms describes the path of evolution of that group. It can show which organism the group evolved from and its relationships with other closely related organisms. It can show when key traits emerged or how environmental changes affected their development. Although our understanding of evolutionary relationships among organisms has improved with the advent of molecular techniques, it continues to be revised as new data becomes available.

APPLYING

6 A phylogenetic tree shows evolutionary relationships and the points at which lineages have diverged. Each fork on a branch marks a point at which new species arise, when populations became so different from other populations of the same species that they could no longer interbreed. This means that each node at a fork represents an ancestor common to all the species above that node.

7 The only clade that includes the bryophytes must include all the other categories because the bryophyte point of cladogenesis was at the earliest common ancestor in the diagram. Bryophytes do not possess any of the three features identified. Every possible clade includes the angiosperms because their point of cladogenesis is at the latest common ancestor, so angiosperms possess all three of the new features identified. Earlier ancestors will be common to the angiosperms as well.

8 Cladistics follows the principle of parsimony in that the simplest explanation is the most likely. It is most likely that seeds as a feature arose once, as shown in Question 7, not twice, as shown in this question. It is less likely that both Gymnosperms and Angiosperms both evolved seeds independently. It is more likely that they inherited the seed development trait from a common ancestor

CHAPTER EXAM

MULTIPLE CHOICE

1 B

2 C

3 C

4 D

5 A

6 D

7 D

8 D

9 B

10 A

SHORT RESPONSE

11 Reasons for agreeing should refer to the strength of cladistics as an organising tool, the fact that class Reptilia is not currently a clade and the reminder that scientific models only stand for as long as evidence supports them. Reasons for disagreeing may include the fact that reclassifying them into clades would require crocodiles to be classed with birds, despite their obvious physiological differences, or for crocodiles to be classified as a new class equivalent to birds and mammals.

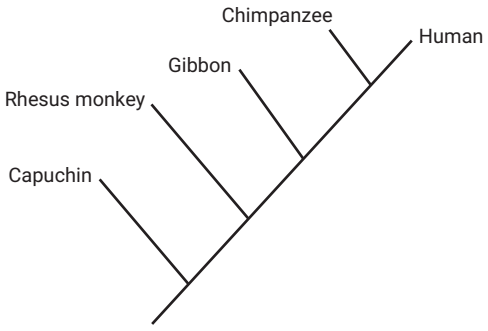
12 The mutation rate estimates the number of differences accumulated per generation, typically using neutral mutations. By counting the total number of differences and comparing it to the estimated number of differences per generation, scientists can estimate the number of generations that occurred between their point of cladogenesis and now.

CROSS-CHAPTER QUESTION

13 The base triplet code for amino acids in a protein sequence incorporates redundancy, meaning that there are multiple triplet codes in the DNA/mRNA that result in the same amino acid. Therefore, a protein that has the same amino acid sequence may have a different base sequence in DNA.

DATA ANALYSIS

14



15 The Rhesus monkey has 91.1% similarity in DNA for this sequence with humans. The protein synthesised from this DNA would not necessarily be exactly the same. Some of the triplet codes would probably result in different amino acids. However, there is a chance that the redundancy of the triplet code could mean the protein may have the same amino acids, even though the DNA sequences are different.

GLOSSARY

5′ cap a molecule added to the 5′ end of an mRNA strand to protect it from degradation and direct it out of the nucleus

A

abiotic factor a non-living component of an ecosystem, including the physical landscape, minerals and weather conditions

agarose gel a gel matrix used for electrophoresis

alleles different versions of the same gene, determined by slightly different DNA sequences at that gene locus

alleles two or more alternative DNA sequences at the same gene locus on homologous chromosomes

allopatric speciation the speciation that is due to geographic isolation

anaerobic in the absence of oxygen

anaphase the third stage of meiosis where chromosomes separate to opposite poles of the cell

aneuploidy when a cell contains an abnormal number of chromosomes for its species, either more or fewer chromosomes than normal

anneal to hydrogen bond, as when two single-stranded sections of complementary DNA align to form a double strand

anticodon a sequence of three nucleotide bases on a tRNA molecule that pairs with complementary bases on an mRNA strand during translation at a ribosome

autosome a chromosome that is the same in both males and females of a species; autosomes do not include sex chromosomes

autotroph (producer) an organism that can produce its own organic compounds from sunlight, water and carbon dioxide

B

binomial nomenclature a naming system in which each individual is given a two-part name; in biology this is genus and species

biodiversity the full range of living things in a particular area or region; it can be described at various levels, including genetic differences, different species or types of ecosystems in a larger area

biological species concept a definition of species as groups of actual, or potentially, interbreeding natural populations that are reproductively isolated from other such populations

biomass the total mass of living matter in an ecosystem

biotic factor a living component of an ecosystem, including animals, plants and bacteria

bivalent visible chromosomes in a cell during prophase I of meiosis, which are made up of two homologous chromosomes joined together

blunt end the flat end of a DNA fragment that is produced after symmetrical cleavage by a restriction enzyme

bottleneck effect when a catastrophic event or a period of adverse conditions drastically reduces the size of a population, reducing genetic variation within the population

C

carrying capacity the greatest density of organisms that an area or a resource can potentially support

centromere the waist-like constriction in a duplicated chromosome required for the movement of chromosomes during cell division

character matrix a table of characteristics used for classification

chiasma the point of contact between homologous chromosomes during prophase I of meiosis

chromatin the complex of proteins and DNA in eukaryotes

chromosome a structure composed of DNA and protein that contains along its length linear arrays of genes carrying genetic information

clade a group consisting of all the descendants of a particular ancestor organism

cladistics a taxonomic technique that arranges organisms by clade

cladogram a phylogenetic tree in which all organisms are grouped according to their most likely evolutionary relationships

class the fourth-highest taxon in Linnaean classification, e.g. Mammalia

climax community the end-point in a community succession when the community has become relatively stable

coding DNA a section of DNA that specifically carries the code for direct translation into a polypeptide

codominant two or more alleles are equally expressed in the phenotype; produces blended phenotypes

codon a series of three adjacent nucleotide bases in DNA and mRNA that codes for a particular amino acid to be added to a polypeptide or signals start or stop

coevolution a process whereby an evolutionary change in one species influences the evolution of another species

common ancestor a species or organism whose offspring diverged over time

community groups of different species in an area and their interactions

comparative genomics the study of DNA similarities across species

competition a species interaction in which two or more individuals, from the same or different species, compete for the same resource in the same area

competitive exclusion principle a key ecological principle that states that no two species can occupy exactly the same niche in an ecosystem

complementary bases nitrogenous bases that bind to each other in DNA (A–T and C–G) and in RNA (A–U and C–G)

conserved sequence a DNA or protein sequence that is preserved across species because it is necessary for optimal function

continuous variation the variation in a trait caused by two or more genes; the range of different phenotypes is wide with small, smooth gradations between differences

convergent evolution a process whereby unrelated organisms evolve similar adaptations in response to similar environmental pressures

crossing over an event during meiosis in which homologous chromosomes exchange segments with one another

cytokinesis the division of the cytoplasm and formation of new cell membranes

D

daughter cell either of the two cells formed when a cell undergoes cell division

decomposer an organism that grows on and absorbs nutrients from dead tissues, e.g. a fungus

deletion the removal of a single nucleotide from a sequence

denaturation (in the polymerase chain reaction), the application of high temperatures to break the hydrogen bonds in DNA, which causes the two strands to separate

density dependent the effect of a factor increases with an increase in population size

density independent the effect of a factor is the same regardless of population size

deoxyribonucleic acid (DNA) an information molecule that is the universal basis of an organism's genetic material; it contains instructions, in chemical code, for the operation of the cell

detritivore an organism that consumes the dead tissues of once-living organisms (detritus), e.g. a worm

dichotomous having two branches, two opposing aspects

dichotomous key a series of choices between two options that results in the classification of an organism

diploid describes a cell or organism that has a genome comprising two copies of each chromosome, represented by $2n$

directional selection a form of selection where one phenotype is favoured, causing the allele frequency to shift in one direction

discontinuous variation the variation in a trait caused by two or more allele variants for a single gene; a narrow set of distinct phenotypes

disjunction the segregation of chromosomes to separate poles of the cell during anaphase

disruptive selection a form of selection that operates in favour of extremes and against intermediate forms

divergent evolution a process whereby related organisms acquire new traits over time, away from the common ancestor, to give rise to new species

division the third-highest taxon in Linnaean classification of plants, e.g. Tracheophyta (vascular plants)

DNA helicase the enzyme that unwinds and separates the two strands of the DNA double helix in DNA replication

DNA ligase an enzyme that catalyses the formation of a sugar–phosphate bond between two pieces of DNA

DNA polymerase the enzyme that forms the complementary strand in DNA replication

DNA profiling a process that compares an individual's genome with another

domain the highest ranking taxon in Linnaean classification, e.g. Eukarya

dominant allele the allele that is expressed in the phenotype when at least one copy occurs in the genotype

E

ecological niche the role and space that an organism fills in an ecosystem, including all its interactions with the biotic and abiotic factors of its environment

ecological pyramid a pyramid diagram that shows the relative proportions of biomass, numbers or energy at each trophic level in an ecosystem

ecosystem a self-sustaining unit consisting of the interactions between the species present and their environment

ectotherm an organism whose internal body temperature reflects and fluctuates along with the surroundings

emigration the movement of individuals of a species out of a place

endosymbiotic theory a theory that suggests that chloroplasts and mitochondria arose from ancient prokaryotic cells that were ingested by other prokaryote host cells

endotherm an organism that regulates and maintains internal body temperature higher than the temperature of the surroundings

environmental gradient a gradual change in an abiotic factor over distance

environmental resistance environmental conditions that limit a species population from growing out of control; includes both biotic and abiotic factors

euchromatin a loosely coiled complex of proteins and DNA that is characterised by many genes and high transcription

euploid when a cell contains the normal number of chromosomes for its species, either *n* haploid or 2*n* diploid

evolution the change in the genetic composition of a population during successive generations, which may result in the development of new species

evolutionary radiation an increase in taxonomic diversity or morphological disparity

exon a section of DNA or mRNA that codes for a polypeptide

exponential population growth (J-curve) the growth of a population in an ideal, unlimited environment

extant currently in existence, not extinct

F

family the sixth-highest (third lowest) taxon in Linnaean classification, e.g. Felidae

fecundity a measure of fertility; the capacity to reproduce

fitness the capacity of an individual to survive and pass on alleles to viable offspring

food chain a chain of organisms where one organism occupying a trophic level is consumed by the next organism in a higher trophic level

food web a diagram of interconnecting food chains that shows how different organisms feed on each other, thereby transferring energy and matter through an ecosystem

founder effect a type of gene flow that occurs when a few individuals that have become isolated from a larger population do not carry all the alleles that were present in the original population

frameshift mutation a mutation that dislocates the translational reading frame

fundamental niche the widest potential niche that a species could occupy without competitors, predators or parasites

G

gamete a cell produced in sexual reproduction, which combines at fertilisation; in humans, the gametes are ova and sperm cells; in flowering plants, pollen grains contain male gametes and ova contain a female gamete

gel electrophoresis a technique that separates DNA fragments according to their size and charge

gene a region of DNA that encompasses the coding and non-coding DNA for a particular protein or protein family

gene expression the process of a gene being transcribed and translated into products (proteins or functional RNA)

gene flow the transfer of alleles that results from emigration and immigration of individuals between populations

gene locus the specific physical location of a gene on a chromosome

gene pool the range of genes and all their alleles present in a population

gene regulation various processes that enable a gene to be expressed (or not) in specific cells at specific times and allow the proteins to be produced at required rates

genetic diversity the combined differences in DNA of all the individuals in a species

genetic drift a change in the gene pool of a population as a result of chance; usually occurs in small populations

genetically modified organism (GMO) an organism that has been modified by incorporating a piece of foreign DNA into its genome

genus the seventh-highest (second lowest) taxon in Linnaean classification; it is always italicised, e.g. *Felis*

geographic isolation when populations of the same species are separated by a type of physical barrier

germ cell a cell that produces gametes

gross primary productivity (GPP) the total organic matter produced annually in an area by photosynthesis

H

habitat a location that meets all of the conditions for an organism's survival

habitat fragmentation the process by which areas of a habitat are lost, resulting in a large continuous habitat being broken up into smaller, more isolated habitats

haploid describes a cell or organism that has a genome that contains one copy of each chromosome, represented by *n*

heredity the study of inheritance; genetic transmission of characteristics from one generation to another

heritable capable of being passed on to the next generation

heterochromatin a tightly coiled complex of proteins and DNA that is characterised by few genes and limited transcription activity

heterotroph (consumer) an organism that cannot convert sunlight to useful energy and must consume other organisms for food

hierarchy a system categorised by the specific arrangement of information into layers

histone a protein that spools DNA in eukaryotic cells

homologous pair a pair of unduplicated chromosomes that are the same size and shape, and have the same genes at the same locations; each member of the pair may carry a different allele for any particular gene

homology a similarity due to a common origin

host an organism that is infected with a pathogen or parasite

housekeeping gene a gene that encodes a polypeptide essential for basic cellular processes

HOX genes a gene family that codes for proteins that regulate the body plan in the developing embryo

hybrid an organism resulting from the interbreeding of two different species

I

immigration the movement of individuals of a species into a place

independent assortment the process by which the paternal and maternal chromosomes of each homologous pair behave independently of the other homologous pairs as they separate in meiosis I

insertion the addition of a single nucleotide within a sequence

interphase the stage of the cell cycle between active divisions

intron a section of DNA or mRNA that does not code for a polypeptide

ion an atom or group of atoms that has either lost or gained valence shell electrons, acquiring a net positive or negative charge

K

karyotype a display of the number and appearance of the chromosomes of an organism or cell observed at metaphase

keystone species a plant or an animal that plays a unique and crucial role in the way an ecosystem functions

kingdom the second-highest taxon in Linnaean classification, e.g. Animalia

L

lagging strand the DNA strand that is already in the 5′ to 3′ direction, so its complement cannot be replicated continuously by DNA polymerase; replication forms Okazaki fragments that must be stitched together by DNA ligase

leading strand the DNA strand that is already in the 5′ to 3′ direction, so its complement cannot replicate continuously by DNA polymerase in the 5′ to 3′ direction because its parent strand is unzipped in the 3′ to 5′ direction

Lincoln index a formula used to estimate animal population sizes through a mark-and-recapture technique

logistic population growth (S-curve) the population growth that levels off as population size approaches carrying capacity

M

macroevolution the variation of allele frequencies at or above the species level, over geological time, resulting in the divergence of taxonomic groups, in which the descendant is in a different taxonomic group from the ancestor

mass extinction a short period of geological time during which a high percentage of species die out

meiosis a two-phase type of cellular division in which the chromosome number of a cell is halved to the haploid number; the basis of gamete formation in animals and spore formation in plants

messenger RNA (mRNA) a ribonucleic acid molecule formed in the nucleus during transcription; its nitrogen base sequence is complementary to the DNA template segment; travels to cytoplasm for translation

metaphase the second stage of meiosis where chromosomes line up at the equator of the cell

metaphase plate the equator of the cell where chromosomes line up during metaphase

microevolution small-scale variation of allele frequencies within a species or population, in which the descendant is of the same taxonomic group as the ancestor

microhabitat a smaller location within a habitat

molecular homology the identification of shared biomolecular elements – generally genes – used to test the relationships between organisms, which can demonstrate common ancestry

molecular size marker a set of pieces of DNA of known length that is used to estimate the size of other DNA fragments in a gel

monoculture the agricultural practice of growing a single crop or species over a wide area for many consecutive years

monosomy when an individual's nuclei contain only one copy of a particular chromosome

morphological species concept a definition of species that is based on physical characteristics

morphology the shape and form of an organism or its parts

mutation a permanent change in a sequence of DNA

mutation rate the estimated number of base pair changes per nucleotide site per generation of a population

N

net primary productivity (NPP) the amount of organic matter made available to herbivores annually; equals gross primary productivity minus the energy required by the producers themselves

nitrogen-fixing bacteria bacteria that absorb elemental nitrogen (N_2) from the atmosphere and convert it to nitrites (NO_2^-), nitrates (NO_3^-) or ammonium ions (NO_4^+)

node a point in a diagram where lines branch or intersect

nodule a small swelling or lump

non-coding DNA a section of DNA that carries information for when, where or how often its associated coding DNA is expressed

non-disjunction when a pair of chromosomes fails to separate during anaphase, with both members of the pair moving to the same pole of the cell

non-template strand the DNA strand complementary to the template strand; does not form the pattern for the synthesis of complementary polynucleotide

nucleosome the basic structural unit of chromatin, comprising a DNA strand wrapped tightly around a group of eight histone proteins

nucleotide the basic building block of nucleic acids (DNA and RNA) linked together by phosphodiester bonds; each nucleotide is made up of a five-carbon sugar molecule, a phosphate group and a nitrogenous base

nudation the development of bare sites with no organisms inhabiting them

nutrient cycle the cyclic movement of key elements and molecules through the biotic and abiotic components of an ecosystem, e.g. the water cycle and carbon cycle; also called biogeochemical cycle

O

Okazaki fragments the DNA fragments caused by the discontinuous replication of DNA on the lagging strand; they are stitched together to make a continuous strand by DNA ligase

oogenesis the process in the ovary that produces female gametes (ovum/egg)

oogonia the stem cells responsible for producing cells that can create eggs

order the fifth-highest taxon in Linnaean classification, e.g. Carnivora

organelle a cellular structure that performs a specific function in a partitioned space within the cell

ovum the female haploid reproductive cell; also called an egg

P

parallel evolution a process whereby related organisms are reproductively isolated but evolve similar adaptations in response to the same environmental pressures

parapatric speciation the speciation that occurs when populations are separated by an extreme change in habitat; populations may interbreed in bordering areas

parasite an organism that causes long-term disease while leaving the host alive, such as protozoa and worms

parental DNA the DNA of the original cell in cell division

percentage cover the percentage of an area occupied by a species

percentage frequency the probability that a particular species will occur in a quadrat; the proportion of quadrats that contain a particular species

phylogenetic relationship an evolutionary relationship that exists between a group of species, often expressed as a tree-like diagram

phylogenetic species concept a definition of species that is based on the smallest group of individuals having a common ancestor, often determined through genetic analysis

phylogenetic tree a branching diagram showing evolutionary relationships

phylogram a phylogenetic tree in which branch length or width represents genetic differences or time since divergence

phylum the third-highest taxon in Linnaean classification of animals, e.g. Chordata

pioneer species an organism capable of invading bare sites and surviving

plasmid a small circular piece of DNA in bacteria that can replicate independently of the cell's chromosomes; plasmids carry antibiotic resistance markers

point mutation a mutation that affects a single base-pair position within a gene

polar body a small structure containing a nucleus and very little cytoplasm, that is produced, dies and is absorbed by the ovary during oogenesis

pollution the introduction of harmful materials into the environment

poly-A tail a section of repeated adenosine bases added to end of an mRNA strand to protect it from degradation

polygenes genes for which different alleles have a small additive effect on a phenotype; contribute to continuous variation in polygenic phenotypes

polygenic inheritance the transmission of characteristics controlled by two or more genes

polymerase chain reaction (PCR) a cyclical reaction in which DNA polymerase is used to copy a DNA sample, making millions of copies of the same piece of DNA

polypeptide a polymer of many amino acids linked by peptide bonds; forms a protein or part of a protein

population a group of individuals of the same species living in a particular place at the same time

predation a species interaction in which one species kills and eats another

predator an organism that kills and consumes all or part of the body of another organism

prey an organism that is hunted by another organism for food

primary oocyte a cell that enters meiosis I in oogenesis

primary spermatocyte a cell that enters meiosis I in spermatogenesis

primary succession the process of a community developing in a barren place

primer a single-stranded DNA molecule that anneals to its complementary sequence on the DNA sample to act as the start of the amplification process

promoter region a non-coding section of DNA upstream of a gene that initiates transcription

promoter region a region of DNA upstream of a gene that binds enzymes that initiate transcription

prophase the first stage of meiosis where chromosomes condense and centrioles form

Punnett square a grid used to graphically illustrate and predict the outcome of a genetic cross

purebred when crossed with each other, offspring all have the parent phenotype

Q

quadrat a frame used to set a standard area for sampling

R

random sampling a sampling method that ensures each part of the sample area has an equal chance of being counted

reading frame the ribosome's division of nucleotides into triplets for translation; shifted by insertion or deletion mutations

realised niche the actual niche that a species occupies, given the restrictions placed on it by interactions with other species

recessive allele the allele that is expressed in the phenotype only if both copies occur in the genotype

recombinant DNA technology the process of transferring a gene from a cell of a member of one species to the cell of a different species

recombinant plasmid a plasmid with foreign DNA inserted into it

reliability (of sampling) whether the sampling methods/techniques produce the same results when repeated

replication fork the junction between the unwound single strands of DNA and the intact double helix during replication

reproductive isolation processes that prevent individuals of separated populations from mating and producing fertile offspring

residue a single unit that makes up a polymer; e.g. a single amino acid in a protein sequence

resource partitioning the creative use of space and time that reduces competition between species and allows many unique ecological niches to exist in the same area

restriction enzyme an enzyme that cuts DNA at a specific restriction site

restriction site a specific nucleotide sequence (usually 4–8 base pairs) that is recognised as a cleaving site for a restriction enzyme

ribonucleic acid (RNA) a short-lived molecule consisting of ribonucleotides; it plays an essential role in protein synthesis (as messenger RNA and transfer RNA) and as a structural component of ribosomes

ribosome the organelle where polypeptide synthesis occurs in all cells

RNA polymerase the enzyme that produces mRNA from the DNA template strand; major enzyme in transcription

RNA splicing the process of removing parts of an mRNA strand, particularly any unnecessary introns, to produce mature mRNA

S

salination increased salt concentration

secondary oocyte a cell produced by meiosis I that enters meiosis II in oogenesis

secondary spermatocyte a cell produced by meiosis I that enters meiosis II in spermatogenesis

secondary succession the recolonisation of disturbed plant communities

selection pressure a factor that influences the survival of an individual within a population

semiconservative replication the production of two new DNA double helix molecules, each consisting of one parental strand and one daughter strand

seres transitional stages that are part of a succession

sex chromosome a chromosome that affects sexual traits; sex chromosomes are different in male and female individuals of the same species

sex-linked a gene located on a sex chromosome; in humans this is usually the X chromosome

sexual reproduction a form of reproduction in which offspring are produced from two parents

short tandem repeat (STR) a short non-coding region of DNA that is repeated many times in the genome of an organism; it is highly variable between individuals and can be used in DNA profiling to identify individuals

Simpson's diversity index (SDI) the combined ratio of individuals in each species to the total individuals in an ecosystem – a quantitative measure of biodiversity

sink an area where atoms naturally accumulate away from the normal nutrient cycle

sister chromatids the two identical copies of a single chromosome, formed by replication and connected by a centromere

somatic of the body, as distinct from the sex cells or sex chromosomes

speciation the evolution of one or more new species from an ancestral species

species evenness (relative species abundance) the number of individuals of each species in an ecosystem

species richness the number of species in an ecosystem

species the lowest taxon in Linnaean classification; it is always italicised and combined with genus, e.g. *catus* in *Felis catus*

spermatid a haploid daughter cell of spermatogenesis

spermatogenesis the continuous production of sperm cells in the testis

spermatogonia the stem cells responsible for producing cells that can create sperm

stabilising selection a form of selection that tends to favour organisms with a phenotype similar to their parents; usually occurs when the environment is very stable and unchanging and selects against extremes of phenotype

start codon the first codon of an mRNA strand translated by a ribosome

sticky end the overhanging end of a DNA fragment that is produced after asymmetrical cleavage by a restriction enzyme

stratified sampling a sampling method that divides an area into strata for separate sampling

stratum a layer or subsection of a whole

substitution when a single nucleotide is swapped for another

succession the progressive change of communities over time

symbiosis a relationship between individuals of two or more species in which at least one organism benefits from the interaction

sympatric speciation the speciation that occurs without spatial or geographic isolation

synapsis the physical pairing of homologous chromosomes

systematic sampling a sampling method that occurs at fixed intervals, typically along an environmental gradient

T

***Taq* polymerase** DNA polymerase from the bacterium *Thermus aquaticus*; used in the polymerase chain reaction because it can withstand the high temperatures used in the process

taxon a level of a hierarchical classification system, e.g. kingdom, family or species

taxonomy a system of classification, particularly biological; or the study of these systems

telomere a region at the end of a chromosome, characterised by repeated sequences of non-coding DNA

telophase the fourth stage of meiosis where membranes form around the two new nuclei

template strand the DNA strand that serves as a pattern for making complementary polynucleotide

transcription the formation of an mRNA molecule against the template strand of a DNA molecule in the nucleus by complementary nucleotide base pairing

transcription factor a regulatory protein whose function is to activate or inhibit transcription of coding DNA by binding to specific non-coding segments near the gene to be expressed or inhibited

transect a narrow section taken straight across an area, along which observations or measurements are made

transfer RNA (tRNA) a ribonucleic acid molecule with a specific RNA codon, paired with a particular amino acid from the cytoplasm, to deliver the amino acid to a growing polypeptide chain inside a ribosome

transform to change from one type to another

translation the joining of amino acids in a specific order to form a polypeptide, according to the mRNA sequence read by ribosomes

trisomy when an individual's nuclei contain three copies of a particular chromosome

trophic level a level in the food chain of an ecosystem based on feeding relationships

V

validity (of sampling) how well a population is accurately represented by the sample collected using the selected methods/techniques

vector a vehicle used to transfer DNA sequences from one organism to another

viability the capacity of an organism to stay alive

W

waterlogging what happens to plants when the water table rises into the root zone; results in anaerobic conditions that may kill some plants; may also increase salinity levels in the soil

INDEX

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