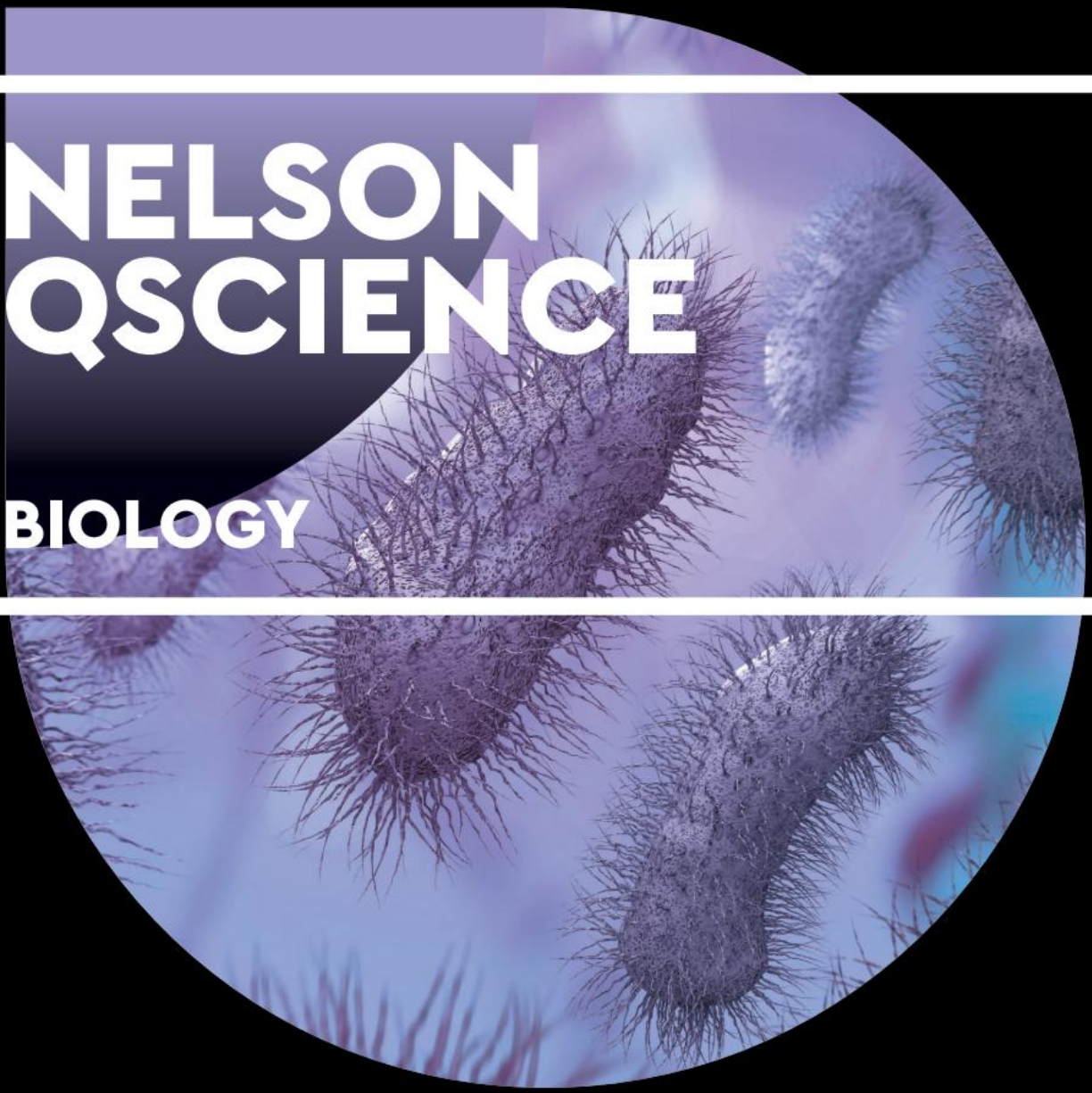
NELSON QSCIENCE

BIOLOGY



UNITS 3 4

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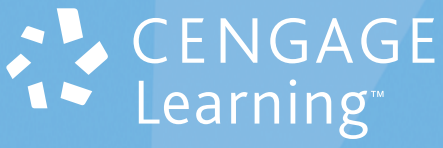

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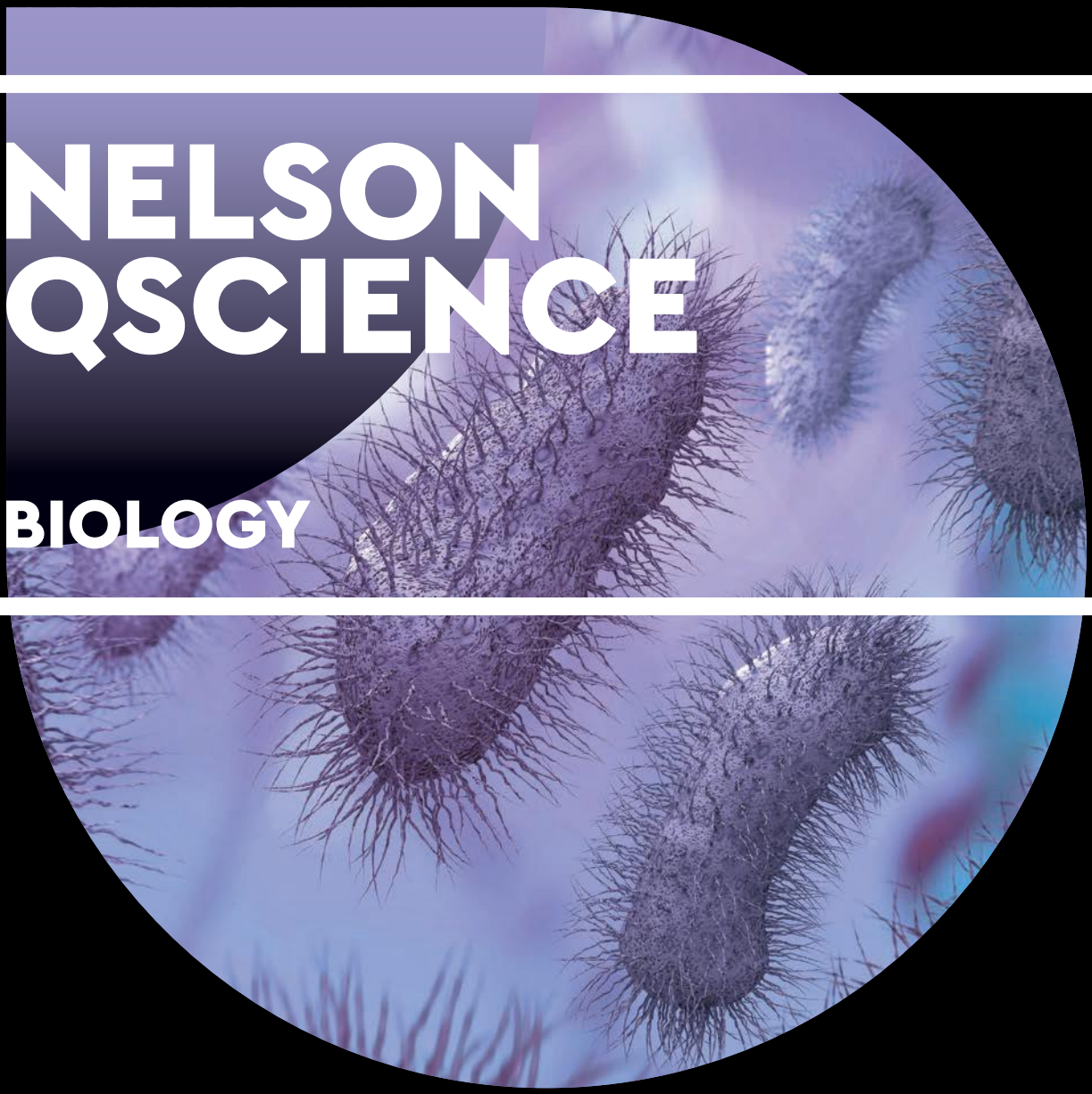

NELSON QSCIENCE

BIOLOGY

UNITS 3 4

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TOPIC 1: DNA, GENES AND THE CONTINUITY OF LIFE

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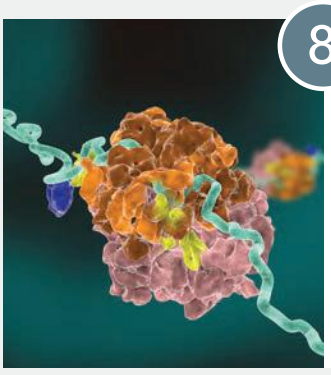

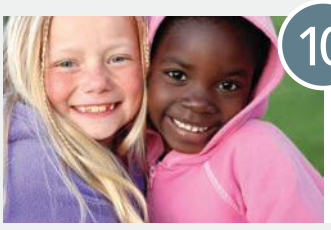

TOPIC 2: CONTINUITY OF LIFE ON EARTH

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PREFACE

Nelson QScience Biology Units 3 & 4 has been written to meet the requirements of the QCAA Senior Secondary Science Syllabus – Biology. Each page has been carefully considered to provide students with all of the information they need to meet the content and skills requirements of the new syllabus.

With the introduction of the QCE external examination, *Nelson QScience Biology* includes features such as practice exams at the end of each section, a Units 3 & 4 practice examination, chapter quizzes (available on *NelsonNet*) and ExamView (available on *NelsonNet*).

nelsonnet

AUTHORS AND REVIEWER TEAM

Nelson QScience Biology Units 3 & 4 has been adapted from the following titles: *Nelson Biology Units 1 & 2 for the Australian Curriculum* by Stephen Bird, Pam Borger, Merrin Evergreen, Genevieve Martin, Xenia Pappas, Katrina Walker, Jim Woolnough and Jane Wright; and *Nelson Biology Units 3 & 4 for the Australian Curriculum* by Pam Borger, Tony Chiovitti, Jacinta Duncan, Wayne Gerdtz, Patrick-Jean Guay, Genevieve Martin, Katrina Walker, Jim Woolnough and Jane Wright, with Sarah Jones.

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SYLLABUS REFERENCE GRID

UNITS AND TOPICS	*NELSON QSCIENCE BIOLOGY UNITS 3 & 4*
UNIT THREE » BIODIVERSITY AND THE INTERCONNECTEDNESS OF LIFE	
TOPIC 1: DESCRIBING BIODIVERSITY	
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Classification process	Chapter 2
TOPIC 2: ECOSYSTEM DYNAMICS	
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Evolution	Chapter 12
Natural selection and microevolution	Chapter 13
Speciation and macroevolution	Chapter 14

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ABOUT THIS BOOK

At the beginning of unit and topic

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

At the beginning of each chapter

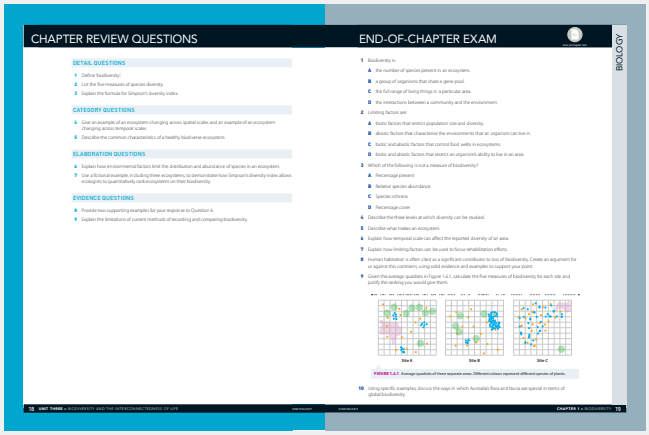
- A short chapter summary introduces students to the key content and skills covered.
- Stimulus questions are relevant to the syllabus.

In each chapter

- **Key formulas** are highlighted in the margin.
- **Key glossary terms** are highlighted in the margin.
- **Science as a Human Endeavour** provides opportunities for students to connect to the importance of science as a human endeavour and develop scientific research skills.
- **Inquiring further** provides opportunities for students to further investigate scientific concepts and develop scientific research skills.
- **Section reviews** are written in the style of Bloom's revised taxonomy.
- **Practical experiments** contain guided instructions on the materials, procedure, collection and analysis of results, and discussion.

At the end of each chapter

- **Chapter review questions** written in the style of Marzano and Simms (2014) questioning sequences.
- **End-of-chapter examinations** help students develop skills in decoding and answering exam-style questions.



At the end of the book

- **Practice exam** questions provide an extended practice of the content and skills learnt across the text.
- **Glossary** provides explanations of all of the new terms introduced in the text.
- **Answers** provides complete short answers for student reference (fully worked solutions are on the teacher website).

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» UNIT THREE

BIODIVERSITY AND THE INTERCONNECTEDNESS OF LIFE

- Topic 1: Describing biodiversity
- Topic 2: Ecosystem dynamics

Species that live together within ecosystems do not live alone. They interact with each other and with the biotic and abiotic components of their environment. Species diversity and population numbers are influenced by the movement of energy and matter between members of an ecosystem and the environment. Ecosystems rarely remain the same. Some changes are regular, while others are caused by natural disasters and human activities. Environmental limiting factors determine the species diversity and population growth. Identifying and classifying organisms and studying interactions between species provides a basis for comparisons between ecosystems in time and space.

UNIT OBJECTIVES

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

1. describe and explain biodiversity and ecosystem dynamics
2. apply understanding of biodiversity and ecosystem dynamics
3. analyse evidence about biodiversity and ecosystem dynamics
4. interpret evidence about biodiversity and ecosystem dynamics
5. investigate phenomena associated with biodiversity and ecosystem dynamics
6. evaluate processes, claims and conclusions about biodiversity and ecosystem dynamics
7. communicate understandings, findings, arguments and conclusions about biodiversity and ecosystem dynamics.

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» UNIT THREE

BIODIVERSITY AND THE INTERCONNECTEDNESS OF LIFE

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Topic 1: Describing biodiversity

Not only do the types of species found in an ecosystem vary, but the ecosystems themselves vary. The environmental conditions in an area can impact upon the type and number of organisms that can live there. Measuring the types, abundance and distribution of species can be used to determine species diversity. Descriptions of the amount and type of biodiversity use species diversity, types of interactions between species, and abiotic factors. These measurements are useful when comparing ecosystems across different areas and over time. Descriptions of species and ecosystem diversity rely on classification processes. Classification of species uses physical features, methods of reproduction and molecular sequences to recognise similarity and relatedness of organisms. Conversely, ecosystems are classified according to the various habitats from which they are composed. Ecosystem classification can inform environmental management strategies and protection plans.

SCIENCE AS A HUMAN ENDEAVOUR

Students should be given opportunities to investigate the interactions between technology and biodiversity, international agreements designed to protect biodiversity, and the setting of biodiversity targets.

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1 BIODIVERSITY

Introduction

We live in a world with amazing forms of life. In many places, there are still more unknown species to be uncovered. In the 18th and 19th centuries, explorers sailed the world on voyages of discovery. Naturalists and collectors took advantage of these voyages and wrote detailed accounts of what they observed. These accounts were widely read back home in Europe by a public fascinated with exotic places and things, and who marvelled at the specimens brought back from expeditions. Wealthy patrons sponsored collectors to bring back live exotic animals and plants, and private menageries and public zoos were created. At the same time, naturalists began to question age-old beliefs about the physical and living world around them. They wondered about the new, previously unknown, species brought back from unseen lands. It was in part due to his own voyage of discovery that Charles Darwin developed his theory of evolution by natural selection. This chapter explores the beautiful diversity of life on Earth.

Stimulus questions

How do you measure biodiversity?

How do environmental factors affect biodiversity?

How are ecosystems defined and compared?

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1.1 The diversity of species and ecosystems

The great variety of living organisms that have evolved on Earth is a source of endless discovery and amazement. This variety of life is called **biodiversity**, and the term can apply to the planet as a whole or to individual locations. When applied to individual locations, biodiversity generally refers to how many different species work together in an **ecosystem**. 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 any physical barrier.

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

Biodiversity used to be nothing more than a source of curiosity, but is now recognised for the vital role it plays in the long-term stability of a species, an ecosystem and the planet as a whole, including the societies in which we live. Consequences for low biodiversity include inbreeding, vulnerability to disease, over-predation and ecosystem breakdown.

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

ecosystem
a self-sustaining unit consisting of the interactions between the species in a community and the environment

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

Diversity of species

Determining the number of species on the planet 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 the number of microscopic species could be in the billions. However, we have more precise estimates for the species that have been discovered. 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 wild in Australia (Figure 1.1.1).

FIGURE 1.1.1 Sir Joseph Banks discovered hundreds of new plant genera in Australia. One plant was named after him – the banksias, such as this *Banksia serrata*.

1.1.1 What is biodiversity and why is it important?
1.1.2 Australia's biodiversity
1.1.3 Australia's biodiversity – summary

INQUIRING FURTHER

Research the voyages of Joseph Banks (HMS *Endeavour*, 1770), Robert Brown (HMS *Investigator*, 1801) or Charles Darwin (HMS *Beagle*, 1836) to find out how many new species each naturalist discovered and the contributions he made to understanding the unique Australian ecology.

SYLLABUS LINK

Chapter 4 also discusses biotic and abiotic factors.

Chapter 3 discusses the transfer and transformation of energy.

biotic factors
the living components of an ecosystem, including animals, plants and bacteria

abiotic factors
the non-living components of an ecosystem, including the physical landscape, minerals and weather conditions

photosynthesis
the process of using light energy to convert carbon dioxide and water into glucose and oxygen

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

species richness
the number of species present in an ecosystem

relative species abundance
the number of individuals present for each species in an ecosystem

percentage cover
the percentage of the quadrat that a species takes up

percentage frequency
the percentage of quadrats in which a species appears

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

quadrat
a 1 m × 1 m square frame that is placed over a location to provide a boundary for sampling in ecology

Diversity of ecosystems

An ecosystem is composed of all the living organisms (**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 by the cycling of nutrients and raw materials within it. These include CO_2, O_2, water, nitrogen, phosphorus and many other minerals, as well as the living organisms that transfer energy through the system. In most systems, the energy is initially transformed from light to chemical energy, through **photosynthesis**, and then transferred between organisms via tightly linked **food webs**. The final transformation of energy is generally to body heat.

SECTION REVIEW 1.1

REMEMBERING

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

2 Describe the three types of biodiversity.

UNDERSTANDING

3 Outline some reasons why Europeans may have been puzzled by different-looking animals and plants collected in Australia.

4 Explain why species diversity is important within an ecosystem.

APPLYING

5 There are 10 000 pure-bred pug dogs registered in the UK, but the entire set of DNA from these dogs amounts to only 50 individuals. Some experts now believe the pug is critically endangered and cannot be saved. Explain two issues that a lack of genetic diversity could be causing in pugs.

1.2 Determining the diversity of species

In order to speak quantitatively about how diverse a particular ecosystem is, ecologists need a measure or scale to compare ecosystems. However, so many factors play a part in biodiversity that five common measures are used, often together, to describe the diversity of the species in an ecosystem; **species richness**, **relative species abundance**, **percentage cover**, **percentage frequency** and **Simpson's diversity index**.

To begin with, the ecosystem must be sampled in a standard way. Usually this is the **quadrat** method, where a 1 m × 1 m square frame is laid on the ground and everything inside the frame is sampled. Taking several quadrats at the same location allows for more accurate average data.

Species richness

Species richness refers to the number of species present in an ecosystem. It is a number from one to infinity and is relatively easy to count out from a quadrat. Although this seems like a good measure of diversity, it does not take into account how many of each species are present or what their interactions are. This can mean that an ecosystem that is almost entirely *Lantana camara* (Figure 1.2.1) but has three other species not yet killed by it, is equal to an ecosystem that has a balance of four different species. To correct this, ecologists also look at the relative species abundance.

FIGURE 1.2.1 *Lantana camara* is a very invasive weed in Queensland.

Relative species abundance

Relative species abundance refers to how many of each species are present. This can be more difficult to count, because many grasses have runners that blur the boundary between individuals (Figure 1.2.2). Regardless, this measure enables ecosystems with one dominant species to be differentiated from more evenly distributed ecosystems. An ecosystem is generally considered healthier if its species are similar in number. For quadrats with particularly difficult species to count, percentage cover is often used instead.

Percentage cover

Percentage cover is an estimate of the percentage of a quadrat that a species is occupying. Grasses and other plants that can be difficult to count are better approximated with this measure. Within a 1 m × 1 m quadrat, every 10 cm × 10 cm square is 1%. Estimating how much of the quadrat is covered by a single species of grass can then be used instead of the relative species abundance.

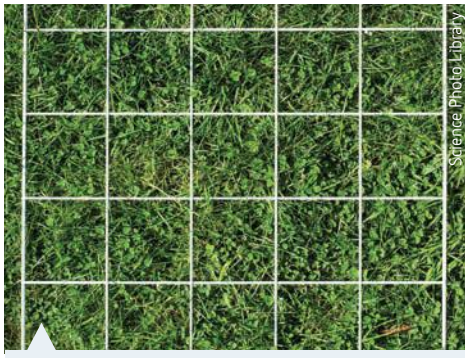

FIGURE 1.2.2 Grasses are particularly difficult to count individually, so the percentage cover method is often used instead.

Percentage frequency

Percentage frequency is the proportion of quadrats that contained a particular species. One limitation of quadrats is that species tend to live together in communities and this may mean that although your quadrat is 80% clover, it may be the only clover in the ecosystem. By noting how many of the quadrats in the 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 (D) gives a number between zero (no diversity) and one (infinite diversity), while accounting for both species richness and relative species abundance. A value closer to 1 denotes good biodiversity. Increased richness increases the index, as does a more even distribution of individuals. Table 1.2.1 (page 10) shows the data gathered for two open forests in Queensland.

KEY FORMULA

Simpson's diversity index

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

where:

n is the number of individuals of each species

N is the total number of individuals at the site.

1.2.1 Simpson's diversity index

TABLE 1.2.1 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	$D = 1-\left(\frac{\sum n(n-1)}{N(N-1)}\right)$ $= 1-\frac{110}{420}$ $= 0.738$			$D = 1-\left(\frac{\sum n(n-1)}{N(N-1)}\right)$ $= 1-\frac{138}{272}$ $= 0.493$		

Simpson's diversity index can be simplified to dividing the sums of individuals of each species by the total number of individuals and subtracting this number from one to enable a logically consistent value. In the example given in Table 1.2.1, 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.

SECTION REVIEW 1.2

REMEMBERING

1. Outline the five indicators used to determine diversity of species.
2. Define 'quadrat method'.
3. Recall and define the formula for Simpson's diversity index.

UNDERSTANDING

4. Explain the difference between species richness and relative species abundance.

APPLYING

5. 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.
6. Create an argument for or against the use of standardised indices in communicating and comparing biodiversity.

1.3 Comparing ecosystems

It can be misleading to give straight comparisons of ecosystems by using only the five measures of biodiversity because these are only representative of the time and place that were sampled. For example, nocturnal animals would not have been counted in a daytime sampling, while bulbs such as daffodils and crocus will be dormant underground during a winter sampling. It can also be misleading to assume that a sampling of the shoreline of Moreton Bay must be the same as one taken out in the bay, where the conditions are very different.

Spatial differentiation

The **spatial scale** of an ecosystem refers to how large an area it covers (Figure 1.3.1). **Macro-level ecosystems** are typically whole oceans or continents, such as the general types of plants and animals found in Australia. **Meso-level ecosystems** are areas within the ocean or continent with more homogeneous climate conditions, such as the Simpson Desert or Lamington National Park. **Micro-level ecosystems** are specific local areas, such as the Antarctic beech forest, warm temperate rainforest and subtropical rainforest within Lamington National Park. Analysing ecosystems any smaller than this usually misses key organisms.

As a general rule, micro-level ecosystems are collectively representative of the macro-level ecosystem, in the same way that sampling quadrats are collectively representative of the whole.

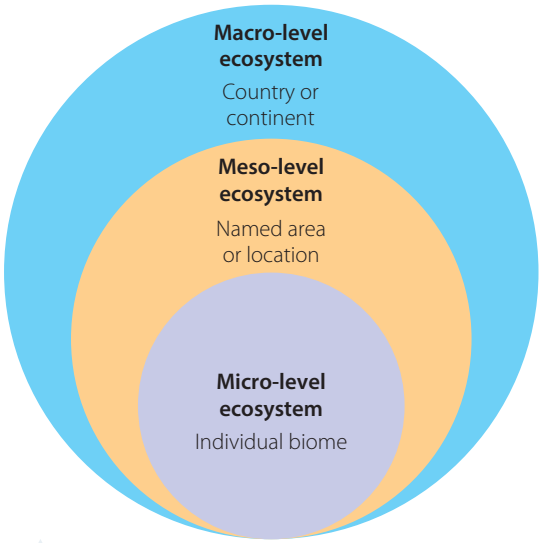

FIGURE 1.3.1 Scale is an important consideration when comparing ecosystems. Ecosystems exist on many different scales, including macro-, meso- and micro-levels.

spatial scale
how much area a studied ecosystem covers

macro-level ecosystem
a large area of land or water (typically a whole continent or ocean) and its inhabitants

meso-level ecosystem
a medium-sized area of land or water (typically a single-named location, such as a desert or lake) and its inhabitants

micro-level ecosystem
a small area of land or water (typically a single biome, such as temperate rainforest) and its inhabitants

SYLLABUS LINK

Section 1.2 discussed Simpson's diversity index (D) in greater detail.

1.3.1 Ecological relationships

Species diversity

A Simpson's diversity index calculation takes into account the size of an ecosystem by including the ratio of new species to the number of individuals present. Hence, a macro-level ecosystem with $D = 0.7$ is equally biodiverse to a micro-level ecosystem with $D = 0.7$.

Species interactions

Species interactions, such as **predation** and **competition**, can be compared across spatial scales in a general manner. The ratios of **producers** to first and second level **consumers** is similar in similarly biodiverse ecosystems, regardless of spatial scale. The interactions between these species, including levels of predation, is also similar. Less biodiverse ecosystems are often skewed one way or the other.

Abiotic factors

Abiotic factors are physical and chemical factors such as temperature, light intensity, rainfall, the texture and pH of the soil or water and the concentration of significant gases in the water or air. Abiotic factors vary considerably across spatial scales. Australia as a whole has a range of February temperatures from 2.6°C (16 February 2016, Mt Wellington Pinnacle, Tasmania) to 47.8°C (12 February 2016, Mardie, Western Australia). This is the difference between snow and heatstroke! It is unusual to find homogeneous abiotic factors within a macro-level ecosystem, so comparisons are usually limited to meso-level and micro-level ecosystems.

Other abiotic factors that vary between ecosystems include soil type and depth, wind speed, light intensity, rainfall, infiltration rate, dissolved oxygen, turbidity and chemical composition. Each of these has the capacity to change what could be considered normal and healthy biodiversity for an ecosystem.

predation
a species interaction in which one species kills and eats another

competition
a species interaction in which two or more individuals (whether the same species or not) compete for the same resource in the same area

producer
an organism, such as a plant, that converts energy to sugars

consumer
an organism that eats other organisms for nutrition

Temporal differentiation

temporal scale
the time period over which an ecosystem is studied

Ecosystems can also be compared across different time periods. **Temporal scales** can be short term, such as over 24 hours, mid-term, such as seasonal changes, or long term, such as years.

Species diversity

Measures of species diversity are often different at different times of day or year. The same ecosystem can give a Simpson's diversity index of 0.4 during the day, but 0.6 at night. This could be caused by human disturbance of **diurnal** organisms during the day while nocturnal organisms are left undisturbed. It can also be entirely natural for locations to have lower biodiversity at night if a large predator population takes advantage of sleeping nocturnal organisms, such as the impact of feral cats on the possum population. This leaves the predators active during the day and fewer nocturnal organisms to be active at night.

diurnal
active during the daylight hours

In places that experience regular winter snow, animals often hibernate or migrate to warmer areas. Insects and other small organisms also find warm places to shelter until the snow melts, or the timing of their life cycles ensures their tiny bodies are not exposed to the extreme cold of winter. This can affect the measures of diversity used to describe the ecosystem at different times of the year.

Species interactions

Species interactions can also change considerably between temporal scales. Healthy ecosystems will be more stable in the long term, so that even as some species move on or die out, others are present to fill the **niche**. Ecosystems with poor biodiversity often have large changes in their species interactions over time.

niche
a specialised position or role

Abiotic factors

Most abiotic factors do not naturally change a lot over time. Temperature and humidity are the two factors that experience considerable short-term change (and thus affect diversity on short time scales), but over longer temporal scales, such as decades and millennia, the smaller changes are only minor fluctuations around an overall stable level of diversity. However, climate change has caused drastic changes to the long-term temperature of the macro-level ecosystem.

Other abiotic factors such as soil type and dissolved oxygen do not change much over short time scales, but can be very different over long time scales (usually millennia), as seas rise and fall, rivers dry up and valleys fill with water.

SECTION REVIEW 1.3

REMEMBERING

1. Define:
   - **a** spatial scales
   - **b** temporal scales.
2. Give an example of how species diversity may differ in the same place at different times.
3. Give an example of how abiotic factors differ between spatial scales of an ecosystem.

UNDERSTANDING

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

APPLYING

5. Choose an ecosystem and describe how its biodiversity would change at three different spatial scales and three different temporal scales. You may like to summarise your response in a 2×3 table.

1.4 Environmental limiting factors

All organisms are limited by their environment, even those that appear perfectly suited to it. If an organism is not limited, its population spirals out of control, such as during algal blooms (Figure 1.4.1). **Limiting factors** are aspects of the environment that restrict an organism's ability to live there. This does not mean that the organism cannot live there; it is just not easy for the organism to live there. For example, koalas live in urban bushland, but their population is restricted by the number of eucalypt trees and the distance between mating individuals. Many ecological efforts to support endangered populations revolve around mitigating limiting factors.

limiting factor an aspect of the environment that restricts an organism's ability to live there

FIGURE 1.4.1 Algal blooms occur when natural limiting factors are removed; for example, the sudden excessive availability of key nutrients such as nitrates from fertiliser run-off.

Almost all biotic and abiotic factors are limiting factors to something. The rainfall in an area limits the number of plants that can grow, the type of soil limits the type of plants that can grow and the local herbivorous animals restrain plant growth through grazing.

As an extreme example, polar bears are well suited to living in the Arctic, but many strongly limiting factors would prevent them from thriving in Queensland. Abiotic limiting factors include high temperature, relatively low shade that may have made the temperature tolerable, no ice to enable their hunting strategies and no snow to enable their den-building strategies. Also, biotic factors, such as a lack of large, fatty game and strong competition for what game there is, make it highly unlikely that any ecological effort to support a local polar bear population in Queensland would be successful. However, in the Arctic many of these factors are becoming more limiting as climate change worsens.

INQUIRING FURTHER

Research the northern hairy-nosed wombat, of which there are only approximately 230 individuals left, located in two reserves in southern Queensland. Discuss three limiting factors for these wombats and suggest a possible solution for each.

MANIPULATIVE SKILLS 1.4.1

Gathering data on environmental factors

The environmental conditions in an area can have a big impact on the type and number of organisms that can live there. Testing the abiotic factors can give ecologists a better idea of how an ecosystem is functioning. Often, improvements to biodiversity can occur when organisms repopulate an area after abiotic factors have been stabilised.

AIM

To use appropriate technology such as data loggers, chemical tests, turbidity tubes and other equipment to measure abiotic factors in the field and in the classroom.

MATERIALS

- data logger with temperature, pH and dissolved oxygen probes
- nitrate test kit (from aquarium or similar)
- universal indicator and colour chart
- turbidity tube
- thermometer
- small bucket
- test tube
- measuring cylinder
- sample tubes with lids
- flask
- evaporating dish
- funnel
- scales
- deionised water
- filter paper
- blank results sheet
- clipboard
- pen

PROCEDURE

1. Choose a field site with a creek or river. Make a brief assessment of the quality of the animal and plant life you can see.
2. Temperature: Measure both the air and water temperature with the thermometer and the temperature probe. Rinse the temperature probe and thermometer with deionised water.
3. Clarity: Fill the small bucket with water from the creek and pour it into the turbidity tube until the mark at the bottom is no longer visible when looking from above. Record the result.
4. pH: Fill the test tube with water from the creek and dip in the pH probe. Record the result before you rinse the probe with deionised water. Then add three drops of universal indicator to the water in the tube. Swirl to combine and compare the colour to the colour chart.
5. Dissolved oxygen: Refill the test tube with fresh water from the creek. Dip in the dissolved oxygen probe and record the result. Rinse the probe with deionised water.
6. Take two 10 mL samples back to class for the nitrate and solids tests.

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7 Nitrates: Follow the instructions on the nitrate test kit to obtain results for the nitrate level in the water sample.

8 Total dissolved solids and suspended solids: Wet the filter paper with a small amount of deionised water and weigh it on the scales. This is your base weight for the suspended solids. Carefully fit the wet filter paper into the funnel without tearing it. Pour the sample through the filter into the flask then reweigh the filter paper. The difference between the base weight and final weight is the total suspended solids. Weigh the evaporating dish. This is your base weight for the total dissolved solids. Pour the filtered sample from the flask into the evaporating dish and allow it to evaporate fully. Reweigh the evaporating dish. The difference between the base weight and final weight of the evaporating dish is the total dissolved solids.

RESULTS

QUALITY OF PLANT AND ANIMAL LIFE	Plant life:	Animal life:	
AIR TEMPERATURE	Thermometer:	Probe:	
WATER TEMPERATURE	Thermometer:	Probe:	
CLARITY			
pH			
DISSOLVED OXYGEN			
NITRATES			
SUSPENDED SOLIDS	Base weight:	Final weight:	Result:
TOTAL DISSOLVED SOLIDS	Base weight:	Final weight:	Result:

QUESTIONS

1 Explain the difference between the thermometer and temperature probe results.

2 Why were both the air temperature and water temperature taken?

3 Describe how low water clarity can affect the plant and animal life in a creek or river.

4 Make an overall assessment of the abiotic factors that you tested. Identify any factors that may be preventing plant and animal life from living in the area. Comment on any factors that may be supporting certain plant and animal life there.

SECTION REVIEW 1.4

REMEMBERING

1 Define 'limiting factors'.

2 Give three biotic and three abiotic factors that could limit species populations.

UNDERSTANDING

3 Explain two limiting factors for the human population in Queensland.

4 Explain two limiting factors for the shark population in Queensland waters.

APPLYING

5 Kangaroos are quickly reaching pest proportions in central and south-west Queensland after 3 years of good rains in the area. Give three previously limiting factors that have been relaxed by the rains and explain whether you think the population will self-limit or require human intervention.

1.5 Mandatory practical

DETERMINING BIODIVERSITY

Introduction

Ecologists are often called upon to advise politicians on local environmental matters, such as the impact of a proposed development or which area needs rehabilitation. 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 them in making accurate, quantifiable assessments.

AIM

To determine species diversity of a group of organisms based on a given index by using the five measures of species biodiversity to compare two ecosystems.

MATERIALS

- two field sites of vegetation (e.g. grassed yard, bushland, rainforest, crop field, garden)
- quadrat frame
- clipboard
- 6 copies of Table 1.5.1
- 2 copies of Table 1.5.2
- 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 1.5.1.
4. Count the number of individuals of this species within the quadrat and record this.
5. Estimate the percentage of the quadrat that the individuals take up in total and record this.
6. Repeat steps 3–5 for all of the species you can identify.
7. Repeat steps 2–6 for at least three quadrats in your area.
8. Repeat steps 1–7 for the second field site. In total, complete at least six copies of Table 1.5.1.
9. Calculate species richness, relative species abundance, percentage cover and percentage frequency for each of the field sites and enter them into Table 1.5.2. You will need to average much of your data.

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RESULTS

TABLE 1.5.1 Field site #_____ Quadrat #_____

SPECIES	NUMBER OF INDIVIDUALS	PERCENTAGE COVER

TABLE 1.5.2 Field site #_____

SPECIES RICHNESS		
SPECIES	RELATIVE SPECIES ABUNDANCE (AVERAGE)	PERCENTAGE COVER (AVERAGE)

DISCUSSION

1. Compare the diversity summaries for each of the field sites (using Table 1.5.2).
2. Comment on the diversity of the first field site. Does it seem diverse? Is this a surprising finding?
3. Comment on the diversity of the second field site. Does it seem diverse? Is this a surprising finding?
4. Calculate Simpson's diversity index for both field sites. What does this mean for your sites?
5. Discuss the implications of your findings for each of the field sites. How have humans impacted the biodiversity of this site? Is intervention needed?

CONCLUSION

1. Use the five measures of species diversity to compare the biodiversity of the two ecosystems studied.

CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1. Define 'biodiversity'.
2. List the five measures of species diversity.
3. Explain the formula for Simpson's diversity index.

CATEGORY QUESTIONS

4. Give an example of an ecosystem changing across spatial scales and an example of an ecosystem changing across temporal scales.
5. Describe the common characteristics of a healthy biodiverse ecosystem.

ELABORATION QUESTIONS

6. Explain how environmental factors limit the distribution and abundance of species in an ecosystem.
7. Use a fictional example, including three ecosystems, to demonstrate how Simpson's diversity index allows ecologists to quantitatively rank ecosystems on their biodiversity.

EVIDENCE QUESTIONS

8. Provide two supporting examples for your response to Question 6.
9. Explain the limitations of current methods of recording and comparing biodiversity.

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END-OF-CHAPTER EXAM

End-of-chapter test

1 Biodiversity is:

- **A** the number of species present 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** abiotic factors that characterise the environments that an organism can live in.
- **C** biotic and abiotic factors that control food webs in ecosystems.
- **D** biotic and abiotic factors that restrict an organism's ability to live in an area.

3 Which of the following is not a measure of biodiversity?

- **A** Percentage present
- **B** Relative species abundance
- **C** Species richness
- **D** Percentage cover

4 Describe the three levels at which diversity can be studied.

5 Describe what makes an ecosystem.

6 Explain how temporal scale can affect the reported diversity of an area.

7 Explain how limiting factors can be used to focus rehabilitation efforts.

8 Human habitation is often cited as a significant contributor to loss of biodiversity. Create an argument for or against this comment, using solid evidence and examples to support your point.

9 Given the average quadrats in Figure 1.6.1, calculate the five measures of biodiversity for each site and justify the ranking you would give them.

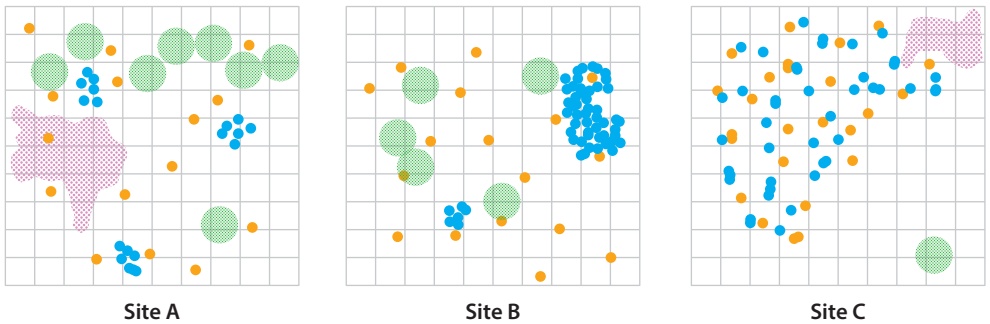

FIGURE 1.6.1 Average quadrats of three separate areas. Different colours represent different species of plants.

10 Using specific examples, discuss the ways in which Australia's flora and fauna are special in terms of global biodiversity.

2 CLASSIFICATION PROCESS

Introduction

At the time of the exploration and settlement of Australia by Europeans, the science of natural history was at its peak. The naturalists who described, collected and classified plants and animals were amazed by the sheer number of new species discovered in Australia. Captain Cook's landing point at Botany Bay was named for the diverse plant life found there. The exploration of Australia provided opportunities, as well as challenges, for the naturalists of the 18th and 19th centuries.

One such challenge was how to make sense of the flora and fauna in Australia. Initially, European explorers described Australian animals in terms of those they were familiar with. They wrote of 'wolves' (dingoes), 'badgers' (wombats) and 'raccoons' (wallabies). Eventually, naturalists realised that the plants and animals of Australia were so different from those of Europe that they needed their own names.

Some naturalists based their work on specimens and sketches brought back from Australia. However, others made the voyage to Australia themselves. British ornithologist John Gould made this journey with his wife Elizabeth – a sketch artist. Over a period of 2 years spent in Australia, the Goulds described around 300 new species of birds. While initially focusing on birds, John Gould became so interested in Australian mammals during his stay that he also spent considerable time describing and classifying them. The Goulds' contribution to the classification of Australian wildlife was phenomenal.

Stimulus questions

How is life classified?

How are ecosystems classified?

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2.1 Biological classification

Biological classification systems or **taxonomies** are methods of sorting living things, so that similar or related organisms are grouped together. The diversity of life on Earth is so large that classifying organisms is the first step in processing the vast amounts of information. By grouping similar organisms together, we can better see the range of life on Earth, observe patterns and trends, and understand relationships between organisms and groups of organisms. Classification then allows biologists to analyse these relationships to better understand how we came to be here and our place in the web of life.

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

2.1.1 A brief history of the kingdoms of life

Why classify?

One of the major benefits of classification is in simplifying and condensing large amounts of information. The numbers from 1 to 1 000 000, for example, would be almost impossible to memorise if not for the decimal place value system. This system groups the numbers into units of 1, 10, 100 and so on, so that each number is related to all the numbers around it. With this system, it is easy to remember that after 845 631 comes 845 632 because they have so much in common. In taxonomy, the vast range of living organisms are collected into categories, such as birds and mammals, based on common features.

To further simplify a wide range of information, classification systems are often hierarchical. Organising the information into layers of relatedness reduces the total number of parts required in your system and allows for deeper analysis. For example, moving from ones to tens and tens to hundreds simply involves adding another layer of numbers and repeating the previous steps. In taxonomy, birds and mammals are different classes but both have internal skeletons, which is used to group them together with other organisms. In **hierarchies**, the upper levels incorporate more information than the lower levels, which, in turn, are more specific (Figure 2.1.1).

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

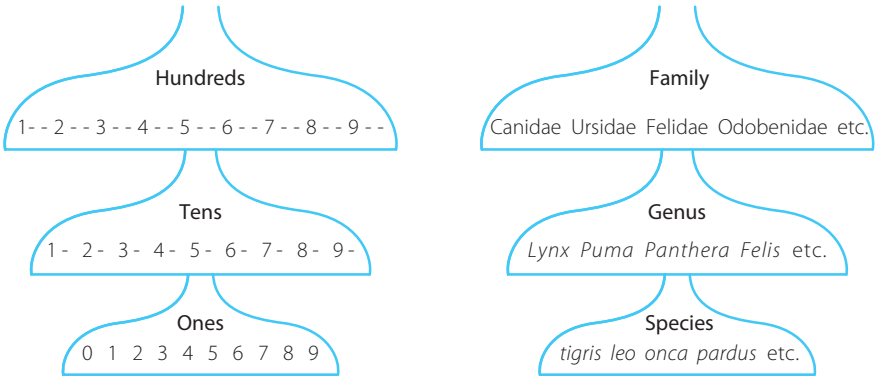

FIGURE 2.1.1 Both the place value system and the currently recognised taxonomy organise information with hierarchies of relatedness.

Limitations of classification

When you simplify information for analysis, you have to make choices. Which features do you group by? If you're counting legs, do you count all limbs or only those used for locomotion? Regardless of what you choose, other people will interpret groupings differently. Even standard systems are open to interpretation and the choices of others in classifying organisms.

Classifying also requires biologists to emphasise major similarities, which means reducing or ignoring minor differences in individuals. The minor differences are what make the range of life on Earth so impossibly complex, which is why classification is needed in the first place – to reduce the complexity to an understandable level. Unfortunately, when you reduce or ignore minor differences, you get a skewed view of reality. For example, race is an arbitrary classification that emphasises the similarities in skin tone and facial features between humans. This classification reduces and ignores the very real differences between individuals who are grouped by race (Figure 2.1.2). It is important to keep in mind that any attempt to group things is a temporary and artificial construct and is imperfect by nature.

FIGURE 2.1.2 Individuals are grouped and classified in many ways. It is important to remember that none of these ways has any meaning outside of the original analysis.

There are no permanent classifications. A taxonomy is built to organise the data for analysis and is directly related to the purpose for which the data will be used. After the analysis, the classification is no longer relevant.

SECTION REVIEW 2.1

REMEMBERING

1 Define 'taxonomy'.

2 List two benefits of classifying organisms.

UNDERSTANDING

3 Explain two limitations of classification.

APPLYING

4 Given the first names of the students in your class, design a way to group them for easier recall. Begin with first letter as a consonant/vowel and continue with two or three more subcategories. Try not to use personality or other characteristics unrelated to their name.

2.2 Classification systems

All living organisms can be classified on the basis of physical traits, reproductive method and/or molecular sequences. 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. The most widely accepted and supported standard taxonomy is currently Linnaean classification.

Classification by physical traits

When Carl Linnaeus wrote *Systema Naturae* in the 1750s, he was trying to create order from the chaos that species identification had become. Each new species had a completely new name that did not reflect any organising principle and naturalists at the time were finding the ever-lengthening names confusing and unwieldy (Figure 2.2.1). *Systema Naturae* detailed both a framework of taxonomic levels that could organise the known species and the rules for its use.

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

FIGURE 2.2.1 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*. Using Linnaeus' binomial taxonomy, it became *Rosa canina*.

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 from the bottom) 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*

eukaryote
a complex type of cell with a nucleus and membrane-bound organelles; a member of domain Eukarya

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

prokaryote
a simple type of cell that lacks a nucleus and membrane-bound organelles; a member of domains Archaea or Bacteria

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 2.2.2). 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. Therefore, each organism can be defined by the taxa to which it belongs.

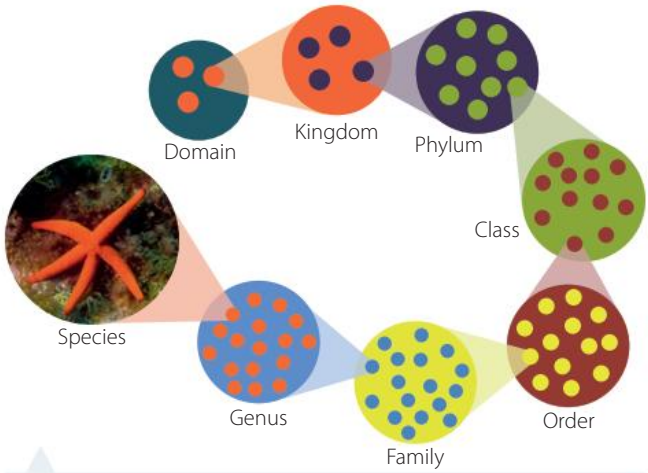

FIGURE 2.2.2 The hierarchy of Linnaean classification involves eight taxa. Thus, each organism on Earth can be identified with just eight words that indicate which taxa it belongs to.

Domains and kingdoms

Although Linnaeus did not have access to cellular information, it is now used to divide life into three domains (Figure 2.2.3). In members of domain Eukarya, called **eukaryotes**, the DNA is contained within a nucleus and there are other membrane-bound compartments, called **organelles**, within their cells. Domains Archaea and Bacteria include **prokaryotes**: organisms that lack these features. Despite this superficial similarity, organisms in Archaea and Bacteria have differences in the way DNA is stored and how proteins are synthesised, which means that they are classified in separate domains. Many of the members of Archaea live in extreme environments (such as areas of high salt or temperature).

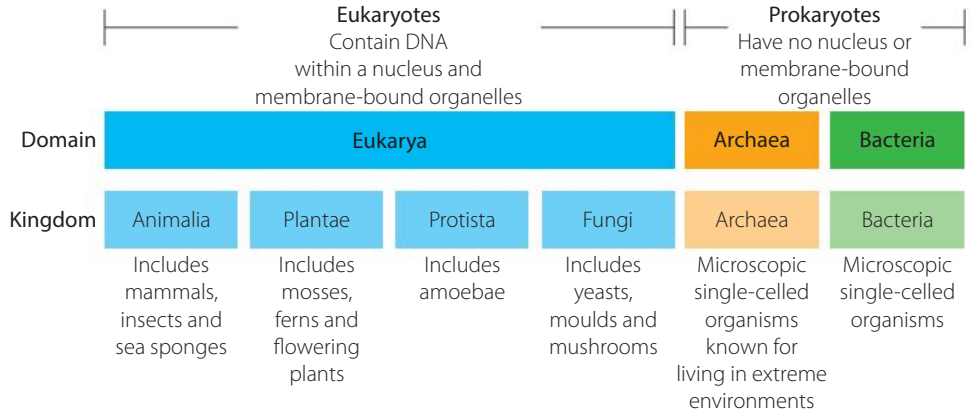

FIGURE 2.2.3 Organisms are classified into three domains on the basis of cell structure (eukaryote/prokaryote) and cell function (Archaea/Bacteria).

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There are four kingdoms in domain Eukarya: Animalia, Plantae, Protista and Fungi. You may be familiar with many of the organisms within these kingdoms. Kingdom Animalia contains all of the animals, including some that are single-celled. Plants (kingdom Plantae) have cell walls that contain cellulose and obtain 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 organisms that are mostly single-celled and live in aqueous environments. Interestingly, taxonomists still debate about how these groups should be divided. The Archaea and Bacteria used to be considered as part of a single kingdom, the Monera, and this terminology is sometimes still used. Other taxonomists have suggested different kingdoms.

Binomial nomenclature

Linnaeus' original work stated that each taxa could only be described with a single Latin word and that the final two levels, genus and species, would be the source of the organism's name. The use of two-part scientific names is called **binomial nomenclature**. To reduce names that were sometimes extremely descriptive down to just two words, Linnaeus relied on the most obvious features. Unfortunately, this heavy reliance on physical characteristics in animals and flower structures in plants resulted in some odd relationships, including grouping together every plant that doesn't have flowers (such as algae and ferns).

binomial nomenclature
a naming system in which each individual is given a two-part name, such as genus and species or first name and surname

KEY SKILLS

Common conventions in nomenclature

- Scientific names are written in italics. The genus is capitalised, but not the species.

  Escherichia coli

- When handwritten, the scientific name is underlined instead of italicised.

  Escherichia coli

- When the full name of a species has already been mentioned, the genus can then be abbreviated to its initial and a full stop.

  First instance: *Escherichia coli*

  Subsequent instances: *E. coli*

- When referring to members of a genus in a general sense, rather than 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*) or *Escherichia* spp. (members of the genus *Escherichia*)

Classification by reproductive methods

eutherian (placental)
a mammal that gives birth to fully developed, or very near fully developed, live young, e.g. dog

Because all living organisms reproduce, their method of reproduction is an important characteristic to use when classifying them. An organism that reproduces sexually, such as kangaroos (Figure 2.2.4) with internal fertilisation and embryos that develop in laid eggs, is quite different from an organism that reproduces asexually by budding. These reproductive differences are used to refine Linnaeus' taxonomy.

Class Mammalia (animals that produce milk for their young and have fur) is separated into three main groups according to where their offspring develop. **Eutherians** (or placentals) give birth to live young after the foetus develops completely inside the mother. Most mammals are included in this group. **Marsupials** give birth to live young at an extremely early developmental stage and the offspring complete their development in a pouch. This group of animals, which are predominantly found in Australia, includes kangaroos, koalas and possums. **Monotremes** are a very small group of mammals whose offspring develop in eggs. This group, only found in Australia, has just two members: echidnas and platypuses.

FIGURE 2.2.4 Many species of animals, including kangaroos, reproduce sexually, though some can reproduce asexually depending on environmental conditions. There is more balance among plant species between sexual, asexual and combined methods.

marsupial
a mammal that gives birth to undeveloped live young, who complete their development in their mother's pouch, e.g. kangaroo

monotreme
a mammal that does not give birth to live young, but lays eggs, e.g. platypus

r/K selection
a form of mathematical classification based on the number of offspring a species produces and the level of parental involvement required to care for them

Another way of classifying organisms is by their behaviour towards their young. Some organisms produce very large numbers of offspring who must survive without parental involvement, while others produce only a handful of offspring who rely on their parents for an extended period of time. This form of classification, called **r/K selection**, stems from mathematical analysis of populations.

Classification by molecular sequences

More recently, the sequences of molecules such as DNA and proteins have also been used to classify organisms. Even though they cannot be directly seen, molecular sequences can be deduced with current biotechnology. Because these sequences are inherited from our ancestors, they can provide clues about whether organisms share an ancestor despite physical differences. Sequences that are more similar show closer evolutionary relationships.

SYLLABUS LINK
Chapter 5 discusses r/K selection in more detail.

DNA sequences

DNA is made up of a sequence of four bases: adenine (A), thymine (T), cytosine (C) and guanine (G). The order of these bases determines the physical and physiological features of an organism. Within a species, there are differences in the order of these bases in individuals, which contributes to individuality. However, these differences are much smaller than the differences in sequence between organisms of different species. By looking at the similarities and differences between DNA sequences, scientists can help to classify organisms.

DNA evidence has been particularly useful to taxonomy when physical evidence is not clear. The classification of the red panda, *Ailurus fulgens* (Figure 2.2.5), was debated for many years. At different points in time it had been considered part of the family Ursidae (bears) and family Procyonidae (raccoons) because it shared physical characteristics with members of both families. DNA evidence has suggested that the red panda is sufficiently different to be considered in its own family, called Ailuridae.

FIGURE 2.2.5 DNA evidence shows that the red panda is neither a bear nor a raccoon. Instead, it is in a family all on its own: family Ailuridae.

INQUIRING FURTHER

The study of DNA similarities is called comparative genomics. This field of science was only invented in 1995, after the first two organisms (both bacteria) had their entire genome sequenced. The impact of genomics on evolutionary theory cannot be understated – it has shown that many apparently similar organisms were not genetically related at all! Learn more about how technology has affected taxonomy and the range of organisms that have now been sequenced.

Protein sequences

amino acid
a simple organic compound that contains both amino ($-NH_2$) and carboxyl ($-COOH$) groups that combine to make proteins

Similar to DNA, protein structure can also be used in classification. Proteins are made up of sequences of **amino acids** and the order of these amino acids can be used to help classify organisms. Table 2.2.1 shows the sequence of the first 38–40 amino acids in the protein cytochrome c for five different animals. Each letter stands for a different amino acid. The sequences of the first four have been stretched (with the dashes) to align with the fifth so that you can compare them. You can see that when an animal has a different amino acid from that in the human sequence, it has been coloured red.

TABLE 2.2.1 The first 38–40 amino acids in the protein cytochrome c. One-letter amino acid codes have been used

SPECIES	AMINO ACIDS			
Human (*Homo sapiens*)	MG— DVEKGK	KIFIMKCSQC	HTVEKGGKHK	TGPNLHGLFG
Chimpanzee (*Pan troglodytes*)	MG— DVEKGK	KIFIMKCSQC	HTVEKGGKHK	TGPNLHGLFG
Emu (*Dromaius novae-hollandiae*)	MG— DIEKGK	KIFVQ KCSQC	HTVEKGGKHK	TGPNLNGLFG
Lamprey (*Lampetra tridentata*)	MG— DVEKGK	KVFVQKCSQC	HTVEKAGKHK	TGPNLSGLFG
Fruit fly (*Drosophila melanogaster*)	MGSGDAENGK	KIFVQKCAQC	HTYEVGGKHK	VGPNLGGVVG

You will notice that the amino acid sequences for humans and chimpanzees are identical. This supports the classification of humans and chimpanzees into the same order (Primates). Humans are less similar to emus than they are to chimpanzees. Thus, although humans and emus are in the same phylum (Chordata), they are in different classes. Emus have four different amino acids in this sequence, supporting their different classification. Fruit flies have 13 different amino acids. This supports the fact that, unlike all the other animals listed, fruit flies are in phylum Arthropoda.

The study of bioinformatics combines mathematical modelling, computer science and biology to compare molecular sequences on a very large scale. The development of specialised computer programs has been very important in enabling scientists to further explore the relationships between organisms.

2.2.1 Classification system

SECTION REVIEW 2.2

REMEMBERING

1 List the eight taxa of Linnaean classification.
2 Outline the four kingdoms in domain Eukarya.
3 List the three different categories of characteristics that are used to classify organisms.

UNDERSTANDING

4 Explain how molecular sequences are used to classify organisms.
5 Give an example of an organism that was reclassified due to reproductive or DNA evidence.

APPLYING

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

2.3 Clades

Common ancestors

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. These slow, incremental changes are referred to as evolution and can result in the formation of new species. Consequently, multiple species can develop from the same common ancestor. The more recently that two species shared a common ancestor, the more closely related they are and the more features they will have in common. When we classify organisms, we are also determining how they are related to one another. For example, two birds within the same genus are more closely related to one another than either bird is to animals in a different class.

common ancestor
a species of organism whose offspring diverged over time

SYLLABUS LINK

Chapter 12 discusses the process of evolution and the relatedness of organisms is discussed in greater detail.

Phylogenetic trees

These relationships can be shown in diagrams called **phylogenetic trees**. Like trees, these diagrams follow a branching pattern. Unlike trees, they are always **dichotomous**, each split having only two branches. You can think of each **extant** organism as a leaf on the tree and each point of divergence representing the most recent common ancestor, who is likely to be but is not always extinct.

Phylogenetic trees are often organised vertically, such as in Figure 2.3.1a,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 2.3.1c 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 the paper more effectively.

phylogenetic tree
a branching diagram showing evolutionary relationships

dichotomous
having two branches, two opposing aspects

extant
currently in existence, not extinct

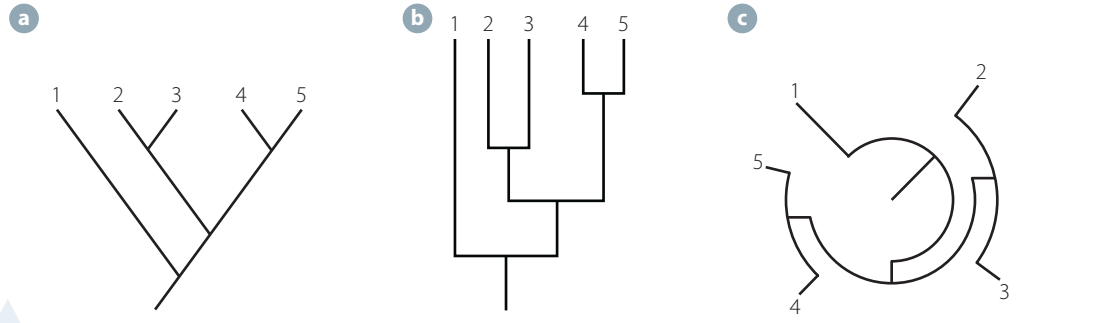


FIGURE 2.3.1 Phylogenetic trees are used to show the relatedness of extant species. This tree is drawn in three ways, showing that species 2 and 3 are closely related and that both of these are more closely related to species 4 and 5 than to species 1.

Clades

With the acknowledgement of common ancestors, taxonomists required a new word to refer to all of the descendants of a particular ancestor organism. In Scottish culture, the descendants of a particular person are called a clan, with Clan McDonnall indicating all of the descendants of McDonnall. In taxonomy, this particular grouping of all of the descendants of an organism is called a **clade**.

Figure 2.3.2 shows the types of groupings that can be considered a clade and those that cannot. Remember, a clade is *all* of the descendants, not just some.

clade
a group comprising all of the descendants of a particular ancestor organism

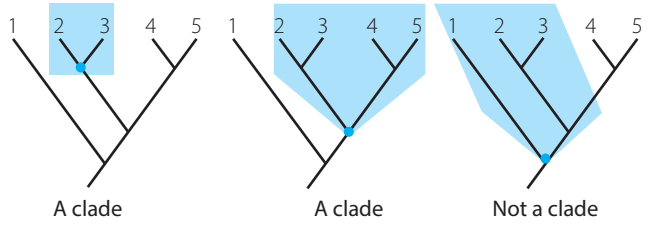


FIGURE 2.3.2 Groupings must include all descendants of a single ancestor to be considered a clade.

SECTION REVIEW 2.3

REMEMBERING

1 Define:

- **a** clade
- **b** common ancestor.

2 Describe how the orientation of a phylogenetic tree aligns with the passage of time.

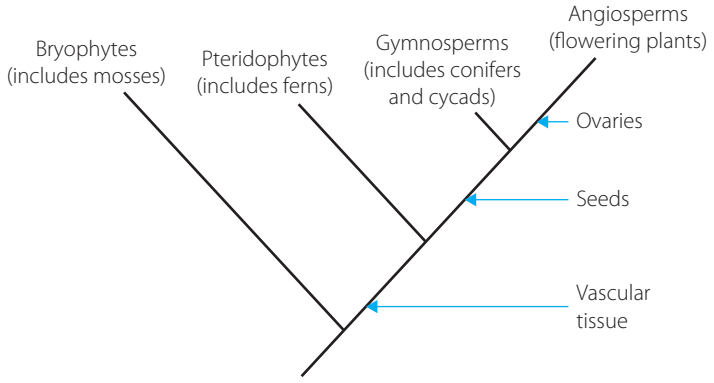
UNDERSTANDING

3 Draw your family tree from your grandparents to you. Explain how this tree is different from a phylogenetic tree.

APPLYING

4 In Figure 2.3.3, explain why there is only one possible clade that includes the bryophytes and yet every possible clade includes the angiosperms.

FIGURE 2.3.3 At each branching point, some of the offspring of the ancestor developed a new feature, while others did not. This evolution of features has created a wide, but interrelated, variety of life on Earth.



2.4 Cladistical methods of classification

Phylogenetic trees are known as **cladograms** when they are constructed by a technique called **cladistics**. Cladistics is the term used for the construction of clades, which requires taxonomists to correctly identify all of the descendants of a particular ancestral species. Due to the uncertain nature of an organism's evolutionary history, most cladograms are considered 'best guesses' and can be disputed among taxonomists.

cladogram
a phylogenetic tree in which all organisms are grouped according to their most likely evolutionary relationships

cladistics
a taxonomic technique that arranges organisms by clade

Cladistics relies on three assumptions.

1 Because all life evolved from a single ancestor, any group of organisms will share a common ancestor at some point in the past.

2 The offspring of an ancestral species diverge dichotomously in a process called cladogenesis.

3 Organisms become increasingly different as they continue evolving from their point of cladogenesis.

The first assumption supports the development of cladograms in the first place. It implies that all organisms are related in some way and that, importantly, we can map that relationship.

The second assumption is a point of contention within the field of taxonomy. It suggests that all speciation events (where a new species develops) are singular splits, that the new generation of a particular organism will either be the same as their parent generation (**plesiomorphic**) or different in only one way (**apomorphic**). Instances where the new generation contains more than one difference significant enough to denote a separate species are extremely rare and often accumulate over time.

plesiomorphic
having characteristics or traits that are common among their evolutionary relatives but are not unique to their clade; e.g. members of class Reptilia usually have legs as do many organisms not in class Reptilia

apomorphic
having a characteristic or trait unique to a particular group of organisms that is different from their evolutionary relatives, e.g. snakes, in class Reptilia, have no legs

The third assumption is a tenet of evolutionary biology, which states that organisms that share more characteristics are likely to be more closely related. This allows for organisms that share characteristics to be grouped separately from organisms that don't share that characteristic. When there are multiple possible ways that organisms can be related, the simplest explanation is the most likely to be correct, because it is more likely that a feature evolved once in a common ancestor rather than evolving independently for each organism.

SECTION REVIEW 2.4

REMEMBERING

1 Summarise the three assumptions of cladistics.

UNDERSTANDING

2 Explain why cladograms are considered best guesses.

3 The vast majority of offspring for a species are plesiomorphic. Explain why this is so.

APPLYING

4 Mistakes happen when scientific developments and 'truths' are taken out of context. Understanding the underlying assumptions of scientific developments and methods enables us to apply them reasonably. Given its assumptions, outline one limitation of cladistics as a method of grouping organisms.

2.5 Interpreting cladograms

character matrix
a table of characteristics used for classification

In order to correctly interpret cladograms, you need to understand how they are constructed. The first step is to create a table of the characteristics, known as a **character matrix**, to be used for classification. These characteristics can be physiological, reproductive or molecular in nature. Within the character matrix, each characteristic is assessed as present or absent in the organism or group of organisms. Table 2.5.1 shows a completed character matrix for the four major plant groups.

TABLE 2.5.1 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 second step is to take the character matrix and determine how the organisms or groups of organisms can be assembled into clades. Clades must share a common ancestor and must include all descendants of that ancestor. For example, the first clade that can be made with Table 2.5.1 contains all of the plants that can perform photosynthesis (all groups). Another clade can be made with all of 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 that can be made include plants that make seeds (both 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.

node
a point in a diagram where lines branch or intersect

Figure 2.5.1 shows the cladogram for the major plant groups. It begins with the common ancestor for all groups, which must have performed photosynthesis since all of the groups share that characteristic. At the first point of cladogenesis, some of the descendants of this common ancestor developed an apomorphy (vascular tissues) and some remained plesiomorphic (without vascular tissues). The plesiomorphic branch has remained very similar to the ancestral species. This group of plants is the bryophytes and they include the mosses and liverworts.

2.5.1 How to make a cladogram

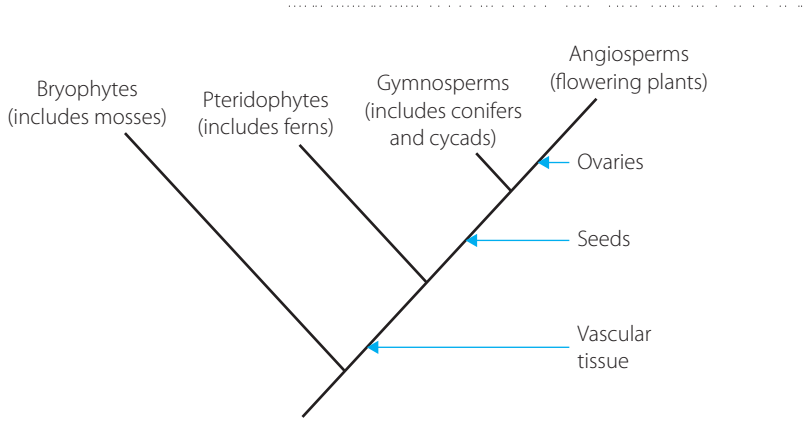


FIGURE 2.5.1
Cladograms are constructed by arranging the clades in order from most organisms in the clade to fewest organisms in the clade.

The second point of cladogenesis occurs in the vascular tissue descendants. Some of the offspring develop an apomorphy (seeds), while some remain plesiomorphic. These plesiomorphic plants are the pteridophytes, which include the ferns. The third point of cladogenesis occurs in the seeded descendants, when some of the offspring develop another apomorphy (ovaries) and some remain plesiomorphic. The seeded plants are known as gymnosperms (including conifers and cycads), while the plants with ovaries are called angiosperms and include all of the flowering plants.

INQUIRING FURTHER

According to the fossil record, the first flowering plants developed ovaries around 130 million years ago. An apomorphy on this scale has not happened since. Research the timeline of plant evolution to determine how much time passed between each point of cladogenesis in Figure 2.5.1.

SECTION REVIEW 2.5

REMEMBERING

1 List the two words used in completing a character matrix.

2 Describe what the nodes in a cladogram represent.

UNDERSTANDING

3 Explain why the relationships between the major plant groups shown in Figure 2.5.2 is not a likely option compared to Figure 2.5.1.

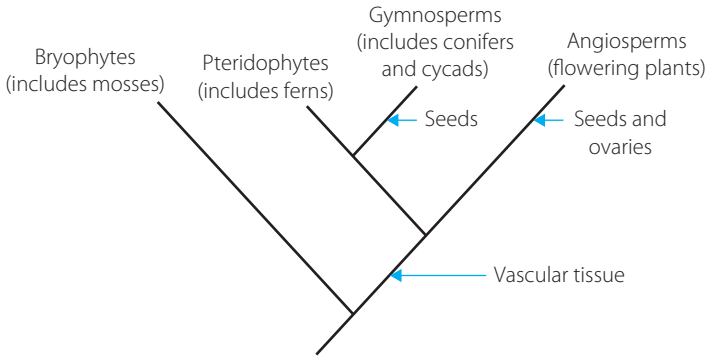
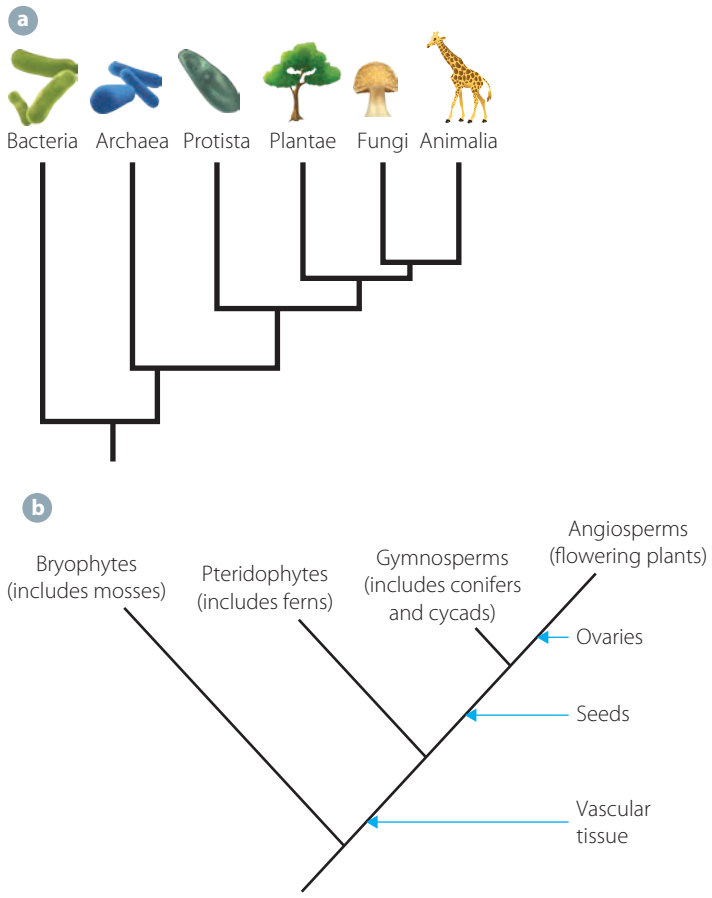


FIGURE 2.5.2 Alternative cladograms, such as this, are possible but are often unlikely.

4 Explain the evolutionary relationships shown in Figure 2.5.3.

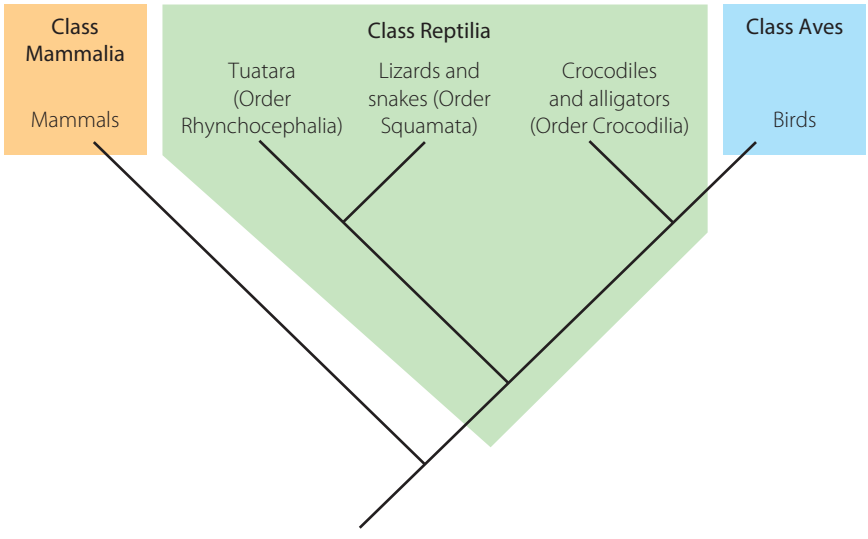
FIGURE 2.5.3
Continued research into comparative genomics allows us to better understand the relationships between life forms on Earth.



APPLYING

5 Figure 2.5.4 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.

FIGURE 2.5.4
Some scientists dislike that class Reptilia is not a clade and have argued for its reclassification.



9780170411677

2.6 Species' evolutionary relatedness

Different organisms share **molecular homologies** as well as structural ones. Both DNA and RNA possess a four-base code that provides the basis for all life; 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 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

Protein conservation

Proteins, and the alleles that encode them, are subject to the same process of evolution by natural selection as the larger traits that individuals possess. A protein that is well suited to its function will be **conserved** through time, while other traits around it may evolve. This is because mutations in this well-suited protein are more likely to hinder its function than improve it, and individuals with the hindered protein will not survive as well as those with the better version. Natural selection is more likely to ignore mutations in proteins that are not so vital to success.

conserved sequence
a DNA or protein sequence that is preserved across species due to optimal function

Since protein sequences that are efficient and effective are generally conserved through time, 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 over time, 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 all of the time. 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 fail to be 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 the vast majority of eukaryotic organisms. Figure 2.6.1 shows part of the sequence for histone H1 in five different mammals. The level of conservation is extremely high; only a few amino acid **residues** are different. The human and chimp 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 chimp 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

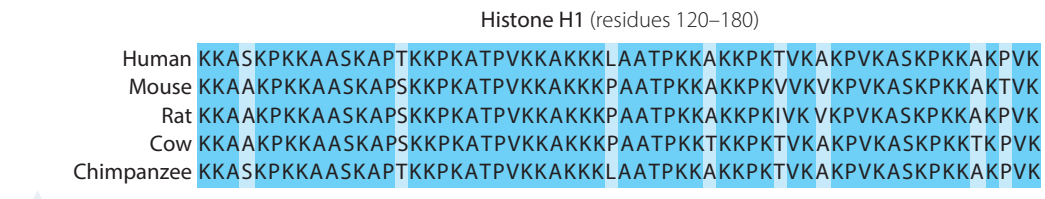


FIGURE 2.6.1 Histone H1 is a common example of protein conservation, given its vital role in the storage and access of DNA. Residues 120–180 are shown here. One-letter amino acid codes have been used.

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 is fairly constant within a species and is called the **mutation rate**. When comparing the genomes of two species, the mutation rate can be used as a molecular clock (section 2.7) 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

Molecular phylogeny

The comparison of genome sequences of different species or individuals gives a very broad picture of DNA sequence conservation and mutation frequencies, making it possible to trace evolutionary processes responsible for the divergence of two genomes. However, this produces huge amounts of data that must be stored and analysed in a logical and meaningful way. Only very recently has it become possible to undertake these analyses, due to advancements in computer science, engineering and mathematics via **bioinformatics**, which has dramatically increased the size, accuracy and scope of data sets, such as those needed for comparative genomics.

bioinformatics
the digital storage, retrieval, organisation and analysis of biological data (e.g. genomic); it is especially important in genomics research because of the large amount of complex data this research generates

molecular phylogeny
the study of evolutionary relationships using comparative genomics

These sequences can be used to build another version of a phylogenetic tree by a technique called **molecular phylogeny**, which is based on the evolution of a single gene or set of genes rather than a species (Figure 2.6.2). For example, the genes that code for 'building eyes' on vertebrates such as humans, called *PAX6*, are more than 78% similar in their protein arrangement to those responsible for building the eyes of an octopus. The similarities in sequence, function and abundance of these genes across a broad spectrum of phyla are yet another example of homology, in this case at a molecular level. It is possible to conclude that as descendent lineages evolved, the *PAX* genes were modified in a variety of ways, giving rise to the diversity of eye-building genes seen in modern animals.

SYLLABUS LINK
Chapter 12 discusses bioinformatics in more detail.

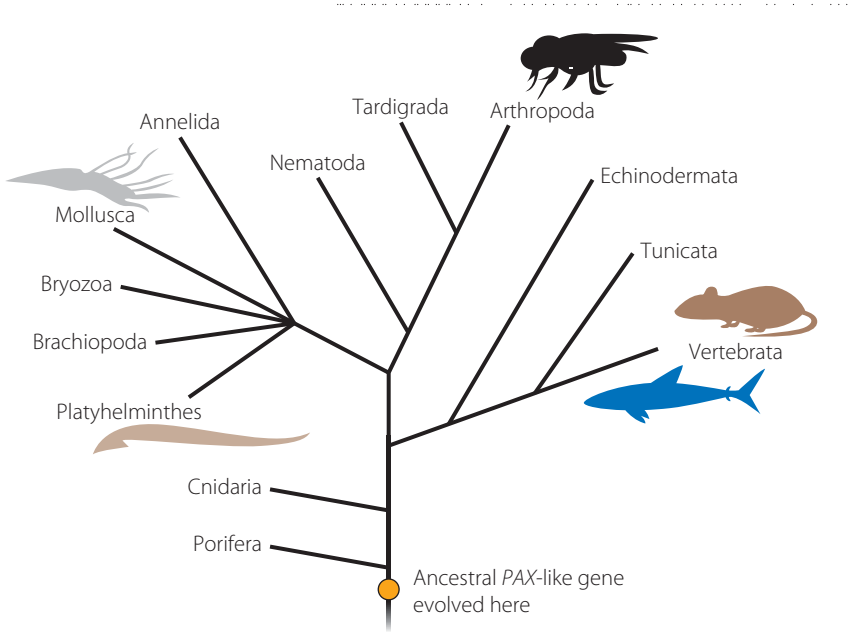


FIGURE 2.6.2
Comparative genomics has found similarities in eye-building genes across all animals with eyes. From this, molecular phylogeny has produced an evolutionary phylogenetic tree.

PRACTICAL ACTIVITY 2.6.1

Data analysis: the molecular clock

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 as a result of fossil records or 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.

2.6.1 The molecular clock and estimating species divergence

QUESTIONS

Short items

1 What is a molecular clock?

2 Why are molecular clocks useful?

3 Construct a formula for calculating the base rate of mutation, based on the second paragraph of the background information.

Calculations

4 Calculate the base rate of mutation for the two species in Table 2.6.1.

TABLE 2.6.1 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	GDVEKGKKIFIMKCSQCHTV
Primates	GSAKKGATLFKTRCLQCHTV

5 Estimate the date of divergence for humans and chimpanzees, using the sequences in Table 2.6.3 and the base rates in Table 2.6.2.

TABLE 2.6.2 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 2.6.3 DNA sequences for human and chimpanzee in non-coding area. One-letter amino acid codes have been used

SPECIES	DNA SEQUENCE
Human	ATGTATCCAGGTAGTGGACGTTACACCTACAACAACGCTGGTGGTAATGG
Chimpanzee	ATGTTTCGAGGTAGTGGTCGTTAGAACTACTACAAGGCTGGTGGTAATTG

Interpreting data

6 Comment on differences between the base rate of mutation for cytochrome c and the approximate base rates of mutation for DNA.

7 Explain whether your estimate of the date of divergence for humans and chimpanzees in Question 5 is reasonable, in light of the date of divergence for primates and yeast and your own knowledge.

Responding to new stimuli

8 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%, outline three limitations of the method that contribute to such enormous uncertainty.

SECTION REVIEW 2.6

REMEMBERING

1 Define 'comparative genomics'.

2 Give an example of a neutral mutation.

UNDERSTANDING

3 Explain why histones are a good candidate for molecular sequence conservation.

4 Outline how mutation rate could be used to determine how long ago two species diverged.

APPLYING

5 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 from residues 195–211 of LDH from a number of organisms have been sequenced, as shown in Table 2.6.4. Use this data to infer the evolutionary relationships of the organisms. You may like to summarise your findings in a phylogenetic tree.

TABLE 2.6.4 LDH sequences (residues 195–211) from seven organisms. One-letter amino acid codes have been used

ORGANISM	LDH SEQUENCE (RESIDUES 195–211)
1	GDQVQCFCCGGKLKNWE
2	GDQVQCFCCGGKLKNWE
3	DDQVQCFCCGGKLKNWE
4	RDHVKCFHCDGGLRNWE
5	LDHVKCVWCNGVIAKWE
6	DDQVQAFCCGGKLKNWE
7	DDNVQCFCCGGGLSGWE

2.7 The need for multiple definitions of species

Biological species concept

In general terms, a species is an interbreeding 'kind'. In biological terms, a species is a group of organisms whose members have the potential to interbreed in nature and produce viable, fertile offspring. This **biological species concept** was proposed by Ernst Mayr around 1942. Most importantly, individuals within a species are reproductively isolated from individuals not belonging to that species. This definition has one very important link to the processes of evolution. Current models suggest that speciation occurs when populations of individuals become unable to naturally interbreed.

biological species concept
the definition of a species based on the capacity of individuals to interbreed

Limitations of biological species concept

While the biological species concept worked well before the development of genetic analysis, there are a number of problems in using this definition now. For example, it is not possible to apply it to fossils of extinct organisms, because it is impossible to really know which individuals could interbreed with another or whether physical differences between specimens denote new species or can be attributed to individual variation.

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 individuals from two different species interbreeding. They generally do not survive well outside restricted hybrid zones and generally do not displace either of the parent species, but they do play an important role within the ecosystem. The existence of hybrids offers evidence that the parents are actually of a single species, since they can clearly interbreed, even though all other markers indicate different species.

hybrid
an organism resulting from the interbreeding of two different species

For example, following the loss of ice sheets in Arctic regions, polar bears have been driven into the more forested regions of Canada where grizzly bears live. Occasionally they interbreed to produce a polar–grizzly bear hybrid. These have been called grolar bears (and some are half grizzly, half grolar; or half grolar, half polar), and seem to survive quite well in the wild. But they do not displace either of the polar bear and grizzly bear parental populations. Strictly speaking, this would make grizzly bears and polar bears the same species because they can interbreed to produce viable, fertile offspring. Yet, there are so many other physiological and behavioural differences that do not fit with this model.

morphological species concept
the definition of a species based on physical characteristics

Other species concepts

When examining fossils, the **morphological species concept** is most commonly applied. This concept characterises a species by its form, or morphology. In the case of the human family tree, it is most often the skull that is best preserved and identified morphologically. However, scientists often disagree about which morphological features should be used, and when the features are sufficiently different to justify the creation of a new group.

SYLLABUS LINK
Chapter 14 also discusses the morphological species concept.

The **phylogenetic species concept** identifies a species as being the smallest clade, or smallest group of organisms who can all trace their origins to a single common ancestor. This is an important feature of all classification systems used today, which are based on cladistics. For example, all members of the species *Homo sapiens* have a common ancestor that existed around 200 000 years ago, while domesticated dogs of the species *Canis familiaris* have a common ancestor that existed around 15 000 years ago. Application of the phylogenetic species concept to extant organisms increasingly uses genetic techniques, and most phylogenetic trees produced today are based almost solely on these.

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

SECTION REVIEW 2.7

REMEMBERING

1 Define the three different species concepts.
2 Which species concept is most useful for fossil classification?
3 Give an example of a hybrid species.

UNDERSTANDING

4 Summarise two limitations of the biological species concept.
5 Explain why the phylogenetic species concept has not replaced the other two concepts as yet.

APPLYING

6 The argument has been made for reclassifying the species *Canis familiaris*, because without human intervention, individuals from several of the smaller breeds would be physically incapable of interbreeding with individuals from the larger breeds. Opponents cite the biological species concept as stating that any individuals who can produce viable, fertile offspring belong in the same species regardless of how unlikely it may be in the wild. Make your own case for or against the reclassification, citing your own evidence.

2.8 Infertile species

In general, species mate with their own species and produce fertile offspring. Species are often prevented from interbreeding by physical incompatibility or behavioural differences, such as nocturnalism or intricate mating rituals. In most cases where species are similar enough in appearance and behaviour to mate, this mating either does not produce offspring or produces infertile offspring that cannot pass on their genes. In some cases, hybrid offspring are fertile, such as with the grizzly–polar bear hybrids (Figure 2.8.1). Classification of fertile hybrids is a sore point of contention in taxonomy.

FIGURE 2.8.1 As global warming forces polar bears from the Arctic into mainland Canada, their encounters with grizzly bears leave behind hybrid offspring. These are fertile because both bear species have 74 chromosomes.

Horse–donkey hybrids

Often when two species mate, their offspring are no more or less suited for survival and they pass away after their lifespan, taking their hybrid genes with them. However, some hybrid species feature the best strengths of their parents and are better suited to human use than either of their parent species. This is the case with horse–donkey hybrids called mules (Figure 2.8.2).

Mules are produced when a female horse is impregnated by a male donkey. Female donkeys impregnated by male horses produce hinnies, but hinnies are harder to bring to term. Mules have the size and carrying capacity of a horse, but are considerably stronger and more resilient. They have the endurance and tenacity of a donkey but are considerably more affectionate and easier to train. They require less food and less attention, and are more resistant to sunburn, insect bites, injury and equine disease than either of their parents. In short, mules are a super-equine, that unfortunately are infertile.

FIGURE 2.8.2 Mules are infertile because their parents have different numbers of chromosomes.

Horses have 64 chromosomes ($n=32$) and donkeys have 62 ($n=31$). Owing to the differences in chromosome numbers, when these two species form a **zygote**, it will have 63 chromosomes. The odd number of chromosomes renders them generally unable to successfully form gametes through meiosis. Without successful gametes, mules cannot produce offspring and must be purposely bred from horse and donkey stock.

zygote
the first cell of a new individual, which is formed by fusion of a sperm and ovum at fertilisation

INQUIRING FURTHER

Research the differences between a horse, donkey, mule and hinny. Recommend which would be most suitable for agricultural/farming use in Australia. Give reasons for your recommendation.

SECTION REVIEW 2.8

REMEMBERING

1. Define 'hybrid'.
2. Give an example of a hybrid species that is infertile and a hybrid species that is fertile.

UNDERSTANDING

3. Explain why mules are infertile.
4. Use an example organism to explain how behavioural differences may inhibit interbreeding.

APPLYING

5. Unlike animals, many plant species can produce fertile hybrids. Bread wheat (*Triticum aestivum*) accounts for 95% of global wheat production and has two sets of chromosomes from each of three different species of wild grass, *Triticum urartu, Aegilops speltoides* and *Aegilops tauschii*. This type of genetic mix-and-match is not uncommon in the plant world. Suggest why plant species are generally fertile, considering this example.

2.9 Species interactions

symbiosis
a relationship between individuals of two or more species in which at least one organism benefits from the interaction

Hybrids are not the only result of different species interacting. Competition, symbiosis, predation and disease are all species interactions that have wide-ranging effects on their ecosystems. For example, imagine what a necklace of parasites could do to a carpet python or what would happen to a karri forest if the fungus it depends on for survival died. Understanding the relationships within and between species can help us understand how an ecosystem works and how we may be able to classify it.

Competition

2.9.1 Species interactions and competition

prey
an organism that is hunted by another organism for food

Many species compete with each other because they require the same resources to fulfil their needs for survival. Competition within and between species is a common feature of all communities. For example, seemingly harmless sea anemones compete with other anemones for the same food source. Both rivals discharge a battery of stinging cells, normally used to paralyse and catch prey (Figure 2.9.1). Eventually, one will be defeated, close up and creep away.

FIGURE 2.9.1 Sea anemones compete for food and oxygen by defending their territory from invading anemones. Their stinging cells deter rivals from creeping within reach.

Symbiosis

Symbiosis is the general term used to describe the relationship in which at least one species benefits from the interaction. There are three main types, depending on the relative benefits and drawbacks:

- parasitism: one species benefits at the expense of the other
- commensalism: one species benefits and the other is neither benefited nor harmed
- mutualism: both species benefit from the interaction.

2.9.2 Symbiosis: mutualism, commensalism and parasitism

INQUIRING FURTHER

Research the effect that coral bleaching is having on symbiosis in the Great Barrier Reef. Predict what may happen to this ecosystem if coral bleaching does not stop.

Predation

One of the most common and overt interactions within an ecosystem is predation. In this relationship, one organism, the predator, kills another organism, the prey, or consumes part of it for its food. Although predators usually have a preferred prey species, it is unusual for a predator to depend on only one species. If one prey species becomes scarce, the predator can turn to others.

The dynamic relationship that exists between predator and prey (Figure 2.9.2) 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, although it usually still remains far below that of the prey. During a period of adverse conditions, the prey population can decrease. When this occurs, there is increased competition within the predator population. Predators turn to alternative prey species and the effect on them can be severe, though it does allow the original prey population to grow again.

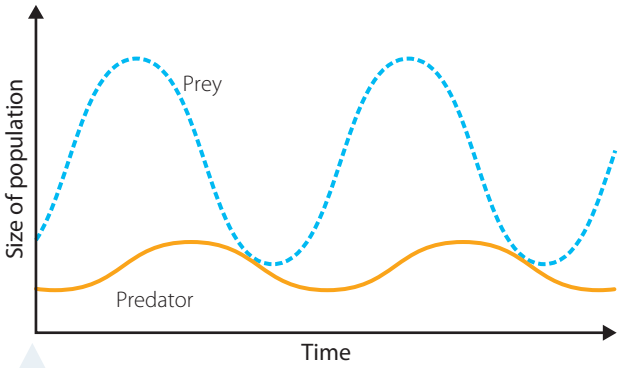


FIGURE 2.9.2 Predator populations are always smaller than their total prey population because a decrease in the availability of prey will result in the starvation of the less healthy predators.

Predation of any sort affects the prey population in an ecosystem. Predation includes animals preying on other animals, plants preying on animals, such as the Venus flytrap or pitcher plants or animals preying on plants (herbivorous predation). For example, seed predators have a large effect on the plant population and their distribution throughout an ecosystem. These animals only feed on the seeds of plants, causing the seeds to become unviable or damaged. Another example of the effect of predation on the biodiversity of an ecosystem is the release of nutrients into the soil from decomposing animal carcasses left behind by predators, which allows for micro-organisms to survive in the ecosystem.

SYLLABUS LINK

Chapter 3 discusses food chains and predator–prey cycles in more detail.

Disease

One of the most overlooked interactions in an ecosystem is that between a disease-causing organism and its **host**. Disease-causing organisms are called **pathogens** when they damage or kill to their host and **parasites** when they leave their host alive, if unwell. For example, the myxoma virus causes myxomatosis, a disease that affects rabbits. In Australia, this virus was successfully introduced to control the rabbit population to allow native animal populations to survive alongside them. Disease can also devastate native populations. Chlamydia is a disease affecting the populations of koalas across Australia. It affects the reproductive tract of the koala, resulting in the failure to produce offspring. In a species that produces few offspring as it is, this has led to a steep decline in koala numbers and genetic diversity.

host
an organism that is infected with a pathogen or parasite

pathogen
an organism that causes disease, resulting in damage or death, such as a bacterium or virus

parasite
an organism that causes long-term disease while leaving the host alive, such as protozoa and worms

PRACTICAL ACTIVITY 2.9.1

Data analysis: Classifying and naming ecosystems

INTRODUCTION

In 1970, Raymond Louis Specht, then Professor of Botany at the University of Queensland, developed an ecological classification system that finally made it practical to account for the variation in Australian landscapes. His system relies on just two factors, the size of the tallest vegetation present and the approximate area that the foliage of this vegetation covers. This was a major improvement on previous systems that required ecologists to identify the particular species of plant that was most abundant and combine that with soil and rainfall data to arrive at a conclusion.

Table 2.9.1 is key to Specht's classification system. Several useful definitions were that trees usually had a single trunk, while shrubs often had multiple stems emerging at ground level, as well as the differences between hummock grasses, tussock grasses and sedges (Figure 2.9.3).

FIGURE 2.9.3 (**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.

TABLE 2.9.1 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

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QUESTIONS

Short items

1 Describe Specht's classification system.

2 Explain how his system was a practical improvement on earlier systems.

3 Using Table 2.9.1, name an ecosystem whose tallest vegetation was 2–3 m shrubs that covered 40% of the land area.

Interpreting data

4 Categorise the ecosystem in Figure 2.9.4. Justify your decision.

FIGURE 2.9.4 Low rainfall limits biodiversity in this area.

5 The ecosystem in Figure 2.9.5 could be categorised in a number of different ways from the information given. Explain why Specht's classification system is not able to be decisive in this case.

FIGURE 2.9.5 Greater biodiversity exists in areas of high rainfall, such as this area in the mountains.

FIGURE 2.9.6 Australia is often defined by the sudden changes in the landscape. This scene shows three different ecosystems all in the same frame.

6 Categorise the three areas in Figure 2.9.6 and justify your decisions.

7 Comment on how sure you are of your classification of each of the ecosystems in Figure 2.9.6.

Responding to new stimuli

8 When naming ecosystems, it is often useful to be a little more specific than Specht's system allows. Modifications to Specht's system include adding the genus or common name of the tallest vegetation. For example, three different forests could be described as a mountain ash forest, a casuarina forest and a eucalypt forest. Describe two benefits that this modification provides for ecology.

SECTION REVIEW 2.9

REMEMBERING

1 Briefly outline the four species interactions.

2 Give one example of competition within a species and one example of competition between two species.

UNDERSTANDING

3 Explain why predator and prey populations follow a predictable and repetitive cycle, as in Figure 2.9.2.

4 Use an example to explain how disease can be an important factor in shaping the biodiversity of an ecosystem.

APPLYING

5 African acacia varieties are often plagued by beetle grubs that destroy their seeds and prevent them from germinating by themselves. This could have had dire consequences for the trees, if not for elephants. Many animals, including elephants, feast on their fruits, but elephants don't chew their food very much so their dung contains a great deal of fibrous matter, including whole, beetle-free acacia seeds. On average, 90% of acacia seeds deposited in elephant dung will germinate. Construct a diagram showing the relationships between acacia trees, beetles and elephants.

2.10 Classification and ecosystem management

SYLLABUS LINK

Chapter 1 discusses abiotic and biotic factors, as well as how these are limiting to organisms in an environment.

Over time, ecology has become a more exact science by using quantitative data measurements and developing models and theories that define the relationships between organisms. Today, ecologists use both qualitative and quantitative data to classify habitats based on their abiotic and biotic factors, such as the organisms present and their interactions with each other. The range of organisms living in a habitat is influenced by the limiting abiotic and biotic factors present.

Ecosystems are then classified according to the various habitats from which they are composed. Classification in this way is most often used to inform environmental management strategies and protection plans.

Terrestrial habitats

terrestrial of land

The distribution of **terrestrial** habitats such as tundras, deserts, open forests and temperate grasslands is based mainly on climatic variation (Figure 2.10.1). Temperature, water, light and wind are the four main elements of climate. Both water and temperature significantly affect the range of organisms that can live in an environment. For example, the climate of the desert differs considerably from that of a tropical rainforest and understanding these differences is the first step in appropriate ecological management.

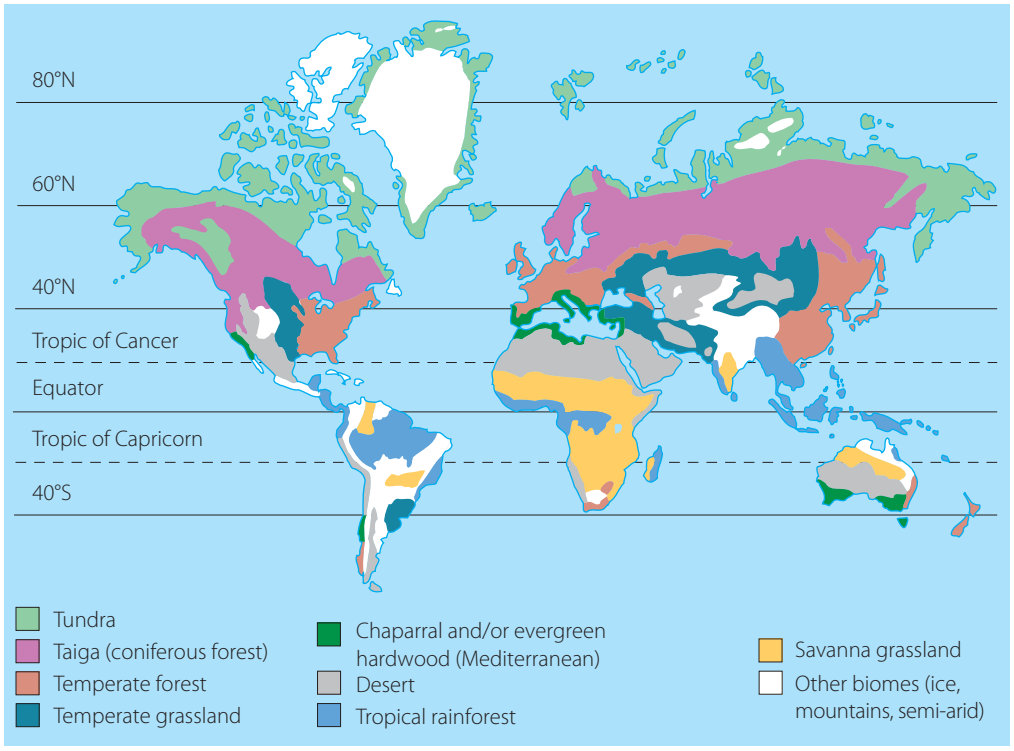

FIGURE 2.10.1 The world's major terrestrial ecosystems are called biomes.

Both deserts and rainforests are generally found close to the equator where the climatic conditions are more intense. Temperatures range widely in the deserts, from below 0°C overnight to above 40°C during the peak of the day, while they remain quite stable in the rainforest, between 20°C at night and 35°C during the day, year round. Rain is generally unpredictable and infrequent in the deserts, with less than 250 mm of precipitation annually, while rainforests commonly receive between 1500 and 2500 mm. However, both habitats are characterised by poor soils. Phosphorus and nitrogen, which nourish plant life, are present in the soil in considerably lower concentrations in the desert than elsewhere, due to a lack of organic detritus called **humus**. In rainforests, the humus and its nutrition are washed through the soil into the water table from the frequent precipitation, leading to characteristically poor soil.

humus
the dark brown organic matter in soil, derived from decomposed plant and animal remains

The biotic factors of deserts and rainforests are very different. Limited numbers of species are found in an Australian desert, including small mammals such as the spinifex hopping mouse (*Notomys alexis*) and the numbat (*Myrmecobius fasciatus*), invertebrate herbivores such as grasshoppers and crickets, and mulga trees (*Acacia aneura*). However, rainforests support nearly 50% of all terrestrial animal and plant life on the planet. The biodiversity of each habitat depends on the severity of the limiting abiotic factors that define it.

Aquatic habitats

Aquatic habitats include both **marine** and freshwater environments and make up the largest part of the biosphere. The oceans alone cover 71% of Earth's surface. Aquatic environments include the moving waters of oceans, bays, estuaries, creeks, streams and rivers, and the still waters of lakes, ponds and swamps.

aquatic
of water

marine
saltwater

Marine habitats are classified according to depth, distance from the shoreline and the way they are formed. The first 200 m of ocean depth is known as the **photic zone**. This is the only part of the water that light can penetrate and accommodate photosynthesising organisms. The temperature ranges from approximately 34°C to 10°C as the depth increases. Approximately 90% of marine life lives in the photic zone.

photic zone
the first 200 m of ocean depth

The deeper you go, the colder and darker it gets, and below about 1000 m, the water is near freezing and no light penetrates at all (Figure 2.10.2). The pressure also increases from regular air pressure at sea level to 100 times this pressure at 1000 m. The bottom of the deepest trench in the ocean is nearly 11 km below sea level and experiences 1000 times the pressure. These abiotic factors severely limit the distribution of marine organisms.

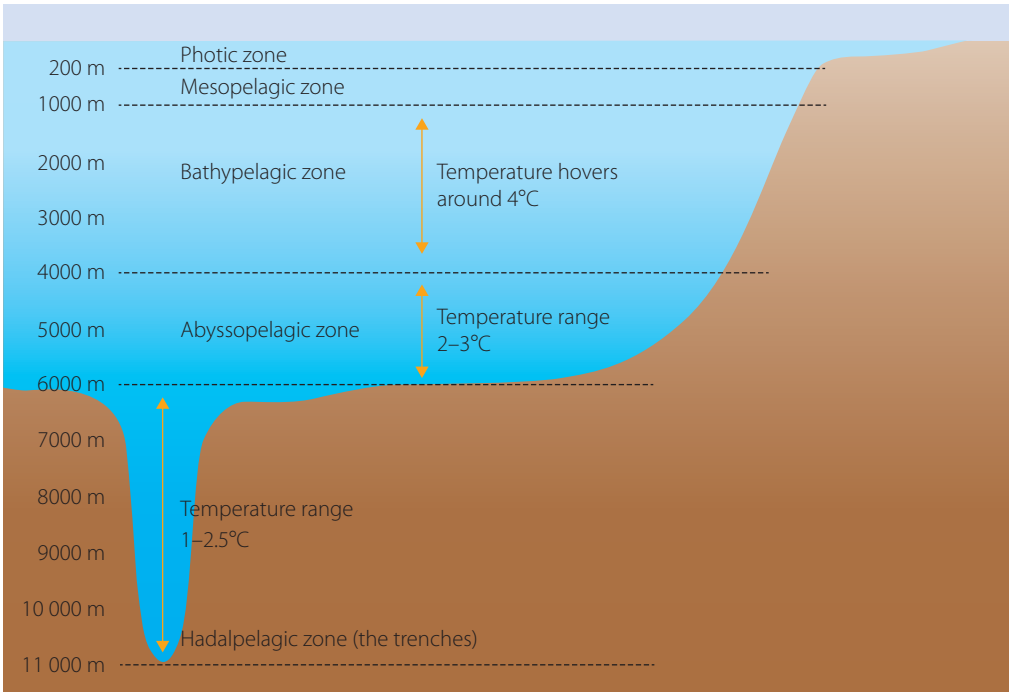

FIGURE 2.10.2 As ocean depth increases, water temperature and available light decrease, while pressure increases. This was originally thought to limit ocean life to the top few kilometres, but strange new deep ocean organisms are being discovered every day.

INQUIRING FURTHER

Research one deep ocean organism discovered off the oceans of Australia; for example, faceless fish, giant sea spiders and blobby sea pigs. Discuss how the organism has adapted to live in the deep ocean.

eutrophication the increased concentration of nutrients, such as phosphates and nitrates, in a waterway that promotes algal bloom

Freshwater environments have two subgroups: standing and moving bodies of water. Deep lakes are also characterised by depth and can be divided into photic and aphotic zones. Freshwater environments are classified according to the production of organic matter. For example, large, deep rivers tend to be nutrient-poor whereas shallow lakes tend to be nutrient-rich but lend themselves to **eutrophication**. The resulting algal bloom can reduce light penetration and oxygen concentration, causing negative effects on local species living in shallow lakes.

Estuaries differ from other aquatic environments in that they have fluctuating salt concentrations. During a high tide, the salt concentration increases to be almost equal to that of the ocean (around 3%) and decreases as the point of low tide approaches. As you move up the estuary, the salt concentration nears that of fresh water (around 1%).

2.10.1 Convention concerning the protection of the world cultural and natural heritage

Managing ecosystems

Australian terrestrial ecosystems are named according to Specht's classification system and then modified with the common name or genus name of the dominant species. This allows ecologists

to group similar ecosystems and habitats for study. For example, Antarctic beech forest is an endangered habitat in eastern Australia. Only a few small pockets of forest are left, and by grouping these areas for study with similar areas in Chile and New Zealand, researchers from all over the world are able to collaborate on its protection. By classifying habitats such as old growth forests and coral reefs, management policies and procedures can be tailored more specifically to the needs of the habitat.

2.10.2 Report on the review of the first five years of Australia's Biodiversity Conservation Strategy

International organisations such as UNESCO have conventions and agreements to protect local, regional and international biodiversity. Research one or more of these agreements and discuss why it is important to protect and maintain global biodiversity

SCIENCE AS A HUMAN ENDEAVOUR

The Australian Government set a 20-year strategy to conserve and protect Australia's biodiversity. Read the review of the first 5 years of the project and suggest ways that the strategy could be improved for the next 5 years.

SCIENCE AS A HUMAN ENDEAVOUR

SECTION REVIEW 2.10

REMEMBERING

1 List two terrestrial biomes and an aquatic biome.

2 Outline three abiotic factors that influence the range of organisms living in a rainforest.

UNDERSTANDING

3 Explain the distribution of ecosystems in Figure 2.10.3.

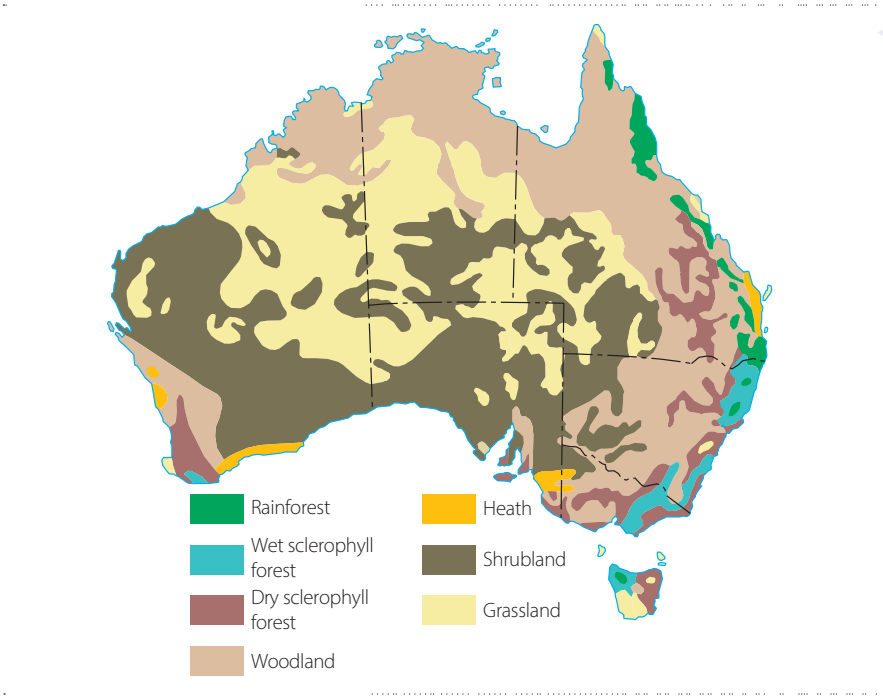

FIGURE 2.10.3 Key vegetation categories form patterns across the Australian continent.

4 Use an example to explain how rainfall can both help and hinder an organism.

APPLYING

5 Koalas (*Phascolarctos cinereus*) are classified as a vulnerable species, with several threats to their survival. These include the continued epidemic of *Chlamydia* infections that cause infertility, loss of eucalypt forest as a habitat and food source and fatal encounters with vehicles while travelling between eucalypt pockets. Outline a potential management plan to preserve the koala population.

2.11 Stratified sampling

stratified sampling
a statistical sampling technique that divides an area into strata for separate sampling

stratum
a layer or subsection of a whole

In ecology, gathering data about an entire population is difficult and statistical sampling techniques must be employed to form accurate estimations. **Stratified sampling** is a statistical sampling technique used primarily for ecosystems or ecoregions that comprised a wide variety of subsections and habitats. 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.

Stratified sampling can be used to accurately estimate population size, density and distribution over an area, as well as to identify and define environmental gradients and habitat zones. To begin, an area is divided into relatively homogeneous subsections called **strata** (singular: stratum). The entire area to be analysed must be divided completely and neighbouring strata cannot overlap (Figure 2.11.1).

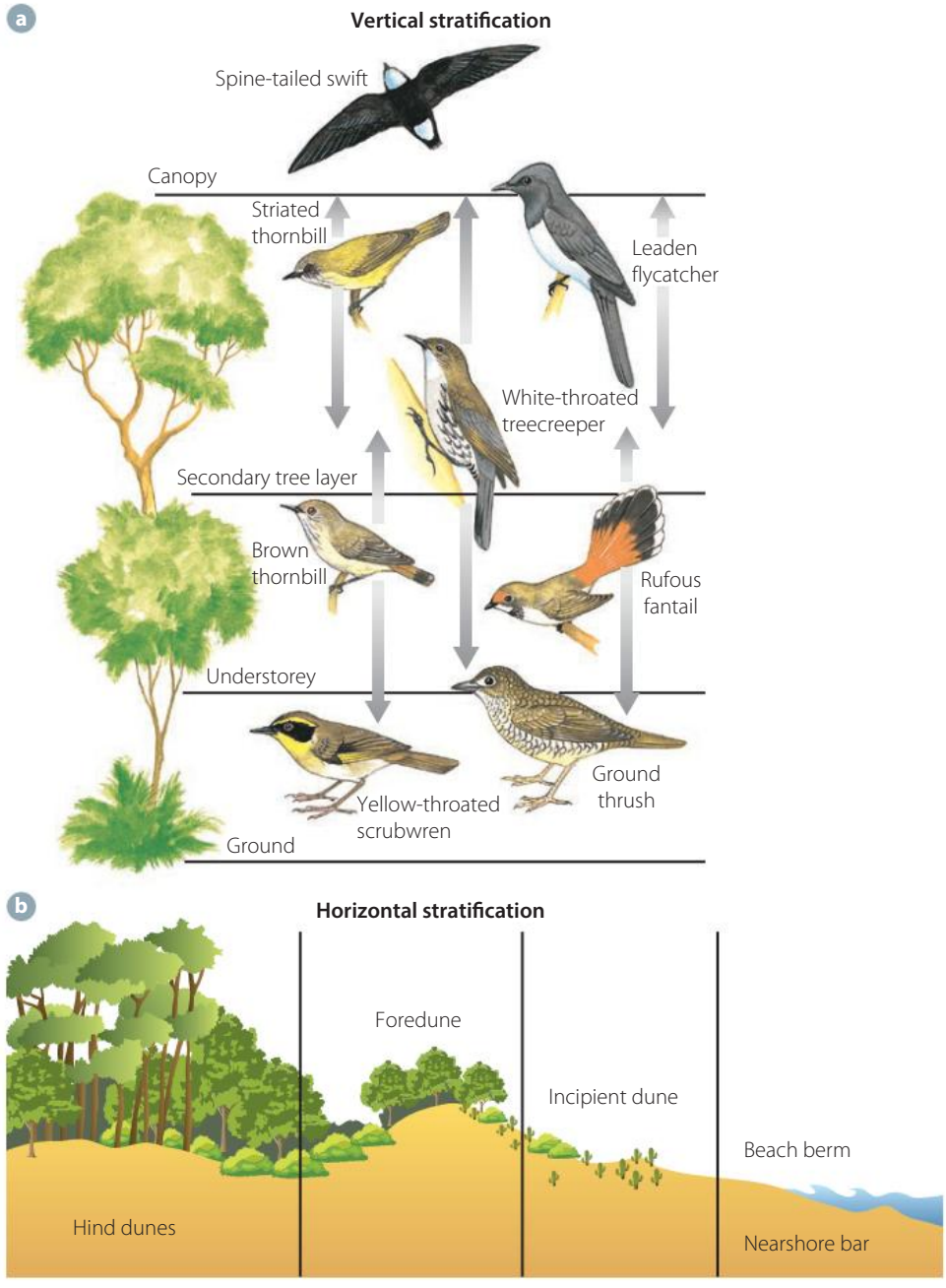

FIGURE 2.11.1
Strata can be arranged (**a**) vertically or (**b**) horizontally but cannot overlap or leave gaps.

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Selecting and sampling strata

When selecting strata, it is important to consider how large an area is appropriate. The boundaries between strata should be as defined as possible; for example, the boundary between high tide mark and the upper beach sands, or between the upper beach sands and the beginning of groundcover over the dunes. Obvious boundaries make it easier to determine if your sampling is going to be representative of the area.

The area within each stratum is then randomly sampled. The number of samples in each stratum should reflect their relative sizes. A habitat that forms only 10% of the total area should be allocated only 10% of the total number of quadrats performed. Figure 2.11.2 gives a comparison of true random sampling with stratified sampling of a river ecosystem.

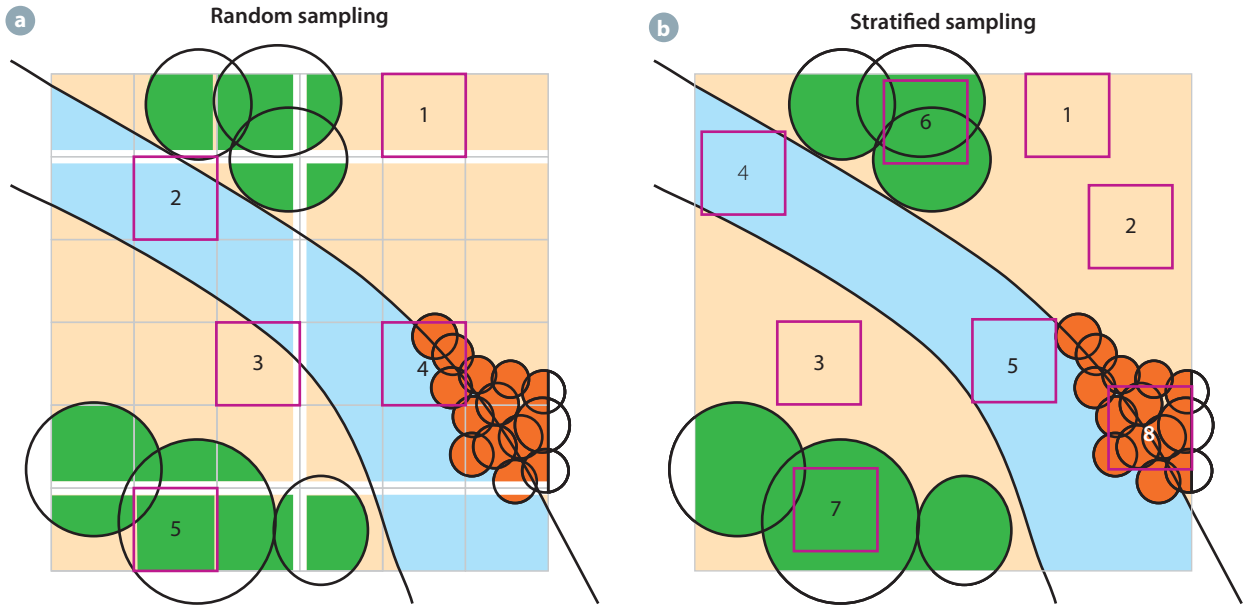


FIGURE 2.11.2 (**a**) Random sampling often produces quadrats of mixed habitat and ignores the relative sizes of those habitats in the ecosystem. In this case, the blue habitat will be sampled in three quadrats, while the much larger brown habitat will also be sampled three times. The data will represent 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 samples within each stratum, which means a more accurate proportion of quadrats can be taken from each habitat area.

Sampling techniques

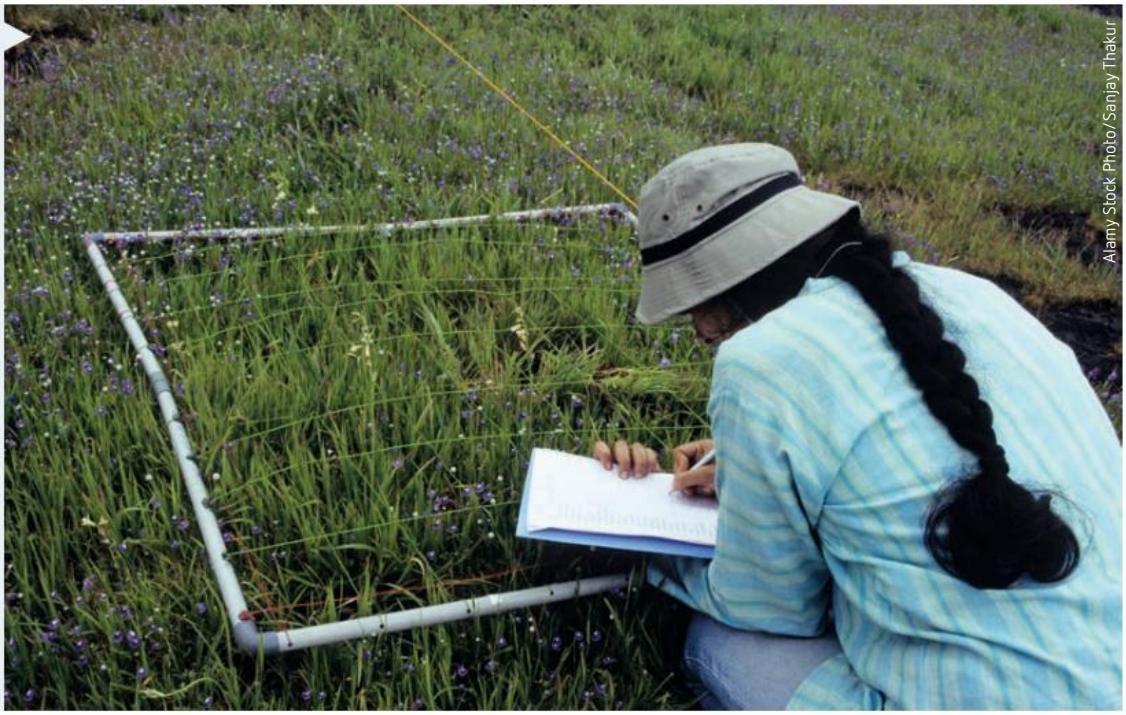
Quadrats

For organisms that are fixed or do not move very much, the quadrat method of sampling can be used to estimate distribution and abundance (Figure 2.11.3). A quadrat is a square, the size of which is determined according to the organism being studied, measured at ground level. It is most often used when measuring plant or fungus species because they are stationary. It is also used along shorelines to record sedentary marine species that may be exposed as the tide changes.

SYLLABUS LINK

Chapter 1 discusses sampling techniques, and calculations are discussed in more detail.

FIGURE 2.11.3
Quadrat sampling is often used to estimate plant population size and density.



For each quadrat, the number of individuals of each species is counted (or estimated in the case of difficulty) and recorded. The data from multiple quadrats is then averaged. By dividing the average number of individuals per quadrat by the size of each quadrat, ecologists can calculate population density. Worked example 2.11.1 shows you how to do this calculation.

KEY FORMULA

$$\text{Population density} = \frac{\text{average number of individuals per quadrat}}{\text{size of each quadrat}}$$

WORKED EXAMPLE 2.11.1

If a total of 35 individuals have been counted in 10 different 2 m^2 quadrats, what is the average density of that species?

ANSWER

- Determine the average number of individuals per quadrat.

$$\text{Average number of individuals per quadrat} = 35 \text{ individuals} \div 10 \text{ quadrats}$$
$$= 3.5 \text{ individuals per quadrat}$$

- Calculate the density by using the key formula.

$$\text{Population density} = \frac{\text{average number of individuals per quadrat}}{\text{size of each quadrat}}$$
$$= \frac{3.5 \text{ individuals per quadrat}}{2 \text{ m}^2}$$
$$= 1.75 \text{ individuals/m}^2$$

Transects

A **transect** is a line drawn through a community to provide a boundary for sampling (Figure 2.11.4). The information gathered about the organisms on this line is used to determine the distribution of species within that community. Again, this is a useful method when species are fixed in place, such as plants and fungi. In order to improve the data collected, quadrats may also be placed at intervals along the transect line and thus data on density in specific locations may also be recorded.

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

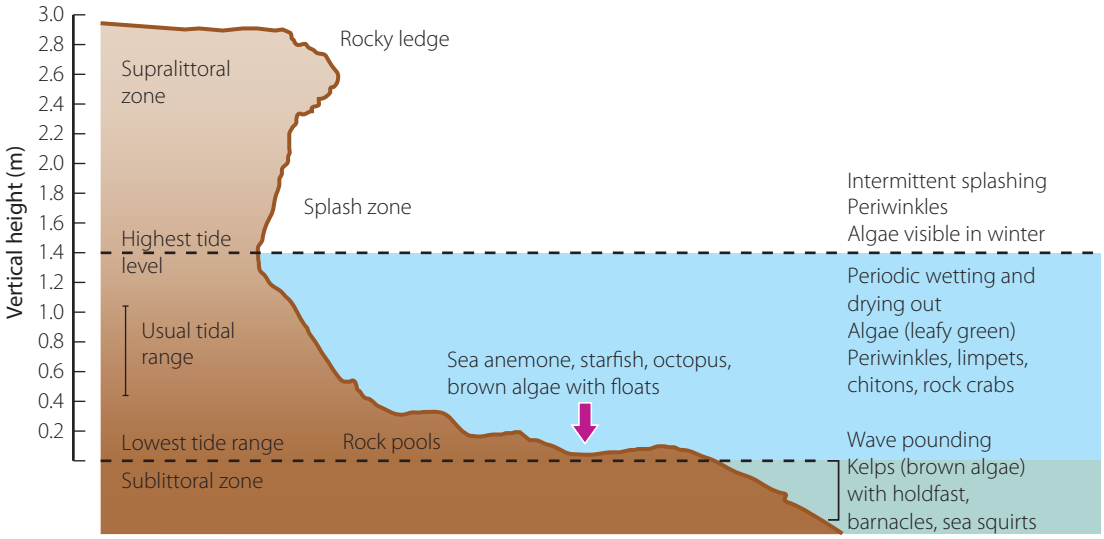


FIGURE 2.11.4 Transects allow ecologists to profile many habitats that would otherwise be too complicated, such as this marine rock platform.

Capture–mark–recapture

One of the most common sampling methods for mobile species, such as animals, is the capture–mark–recapture method. This method involves capturing a number of individuals, marking them and releasing them. At a later date, the same number of individuals is recaptured and the proportion of marked to unmarked individuals is used to estimate the population size.

SYLLABUS LINK

Chapter 4 discusses the capture–mark–recapture method and other applications of sampling are discussed in greater detail.

Minimising error

As with all sampling techniques, stratified sampling has a certain degree of error. However, this bias can be minimised in a number of ways. First, sufficient quadrats should be taken in each stratum to ensure the sample is representative. However, the number of quadrats from each stratum should be proportional to the relative size of each habitat. It is easiest to begin with the smallest stratum and allocate sufficient quadrats to that area before scaling up to the larger habitats.

A second process for minimising bias in stratified samples is to use a random number generator to determine the position of quadrats taken within a stratum, to follow strict criteria for what constitutes an individual in the case of groundcover plants where individuality is difficult to determine and how much of the plant must be within the quadrat to count it. Any equipment used for abiotic sampling should be calibrated immediately before use and the associated precision of the instrument should be noted in the data.

Presenting sampled data

Sampled data can be presented in a number of ways. The simplest is in table form, although it is easier to see patterns and trends when data is in a visual format, such as a graph.

Graphs should always be constructed for a purpose. First, determine which two variables you would like to analyse for a relationship. In the case of stratified sampling, this could be how the density of forest lichen changes as you get further from the ground (Figure 2.11.5), or how the ratio of native to non-native species changes in different habitats. These two variables will become your two axes, and will ensure that your graph means something and will provide you with an answer when analysed.

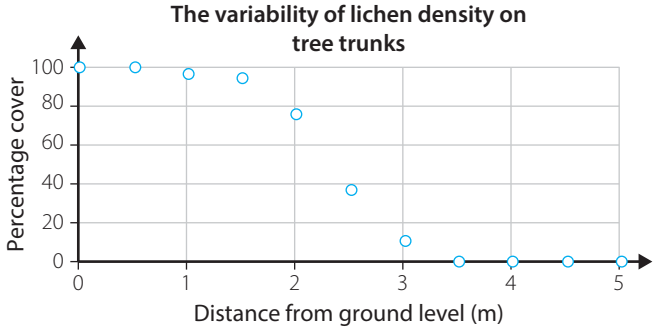


FIGURE 2.11.5
Graphs that are constructed to answer a specific question are much clearer and more meaningful than those constructed by mashing data onto a set of axes. This graph clearly shows that lichen is abundant on the bottom 1.5 m of a tree trunk and this drops off sharply between 2 m and 3 m above the ground.

SECTION REVIEW 2.11

REMEMBERING

1. Define 'stratified sampling'.
2. Outline the main features of the quadrat and transect sampling methods.
3. List two ways to minimise bias in stratified sampling.

UNDERSTANDING

4. Explain why quadrat and transect sampling are not generally useful for sampling animals.
5. Calculate the density of the following sampled species.
   - **a** An average of four individuals per 3 m^2 quadrat
   - **b** 14 individuals counted in two different 1 m^2 quadrats
   - **c** 32 individuals counted in eight different 2 m^2 quadrats
6. Give two reasons why stratified sampling is more accurate than true random sampling for ecosystems with a wide variety of habitats.

APPLYING

7. Complete the following to determine the average density.
   - **a** 65 individuals in 24 different 2 m^2 quadrats
   - **b** 110 individuals in 12 different 5 m^2 quadrats

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2.12 Mandatory practical

STRATIFIED SAMPLING

Introduction

When collecting data about local waterways, ecologists often use a combination of stratified sampling techniques. Transects allow them to analyse positional data, which is useful in monitoring the conditions along a waterway, while quadrats can provide data on the abundance and density of plants and organisms along the transect line. This information is vital to the ongoing management of our local creeks and rivers.

Aim

To analyse the conditions of a local waterway to classify it using the Australian National Aquatic Ecosystem (ANAE) classification framework.

Materials

- a local waterway with at least three access points
- a topographic map of the waterway
- datalogger with pH probe and conductivity probe
- quadrat frame
- clipboard
- note paper
- pen

Procedure

1. On the topographic map of the waterway, mark at least three access points and measure the distance between them.
2. Access the first site and observe it to record data for the first six sections of Table 2.13.1.
3. Use the datalogger and probes to determine and record the pH and electrical conductivity (EC) of the water at the site.
4. Convert EC to a total dissolved solids (TDS) estimate to determine the approximate salinity of the water. Record this calculation.

KEY FORMULA

Converting electrical conductivity (EC) to a total dissolved solids (TDS) estimate

$TDS = EC \times 640$

where:

TDS is the total dissolved solids and EC is the electrical conductivity.

5. Lay the quadrat frame over a section of the waterway bank. This will be quadrat 1 for this site.
6. Identify the first species and note it on Table 2.13.2.
7. Estimate the percentage of the quadrat that the individuals take up in total and record this.
8. Repeat steps 6 and 7 for all of the species you can identify.
9. Repeat steps 2–9 at each site.

»

Results

TABLE 2.13.1 Field site #_____ Abiotic data #_____

ATTRIBUTE	RESULT
LANDFORM How sloping is the land around this site? Steep, sloped or shallow How sloping is the water course at this site? Steep, sloped or shallow	
CONFINEMENT How deep is the water course channel? How easily would it erode in a flood event? Confined (non-floodplain), semi-confined (discontinuous floodplain) or unconfined (floodplain)	
SOIL/SUBSTRATE If there is soil, how soft is it? Does it contain organic matter? Peat (organic), mineral (soft, non-organic) or sand (hard) If there is no soil, what is the bedrock made of? Clay, chemical sediment, detrital sediment or volcanic rock	
VEGETATION What general type of vegetation is present at the site? Forested, shrub, sedges/grasses/flowers, or none	
WATER SOURCE Where does the water at this site come from? Surface water, groundwater or localised rainfall	
WATER REGIME How often does this waterway have water in it? Permanently inundated, seasonally inundated, periodically inundated	
WATER TYPE Determine the salinity and pH of the water at this site. Salinity: fresh (<100 mg/L), brackish (1000–3000 mg/L) or saline (>3000 mg/L). pH: acidic (<6), neutral (6–8) or alkaline (>8)	

Adapted from Aquatic Ecosystems Task Group (2012). Aquatic Ecosystems Toolkit. Module 2. Interim Australian National Aquatic Ecosystem Classification Framework. Australian Government Department of Sustainability, Environment, Water, Population and Communities, Canberra.

TABLE 2.13.2 Field site #_____ Biotic data Quadrat #_____

SPECIES	PERCENTAGE COVER

Discussion

1. Compare the general attributes of the waterway (Table 2.13.1) at each of the three sites. Is it similar along its length?
2. Comment on the salinity and pH of the water at each site. Is it similar or are there differences? Can you account for any differences? Is this a surprising finding? How will this affect organisms wishing to live here?
3. Comment on the biodiversity at each site. Does it appear to support a healthy diversity of species?
4. Research the ANAE classification framework and use it to classify this waterway.
5. Discuss the implications of your findings. Does this waterway seem to be healthy for its classification?

Conclusion

1. Summarise the condition of the waterway at each of the sites along its length and state how these support its classification.

CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1. Describe the two fundamental principles of Linnaean taxonomy.
2. Outline the four species interactions.
3. Who developed the first system for classifying the diversity of Australian ecosystems?

CATEGORY QUESTIONS

4. Explain how cladistics is different from and an improvement on Linnaean taxonomy.
5. Give an example of an infertile species, and how its interactions with the ecosystem would differ from fertile species.

ELABORATION QUESTIONS

6. Explain the benefits of classifying the species and ecosystems around us.
7. Suggest how the quadrat method might be modified to incorporate mobile animals.

EVIDENCE QUESTIONS

8. Provide a supporting example for your response to Question 6.
9. Explain any practical limitations to implementing your suggestion in Question 7.

END-OF-CHAPTER EXAM

End-of-chapter test

1 Which of the following is not one of Linnaeus' taxa?

A Phylum

B Clade

C Species

D Family

2 An infertile organism produced by the interbreeding of separate species is called a:

A hybrid.

B hubris.

C hagrid.

D humus.

3 Which of the following is not an assumption of cladistics?

A Common ancestry

B Dichotomous cladogenesis

C Ever-widening difference

D Interspecies competition

4 Describe what a common ancestor is.

5 Figure 2.14.1 shows a cladogram for several primate groups.

a State whether the circled group is a clade.

b List all members of the clade that contains macaques and gibbons, but not marmosets.

c State which other primate is also descended from the most recent common ancestor of gibbons and humans.

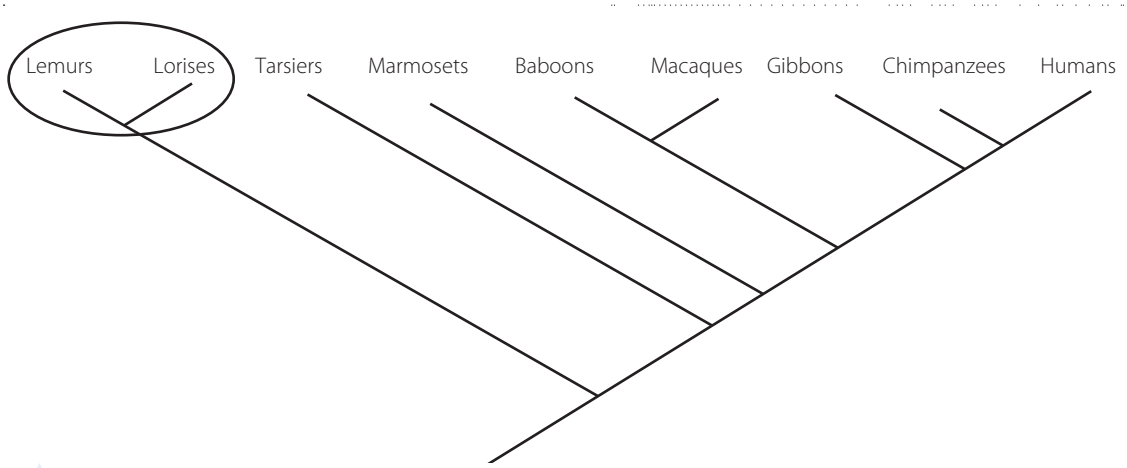

FIGURE 2.14.1 Primate ancestry is not well supported by the fossil record, and must be supplemented with comparative genomics.

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6 Outline the process of determining relatedness in organisms through molecular sequencing.

7 Explain why different species have significantly different base rates of mutation.

EXTENDED RESPONSE

8 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.

9 Outline how technology has changed the scientific classification of organisms.

10 Figure 2.14.2 shows 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, using Table 2.9.1.
- **e** Explain the limitations of only using one sample plot.

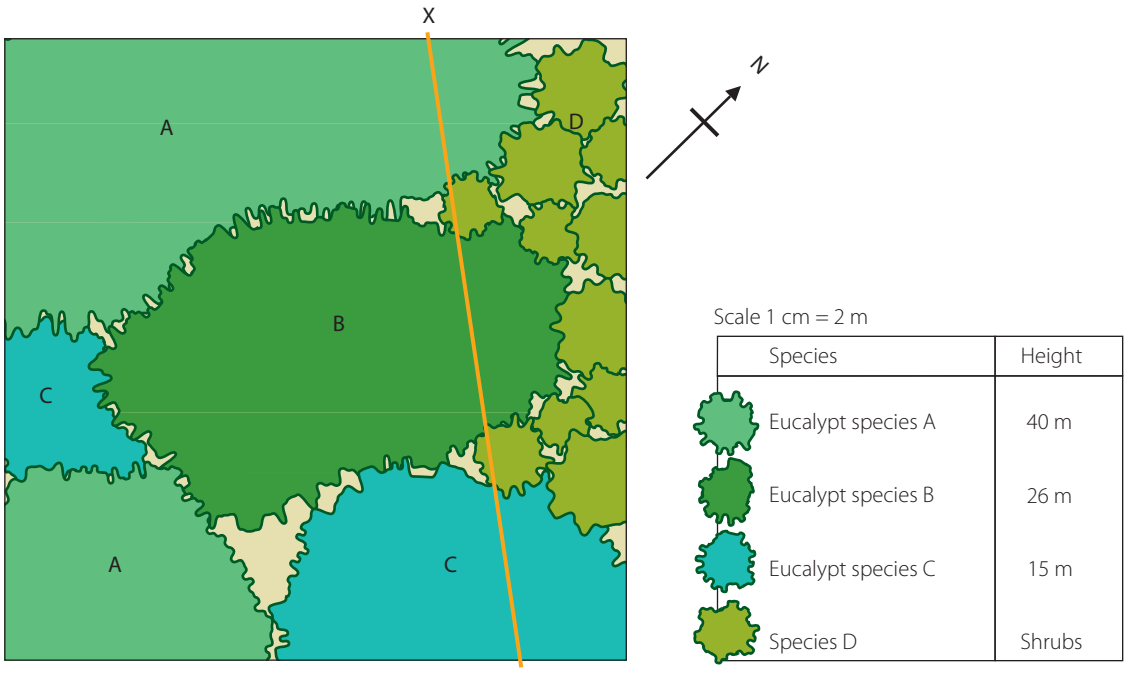

FIGURE 2.14.2 Plots of ecosystems often employ surface maps that show a rough aerial view of the area.

» UNIT THREE

BIODIVERSITY AND THE INTERCONNECTEDNESS OF LIFE

Alamy Stock Photo/Siegfried Schnepf

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Topic 2: Ecosystem dynamics

Each ecosystem has features that are different from those of other ecosystems, as well as features that differ over time. Measurements of the transfer and transformation of energy and matter can be used to study an ecosystem's diversity and functioning. A species' interaction with both biotic and abiotic components of their ecosystem limits where and how they live and how successful they are. Changes in biotic and abiotic factors affect the types of communities and population growth rates. Calculation and analysis of population numbers can be used to compare ecosystems over time and space.

SCIENCE AS A HUMAN ENDEAVOUR

Students should be given opportunities to investigate Aboriginal and Torres Strait Islander knowledge of the local ecosystem and how this knowledge can be used for conservation; the role of technology and data collection in the analysis of marine reserves and their effectiveness and the role of keystone species in conservation.

KEY FORMULA

Population size by the capture–recapture measure is the Lincoln index, shown as:

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

where:

M = number of individuals caught, marked and released initially

n = number of individuals caught on second sampling

m = number of individuals captured that were marked

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3 FUNCTIONING ECOSYSTEMS

Introduction

Wherever life exists, in the deep-sea trenches kilometres below the surface of the oceans, in the geothermal springs of New Zealand or in the Antarctic, life 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. The winds, the tides and the circulation of the oceans in one part of the world affect what happens in another part of the world.

This chapter explores the transfer and transformation of this energy and matter as it is cycled and recycled through the biosphere.

Stimulus questions

How does energy move through an ecosystem?

How are nutrients cycled through an ecosystem?

How do different species live harmoniously with finite resources?

Alamy Stock Photo / Mike Greenslade / Australia

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3.1 Transfer and transformation of solar energy

All complex systems on Earth require a constant supply of energy to drive them. It is the supply of energy that allows matter to be combined into an almost infinite range of complex structures. For example, the developing offspring of a mammal begins with the fusion of two cells, one from each parent, eventually forming a complete and independent organism. The energy that drives this process is provided to the growing offspring through a series of transfers and transformations originating with the Sun.

3.1.1 Solar energy
3.1.2 Using solar energy

Sources of energy

The Sun (Figure 3.1.1) provides most of 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, tides, weather systems and ocean currents. The amount of energy depends on the wavelength of the incoming light. Because the Sun emits all visible, infrared and ultraviolet radiation, the total amount of energy is very large. Even so, it is of little use to a living organism unless the organism is equipped to capture this energy and transform it into a more useful form.

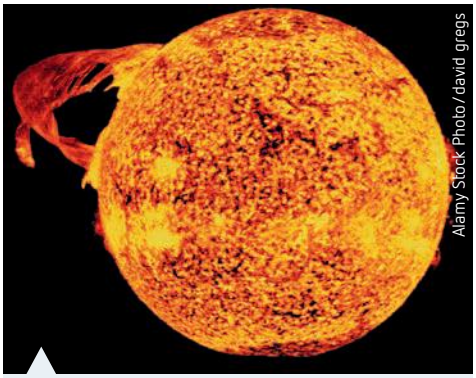

FIGURE 3.1.1 The Sun provides almost all energy to all planets of the solar system. The only other energy comes from the subtle bending and flexing of the planet as it orbits the Sun and is orbited by moons.

transform
to change from one type to another

INQUIRING FURTHER

Hydrothermal vents are regions in the deep ocean where volcanic magma heats seawater to more than 300°C, and yet these entirely dark, hot, acidic environments are home to diverse communities. Research how chemotrophic bacteria support these ecosystems under such extreme conditions.

Conversion of light to chemical energy

Plants and algae have evolved photosynthesis (Figure 3.1.2) as a way to utilise the Sun's energy and establish an energy structure upon which all organisms depend. Photosynthesis involves harnessing the light energy from the Sun to bind molecules of water and carbon dioxide into glucose molecules. The Sun's light energy is transformed into chemical energy during this process and then locked in the high-energy chemical bonds formed in the glucose molecules. This energy is made available for the life processes of metabolism when it is released through cellular respiration, a complementary process to photosynthesis, which breaks down the glucose molecules back into their component parts.

cellular respiration
the process of releasing chemical energy from the bonds of glucose molecules

$$C_6H_{12}O_6 + 6O_2 \underset{\text{Photosynthesis}}{\overset{\text{Cellular respiration}}{\rightleftharpoons}} 6CO_2 + 6H_2O + \text{energy}$$

FIGURE 3.1.2 In terms of gross products, photosynthesis and cellular respiration are a pair of simple inverse reactions. However, the biochemical pathways required in each process are very different.

SYLLABUS LINK

Nelson QScience Biology Units 1 & 2, Chapter 4 discusses photosynthesis and cellular respiration in more detail.

Producing biomass

autotroph (producer)
an organism that can produce its own organic compounds from sunlight, water and carbon dioxide

trophic level
a level in the food chain of an ecosystem based on feeding relationships

biomass
the total mass of living matter in an ecosystem

photosynthetic efficiency
how well a producer converts light energy into the chemical energy of carbohydrates

gross primary productivity (GPP)
the total organic matter produced annually in an area by photosynthesis

Organisms that can capture the Sun's energy in the bonds of glucose molecules are termed **autotrophs** because they do not rely on any other organism for their energy needs. Autotrophs (also known as producers) are the basis of all organic matter and form the base **trophic level** of **biomass** in every ecosystem.

Not all producers make the same amount of biomass. How well a producer converts light energy into carbohydrates during photosynthesis is referred to as its **photosynthetic efficiency**. This depends on the availability of raw materials and sunlight, but also on temperature, light intensity and the nature of the organism. For example, an area covered in trees will produce significantly more biomass than the same area covered with grass (Figure 3.1.3). Tropical forests cover only about 4% of Earth's surface but contribute about 25% of the world's yearly **gross primary productivity (GPP)** of organic matter.

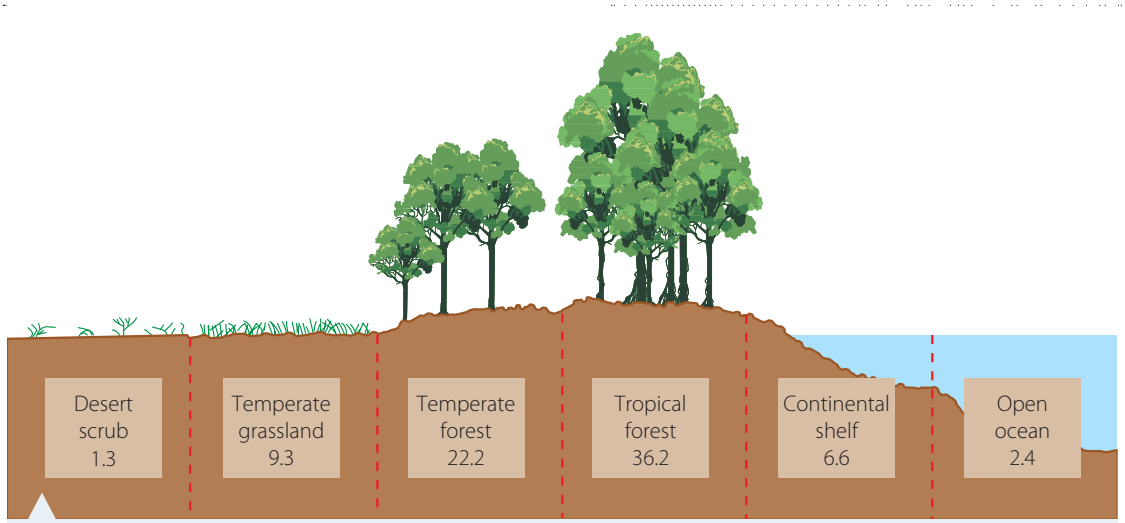

FIGURE 3.1.3 Different autotrophs have different primary productivity rates. The numbers in this diagram refer to the amount of chemical energy converted from sunlight per square metre each year (kJ/m^2/year)

3.1.3 What is biomass?
3.1.4 Biomass explained
3.1.5 Bioenergy

Ocean ecosystems also depend on producers such as phytoplankton to transform light energy into vast amounts of organic material. However, their primary production is not as efficient as that of terrestrial ecosystems because light does not penetrate deep water and other nutrients are not abundantly available. 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. So 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.

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

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Subsequent trophic levels

From the base autotrophic level rise other trophic levels populated by **heterotrophs**, organisms that cannot photosynthesise and, therefore, must obtain their energy either directly or indirectly from organisms that can. Heterotrophs are also called consumers because they must consume other organisms for energy. A **biomass pyramid** (Figure 3.1.4) shows the relationships between the amounts of autotrophic matter and heterotrophic matter. A balanced and healthy ecosystem must have a stable pyramid, with decreasing mass of organisms in each successive trophic level.

heterotroph (consumer)
an organism that cannot convert sunlight to useful energy, and must consume other organisms for food

biomass pyramid
a pyramid diagram that shows the relative proportions of each trophic level in an ecosystem

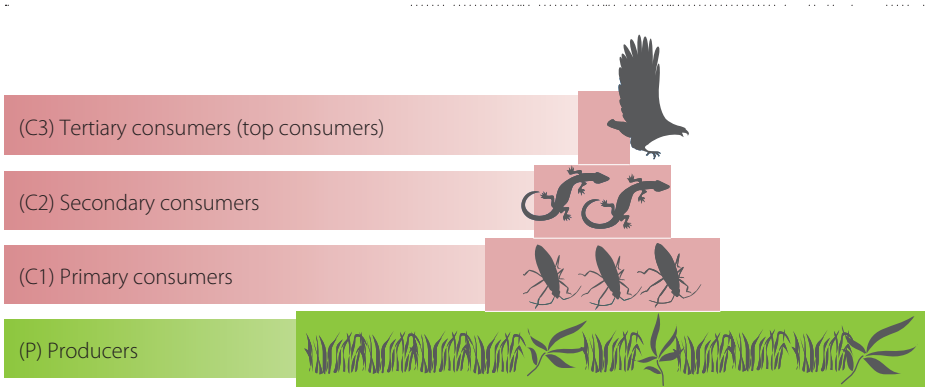

FIGURE 3.1.4 The width of each level in a biomass pyramid indicates the relative mass of living matter at that level.

3.1.6 Pyramids of numbers and biomass

SECTION REVIEW 3.1

REMEMBERING

1 Define:
   - **a** autotroph
   - **b** heterotroph.

UNDERSTANDING

2 Outline the process of producing biomass from sunlight.

3 Explain the difference between GPP and NPP.

4 Discuss the statement: 'The Sun is the primary source of all energy on the planet'.

APPLYING

5 Biomass pyramids are often constructed as part of the information-gathering process used to inform ecosystem management strategies. Demonstrate the benefits and limitations of basing ecological decisions on a biomass pyramid.

3.2 Calculating energy transfers and transformations

Energy is required for animals to carry out work. This may include foraging for food, avoiding predators, migrating or keeping warm. Some energy is used to keep bodily functions working, building or repairing new tissues, and for the production of gametes in reproduction (Figure 3.2.1).

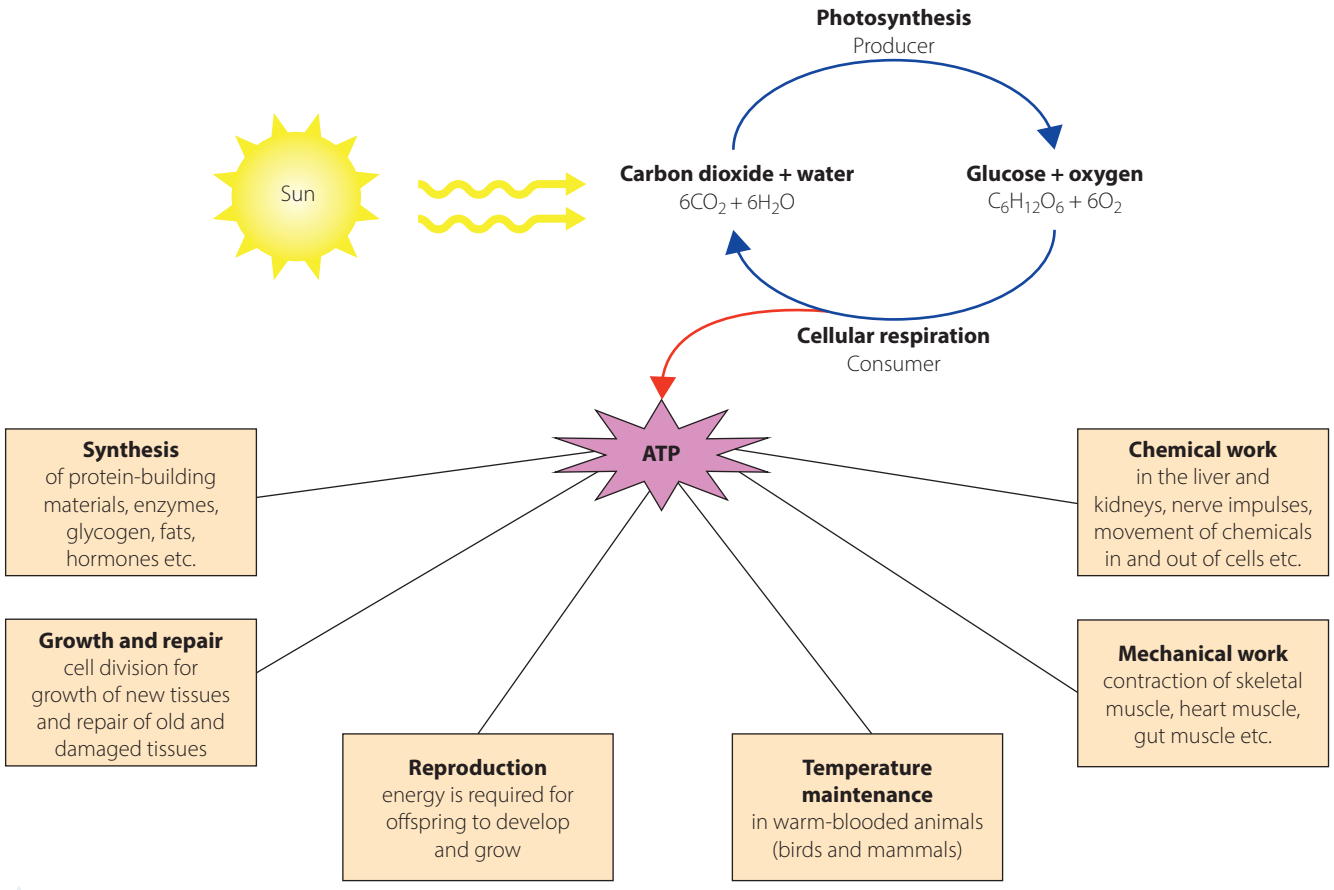

FIGURE 3.2.1 The energy originating from the Sun is used by organisms to perform work, whether they obtain it directly from sunlight or indirectly through consuming others.

food chain
a chain of organisms where one organism occupying a trophic level is consumed by the next organism in a higher trophic level

Energy transfers

Food chains and food webs are examples of qualitative and predictive models that allow ecologists to monitor the energy flow within an ecosystem. The chains have their own internal order, with each organism in the chain occupying a position or trophic level (Figure 3.2.2).

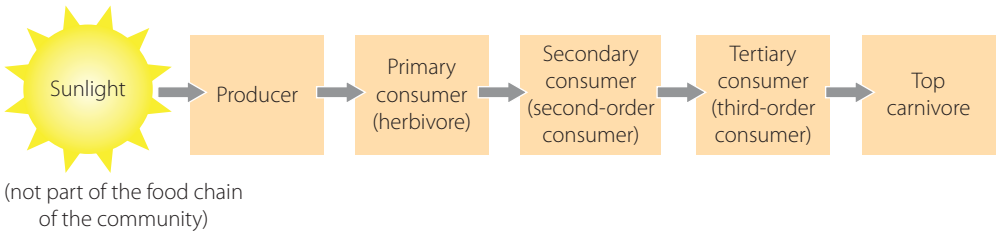

FIGURE 3.2.2 Food chains begin with the Sun as the original source of all energy in the chain.

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Beginning with the Sun as the source of energy, the first organism in every food chain receives its energy directly from the Sun. This is shown with arrows that represent the flow of energy from one trophic level to another. Each organism in the chain receives energy from the preceding one, generally by eating it (Figure 3.2.3). 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.

3.2.1 Food chains and food webs

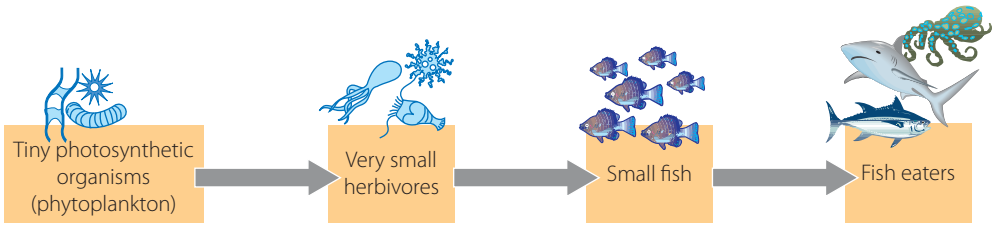

FIGURE 3.2.3 In general, food chains simplify feeding relationships by focusing on one organism or group of organisms at each trophic level.

Energy losses

A useful rule in ecology is that about 10% of the energy at one trophic level is passed on to the next level. The remaining 90% 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 3.2.4). **Endothermic** animals, such as mammals and birds, lose comparatively more energy through heat radiation than **ectothermic** animals, who do not maintain a high internal body temperature.

endothermic when the internal body temperature of an organism is regulated and maintained higher than the temperature of the surroundings

ectothermic when the internal body temperature of an organism reflects and fluctuates along with the surroundings

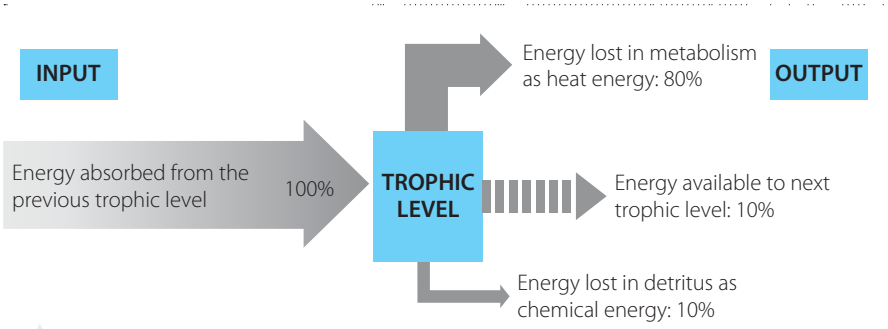

FIGURE 3.2.4 Trophic efficiency describes the proportion of energy that is available to the next trophic level within a food chain.

3.2.2 Endotherms and exotherms

Consumers differ considerably in how efficiently they pass on the energy from the food that they eat, varying from less than 0.1% to more than 10%. For example, lizards are smaller and internally cooler than possums. Therefore, lizards require relatively less of the total energy taken from insects to maintain their body cells. A feral cat, which would eat both lizards and possums, would obtain a higher percentage of the Sun's energy from the lizards. In fact, if the possum had eaten the lizards before it became a meal for the cat, the energy efficiency would be even worse. This loss of energy limits the number of trophic levels possible in an ecosystem, and forces consumers at higher trophic levels to eat larger proportions of prey.

Calculating energy efficiency

Ecologists calculate energy efficiency to identify and study energy bottlenecks and the species that contribute to the sustainability of an ecosystem. Generally, this begins by gathering information on the bulk mass and energy production of each species, each year, and organising them into trophic levels. This can be quite difficult for complex food webs because some organisms occupy three different trophic levels depending on their food source. With simpler food webs, it is considerably easier (Figure 3.2.5).

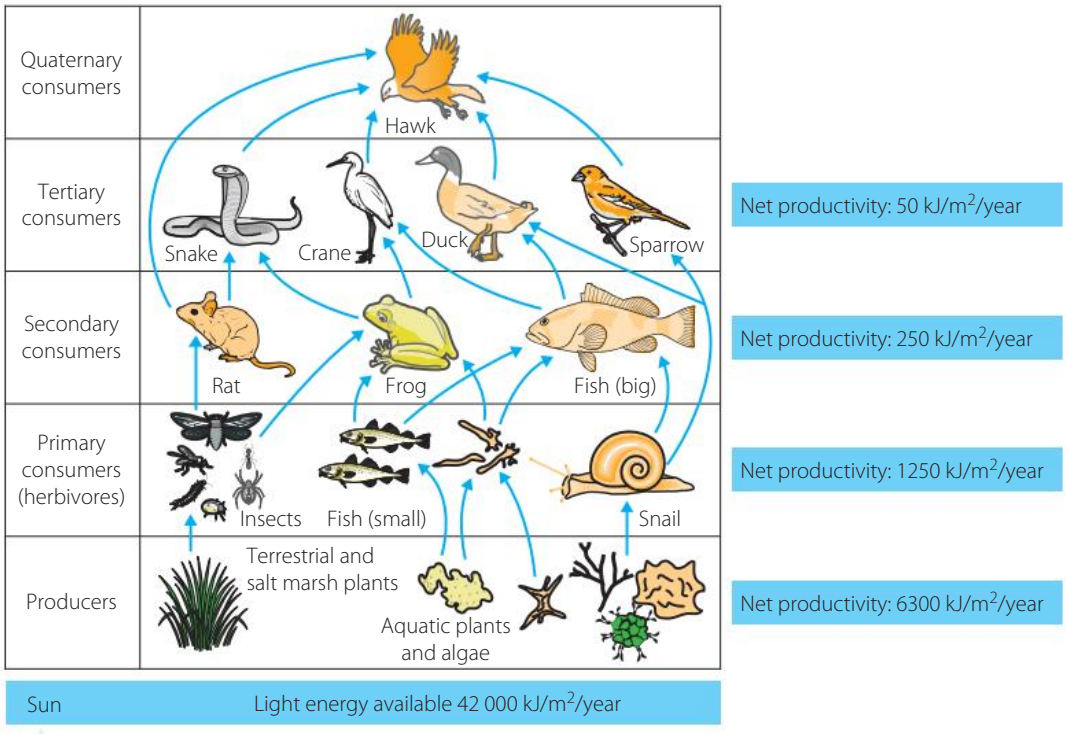

FIGURE 3.2.5 The net productivity at each trophic level includes the total amount of energy that the organisms produce in edible parts per square metre of space in a year.

INQUIRING FURTHER

Ecologists can estimate the size of the home range for territorial animals by calculating the net productivity of their prey and extrapolating how many square metres they would need to hold to obtain sufficient energy each year for their needs. Investigate the net productivity of eucalypt forests and the energy needs of a koala to estimate the size of territory that a single koala needs to survive.

To calculate energy efficiency, the energy produced by the organism is divided by the energy available from the previous trophic level. This is often converted from a decimal to a percentage for clarity. Worked example 3.2.1 (page 69) shows you how to do this calculation.

KEY FORMULA

Trophic energy efficiency

$$\text{Percentage efficiency} = \frac{\text{net productivity of the organism}}{\text{net productivity of the previous trophic level}} \times 100$$

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WORKED EXAMPLE 3.2.1

Calculate the percentage efficiency of the producers in Figure 3.2.5.

ANSWER

- Substitute the values for producers and available light into the key formula.

$$\text{Percentage efficiency} = \frac{\text{net productivity of the organism}}{\text{net productivity of the previous trophic level}} \times 100$$

$$= \frac{6300}{42\,000} \times 100$$

$$= 15\%$$

SECTION REVIEW 3.2

REMEMBERING

1. Write three reasons why energy transfers between trophic levels are not 100% efficient.
2. State the formula for calculating percentage efficiency.

CREATING

3. Create 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 and 75 g/m^2 of tertiary consumers. Begin with producers as a bar 20 cm wide.

UNDERSTANDING

4. Explain which trophic levels in Question 3 are the most efficient and which are the least efficient.

APPLYING

5. Calculate the total energy lost to metabolism and wastes in Figure 3.2.5.
6. Calculate the percentage efficiency of each of the trophic levels in Figure 3.2.5.
7. Calculate the percentage efficiency between the total energy originally available from the Sun and the amount available to the top predator in Figure 3.2.5.
8. An omnivore eats a range of foods, including plant and animal matter. Construct an argument for or against this statement: 'A vegan diet is a more efficient use of our natural resources than an omnivorous one'.

3.3 Energy flow diagrams

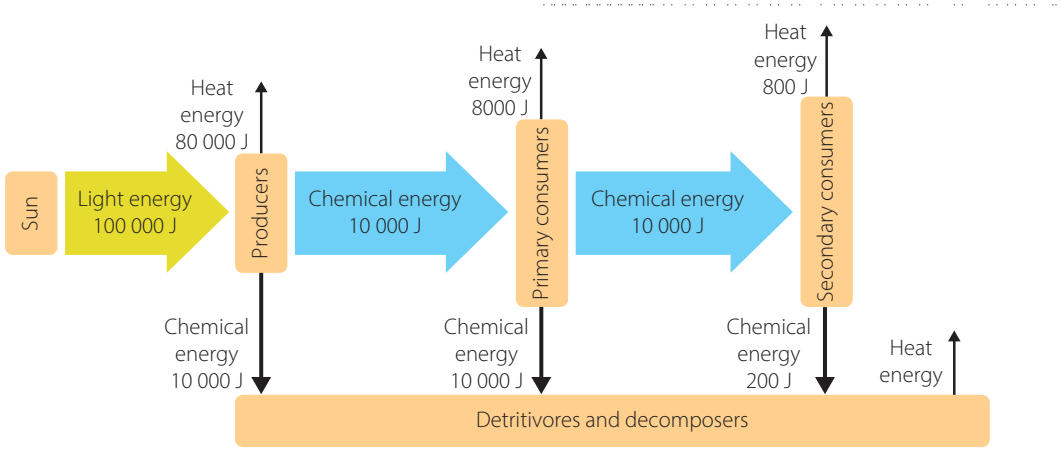
Energy flow diagrams (Figure 3.3.1, page 70) map the path of the Sun's energy as it transfers through the trophic levels of an ecosystem and is transformed into heat by metabolism. Several key principles govern the construction of these diagrams.

1. Arrows show the direction of energy flow and are labelled with the form and quantity of energy they carry.
2. Boxes are used to represent trophic levels in sequence.
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.
5. Total heat energy lost must equal the amount of chemical energy brought into the system by producers.

detritivore
an organism, such as a worm, that consumes detritus, the dead tissues of once-living organisms

decomposer
an organism, such as a fungus, that grows on and absorbs nutrients from dead tissues

FIGURE 3.3.1
Energy flow diagrams illustrate the movement of energy through ecosystems.



SECTION REVIEW 3.3

REMEMBERING

1 Summarise the five principles of constructing an energy flow diagram.

UNDERSTANDING

2 Explain the role that detritivores and decomposers play in the energy flow of an ecosystem.

3 Construct an energy flow diagram for an ecosystem in which 400 000 kJ of chemical energy is brought into the system by producers, which are 13% efficient. The primary consumers are 15% efficient and the secondary consumers are 18% efficient. Heat lost by each trophic level is 10%.

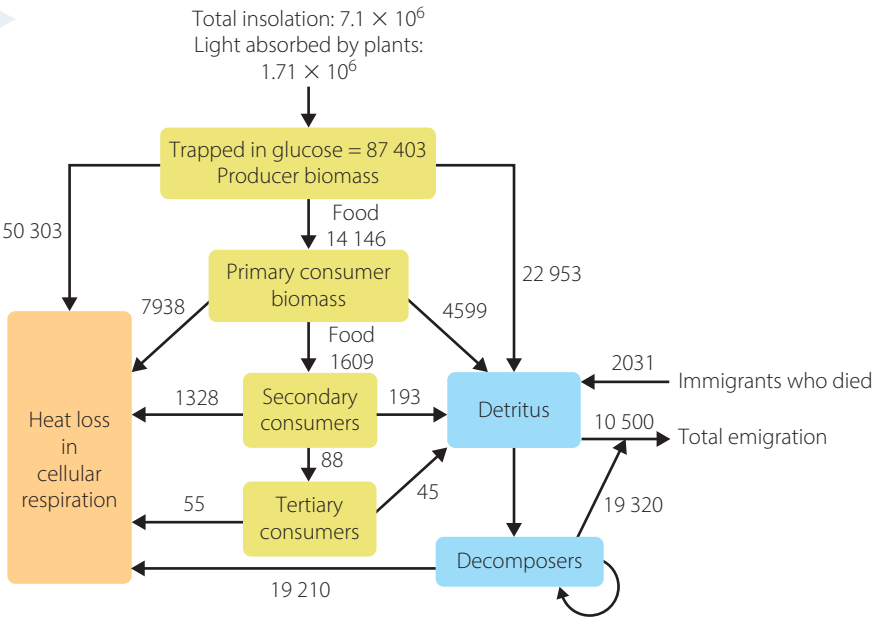
APPLYING

4 Figure 3.3.2 shows an energy flow diagram for a community in Silver Springs – a spring-fed stream in Florida, USA.

- **a** Calculate the efficiency of the primary consumers in this community.
- **b** Determine why immigration and emigration was included at the right of the diagram.
- **c** Determine if heat losses equal the total energy brought into the system by producers. Comment on your result.

5 In general, humans throughout the world rarely eat carnivores. Discuss why this may be so.

FIGURE 3.3.2
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.



Odum, H. T. (1957) Tropic Structure and Productivity in the Silver Springs Community, Florida. *Ecological Monographs*, 27(1), pp. 55–112.

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3.4 Transfer and transformation of matter

The difference between energy and matter in ecosystems is that the Sun provides a constant, external supply of energy while the total matter that exists on Earth is a fixed resource and therefore must be recycled. The matter that makes up a living organism is recycled by 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 is able to 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:

- a biological component that follows how the element cycles through organisms
- a geochemical component showing how the element cycles through soils, rocks, water and the atmosphere.

Given the interdependent manner in which these components are related, nutrient cycles are also called biogeochemical cycles.

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 cycles

Carbon cycle

Carbon atoms circulate between the organic compounds of living things and their non-living surroundings through a number of pathways, and together these form the carbon cycle (Figure 3.4.1).

3.4.1 Biogeochemical cycles overview

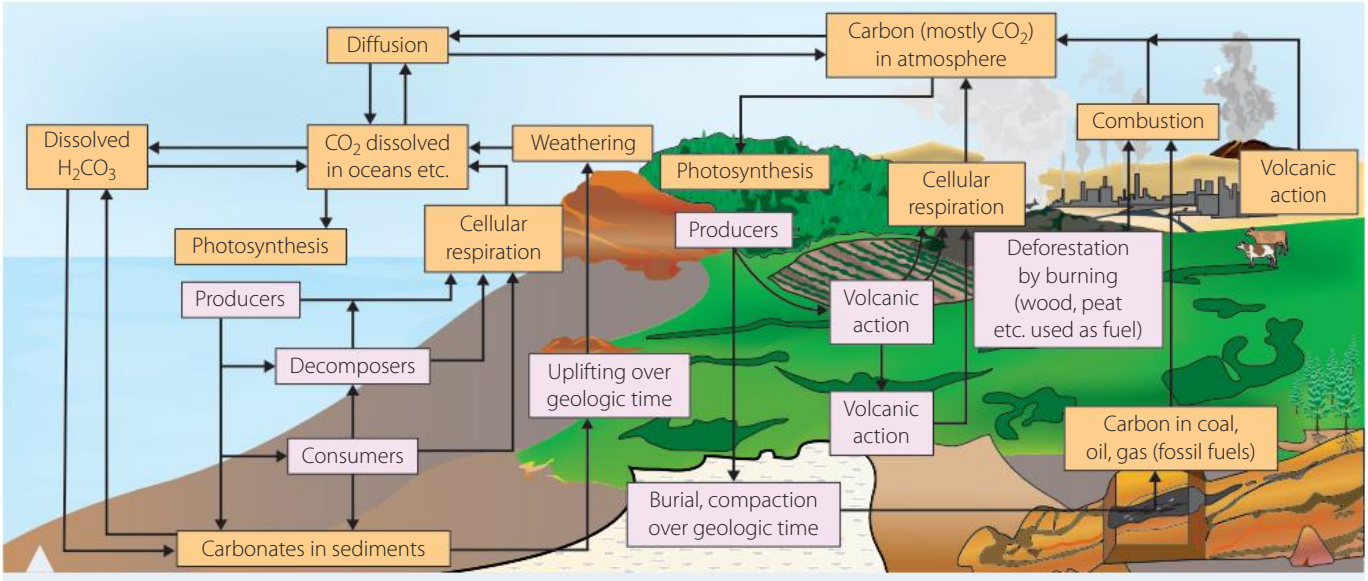

FIGURE 3.4.1 Carbon atoms in atmospheric carbon dioxide are incorporated into carbohydrates during photosynthesis. This carbon is eventually released through cellular respiration or combustion, both of which convert the organic compounds back to carbon dioxide.

The carbon cycle is unique among nutrient cycles because it does not necessarily involve decomposers. In the absence of any decomposers, carbon would still be able to circulate for some time within an ecosystem because carbon is incorporated into and released from glucose through photosynthesis and cellular respiration.

anaerobic
in the absence of oxygen

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.

sink
an area where atoms naturally accumulate away from the normal nutrient cycle

The amount of carbon dioxide in the atmosphere is maintained largely by a balance between photosynthesis, which withdraws it from the atmosphere, and cellular respiration and combustion, which release it to the atmosphere. Unfortunately, due to 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 and reintroduce their carbon to the cycle by combusting them as a source of energy. The surplus disrupts the natural balance between photosynthesis and cellular respiration. Even though plants photosynthesise more rapidly with the increased availability of carbon dioxide in the atmosphere, it is not being taken in fast enough because humans have also cleared vast areas of forest over the last century.

3.4.2 The carbon cycle

Changes to ocean temperatures have also affected the cycling of carbon. The temperature of the 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.

Nitrogen cycle

nitrogen-fixing bacteria
bacteria that absorb elemental nitrogen (N_2) from the atmosphere and convert it to nitrates (NO_3^-) or ammonium ions (NH_4^+)

Nitrogen is an essential element for living organisms. It is a key element in making proteins, including structural proteins and enzymes. These molecules have many different roles in cells and play an essential part in controlling cell activities and growth. Without nitrogen atoms, cells of all kinds would cease to function.

ion
an atom or group of atoms that has either lost or gained valence shell electrons, acquiring a net positive or negative charge

Unlike carbon, nitrogen atoms do not have a direct link between the atmosphere and most living organisms. Even though the atmosphere is 78% nitrogen, it is elemental nitrogen (N_2). Plants and animals are unable to absorb nitrogen in this form. Instead, plants rely on **nitrogen-fixing bacteria** to convert elemental nitrogen into **ions** such as nitrate (NO_3^-) and ammonium (NH_4^+), which they can absorb. Animals absorb nitrogen from the nitrates in plants.

The nitrogen cycle (Figure 3.4.2) is a combination of two cycles:

- the elemental cycle, in which N_2 is absorbed from the atmosphere by nitrogen-fixing bacteria and released back to the atmosphere by denitrifying bacteria and volcanic activity
- the ionic cycle, in which nitrogen-containing ions such as nitrate (NO_3^-) and ammonium (NH_4^+) are passed between organisms in the biosphere.

3.4.3 The nitrogen cycle

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 *Casuarinas*, *Acacias* and legumes, including clover, peas and beans. Instead of living free in the soil, these bacteria are accommodated in special root organs called **nodules** (Figure 3.4.3). In exchange for providing protected living space for the bacteria, the plants have a ready source of ionic nitrogen at their disposal.

nodule
a small swelling or lump

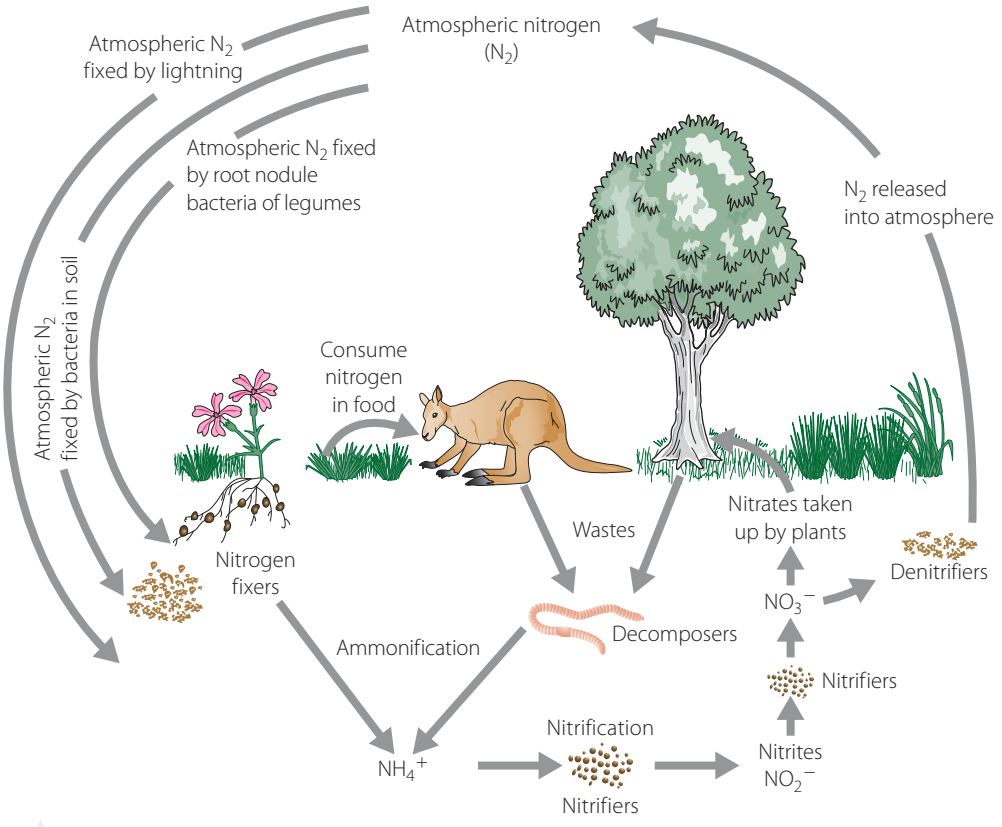

FIGURE 3.4.2 The balance between atmospheric nitrogen and ionic nitrogen is maintained by a set of key bacteria, including nitrogen fixers and denitrifiers.

FIGURE 3.4.3 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.

3.4.4 The water cycle

Water cycle

Water is considered a nutrient although it has no specific nutritional value. Water provides a habitat for a diverse range of living things and it fills the cellular environment in which all metabolic processes occur. The water cycle (Figure 3.4.4) is also known as the hydrological cycle and is driven by two energy sources: the Sun and gravity.

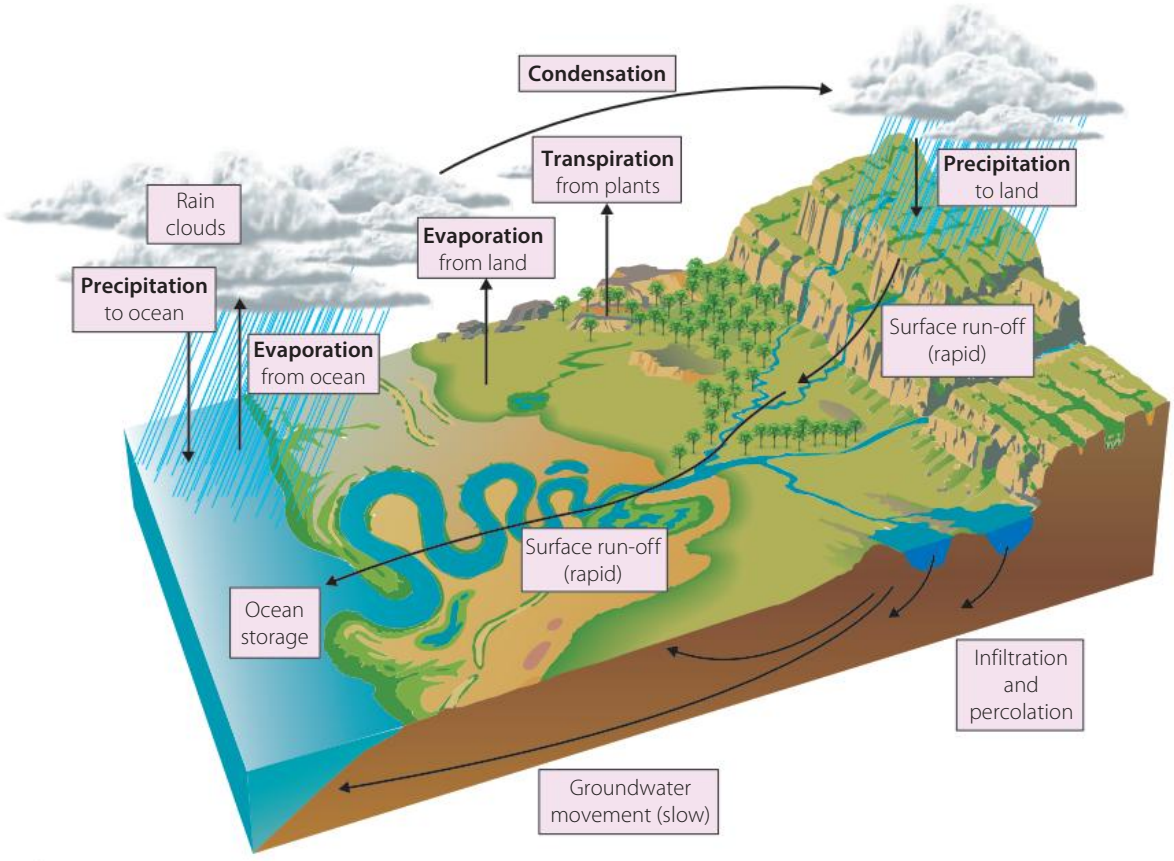

FIGURE 3.4.4 The water cycle follows water molecules between the abiotic and biotic components of an ecosystem, as well as between the three states of matter: solid, liquid and gas.

3.4.5 The phosphorus cycle

Phosphorus cycle

The phosphorus cycle (Figure 3.4.5) is also essential for life on Earth. Most phosphorus is in ionic form as phosphate (PO_4^{3-}), in both the biotic and abiotic components of the cycle. Phosphate is a key ion in the construction of DNA, RNA and ATP and each new cell requires a lot of it. Volcanic action and earthquakes unlock phosphate sinks from deep underground and reintroduce it to the surface environment. Mechanical weathering by wind and rain releases phosphates to the soil and water. This makes phosphate available as an essential nutrient to plants and it enters the food chain for consumption by consumers. After cycling through the food chain, phosphorus is returned to abiotic reservoirs as calcium phosphates in bones, shells, hard parts of aquatic animals and detritus in the oceans.

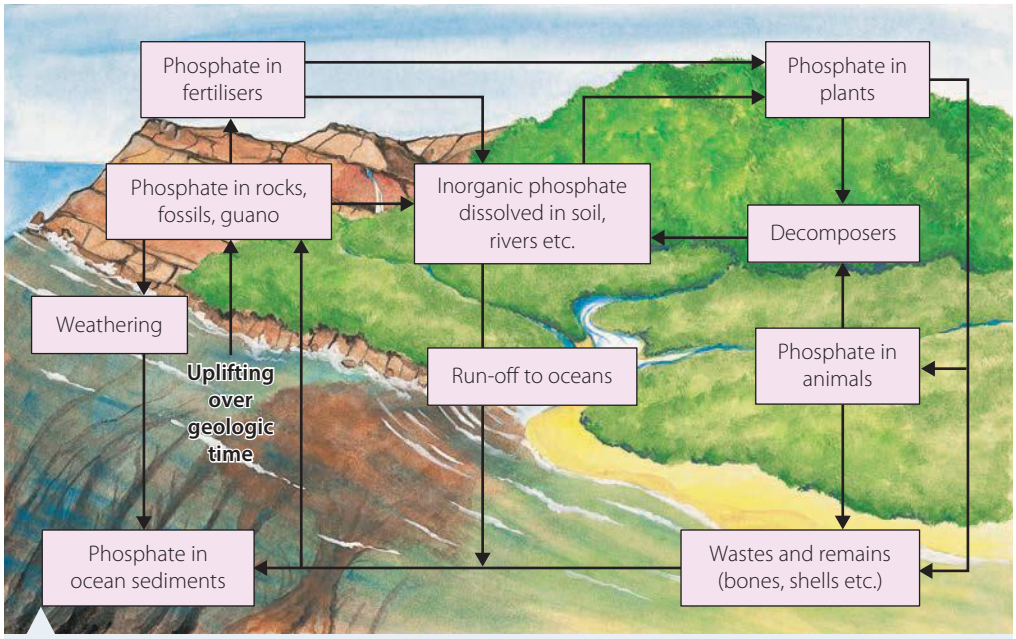

FIGURE 3.4.5 The phosphorus cycle plays a vital role in an organism's access to phosphate for the construction of new nucleic acids.

SECTION REVIEW 3.4

REMEMBERING

1 List four biogeochemical cycles.

2 Summarise the two parts of the nitrogen cycle.

UNDERSTANDING

3 Explain what would happen if large volumes of nitrogen-fixing bacteria were killed off.

4 Explain why deforestation and the excavation and burning of fossil fuels are affecting the carbon cycle.

5 Outline the two biological processes that cycle carbon between the atmosphere and living organisms.

APPLYING

6 Use your knowledge of the water cycle to justify the saying: 'It's always raining somewhere'.

3.5 Ecological niche

Ecosystems across the world are unique and diverse in their own ways. The organisms that inhabit a particular ecosystem survive because of the particular set of biotic and abiotic factors present. The way in which species function within their environment (for example, the time 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) an American biologist at the University of Georgia, made the analogy that if the species' habitat was its home address, then its ecological niche was its profession in that location. If two species attempt to occupy the same niche (that is, practise the same profession in the same location), one will eventually out-compete the other until only one remains.

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 ecological niche of an organism is how it 'fits into' the ecosystem. For example, the niche of the saddle-back tamarin monkey (*Saguinus fuscicollis*) of the Amazonian rainforest includes being diurnal, **arboreal** and feeding on fruits and insects from the trunks of trees up to a height of 10 m above ground level. Saddle-back tamarin monkeys live in groups of 2–12 individuals, in which there is generally only one primary female who will copulate to produce offspring. After a gestation period of around 155 days, she gives birth, usually to twins, when food resources are abundant.

arboreal
mostly tree-dwelling

Emperor tamarin monkeys (*Saguinus imperator*) fill a niche where they are also diurnal and arboreal. However, as well as fruits and insects, they also feed on green leafy plants, eggs and tree sap from trees 10–30 m above ground level. They live in a troop of around 2–8 family members and breed between the months of April and July when the dominant female gives birth around 140 days later, generally to twins.

Despite living in the same range, the saddle-back tamarin and emperor tamarin exhibit different ways of life and thus occupy their own niches (Figure 3.5.1).

FIGURE 3.5.1 Saddle-back tamarins (*Saguinus fuscicollis*) occupy an overlapping but ultimately different ecological niche from that of their cousins, the emperor tamarins (*Saguinus imperator*).

Fundamental versus realised niches

An American zoologist, G.E. Hutchinson, distinguished between the **fundamental niche** and the **realised niche**. The fundamental niche is the ideal niche a species would occupy if there were no competitors, predators or parasites. It is the widest set of potential relationships and interactions possible. The realised niche is narrower and represents only the actual relationships and interactions. The discrepancy results from an organism's inability to fully exploit the resources of its habitat because of restrictions imposed by other organisms. In this way, a species may not be distributed evenly throughout its potential geographic range, nor will its diet be an even balance of all of its potential prey.

fundamental niche
the widest potential niche that a species could ideally 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

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 including Tasmania. However, the species is not distributed evenly throughout this geographical range because successful competitors, such as the blue-winged kookaburra, occupy its niche in certain areas.

Resource partitioning

To alleviate competition for niches, some organisms use a method called **resource partitioning**. Because organisms within an ecosystem cannot feed on the same food sources at the same time, they differ in their use of space and even the timing of their activities. Different forest birds feed on the same trees at different heights above the ground (Figure 3.5.2), and some animals feed at night while others feed during the day. Different species of shorebirds have different leg lengths and beak shapes, which allows them to exploit different parts of the mud flats and feed at different depths. These differences reduce competition and allow a larger number of species to live in the same habitat.

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

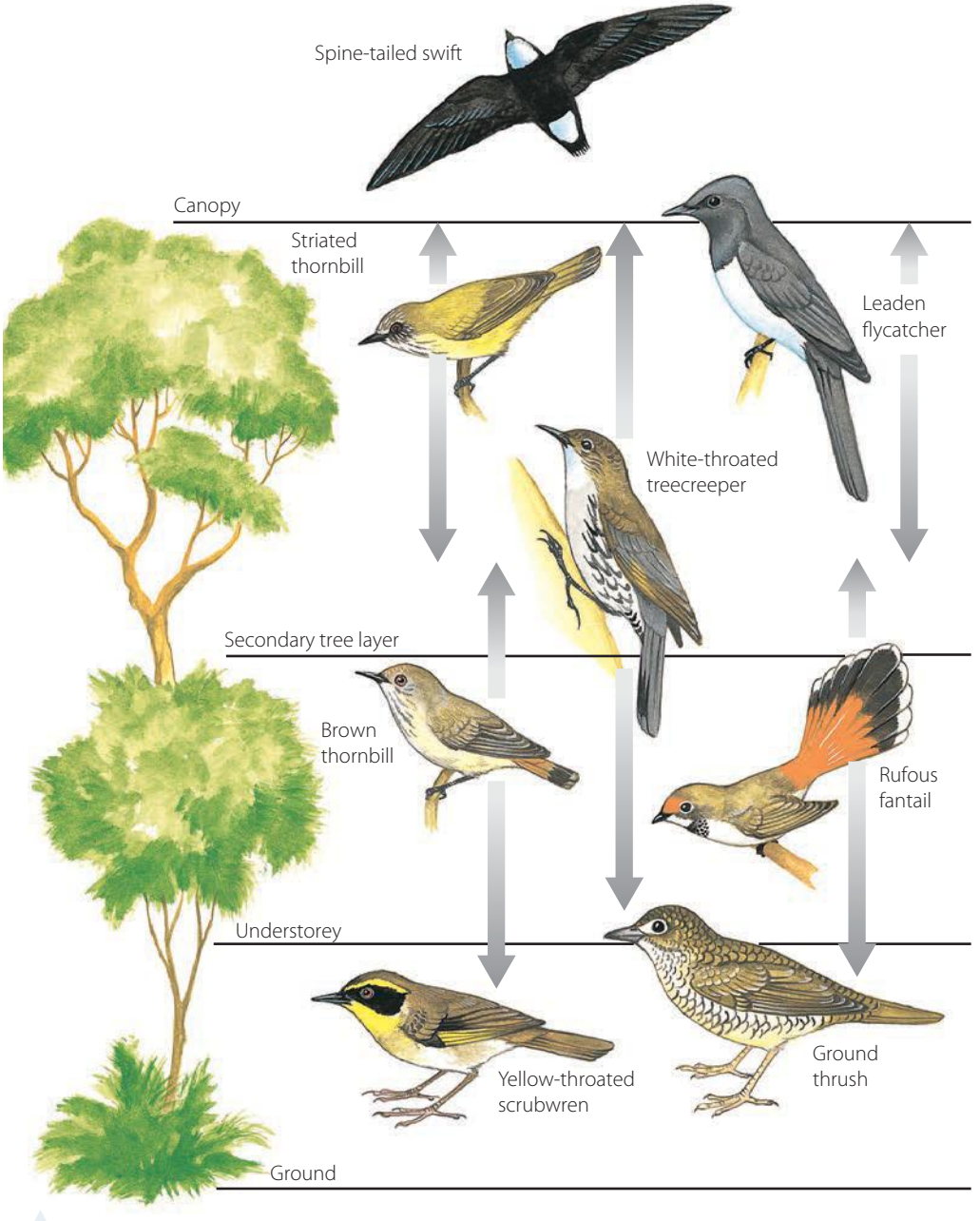

FIGURE 3.5.2 Resource partitioning reduces feeding competition between these bird species, which would otherwise occupy the same ecological niche in an eastern Australian eucalypt forest.

SECTION REVIEW 3.5

REMEMBERING

1 Define 'ecological niche' and provide an example.

2 Describe the difference between a fundamental niche and a realised niche.

UNDERSTANDING

3 Explain how resource partitioning allows more species to inhabit the same area than would otherwise be possible.

4 Briefly outline the realised ecological niche of the Torresian crow (Figure 3.5.3).

FIGURE 3.5.3
Torresian crows (*Corvus orru*) are one of the most common birds in Australian urban settings and make a nuisance of themselves with loud, raucous calls and rubbish bin riffling.

APPLYING

5 American ecologist Joseph Connell conducted an experiment to determine the fundamental and realised niches of two different species of barnacle, *Balanus balanoides* and *Chthamalus stellatus*. The two barnacles inhabited the same rock face but *C. stellatus* was found on higher rocks and *B. balanoides* was found 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*.

3.6 Competitive exclusion principle

competitive exclusion principle
a key ecological principle that states that no two species can occupy exactly the same niche in an ecosystem

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. Competitive exclusion is one of the main reasons for the difference between fundamental and realised niches.

In 1934, Russian ecologist, G.F. Gause completed an experiment between *Paramecium aurelia* and *Paramecium caudatum*, two closely related species of protists. Gause found that when he grew each species as two separate cultures, with a constant source of food, the population numbers increased

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exponentially until they reached the **carrying capacity** of the culture – the greatest density of organisms that the culture can potentially support. However, he found that when the two species were grown in the same culture, *P. aurelia* had a competitive advantage. *P. aurelia* was able to obtain the food more effectively than *P. caudatum* and drove it to extinction.

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

Based on the interpretation of the data collected (Figure 3.6.1), Gause concluded that two similar species competing for the same resource cannot coexist in the same community. One will be able to obtain and use the resource more effectively and in turn reproduce more quickly than the other. Further models and experimentation supported Gause's idea, which became the basis of the competitive exclusion principle. However, the principle has since been modified by evidence that two ecologically similar species are able to coexist in the same community as long as they have at least one considerable difference in their niches.

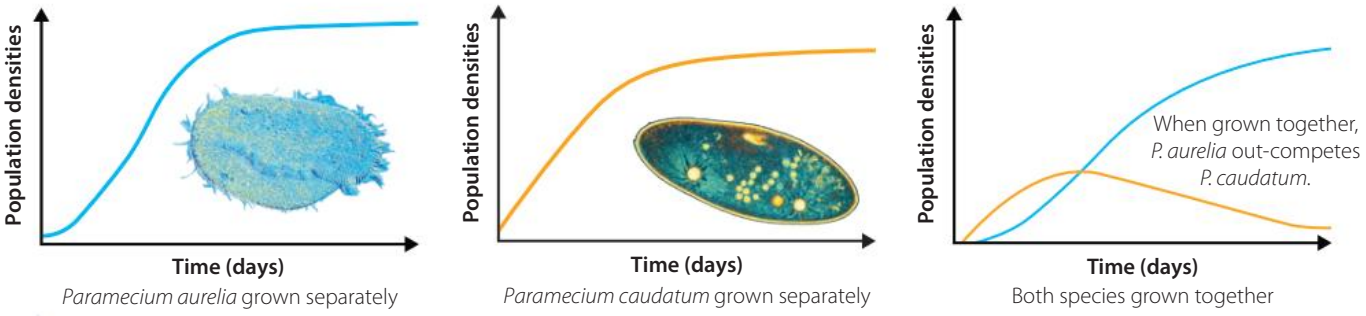

FIGURE 3.6.1 Gause discovered that two similar species of *Paramecium* occupying the same niche in the same community compete with each other to extinction.

PRACTICAL ACTIVITY 3.6.1

Data analysis: species identification

INTRODUCTION

The competitive exclusion principle postulates that no two species can occupy the same niche in the same environment for an extended period of time. Experiments can be used to test this principle and produce models of this interaction, which can then be used to make predictions about the effect of changes within an ecosystem on biodiversity.

A team of scientists investigated Gause's competitive exclusion principle by conducting a field experiment. They studied two **sessile** species, A and B, introduced onto an intertidal rock face. Over a period of 18 months, population density data was collected within the test quadrats and compiled in Table 3.6.1.

sessile fixed or non-moving, as in a species that remains fixed in one place for its lifespan

TABLE 3.6.1 Population density of two sessile species over 18 months on an intertidal rock face

TIME (MONTHS)	POPULATION DENSITY (INDIVIDUALS/m^2)	
	SPECIES A	SPECIES B
0	5	5
1	12	8
2	17	14
3	36	24
4	55	60
5	50	67
6	43	62
7	45	104
8	50	100
9	38	104
10	25	115
11	30	119
12	16	125
13	18	133
14	21	139
15	14	158
16	8	141
17	0	158
18	0	164

QUESTIONS

Short items

1 Sketch a rough graph of the data in Table 3.6.1.

2 Which species had the competitive advantage in the first 3 months?

3 How long did the two species coexist before the competitive exclusion principle began to take effect?

4 Which species had the overall competitive advantage after 18 months?

Interpreting data

5 Outline what occurred to species A throughout the experimental period.

6 Both of these species were introduced to the rock face community. Predict the consequences of this experiment on the biodiversity of the rock face in general.

7 If a disease were to affect the reproductive success of species B at 10 months, predict what would happen to the populations of both species by 18 months.

8 Assess the validity of Gause's competitive exclusion principle when applied in this experiment.

Responding to new stimuli

9 Another species, species C, competes for the same resources as species A and species B, but has a shorter maturation period. Predict the impact on the populations of all three species if species C was introduced to the rock face at the beginning of the experiment.

SECTION REVIEW 3.6

REMEMBERING

1 Summarise how Gause developed his idea of competitive exclusion.

UNDERSTANDING

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. Give an example of an animal that would:

- **a** competitively exclude this species
- **b** compete with this species in some aspects, but would likely not competitively exclude them.

3 Explain why ecologists are so concerned about the impact of feral cats on the continued existence of many Australian native animals and birds.

APPLYING

4 The competitive exclusion principle also applies to much 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.

3.7 Keystone species

The limitations that competition, predation and disease place on a species force it to compromise on its fundamental niche, resulting in a much narrower realised niche. Narrow niches are good for biodiversity because they allow the time, space and resources to support a larger number of species in the community. Changes to species interactions, including the addition or removal of other species, can reduce the pressure on a species to remain in its realised niche. This can have lasting consequences for the ecosystem.

The purple sea star (*Pisaster ochraceus*) is a natural predator of mussels in the intertidal zones of Pacific Ocean seashores (Figure 3.7.1). When researcher Robert Paine removed purple sea stars from this environment, the resident mussels were no longer affected by predation and their population expanded. The mussels displaced the other sessile organisms, such as barnacles and limpets, as they spread. The diversity of species in the area decreased from 15–20 invertebrates and algae to fewer than five over the period of 3 years. When the sea stars were returned, the mussels were again preyed upon and the barnacles, limpets and other species were able to re-occupy the space they left behind.

FIGURE 3.7.1 Purple sea stars (*Pisaster ochraceus*) are a keystone species in intertidal rock pools, where they keep the mussel population under control.

In this community, the presence of the predator, *P. ochraceus*, allowed the stable coexistence of a large number of species with the same requirements for food and space, by limiting the mussel population to a narrower niche. Without the sea stars, the mussels were no longer as restricted, and their expansion into niches held by other species triggered the competitive exclusion principle. Biodiversity plummeted as species after species were outcompeted by the mussels. The ecosystem restabilised after the predators were reintroduced and the mussels were forced back into their original niche.

keystone species a plant or an animal that plays a unique and crucial role in the way an ecosystem functions

The purple sea star in this community is known as a **keystone species.** Keystone species have a 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, nor necessarily the top-level predator, but their presence prevents any one species from monopolising space and resources in the area.

Over time, scientists have recommended policies in a bid to conserve biodiversity. Conservation of a single keystone species should be the central point for the management strategies of an entire community. Scientists have also argued that keystone species are essential in the re-establishment of ecological structure and sustainability.

A keystone species prevents organisms from lower trophic levels from monopolising food resources and space.

INQUIRING FURTHER

Reintroduction of a keystone species

The idea that 'apex predator' is synonymous with 'keystone species' causes issues, including when grey wolves were reintroduced to Yellowstone National Park, USA, in 1995, after an absence of nearly 50 years. They were originally thought to be saviours of the park, which was suffering from a serious overpopulation of elk, who were destroying the native willow population. Compare the enthusiasm of scientists just after their reintroduction with the comments of scientists now, when the willow population still has yet to recover.

PRACTICAL ACTIVITY 3.7.1

Data analysis: Australian keystone species

INTRODUCTION

There are five general types of keystone species: predators, prey, plants, links and modifiers. Keystone predators keep populations in the lower trophic levels under control and within narrow niches. Keystone prey provide a simple and abundant food source for organisms in the higher trophic levels, protecting more fragile species in the lower trophic levels from overpredation. Keystone plants provide food and shelter for a large percentage of the organisms in the ecosystem and are often the only source of food and shelter for a number of them. Keystone links are organisms that provide essential services for a wide range of species in the ecosystem, such as seed dispersal. Keystone modifiers play a major role in shaping the environment to suit the diversity of species present, such as dam-building and other structural or chemical modifications.

Stimulus data

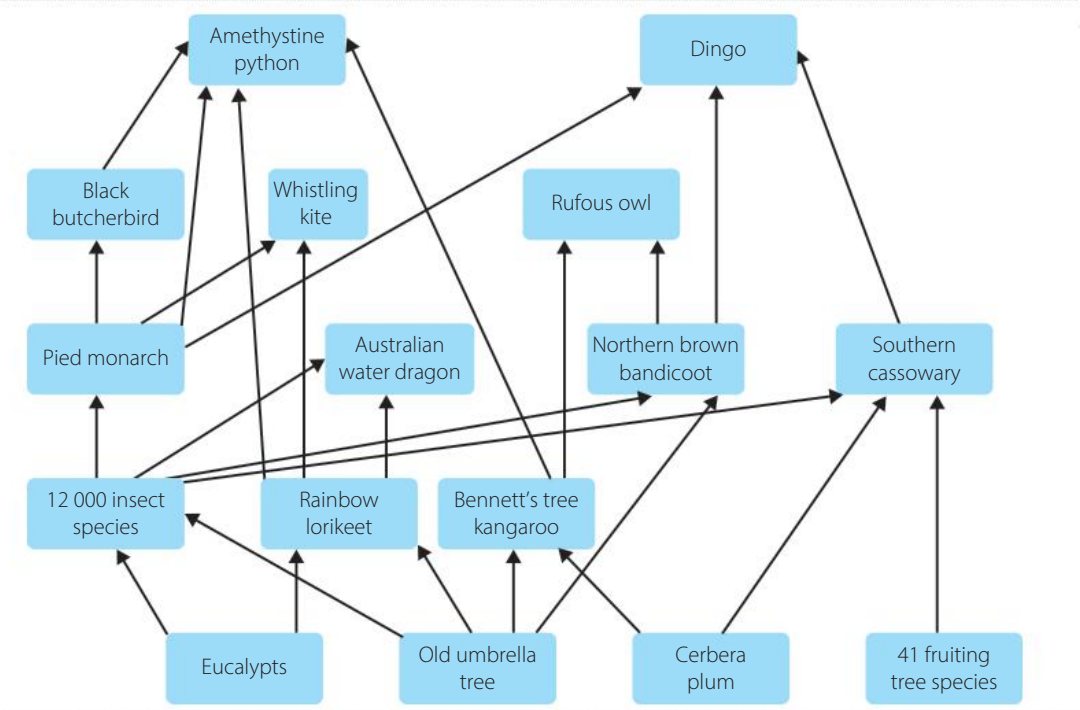

FIGURE 3.7.2 The Daintree lowland rainforest in Far North Queensland has an ecosystem too complex to fit in a single food web. Simplified food webs, such as this one, include many of the important components.

TABLE 3.7.1 Ecological profile of the Daintree lowland rainforest

PROFILE COMPONENT	COMMENTS
Access to shelter	The vast majority of the rainforest is composed 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 allows limited light to the forest floor, though this does not hamper the rain.
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.

QUESTIONS

Refer to both Figure 3.7.2 and Table 3.7.1 when completing the analysis questions.

Short items

1 Name two top predators in the Daintree lowland rainforest.

2 List the food sources of the rufous owl.

3 Explain where the nutrients from the rainforest soil come from.

Interpreting data

4 Referring to Table 3.7.1, comment on the chances of a seed germinating on the forest floor.

5 Predict the effect on the ecosystem if the black butcherbird were to be removed.

6 a Identify one keystone species from this data. Justify your choice.

b Explain which type of keystone species it is.

c Predict the outcomes of removing this species from the ecosystem.

Responding to new stimuli

7 Due to a crocodile cull on the coastline, saltwater crocodiles have been moving further into the Daintree lowland rainforest. Determine where they would fit in the food web and the effects on your keystone species.

SECTION REVIEW 3.7

REMEMBERING

1. Define 'keystone species'.
2. Describe the role that purple sea stars play in their community.

UNDERSTANDING

3. Explain why narrow niches are good for biodiversity.
4. Compare and contrast the terms 'dominant species' and 'keystone species'.
5. Southern cassowaries (*Casuarius casuarius*) are considered a keystone species in the northern Queensland rainforests. They eat fruits from more than 100 rainforest plant species, and are the main seed disperser for most of them. Predict what would happen to the animals and plants in the rainforest if the cassowary died out.

APPLYING

6. Many ecologists believe that keystone species should be central to the efforts to amplify biodiversity. However, others are of the opinion that the definition of a keystone species is not yet refined enough to form the basis of conservation efforts. They speculate that this process could be detrimental to species that are not considered key to biodiversity, and yet are indicators of habitat health. Justify your opinion on the issue.

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CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1 Briefly sketch an outline of the following biogeochemical cycles.

- **a** Carbon cycle
- **b** Water cycle
- **c** Nitrogen cycle
- **d** Phosphorus cycle

2 Calculate the transfer efficiency of energy in the food chain shown in Figure 3.8.1.

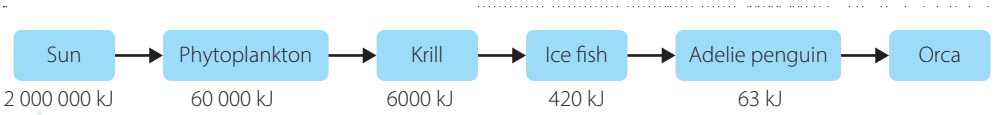

FIGURE 3.8.1 Ocean ecosystems are often less efficient at converting sunlight into chemical energy because of the reduced light intensity below the water's surface.

3 **a** Define 'ecological niche'.

b Explain how the competitive exclusion principle ensures only one species occupies a niche at a time.

CATEGORY QUESTIONS

4 Compare and contrast the carbon and nitrogen cycles.

5 Describe the common characteristics of keystone species.

ELABORATION QUESTIONS

6 Explain how keystone species affect the realised niches of the other organisms in their ecosystem.

7 Predict what would happen to the human food supply if scientists were able to engineer a species of rice that was 70% efficient at converting sunlight to chemical energy.

EVIDENCE QUESTIONS

8 Provide two examples of keystone species and their effects to support your response to Question 6.

9 Explain one negative effect of your scenario in Question 7.

END-OF-CHAPTER EXAM

End-of-chapter test

1 Producers can also be categorised as:

A homotrophs.

B heterotrophs.

C autotrophs.

D chemotrophs.

2 In the nitrogen cycle, nitrogen can be found in all of these variations except:

A N

B N_2

C NO_3^-

D NH_4^+

3 An organism's ecological niche is a combination of all of these except:

A feeding relationships.

B species interactions.

C structural adaptations.

D behavioural adaptations.

4 Draw a food chain with four organisms, showing their trophic levels and the flow of energy.

5 Draw a biomass pyramid for an ecosystem with 7000 kg of sea grass, two 500 kg dugong, 400 kg of small fish and a 90 kg shark.

6 Explain whether the ecosystem in Question 5 is well balanced.

7 Give an example of a keystone species and describe its role in its community.

8 Discuss the advantages and disadvantages of identifying keystone species during conservation efforts.

9 Outline three separate interventions that would offset the increase in atmospheric CO_2 from burning fossil fuels. Refer specifically to the carbon cycle in your response.

10 Discuss the implications of narrow niches on the general health of an ecosystem.

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4 POPULATION ECOLOGY

Introduction

The black swan (*Cygnus atratus*) is a nomadic species of waterbird native to the waterways of Australia, including fresh water, brackish (briny) water and seawater. In times of plentiful rain, food is abundant. Adult swans will migrate to areas that have received the heaviest rain and will reproduce. These waterways often have a small resident population, which will quickly increase in number due to the increased birth and immigration rates. When the environmental conditions return to their previous levels, resources are depleted. Most of the swans will leave and some will die because of the lack of food. Because of the increased emigration and death rates, the local population size is reduced to a level that the environment can support at that time.

Stimulus questions

How is the size of a population measured?

What limits the population size and rate of growth in an ecosystem?

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4.1 Carrying capacity of populations

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

Populations are defined as the total number of a particular species in a particular place at a particular time – for example, the number of manna gums (*Eucalyptus viminalis*) in a heathland community, the number of straw-necked ibises (*Threskiornis spinicollis*) in a wetland in a particular month, or even the number of possums in an urban area. Populations in an ecosystem are dynamic. You might have noticed changes in the number and kind of plants or insects in your neighbourhood from one season to another or from year to year.

Knowing the size of populations helps scientists and ecologists understand the habits and needs of organisms. This enables humans to sustain and ensure that vulnerable species persist and contribute to the planet's biodiversity. Determining the size of various populations addresses many needs, whether it is to help understand how a vulnerable species such as the flatback turtle (*Natator depressus*) is able to survive disturbances from uncontrolled vehicles and coastal development in its Queensland nesting beaches, or to determine how many minke whales Iceland may hunt 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 ensure that Earth's biodiversity is maintained? The factors that would require consideration vary greatly between species. For example, a minke whale population in any area may be as small as six animals or as large as 50–100 animals where food is plentiful. Even the six whales are enough to maintain the population consisting of two mature females, one mature adult male and two or three immature animals. Krill (the food of many baleen whales, such as minke whales) are considered to be at risk with a population size of fewer than one million individuals.

4.1.1 Population ecology

Limiting factors

There is a limit to the number of individuals who can occupy an environment. As population size increases, the demand for resources, such as food, water, shelter and space, also increases. Eventually, there will not be enough resources for each individual. The **carrying capacity** describes the maximum population size of a species that can be supported in a given environment.

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

Populations rely on balanced relationships between their biotic and abiotic components. These factors can vary over space and time. The maximum populations that a particular environment can sustain depend on the biotic and abiotic limiting factors at any given place and point in time.

Biotic factors

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

Changes to biotic factors can affect the carrying capacity of the ecosystem. For example, the availability of food affects the number of young that are born to female kangaroos (Figure 4.1.1). When food is plentiful, the female may have up to three young at various stages of development: a joey that has mostly left the pouch and no longer depends on the mother for nourishment; a young 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 is able to abandon any one of the three young kangaroos. Without her protection, they most certainly perish. This may seem harsh but is ensures that a sustainable population size is maintained. In the long term, this offers stability to the ecosystem and equilibrium to the populations that exist within it.

The loss or introduction of a species can change the carrying capacity for other species in that environment. For example, removal of rabbits (*Oryctolagus cuniculus*) on a farmer's land by introduction of calicivirus increases the carrying capacity for sheep.

FIGURE 4.1.1 The kangaroo-carrying capacity of an environment is affected by the amount of food available.

Abiotic factors

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*) 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. In its specific habitat, this ensures survival of the species. However, 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 used 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.

SECTION REVIEW 4.1

REMEMBERING

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

2 Provide two examples of how ecologists can use knowledge of population size.

UNDERSTANDING

3 Identify and discuss four biotic limiting factors that can affect carrying capacity. Choose two of these factors to explain how carrying capacity is affected.

4 Identify and discuss four abiotic limiting factors than can affect carrying capacity. Choose one of these factors to explain how carrying capacity is affected.

5 Predict the effect of a flood or fire on the carrying capacity of an area.

4.2 Population changes

Platypus (*Ornithorhynchus anatinus*) numbers in the eastern states of Australia have fluctuated over recent times. One method of determining their numbers includes enlisting the help of the public in reporting any sightings to a national database. The information gathered has been used to determine the health and sustainability issues for existing populations. The biggest impact on numbers in water bodies is human activity, specifically dumping rubbish that finds its way into the waterways and freshwater habitats of the platypus. Relationships between organisms can change. At the same time that humans are assisting in the data collection, their activities are impacting directly on platypus numbers. Studying populations can help us predict such changes to their numbers and the far-reaching consequences to the ecosystem they inhabit.

Getty Images/Simone Mueller

FIGURE 4.2.1 Black swan numbers can greatly increase in waterways after heavy rain.

migration
the movement of individuals of a species from one place to another

Population growth

The population size changes seen in the nomadic black swan (*Cygnus atratus*) waterbird (Figure 4.2.1) is an example of an open ecosystem, where **migration** between populations of animals (and occasionally plants) can occur. This migration will affect overall numbers in the ecosystems involved, their distribution and, in the longer term, birth and death rates.

In the Queensland rainforests located between Townsville and Cooktown, a small number of bird species exist that are not found in any other areas. All of their survival and reproductive needs must be met within this rainforest habitat. Victoria's riflebird (*Ptiloris victoriae*) is another example of a species existing in only one area. The population is in decline as its growth rate depends only on birth and death rates. There is no migration because other members of the species will not move into an area where their species is under threat. The decline also reflects habitat loss and hunting pressures. However, the species is abundant throughout its range. This is an example of a closed ecosystem, where migration does not impact at all on population size. A population is therefore increasing if the birth rate and/or **immigration** rate exceeds the death rate and/or **emigration** rate. Rate refers to the number of individuals per hundred, per thousand or whatever unit is appropriate.

Conversely, a population decreases when the death and emigration rates exceed the birth and immigration rates. The decline in the numbers of the common sparrow in Indian urban settings is one such example (Figure 4.2.2). As the wetland habitat of these birds is reduced due to increased

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FIGURE 4.2.2 In India, house sparrow numbers have declined as a result of urbanisation.

immigration
the movement of individuals of a species into a place

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

urbanisation, emigration may occur in the first instance, but the carrying capacity is reached at their destination and therefore the birds just die. The reduction in abiotic and biotic factors in its habitat affects many aspects of the sparrow's needs, including availability of nesting sites, food, water and shelter, which together lead to a reduced birth rate. Interestingly, the sparrow is also an indicator of urban ecosystem health. Urban ecosystems are defined as ecosystems of towns and cities – essentially those constructed by humans. They can have both positive and negative impacts on the surrounding ecosystems of the natural world. After initial establishment issues, wildlife, in particular, have been able to adapt and thrive in these environments. How well they integrate into the setting helps determine the general health and growth of this human-made ecosystem. Therefore, the decrease in sparrow numbers does not bode well for the future of this specific ecosystem.

KEY FORMULA

Population growth rate

Population growth rate = (birth rate + immigration rate) – (death rate + emigration rate)

= (br + ir) – (dr + er)

WORKED EXAMPLE 4.2.1

Calculate the growth rate of a population of 1000 individuals where, every year, 100 individuals are born, 65 individuals immigrate into the population, 37 individuals die and 25 individuals emigrate to another population.

- Substitute the numbers of individuals into the key formula.

ANSWER

Growth rate = (br + ir) – (dr + er)

= (100 per 1000 + 65 per 1000) – (37 per 1000 + 25 per 1000)

= 103

Therefore, the population has grown by 103 individuals per 1000. Growth rates can also be expressed as a percentage: +10.3% if there is an increase or –10.3% if there is a decrease.

4.2.1: Crash Course Ecology #2: The Texas mosquito mystery

4.2.2: Crash Course Ecology #3: Human population growth

SECTION REVIEW 4.2

REMEMBERING

1. List the characteristics of populations that are usually studied when calculating the growth rate.
2. Distinguish between migration, immigration and emigration.

UNDERSTANDING

3. Ecosystems can be open or closed to particular species. Describe what effect this has on growth of a population.

APPLYING

4. Predict if a population's size is increasing or decreasing when (br + ir) is greater than (dr + er).
5. A particular population of kangaroos has 1000 births during the year; 72 individuals join the population, 108 leave and 345 die. Work out the growth rate for this population of kangaroos for the year.
6. Calculate the growth rate of a population if, for every 1000 individuals, there are 59 born, 105 immigrants, 86 deaths and 40 emigrants.
7. Calculate the growth rate of a population if, for every 1000 individuals, there are 150 born, 59 immigrants, 29 deaths and 30 emigrants.

4.3 Measuring populations

direct observation
a method used to measure abundance, e.g. recording sightings at particular intervals; can be time-consuming and dangerous

It might be possible to measure populations by making **direct observations** and recording sightings at particular intervals, but this is time-consuming and can sometimes be dangerous; for example, in the case of male fur seals in the breeding season on windswept shores. Satellite images have been used to determine percentage vegetation cover in relatively inaccessible regions. In aquatic ecosystems, plankton nets are used to 'sweep' the organisms, and aircraft traverse areas to count kangaroos and other large mammals like musk ox in the Arctic and antelope on African savannahs.

GPS tracking is also used to track the movements of migrating animals such as birds and caribou, and is most efficient when tracking water animals such as whales, sharks, sea turtles and many sea birds. The signal is received by a satellite that ensures the animals are tracked when not in sight.

UAVs (unmanned aerial vehicles) or 'drones' are becoming a more common way to monitor wildlife populations (Figure 4.3.1). Drones collect data with better spatial and temporal resolution. Computer technology can be linked to drone images to identify and count targeted species automatically. Some people are concerned that drones may place undue stress on animals. However, it is generally thought that the data collected by drones could substantially improve the accuracy of population estimates, particularly in places that may be inaccessible to humans on foot.

FIGURE 4.3.1 Drones are an efficient and accurate way to estimate wildlife numbers, especially in remote areas that are hard to access.

To determine the population numbers of nocturnal species, scientists need to use specialist equipment. For example, researchers in New Zealand use spotlights with a red filter to determine the number of fish in a measured and netted area of a river. The filter reduces the impact on the fish and counting can be carried out reliably.

It is not always possible or necessary to determine the population size of a species by direct observation. Birds and insects are constantly on the move, and some animals move too fast to be counted. Other sampling techniques can be used to make estimates of a population. A **sample** is a small group of organisms selected from the total population in a given area or volume. This sample represents the whole population.

sample
a small group of organisms selected from the total population; is representative of the whole population

Choosing a particular site because it is easy to get to or is more interesting, or selecting only two sample specimens, reduces the reliability of the data obtained. It does not give a true picture of the whole population. To represent the population as a whole reliably, the samples must be collected in an unbiased way.

Lincoln index

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

capture–mark–recapture
an ecological surveying technique used to measure animal populations, in which individual animals are captured, marked and released; after a time, the population is re-sampled and the number of marked animals caught gives an indication of population size

The **Lincoln index** is commonly used to sample mobile species. A random sample of individuals of a species is taken and an overall estimation of the abundance of the species is made. This method is also referred to as the **capture–mark–recapture** method.

KEY FORMULA

Lincoln index

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

where N = the total population

M = the number of individuals caught, marked and released initially

n = the number of individuals caught on second sampling

m = the number of individuals recaptured that were marked

- **Step 1 Capture.** Animals are caught randomly without hurting them. Small animals are trapped in cages or pitfalls in the ground, birds are trapped in fine nets and some animals are caught easily when they 'freeze' in spotlights. Flying insects are attracted to light traps.
- **Step 2 Mark and release.** Each captured animal is marked so that the mark is not obvious to predators or harmful to the organism (Figure 4.3.2). Insects are usually marked with a blob of paint, whereas birds are tagged on the leg or wing. The animals are returned to their habitat and left to mix with the unmarked individuals.
- **Step 3 Recapture.** A random sample is taken and the number of marked individuals is counted. The timing of recapture needs to be appropriate to capture a random mixture of individuals, but before the original marked individuals have died. From this information the total population can be estimated. The procedure has to be planned carefully so that the chances of each individual being caught are equal. Sometimes 'trap happy' individuals will be sampled repeatedly.

FIGURE 4.3.2 Tagging a turtle is a way of marking captured animals, who will then be released and possibly recaptured.

The Lincoln index method of estimating populations is demonstrated in Worked example 4.3.1.

4.3.1 Investigating ecosystems

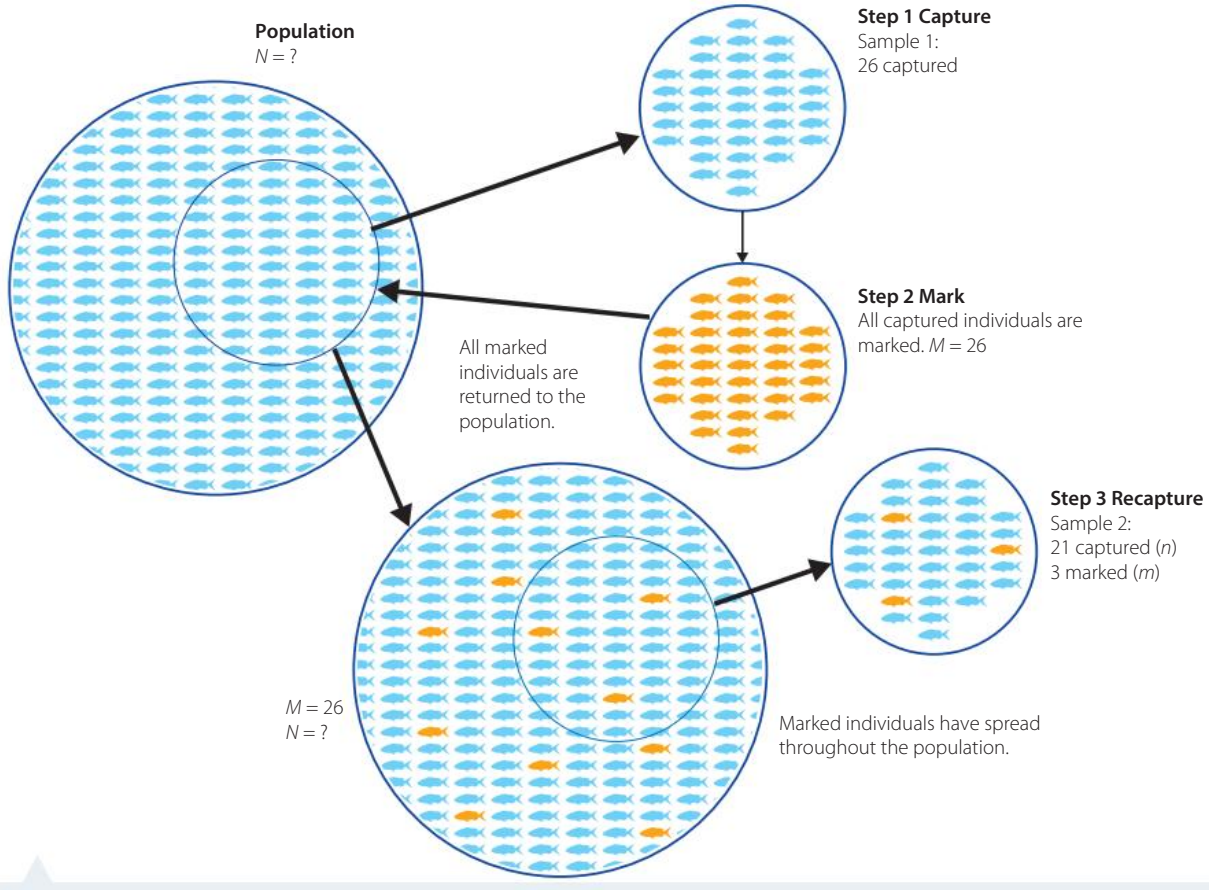

FIGURE 4.3.3 The Lincoln index method of estimating population numbers

WORKED EXAMPLE 4.3.1

If 20 individuals were marked and released and 50 individuals were recaptured, 10 of which were marked, what is the total population?

- Substitute the numbers of individuals caught and marked into the key formula

ANSWER

$$N = \frac{M \times n}{m}$$
$$= \frac{20 \times 50}{10}$$
$$= \frac{1000}{10}$$
$$= 100 \text{ individuals in the total population}$$

INVESTIGATION 4.3.1

Estimation of population size

When you study a population of organisms, whether it is a school of fish or a population of wombats in a certain area, it is not possible or even necessary to count all members of a given population. Therefore, estimates of numbers within the population are made on the basis of various sampling techniques. A sample is a small group of organisms, selected from the total population, which is representative of the whole population. But just how reliable are these methods of estimating population size?

AIM

To estimate the size of a non-living population using the Lincoln index and to comment on its reliability as a technique.

MATERIALS

Each student requires:

- 160 white or black buttons (beads or matches may be substituted)
- plastic cup to mix or shake the buttons

PROCEDURE

1. Using a marker pen, mark 40 of the buttons with an 'X'. Alternatively, use buttons that are a different colour from the rest; for example, 40 yellow buttons among all the black or white ones.
2. Thoroughly mix the marked buttons with the rest of the buttons by shaking them in the cup.
3. Take out a sample of 20 buttons and count the number of marked ones.
4. Assume that if the sample taken is representative of the whole population, then the ratio of marked objects will be the same in both the sample and the whole population:

$$\frac{\text{total marked}}{\text{total population (marked and unmarked)}} = \frac{\text{number marked in sample}}{\text{number (marked and unmarked) in sample}}$$

$$\frac{\text{40 marked}}{\text{out of 160 total}} \text{ should produce } \frac{\text{5 marked}}{\text{out of 20 in a sample}}$$

$$\text{So the total population} = \frac{\text{number in sample} \times \text{total number marked}}{\text{number marked in sample}}$$

$$\text{In this example, the total} = \frac{20 \times 40}{5}$$
$$= 160$$

5 Calculate your estimate of the population in your Results.

6 Repeat the procedure an additional nine times, each time returning the sample and mixing to get a reasonable average. You should now have 10 population estimates based on 10 samples.

7 Draw a table and record your results.

8 Finally, count all the objects in your population.

RESULTS

1 Record your calculations: 10 estimates of population size.

2 Record your table of results.

3 Write your average estimated population size.

DISCUSSION

1 According to your calculations, explain how reliable this technique is at estimating population size.

2 Can you suggest any ways of improving the accuracy of this technique in this experiment? Explain.

3 Discuss the advantages and disadvantages of using the Lincoln index to estimate a wild population of mice or blue whales.

CONCLUSION

1 Refer back to the aim of this experiment. Have you achieved this aim? Write a conclusion based on what you have learned.

Measuring distribution

It is not only important to know the population size, it is also important to know the distribution – exactly where in the physical space members of the different species are found.

Members of a population are seldom spread evenly throughout the entire ecosystem. There are patterns in the way populations are distributed.

- **Random distribution**: organisms are spaced irregularly; the location of an organism does not affect the location of another organism (more common for plants than for animals).
- **Uniform (continuous) distribution**: organisms are evenly spaced; the presence of one organism determines how close or distant another will be. It is common in relatively high-density populations of some animals that set up breeding territories.
- **Clumped (grouped) distribution**: a number of individuals are grouped together and the groups make up the population as a whole. This is sometimes related to social behaviour, such as in schools of fish, or clumping of vegetation in mini-habitats where biotic and/or abiotic factors are favourable.

random distribution
a measurement of distribution in which organisms are spaced irregularly

uniform (continuous) distribution
a measurement of distribution in which organisms are evenly spaced

clumped (grouped) distribution
a measurement of distribution in which individuals are grouped together when biotic and/or abiotic factors are favourable; can be social (e.g. schools of fish) or clumping of vegetation

Knowing the distribution and abundance of a species can help keep track of populations of significance. Knowledge of particular plant species can give clues about the distribution and abundance of animals that depend on them. The forestry industry needs to know about the distribution and abundance of valuable tree species, and the fishing industry needs to know about fish stocks. Keeping track of pest and plague species, such as mice and locusts, gives forewarning of potential outbreaks that would require management.

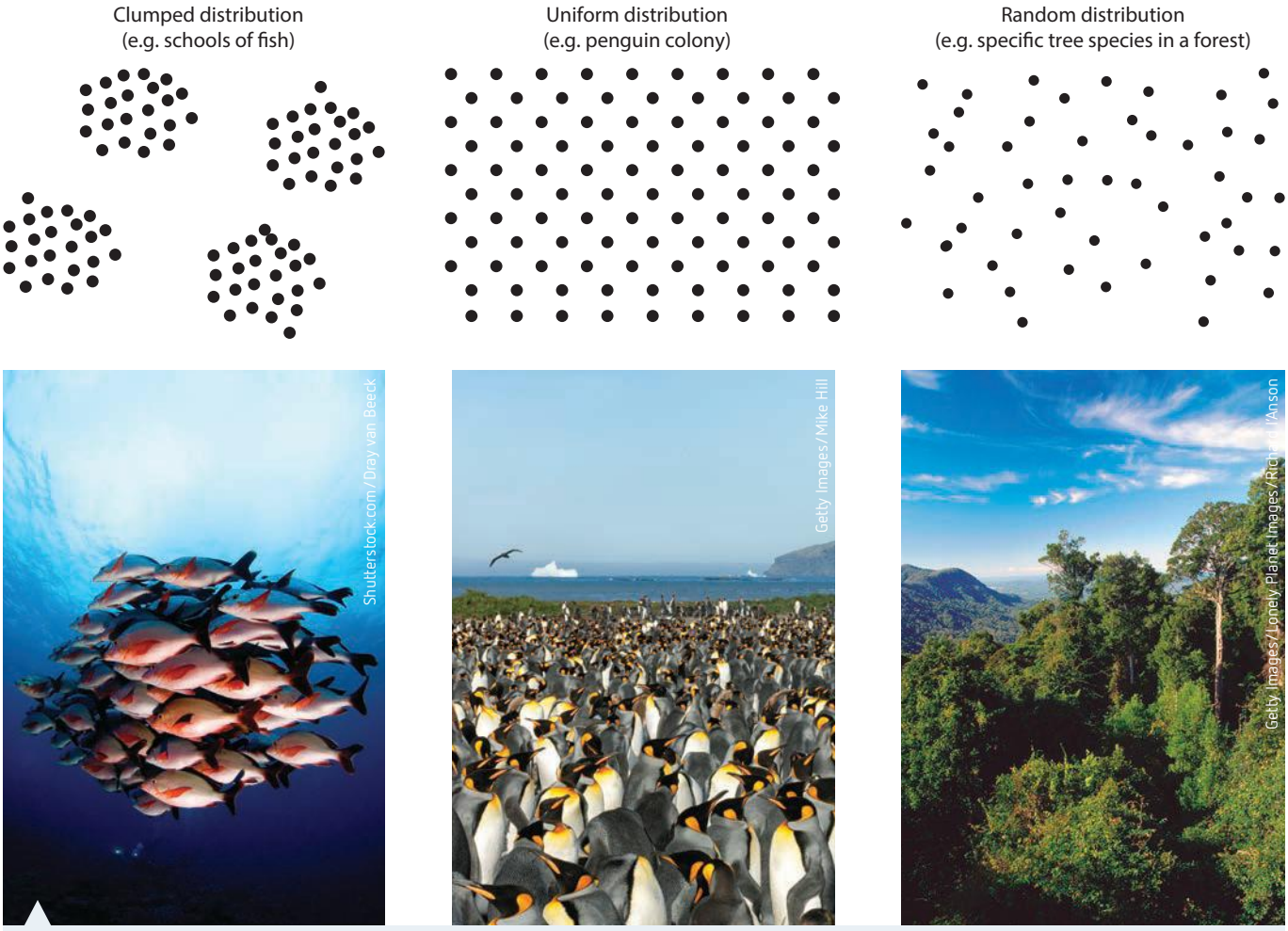

FIGURE 4.3.4 Distribution patterns: clumped, uniform and random

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SCIENCE AS A HUMAN ENDEAVOUR

One of the seven natural wonders of the modern world, the Great Barrier Reef stretches over 3000 km from near Bundaberg to past the northern tip of Cape York. It is the richest and most diverse natural ecosystem on the planet.

GBROOS (Great Barrier Reef Ocean Observing System) is an observing system that collects data such as temperature and salinity profiles, waves and currents in the marine park. Marine ecologists from the CSIRO are applying survey data and using technologies such as underwater instrumentation, airborne and satellite remote sensing, oceanographic datasets and model outputs to provide insights for scientific understanding and management.

Research how data collection is contributing to our understanding of coral bleaching and how the data is used to inform government policies on conservation in the Great Barrier Reef.

INQUIRING FURTHER

The Great Barrier Reef is under threat from both natural and human activities. Determine what these threats are and what is being done to monitor and reduce them and to minimise their impacts.

4.3.2 Great Barrier Reef Foundation

4.3.3 Managing the reef

4.3.4 Science and the Great Barrier Reef.

SECTION REVIEW 4.3

REMEMBERING

1 Write out the Lincoln index formula in both notation and word form.

2 Describe three basic patterns of distribution of populations of organisms.

UNDERSTANDING

3 Distinguish between the abundance and distribution of a species.

4 Explain why direct observations are not always possible or ideal when calculating population size.

5 Describe a circumstance under which the Lincoln index method of population sampling would be used.

APPLYING

6 An ecologist records the abundance of turtles in the Great Barrier Reef by using the Lincoln index. In the first sample, 30 individuals were marked. In the second sample, 50 individuals were recaptured and 10 of these were marked. What is the total population?

7 The ecologist in Question 6 moved to another location and recorded turtle abundance. In the first sample, 100 individuals were marked. In the second sample, 200 individuals were recaptured and 50 of these were marked. What is the total population?

ANALYSING

8 Briefly explain how the ecologist in Questions 6 and 7 would record the abundance of turtles in the Great Barrier Reef by using the Lincoln index.

9 Explain how an emerging technology is used to estimate abundance and distribution of populations. Find one advantage and one disadvantage of this technology.

4.4 Mode of population growth

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

Exponential growth J-curve

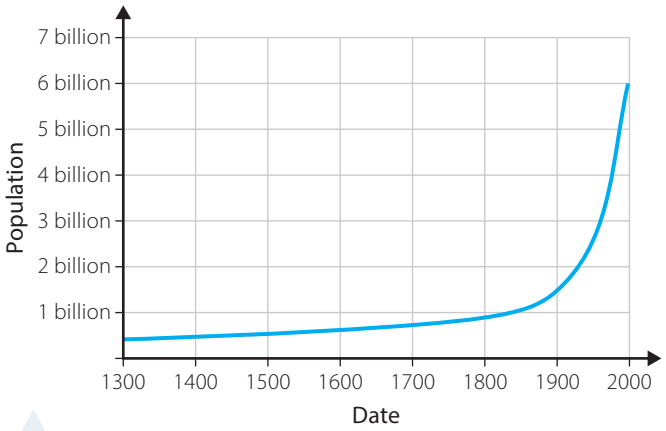

FIGURE 4.4.1 Exponential human population growth results in a J-shaped curve.

In unstable, unpredictable ecosystems, such as after a fire or land-clearing, opportunistic species move in and colonise as quickly as they can. In these environmental conditions, population explosions of these colonisers follow. In order to survive, these types of species must colonise new environments quickly, and be able to reproduce rapidly and in relatively large numbers. Population increase in these conditions is called **exponential population growth**.

The size of a population that is growing exponentially increases at a constant rate, resulting in a J-shaped growth curve (Figure 4.4.1) when population size is plotted over time. Under ideal conditions with unlimited resources, every population has a particular maximum potential for growth. The size of the population after a period of time has passed is estimated by the exponential growth model.

The world's human population is a good example of exponential population growth. The human species is thought to have evolved about 200 000 years ago. For most of the time since then, humans lived a precarious existence as hunters and gatherers. This kept their total population number less than 10 million. Development of agriculture allowed communities to develop that could support more people and population growth rate began to increase. After the start of the Industrial Revolution in the 1700s, living standards rose and widespread famines and epidemics diminished in some areas. Population growth rate increased rapidly and is continuing to increase as new technologies and resources increase Earth's carrying capacity.

exponential population growth
the growth of a population in an ideal, unlimited environment

Logistic growth S-curve

When a few members of a species colonise a new and favourable habitat, the population increases rapidly. However, this population growth cannot be sustained; resources are used and the population begins to level off. Despite minor fluctuations in populations, there tend to be upper and lower limits. For a given species in a particular habitat, there is a certain equilibrium population that the ecosystem can support. In the **logistic population growth** model, the rate of population increase approaches zero as the population size nears the carrying capacity. When the logistic model is graphed, it produces an S-curve (Figure 4.4.2).

Factors in the environment, collectively referred to as **environmental resistance**, act on a population. If the population rises above the equilibrium, competition for resources such as food and space begins to take effect. The increased ability of disease-causing organisms and parasites to spread also increases deaths and possibly reduces breeding. This could be to such an extent that the population falls. If it falls below the equilibrium, there is less competition and the population begins to rise again. This kind of negative feedback process, or homeostatic control, keeps the population more or less constant.

logistic population growth
the population growth that levels off as population size approaches carrying capacity

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

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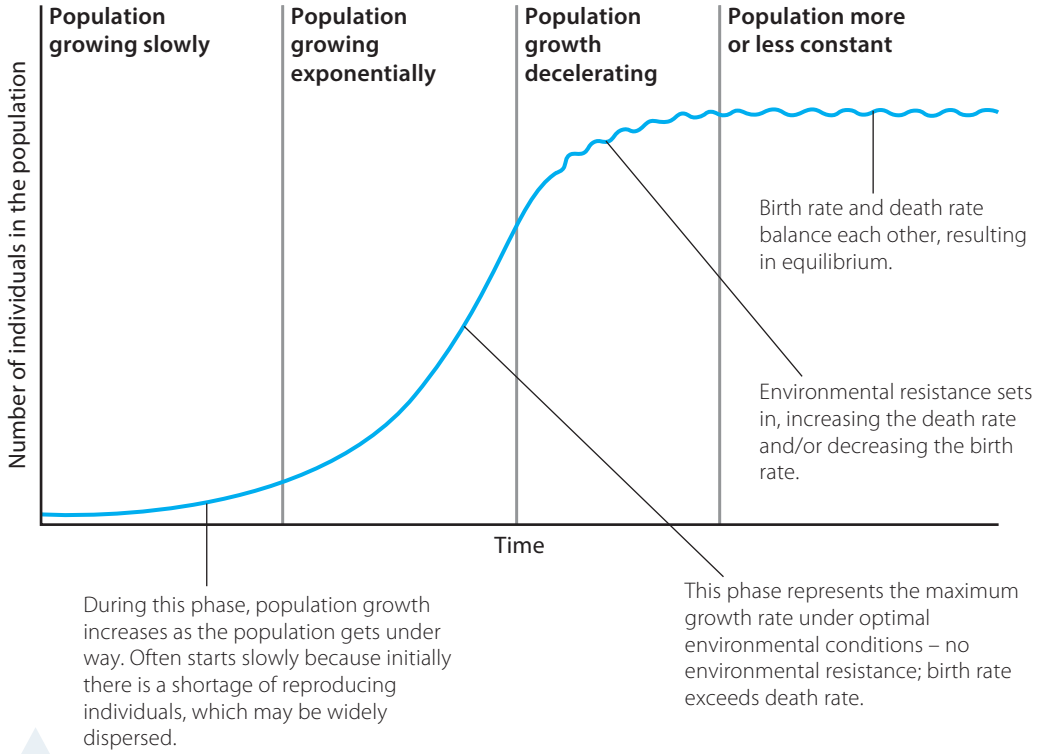

FIGURE 4.4.2 The S-curve is a generalised graph of population growth.

SECTION REVIEW 4.4

REMEMBERING

1 Describe the shape of a logistic population growth curve.

UNDERSTANDING

2 Distinguish between exponential population growth and logistic population growth.

3 Explain 'environmental resistance'.

4 Explain why an exponential growth curve is not typical of a population.

APPLYING

5 Consider two areas of forest in 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. Explain your reasoning.

4.5 Mandatory practical

DISTRIBUTION AND ABUNDANCE OF PLANTS

Introduction

Determining plant numbers and species is a lot easier than determining animal numbers and species. Plants do not move! Two sampling strategies work well. One is used to determine the density and total number of plants in a given area. Another method allows you to determine the distribution of a range of species within a defined space. You will be using both in this practical.

Aim

To investigate the distribution and abundance of local plants.

Materials

- 10 m tape measure
- three 1 m rulers
- pencil and eraser
- note pad

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.

Procedure

1. Select two sites to investigate: a school oval, and a forested area at least 10 m in length.
2. **a** On the oval, collect data about the number of plants on the total oval surface using a 1 m^2 quadrat.
   b In the forested area, collect data about the type and distribution of plants along a 10 m transect.
3. Record the amount of light (full sun, semishade, full shade) and water (moist, damp, dry) for each sample area.

Results

1. Using your collected data, determine the species types and number.
2. Research to determine the needs of each species.
3. Record your results in a table.
4. Compare your results with data from other groups.

Discussion

1. Account for any differences between the data from your group and data from other groups.
2. Decide whether your group's data or combined data from all groups would be more accurate. Explain reasons for your answer.
3. Discuss the effect of different amounts of light and water on weed density.

Conclusion

Make sure your conclusion includes quantitative data that relates directly to the measurable quantities you mentioned in your aim. If possible, make an estimate of the uncertainty in your results.

CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1. What is the carrying capacity of a population?
2. What factors determine population growth rate?
3. What patterns of population growth are there?
4. What limiting factors affect the carrying capacity?

CATEGORY QUESTIONS

5. How do limiting factors affect the carrying capacity of a population?
6. How is population growth rate calculated?
7. What methods are used to calculate population size and distribution?
8. Under what conditions do populations increase exponentially?

ELABORATION QUESTIONS

9. Why do populations not continue to increase exponentially?
10. What would happen to population size and distribution if biotic and abiotic factors changed? Provide examples.
11. Why are direct observations not commonly used to measure populations? Provide examples.

EVIDENCE QUESTIONS

12. What, if any, external sources did you use to support your answers to questions 9–11?
13. Explain your reasoning behind your answers to questions 9–11.
14. What other factors could affect population size and growth?
15. How could your answers to questions 9–11 be improved?
16. What further evidence could be used to support your answers to questions 9–11?

END-OF-CHAPTER EXAM

End-of-chapter test

1 The 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 rate of increase of this population is:

A 13 individuals/year.

B 174 individuals/year.

C 200 individuals/year.

D 187 individuals/year.

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 total population of possums?

A 20 individuals

B 600 individuals

C 216 individuals

D 28 individuals

5 Define:

a exponential population growth

b logistic population growth.

6 Distinguish between biotic and abiotic limiting factors.

7 Relate how resources are distributed in an area to each of the population distribution patterns.

8 The Lincoln index or capture–mark–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 second recapture.

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9 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

10 Predict the effect on the carrying capacity for a population of rabbits if:

- **a** there were no predators in the areas where the rabbits lived
- **b** a predator such as a fox was introduced.

11 Describe the attributes that would indicate that a population is increasing in size.

12 A student is asked to estimate the population size of beetles in an area by using the Lincoln index method. Detail the steps involved.

13 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/m^2 have been recorded.

- **a** Outline the biotic and abiotic conditions that may give rise to locust outbreaks.
- **b** Name 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.

5 CHANGING ECOSYSTEMS

Introduction

Riversleigh in Queensland was once a lush rainforest. Today it is part of the driest vegetated continent on Earth. A few million years ago, there were no eucalypt trees to provide shade. The landscape was dominated by towering tea trees and pandanus that lined deep river pools where freshwater crocodiles swam and large wombat-like creatures called diprotodonts came to drink.

Today, the temperature soars above 40°C at midday, there is very little wind and everywhere you look it is dry, dusty and seemingly lifeless. Yet within a day, as Earth turns away from the Sun, the temperature drops dramatically. The scrublands come alive with nocturnal animals such as geckos, small mammals and a rich diversity of insect life. During the rainy season, Riversleigh is exposed to flooding rains, which transform the area into an inland freshwater wetland that forms a temporary home for thousands of water birds on their migratory routes.

These daily and seasonal changes are examples of relatively short-term change. Riversleigh, like other ecosystems, is always changing. Ecosystems have changed from what they were millions of years ago and will continue to change annually, seasonally and daily. Ecosystems are dynamic in nature.

Stimulus questions

How do communities change progressively over time?

Is there any difference in the biotic factors of disturbed and undisturbed areas?

What impact has human activity had on biodiversity and ecosystem changes?

Alamy Stock Photo / petpics

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5.1 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. Communities change progressively over time, with one community being replaced by the next in serial replacement known as **succession**.

succession
the progressive change of communities over time

Shutterstock.com/mark higgins

FIGURE 5.1.1 Riversleigh, Queensland, was once a lush rainforest supporting an enormous array of plants and animals. This fossil site is now part of the driest vegetated continent on Earth.

Primary succession

Catastrophic events such as volcanic eruptions, cyclones, earthquakes and tsunamis can cause the development of bare sites with no organisms inhabiting them. This process, called **nudation**, starts a long-term process of change, generally involving three stages.

nudation
the development of bare sites with no organisms inhabiting them

The first stage is known as **primary succession**. **Pioneer plants** begin to colonise the area. The particular species of pioneer plants depends on the environmental factors in the habitat, such as whether it is coastal sand dunes, mangroves, or newly formed islands rising from the sea as a result of volcanic activity.

primary succession
the colonisation of plants in a barren place

Autotrophic organisms such as lichens are usually the first to become established in harsh, bare surroundings, such as after glacial retreat. Acids secreted by the lichens attack the rocky surface in the process of weathering, allowing windblown dust particles to settle in the cracks and form 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, bacteria, fungi and invertebrates are able to form a simple community. At various stages, there is enough soil for grasses, ferns and shrubby herbaceous plants to become established; they grow upwards and outwards, shading those below, their roots speeding up the process of weathering.

pioneer plant
a plant capable of invading bare sites, such as a newly exposed soil surface

r-selected species
a fast-growing and reproducing organism, often the first to occupy unused resources and living space

These early colonising pioneer plants are hardy enough that they can live under extreme conditions. They are able to grow in poor soils with low nutrient levels. As they grow, these plants have the ability to fix nitrogen into the soil through their relationship with specialised bacteria growing in root nodules. Pioneer species are normally small and photosynthetic. They have characteristics that make them successful: effective seed dispersal, rapid growth and rapid reproduction. They are generally fast-growing and typical of **r-selected species**. The J-shaped curve of exponential growth is characteristic of r-selected species.

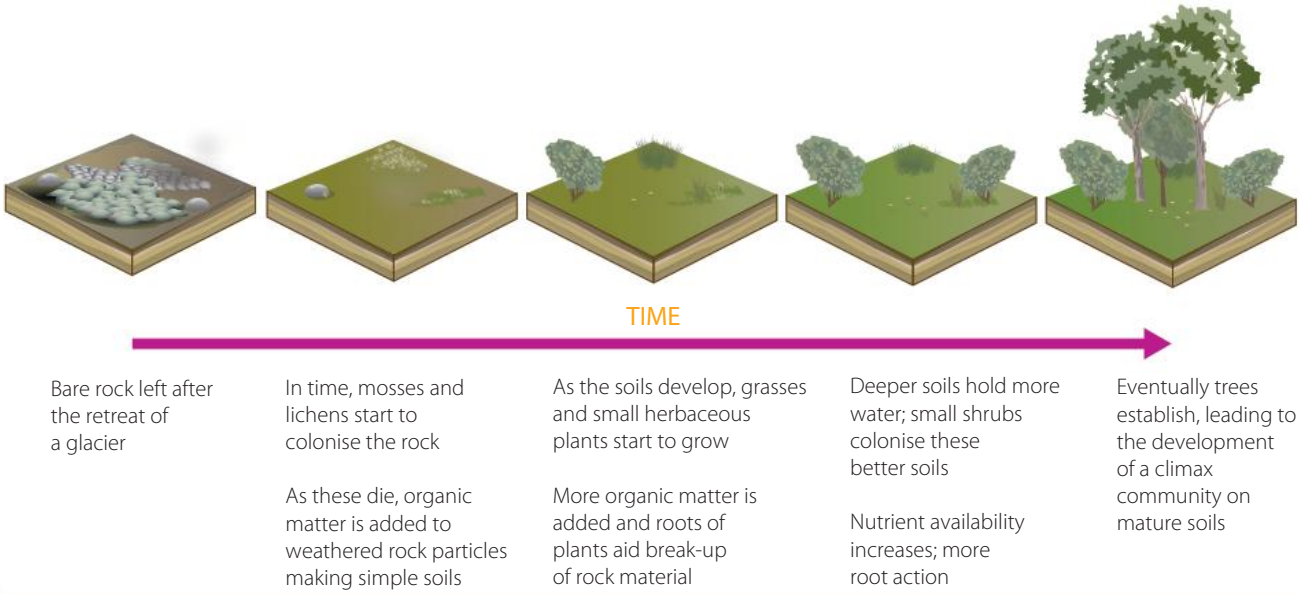


FIGURE 5.1.2 Primary succession following glacial retreat

Temporary environments such as pools formed after heavy rain also attract r-selected species. These species are often the first to occupy the unused resources and living space. Their numbers increase rapidly but often decline just as rapidly when more competitive species move in.

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. Gradually, a new community forms, colonised by immigrants from the surrounding areas. Immigrants survive or stay only if they can obtain the resources that they need for survival.

Secondary succession

secondary succession
the recolonisation of disturbed plant communities

Through fire and flood, or through human intervention by logging and land clearing for agriculture, dramatic changes to ecosystems occur. The cycling of matter and the flow of energy are interrupted as the components of the ecosystems are affected. Organisms can recolonise recently disturbed communities via **secondary succession**, regaining equilibrium, although the number and kinds of organisms present may be different from the original ecosystem (Figure 5.1.3).

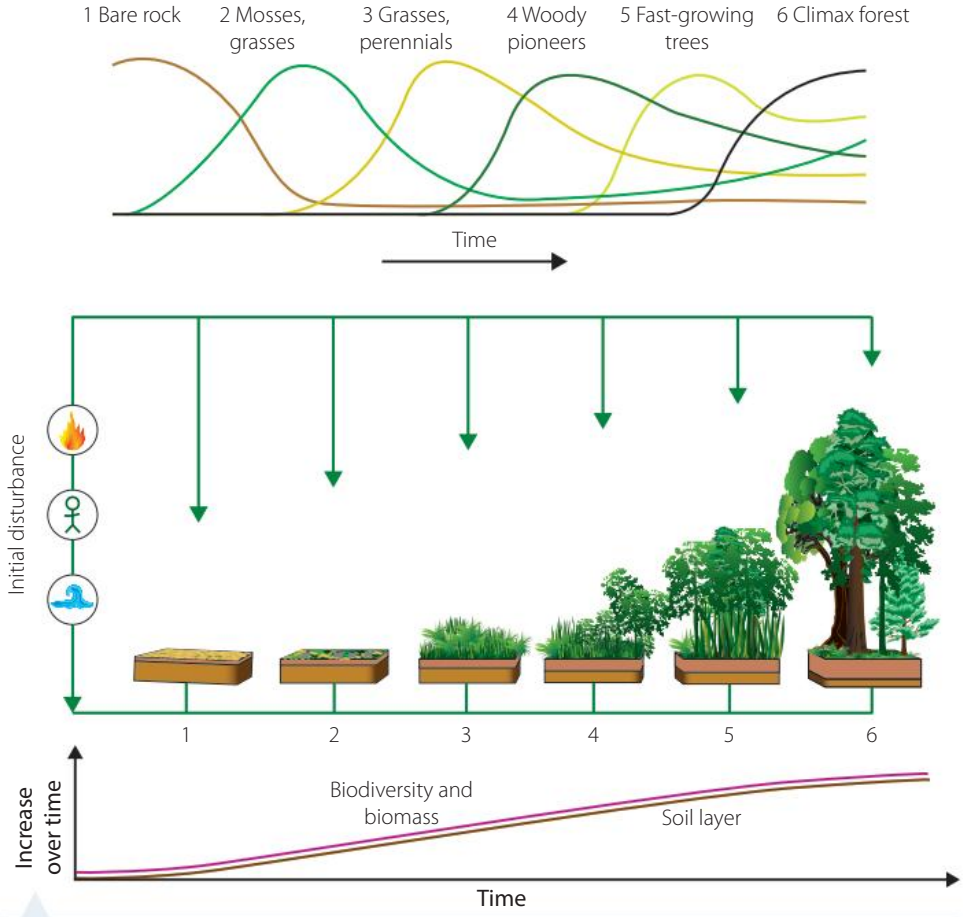


FIGURE 5.1.3 Forest succession over time in six stages

Climax community

The end of succession is marked by a **climax community**. The old-growth forests of Cooloola National Park in south-east Queensland (Figure 5.1.4) and the temperate rainforest pockets scattered throughout the east coast of Australia are examples of climax communities. Such communities tend to be made up of slow-growing, long-lived **K-selected species**. These species, living in more stable environments than r-selected species, out-compete the others around them. They are often tall trees such as oaks or large conifers in the northern hemisphere, and trees such as kauri or mountain ash in Australia.

Not all successions reach a climax community. For example, a combination of factors such as fire and selective grazing by herbivores helps to create conditions that allow grasslands to persist.

FIGURE 5.1.4 The rainforests of south-east Queensland are an example of a climax community.

climax community
the end-point in a community succession where the community has become relatively stable, e.g. old-growth forests and rainforests

K-selected species
a slow-growing, long-lived species typical of those in a climax community

Predictions of succession

To predict the stage of succession in a habitat, data on a number of features is collected and analysed (Table 5.1.1).

TABLE 5.1.1 Features in a habitat that can be used to predict the stage of succession

FEATURE	PRIMARY SUCCESSION	SECONDARY SUCCESSION
Type of species present	r-selected; small size of organisms; fast growing	K-selected; organisms larger in size; slow growing
Biodiversity	Low	High
Biomass	Low	High
Biotic interactions	Simple interactions, food chains common	Complex interactions, food webs operate
Abiotic interactions	Small amounts of poor-quality soil; low nutrient levels; unused resources and living spaces; conditions unstable	Large amounts of good-quality soil and nutrients; resources and living spaces in demand; stable conditions

SECTION REVIEW 5.1

REMEMBERING

1 Describe factors that may prevent succession from reaching a climax community.

UNDERSTANDING

2 Distinguish between primary and secondary succession.

3 Draw an annotated timeline to show the sequence of stages in primary succession.

4 Predict the stages of succession where the majority of species are:

- **a** r-selected species
- **b** K-selected species.

5 Relate the characteristic features of r-selected species and K-selected species to the stages of succession they are most likely to be found in.

5.2.1 The discovery of Dinosaur Cove

5.2 Ecosystems can change dramatically over time

In the early 1980s, palaeontologists studying the 110-million-year-old rock sequences at Dinosaur Cove in Victoria pieced together evidence of a different land. Australia, Africa and Antarctica did not exist 110 million years ago (mya). In fact, none of the continents we know today existed at that time; they were all joined together to form a supercontinent called Pangaea.

Pangaea initially split into two large landmasses, Laurasia to the north and Gondwana to the south. The great southern continent of Gondwana contained what was to become the Australian landmass. By 110 mya, Gondwana was beginning to break up. South America was separating from Africa, and India was beginning its long trek north. This was an important stage in the physical isolation that was to give Australia's biota (plants, animals and other organisms) such distinctive characteristics.

palaeontologist a scientist who studies palaeontology, the science of the forms of life that existed over the course of Earth's history (e.g. the study of fossils)

Pangaea the supercontinent consisting of all of Earth's land masses; it existed from the Permian through the Jurassic period before breaking up during the late Triassic period

Evidence of changes in past ecosystems

Comparing present biota with those in the fossil record helps us to understand changes in living components of ecosystems over time. Changes in abiotic factors can also be deduced by studying soils, rocks and even ice cores.

Laurasia
the northern supercontinent formed after the break up of Pangaea; it included what is now North America, Europe, Asia, Greenland and Iceland

Gondwana
the southern supercontinent formed after the break up of Pangaea; it included what is now Antarctica, India, Africa, Australia and South America

biota
the living organisms in a region

FIGURE 5.2.1 An artist's impression of Riversleigh as it may have appeared 15 mya based on fossils preserved in the limestone rocks of the area.

5.2.2 Evidence of plate tectonics
5.2.3 The Pangaea pop-up

Scientists can accurately predict and describe Riversleigh's ecosystem 25–15 mya because many of the more than 250 sites at Riversleigh that are rich in fossils are well preserved (Figure 5.2.1). These sites are supplying a detailed and continuous fossil record of the changes in biota. 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. Scientists are using the characteristics of the grey limestone deposited 25–15 mya. Early relatives of today's fauna were preserved in the lime-rich sediments of the wetlands that flourished at this time. This layer lies on top of older limestone without the fossil remnants and without sedimentation patterns characteristic of a wet climate.

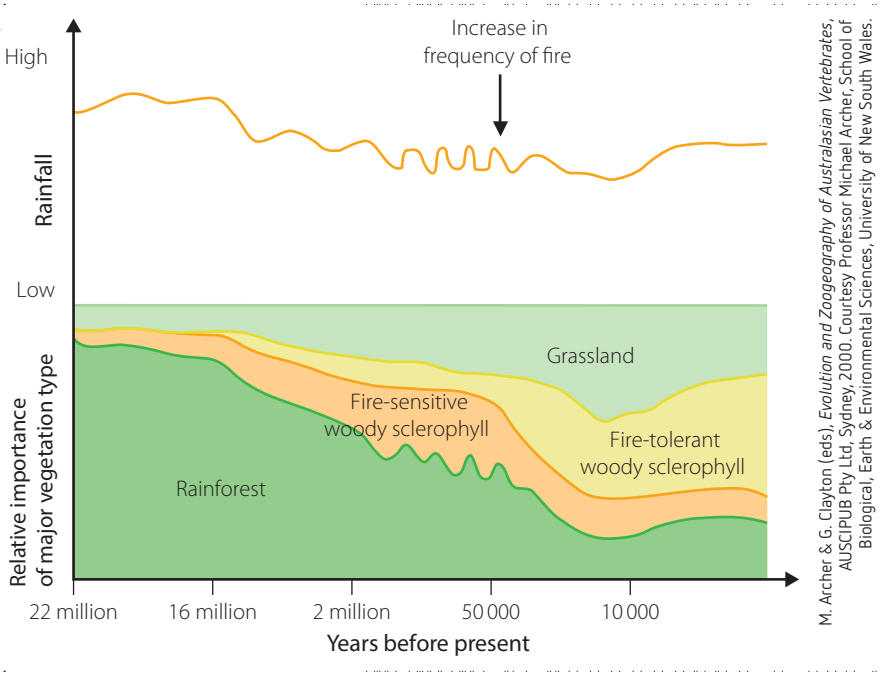
Ice cores as evidence of change

Drilling down into the ice at the poles and within large glaciers produces cores that have preserved a continuous record of past climatic conditions (Figure 5.2.2). 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 15 000–18 000 years ago.

FIGURE 5.2.2 An ice-drilling site in Antarctica.

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. Reduced global temperatures and lower evaporation rates also affected the water cycle – lower levels of atmospheric water meant lower rainfall (Figure 5.2.3). A little more than 15 000 years ago Australia became a desert: windblown, dry and, for more than three-quarters of the continent, treeless. Two-thirds was covered in sand dunes and the top soil was heavily wind-eroded.



M. Archer & G. Clayton (eds), *Evolution and Zoogeography of Australasian Vertebrates*, AUSCIPUB Pty Ltd, Sydney, 2000. Courtesy Professor Michael Archer, School of Biological, Earth & Environmental Sciences, University of New South Wales.

FIGURE 5.2.3
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.

Analysing data to predict successional changes

To better understand successional changes in ecosystems, ecological data is used to develop models. The development of models of interactions between components of ecosystems has advanced rapidly over the last few decades.

spatio-temporal
relating to space and time

Models, such as those demonstrating successional changes over space and time (**spatio-temporal**), are built from data gathered and the interpretation of that data. The most accurate and comprehensive data set would entail 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 random sampling. The reliability of the model is determined by the representativeness of the sampling.

Ecosystem models are useful representations of elements within the ecosystem, the relationship between the elements and the relationship with surrounding ecosystems. Ecosystem models are very useful for simulating and analysing the long-term dynamics and properties of complex ecosystems. They allow information from different disciplines as well as analysing, interpreting and understanding field observations. This provides a basis for predictions of the impacts of changes in real ecosystems, the development of tools for management support and policy advice.

One of the most widely used models is that of ecological succession. The concept of secondary succession is applied to restoration ecology projects worldwide in an effort 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.

SECTION REVIEW 5.2

REMEMBERING

1 Describe the relative changes in vegetation types in Australia over the past 22 million years.

UNDERSTANDING

2 Describe how models of successional changes over space and time are developed.

3 Discuss how the well-preserved fossils and surrounding sedimentary rock at Riversleigh have been used by scientists to determine the ecosystem of 15 mya.

APPLYING

4 Explain how sampling ice cores can be used to give evidence of climatic change.

5 Explain the effects of the last ice age on Australia's climate. Suggest how the drop in sea level would have helped to preserve biodiversity.

5.3 Impact of human activity

Until a few tens of thousands of years ago, humans were just one species among countless others. Today, there are few areas in the world that have not been influenced by our activities. Within a relatively short span of time, our activities have been changing the character of the land, ocean, atmosphere and even the genetic character of species. We now have the population size, technology and cultural inclination to use up energy and modify the environment at rapid rates.

Maintaining our standard of living is important, but the effects of this need to be evaluated against the overall sustainability of global ecosystems. It is ecosystems that maintain all life, including ours, on our planet. The variety of organisms, such as the genes they carry and the populations and ecosystems of which they are a part, is a measure of biodiversity. This also includes the ways in which the various components of biological diversity work together to sustain the biosphere. Maintaining a high level of biodiversity is a key to survival.

Australia's biodiversity is unique and globally significant, but humans have significantly impacted on its natural environment. Australia is recognised as one of only 17 'megadiverse' countries, with ecosystems of exceptional variety and uniqueness. This group of megadiverse countries covers less than 10% of the global surface, but supports more than 70% of Earth's biological diversity. Scientists are interested in exploring this biodiversity for natural compounds with medicinal potential. Unfortunately, this biodiversity also attracts people who would exploit it for illegal purposes, such as for the illegal trading of unusual collector items.

Australia's first human inhabitants

Aboriginal and Torres Strait Islander peoples came from the north through South-East Asia at a time when the sea level was lower than it is today. By at least 20 000 years ago, they had travelled through much of Australia's inland waterways and desert areas, and inhabited coastal areas and their hinterland. The first Australians were predominantly hunter–gatherers, obtaining their requirements from the land and water and adapting to the various climates and resources available. Like all humans, they exploited their environment to improve their own well-being, modifying their particular environment in the process.

Throughout much of Australia they changed a regime of fire induced by lightning to fire induced by humans to manage and sustain the productivity of the land. In the process, the distribution and abundance of different species of plants changed to ones that became more fire-tolerant. This in turn produced changes in wildlife.

megafauna
large animals

5.3.1 The age of megafauna

5.3.2 Megafauna

The demise of Australia's **megafauna** between 10 000 and 20 000 years ago has been attributed to continuous hunting and exploitation by first Australians, but this is still open to scientific debate. Extinct megafauna includes the *Diprotodon*, a giant wombat-like marsupial, and other large creatures such as a 6 m-long goanna and a 7 m-long python. Climate change, the use of fire and interrelated factors are likely to have contributed to their demise. Hunting megafauna would have removed the natural fertiliser of soils, estimated at 100 kg per adult per day, disturbing the cycling of matter between the living and non-living components of ecosystems and reducing the fertility of the soils, resulting in soils in which more fire-tolerant plants were able to grow. Climate change and fire would have changed the habitat and affected vegetation. Broad-leaved plants that were integral to cycling of water would have decreased in numbers, resulting in less rain and a more arid environment. Competition for resources would have been so severe that populations of the various megafauna would have become unsustainable.

SCIENCE AS A HUMAN ENDEAVOUR

INDIGENOUS ECOLOGICAL KNOWLEDGE: THE GUNDITJ MIRRING PARTNERSHIP PROJECT

The Budj Bim landscape in south-west Victoria 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.

It 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.

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 sharing and use of this resource will offer valuable insights for the protection and management of the environment today and in the future.

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 view that Indigenous communities have the potential to provide new and unique viewpoints on land management.

Identify reasons why it is important to conserve Aboriginal knowledge of species and ecological processes. Discuss the threats to the continuation of indigenous ecological knowledge.

FIGURE 5.3.1 Australia's early settlers tried to impose their foreign agricultural practices on a country that could not cope with them, irreparably damaging the landscape.

European settlement

Whatever the impact of Aboriginal and Torres Strait Islander peoples on the environment across Australia, they continued to survive and lived sustainably for tens of thousands of years. The effects of European modification of the landscape were much less subtle. As Europeans colonised more and more land, they tried to impose their agricultural practices on a country that did not have the soil, water or climatic stability for it. European settlers had little to no understanding of fire as a management tool, nor did they appreciate how well-adapted animals and plants could be used as food.

In early 1853, a settler by the name of John Robertson wrote to Governor La Trobe of Victoria of his concerns about the

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impacts sheep were having on the landscape. He noted that some plants had begun to disappear, clay (denuded) hills were slipping, springs of salt water were appearing and erosion from rainfall was becoming evident.

The rate of change to the environment after European colonisation had increased dramatically. Worldwide, the effect of human activity is marked. Destruction of land habitats, changes to the atmosphere and water, the stripping of vegetation and the exploitation of wildlife have all contributed to the extinction of thousands of species. The equilibrium of ecosystems and the biosphere as a whole has been upset, irreparably in places, in what has come to be described as the sixth extinction.

Human impact on ecosystems today

As Australia's population approaches 30 million, there is continued competition for both renewable and **non-renewable** resources. This parallels the effect of the global increase in population. Competition for land use is considerable: for agriculture; for habitats for native biota; for industrial and domestic constructions; for roads, waste disposal and the spreading urban development; and for minerals, matter and fuels that sustain a consumer society.

non-renewable a resource that exists in limited supply and cannot be replaced if it is used up within normal human timescales

Urbanisation

The community of urban ecosystems has reduced biodiversity and is dominated by people. There is little recycling of matter between the community and the non-living surroundings. Additional inputs of energy and matter are needed from other ecosystems to maintain modern standards of living. There is an increase in output of gaseous and material wastes of many kinds that are disposed of into the atmosphere, on the land and in the water of other ecosystems, which in turn become subject to change. For example, scarce landfill sites are being filled with material that could be recycled. Food scraps and other organic materials in landfill produce methane, a 'greenhouse gas' that could be tapped as a fuel, and of the seven kinds of plastic used for consumable items only two are accepted for recycling.

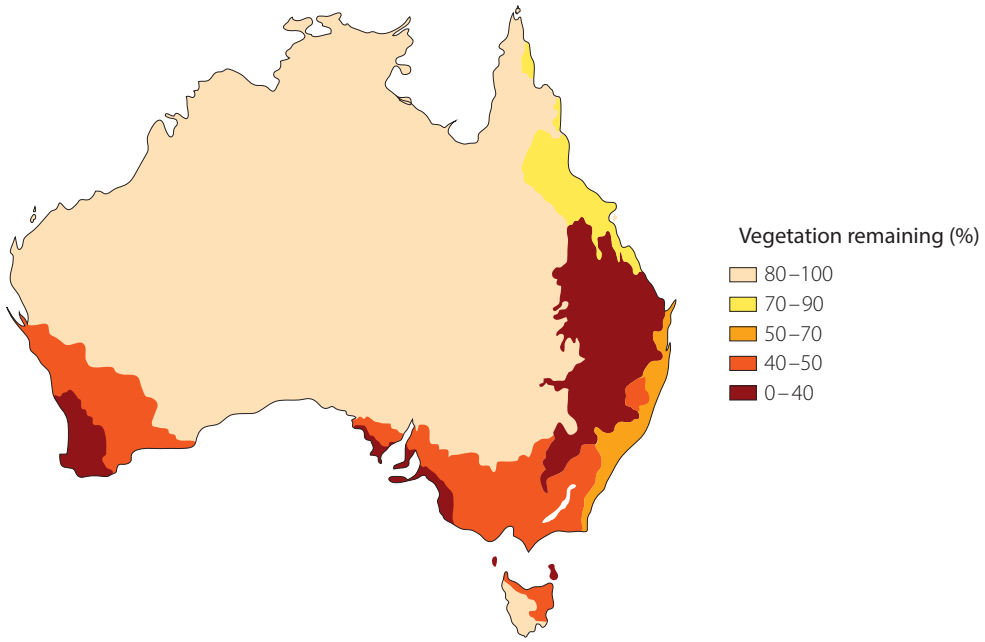
About 6.9 billion plastic shopping bags are used in Australia each year, and a great number of these end up in waterways and eventually the ocean. There they can take up to 500 years to break down and in the meantime cause a great deal of damage to marine ecosystems.

Urbanisation can cause rapid changes of large magnitude to an ecosystem. Local biodiversity is reduced and, even though new species may potentially move into an urban area, the ecosystem is changed for a very long time, often permanently.

Habitat destruction

Biodiversity is constantly changing, but is reduced by processes such as habitat degradation. Habitat degradation resulting from human activity has put many species at risk, with the clearance of native vegetation a significant threat to biodiversity. Since 1750, more than 20% of Australia's forests have been cleared for crops and grazing, with nearly 90% of the vegetation cleared in the more fertile areas of southeastern Australia. It is estimated that at the turn of this century we, as a nation, were clearing the equivalent of 740 football fields of land, each the size of an international cricket ground, per day.

The pattern of native vegetation loss shown in Figure 5.3.2 reflects that of European settlement and land use. The greatest reductions in native vegetation have been in eastern, southeastern and southwestern Australia, where post-1750 human settlement and agricultural land use has been the most widespread.



Hutchinson M, McIntyre S, Hobbs R, Stein J, Garnett S, Kinloch J. 'Integrating a global agro-climatic classification with bioregional boundaries in Australia', *Global Ecology and Biogeography*, 2005; 14:197–212.

FIGURE 5.3.2 Percentage of Australian native vegetation remaining since 1750

5.3.3 Threatened species and ecological communities in Australia

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

When native vegetation is cleared, habitats that were once continuous become fragmented. After intensive clearing, the separate fragments tend to be very small islands isolated from each other by cropland and pasture. This process is known as **habitat fragmentation**. Small fragments can support only small populations of fauna and flora, and these small populations are more vulnerable to extinction. Those that are separated from each other are unlikely to be recolonised and they do not support species that require large home ranges to obtain resources and locate mates.

Land and soil degradation

Settler John Robertson's records indicate a holding of more than 11 000 sheep on a property of just under 5000 ha, a little more than two sheep per hectare. While this may not sound like a significant number, it is well above the normal carrying capacity for such a large herbivore. Sheep and some other introduced domestic animals have hard hooves as opposed to the soft-footed structures of native animals, and so compact the soil when they graze. This creates opportunities for invasive, shallow-rooted, introduced plants at the expense of the deep-rooted native grasses. With significantly reduced tree cover and increases in shallow-rooted grasses, the topsoil becomes more exposed to the abiotic elements, in particular wind and rain. Sheep graze selectively, eating some plants in preference to others. The vegetation gradually changes in response to these pressures.

SYLLABUS LINK
Chapter 14 discusses the effect of habitat fragmentation as a mechanism of population isolation.

The degradation that happened on John Robertson's property has happened over much of Australia. While soil is the most basic of our agricultural resources, it is also finite. When measured against human lifetimes, soil is a non-renewable resource. To farmers, soil loss by wind or water means production loss (Figure 5.3.3). To the animals, plants and other organisms that live in that environment, it means death.

Past land clearance practices, the move to shallow-rooted pastoral grasses and the overuse of fertilisers that have affected soil organisms have placed enormous pressures on the structure of the soil and the ability of the land to hold its topsoil. Farming practices that rely on large and heavy machinery for efficiency have added to the problem by compacting soil, as is evident when removal of topsoil by wind or water exposes the deep, hard ruts in paddocks. Modern agricultural practices can cause rapid changes to the abiotic components of the ecosystem, in turn rapidly changing the biotic components. If there is significant change or loss of topsoil, the ecosystem may be permanently changed.

5.3.4 Australian actions to combat desertification and land degradation
5.3.5 Land degradation: measuring Australia's progress
5.3.6 Land degradation and the Australian agricultural Industry

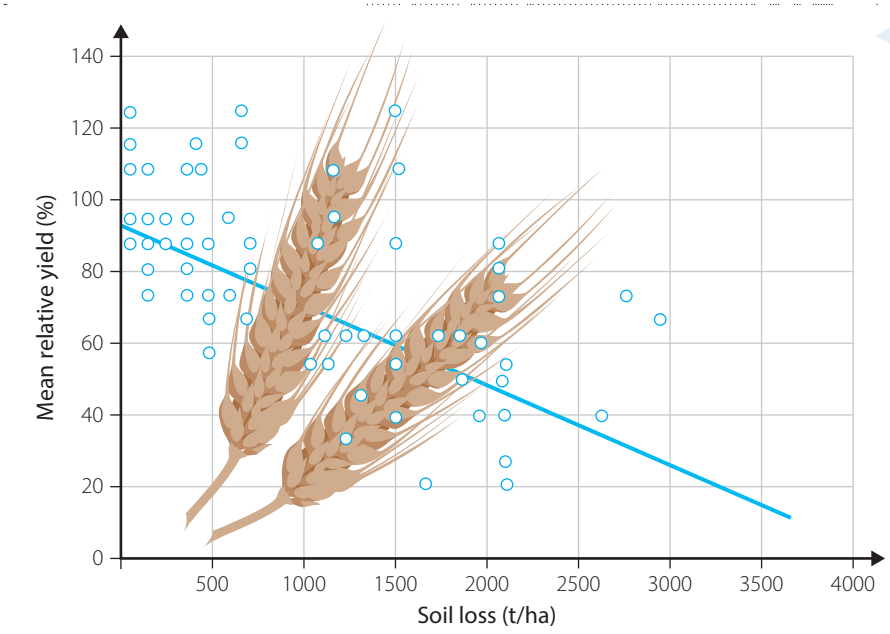


FIGURE 5.3.3 Soil loss means reduced farm productivity.

Salinity

One of the most significant problems associated with replacing natural vegetation with crops that require irrigation is salinity. Farm dams and irrigation channels can become important local sites of biodiversity, but irrigation contributes significantly to increasing groundwater. This raises the water table, and its often high salt content, to the surface (Figure 5.3.4). In the first instance, this can cause **waterlogging** and, 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, the salination problem is not solved but simply moved to another location. Like all run-off, it inevitably ends up in a stream.

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 cause salinity levels in the soil to rise

salination
increased salt concentration

FIGURE 5.3.4 Salination of land. Dry-land salinity caused by a combination of land clearing and irrigation practices can reduce biodiversity and devastate ecosystems.

Monoculture practices

A biologically diverse ecosystem, such as an old-growth forest or a tropical rainforest, is healthy, complex and stable. Nature tends to increase diversity through the process of succession. However, modern agricultural practice often reduces the number of crop or livestock species. Crops are grown over a wide area for a large number of consecutive years. This allows large harvests with minimal labour.

monoculture
the agricultural practice of growing a single crop or plant species over a wide area for a large number of consecutive years

When only one species of organism is grown, such as a wheat field, biodiversity is reduced. This type of farming resulting in a **monoculture** often requires extensive use of fertilisers along with pesticides and herbicides to reduce the natural tendency of the community to diversify. Another downside of this practice is the spread of disease and susceptibility to changing environmental conditions. Cultivated plants grown in genetically homogeneous monocultures do not have the necessary ecological defence mechanisms to tolerate the impact of pest outbreaks.

As a result of reduced biodiversity in monocultures, natural enemies of pests are no longer present. 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.

FIGURE 5.3.5 A pine plantation is an example of a monoculture.

SECTION REVIEW 5.3

REMEMBERING

1. Summarise the consequences of land clearance.
2. Describe methods that could restore damaged land.

UNDERSTANDING

3. Suggest some agricultural practices that can contribute to salination.
4. Summarise the activities of early European settlers and the impacts these activities had on ecosystems.

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5.4 Mandatory practical

USING ECOLOGICAL SURVEYING TECHNIQUES TO ANALYSE SPECIES DIVERSITY

Introduction

Primary data collection is important in all ecological work. Good-quality survey data is necessary. A wide range of survey techniques is available for different purposes and circumstances. Selecting appropriate survey techniques is determined by a variety of factors such as the season, time frame, accessibility, legal requirements and finances.

Aim

To select and appraise ecological surveying tools in order to compare species diversity in a disturbed and undisturbed ecosystem.

Method

1. Choose an ecosystem in which it is possible for you to survey species diversity. Within this ecosystem there should be an undisturbed area identified as a climax community and a disturbed area identified as a pioneer community.
2. Select a surveying technique that you will use. Choose one of:
   - total count
   - quadrat
   - transect
   - Lincoln index (capture–mark–recapture) method
   - fixed point photography.
3. For your chosen surveying technique discuss and answer the following questions.
   - Is the method likely to damage the environment?
   - Are samples required?
   - Will the method provide the appropriate type of measurement?
   - Can the technique be used in the ecosystem conditions?
4. Design the surveying strategy. Write a proposal to present to your teacher, describing the two sites in the area you have chosen and how you propose to carry out the survey. Include:
   - a risk assessment table
   - a list of suitable materials and equipment to carry out your investigation
   - what data you will record and how it will be presented.
5. Conduct the ecological survey.
6. Record your results.
7. Analyse your results by using Simpson's diversity index (Chapter 1).

Results

1 Present your results in the form you have chosen.
2 Using Simpson's diversity index, calculate species diversity for both sites.

Discussion

1 Describe any problems you experienced in conducting your survey. Explain how you overcame them.
2 Complete Table 5.4.2 by considering five different ecological surveying techniques.

TABLE 5.4.2

TECHNIQUE	ACCURACY	ADVANTAGES	DISADVANTAGES
Total count			
Quadrat			
Transect			
Lincoln index method			
Fixed point photography			

Conclusion

Discuss the difference in species diversity between a pioneer and climax community. Evaluate the different types of ecological surveying techniques.

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CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1. What are the stages of ecological succession?
2. What are the features of pioneer species?
3. How can fossil records be used to describe past ecosystems and changes in biotic and abiotic components?
4. What sorts of human activity reduce biodiversity?

CATEGORY QUESTIONS

5. What are the differences between primary and secondary succession?
6. What ecological data can be used to predict temporal and spatial successional changes?
7. What impact did Australia's first human inhabitants have on ecosystem change?
8. How did European colonisation of Australia affect environmental change?

ELABORATION QUESTIONS

9. What changes would be expected to a climax community following a catastrophic event such as a volcanic eruption or cyclone?
10. What evidence is there that humans in Australia today are reducing biodiversity?
11. Why are current agricultural practices increasing the magnitude, duration and speed of ecosystem change?

EVIDENCE QUESTIONS

12. What, if any, external sources did you use to support your answers to questions 9–11?
13. Explain your reasoning behind your answers to questions 9–11.
14. What other factors could cause ecosystems to change?
15. How could your answers to questions 9–11 be improved?
16. What further evidence could be used to support your answers to questions 9–11?

END-OF-CHAPTER EXAM

End-of-chapter test

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 creates different physical environments, suiting different species.

2 The fossil record, rocks, soil and ice cores provide information on the nature of past ecosystems and changes in the components of those ecosystems. Choose the incorrect statement.

At Riversleigh in Queensland:

A there are rich, well-preserved fossils that demonstrate extensive biodiversity and point to a climate very different from today's dry and hot habitat.

B sedimentary rocks indicate changes in abiotic factors, suggesting that the climate was wetter in the past.

C trapped gas bubbles in ice cores reveal information about changes in temperature and relative concentrations of atmospheric gases.

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 from the following.

A A plant growing in early succession would have an abundance of resources and would be an r-selected species.

B Many 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 A practical approach to modelling an ecosystem is to examine parts of that ecosystem by random sampling. Before sampling and collecting data, the process includes these stages.

1 Specify the type of data to measure.

2 Determine the number of samples.

3 Describe a sampling method.

4 Define the population of interest.

Choose the order in which these steps should be carried out.

A 2, 3, 4, 1

B 4, 1, 3, 2

C 3, 1, 4, 2

D 4, 2, 3, 1

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5 In modern agricultural practice, large areas of a single crop are grown for many consecutive years in monocultures. This practice:

A results in reduced biodiversity so that natural enemies of pests are no longer present.

B may cause a change in environmental conditions.

C reduces the need for the use of fertilisers, pesticides and herbicides.

D means that if pest outbreaks occur, beneficial populations of insects exist as predators.

6 Name the type of succession that occurs after a landslide.

7 Identify three features characteristic of a pioneer species that make them effective colonisers.

8 Describe two main differences between an urban ecosystem and a natural ecosystem.

9 Describe and explain reasons for the rate of environmental change after European settlement in Australia.

10 Explain how the fossil record and sedimentary rock characteristics provide evidence of past ecosystems.

11 Identify the r-selected and K-selected species in the graph in Figure 5.5.1. Give reasons for your answer.

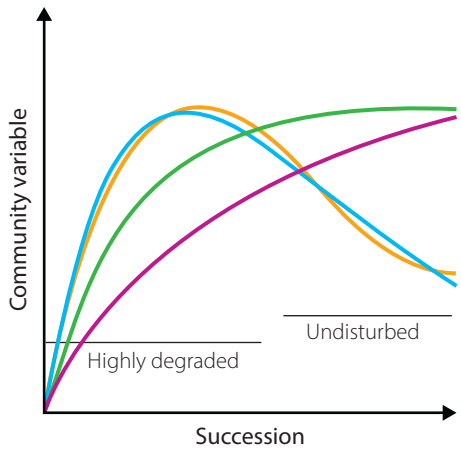

FIGURE 5.5.1
Change in communities in the process of succession

» UNIT FOUR

HEREDITY AND THE CONTINUITY OF LIFE

- Topic 1: DNA, genes and the continuity of life
- Topic 2: Continuity of life on Earth

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 kinds of 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 and explain DNA, genes and the continuity of life, and the continuity of life on Earth.
2. apply understanding of DNA, genes and the continuity of life, and the continuity of life on Earth
3. analyse evidence about DNA, genes and the continuity of life, and the continuity of life on Earth
4. interpret evidence about DNA, genes and the continuity of life, and the continuity of life on Earth
5. investigate DNA, genes and the continuity of life, and the continuity of life on Earth
6. evaluate processes, claims and conclusions about DNA, genes and the continuity of life, and the continuity of life on Earth
7. communicate understandings, findings, arguments and conclusions about DNA, genes and the continuity of life, and the continuity of life on Earth.

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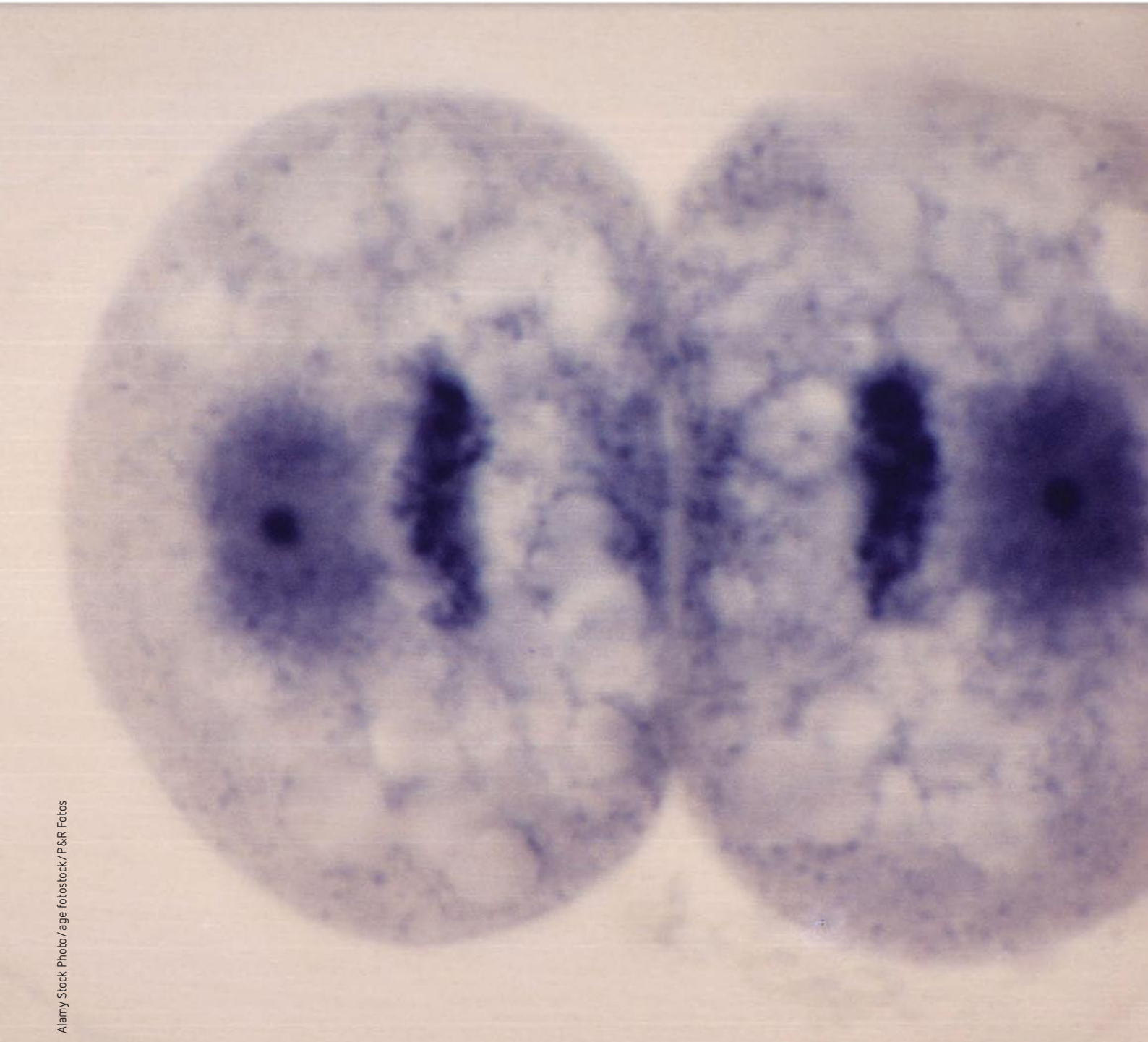
HEREDITY AND THE CONTINUITY OF LIFE



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Topic 1: DNA, genes and the continuity of life

The continuity of life depends on reproduction. Through cell division, parents produce a new generation of cells like themselves. DNA, packaged in chromosomes, undergoes replication during cell division. DNA molecules contain information about heritable traits. The information is encoded in the particular sequence of nucleotide bases known as genes. Gene products are synthesised when genes are expressed. Patterns of inheritance can be explained using information about genes and chromosomes. Chromosome structure and chromosome number rarely change. However, the combination of parental chromosomes can change through the process of gamete formation. Permanent errors in genes and chromosomes sometimes occur. These mutations may lead to differences in offspring. Biotechnology offers the opportunity for humans to manipulate DNA.

SCIENCE AS A HUMAN ENDEAVOUR

Students should be given opportunities to investigate the use of bioinformatics, economical genome sequences and the genetic modification of organisms.

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6 DNA STRUCTURE AND REPLICATION

Introduction

Deoxyribonucleic acid, DNA, is the cellular genetic material that contains the instructions for growth, development and functioning of all organisms, whether they are prokaryotes, eukaryotes, unicellular or multicellular organisms. The story of the discovery of the structure of DNA is more than just the details of DNA structure and function. It reveals how scientists work and how scientific discoveries can be made. It shows scientists sharing what they understand and what they do not understand. Even when an experiment fails to produce the expected results, it may reveal interesting information that other scientists can use to answer their questions.

One of the most exciting aspects of the discovery of the structure of DNA was that the proposed specific base-pairing immediately suggested a possible copying mechanism for the genetic material. After all, cells originate from pre-existing cells and for genetic information to be transferred to the next generation, DNA must be copied.

Stimulus questions

In what way is the DNA of prokaryotes and eukaryotes similar and different?

What structural features of DNA make it suitable to carry information from one generation to the next?

How is DNA copied to enable transmission to the next generation?

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6.1 Understanding DNA

All living things inherit **deoxyribonucleic acid (DNA)** from their parents. DNA (Figure 6.1.1) is the common genetic material for all organisms and carries the information coded in **genes**.

Genes are sections of DNA. One gene is one 'unit' of genetic information, which can be read and switched on or off independently of other genes. When a gene is switched on, the cellular machinery will 'read' the gene and produce, for example, a specific protein. The gene is then said to be 'expressed'.

DNA has the same basic structure in all organisms, but small differences in the sequence of subunits make individual genes different and species distinct from one another. It is clear that this special molecule is capable of holding very complex information.

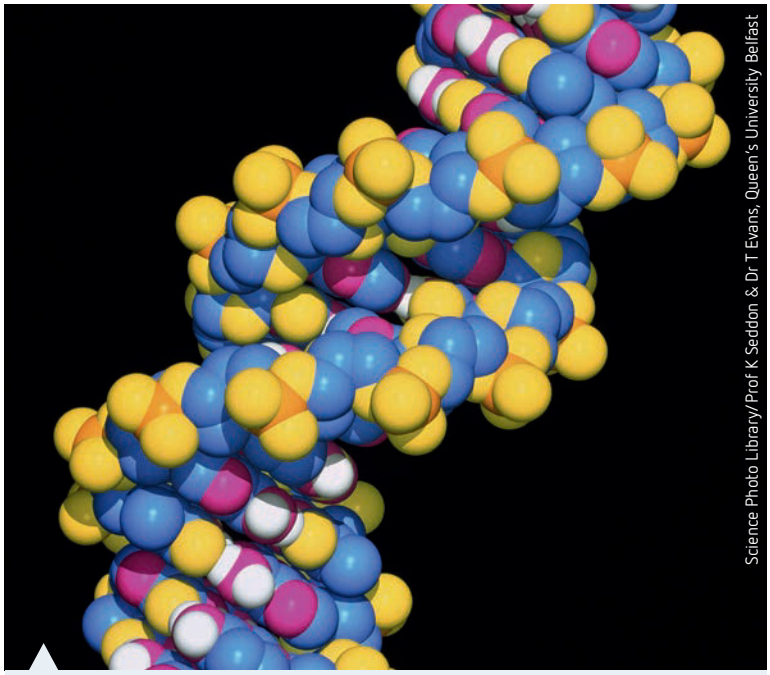

FIGURE 6.1.1 This model of the DNA molecule shows its twisted helical structure.

deoxyribonucleic acid (DNA)
an information molecule that is the universal basis of an organism's genetic material; it contains instructions, written in a chemical code, for the production of proteins by the cell

gene
a unit of heredity that transmits information from one generation to the next; a segment of DNA that codes for polypeptide

6.1.1 DNA: the book of you

DNA in eukaryotes

Eukaryotes are complex cells containing membrane-bound organelles. In these types of cells, DNA is found in the nucleus, chloroplasts and mitochondria.

DNA in the nucleus of eukaryotes

In the nucleus of a eukaryotic non-dividing cell, DNA is only visible as a grainy substance without detail. Early microscopists named this seemingly diffuse, grainy substance **chromatin** (Figure 6.1.2). Scientists now use the term to describe the cell's DNA together with all the proteins associated with it. When the cell prepares to divide, the chromatin condenses by coiling up, eventually becoming thick enough to be seen, when stained, as a number of separate structures called **chromosomes** (from 'chromo' meaning colour, and 'soma' meaning body). A chromosome is one DNA molecule with its associated proteins.

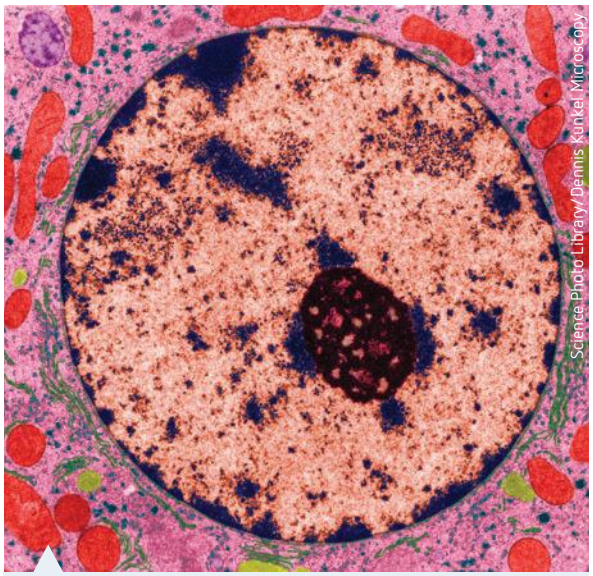

FIGURE 6.1.2 A coloured transmission electron micrograph of part of a liver cell, showing a large central nucleus (orange) containing a nucleolus (burgundy) and patches of grainy chromatin (purple).

chromatin
a complex of proteins and DNA in eukaryotic chromosomes

chromosome
a structure composed of DNA and protein that contains along its length linear arrays of genes carrying genetic information; prokaryotes have one circular chromosome whereas eukaryotes have a number of linear chromosomes

histone
a protein that DNA winds around in eukaryotic cells

sister chromatids
the two identical copies of a single chromosome, formed by replication and connected by a centromere

centromere
the waist-like constriction in a chromosome required for the movement of chromosomes during cell division

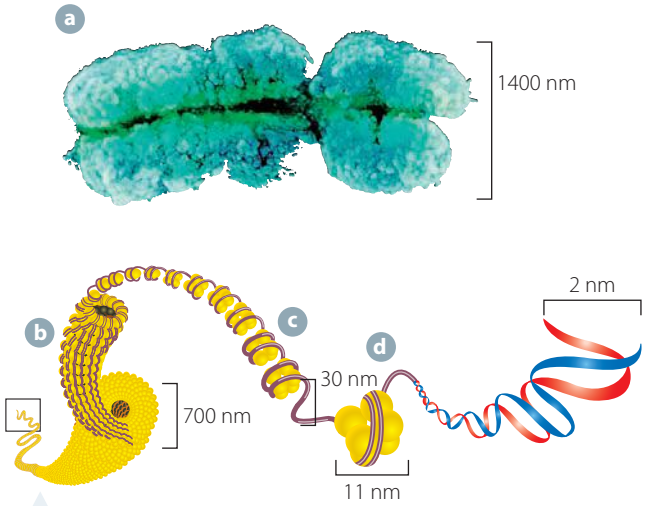

FIGURE 6.1.3 Levels of organisation in a human chromosome. (**a**) A tightly coiled and condensed human chromosome is only visible when stained during cell division, after DNA replication. (**b**) Interacting proteins package loops of coiled DNA into a 'supercoil', to produce chromatin, which is organised as a cylindrical fibre. (**c**) The loops of coiled DNA are wound around a core of eight histone proteins to produce a nucleosome. (**d**) A nucleosome consists of a section of DNA molecule looped twice around a core of histones.

For most of the time, chromosomes are unduplicated. An unduplicated chromosome is a single, long DNA double helix molecule coiled around **histone** proteins (Figure 6.1.3). By contrast, duplicated chromosomes, which have undergone DNA replication in preparation for cell division, contain two identical copies, called **sister chromatids**. Sister chromatids are joined by a **centromere**, making them an 'X' shape (Figure 6.1.4a). The position of the centromere can vary in different chromosomes and descriptive names are given according to their position (Figure 6.1.4b). Since chromosomes only become visible just prior to cell division and after replication has occurred, most images and drawings of chromosomes show them in the duplicated form.

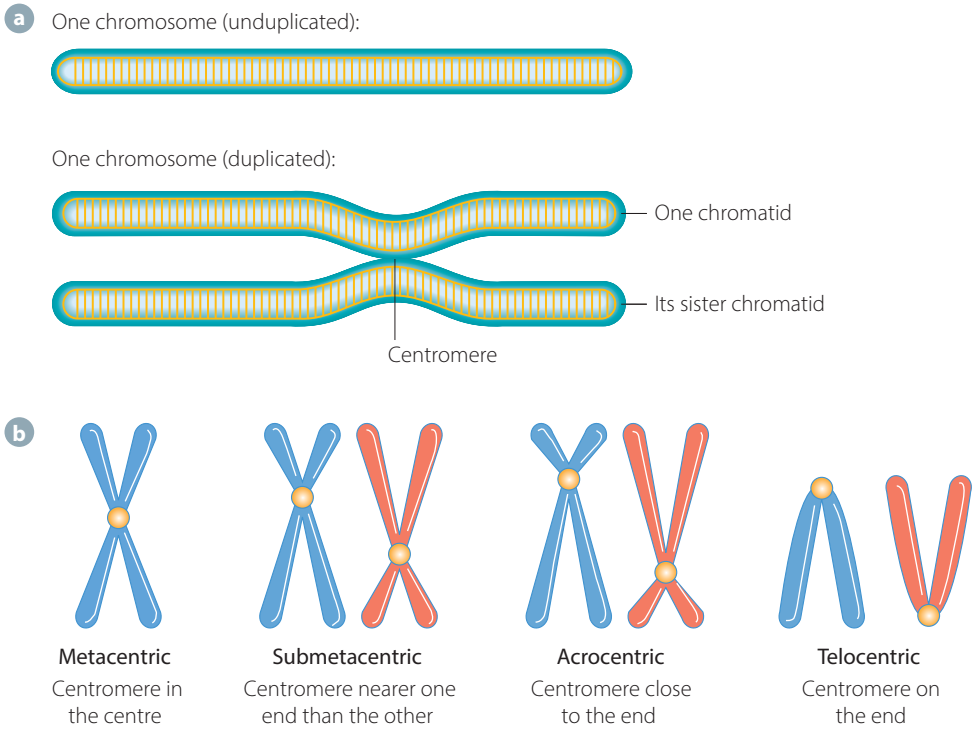

FIGURE 6.1.4 (**a**) An unduplicated chromosome and a duplicated chromosome, showing the position of the centromere. (**b**) Centromeres can be in different positions along chromosomes.

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Microscopic examination of a stained eukaryotic cell in the process of nuclear division reveals a jumbled cluster of chromosomes that exist in pairs, called **homologous chromosomes**. In homologous pairs, one chromosome is inherited from each parent. Photographic images of chromosomes are arranged into matched and ordered pairs to create a **karyotype**, the standard way of displaying and analysing chromosomes (Figure 6.1.5). Chromosomes are ordered by length, from largest to smallest, with members of each homologous pair sharing characteristic banding patterns. The exception is the sex chromosomes, which in one sex, usually the male, are not homologous. Figure 6.1.5 shows a karyotype of a male mouse with an X and a Y chromosome. Each species of organism has a particular number of chromosomes in its cells. Mice have 40 chromosomes (20 pairs) and humans have 46 (23 pairs).

homologous chromosomes
a pair of chromosomes that have the same size, shape and genes at the same locations

karyotype
a display of the number and appearance of the chromosomes of an organism or cell observed at metaphase

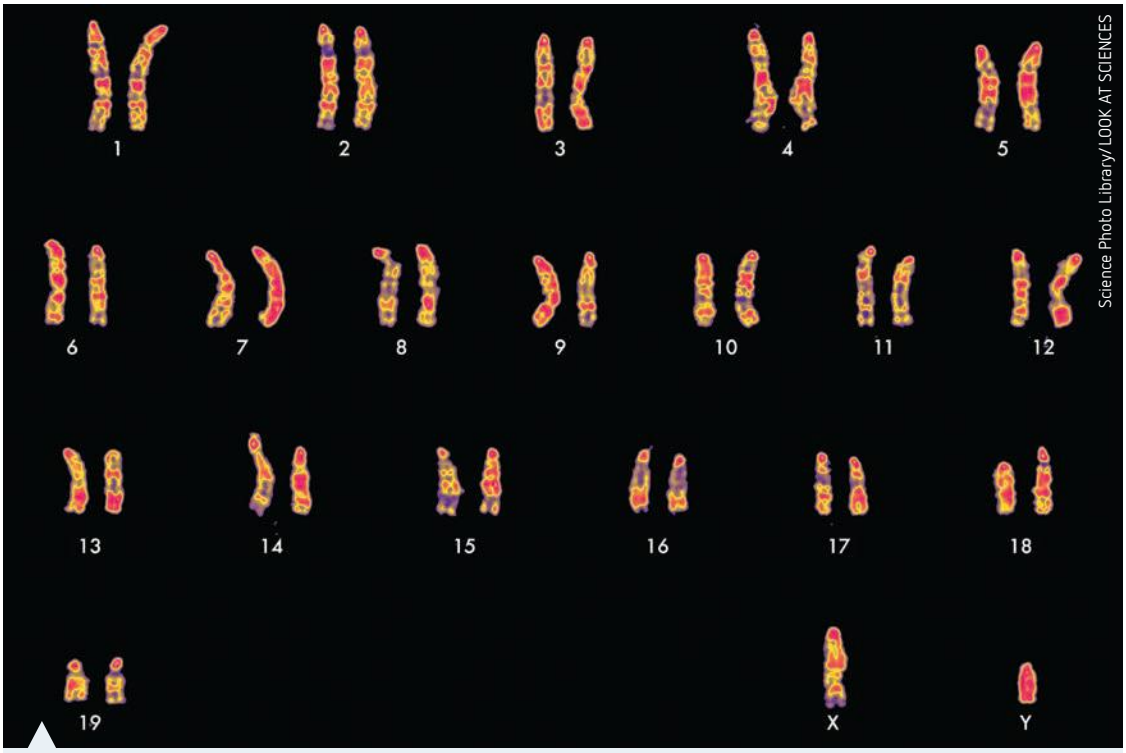


FIGURE 6.1.5 A karyotype of a mouse

DNA in mitochondria and chloroplasts of eukaryotic cells

The DNA of both mitochondria and chloroplasts is similar to the single, circular chromosomes in prokaryotic cells. This feature provides strong evidence for the **endosymbiotic theory**. The endosymbiotic theory proposes that eukaryote cells were formed when a bacterial cell was ingested by another primitive prokaryotic cell.

Mitochondria and chloroplasts can only arise from pre-existing mitochondria and chloroplasts. Although egg cells only contain a few mitochondria, it is these mitochondria that, after fertilisation, divide to populate the cells of the adult organism. Similarly, for most flowering plants, chloroplasts are inherited from the female plant. This inheritance, which is only from mothers, is known as **maternal inheritance**.

endosymbiotic theory
a theory that suggests that chloroplasts and mitochondria arose from ancient prokaryote cells that were ingested by other prokaryote host cells

maternal inheritance
inheritance only from mothers; any trait that is encoded by organelle DNA is contributed by the female

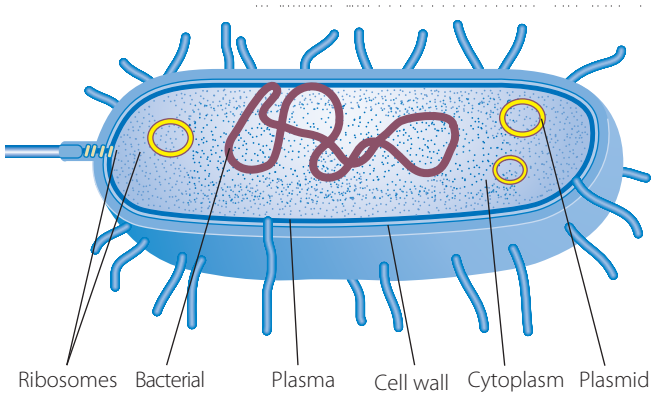
DNA in prokaryotes

nucleoid
the region within a prokaryotic cell that contains the genetic material

plasmid
a small circular piece of DNA, found in bacteria, which can replicate independently of the cell's chromosomes; plasmids carry antibiotic resistance markers

Membrane-bound organelles, such as the nucleus, are not present in prokaryotes. The DNA within these cells generally forms a single circular chromosome that lies in direct contact with the cytoplasm (Figure 6.1.6). Chromosomes are often joined to the plasma membrane at a single point. Although not contained by any internal structure, in prokaryotes a chromosome can be in a distinct region of the cell called a **nucleoid**. Additional numerous small rings of DNA, called **plasmids**, may also be present in the cytoplasm. Non-essential genes are commonly encoded on these plasmids. 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 and replicate rapidly.

FIGURE 6.1.6 DNA in a prokaryote cell



SYLLABUS LINK

Chapter 2 of *Nelson QScience Biology Units 1 & 2* discusses the endosymbiotic theory.

Like eukaryotic chromosomes, the DNA of prokaryotic chromosomes needs to fit into a small area. This can be achieved by supercoiling, where a number of architectural proteins act together to fold and condense the DNA. Prokaryotic cells are generally haploid – they only contain one copy of each gene. Furthermore, prokaryotic DNA contains very little repetitive and non-coding DNA.

SECTION REVIEW 6.1

REMEMBERING

1 Name the place where DNA is located in a eukaryotic cell.
2 Identify the components of a chromosome from a eukaryotic cell.

UNDERSTANDING

3 Explain the meaning of the following terms.
   - **a** Homologous
   - **b** Sister chromatid
   - **c** Endosymbiotic theory
   - **d** Centromere
4 Describe the DNA in the mitochondria and chloroplasts of eukaryotic cells.
5 Discuss how you would know whether two number 21 chromosomes in humans are homologous.
6 Construct a table to show the similarities and differences in the nuclear chromosomes of eukaryotic and the chromosomes of prokaryotic cells.
7 Describe how a karyotype is made and identify how chromosomes are ordered.
8 Explain whether all human chromosomes have a homologous pair.

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6.2 The structure of DNA

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 has only been within the last 70 years that the mechanism of inheritance has been explained. Amazing discoveries have been made in recent years and are continuing to be made about the structure and function of DNA and genes.

Watson and Crick's model of DNA

In 1953, James Watson and Francis Crick, working in Cambridge, England, suggested a possible structure for DNA (Figure 6.2.1). Like many other important scientific discoveries, their model was based on the crucial contributions and ideas of other scientists past and present.

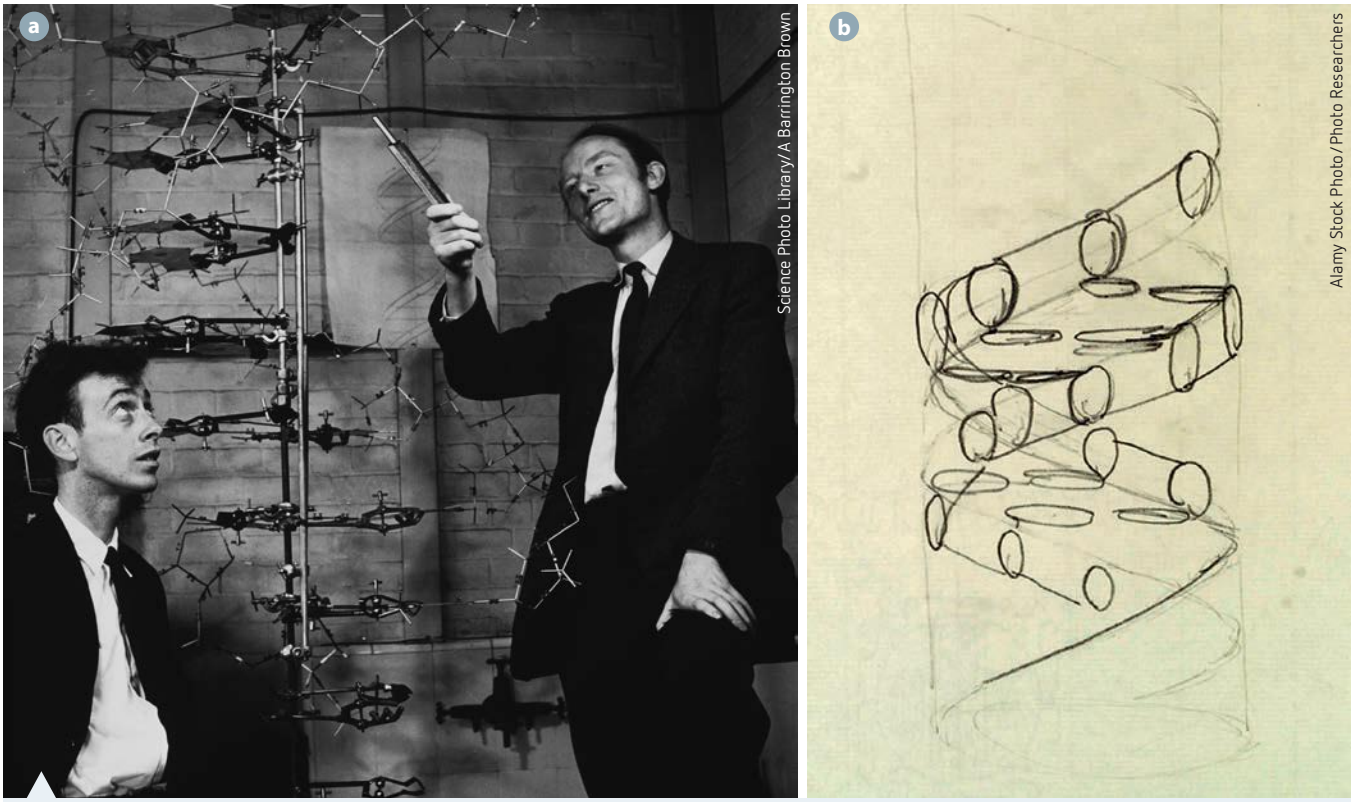

FIGURE 6.2.1 (**a**) Watson and Crick come up with a structure for DNA. (**b**) Crick's sketch of a double helix.

Maurice Wilkins began using spectroscopy to study DNA in the late 1940s. In 1950, he and Ray Gosling obtained the first clear crystalline X-ray diffraction patterns from DNA fibres. Their colleague Alec Stokes suggested that the patterns indicated that DNA was helical in structure.

6.2.1 How I discovered DNA

6.2.2 Rosalind Franklin: DNA's unsung hero

In 1952, Rosalind Franklin (Figure 6.2.2), working alongside Wilkins in his laboratory in England, obtained some clear X-ray diffraction images of DNA (Figure 6.2.3). This was not an easy task because of the complexity and size of DNA and its reluctance to crystallise.

Using these results and other accumulated evidence, Watson and Crick suggested that DNA consisted of the now familiar two chains joined and twisted around each other to form a double helix ladder.

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.

FIGURE 6.2.2 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.

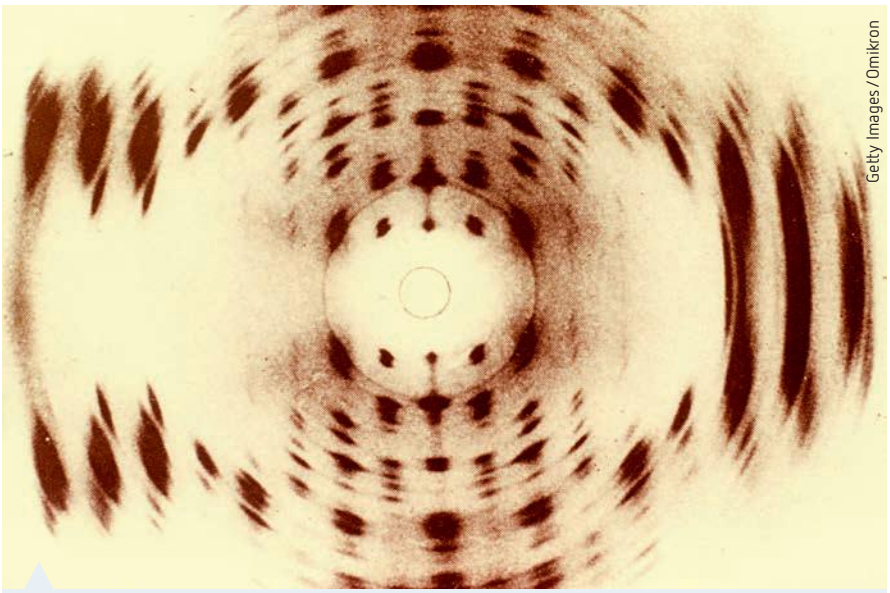

FIGURE 6.2.3 An X-ray diffraction photograph of DNA. The DNA molecule was too small to see physically by conventional methods, so X-rays were used. The image produced an accurate three-dimensional shape.

INQUIRING FURTHER

There has been a continued debate about whether Rosalind Franklin should also have been awarded the Nobel Prize in 1962 because Watson and Crick admitted to basing their ideas on her results without her knowledge. Research the awarding of the prize and present an argument for or against including Rosalind Franklin.

The detailed 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, 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 6.2.4):

- a five-carbon sugar (deoxyribose in DNA)
- a negatively charged phosphate group
- an organic nitrogen-containing compound called a base.

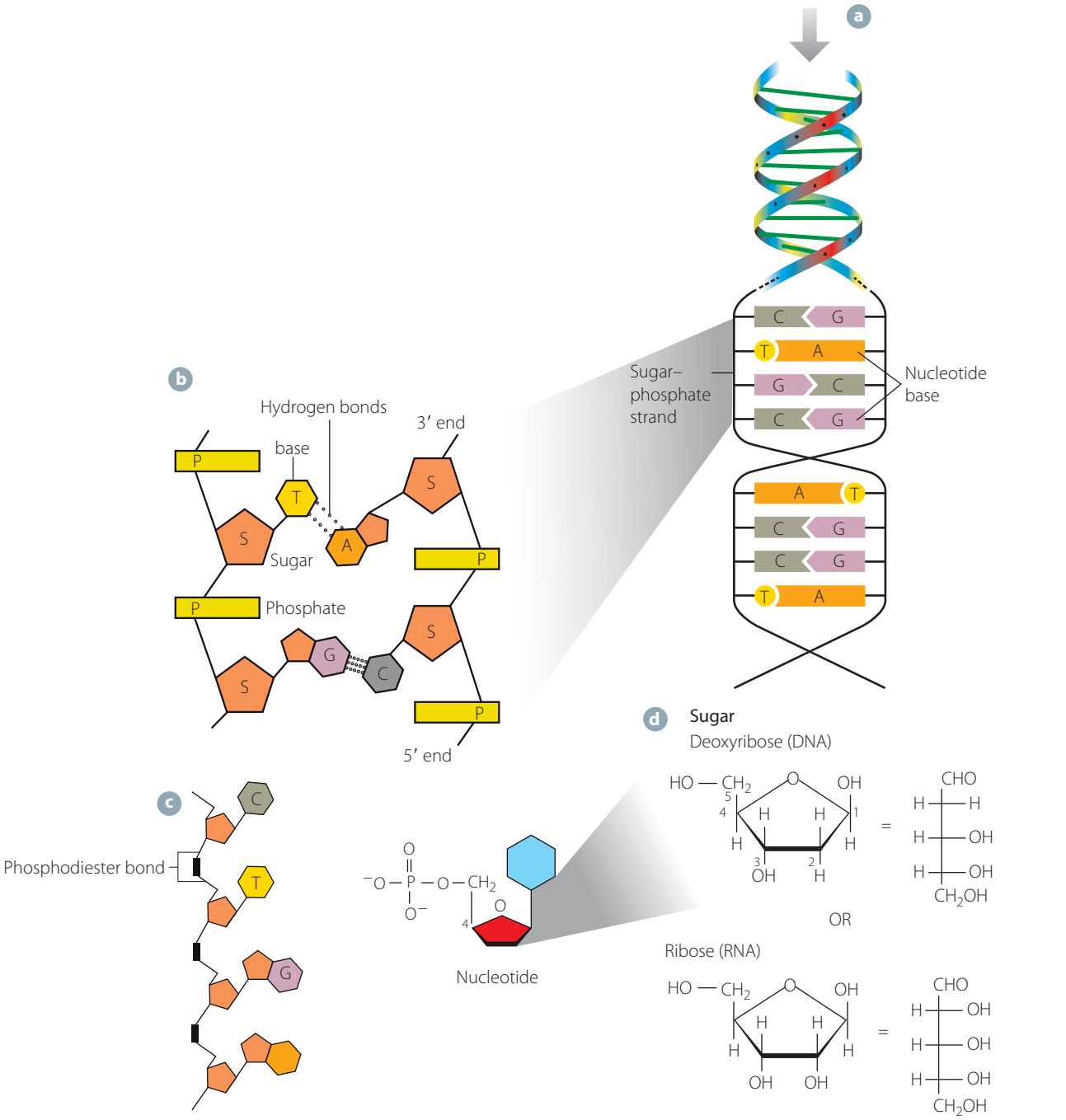

FIGURE 6.2.4 (**a**) The DNA helix is a double-stranded molecule. (**b**) The two strands are held together by hydrogen bonding between complementary nitrogenous bases. (**c**) As well as nitrogenous bases, nucleotides have a sugar phosphate backbone linked by phosphodiester bonds. (**d**) DNA contains deoxyribose sugars and RNA contains ribose sugars.

There are four kinds of nitrogenous (nitrogen-containing) bases in DNA:

- adenine (A)
- thymine (T)
- guanine (G)
- cytosine (C).

complementary bases
nitrogenous bases on nucleotides that bind to each other (e.g. A–T and C–G)

ribonucleic acid (RNA)
a molecule consisting of a single strand of nucleotides; it plays an essential role in protein synthesis (as messenger RNA and transfer RNA) and as a structural component of ribosomes

In each nucleotide 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 and opposite the nitrogenous base of the second strand. Hydrogen bonds between the opposing pairs of nitrogenous bases hold the double helix together. The bonding of the nitrogenous bases does not happen by chance. According to the base-pairing rule, A bonds with T and C bonds with G. Put another way, A and T, and C and G are said to be **complementary base** pairs. The two strands of the double helix are antiparallel, which means that they run in opposite directions.

Ribonucleic acid (RNA) is a nucleic acid related to DNA, but with three major differences. RNA is composed of a single chain of nucleotides, making it single stranded; the base thymine is replaced by the base uracil (U); and ribose sugar replaces the deoxyribose of DNA. RNA has important functions in protein synthesis.

SECTION REVIEW 6.2

REMEMBERING

1 List the scientists who contributed to the discovery of the structure of DNA.
2 Describe a nucleotide.
3 State the rule for the pairing of nitrogen-containing bases in the DNA molecule.
4 State the type of chemical bond that holds strands of DNA together.

UNDERSTANDING

5 Predict the nucleotide sequence for the complementary strand of a fragment of a DNA chain with the nucleotide bases GCCTATTGCA.
6 Compare and contrast the nucleotides of DNA and RNA.
7 Describe the current model of DNA.

APPLYING

8 The 1997 science fiction film *Gattaca* is about exploring the use of genetics to predict potential health and ability. Identify the link between the film title and DNA composition.

SYLLABUS LINK
Chapter 8 discusses RNA and uracil in more detail.

6.3 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 when the organism reproduces. Before they divide, cells must replicate (copy) their DNA to ensure that each **daughter cell** receives the instructions for the proper functioning of that cell.

daughter cell
either of the two cells formed when a cell undergoes cell division

The sequence of events from one cell division to another is called the cell cycle (Figure 6.3.1a). The stage of nuclear division (M) is a small part of the cycle. The stage between nuclear divisions is called interphase. It includes a period of active growth, (G1 phase), synthesis of DNA (S phase) and preparation for the next division (G2 phase). Figure 6.3.1b shows how the amount of DNA in a cell changes during the cell cycle.

DNA replication begins with the enzyme **DNA helicase**. DNA helicase unzips the long, helical molecule of double-stranded DNA by breaking the weak hydrogen bonds between the nucleotides and thus exposing the nucleotide bases. This separation of the **parental DNA** strands happens along a small section at a time. The hydrogen bonds that hold the two strands of the DNA molecule are weak and the enzyme is easily able to separate them.

DNA helicase
an enzyme that helps the two strands of the DNA double helix unwind and separate

parental DNA
in cell division the DNA of the original cell

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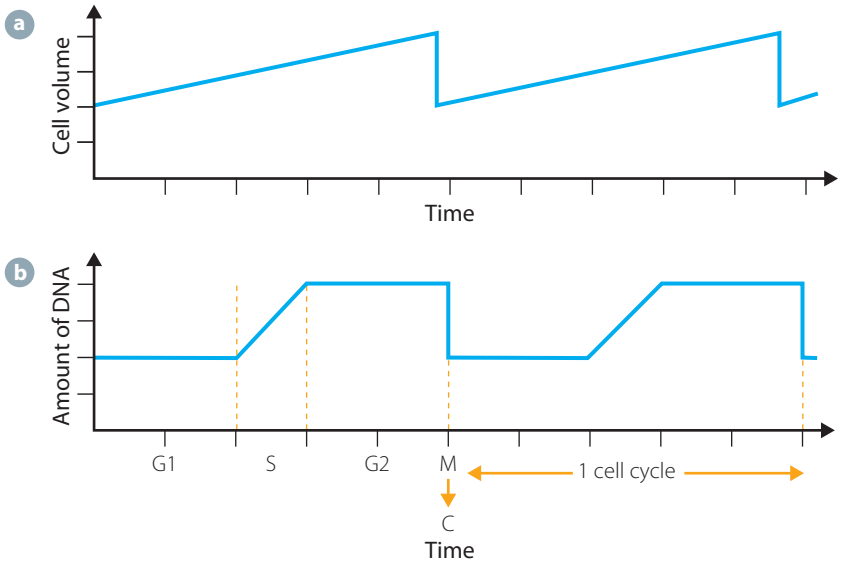

FIGURE 6.3.1 (**a**) The cell volume and (**b**) amount of nuclear DNA change during a cell cycle reflects the different activities during the cell cycle. M stands for mitosis, S stands for synthesis and G1 and G2 are growth phases.

replication fork the junction between the unwound single strands of DNA and the intact double helix during replication

DNA polymerase an enzyme capable of making exact copies of fragments of DNA

semiconservative replication the production of two new DNA double helix molecules, each consisting of one parental strand and one daughter strand

The junction between the unwound single strands of DNA and the intact double helix is called the **replication fork**. The replication fork moves along the DNA so that there is a continuous unwinding of the parental strands (Figure 6.3.2). Stockpiles of free nucleotides attach to the exposed bases according to the base-pairing rule (Figure 6.3.3) with the help of the enzyme **DNA polymerase**, which then joins the nucleotides to form a new complementary strand. Both strands act as templates for the production of new DNA strands, with nucleotides being linked together in what is termed a 5′ to 3′ direction.

The outcome of DNA replication is two double helix DNA molecules, each consisting of one original parental strand and one new strand. Thus, one of the two strands is conserved, or retained, from one generation to the next, while the other strand is new. This process is referred to as **semiconservative replication**.

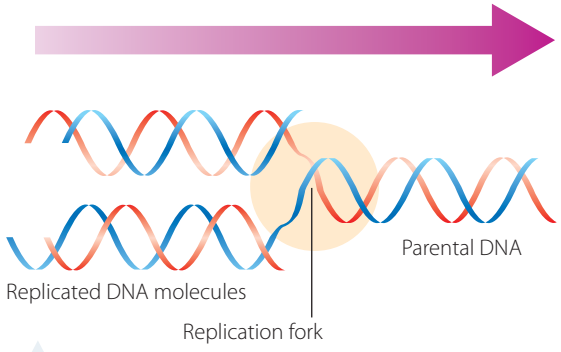

FIGURE 6.3.2 Movement of the replication fork along parental DNA causes unwinding of DNA strands and rewinding of newly replicated strands.

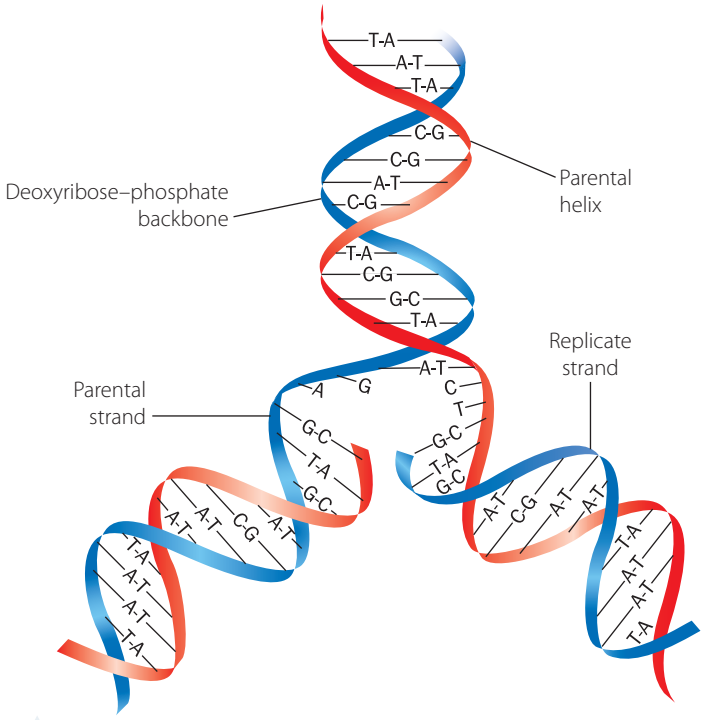

FIGURE 6.3.3 Replication of DNA. The two strands of the double helix separate and free nucleotides align themselves along each of the two strands. The specific relationship between A and T and between C and G ensures that the sequence of bases in the daughter DNA is exactly the same as in the parental DNA.

SECTION REVIEW 6.3

REMEMBERING

1 Describe the role of the enzymes helicase and DNA polymerase in DNA replication.

2 List three processes that require cells to replicate their DNA.

UNDERSTANDING

3 Describe what it means to say that the two strands of DNA are complementary.

4 Describe the process of DNA replication.

5 Explain why DNA replication is referred to as semiconservative replication.

APPLYING

6 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 6.3.4.

FIGURE 6.3.4 A section of DNA undergoing replication

After the cell replicates, one of the daughter cells is normal and the other carries the mutation. Identify what mistake was made and develop a hypothesis to explain the results.

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CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1 What places in the cell are associated with DNA?

2 What happens during DNA replication?

3 What is the purpose of DNA replication?

CATEGORY QUESTIONS

4 What two major processes are associated with the nucleic acid DNA?

5 What place is associated with the category of DNA in eukaryotic cells?

6 What purpose is associated with the category of DNA in eukaryotic organelles?

ELABORATION QUESTIONS

7 Predict how living organisms would be different if prokaryotes had not developed a nucleus.

8 Predict what would happen if the DNA helicase in a cell stopped working.

EVIDENCE QUESTIONS

9 Provide evidence to support your answer to Question 7.

10 One early model of the structure of DNA was that the bases stuck outwards from the nucleotide strand, not inwards. Use evidence to explain why this was quickly discredited.

11 Use Table 6.3.1 to provide evidence that supports the base-pairing rule.

TABLE 6.3.1 Data on the base nucleotides in DNA from several sources

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

END-OF-CHAPTER EXAM

End-of-chapter test

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 Choose the incorrect alternative. The sequence of events from one cell division to another includes:

- **A** synthesis of DNA before nuclear division.
- **B** a small part of the cycle (M) in which the nucleus divides.
- **C** a stage between nuclear divisions called interphase.
- **D** a doubling of the amount of DNA before active growth in G1 phase.

3 If 35% of the bases of a molecule of DNA are thymine, it will also contain:

- **A** 15% guanine.
- **B** 35% cytosine.
- **C** 30% uracil.
- **D** 25% adenine.

4 Which one of the following is correct?

- **A** One strand of DNA is maternal and one strand is paternal.
- **B** Each chromosome is made up of many molecules of DNA.
- **C** A chromosome is composed of DNA and proteins.
- **D** The different cell types in an organism have different DNA.

5 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.

6 Name the enzyme responsible for separating the strands of DNA during replication.

7 Name the junction between the unwound single strands of DNA and the intact double helix.

8 Distinguish between a nucleotide and a nitrogenous base.

9 Define 'homologous chromosomes'.

10 Explain what it means to say that not all homologous chromosomes are homologous.

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7 CELLULAR REPLICATION AND VARIATION

Introduction

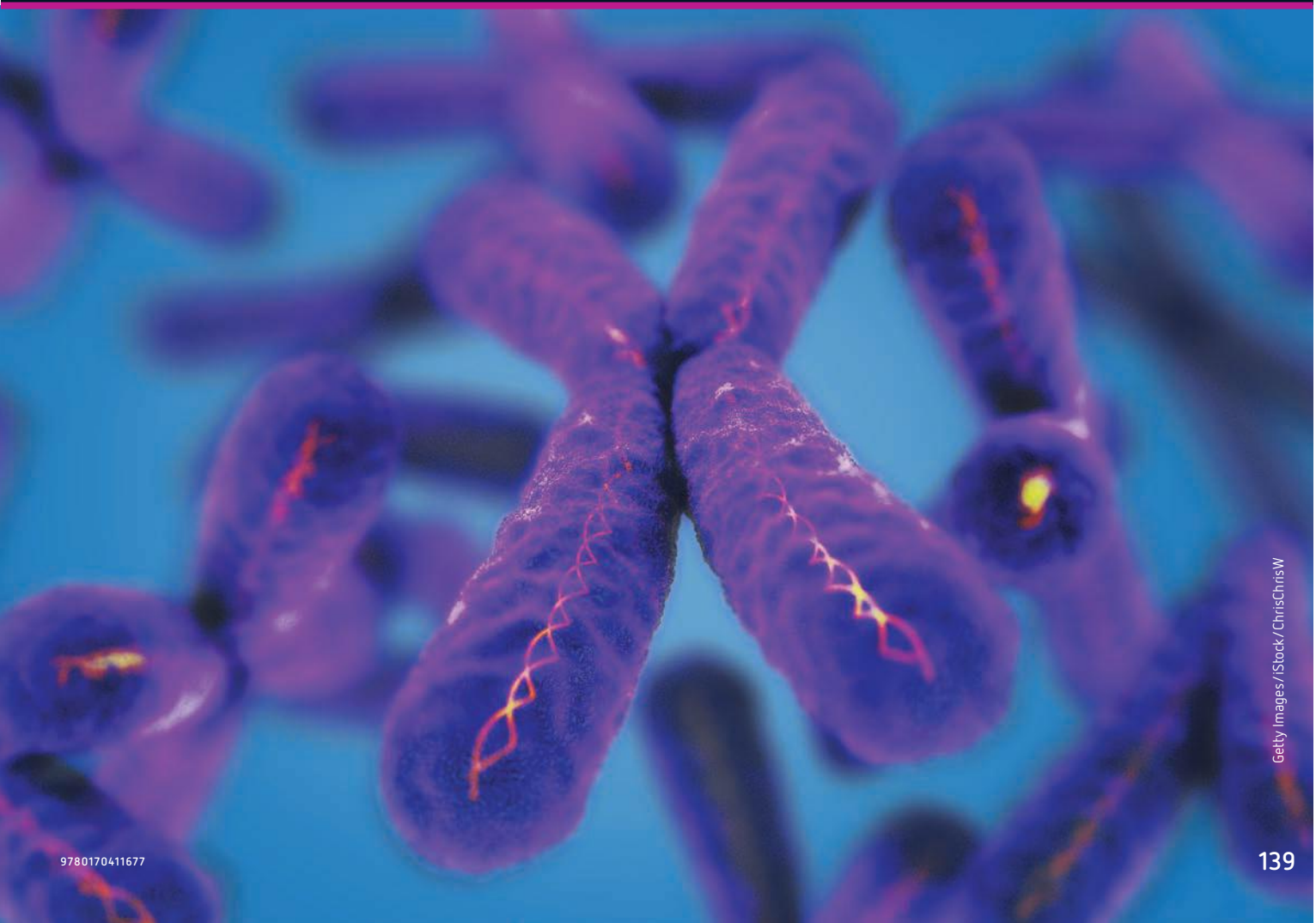
All organisms have a life span and eventually die, but species continue because some members reproduce. Instructions are passed on, embedded in DNA, for the development of characteristics that define the species: the characteristics that appear in successive generations.

At a family gathering, we can be struck by how much we resemble some of our relatives but how different we are from others. Characteristics from mothers or fathers may be evident in the next generation, or they can be missing entirely.

In this chapter, the special type of cell division that is responsible for the transmission of characteristics from one generation to the next will be explored.

Stimulus questions

- How is DNA transmitted to the next generation?
- In what ways are the processes of egg and sperm formation similar and different?
- What cellular events enable information to be carried from one generation to the next?
- What processes allow different combinations of characteristics to arise between one generation and the next?



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7.1 The process of meiosis

asexual reproduction
a form of reproduction in which offspring are produced from a single parent

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; meiosis is 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

locus
the position a gene occupies in a chromosome

allele
one of different versions of the same gene (at the same locus) determined by small differences in the DNA sequence of the gene

genotype
the alleles present in the cells of an organism

Some living things originate from one parent by a process called **asexual reproduction**. An example is bacteria dividing to form two new individuals. Because they have only one source of hereditary information, the offspring usually closely resemble their parent. Other organisms inherit hereditary material from two different parents by **sexual reproduction**. In these organisms, the difference in characteristics between one generation and the next is greater than in organisms that reproduce asexually.

Meiosis is a form of eukaryotic cell division that is involved in sexual reproduction. In meiosis, nuclear division results in the formation of four daughter cells, each containing half the number of chromosomes of the original nucleus. At fertilisation, two sex cells, called **gametes**, usually from different individuals, combine to restore the original chromosome number.

Homologous chromosomes

Genes, alleles and genotype

Along the length of each DNA molecule, particular regions called genes code for different proteins that can determine particular characteristics or traits (Figure 7.1.1). The location of a particular gene on a chromosome is referred to as its **locus** (plural: loci). Eukaryotic cells have two copies of every gene, each copy residing on one of a pair of homologous chromosomes. However, each copy of a particular gene is not necessarily identical. Small differences in the DNA sequence between one copy and the other create alternative forms of the gene called **alleles**. For some genes, different alleles give individuals distinct traits; for example, blue or brown eye colour. The genetic composition of an organism is known as its **genotype**. In essence, the genotype is the sum of all the alleles present in the cells of an organism.

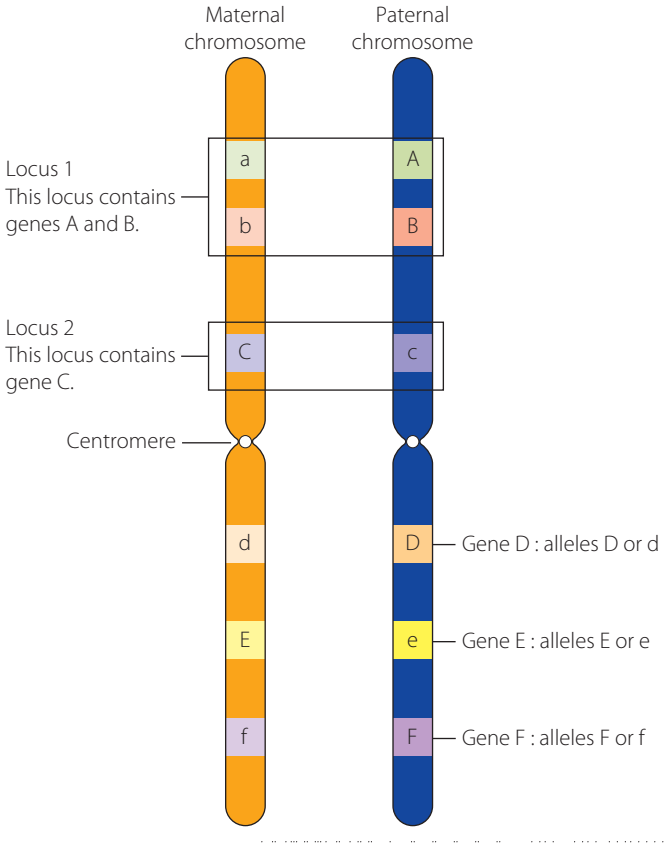

FIGURE 7.1.1
A stylised representation of a pair of chromosomes. Chromosomes exist in pairs in somatic cells, with one of the pair coming from the male parent and the other from the female parent.

7.1.1 Asexual reproduction
7.1.2 Sexual reproduction
7.1.3 What is meiosis?
7.1.4 Meiosis

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Karyotypes

A karyotype is the standard way of displaying and analysing chromosomes. The chromosomes are ordered by length, from largest to smallest, with members of each homologous pair sharing characteristic banding patterns. As DNA replication has already occurred, the chromosomes are seen as pairs of sister chromatids, joined at the centromere (Figure 7.1.2).

SYLLABUS LINK

Chapter 6 also discusses karyotypes.

chromatid
a daughter strand of a duplicated chromosome that is joined to a sister chromatid by a centromere

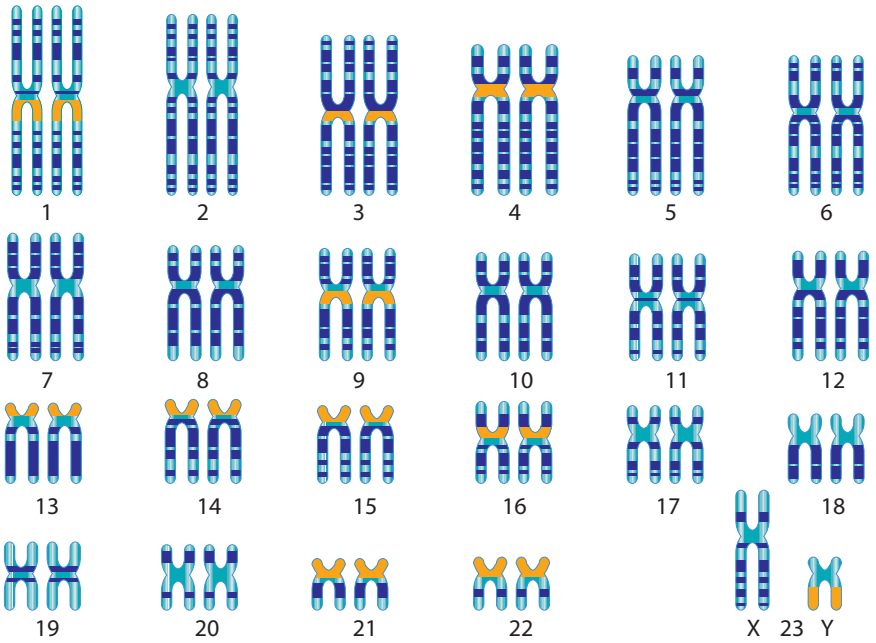

FIGURE 7.1.2 The 46 human chromosomes form 23 pairs. Individual chromosomes can be recognised by their size, position of centromere and banding pattern: the karyotype. The bands correspond to large groups of genes.

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, one sex having homologous sex chromosomes, the other sex having a dissimilar set

The nucleus of each somatic or body cell of a human contains 46 chromosomes, which form 23 pairs, of which 22 are matched or homologous. One chromosome of each pair comes from the female parent via the egg cell (ovum) and the other from the male parent via the sperm cell. 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).

This arrangement of a pair of each of the chromosomes is called the diploid number and is represented as $2n$. For example, a human somatic cell has 23 pairs of chromosomes so its diploid number is $2n = 46$. After meiosis, the gametes contain only one chromosome of each homologous pair. They are said to be haploid, denoted n. Human gametes, better known as eggs and sperm, are haploid with $n = 23$ chromosomes.

diploid ($2n$)
describes a cell or organism that has a genome comprising two copies of each chromosome, represented by $2n$

haploid (n)
describes a cell or organism that has a genome that contains one copy of each chromosome, represented by n

Mechanics of meiosis

During sexual reproduction, haploid sex cells or gametes are produced that contain just one of each pair of chromosomes. Meiosis is the nuclear division that reduces the chromosome number from $2n$ to n to produce haploid gametes, in animals called eggs and sperm. In flowering plants, pollen grains contain cells that are male gametes and ova contain an egg cell or female gamete. When the gametes fuse at fertilisation to form a zygote, the diploid number of chromosomes is restored (Figure 7.1.3, page 142).

Meiosis occurs in specialised organs of sexually reproducing animals and plants. In mammals, meiosis occurs in the ovaries and testes. In plants, meiosis occurs in the female and male parts of flowers.

interphase
the stage between nuclear divisions

SYLLABUS LINK
Chapter 6 describes DNA replication.

Interphase is the stage between nuclear divisions. It is during this phase that DNA replication occurs, resulting in identical sister chromatids attached at the centromere. At this time, the chromosomes cannot be distinguished under a light or electron microscope.

Overview of meiosis

Two divisions of the nucleus of the parent cell take place during meiosis. In the first division, meiosis I, each chromosome of a pair separates and goes to each end (pole) of the cell. This is called the reduction division because the two cells produced are haploid. In the second division, meiosis II, the chromatids of each chromosome separate from each other, again moving to the poles. Four gametes are thus produced, each carrying half the original number of chromosomes. These daughter cells are haploid.

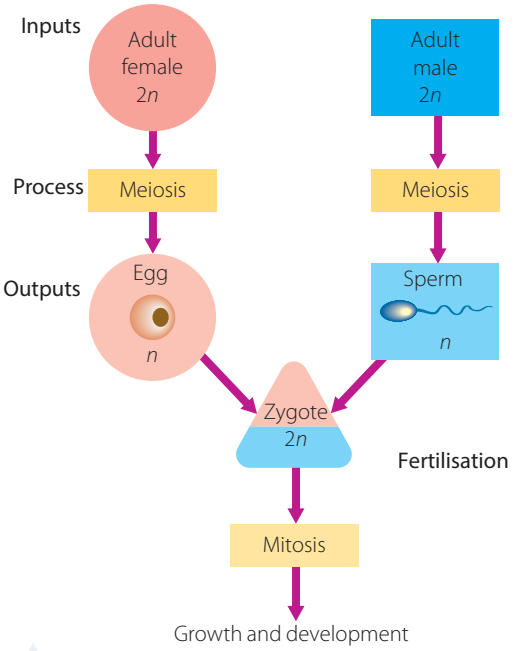

FIGURE 7.1.3 The inputs and outputs of meiosis.

Meiosis I

As the cell leaves interphase and enters the first stage of meiosis, called prophase I, the chromatin threads shorten and thicken (condense) and chromosomes become visible (Figure 7.1.4). A spindle begins to form, originating from the centrioles, if present, and attached to the centromere of each chromosome. Homologous chromosomes come to lie side by side, in a process known as **synapsis**. The pairs of homologous chromosomes, one maternal and the other paternal, may coil around each other intimately and are now called a **bivalent**. Later, they move apart but the non-sister chromatids remain in contact at certain points called **chiasmata** (singular: chiasma). At the end of prophase, the nuclear membrane breaks down.

synapsis
the pairing of homologous chromosomes

bivalent
visible bodies in a cell during prophase I of meiosis, which are made up of two homologous chromosomes joined together

chiasmata
the point of contact between homologous chromosomes during prophase I of meiosis

disjunction
the moving apart of homologous chromosomes during anaphase of meiosis

cytokinesis
the division of the cytoplasm

In metaphase I, the homologous chromosomes move together to line up across the equator of the spindle, still attached at chiasmata. Then in anaphase I, the maternal and paternal chromosomes of homologous pairs are pulled towards opposite poles of the cell by the spindle fibres. 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.

In telophase I, a haploid set of chromosomes is seen at each pole, but each chromosome still has two sister chromatids. The spindle breaks down, the cell starts to separate across its middle, and nuclear envelopes form around the two new nuclei. **Cytokinesis**, the division of the cytoplasm, completes the first stage of meiosis. At the end of meiosis I, a brief interphase usually occurs. DNA does not duplicate during this interphase.

Meiosis II

The cell then enters the second meiotic division. In prophase II, a new spindle forms; then in metaphase II the chromosomes move to the equator of the cell. The sister chromatids separate and move apart from each other to opposite poles of the cell in anaphase II. Once at the poles, the chromatids become the chromosomes of the daughter cells and the cells enter telophase II. The spindle apparatus disappears, the chromosomes de-condense to their thread-like form and new nuclear envelopes form.

With meiosis completed, cytoplasmic division follows, with four haploid cells being formed from the original single diploid parent cell. In humans, females produce an ovum containing 22 autosomes

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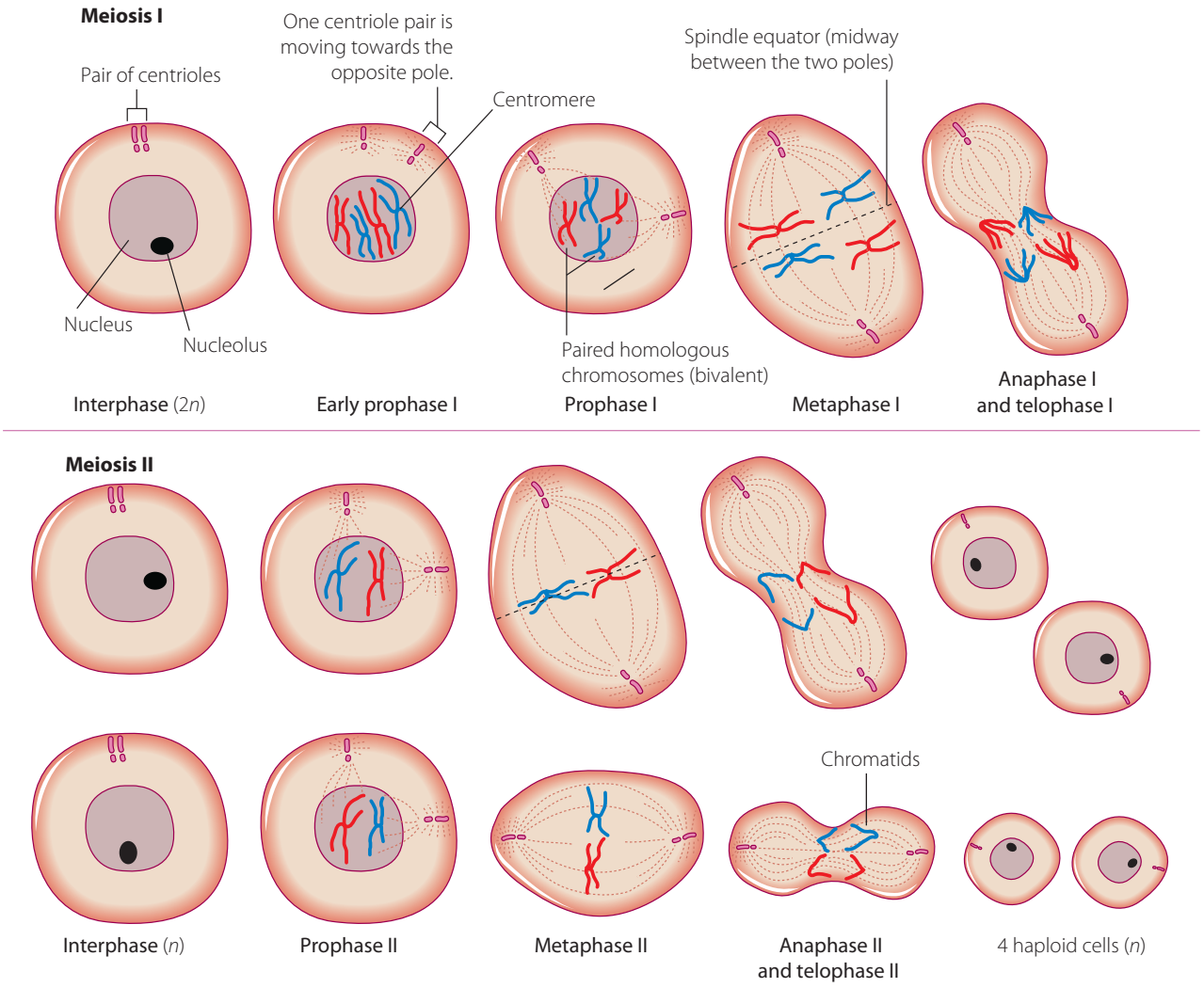


FIGURE 7.1.4 The stages of meiosis

and one X chromosome, and males produce sperm containing 22 autosomes and either an X or a Y chromosome.

Crossing over and recombination

An important event involving homologous chromosomes during meiosis is crossing over. During synapsis in prophase I, when the pairs of homologous chromosomes coil around each other to form a bivalent, the non-sister chromatids become attached at points called chiasmata. Here they may exchange segments of genetic material with one another in a process called **crossing over**. This recombination scrambles pieces of maternal and paternal genes and rearranges the combinations of alleles available on each homologous chromosome. The resultant recombinant chromosomes produce new combinations of genes, which increases the genetic diversity in the offspring.

crossing over an event during meiosis in which homologous chromosomes exchange segments with one another

An example of new combinations of alleles can be seen in Figure 7.1.5 (page 144). Without crossing over, two sex cells, for example two sperm, would contain genes A and B and two would contain a and b. After crossing over, the four cells will contain A and B, a and b, A and b, and a and B. This means that some haploid sex cells contain a mixture of genes from both the mother and father.

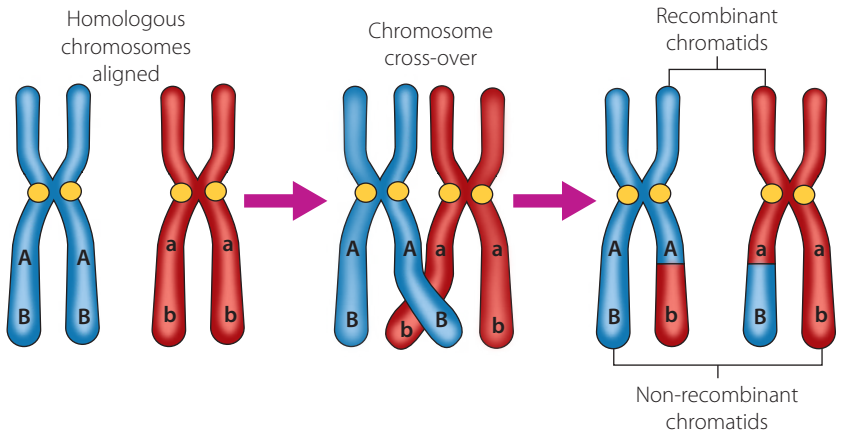


FIGURE 7.1.5 During crossing over, non-sister chromatids exchange segments with one another to rearrange combinations of alleles.

Oogenesis and spermatogenesis

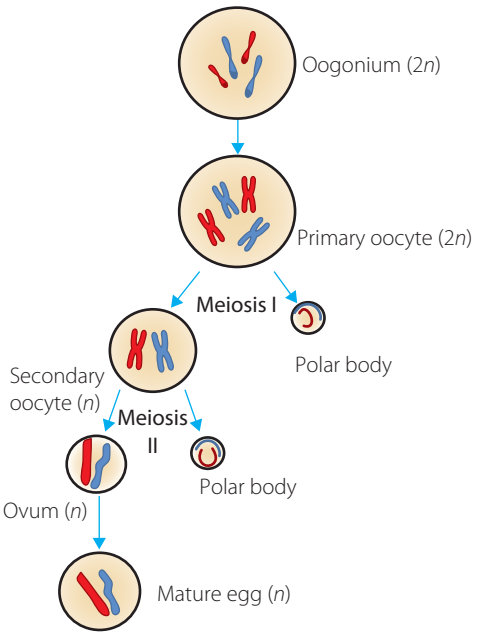
oogenesis
the process in the ovary that results in the production of female gametes

polar body
a very small cell produced during oogenesis, containing a nucleus, but very little cytoplasm

In females and males, the process of meiosis is very similar, but there are some important differences.

The process of **oogenesis** (Figure 7.1.6) begins in the ovaries of females during embryonic development, before a woman is born. There, primary oocytes begin meiosis, but remain in prophase I until the female matures sexually. After that time, a primary oocyte completes meiosis I each month to form a secondary oocyte and a structure called a **polar body**. Cytokinesis is unequal, with almost all of cytoplasm going into the secondary oocyte. The polar body degenerates. The second meiotic division, which produces a haploid ovum (egg) and a second polar body, occurs only if a sperm fertilises the egg.

FIGURE 7.1.6
Oogenesis in the ovary. Meiosis results in the haploid number of chromosomes in the egg cell.



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The production of sperm in males is called **spermatogenesis** (Figure 7.1.7). Stem cells in the testes undergo mitotic division, each time producing a new stem cell that continues to divide, and a diploid primary spermatocyte. The latter divides in meiosis I to form two secondary spermatocytes, which in turn divide in meiosis II to form four spermatids, which are haploid and develop into four sperm cells. This process occurs throughout a male's lifetime and is capable of producing, in humans, at least 3 million sperm every day.

spermatogenesis the continuous production of sperm cells in the testis

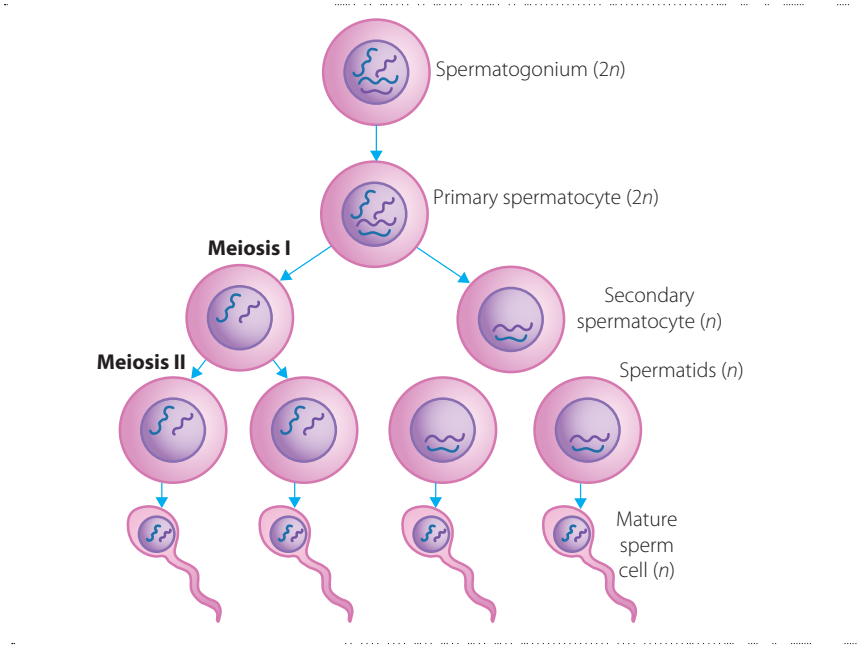

FIGURE 7.1.7 Spermatogenesis in the testis. Meiosis results in the haploid number of chromosomes in the sperm.

Oogenesis and spermatogenesis differ in three main ways.

- In oogenesis, cytokinesis in both meiosis I and II is unequal and produces only a single egg and small polar bodies that degenerate. By contrast, meiosis in spermatogenesis produces four sperm.
- At birth, an ovary contains all the cells that will ever develop into eggs. Once puberty is reached, sperm are produced throughout a man's lifetime.
- Sperm are produced continuously, whereas oogenesis has long breaks between stages of division. In fact, it may be more than 40 years between the beginning and end of meiosis I. This is because all primary oocytes begin meiosis in the female embryo, but some eggs will not complete meiosis I until the woman reaches menopause usually between the ages of 45 and 50 years.

Fertilisation

In the process of fertilisation, haploid sex cells fuse to produce a diploid zygote. Human gametes produced by meiosis each contain $n = 23$ chromosomes. Fertilisation restores the chromosome number to $2n = 46$. Different species have different numbers of chromosomes.

The role of the sex chromosomes

As well as 22 autosomes, human eggs contain an X chromosome. Sperm have 22 autosomes; half will also contain a Y chromosome and the other half will contain an X chromosome. This means there is a 50% chance that a sperm cell bearing a Y chromosome will fuse with an egg cell, resulting in a male (XY), and a 50% chance that a sperm cell carrying an X chromosome will fuse with an egg cell, resulting in a female (XX).

In other species, it is not always the male that has the unmatched sex chromosomes. For example, in birds, males are XX and females are XY. In some insects, females are XX and males are XO, with O denoting the absence of a chromosome, so the female cells must have two sex chromosomes but those of males have only one unmatched sex chromosome. In certain other social insects, such as bees, females develop from fertilised eggs and are diploid, and males develop from unfertilised eggs and are haploid.

SECTION REVIEW 7.1

REMEMBERING

1 Distinguish between:
   - **a** diploid and haploid
   - **b** gamete and zygote
   - **c** autosome and sex chromosome.

2 **a** In humans, the diploid number is $2n = 46$. State what n equals.
   - **b** State what type of cells have the $2n$ number of chromosomes.

3 Describe what happens in cytokinesis.

4 Compare and contrast spermatogenesis and oogenesis.

UNDERSTANDING

5 Explain the relationship between genes and alleles.

6 Describe the events in meiosis I, including any changes to the chromosome number.

7 It has been said that King Henry VIII of England was wrong to blame his wives for not having any sons. Comment on this statement and provide evidence to support your position.

8 Explain how crossing over and recombination contributes to genetic variation.

APPLYING

9 A cell from an unknown source has been prepared and stained, and a karyotype has been displayed. Explain how you could tell if it was likely to be from a human and what sex they were.

7.2 Independent assortment and random fertilisation

During metaphase I of meiosis, the chromosomes line up in homologous pairs across the equator of the cell (Figure 7.2.1). Each pair consists of one maternal and one paternal chromosome and the way they line up is independent of the way the other pairs orient themselves. When the chromosome pairs separate and move to opposite poles in anaphase I, the original maternal and paternal chromosomes are distributed randomly to the gametes instead of as a predefined set from either parent. This process is called **independent assortment**.

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

Independent assortment ensures that each resultant haploid cell contains a mixture of genes from the organism's mother and father. As the homologous pairs carry different genetic information, independent assortment increases the number of different combinations of genes carried by the gametes. The number of different combinations of chromosomes can be calculated as 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.

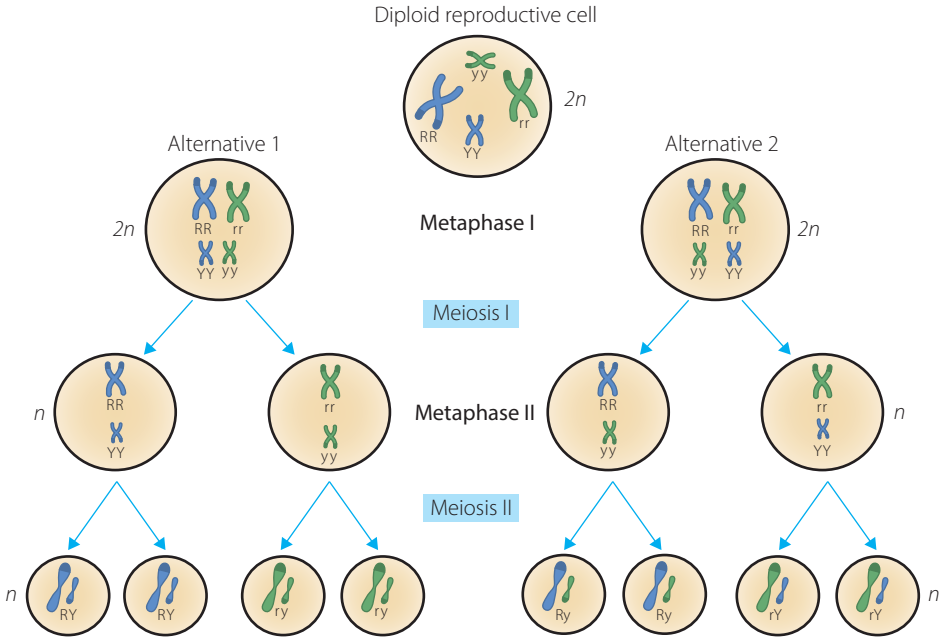

FIGURE 7.2.1 Independent assortment of chromosomes in meiosis increases the genetic variability of the offspring.

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. This greatly increases the potential for variation in the genotypes of the offspring.

SECTION REVIEW 7.2

REMEMBERING

1. State the stage of meiosis in which homologous chromosomes line up at the equator of the cell.
2. State how many combinations of paternal and maternal chromosomes are possible in humans where $2n = 46$.

UNDERSTANDING

3. Describe independent assortment.
4. Describe random fertilisation.
5. Explain the importance of independent assortment.

APPLYING

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. Compare the amount of variation that would be expected in eggs and sperm.

CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1. What place is associated with the process of meiosis?
2. Describe the time period associated with meiosis.
3. What is the purpose of meiosis?

CATEGORY QUESTIONS

4. What components are associated with the category of chromosomes?
5. What two processes are associated with sexual reproduction?

ELABORATION QUESTIONS

6. Predict, with reasons, whether sexual reproduction would be possible in a haploid organism.
7. Predict what would happen if a chemical that interfered with the contraction of the spindle was added to a culture of cells undergoing meiosis.

EVIDENCE QUESTIONS

8. Provide evidence to support or refute the statement: 'In sexually reproducing organisms, half of the organism's body cells contain DNA from the mother and half contain DNA from the father'.
9. Explain the reasoning behind the statement: 'Sexual reproduction produces genetic variation among offspring'.

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END-OF-CHAPTER EXAM

End-of-chapter test

1 Crossing over contributes to genetic variation because chromosomal fragments are exchanged between:

A chromatids of non-homologous chromosomes.

B sister chromatids of a chromosome.

C non-sister chromatids of homologous chromosomes.

D autosomes and sex chromosomes.

2 The DNA content of a diploid cell that is $2n = 4$ is measured. If the DNA content of this cell is x, then the DNA content of the same cell at metaphase of meiosis II would be:

A $0.5x$

B x

C $2x$

D $4x$

3 The points of contact between homologous chromosomes in prophase I of meiosis is called:

A centromeres.

B chiasmata.

C disjunctions.

D bivalency.

4 Cell B was found to contain twice the amount of DNA as a normal body cell C.

a Name a phase of meiosis that cell B could be in.

b If cell C has 16 chromosomes, calculate how many chromatids you would find in cell B.

5 What name is given to a display of the number and appearance of the chromosomes of a cell observed at metaphase?

6 Scientists from the Australian Museum and Queensland University of Technology have sequenced the koala genome. Analysis of the data should reveal between 12 000 and 20 000 genes on the 16 chromosomes. Explain, with reasons, whether you would expect the sequence of DNA to be exactly the same in all members of the koala species.

7 A group of cells being studied was never observed to undergo meiosis. Predict if this means the cells were dead. Justify your answer.

8 GENE EXPRESSION

Introduction

Every cell in any individual of any multicellular species has exactly the same chromosomes, yet each differentiated cell type has its own particular structure and function. Differences between specialised cells are determined by which of the genes on those same chromosomes are active or 'expressed'.

Some genes control functions common to all cell types; for example, cellular respiration reactions. These genes must be active in all varieties of cells at all times. However, most genes are regulated; that is, their production is controlled. In any particular specialised cell, at any particular time, regulated genes may or may not be expressed.

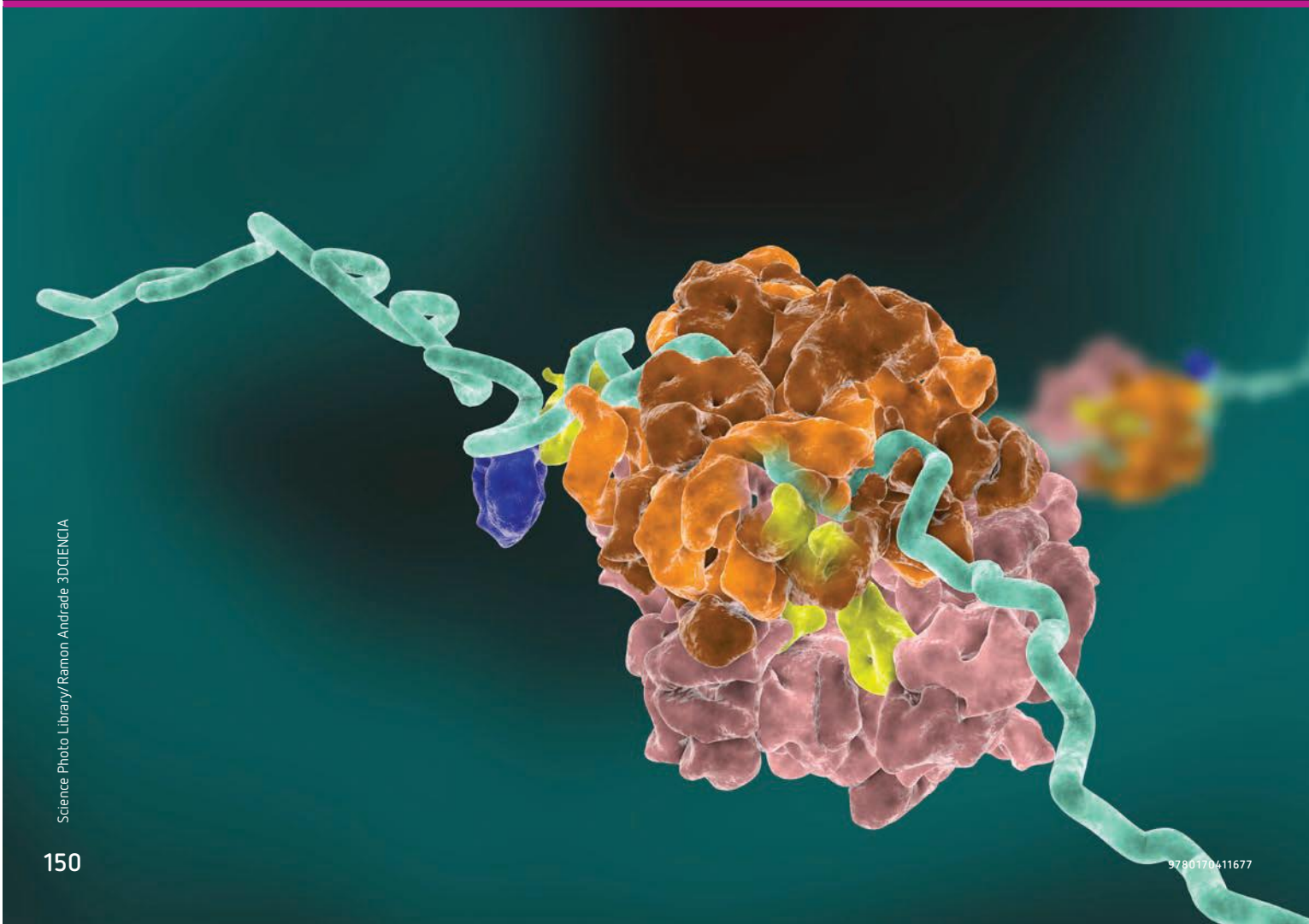
Stimulus questions

What determines which genes are active in a particular specialised cell type?

Are there several different factors that determine which genes are active in a particular cell type?

How can genes be active sometimes and inactive at other times in an organism?

Are the factors that affect gene expression internal to an organism, or environmental, or both?



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8.1 Genome and genes

The DNA molecule can be considered to be the most important molecule in all organisms, and distinguishes living things from non-living substances. The total of all the DNA in an organism's cells, including that in the nucleus and in mitochondria and chloroplasts (if present), is called its **genome**. It is this genetic material that makes each organism different from any other.

Genes are particular sections of the genome that carry instructions in the form of a code. Genes are composed of particular sequences of the nucleotide units constituting the DNA molecules. Genes 'direct' the production of polypeptides that make up proteins, or of ribonucleic acids (RNAs) involved in the synthesis of these proteins. In combination with regulating factors that determine *which* proteins are produced in *which* particular cells and *when*, gene-coded proteins determine every characteristic of every individual organism.

genome
all genetic material contained in an organism or a cell, including DNA existing as chromosomes within the nucleus, and DNA in mitochondria and chloroplasts (if present)

Genomics

The study of the genomes of organisms, which differ between species but also have universal commonalities, is termed 'genomics'. This significant branch of molecular biology has been made possible by advances in technologies, particularly in robotics and 'bioinformatics' – the science of managing and analysing huge amounts of complex biological data using advanced computing techniques.

These technologies have become much further developed since first assisting in the momentous task of mapping the human genome; that is, determining the complete sequence of over 3000000000 nucleotide bases in human DNA. The Human Genome Project team, collaborating scientists from several countries, after more than a decade of painstaking work, published the 90% completed draft sequence in the scientific journal *Nature* in 2001. Such sequencing with today's technology could be completed in days to weeks, and at a minuscule fraction of the cost.

SYLLABUS LINK

Chapter 6 describes the structure of DNA.

8.1.1 Genome sequencing

8.1.2 IGSR and the 1000 Genomes Project

ENCODE

In 2003, a research project called ENCODE (Encyclopedia of DNA Elements) was initiated by the United States National Human Research Institute to learn as much as possible about the human genome sequence. The ENCODE production effort is organised as an open consortium and includes investigators with diverse backgrounds and expertise in the production and analysis of data. The project continues to this day, and all data generated by ENCODE participants is rapidly released into the public domain.

INQUIRING FURTHER

Investigate the time taken to complete the Human Genome Project and the approximate cost.

Research the types of DNA testing that are available today to private individuals.

Summarise the approximate costs of each of these tests, and the time taken for each to be completed.

Comment on the progress in the areas of genomics and bioinformatics, since the Human Genome Project.

The human genome

As discovered during the Human Genome Project, the human genome contains about 3.1 billion nitrogen base pairs. There are 19000–20000 genes that code for the production of proteins, and over 25000 genes that are not protein-coding genes, but include genes that code for ribosomal RNA and transfer RNA, which are involved in the synthesis of proteins.

SYLLABUS LINK

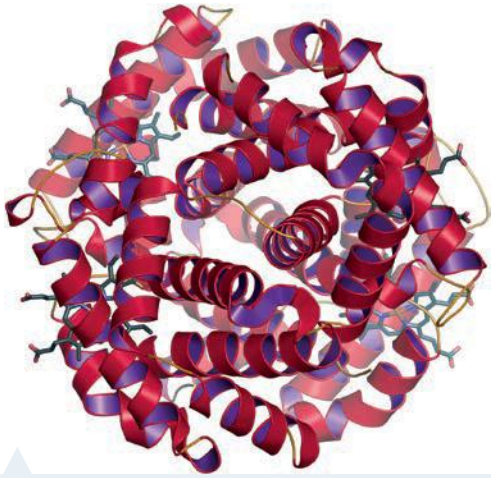
Section 8.3 discusses coding and non-coding genes.

SECTION REVIEW 8.1

REMEMBERING

1 Briefly explain the relationships between DNA, genes and a genome.
2 Define:
   a genomics
   b bioinformatics.
3 Briefly describe what the Human Genome Project was.

8.2 Protein synthesis



Dreamstime.com / Johannes Kaestner

FIGURE 8.2.1 A computer-generated representation of a haemoglobin molecule. Coiled flat purple-red ribbons represent polypeptide chains that make up haemoglobin, and the innermost smaller red coils indicate bonding sites for oxygen. Additional components of the molecule are also illustrated.

Proteins are essential in cells: the structure and the function of each and every specialised cell in multicellular organisms are due to the suite of proteins produced within it.

For example, in humans a red blood cell, during its development, must accumulate haemoglobin protein (Figure 8.2.1) to carry oxygen, but it has no need for keratin, a type of fibrous protein in protective tissue structures such as skin, hair and toe and fingernails. Muscle cells need to produce large amounts of actin and myosin proteins, arranged in highly ordered arrays, for muscle contraction and thus movement of body structures. Some cells of the pituitary gland synthesise growth hormone, a protein that is released during childhood and adolescence to promote bone growth.

Enzymes are vital functional proteins because they speed up every chemical reaction in every cell. Without enzymes, reactions would be so slow as to hardly proceed at all; this would be incompatible with the maintenance of life itself.

Everything a cell does – what it develops into, what it synthesises and how it operates – is determined, more than anything, by the proteins it produces, and the cell's genome directs the production of these proteins.

DNA directs protein production

polypeptide
a polymer of many amino acids linked by peptide bonds; forms a protein or part of a protein

A protein consists of one or more **polypeptide** chains arranged into a three-dimensional shape, which can be amazingly intricate, such as haemoglobin (Figure 8.2.1). Polypeptide molecules consist of subsets of 20 different amino acid subunits. It is the order in which the amino acids are arranged, and the relative abundance of each, that give a particular polypeptide, and thus the protein that it and other polypeptides are constituents of, its individuality and functionality.

codon
a series of three adjacent nucleotide bases in DNA and mRNA; each codon specifies a particular amino acid to be added when a polypeptide is assembled; start and stop codons also occur

DNA, with its four different nucleotide bases of adenine (A), thymine (T), cytosine (C) and guanine (G), determines which particular amino acids (in which sequence) are assembled into polypeptides at ribosomes.

However, it cannot be just one of these nucleotide bases that codes for one particular amino acid because then only four different amino acids could be specified. Two sequential bases allow for 16 different combinations of the 4 bases: 4×4. A sequence of three bases though, with a total of $4 \times 4 \times 4 = 64$ combinations, is more than sufficient to account for the 20 different amino acids commonly found in cells. Each 'triplet' of bases is known as a **codon**.

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DNA, mRNA and ribosomes

Although it is DNA in the nucleus that contains the sets of instructions for polypeptide production, it is **ribosome** organelles, in the cytoplasm, that carry out these instructions. The DNA molecules act as templates or masters for the production of another sort of nucleic acid, called **messenger RNA (mRNA)**, which carries the instructions from the nucleus out to the cytoplasm. Like DNA, mRNA consists of a string of nucleotides. However, RNA differs from DNA in four ways, as shown in Table 8.2.1.

8.2.1 Translation: DNA to mRNA to protein

ribosome organelle where polypeptide synthesis occurs in all cells; locks onto mRNA molecule and moves along it to translate its code and link amino acids; formed in nucleolus

messenger RNA (mRNA) a ribonucleic acid molecule formed in the nucleus during gene transcription; has nitrogen base sequence complementary to DNA template segment; travels to cytoplasm where ribosomes attach

TABLE 8.2.1 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 of DNA into mRNA

The single-stranded mRNA molecule is generated from the **template strand** of the 'unwound' DNA double helix. This process is called **transcription**. It is accomplished through complementary pairing or chemical bonding between nucleotide bases: cytosine (C) with guanine (G) and adenine (A) with uracil (U). As shown in Table 8.2.1, the RNA strand contains the nitrogen base uracil (U) in place of thymine in DNA. U and T are so similar in chemical structure though, that U pairs with A in RNA, just as T pairs with A in the double strands of the DNA molecule, and in the DNA replication process.

The first step in the process of transcription, as seen in Figure 8.2.2, occurs when DNA in the region of a gene unwinds, and then unzips, exposing the nucleotide bases of both DNA strands. However, only the template strand is used to direct the synthesis of mRNA. The other strand of DNA is called the **non-template strand**, or complementary strand.

template strand the DNA strand that serves as pattern for making complementary polynucleotide

transcription the formation of an mRNA molecule against the template strand of DNA molecule in the nucleus by complementary nucleotide base pairing

non-template strand the DNA strand complementary to template strand; does not form the pattern for the synthesis of complementary polynucleotide

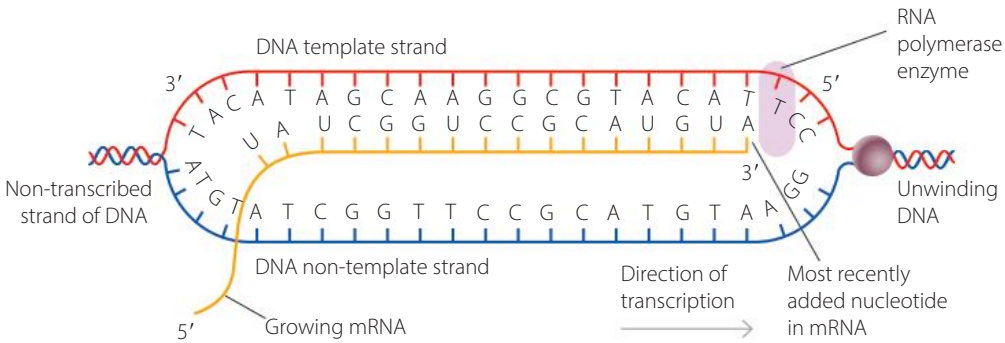


FIGURE 8.2.2 Transcription of mRNA from the DNA template. The double-stranded DNA molecule unwinds and RNA nucleotides pair with the exposed bases on the template strand. These RNA nucleotides are then joined together by the enzyme RNA polymerase, resulting in mRNA.

A particular nucleotide sequence at the beginning of the unzipped section of DNA signals the start of a gene to be transcribed. Complementary RNA nucleotides are progressively joined together by RNA polymerase enzyme moving along the length of DNA. A base sequence at the end of the gene serves as a stop signal and the mRNA is released as a single strand. The DNA 'zips up' again and twists itself back into a double helix once the mRNA molecule has peeled off.

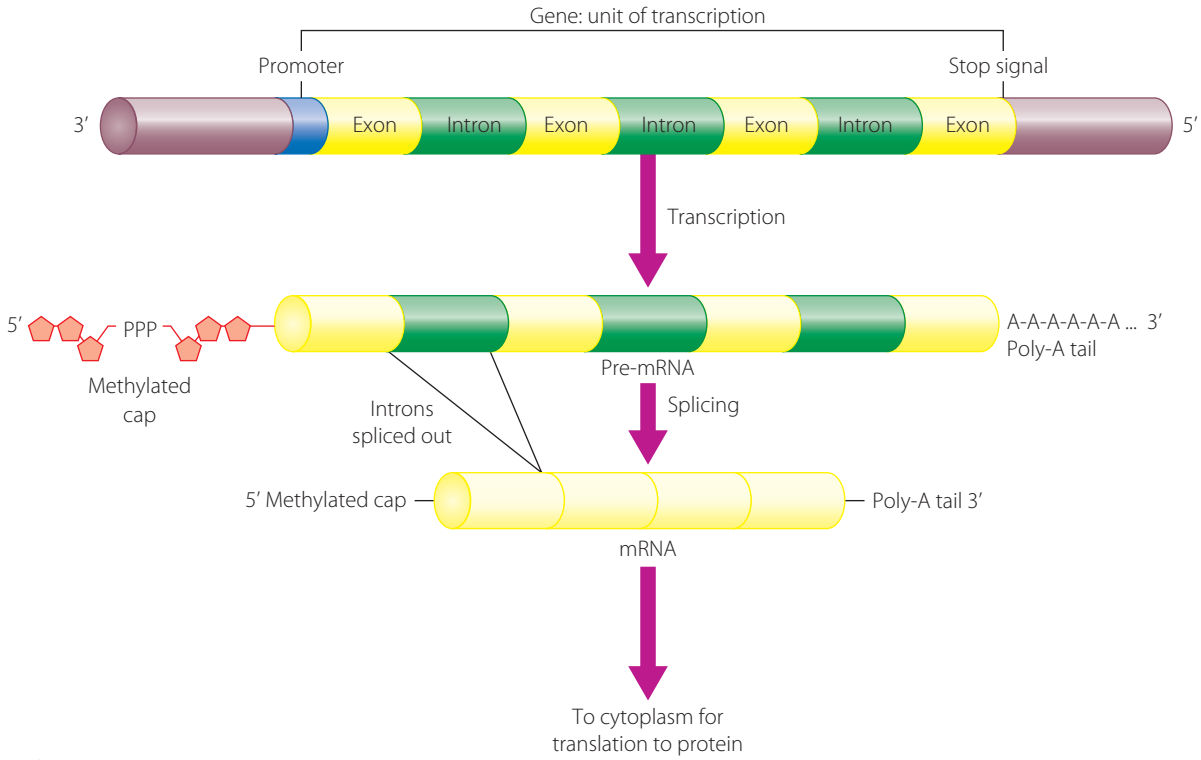


FIGURE 8.2.3 Modification of mRNA molecules occurs in the nucleus of a cell before they are exported to the cytoplasm for translation into polypeptides at ribosomes.

pre-mRNA
an unmodified 'immature' mRNA molecule that contains introns

intron
a section of DNA or pre-mRNA that does not code for a polypeptide; is removed (spliced) from pre-mRNA to form mature mRNA molecule

exon
a section of DNA, pre-mRNA or mRNA that codes for a polypeptide

mature mRNA
a modified pre-mRNA molecule with introns removed; ready to move out of nucleus to cytoplasm

Adjustments to the newly formed mRNA molecule

The mRNA strand at this stage is called **pre-mRNA**. Before it leaves the nucleus, it is modified by certain chemical additions to its ends that ensure the stability of the mRNA molecule as it moves out of the nucleus (Figure 8.2.3). Also, some segments of the mRNA molecule, called **introns**, are removed. Introns are regions of base sequences that do not code for polypeptide production. Introns are interspersed with regions of DNA called **exons**, which *are* coding regions and *do* contain the information for polypeptide formation.

Both the exons and introns are transcribed into pre-mRNA, but introns are removed and exons joined back together, in a process called splicing, before the **mature mRNA** leaves the nucleus.

Different versions of produced proteins

When exons from the same pre-mRNA segments are spliced together differently, alternative forms of the mature mRNA are created, and are then translated into different versions of the polypeptides, and thus different final proteins. Introns direct this alternative splicing.

In this way, particular tissue types in multicellular organisms contain uniquely different versions of proteins that have all been encoded by the same gene. Alternative splicing such as this occurs in the processing of 95% of human genes.

Translation of mRNA into polypeptides

When mature mRNA moves from the nucleus into the cytoplasm, a ribosome attaches to it, and moves along until it comes to an AUG **start codon**. This start codon is the signal to begin the process of assembling amino acids into the polypeptide chain specific to the particular nucleotide sequence in the mRNA. This process is known as **translation**. Figure 8.2.4 illustrates a polypeptide being translated at a ribosome.

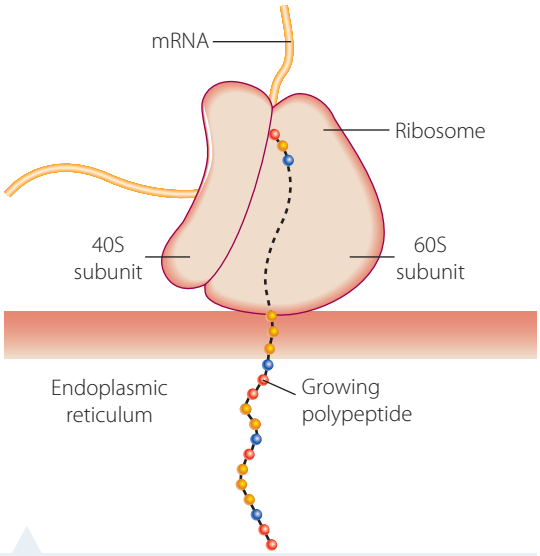


FIGURE 8.2.4 A representation of a ribosome, composed of two subunits; 40S and 60S (S is a unit of size). The ribosome is shown attached to endoplasmic reticulum membrane, and is synthesising a polypeptide chain.

Transfer RNA

Another type of RNA, called **transfer RNA (tRNA)**, is also necessary in translation. tRNA transfers or carries amino acids to ribosomes. tRNA molecules are folded back on themselves to form a compact three-dimensional structure rather like a clover leaf.

As illustrated in Figure 8.2.5, each tRNA molecule has a three-base nucleotide sequence, called the **anticodon**, at one end, which bonds to the complementary codon on the mRNA strand. Each of the 20 amino acids can bond to at least one and up to four different tRNA molecules at the end opposite the anticodon, called the **amino acid binding site**. The ability of an amino acid to bond to a particular tRNA is associated with which anticodon is present in that tRNA molecule. When the tRNA anticodon is bonded with the complementary codon on the mRNA, the amino acid at the binding site is in a position to be joined to the growing chain of amino acids by a **peptide bond**.

The ribosome continues moving along the mRNA strand, facilitating the tRNA delivery of an amino acid, and its bonding to the growing chain, until it comes to a **stop codon**, for which there is no corresponding tRNA molecule. At this point, the synthesis of the specific polypeptide molecule is complete.

Each tRNA molecule peels off from the mRNA, and, along with other tRNA molecules in the cytoplasm, can subsequently pick up specific amino acids again and again when required. Also, the mRNA strand, released from the ribosome, is subsequently broken down by the cell, enabling the RNA nucleotides to be re-used over and over again.

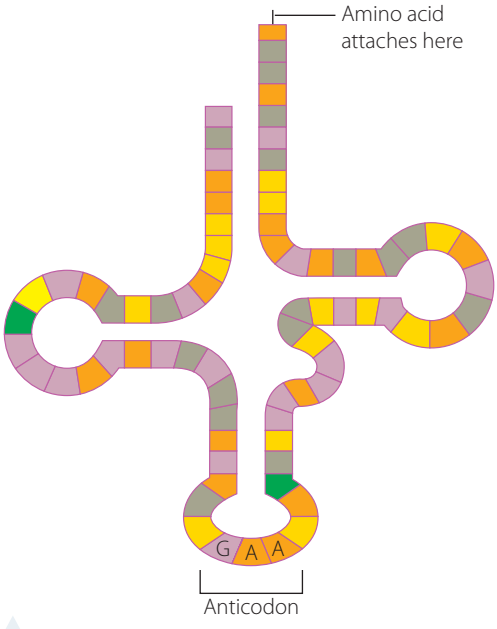


FIGURE 8.2.5 The structure of transfer RNA. The diagram shows the molecule as a flat molecule shaped like a clover leaf. The three bases shown at the bottom, called the anticodon, are attracted to the complementary mRNA codon. The amino acid binding site is shown at the top of the molecule.

start codon
the first codon of an mRNA transcript translated by a ribosome; signals ribosome to start translating mRNA

translation
the joining of amino acids in a specific order, according to information in mRNA 'read' by ribosome, to form polypeptide

transfer RNA (tRNA)
an RNA molecule that picks up a particular amino acid from the cytoplasm and then pairs with a specific mRNA codon to deliver the amino acid to the growing polypeptide chain

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

amino acid binding site
the site of attachment of an amino acid to a tRNA molecule

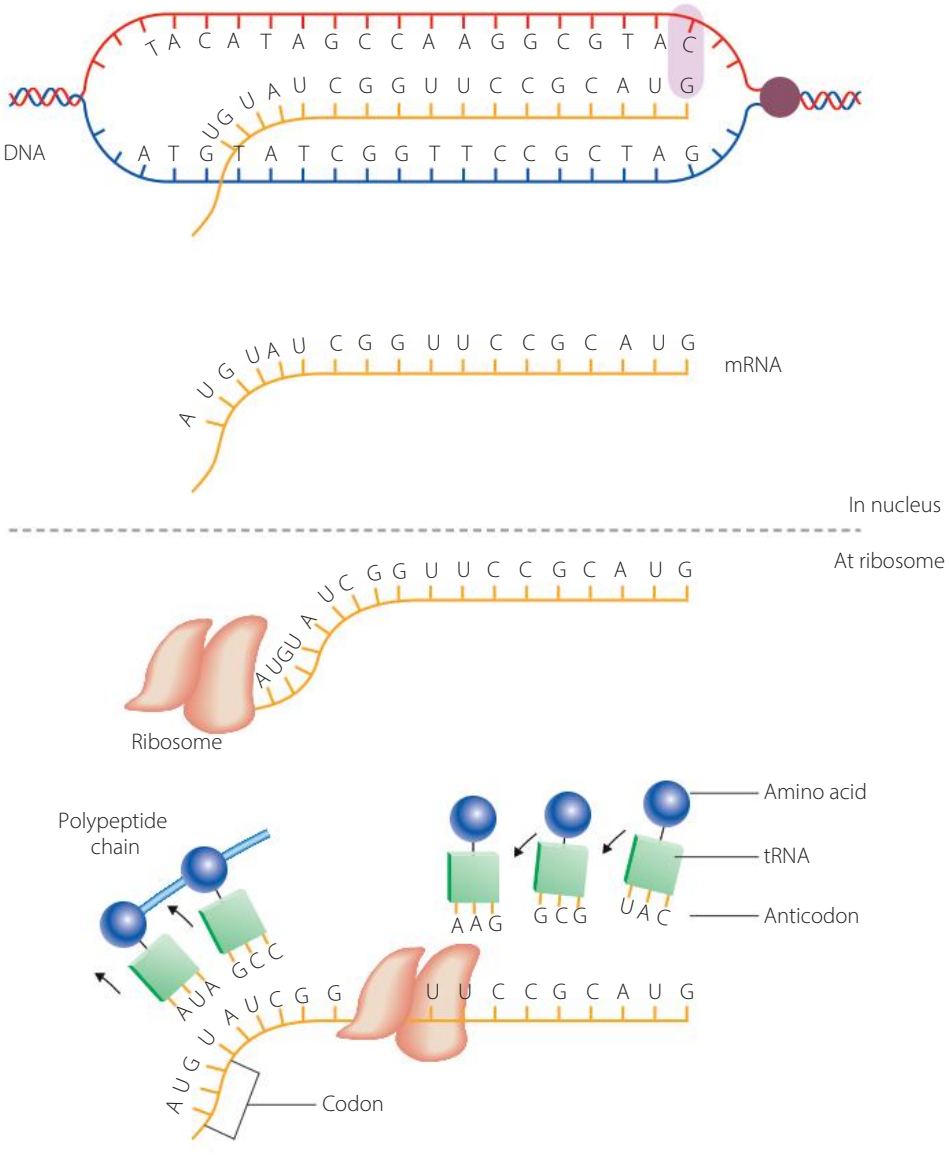
peptide bond
the bond that forms between adjacent amino acid monomers

stop codon
the codon that discontinues the synthesis of the polypeptide chain

In this way, the amino acids are linked in an order corresponding to the sequence of nucleotide base codons in the mRNA. As the mRNA base sequence is determined by the sequence of base codons in the original DNA, it follows that the base sequence in the DNA determines the order in which amino acids line up.

The whole polypeptide synthesis process, starting with the DNA in the nucleus, is summarised and illustrated in Figure 8.2.6.

A protein molecule is later formed from one or more polypeptide chains joined together to form a specific, and often very intricate, three-dimensional structure, such as that of haemoglobin illustrated in Figure 8.2.1.



Through the action of tRNA, the mRNA dictates the order in which amino acids link up to form the polypeptide chain.

The anticodons at the ends of tRNA molecules complement the codons in the mRNA.

FIGURE 8.2.6 The process of polypeptide formation

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The genetic code

The genetic code (Figure 8.2.7) shows the relationship between the codons on the mRNA molecule and the amino acids that are delivered by tRNA to form the polypeptide chain. From the genetic code, it is also possible to work out the relationship between the bases in the original DNA and the amino acids that result.

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

First base \ Second base	U	C	A	G	Third base
U	UUU, UUC: Phe; UUA, UUG: Leu	UCU, UCC, UCA, UCG: Ser	UAU, UAC: Tyr; UAA: Stop; UAG: Stop	UGU, UGC: Cys; UGA: Stop; UGG: Trp	U C A G
C	CUU, CUC, CUA, CUG: Leu	CCU, CCC, CCA, CCG: Pro	CAU, CAC: His; CAA, CAG: Gln	CGU, CGC, CGA, CGG: Arg	U C A G
A	AUU, AUC, AUA: Ile; AUG: Met/Start	ACU, ACC, ACA, ACG: Thr	AAU, AAC: Asn; AAA, AAG: Lys	AGU, AGC: Ser; AGA, AGG: Arg	U C A G
G	GUU, GUC, GUA, GUG: Val	GCU, GCC, GCA, GCG: Ala	GAU, GAC: Asp; GAA, GAG: Glu	GGU, GGC, GGA, GGG: Gly	U C A G

FIGURE 8.2.7 The genetic code. The mRNA codons shown correspond to the 20 amino acids assembled by translation on the ribosomes, and three codons act as stop codons, with the AUG codon initiating polypeptide synthesis in specific circumstances.

Most of the amino acids are coded for by more than one codon. Three codons, UAA, UAG and UGA, do not actually code for an amino acid. Instead they act as termination or 'stop' signals, disengaging the completed polypeptide chain at that point. Also, the AUG codon initiates polypeptide synthesis under certain conditions.

The genetic code is often referred to as the 'universal genetic code' because it applies to almost all known organisms, except for certain bacteria and mitochondrial DNA. DNA can also generally be said to be a 'universal indicator of life'.

SECTION REVIEW 8.2

REMEMBERING

1 Briefly describe:
   - **a** three examples of proteins with different roles in cells
   - **b** the importance of enzyme proteins
   - **c** messenger RNA (mRNA) and its role.

UNDERSTANDING

2 Describe the relationship between proteins, polypeptides and amino acids.

3 Distinguish between:
   - **a** transcription and translation
   - **b** pre-mRNA and mature mRNA.

4 Write one sentence describing transcription, using the terms 'gene', 'exon' and 'intron'.

5 **a** Describe the outcome of alternative splicing of mRNA.
   - **b** Explain its significance in specialised cell structure and function.

APPLYING

6 **a** Referring to the genetic code in Figure 8.2.7, name the:
   - **i** start codon
   - **ii** termination codons.

   b If the DNA template strand has the base sequence AGC TAT CGA GTC AAA:
   - **i** write the complementary mRNA sequence
   - **ii** write the sequence of bases on the non-template DNA strand
   - **iii** identify the five amino acids specified by your answer to part i.

8.3 Coding and non-coding DNA

Before the human genome sequence was published in 2003, it was estimated that it would contain about 100 000 protein-coding genes. This was a reflection of the huge number of different types of proteins produced in the human body. When the sequence was finally published, it contained about 20 000 protein-coding genes, about one-fifth of the original estimate. How could such a comparatively small genome code for all the known proteins? (A proportion of this protein variety results from splicing, explained in section 8.2, when exons are re-joined in different ways in the production of mature mRNA to produce variation in the polypeptides, and thus proteins, synthesised from just one gene.)

Considering the very large number of functional proteins synthesised in human cells, it now seems likely that our 'DNA → RNA → protein' definition of protein synthesis has to be questioned.

Central dogma of molecular biology

Originally stated by Francis Crick in 1958, the term 'central dogma of molecular biology' (Figure 8.3.1) is used to describe the one-way sequence of information transfer where:

- DNA acts as a template for its own replication, and also as a template for the production of mRNA
- the newly formed mRNA is modified to become mature mRNA, before mature mRNA moves out to the cytoplasm to act as template for the compilation of amino acids into a polypeptide by a ribosome.

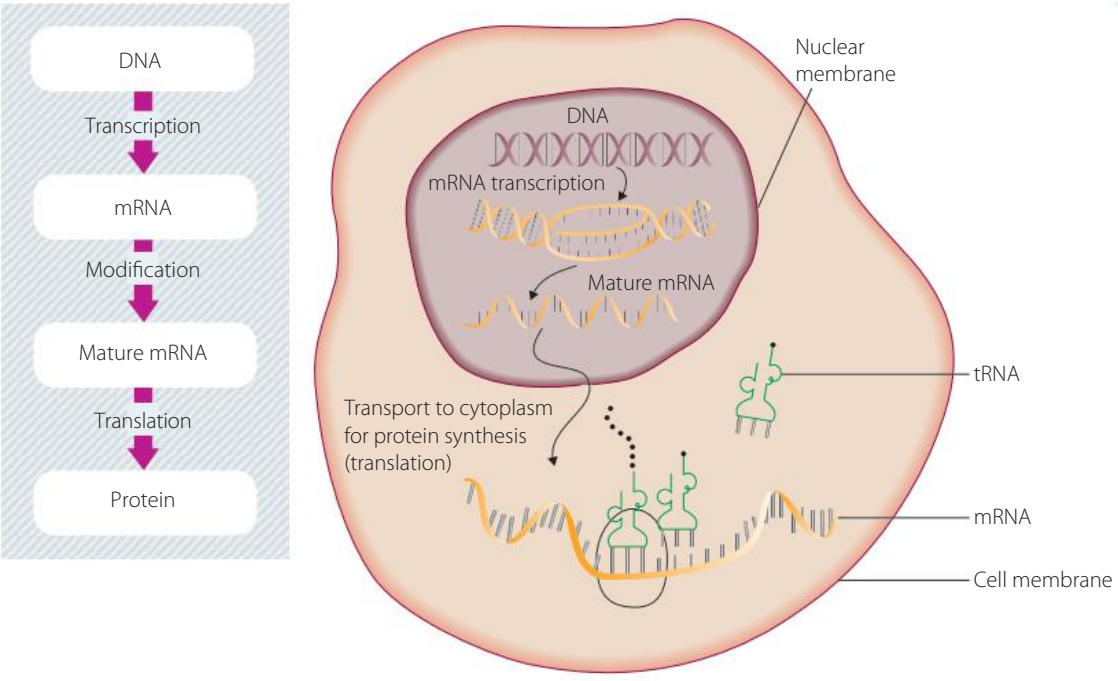

Illustration adapted from the National Human Genome Research Institute (NHGRI)

FIGURE 8.3.1 The classic view of the central dogma of molecular biology

There are many examples to show that this one-way sequence of information is no longer the only possibility. For example, a group of viruses called retroviruses uses the enzyme reverse transcriptase to produce DNA from the RNA genome. Human immunodeficiency virus (HIV) is an example of a retrovirus.

Some discoveries are also at odds with the central dogma. These include: only a tiny fraction of the genome results in polypeptide production; chemical modification of DNA can affect the expression of genes; and genes work together in networks.

The genome consists of coding and non-coding DNA

Eukaryotic genomes are comparatively very large (Table 8.3.1). For example, as previously stated, the human genome consists of 3.1 billion nucleotide pairs. However, only a small fraction of the genome actually codes for protein. **Coding DNA** sequences, transcribed into mRNA and then translated into polypeptides and then proteins, are the most well-known part of the genome. However, these sequences actually make up less than 2% of the human genome: the vast majority is made up of **non-coding DNA**. Determining all the functions of the non-coding DNA is an ongoing area of research.

coding DNA the small part of DNA used as a template for mRNA synthesis and thus for polypeptide synthesis; also known as a gene

non-coding DNA all DNA sequences within the genome that are not found within mRNA-coding exons, i.e. do not code for polypeptides

TABLE 8.3.1 Genome sizes of some eukaryotic species

ORGANISM	SIZE OF GENOME (BASE PAIRS)
Human	3 100 000
Fruitfly	168 700
Nematode worm	100 300
Yeast	12 200

Non-coding DNA

ribosomal RNA (rRNA)
a folded molecule of RNA that combines with proteins to form ribosomes; formed in nucleolus of eukaryotic cells

telomere
hundreds to thousands of repeated short DNA sequences at the ends of chromosomes to help maintain them; short lengths lost with each replication of DNA

At least some sections of the non-coding DNA have specific functions in switching gene function on or off; that is, in regulating which genes are active in which cells and under what circumstances.

Much of the non-coding DNA is made up of repetitive sequences. A considerable proportion of these sequences is transcribed into functional RNA, including **ribosomal RNA (rRNA)** and transfer RNA (tRNA), both of which are necessary for protein synthesis.

The ENCODE project, at initial analysis, revealed that at least 80% of the human genome is transcribed at one time or another, for some useful purpose. Genes for non-coding RNA (e.g. rRNA, tRNA), regulatory DNA and genes producing introns are just some of the types of non-coding DNA that control how genetic instructions are interpreted.

Centromeres and **telomeres** are also segments of non-coding DNA. Centromeres hold duplicated chromosomes (sister chromatids) together, and are the site of attachment for spindle fibres to move chromosomes in cell division. Telomeres are extensions of DNA at the ends of chromosomes that act to prolong the life of chromosomes. At each replication of a DNA molecule, some of the repeating segments making up the telomeres are lost, but the coding sections are preserved.

8.3.1 What are the relationships between the coding and non-coding strands of DNA?

SYLLABUS LINK

Chapter 6 discusses the structure of DNA, including centromeres of chromosomes.

SECTION REVIEW 8.3

REMEMBERING

1. Briefly describe what is meant by 'central dogma of molecular biology'.
2. **a** Define:
   - **i** coding DNA
   - **ii** non-coding DNA.

   b List three examples of non-coding DNA.

UNDERSTANDING

3. Explain what it means for non-coding DNA to be transcribed or not.
4. tRNA and rRNA are described as 'functional RNA'. Explain what this means.
5. Centromeres and telomeres are examples of non-coding DNA. Introns are transcribed by non-coding DNA. Briefly describe their functions.

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8.4 The purpose of gene expression

During the progressive development of an individual – such as from a fertilised egg or asexual spore, or from a juvenile to an adult – many different changes to cells occur. Cells can become specialised to carry out particular functions, and biochemical activities can change at various times. Cells in any individual have the same DNA content, and the DNA specifies each cell's activities and characteristics, due largely to the proteins determined by their genes. Specialised cell types become so different from each other, and different *within* types at different times, because they do not express all the genes of their genome at any particular time.

Rather, at any given time, genes that code for required time-specific and/or cell type-specific proteins in a cell may be active, while genes coding for non-required proteins are inactive. This ensures the cell does not waste energy and resources producing unwanted proteins, as well as ensuring the cell does not produce proteins whose functions may interfere with the cell properly performing its specialised role.

Even when genes *are* expressed, there are controls over how fast specific genes are transcribed and translated. Whether genes are expressed seems to depend on the type of cell, its stage of development and conditions within and around the cell.

Gene expression refers to a gene being transcribed into mRNA and translated into a polypeptide, or transcribed into functional RNA. **Gene regulation** refers to the processes within cells that enable a gene to be expressed just in particular cells and at certain specific times and rates. These capabilities are present in all known life on Earth.

In eukaryotic cells, it seems the default state of gene expression is 'off'. However, some genes that encode proteins that serve to maintain basic cellular processes are continually expressed at some level to maintain cell function. These can be called **housekeeping genes**. For example, genes that express proteins for glycolysis or for biosynthesis of essential macromolecules are housekeeping genes. It is only when specific DNA sequences are in an open configuration on the chromatin, and accessible for specific proteins to bind to, that gene expression is 'on'.

gene expression
the process in which information encoded in genes directs the production of RNA molecules (mRNA, tRNA and rRNA) for polypeptide and thus protein synthesis

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

housekeeping gene
a gene that encodes a polypeptide as part of a protein (often an enzyme) required to maintain basic cellular processes

SECTION REVIEW 8.4

REMEMBERING

1 Why do cells not express all genes in their genome all the time?

2 Define:
- **a** gene expression
- **b** gene regulation.

3 **a** Briefly explain what a housekeeping gene is.
- **b** Suggest examples of functions such genes may have.

UNDERSTANDING

4 The default state of expression of many genes in eukaryotic cells is said to be 'off'. Discuss what this means.

8.5 Factors regulating the phenotypic expression of genes

Overall, there are two major categories of gene regulation: short-term regulation and long-term regulation (section 8.6). Short-term regulation ensures that all of the different varieties of specialised cells can carry out their regular everyday functions. Long-term regulation in multicellular organisms determines the development of the organism through all the different life stages, including the differentiation of specialised cells.

Regulation of genes occurs at several levels. The major regulatory effects, carried out by several different factors, occur at gene transcription stage, where genes will actually be activated so that mRNA is produced, and later polypeptides also at the ribosomes. Additional controls occur during the conversion of pre-mRNA to mature mRNA (after transcription), in the translation of mature mRNA into polypeptides, and even post-translationally.

Chemical modification of chromatin at transcription stage

nucleosome basic structural unit of chromatin comprising DNA strand wrapped around a group of 8 histone molecules

DNA is packaged with histone proteins to form the DNA–protein complex referred to as chromatin. The most fundamental unit of chromatin is the **nucleosome**, in which the double-helical DNA is wound twice around eight histone proteins that are arranged in a ball shape. Nucleosomes form the scaffold for the packaging of DNA molecules. Each of the histones has a tail that extends out from the nucleosome.

When DNA is packaged and coiled into chromatin, the genes within the DNA are not available for expression because they are wrapped and coiled tightly into a very condensed structure. RNA polymerase cannot access the DNA in the chromatin to begin transcription of the mRNA molecule from the DNA template strand. In essence, such genes are 'switched off' and the corresponding polypeptides are not made.

SYLLABUS LINK
Chapter 6 details the structure of DNA.

However, chromatin can be 'chemically remodelled' to allow segments of DNA containing genes to become unwrapped and exposed, so that transcription can occur. The addition of acetyl chemical groups, 'histone acetylation', to specific amino acids in the histone protein tails (Figure 8.5.1) results in a loosening of the association of the histones with DNA, so that transcription of the exposed DNA can occur. Conversely, the addition of methyl groups, 'histone methylation', results in gene inactivation, due to attraction between the methylated histones and DNA that block transcription. This is just one of many ways that chemical modification exerts control over the phenotypic expression of genes.

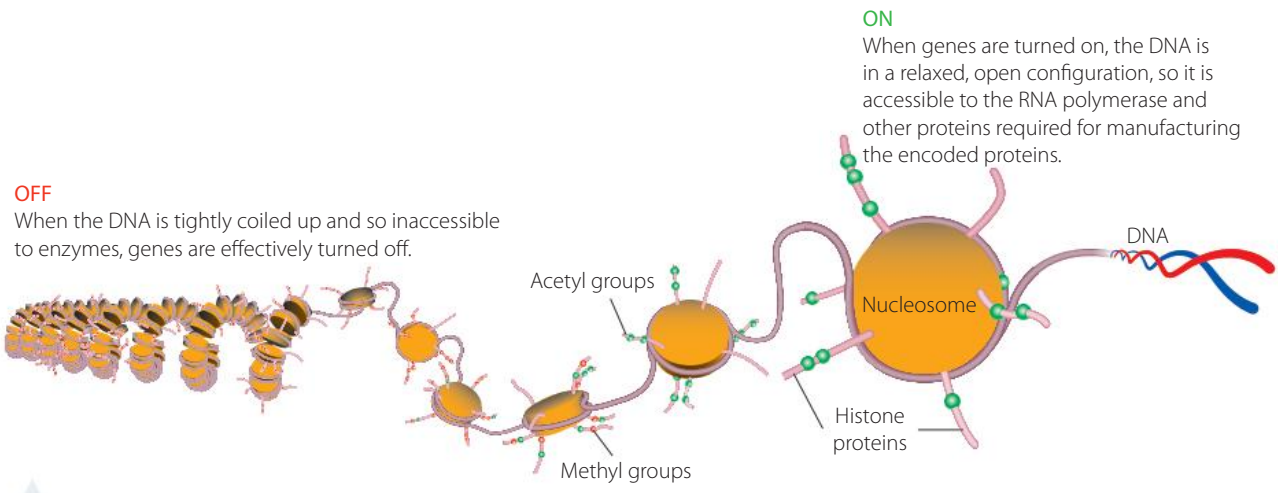

FIGURE 8.5.1 The process of switching genes on and off, by chemical modification of chromatin. Acetyl groups are shown in green and methyl groups are shown in red.

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Direct chemical modification of DNA at transcription

Methylation and acetylation can also occur directly to chromosomal DNA, rather than to the histone protein tails, to either disable or stimulate the transcription of DNA to mRNA. It has been discovered that the addition of other chemicals, including phosphate groups and small proteins, also acts to regulate transcription in this way. Research in this area is actively continuing.

One classic example of regulation of phenotypic gene expression by DNA methylation is 'X-inactivation'. DNA methylation is used to deactivate one of the two X chromosomes in the body cells of female mammals. In tortoiseshell cats (Figure 8.5.2), one X chromosome carries the orange alternative of the fur colour gene, and the other X chromosome carries the black alternative of the fur colour gene. Depending on which of the X chromosomes is inactivated early in embryonic development, patches of fur descending from these original embryonic cells only express the colour from the X chromosome that is still active.

FIGURE 8.5.2 The patchwork fur pattern in this female tortoiseshell cat is a result of chemical modification and thus deactivation of the DNA segment coding for black or orange fur colour on one of the two X chromosomes in embryonic cells of the cat.

8.5.1
X-inactivation

Regulation of gene expression by products of other genes at transcription

Transcription can also be influenced by the genome itself. **Regulatory proteins** are products of genes that regulate the expression of genes other than their own. Specific regulatory proteins that bind to the DNA are called **transcription factors**. Most of these activate gene expression but some repress it. Activating proteins bind to a section of non-coding DNA and enable it to unwind from histone proteins. Genes near this unwound DNA can then be transcribed. Activators also assist the binding of RNA polymerase to coding DNA segments to begin their transcription to mRNA. They may bind to several different specialised segments of the DNA, and even to introns. Some activating transcription factors can turn on multiple genes at the same time.

regulatory protein
a protein that binds to DNA to switch a gene on or off

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 repressed

Regulatory proteins that repress gene expression may bind to a particular region on the DNA and block the RNA polymerase from attaching for transcription (Figure 8.5.3).

Another role of regulatory proteins is to interact with other proteins, including signalling molecules such as hormones, that relay information about the physiological or developmental state of the organism.

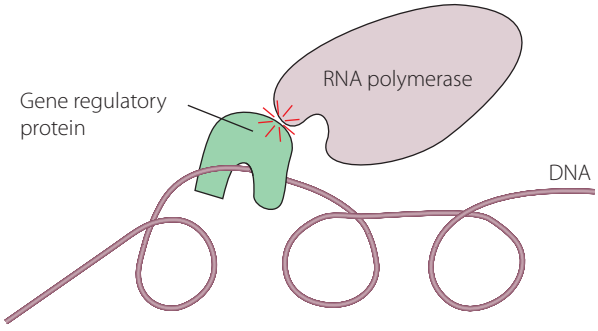

FIGURE 8.5.3 A gene regulatory protein blocks RNA polymerase from attaching to and copying a gene.

Environmental influences on gene expression

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FIGURE 8.5.4 The Himalayan rabbit normally has black hair only on its long ears, nose, tail and lower leg limbs. In an experiment, a patch of a rabbit's white fur was removed, and then an icepack was secured over the hairless patch. Black hairs grew back where the colder temperature had been maintained.

Even though identical twins have the same genes, they often show different characteristics, such as different weights and heights. This is due to environmental conditions affecting gene expression.

A demonstration of the influence of the environment on gene expression is demonstrated by fur colour in the Himalayan rabbit, which has a white body with black ears, nose, feet and tail (Figure 8.5.4). A simple experiment demonstrates that this patterning is not entirely under genetic control. If a cold pad is fixed to the rabbit's back, left in position for a certain minimum time and kept cold, black hair starts to develop beneath the pad.

When heat on a body part is present, the development of the black pigment is prevented. Black fur only grows on those parts of the body that are cool enough; that is, the extremities. This is an adaptation that allows the black fur to absorb more of the Sun's heat in cold weather. The same can occur in sealpoint Siamese cats. In winter, black areas of the coat enlarge, only to get smaller again in warmer weather.

There are many other cases of the environment influencing an organism's characteristics. For example, in plants, chlorophyll will only develop if light is available, and flowers will only appear if the day length is of certain duration and the temperature is suitable.

Development in organisms is the result of subtle and complex interactions between their genome and the environment.

Influences on phenotypic expression of genes that can be passed to offspring

By Randy Jirtle and Dana Dolinoy (Emailed by author) [CC BY 3.0 (http://creativecommons.org/licenses/by/3.0)], via Wikimedia Commons

FIGURE 8.5.5 The agouti gene is switched off by methylation. These inbred agouti mice are genetically identical. The mother of the mouse on the left ate a normal mouse diet. The mother of the mouse on the right ate a diet supplemented with methyl groups, including folic acid and vitamin B12. Instead of giving birth to a pup similar to herself and her mate (yellow, fat and prone to obesity, diabetes and cancer) the second mother produced a normal-sized, brown pup. Methylation of the agouti gene produced the brown phenotype in the offspring even though it was genetically identical to its yellow sibling: an example of epigenic inheritance.

epigenetics
the study of chemical modifications to gene function that are not due to a change in the DNA sequences

There is a great deal of evidence that environmental contaminants such as arsenic, heavy metals and some organic pollutants affect gene expression. It is also thought that lifestyle, such as stress levels, and even types of food consumed, can influence how genes are expressed, and can lead to changes that can be passed to the following generation.

These epigenetic forms of chemical gene regulation, which can be passed on through gametes to offspring, are actually an alternative form of inheritance. The study of the acquisition and inheritance of these chemical modifications, without involving changes in DNA sequences, is called **epigenetics**. Epigenetic mechanisms include DNA methylation, histone modification, non-coding RNA and post-translational modifications.

The agouti gene, causing yellowish banding or stripes on the hair shaft, is found in a range of animals. In an agouti-type mouse, coat colour of offspring can range from yellow to dark brown (Figure 8.5.5).

If pregnant mice are given a diet high in methyl groups, they give birth to a higher proportion of mice with brown fur and normal weight and size. The agouti gene is methylated, and thus switched off. When methylation is low, the agouti gene has a high expression of its protein product, producing yellow mice, with other disadvantageous phenotypical features, including obesity, and a higher risk of cancer and diabetes. This is an example of epigenetic inheritance.

Regulation of gene expression at translation

A further level of regulation can be achieved after a gene is transcribed and processed into mRNA. The mRNA is prevented from being translated into a polypeptide, so expression is switched off in that way. It can be achieved in a couple of different ways.

mRNA-binding proteins can attach to the mRNA and block ribosomes from being able to translate it. These proteins bind to specific non-coding RNA sequences near to the coding region, in a similar way to the transcription factors (described on page 163) that can bind to DNA to block transcription.

These repressor proteins may bind to the mRNA of many different genes at the same time, and thus shut down the expression of a number of genes simultaneously.

A second method of repression of translation is achieved by another type of RNA called **microRNA (miRNA)**. These miRNA molecules are transcribed from non-coding DNA and processed into short segments of around 20 nucleotides in length. When these miRNAs, which are complementary to sequences within mRNA, base-pair with the mRNA sequences, double-stranded RNA is formed, which prevents translation.

microRNA (miRNA)
a small non-coding segment of RNA that plays a role in regulating gene expression at the post-transcription level

In many cases, particularly in plants, double-stranded RNA is a trigger for the cell to digest and destroy the RNA molecules.

SECTION REVIEW 8.5

REMEMBERING

1 Define:
   - **a** chromatin
   - **b** nucleosome
   - **c** histone
   - **d** regulatory protein
   - **e** epigenetics.

2 Use your definitions for Question 1a–c to explain how genes can be switched on and off.

3 Use Himalayan rabbits as an example to describe how environmental factors can affect phenotypic gene expression.

4 At which stage in protein synthesis does most gene regulation occur?

UNDERSTANDING

5 Discuss how tortoiseshell coat pattern is caused by gene regulation in female cats.

6 Discuss how mice carrying the agouti gene can inherit characteristics from their parents epigenetically.

7 **a** Describe two different mechanisms by which genes can be regulated at the translation stage.
   b List how these processes are:
      - **i** similar to
      - **ii** different from

   a similar type of gene regulation at transcription.

8.6 Regulation of morphology and cell differentiation by transcription factors

morphology
the shape and form of an organism or its part

Understanding how genes regulate growth and development to produce the particular **morphology** (structural form and shape) of an organism is the subject of long-standing yet still current research. Early clues to the influence of individual genes in this process came with observations made in the late 1800s to early 1900s of naturally occurring mutant fruit flies. Research in this field continues to develop today, with more sophisticated biochemical methods for analysing genes and the availability of whole genome sequences for organisms.

Past studies have demonstrated how a single nucleic acid copying 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 8.6.1). These observations have provided insights into how different body parts are controlled by similar genetic processes. Furthermore, studies of model organisms have shown that the same sorts of processes are at work in most eukaryotic organisms, including humans.

SYLLABUS LINK

Chapter 9 discusses mutations, or 'changed' genetic material.

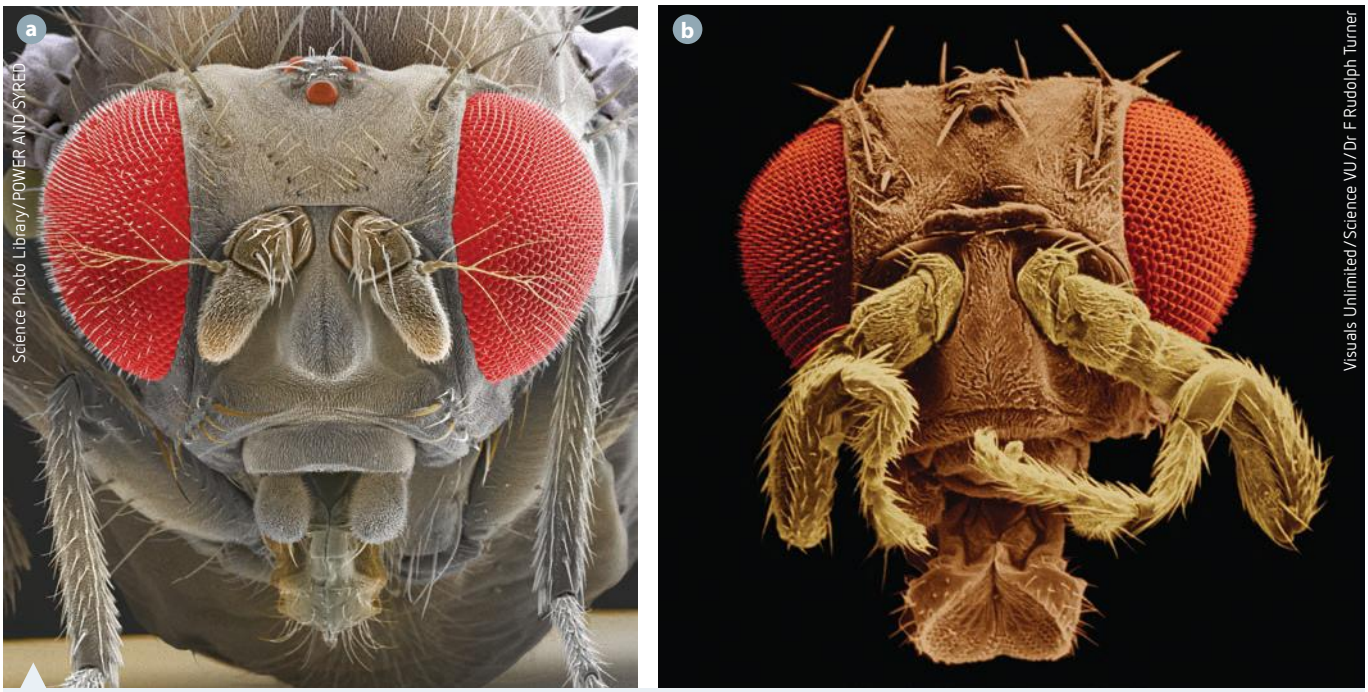

FIGURE 8.6.1 (**a**) A normal fruit fly (*Drosophila melanogaster*) and (**b**) a fruit fly showing abnormal development of legs at the sites where antennae should be

Homeobox genes

homeobox gene
a gene of a group that code for proteins that regulate body formation and patterning in the developing embryo

Previous scientific work has shown that embryonic development is orchestrated by a small subset of genes. For example, of the 13 000 genes in the genome of a fruit fly, as few as eight key genes are responsible for determining its fundamental body structure. A few dozen more are involved in determining the body's axes of symmetry when viewed from the front, rear, top or bottom, or when left and right sides are compared. These genes are referred to as **homeobox genes**, or toolkit genes. Each one of the toolkit genes is expressed precisely in specific parts of the embryo during development (Figure 8.6.2).

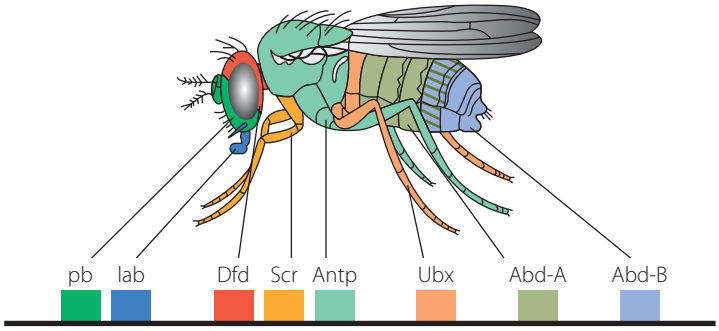

FIGURE 8.6.2 Eight genes regulate the formation of the fruit fly body plan. Each is expressed in a precise location within the animal during development.

This distinctive localised gene expression is accomplished through specific proteins produced in the egg before fertilisation. These proteins (called maternal-effect proteins) diffuse across the egg, forming concentration gradients that convey positional information in the egg (Figure 8.6.3a). 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 such proteins create concentration gradients that mark positions within the egg (Figure 8.6.3b).

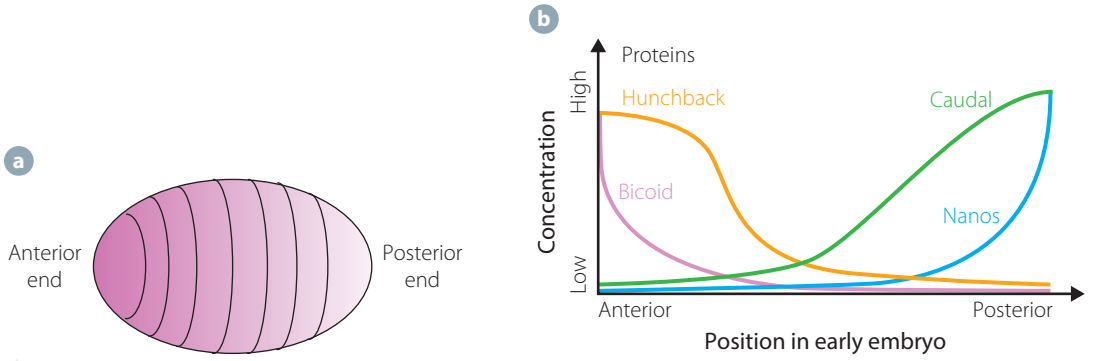

FIGURE 8.6.3 (**a**) Bicoid protein in a fruit fly egg diffuses to create a concentration gradient. The highest concentration marks the future embryo's anterior end. (**b**) The relative concentrations of four different proteins conveying positional information in the developing fruit fly embryo.

These protein concentration gradients are preserved during the early rounds of cell divisions in the zygote, after fertilisation, so that positional information is retained by later generations of daughter cells in the developing embryo. These maternal-effect proteins interact with non-coding DNA regions immediately adjacent to the homeobox genes to either activate or repress gene expression. For example, high concentrations of Bicoid protein will activate homeobox genes that initiate development of the front half of the animal but repress homeobox genes that are required for development of the animal's rear body parts. Therefore, each homeobox gene is activated by specific combinations of positional proteins. The pattern of expression of the homeobox genes ultimately reflects the concentrations of the positional proteins within the developing embryo as it undergoes cell division.

Once expressed, the product of each homeobox gene is a protein that binds to DNA to activate gene expression. These proteins activate expression of collections of many other genes within the genome. The group of genes that are expressed are all those required for the formation of the intended organ or body part at that position within the developing embryo. These homeobox proteins are thus regulatory proteins with wide-ranging effect.

Sex determination: the role of the Y chromosome

At a certain stage of embryonic development, either male or female sexual characteristics are produced. In mammals, gender is determined by the sex chromosomes present in every cell; typically, an individual with two X chromosomes is female, and an individual with one X and one Y chromosome is male.

The Y chromosome clearly must have genes that set the organism on the path to developing into a male. The single most influential gene in this process is the SRY gene (sex-determining region of the Y chromosome), located on the small arm of the Y chromosome. The gene encodes a protein that, like homeobox genes, binds to DNA to activate the expression of many genes. The SRY protein is a regulatory protein that primarily launches the genetic program for testes development. As the testes develop, they produce hormones, including testosterone, that steer the embryo towards the differentiation of male features, ultimately including formation of the penis and other components of the male reproductive system.

If the individual lacks a Y chromosome and is unaffected by the SRY gene, they begin the course towards developing into a female. Proper female development relies on the presence of both X chromosomes to direct the formation of fully functional ovaries.

SECTION REVIEW 8.6

REMEMBERING

1 Define 'morphology'.

2 Briefly describe the role of the homeobox genes in fruit flies.

UNDERSTANDING

3 Describe how maternal-effect proteins convey positional information.

4 **a** Name the most influential gene in the sex-determining region of the Y chromosome.

b What is the name of the protein produced by this gene?

c Outline how it functions.

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CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1 What is a gene?

2 What does it mean to say a gene is 'expressed'?

3 What is gene regulation?

CATEGORY QUESTIONS

4 What are the two main types of products of gene expression?

5 **a** Explain the difference between coding and non-coding DNA.

b List some of the types and functions of non-coding DNA.

6 Name all the stages in protein synthesis and briefly describe what happens at each stage.

7 At which stages of protein synthesis can gene regulation occur? Give an example of regulation occurring at each.

8 List all the types of nucleic acids and state whether they function in gene expression and/or regulation.

9 Describe two different examples illustrating how environmental influences can produce different phenotypic expression of genes in individuals with the same genetic information.

ELABORATION QUESTIONS

10 Explain what discoveries have led to the 'central dogma of molecular biology' being questioned.

11 A section of nucleic acid is isolated and examined. Describe features you would look for to determine whether it is DNA or RNA. List any other information that would be useful in your determination.

12 A particular polypeptide has 100 amino acids.

a How many codons are there in the mRNA strand that codes for this polypeptide?

b How many nucleotide bases are there in the DNA strand that coded for the mRNA?

c If the template DNA strand contains 63 adenine nucleotides, how many thymine molecules are in the non-template strand?

d Is it possible to predict how many guanine molecules are in the non-template strand?

13 In the construction of a house, a carpenter refers to the house plans and uses the plans to construct a kitchen. The carpenter uses timber, hammers and nails. In this analogy, match house plans, timber, hammers and nails to the processes of DNA transcription and translation.

EVIDENCE QUESTIONS

14 Explain how you worked out each of your answers to Question 13.

15 Answer Question 12a and b for the hypothetical case of a four nucleotide base code instead of the three-base code.

16 Provide reasons for your decisions in Question 15.

END-OF-CHAPTER EXAM

End-of-chapter test

1 Choose the correct relationship hierarchy.

- **A** Genes are contained within DNA molecules within genomes.
- **B** DNA is contained within genes within genomes.
- **C** Genomes are contained within DNA within genes.
- **D** None of the above.

2 Introns are:

- **A** coding sections in pre-mRNA that are removed in mature mRNA.
- **B** non-coding sections in pre-mRNA that are removed in mature RNA.
- **C** coding sections in pre-mRNA that remain in mature mRNA.
- **D** non-coding sections in pre-mRNA that remain in mRNA.

3 The correct sequence of processes in polypeptide synthesis for subsequent protein production is:

- **A** translation of mature mRNA, modification of pre-mRNA, transcription.
- **B** modification of pre-mRNA, translation of mature mRNA, transcription.
- **C** transcription, modification of pre-mRNA, translation of mature mRNA.
- **D** none of the above.

4 Choose the correct statement.

- **A** Codons occur in DNA, mRNA and tRNA.
- **B** Codons specify amino acids, anticodons specify stop and start signals.
- **C** Codons occur in DNA, anticodons in RNA.
- **D** Codons occur in DNA and mRNA, anticodons occur in tRNA.

5 The SRY gene on the Y chromosome is responsible for the development of male sex characteristics. It functions:

- **A** only if there are no X chromosomes present in the embryo.
- **B** only if the X chromosome is inactivated in the embryo.
- **C** by encoding a protein that binds to the Y chromosome DNA to activate several other genes that promote the development of the testes.
- **D** by encoding a protein that digests the segments of the X chromosome that code for ovary production so testes can develop instead.

6 Use a sentence to briefly explain gene:

- **a** expression
- **b** regulation.

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7 Refer to the genetic code (Figure 8.2.7) to complete the following table. It indicates the relationships between nucleic acid nucleotide base sequences and the component amino acids in the process of polypeptide synthesis.

DNA	NON-TEMPLATE STRAND										T	C	A
	TEMPLATE STRAND				G								
mRNA CODON						A	C						
tRNA ANTICODON								C	C	U			
AMINO ACID		Tryptophan											

8 Supply words or phrases to complete the following paragraph.

A very high percentage of the genomes of multicellular organisms consist of non-coding DNA; that is, nucleotide sequences that do not result in the production of _____ chains – the components of proteins. However, much of this non-coding DNA is transcribed into useful products, including two types of RNA: tRNA and _____, which are referred to as 'functional RNA', due to the vital roles they play in protein synthesis. The function of tRNA is to carry the _____ to the mRNA strand, where ribosomes are attached to translate the mRNA. The role of the second type of functional RNA is to combine with proteins to form the _____ organelles.

Centromeres, which function in the cell _____ process, and telomeres, which are long repetitive extensions at the end of chromosomes that protect or buffer the chromosome, are both examples of non-coding DNA.

9 One function of introns is to direct splicing of the exons from mRNA in the nucleus before it migrates out to the cytoplasm to be translated.

a Describe what splicing is.

b Explain how splicing can produce a number of variations of a protein from the one gene.

10 Briefly describe how chemical modification of chromatin can switch genes on or off.

11 **a** Name an animal exhibiting phenotypic gene expression in its fur colour and patterning due to chemical modification, in fact inactivation, of all segments of one of the pair of X-chromosomes in cells. The X-inactivation occurs at a very early embryonic stage.

b Which stage of protein synthesis would be affected in this case?

12 mRNA-binding proteins, produced by unrelated genes, can attach to the mRNA and block ribosomes from carrying out their function in polypeptide synthesis. Which stage of protein synthesis is affected in this case?

13 Describe an example where an environmental factor affects the phenotypic expression of a gene.

14 In a short paragraph, explain how maternal-effect proteins, produced in the egg of the female parent fruit fly before fertilisation, actually regulate the homeobox genes responsible for development in the embryonic fruit fly offspring.

9 MUTATIONS

Introduction

Organisms within the same species have a consistently recognisable suite of common characteristics, determined by the same set of chromosomes in cells of members of that species. Each corresponding chromosome pair in each individual's cells also has the same particular sequence of genes. Despite this, characteristics of individuals within species are not uniform; intraspecific variation occurs. Variation in characteristics is determined largely by small differences in the DNA nucleotide base sequences within specific genes (the genotype) of each individual organism's cells; that is, the particular sets of allele pairs inherited from the parents of that unique individual of the species.

Stimulus questions

Where do different alleles come from?

How are different alleles formed?

Sometimes new variations suddenly occur in a species. Sometimes new species appear over time. Does this mean that new alleles are continually being formed?

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9.1 Identifying errors in genes and chromosomes

For new variations to arise among members of a species (i.e. when **intraspecific variation** is increased), new, different alleles must be created, altering the genotypes of these individuals. The different coloured Gouldian finches in Figure 9.1.1 are demonstrating intraspecific variation. There must be changes in the DNA of the offspring that produce the novel characteristics in the offspring phenotype. Changes to DNA are called **mutations**. Mutations may arise spontaneously during the DNA replication part of the cell cycle, or during cell division. The rate at which mutations occur can be increased by physical or chemical **mutagens**.

Mutations are persistent. They tend to be transmitted through many cell divisions without further change, although there is always the possibility that mutation may occur again, either producing another new feature or causing the original condition to revert.

intraspecific variation
differences between characteristics or phenotypes of individuals of same species

mutation
a change in a gene or a chromosome relative to original; may also refer to process of generating change

mutagen
any agent capable of inducing mutation

FIGURE 9.1.1 The three forms of the Gouldian finch species (*Erythrura gouldiae*), illustrating intraspecific colour variation.

SYLLABUS LINK

Chapter 6 discusses chromosomes and their genes.

Chapter 7 discusses alleles, genotypes and variation.

Chapter 8 discusses how genes bring about individual characteristics or phenotypes.

Chapter 10 explores how genetic traits are inherited.

Chapter 13 and 14 discuss allele frequency and formation of new species.

DNA replication errors

Spontaneous mutations may occur during the non-dividing S (synthesis) phase of the cell cycle, when the DNA is unwound for replication and is exposed and vulnerable to damage. For example, adenine normally base pairs with thymine but may, for no apparent reason, undergo a chemical change to another form. This altered adenine may chemically resemble cytosine, which pairs with guanine. During DNA replication, this alternative form of adenine may be mistaken as cytosine, resulting in a guanine nucleotide unit being introduced into the newly produced DNA sequence instead of a thymine. This process is illustrated in Figure 9.1.2.

spontaneous mutation
a mutation occurring in the absence of exposure to mutagens

SYLLABUS LINK

Chapter 6 details the cell cycle and its different phases.

9.1.1 Spontaneous mutations

point mutation
a mutation that affects a single base-pair position within a gene

single nucleotide polymorphism (SNP)
a nucleotide difference that occurs at one given position in the gene

substitution mutation
a mutation in which a single nucleotide is swapped for another

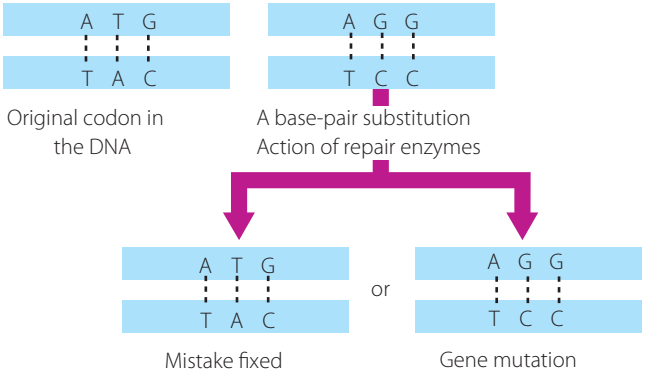

FIGURE 9.1.2 A spontaneous mutation. During DNA replication, adenine may spontaneously change to resemble cytosine. This may result in guanine pairing with it, and thus being incorporated into the new DNA strand instead of thymine.

Point mutations

An error where just a single nucleotide unit within the original DNA is affected is a **point mutation**. Point mutations can also be called **single nucleotide polymorphisms** (or **SNP**s, often pronounced as 'snips').

Point mutations caused by substitution of a nucleotide

A **substitution mutation** is a point mutation where one nucleotide is replaced by another, as in Figure 9.1.2. If the point mutation occurs in a gene coding for a polypeptide chain, a number of different effects on the resulting protein produced may result, ranging from no effect to a significant effect on its structure and function. This depends on the particular codon affected, and on the particular amino acid that may consequently be substituted.

Most amino acids are represented by several different codons, so a substituted nucleotide in one triplet base sequence of a gene may still code for the same amino acid. However, if the mutated codon determines a different amino acid, the effect on the resulting protein would depend on how different the two amino acids are chemically.

DNA repair mechanisms

During the cell cycle, after DNA has been replicated and before cell division occurs, DNA is proofread and any errors that are detected are repaired. Repair usually relies on one of the DNA strands being intact. The intact strand serves as a template for proofreading and restoration of the damaged complementary strand. However, if a mutation is not repaired, or it is improperly repaired, the mutation becomes part of the DNA sequence and persists through subsequent cell divisions.

DNA repair mechanisms are usually highly effective, so mutations are comparatively rare. However, mutation rates vary for different organisms, and across the genome of each organism (Table 9.1.1). The usually low mutation rates are evidence for the remarkable accuracy with which DNA is replicated.

TABLE 9.1.1 Estimated mutation rates for four species

ORGANISM	GENOME SIZE (NUCLEOTIDE PAIRS × MILLION)	MUTATION RATE (MUTATIONS PER GENOME PER CELL REPLICATION)
Roundworm	97	0.018
Fruit fly	180	0.058
Mouse	2600	0.49
Human	3100	0.16

indel
a collective term for mutations caused by insertions and/or deletions

frameshift mutation
a mutation that dislocates the translational reading frame

Mutations causing a frameshift

An insertion mutation occurs when one or more nucleotides are added at a site within the original gene sequence. A deletion mutation is the loss of one or more nucleotides from a locus within the gene. Collectively these can be referred to as '**indels**', an abbreviation for 'insertion' and 'deletion'. The effect of the indel is usually a **frameshift mutation** in which the starting point for the reading of the triplet code sequences for the amino acids to be included in a polypeptide chain is shifted away from the original position. As a result, all the codons 'downstream' of the mutation are affected. (However, note that if there

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was an indel of three or a multiple of three nucleotides, the original sequence of codons beyond the indel would be restored, and there would not be a reading frameshift for translation of the remainder of the nucleotide sequence.)

In the polypeptide produced with a frameshift mutation, the amino acid sequence beyond the location of the mutation bears no resemblance to those in the polypeptide that would have originally been produced. This is illustrated in Figure 9.1.3. Under such circumstances, even a single nucleotide insertion or deletion can have a profound effect on the corresponding protein produced.

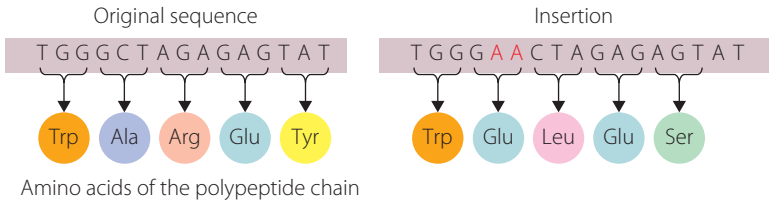


FIGURE 9.1.3 A frameshift mutation occurs after an insertion in the gene sequence, such as AA shown in red. The amino acid sequence in the synthesised polypeptide chain is usually very different from what was originally coded for.

Damage to DNA by mutagens

The amazingly low mutation rates in organisms originally made it difficult for geneticists to investigate mutations until a discovery in 1927 by American biologist H.J. Muller. He found that the mutation rate in the fruit fly species *Drosophila melanogaster* can be greatly accelerated by irradiation with X-rays. Since then, scientists have discovered many other environmental mutagens that speed up mutation rates. These environmental mutagens can be classified as either chemical or physical.

Mutations arise spontaneously and are in no sense 'directed' by the environment. Environmental influences can greatly increase the rate of mutation but they cannot induce a particular mutation to occur. The kind of genetic change is random.

Chemical mutagens

There are many known mutagenic chemicals. The mechanisms by which they exert their effects vary, as shown in Table 9.1.2.

TABLE 9.1.2 Some chemical mutagens and their effects

CHEMICAL MUTAGEN	EFFECT
Acridine orange	Bases in DNA are added or removed
Aflatoxin A, ethidium bromide	Disruption of packing of DNA by slipping between nitrogen bases
Polycyclic aromatic hydrocarbons	Cross-link with adenine and guanine to block DNA repair
2-Aminopurine, 5-bromouracil	Nucleotide substitution
Colchicine	Prevents spindle formation in mitosis and so doubles chromosome number
Cyclamate	Chromosome aberrations
Ethyl methanesulfonate, nitrosoguanidine	Nitrogen bases are chemically modified
Mustard gas	Guanine in DNA is replaced by other bases
Nitric acid	Adenine in DNA is deaminated so it behaves like guanine

Physical mutagens

ionising radiation radiation that is strong enough to break chemical bonds in molecules, and remove tightly bound electrons from the orbits of individual atoms, causing atoms to become charged or ionised

DNA damage can also be caused by **ionising radiation**, such as high-frequency ultraviolet (UV) light, and certainly by even higher energy radiation, such as X-rays, gamma rays and nuclear radiation (Figure 9.1.4). UV light is a natural component of the energy emitted by the Sun. X-rays are also emitted from the Sun's intensely hot outer corona.

9.1.2 Effects of ionising radiation on DNA

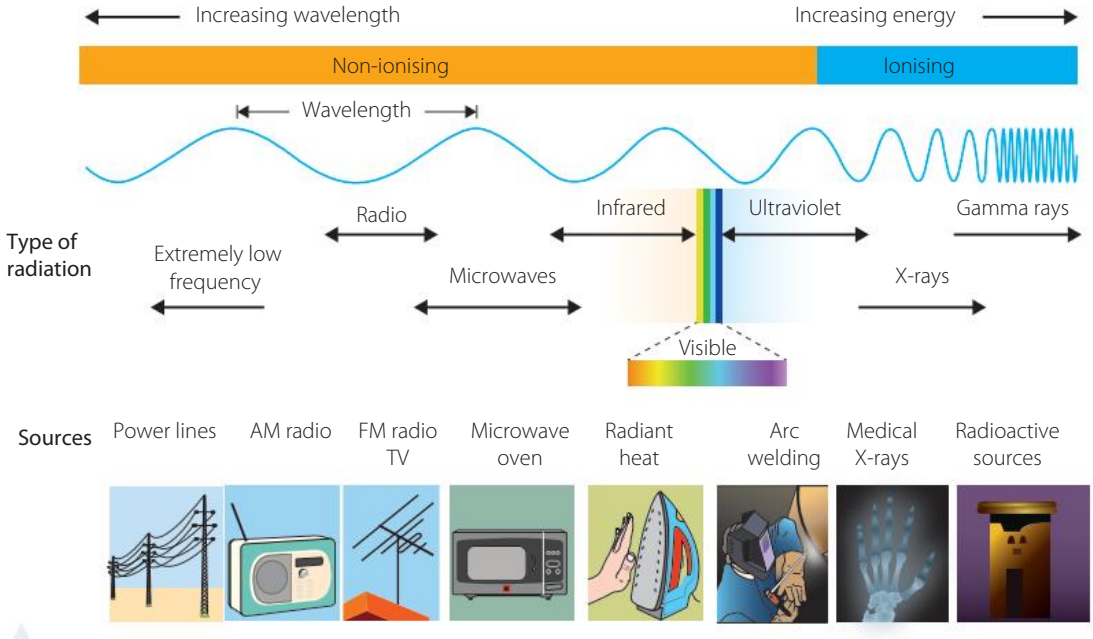


FIGURE 9.1.4 The non-ionising and ionising parts of the electromagnetic spectrum. Ionising radiation can damage DNA.

double-strand break a mutation involving breaks in both of the sugar–phosphate backbones at the same nucleotide pair, resulting in the complete breakage of a chromosome

apoptosis a programmed series of events that lead to natural cell death when the internal contents of the cell are dismantled by various enzymes

Public awareness campaigns have drawn attention to the risks of excessive exposure to UV light, such as increased risk of skin cancer. Higher frequency UV light can affect the chemical structure of the nitrogen bases, fusing adjacent thymine or cytosine bases in the DNA sequence. X-rays cause the deletion of adenine and guanine bases, creating gaps in the double helix. These aberrations disrupt complementary base pairing during DNA replication, potentially causing serious mutations.

Nuclear radiation is one physical mutagen that actually causes **double-strand breaks** in chromosomes. These kinds of anomalies result in large segments of the chromosome being rearranged. A cell can 'put the brakes on' during cell division to give it time to repair breaks and mutations before it divides, but an accumulation of double-stranded breaks upon intense exposure to physical mutagens is often lethal to the cell. **Apoptosis** of the cell in this situation is a mechanism to guard against cancer formation.

SECTION REVIEW 9.1

REMEMBERING

1. Define 'intraspecific variation'.
2. Define 'mutation'.
3. During which two processes of the cell cycle can spontaneous mutations occur?
4. Define:
   - **a** point mutation
   - **b** phase shift mutation.
5. **a** Define 'mutagen'.
   - **b** Describe the difference between a chemical mutagen and a physical mutagen.

UNDERSTANDING

6 Briefly describe the differences between the following types of mutation: substitution, insertion and deletion.

APPLYING

7 Explain why a phase shift mutation can potentially have a much greater effect than a substitution mutation.

8 Classify each of the following as relating to a chemical or physical mutagen.

- **a** Products containing a certain preservative are removed from supermarket shelves after cancers developed in laboratory test mice consuming it.
- **b** Exposure to cosmic radiation during space flight is considered a health risk.
- **c** Radiotherapy is used in treating a primary tumour.

9.2 Aneuploidy

Genetic mutations can involve changes to whole chromosomes, or large parts of them. Chromosome alterations such as these contrast with single-point mutations because they can affect a huge number of genes simultaneously. These anomalies can occur during mitotic cell division in body cells and also during the formation of gametes in meiosis.

As with some other genetic mutations, these errors often have dire consequences for an organism. However, occasionally the transformation can be beneficial and confer a survival advantage upon the recipient.

9.2.1 Aneuploidy and chromosomal rearrangements

Identifying chromosome mutations from karyotypes

Chromosome alterations 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 pairs matched for size and banding pattern (homologous pairs), and ordered from largest to smallest, to create a karyotype – the standard form used to display and analyse chromosomes. Figure 9.2.1 shows a human female karyotype.

SYLLABUS LINK
Chapter 7 also discusses the human karyotype.

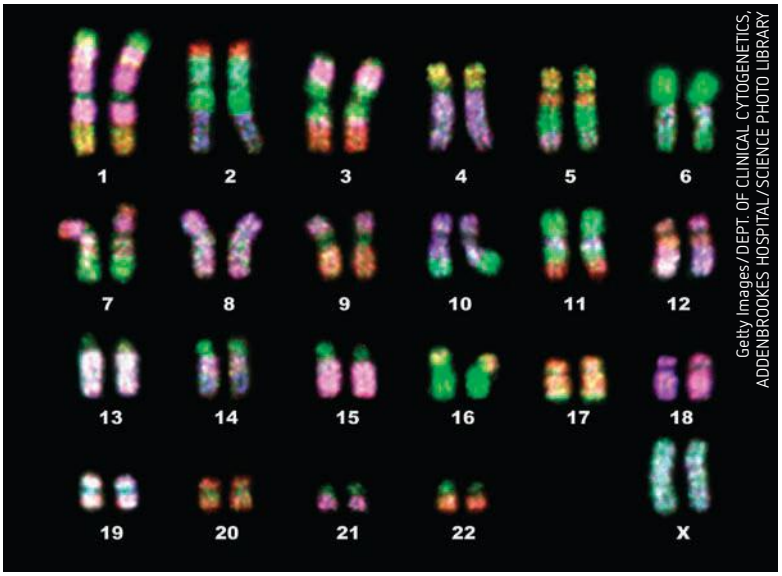
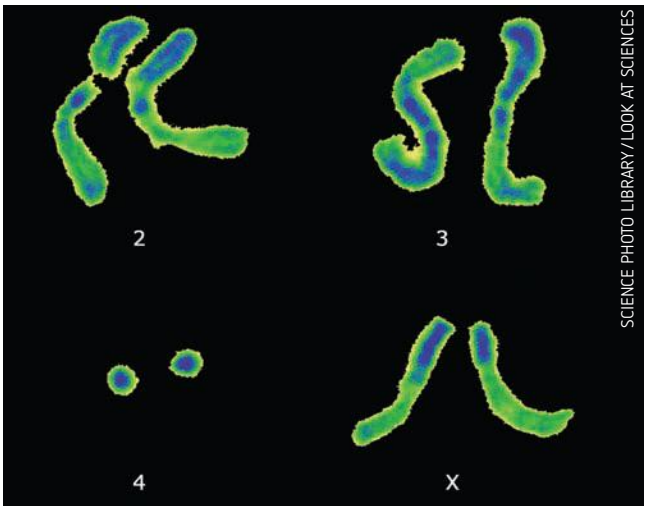


FIGURE 9.2.1 This human female karyotype has been produced from fluorescent chromosome photographs.

Each species of organism is characterised by a particular number of chromosomes in every cell. Figure 9.2.2 shows the karyotype of a female fruit fly.

FIGURE 9.2.2 A karyotype of a female fruit fly



Variations in chromosome number within a species

In most multicellular eukaryotic organisms, the somatic cells are diploid ($2n$) – they contain two sets of chromosomes, one set inherited from each parent. The gametes are haploid (n). There can be serious implications for organisms when the complement of chromosomes in the somatic cells varies from the usual diploid state.

aneuploidy a genome variant having unconventional chromosome number due to loss or addition of one or a small number of chromosomes

An example of a disadvantageous variation in chromosome number in a species is **aneuploidy**. In organisms with this condition, there is an addition or loss of one chromosome from a body cell (i.e. $2n + 1$ or $2n - 1$). Occasionally, the anomaly may even involve more than one chromosome.

It is reasonably common for a pregnancy to end in miscarriage, and it has been found that many of these non-surviving embryos are aneuploids. To understand how aneuploidy comes about, consider the process of meiosis.

Normally, in the first division of meiosis, homologous chromosome pairs come together and then segregate (into what eventuates as separate cells) during anaphase, so that the resulting gametes have only one of each pair of chromosomes. However, occasionally the two members of the chromosome pair go into the same cell during meiosis I instead of separating. This is known as **non-disjunction**. It results in the formation of two types of gametes in equal proportions; one type has two copies of a particular chromosome and the other type has none, as shown in Figure 9.2.3.

non-disjunction the failure of homologous partner chromosomes in meiotic cell division or sister chromatids in mitotic division to separate to opposite poles

Non-disjunction can also occur during meoisis II when sister chromatids fail to segregate into separate cells. If non-disjunction at meoisis II occurs in only one of the two dividing cells resulting from meiosis I, a gamete with two of the affected chromosomes and a gamete without that chromosome will be produced. From the second cell resulting from meoisis I, that divides normally in meiosis II, two gametes each with one of the particular chromosomes will result.

trisomy when somatic cells contain three copies of a particular chromosome

monosomy when somatic cells contain only one copy of a particular chromosome pair

The fusion of a gamete containing two homologous chromosomes from one parent, with a normal gamete, containing one of the same numbered chromosome from the other parent, gives a zygote with three such chromosomes ($3n$), instead of a normal diploid zygote. This condition is called **trisomy**. Fusion of a gamete without a particular chromosome with a normal gamete with only one results in an individual with only one of this particular type of chromosome ($1n$) in each cell. This condition is called **monosomy**.

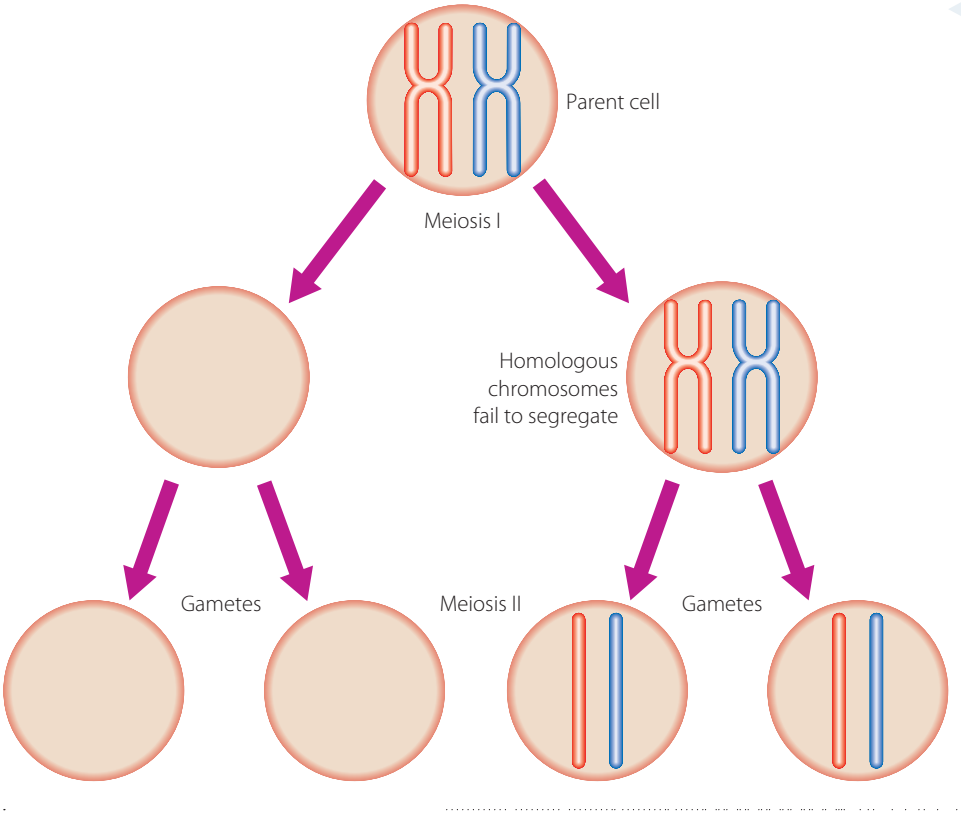


FIGURE 9.2.3 When non-disjunction occurs during meiosis I, the homologous chromosome pairs fail to segregate, so half the gametes contain two chromosomes of a pair each, and half contain no chromosomes at all. Generally, non-disjunction only takes place with one pair of homologous chromosomes of the whole set, while the rest behave normally. Non-disjunction of sister chromatids can also occur during the second meiotic division, but this is not illustrated here.

Non-disjunction of autosomal chromosomes in meiosis

Some types of aneuploidy survive in humans. The most common example, Down syndrome, is caused by the presence of an extra chromosome 21 (one of the smallest chromosomes) in every cell, thus giving three copies of this chromosome. Children with trisomy 21, causing Down syndrome, vary in their symptoms but most show moderate-to-severe delayed development, characteristic almond-shaped eyes and round face, shortened body parts, loose joints, and weak muscles and muscle reflexes. About 40% of people with Down syndrome develop heart defects and are also more susceptible to infections. These afflictions often shorten their life expectancy. Some very positive characteristics of the Down syndrome phenotype include an affectionate and cheerful personality, and often a great appreciation of music and dancing, so that much pleasure is derived from them.

Down syndrome is an example of autosomal trisomy; an extra non-sex chromosome is present, as shown in Figure 9.2.4. Its incidence increases with increasing age of the mother (Table 9.2.1). Older men are also more likely to father a Down syndrome child but their age has less effect on the chances of producing a trisomy 21 baby than does the mother's age.

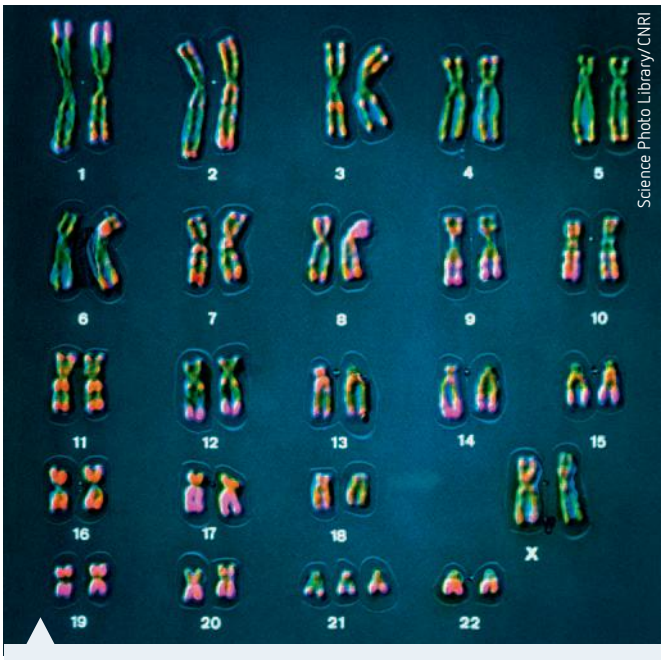


FIGURE 9.2.4 A false-colour (coloured stain used) karyotype from a Down syndrome female. The syndrome is the result of cells having three copies of chromosome number 21. This condition is also known as trisomy 21.

TABLE 9.2.1 The chance of a child being born with Down syndrome increases with the mother's increasing age

MATERNAL AGE AT BIRTH OF CHILD (YEARS)	CHANCE OF CHILD HAVING DOWN SYNDROME
20	1 in 1925
25	1 in 1205
30	1 in 885
35	1 in 365
40	1 in 110
45	1 in 32
50	1 in 12

Non-disjunction of sex chromosomes in meiosis

Non-disjunction also causes various sex chromosome abnormalities in humans. For example, approximately two in every 1000 men have the genotype XXY for their sex chromosomes. This anomaly is known as Klinefelter syndrome, and may result from either the fusion of a Y sperm with an XX egg or the fusion of an XY sperm with an X egg. Although XXY individuals are phenotypically men, they have very small genitals and are infertile. In addition, they may develop breasts, but testosterone therapy at puberty can often help alleviate this symptom.

Turner syndrome is due to the absence of one of the sex chromosomes. Foetuses with 22 normal pairs of autosomes and a single Y chromosome never survive to birth. However, children may be born with 22 normal pairs of autosomes and a single X chromosome. Such individuals have the genetic constitution XO. They are females and occur with an incidence of approximately 0.4 per 1000 live-born girls. The phenotypic effects of Turner syndrome are relatively minor but the person is infertile. Individuals are usually shorter than normal with a characteristic webbed neck. Oestrogen replacement therapy can allow normal pubertal development, and growth can be stimulated with growth hormone.

9.2.2 Klinefelter syndrome

9.2.3 Turner syndrome

PRACTICAL ACTIVITY 9.2.1

Using a karyotype

Genetic mutations that involve alterations to whole chromosomes or significant sections of chromosomes can be studied using karyotypes.

THE HUMAN KARYOTYPE

The human karyotype has 22 pairs of homologous autosomes, each pair with its own characteristic shape, due to the location of the centromere holding each of the two sister chromatids of each chromosome together. For instance, chromosome sets 1 and 3 have centromeres centrally located, so their 'arms' are symmetrical. In other chromosomes, the centromere positions can range from slightly off centre to much closer to one end of the chromosomes, resulting in asymmetrical shapes with long and short arms.

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, the sex chromosomes, may be matching, with banding unique to the pair, as in the case of females with XX genotype. In males, the chromosomes of the 23rd pair are un-matched; the genotype of sex chromosomes are XY, with the Y chromosome being much shorter than the X.

DOWN SYNDROME – A HUMAN ANEUPLOIDY CONDITION

Examine Figures 9.2.1 and 9.2.4. Figure 9.2.1 illustrates the karyotype for a normal human female. Figure 9.2.4 shows the karyotype for a female with Down syndrome also known as trisomy 21.

Identifying ploidy changes and predicting genetic disorders from karyotypes

Examine Figures 9.2.5–9.2.8, and then practise analysing human karyotypes by answering each of the questions following the illustration. Finally, check your conclusions against the answers provided.

1 Determine which of the four karyotypes is normal, and identify the sex of the individual, justifying your answer.

2 Briefly describe the aberrations in the other three karyotypes.

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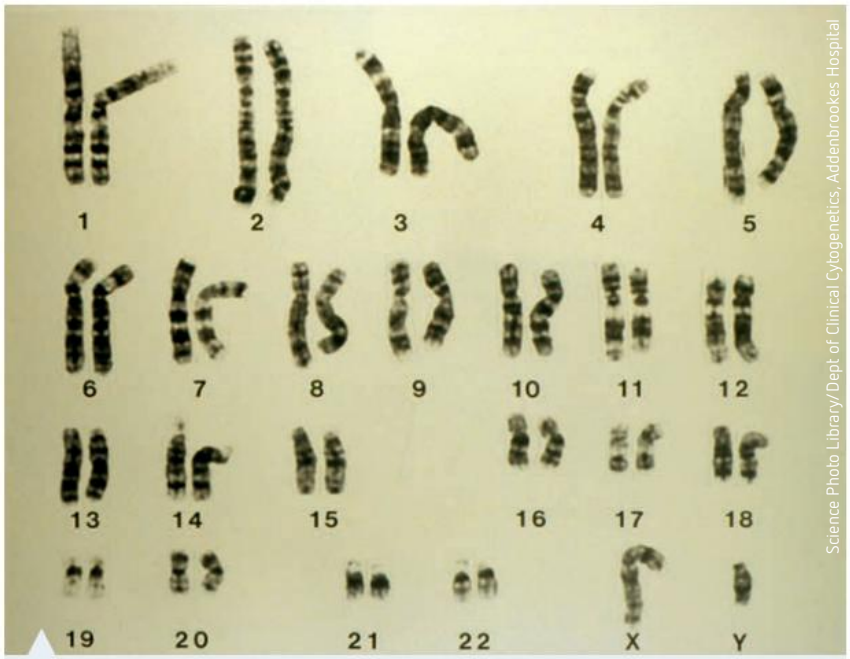

FIGURE 9.2.5 A human karyotype

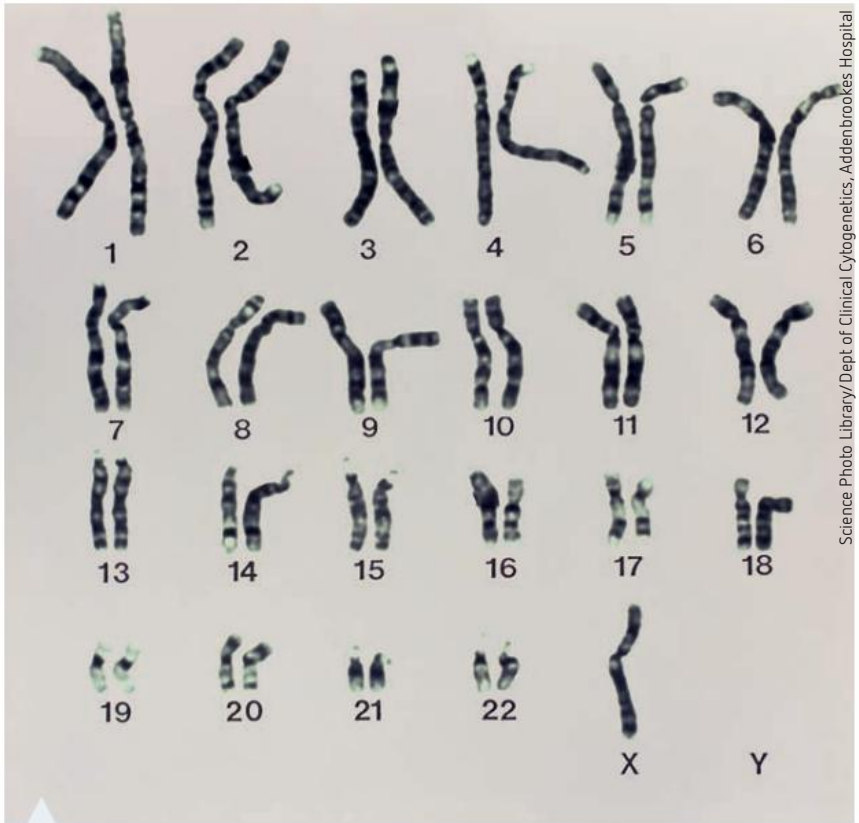

FIGURE 9.2.6 A human karyotype

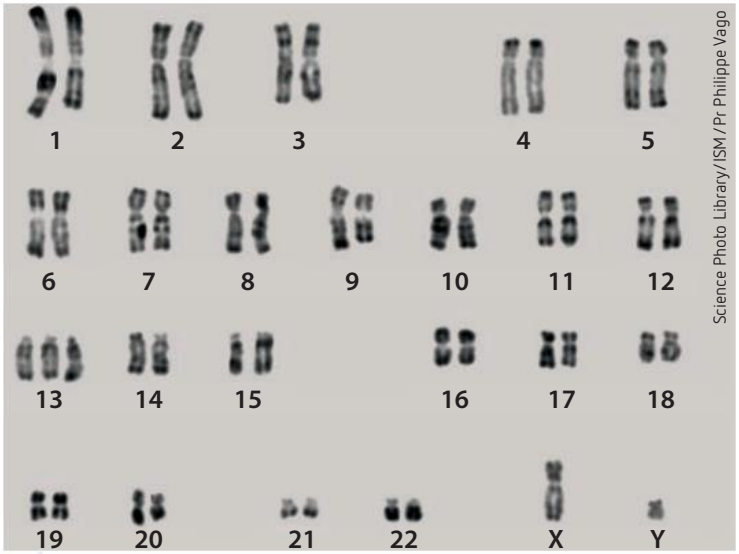

FIGURE 9.2.7 A human karyotype

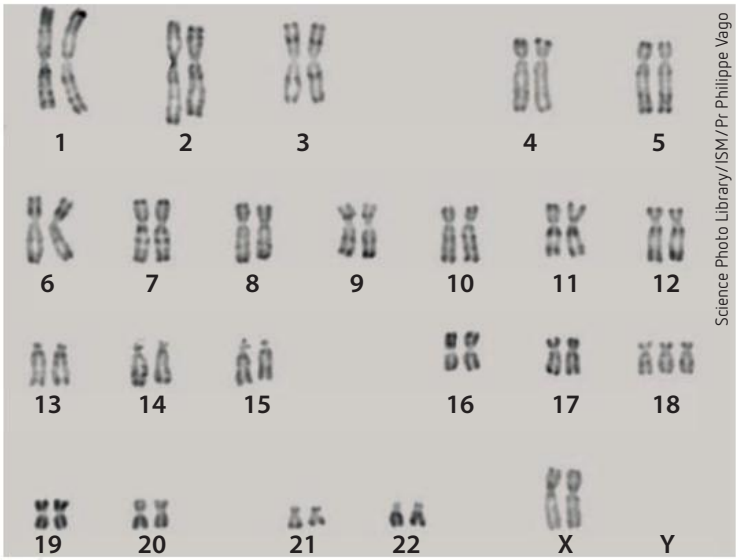

FIGURE 9.2.8 A human karyotype

3 Explain how each of the three mutations could have occurred.

4 After reviewing the information on sex chromosome non-disjunction in section 9.2, do you consider the condition displayed in Figure 9.2.6 to be Klinefelter or Turner syndrome? Justify your choice.

5 Based on the alternative name for Down syndrome, suggest different appropriate names for the mutations in Figure 9.2.7 and Figure 9.2.8.

6 Which of the karyotypes in Figures 9.2.5–9.2.8 indicate individuals with the following two aneuploidy syndromes?

- i Babies born with Patau syndrome (trisomy 13) have many abnormalities, involving nearly every organ system in the body, as well as developmental delay. Only 50% of live-born babies survive beyond about 2 weeks of age, with approximately 20% surviving to one year old, and around 13% to 10 years old.
- ii Edwards syndrome is a chromosomal abnormality characterised by the presence of an extra 18th chromosome or part of it. Children born with this condition have deformities, including of the face

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and hands, heart defects and intellectual disability. This syndrome is the second most common human trisomy syndrome, with most surviving babies being female. Many individuals die before birth with 5–25% of children surviving longer than a year.

Correct conclusions from karyotype analyses

1 Figure 9.2.5 shows the normal karyotype of a male: with one Y and one X chromosome, and 22 pairs of homologous autosomes.

2 Figure 9.2.6 has only one sex chromosome, X; possibly with extra chromosomal material attached

Figure 9.2.7 has three number 13 chromosomes

Figure 9.2.8 has three number 18 chromosomes.

3 Figure 9.2.6 formed from the union of one gamete with no sex chromosome and another gamete with one X chromosome, the gamete with no sex chromosome resulting from non-disjunction of the sex chromosomes at metaphase of meiosis.

Figure 9.2.7 formed from the union of a normal gamete with one chromosome 13, and another gamete with two number 13 chromosomes, the second gamete resulting from non-disjunction of chromosome pair 13 at metaphase of meiosis.

Figure 9.2.8 formed by the same process as in Figure 9.2.7 except the abnormal gamete with extra chromosome formed from chromosome number 18.

4 Turner syndrome: genotype XO

5 Figure 9.2.7, trisomy 13; Figure 9.2.8, trisomy 18

6 i Figure 9.2.7, Patau syndrome

ii Figure 9.2.8, Edwards syndrome

SECTION REVIEW 9.2

REMEMBERING

1 Describe the order in which the chromosomes are arranged in a karyotype.

2 **a** Define 'aneuploidy'.

b During which cell cycle process do errors resulting in aneuploidy occur?

3 Define 'non-disjunction'.

4 **a** Distinguish between monosomy and trisomy in somatic cells.

b Name an example of a human condition that results from trisomy.

UNDERSTANDING

5 At what stage in meiosis are chromosomes photographed to create a karyotype? Explain why.

6 Using just one pair of chromosomes, draw diagrams to illustrate how:

a non-disjunction at both **i** meiosis I and **ii** meiosis II leads to different chromosome numbers in gametes.

b different chromosome numbers in gametes leads to aneuploidy in new individuals.

7 If diploid cells can be represented as 2***n*** and haploid as ***n***, what symbol(s) would you use for aneuploid cells?

8 Complete the following table to summarise the human genetic abnormalities listed.

GENETIC ABNORMALITY	SEX CHROMOSOME COMBINATION/S	MALE OR FEMALE?	PHENOTYPIC ABNORMALITIES
Klinefelter syndrome			
Turner syndrome			

APPLYING

9 Do you consider 'triploid' to be an acceptable alternative term for trisomy? Explain why or why not.

9.3 Inherited mutations

Mutations that occur in genes often affect the translated proteins they code for. These effects are sometimes subtle, but more often they are severe, with potentially catastrophic effects for the survival of the organism. This is especially true for whole chromosome mutations, or those involving large segments of chromosomes.

Most mutations confer disadvantages on the organisms that inherit them. The premature death of organisms with harmful mutations, before reproductive age, prevents these mutations accumulating in populations.

Useful mutations are extremely rare, and their transmission to future generations is even more rare. To be beneficial, and thus be passed on to future generations, the mutation would have to enhance the function of the protein produced by the gene in which it occurs. This enhanced protein, in turn, would need to make the organism better suited to its environment, so that it could compete more successfully with other members in its population.

Cell type and effect of mutation

somatic
a body cell that will not pass its genes onto next generation

mitosis
a type of nuclear division that produces daughter cells with the same chromosomal content as the parent cells; the basis for growth and repair in multicellular individuals, and for asexual reproduction in many eukaryotic species

germ-line
the cell line in eukaryotic organisms from which sex cells are produced

The effect of a mutation depends upon whether it has occurred in non-reproductive (body, somatic) cells, which are produced by mitosis, or in reproductive (germ-line) cells, which are produced by meiosis.

As shown in Figure 9.3.1, a mutation in a somatic cell occurs only in that affected cell and the daughter cells produced from that cell. Cancer is a critically detrimental consequence of mutations in somatic cells. Mutations causing cancer accumulate in particular genes or regions of the cell's DNA that accelerate the rate of division of that cell. These mutations destroy that cell's ability to undergo apoptosis (natural cell death), and may also increase the rate of mutations within that cell.

Mutations that affect gametes can be inherited, or passed on to the next generation, as illustrated in Figure 9.3.1. These mutations are incorporated into every cell of the offspring. Often, the germ-line mutation results in developmental abnormalities that cause the embryo or foetus to be spontaneously aborted. If carried through to birth, these mutations usually result in congenital disorders with varying severity in the offspring.

Occasionally, a gene mutation enhances the function of the encoded protein, which, if circumstances suit, also enhances the chance of survival of the organism above others in its species. If the mutation is consistently passed on from one generation to the next, a new allele has entered the population.

Variation as a result of inherited mutations

SYLLABUS LINK
Chapter 7 details the process of meiosis.

congenital
present at birth; may or may not be inherited genetically

Variation in the characteristics (phenotype) of each individual in a species is largely determined by the unique paired combinations of alleles in its coding genes; that is, its genotype. These alleles arise via mutation. Mutations in coding genes cause changes in proteins produced, and a protein's function depends on its (often intricate) structure.

Classification of mutations

Mutations can therefore be classified according to the impact of the mutation on the protein's function, and thus the organism's survival. Protein function may be unchanged, changed for the worse, or changed for the better.

If the protein product is unchanged compared with the original, thus does not affect the organism's survival, it is a neutral mutation. For example, in the human ABCA1 gene, which codes for a protein involved in cholesterol transport, a substitution in a single GAA codon generates a GAC codon, and causes the amino acid glutamic acid to be replaced by aspartic acid. However, both amino acids are

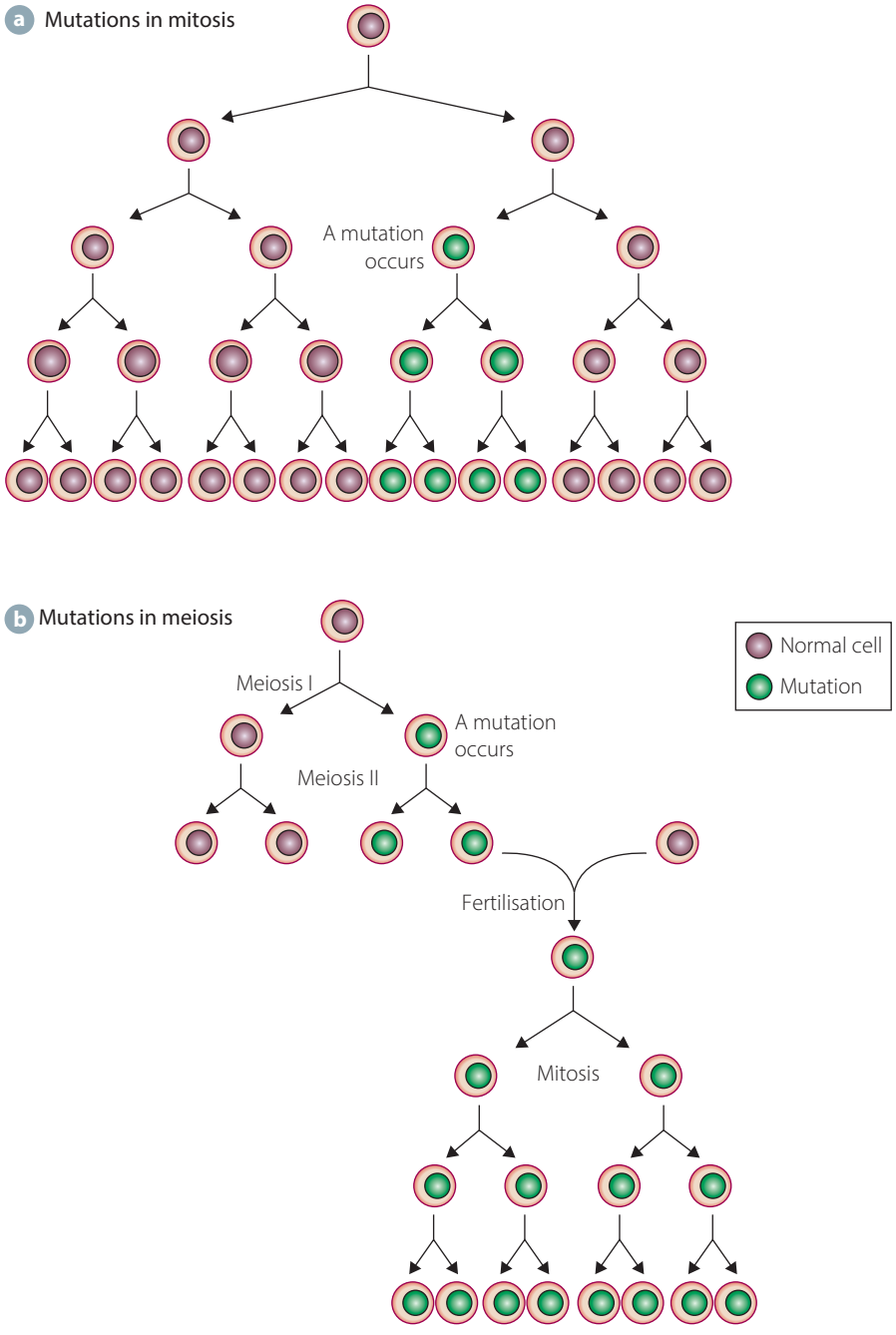

FIGURE 9.3.1 (**a**) Mutations in somatic cells only affect the cell in which they occur and all daughter cells. (**b**) Mutations in germ-line cells affect all body cells of the offspring that inherits them.

negatively charged and occur on the surface of the protein, where they interact with surrounding water, so the important properties and function of the protein remain essentially the same.

A living organism can be compared with a complex product of engineering, such as an aeroplane, in which the components are so intricately integrated that an indiscriminate change to any one component harms the overall operation of the aircraft. Similarly, random mutations may disrupt the function of an encoded polypeptide and the resulting protein. This negatively affects the organism's overall ability to

SYLLABUS LINK

Chapter 10 details the patterns of inheritance of genes.

carry out its basic processes and survive. Such mutations are referred to as deleterious mutations and include most mutations.

However, these deleterious mutations may persist and be passed on, if the individual carrying them also has a copy of the normal allele that codes for the functional version of the protein. The deleterious mutation is thus masked within the organism's phenotype. But if the organism has only non-functional alleles for a particular gene, usually they will die.

Occasionally, mutations lead to a new allele that benefits the survival of the organism, and perhaps of the species in the long term. A beneficial mutation could improve the function of the original protein, or it could eliminate a protein that may have been harmful to the organism in some circumstances.

Phenotypic variation in Gouldian finches

Figure 9.1.1 (page 173) displays some of the striking colour variations in the Gouldian finch species. Table 9.3.1 shows other types of phenotypic variation that may not be so externally obvious.

TABLE 9.3.1 Different types of phenotypic variation in the Gouldian finch

TYPE OF VARIATION	DESCRIPTION	EXAMPLE
Morphological	Variation in organism's shape and structure, including internal anatomy	Size and shape of bird
Biochemical	Variation in organism's chemical structure and composition, including differences in specific types of proteins, lipids and carbohydrates, and of other specialised molecules, such as pigments and hormones	Expression of enzymes creating pigments and resulting colour of head feathers
Physiological	Variations in how individuals carry out metabolism and maintain bodily processes	Sensitivity to lack of food; affects egg production
Behavioural	Differences in ways individuals perceive, think and react, including mental processes (cognition) and translation of thoughts and corresponding emotional responses into action (behaviour)	Aggression, inquisitiveness, mate selection

All phenotypic variation is affected by the presence or absence of specific proteins and the action of those proteins.

Environmental influences on phenotype

The size to which a bird grows, and the physiology of the animal are also influenced by the availability of food. Breeding behaviour and outcomes are affected by the availability of potential mates. To some extent then, an organism's environment also plays a part in determining its characteristics.

SECTION REVIEW 9.3

REMEMBERING

1 Define:
- **a** apoptosis
- **b** allele
- **c** genotype
- **d** phenotype
- **e** variation.

2 Briefly explain the difference between a germ-line cell and a somatic cell.

3 List and briefly describe four different types of phenotypic variation.

4 Briefly describe an example of an environmental influence on an organism's phenotype.

UNDERSTANDING

5 Compare and contrast mitosis and meiosis.

6 Compare the consequences of a mutation in a germ-line cell with that in a somatic cell.

7 Describe how alleles contribute to phenotypic variation.

APPLYING

8 Briefly describe a phenotypic variation between you and your sibling/parent for each of the four categories of variations: morphological, biochemical, physiological and behavioural.

CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1 Define:
- **a** spontaneous mutation
- **b** point mutation
- **c** frameshift mutation
- **d** whole chromosome mutation
- **e** mutagen.

2 Define 'karyotype'.

3 Define:
- **a** aneuploidy
- **b** non-disjunction.

4 Briefly explain the difference between a somatic cell and a germ-line cell.

CATEGORY QUESTIONS

5 During which two phases of the cell cycle can spontaneous mutations occur?

6 Illustrate the differences between the following types of mutations by copying the DNA nucleotide sequence GTACATGGC and then 'mutating' it at the first C for each.
- **a** Substitution
- **b** Insertion
- **c** Deletion

7 During which phase(s) of the cell cycle can whole chromosome mutations take place?

8 Briefly describe three different effects of:
- **a** chemical mutagens
- **b** physical mutagens.

9 Name the two main characteristics of chromosome pairs that allow them to be distinguished from each other in a karyotype.

10 Why are the consequences of a mutation in a germ-line cell more concerning than those of a mutation in a somatic cell?

ELABORATION QUESTIONS

11 Use a simple diagram to explain why a frameshift mutation has a greater effect than a substitution mutation.

12 Explain why a chromosomal mutation has a greater effect than a gene mutation.

13 Briefly explain what each of the two parts of the name 'trisomy 21' mean.

14 Describe briefly the meaning of:
- **a** monoploid
- **b** triploid
- **c** polyploid.

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15 Draw a male karyotype for an imaginary organism with three autosomes and the same sex determination and similarly proportioned sex chromosomes as in the human species.

16 Explain with the use of diagrams how a child may have come to have trisomy 13.

EVIDENCE QUESTIONS

17 It is possible for one chromosome of a homologous pair to have some additional chromosomal material attached. This attachment must have broken away from a chromosome of a different homologous pair. Describe how it may be possible to identify the chromosome from which this detached material came.

END-OF-CHAPTER EXAM

End-of-chapter test

1 Indel is an abbreviated name for a mutation type standing for:

A indefinite number of nucleotide units affected.

B insertion or deletion of a nucleotide unit.

C indescribable type of mutation.

D frameshift mutation.

2 Choose the correct statement.

A A substitution mutation is an example in the frameshift category.

B A point mutation is an example of a substitution mutation.

C A substitution mutation is an example of a point mutation.

D A whole chromosome mutation is an example of a point mutation.

3 A neutral mutation produces a protein that:

A is unchanged compared to original.

B has improved properties compared to original.

C has less useful properties than the original.

D has neither a positive nor a negative effect compared to the original.

4 Choose the correct statement.

A Non-disjunction occurs only in mitosis.

B Non-disjunction occurs only in meiosis.

C Non-disjunction can occur in mitosis or meiosis.

D Non-disjunction occurs during DNA replication.

5 Aneuploidy with respect to sex chromosomes happens:

A during DNA replication.

B in gamete cells and not somatic cells.

C in somatic cells and not gamete cells.

D in both gamete and somatic cells.

6 Complete the following statement.

Non-disjunction of homologous chromosomes during meiosis forms gametes with abnormalities in chromosomes referred to as_____, where there are more or less than the usual number of chromosomes present. Non-disjunction of sex chromosomes during meiosis results in offspring with abnormal numbers of chromosomes in all _____ (insert 'somatic' and/or 'gamete') cells of the body.

Klinefelter syndrome is one example of this, where individuals have genotype XXY, with respect to their sex chromosomes. This may have resulted from the fertilisation by a Y sperm of an egg with _____ chromosomes, or by the fusion of an _____ egg with an XY sperm.

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If the normal chromosome number with respect to body cells is diploid (2*n*), the term used for chromosome number in somatic cells of people with Klinefelter syndrome would be: _____, and signified by symbol: _____.

7 Briefly explain, in a short paragraph, with respect to protein production, how inherited mutations in the form of different alleles produce phenotypic variation. Include examples in your explanation.

8 Name the four different types of phenotypic variations, and for each use a sentence to describe an example of a variation of that type shown by a pet or any domestic animal.

9 Briefly describe an example of how environment can affect an organism's phenotype, in addition to the genotypic influence.

10 Briefly describe in a short paragraph why:

a radiographers taking X-rays as diagnostic tools in medicine leave the room and stand behind a protective screen.

b pregnant woman are not allowed to have X-ray images taken.

11 Consider the mutations (i) CC* CCC ACC CAC C_ _, where A is inserted at *, and (ii) CCC CCA CCC ACC, where the second C is deleted. Determine which mutation would cause the greatest chemical difference to a polypeptide that is normally produced by the unmutated DNA template nucleotide sequence CCC CCA CCC ACC. Use the genetic code, and include simple diagrams of both the resulting mutations and resulting amino acid sequences to justify your decision.

10 INHERITANCE

Introduction

The study of inheritance of characteristics or how genetic material is passed from one generation to the next can be called heredity. Gregor Mendel made significant contributions to the study of inheritance, which have been recognised by the term 'Mendelian genetics', used today to describe the patterns of inheritance he discovered.

Stimulus questions

What genotypes and phenotypes are expected in offspring when different inheritance patterns are considered, including autosomal, sex-linked and multiple alleles?

Why do some characteristics have only a small number of different phenotypes, but others have many variations?

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10.1 Patterns of inheritance

The principles and patterns of inheritance were first proposed by Gregor Mendel (1822–84), an Austrian monk, who was unique in his time (Figure 10.1.1). Genetics or **heredity** may be thought of as the study of how genes are passed on. Genes occur on chromosomes of two types: autosomes (non-sex chromosomes) and sex chromosomes. 'Single autosomal gene inheritance' is when a characteristic is determined by one gene locus on an autosomal chromosome pair. It was this most straightforward inheritance pattern, with one allele of the gene dominating over the other, that governed the genetics of the pea plant characteristics that Mendel chose to study. There are other patterns of inheritance that are not so straightforward; several of these are discussed in this chapter. A simple type of genetics cross is a **monohybrid cross** in which inheritance of only one ('mono') characteristic, exhibiting contrasting phenotypes ('hybrid'), is considered.


Getty Images/Time Life Pictures

FIGURE 10.1.1 Mendel discovered key principles of inheritance that are the basis of all modern knowledge from experimentation in his pea garden.

heredity
study of inheritance; genetic transmission of characteristics from one generation to another

monohybrid cross
only one characteristic with contrasting phenotypes is considered

SYLLABUS LINK
Chapter 7 discusses meiosis.

Single autosomal gene inheritance

In diploid body cells, alleles occur in pairs. One of each pair is located on each of two homologous chromosomes (Figure 10.1.2). One chromosome of every homologous pair was originally inherited from the female parent, via the egg, and the other was inherited from the male parent, via the sperm. The union of egg and sperm (fertilisation) forms the zygote – the first cell of the new individual. Repeated mitotic division then continues, to produce the embryo, foetus and eventually the adult individual.

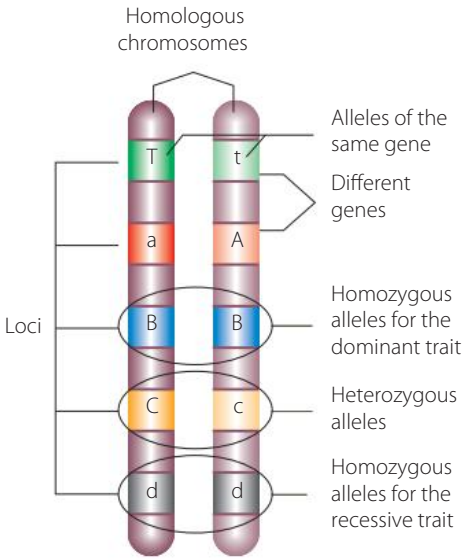

FIGURE 10.1.2 Homologous chromosomes have paired alleles. Each chromosome of each pair, with its assortment of different alleles, is inherited from either the male or female parent. Here are representations of some different combinations of alleles that may occur.

Monohybrid cross

purebreeding when crossed with each other, offspring all have parental phenotype

parental generation (P) two individual organisms originally crossed in breeding experiment; their offspring are the F_1 generation

first filial generation (F_1) the first generation of offspring produced from a cross between two parents (P)

second filial generation (F_2) the offspring of F_1 generation; second generation produced from original cross between two parents (P)

An example of a monohybrid cross involving single autosomal gene inheritance is the cross between **purebreeding** tall and short pea plants, studied by Mendel, incidentally. Purebreeding plants, when crossed among themselves, always give rise to offspring like the parents. All offspring from a cross between tall and short purebreds are tall.

In these crosses, the original purebreeding parent plants are typically referred to as the **parental generation (P)**, and their offspring as the **first filial generation (F_1)**, as in Figures 10.1.3 and 10.1.4.

When F_1 plants are self-pollinated, offspring, belonging to the **second filial generation (F_2)**, are a mix of tall and short. Approximately three-quarters of the F_2 generation are tall and one-quarter are short. In other words, the ratio of tall to short plants is approximately 3:1. Figure 10.1.4 summarises a cross between purebred tall and short pea plants.

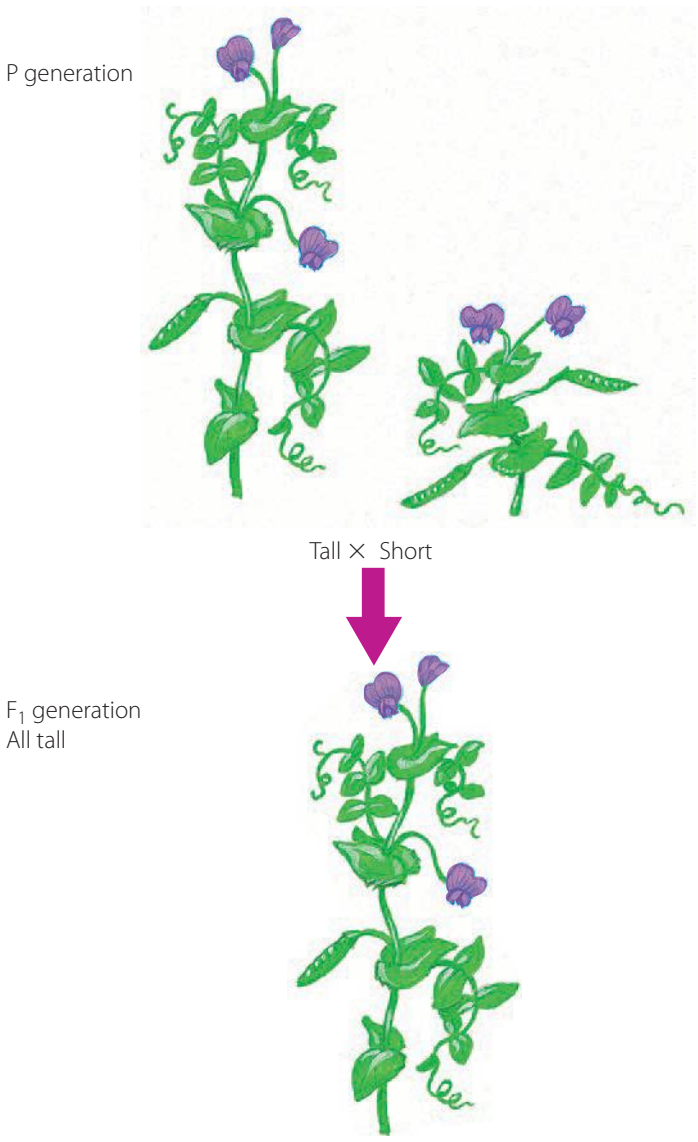

FIGURE 10.1.3 Tall and short pea plants: two different plant height phenotypes

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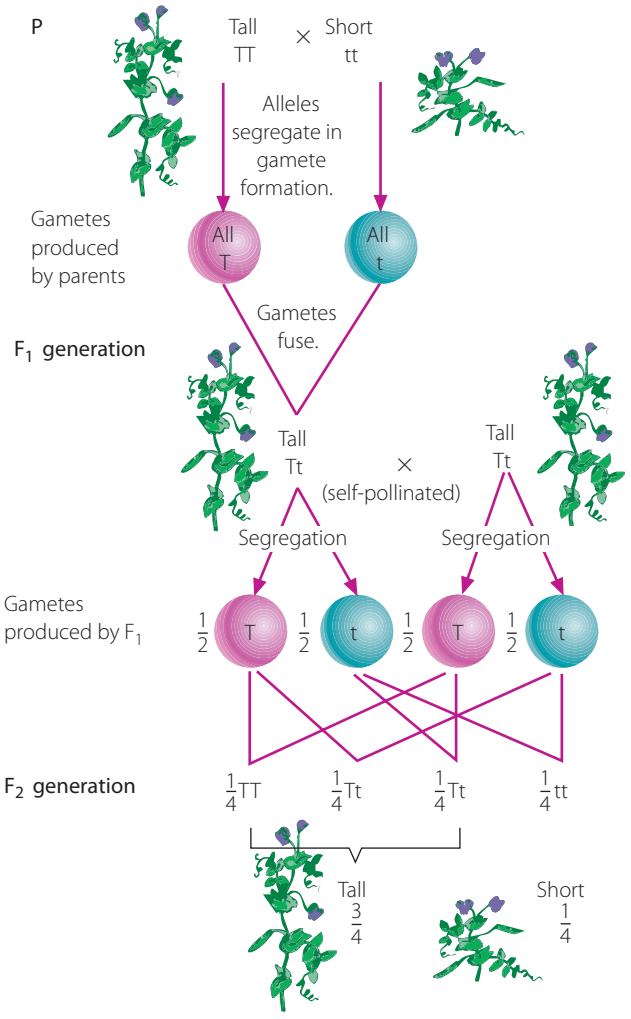

FIGURE 10.1.4 Summary of a cross between tall and short pea plants, both purebred, illustrating expected proportions of two generations of offspring. Upper-case letter 'T' represents the dominant allele for height; lower-case 't' represents the recessive allele. The genotypes of the P, F_1 and F_2 generations are represented as TT, Tt or tt.

The short form (allele) of the height gene, which fails to show itself in the F_1 generation, must be masked in some way by the tall allele. Only in the absence of this tall allele will the short allele be expressed in the outward appearance of the plant. In other words, the allele for tallness is **dominant** to the allele for shortness. Shortness is described as **recessive**.

In Figure 10.1.4, the tallness allele is represented by T, and the shortness allele is represented by t. It is assumed that each purebreeding parent (P) plant (or, more strictly, each somatic cell of each P plant) contains a pair of identical alleles: TT in the case of the tall parent and tt in the case of the short parent.

When an organism contains identical alleles like this it is called **homozygous**. In the pea plants, this describes the genetic make-up of the P plants, or at least the parts of them that determine the plant heights. An organism's genetic composition is known as its genotype. In essence, the genotype describes the alleles that a cell or organism has at a particular gene locus for a particular **trait**.

The way genes are expressed in the characteristics of the organism is known as its phenotype. For the P generation of pea plants described earlier, plant height is the phenotype. Purebreeding pea plants with the 'tall' phenotype have the genotype TT. Pea plants with the 'short' phenotype must have the genotype tt.

dominant
the phenotype expressed when at least one copy of its dominant allele occurs in genotype

recessive
the phenotype only expressed if both copies of its recessive allele occur in genotype

homozygous
a genotype with two identical alleles for single gene locus; purebreeding

trait
heritable characteristic; phenotype

The T allele is present in each of the gametes produced by the tall purebreeding P plant and the t allele is present in each of the gametes of the short purebreeding P plant. Fertilisation brings the T and t alleles together, so that all the F_1 offspring have the genotype Tt. Phenotypically, all F_1 plants are tall, because tallness is dominant to shortness. When an organism contains two dissimilar alleles, it is termed **heterozygous**. In this instance, the T allele expresses itself in the phenotype and the expression of the t allele is blocked by the expression of the dominant T allele.

heterozygous
a genotype with two different alleles for single gene locus

Punnett squares

Punnett square
a grid used to graphically illustrate and predict the outcome of a genetic cross

The **Punnett square** is a relatively simple but highly effective method of predicting all possible genotypes, and thus phenotypes, and proportions of each in a genetic cross. Initially, all possible gametes that can be produced by both parents are written in the square, and then all possible combinations of these are investigated. In a Punnett square, the alleles in the gametes of one parent are written along the top of the boxes and the alleles in the gametes of the other parent are written down the side. The products of the various unions of gametes are written in the corresponding boxes, along with the expected proportion or frequency of occurrence of each combination.

Worked example 10.1.1 demonstrates how a Punnett square can be used, along with other logical thinking, to predict expected frequencies of genotypes and phenotypes.

WORKED EXAMPLE 10.1.1

Consider a pea plant purebred for green pea pods that is crossed with a purebred yellow-podded plant. All F_1 offspring produce green pods. If 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

- Green pods must be dominant to yellow. Therefore, assign alleles G = green, g = yellow.
- Draw a Punnett square for the P generation cross to illustrate the F_1 genotypes.

		Green parent gametes
		All G
Yellow parent gametes	All g	All F_1 Gg green

- Draw a Punnett square for the F_1 cross to predict the F_2 genotypes.

		F_1 parent gametes	
		$\frac{1}{2}$ G	$\frac{1}{2}$ g
F_1 parent gametes	$\frac{1}{2}$ G	$\frac{1}{4}$ GG green	$\frac{1}{4}$ Gg green
	$\frac{1}{2}$ g	$\frac{1}{4}$ Gg green	$\frac{1}{4}$ gg yellow

From this Punnett square, it is expected that $\frac{3}{4}$ of the F_2 generation will have green pea pods.

Whenever a monohybrid cross occurs between two purebreeding phenotypically contrasting parents, involving a dominant autosomal allele and its recessive alternative, the same F_2 phenotypic ratio of 3:1, for the dominant versus recessive phenotypes, will result. (This is often referred to as the 'monohybrid ratio'.)

Incomplete dominance

Some phenotypic variations show offspring characteristics that are intermediate to contrasting parent characteristics.

If a purebreeding red-flowered plant is crossed with a purebreeding white-flowered plant, the F_1 offspring all have pink flowers (Figure 10.1.5). When these F_1 pink plants are crossed with each other, the F_2 offspring have flowers in the ratio of 1 red : 2 pink : 1 white. This is known as **incomplete** or **partial dominance** because one trait is not fully dominant over its partner and the heterozygous phenotype (pink) is intermediate between both homozygous parental phenotypes (red and white).

Special notation is used to indicate inheritance of partially dominant traits. A suitable upper-case letter designates the gene for the trait (e.g. C for colour) and upper-case superscript letters indicate the alleles (e.g. C^R = red colour, C^W = white colour). Figure 10.1.6 illustrates colour inheritance in snapdragons. Worked example 10.1.2 demonstrates how to use a Punnett square to investigate a cross involving incomplete dominance.

FIGURE 10.1.5 In crosses between purebreeding red-flowered and white-flowered plants, incomplete or partial dominance of red and white flower colours results in pink colour.

incomplete dominance
when a heterozygous individual has a phenotype intermediate to those of corresponding homozygous individuals

partial dominance
an alternative term to incomplete dominance

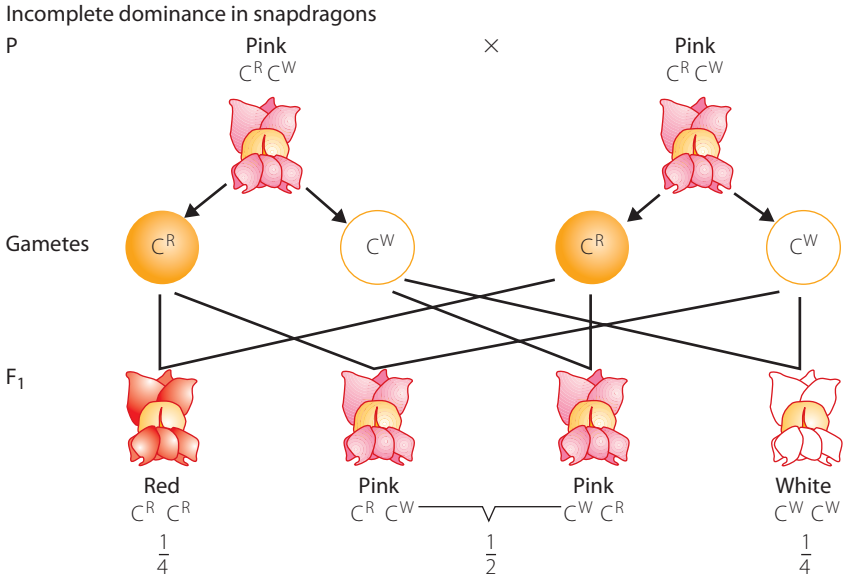

FIGURE 10.1.6 Incomplete dominance in snapdragons. The result of crossing pink snapdragon flowers among themselves. A phenotypic ratio of approximately 1 red : 2 pink : 1 white results.

WORKED EXAMPLE 10.1.2

Predict the genotype and phenotype frequencies in a cross between red and pink snapdragon plants.

- We know that flower colour inheritance in snapdragons demonstrates an incomplete dominance pattern. Therefore, assume that the pink phenotype is produced by the heterozygous genotype and the red phenotype is produced by one of the two homozygous genotypes.

ANSWER

Assign alleles according to convention:

C^R = red colour, C^W = white colour

- Draw a Punnett square for the cross between red and pink snapdragon plants.

		Red parent gametes
		All C^R
Pink parent gametes	$\frac{1}{2}$ **C^R**	$\frac{1}{2}$ C^RC^R red
	$\frac{1}{2}$ **C^W**	$\frac{1}{2}$ C^RC^W pink

From this Punnett square, it is expected that the frequencies of red (C^RC^R) and pink (C^RC^W) phenotypes in offspring would be equal, at 50% or $\frac{1}{2}$ each.

Codominance

codominant when both alleles of heterozygous individual are fully expressed in phenotype

The study of certain coat colours in horses and cattle reveals another type of dominance relationship in which *both* alleles in the genotype are fully expressed in the heterozygote. Such traits are called **codominant**. In shorthorn cattle, coat colour alleles are inherited in this way; the two alleles are expressed as red (C^R) and white (C^W). This is similar to the incomplete dominance shown in snapdragons but, in this case, the offspring of purebreeding red and white parents have roan coats (C^WC^R), a mixture of both red and white hair. The codominant inheritance of coat colour in shorthorn cattle is represented in Figure 10.1.7.

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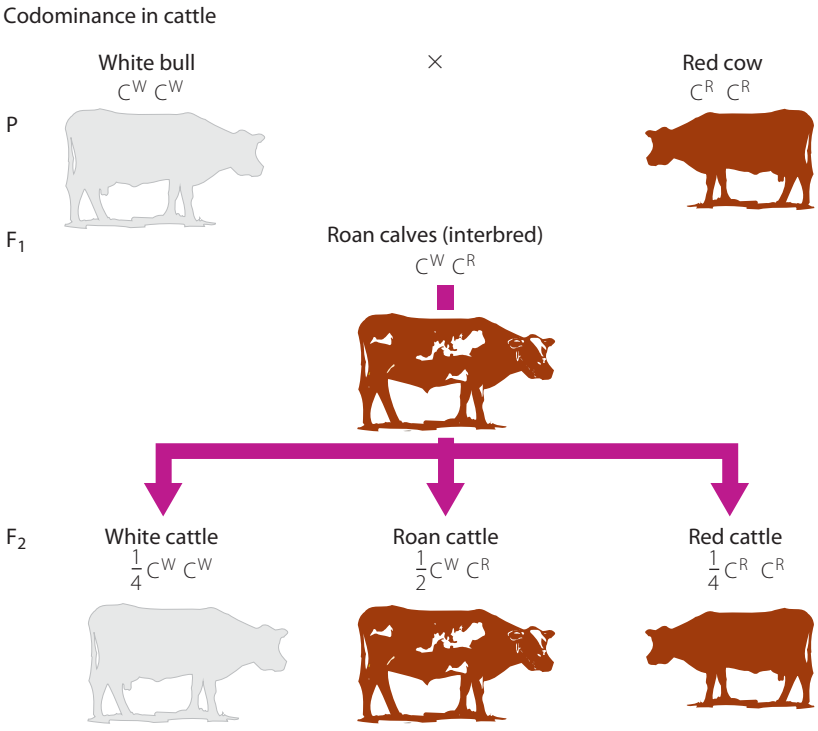

FIGURE 10.1.7 Codominance in cattle. In shorthorn cattle, codominant inheritance results in roan coat colour in offspring of purebreeding red and white parents.

Frequency histograms

Frequency histograms can also be used to illustrate proportions of offspring genotypes and phenotypes, as illustrated in Figure 10.1.8 for the F_2 generation in the shorthorn cattle F_1 cross in Figure 10.1.7.

For both incomplete and codominance inheritance patterns, as shown in Figures 10.1.6 and 10.1.7 with purebreeding parents of contrasting phenotypes, the F_2 generation phenotypic (and genotypic) ratio is always 1:2:1 for one purebreeding phenotype/genotype : heterozygote : other purebreeding phenotype/genotype.

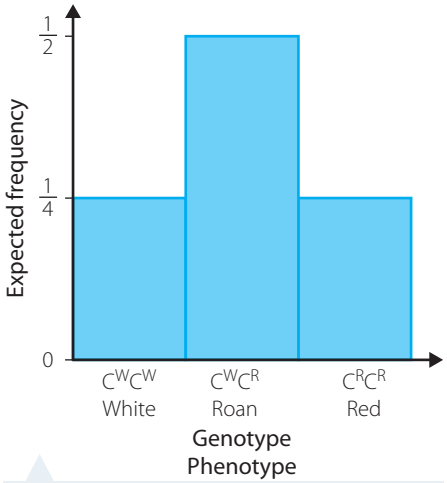

FIGURE 10.1.8 Frequency histogram illustrating expected genotype and phenotype frequencies of offspring from an F_1 cross between a roan cow and a roan bull.

frequency histogram
a specialised column graph illustrating frequencies or proportions on vertical axis of different items (genotypes and phenotypes) on horizontal axis

Sex-linked inheritance

In humans, normally all female gametes contain 22 autosomes and an X sex chromosome. Half of male gametes contain 22 autosomes and a Y sex chromosome and the other half contain 22 autosomes and an X chromosome. Thus, in humans there is a 50% chance that, in fertilisation, a sperm cell bearing a Y chromosome will fuse with an egg cell, resulting in a male (XY), and a 50% chance that a sperm cell carrying an X chromosome will fuse with an egg cell, resulting in a female (XX).

Differential (non-common) regions of the X and Y chromosomes are unique to each chromosome. In males, genes found in the differential regions of the chromosomes are **hemizygous**, meaning there is only a single copy of each gene.

hemizygous
a gene that occurs only as single copy in diploid organism or cell

Genes within these differential regions of the sex chromosomes show inheritance patterns that can be described as **sex-linked**. Sex-linked inheritance presents as phenotypes that have different frequencies between males and females.

sex-linked
a gene located on sex chromosome

Sex-linked inheritance in fruit flies

Whenever there is a difference in the phenotypic proportions between female and male offspring, the gene involved must occur on a sex chromosome, most likely the X chromosome.

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, indicating that red is dominant to white. If males and females of this F_1 generation are mated, $\frac{3}{4}$ of all of the F_2 fruit flies have red eyes, including all the females and half the males, with the other half of the males ($\frac{1}{4}$ of the whole F_2 population) having white eyes. Alternatively, if the initial P cross is between a red-eyed male and white-eyed female, all F_1 males have white eyes and all F_1 females are red-eyed.

These observations make sense if the eye colour gene is carried on the X chromosome. In the first cross, represented in Figure 10.1.9a, between the white-eyed male and the red-eyed female, the male is hemizygous for the white allele. The female must be homozygous dominant for the red allele, symbolised by X^RX^R. In the F_1 generation, all the females are heterozygous for the red phenotype (X^RX^r). However, the males can only inherit one X chromosome from their mother, and so are hemizygous with the red eye allele (X^RY).

When the F_1 generation males and females are crossed (Figure 10.1.9b), all resulting F_2 females are red-eyed, having inherited at least one allele for red eyes; their father only had a red X to pass on. On the other hand, F_2 males inherit only one X chromosome from their heterozygous mother; half get the red allele, half get the white allele, so half the F_2 males are red-eyed (X^RY) and half are white-eyed (X^rY).

In the alternative P cross (Figure 10.1.8c) between a red-eyed male (X^RY) and a white-eyed female (X^rX^r), all the F_1 females inherit an X^R from their father, but receive an X^r from their mother, so are red-eyed (X^RX^r). All the F_1 males inherit an X^r from their mother, and are all white-eyed (X^rY).

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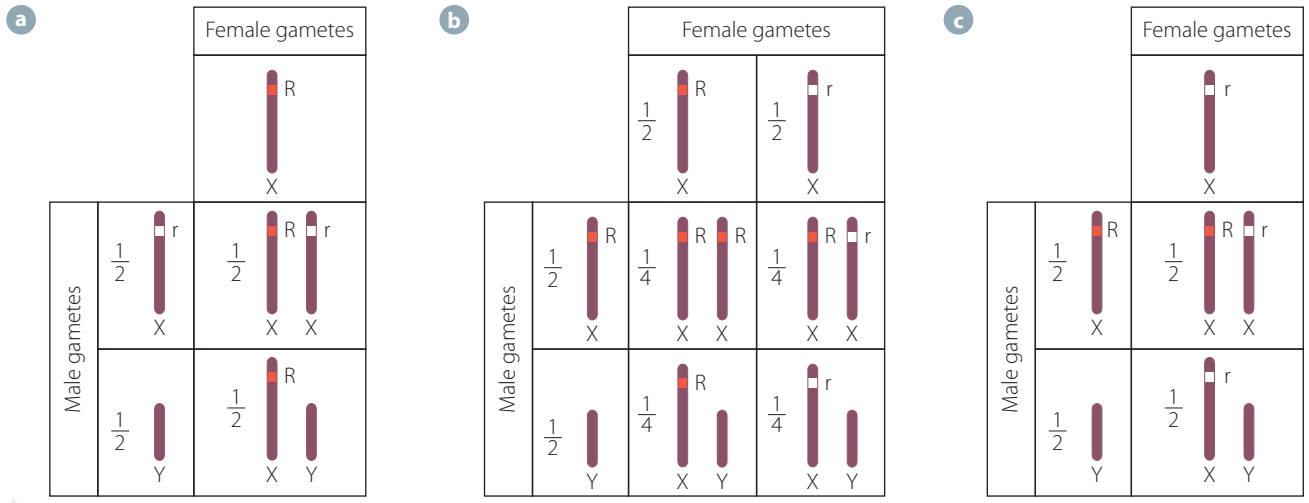

FIGURE 10.1.9 White eye colour in fruit flies is an X-linked recessive phenotype. The three fruit fly crosses described in the text are illustrated in Punnett squares. (**a**) The P generation cross between a homozygous red-eyed female and a white-eyed male. (**b**) The F_1 generation cross between a heterozygous red-eyed female and a red-eyed male. (**c**) A different P generation cross between a red-eyed male and a white-eyed female.

X-linked recessive

When a recessive phenotype is determined by an allele on the X chromosome, it is said to be an **X-linked recessive** phenotype. Males that have the recessive allele on their X chromosome will always express the recessive phenotype because they only have one X chromosome. Females will only express the recessive phenotype when both X chromosomes have the affected allele. A heterozygous female will be a **carrier**.

X-linked recessive
a phenotype that is determined by a recessive allele on X chromosome

carrier
a non-affected, heterozygous organism carrying an allele for a recessive phenotype; organism may transmit recessive allele to its offspring

To express the phenotype, males only need one copy of the affected allele, whereas females must have two. Consequently, males show X-linked recessive phenotypes much more often than females do. Red–green colour blindness and haemophilia are two recessive conditions in humans that are transmitted to offspring through X-linked inheritance.

In this type of inheritance, a male with the phenotype cannot pass on the trait to his sons, because they inherit his Y chromosome only. His daughters will get the affected X chromosome but they will only show the phenotype if they inherit another affected X chromosome from their mother. As with autosomal recessive phenotype, some generations may not have any members showing the phenotype.

X-linked dominant

In **X-linked dominant** inheritance, heterozygous females will always show the phenotype and any individuals showing the trait must have a parent with the phenotype. Males showing the phenotype will not pass the affected allele on to their sons (because their sons inherit their father's Y chromosome) but they will pass the dominant allele on to all their daughters, who will also show the phenotype. A heterozygous female is expected to pass on the allele, and thus the phenotype, to 50% of her offspring regardless of their sex. Inheritance of this type is rare in humans.

X-linked dominant
a phenotype that is determined by a dominant allele on X chromosome

Multiple allelic inheritance

Sometimes there are more than two allele types for a gene, although only two of them occur together at any given locus on the homologous pairs of chromosomes. When three or more alleles of a gene exist among the members of a population, it is called a multiple allele system of inheritance.

An example of this is seen in the ABO blood group (or blood type) system in humans. Allele I^A produces A type marker molecules on the outside of the red blood cell membranes, and the I^B allele produces B markers. The I^A allele is codominant with I^B. A third allele, i, is recessive to both I^A and I^B alleles, and produces no (or 'zero') markers on the blood cell, but is referred to as the (letter) O allele.

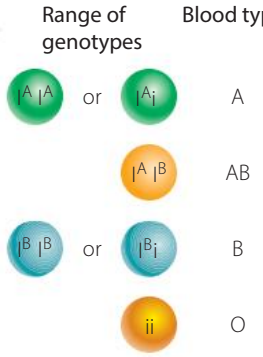

FIGURE 10.1.10
Different blood types found in humans due to different combinations of multiple alleles. Blood type O, can be taken to mean 'zero', due to there being 'zero' markers on the blood cells.

Figure 10.1.10 summarises the range of genotypes and the resulting phenotypes (blood groups/types).

A child whose parents are both blood group O must be blood group O. However, consider what happens when two parents, one of whom is blood type A and the other blood type O, have children. The genotypes of the children depend on the genotype of the A parent. If he or she is homozygous with the genotype I^AI^A, the children can only have the genotype I^Ai and be blood type A. However, if the type A parent is heterozygous with the genotype I^Ai, each child has a 50% chance of being blood type A (I^Ai) or blood type O (ii).

Worked example 10.1.3 illustrates the solution to a proposed blood-type question.

WORKED EXAMPLE 10.1.3

Parents, both of whom have A type blood, produced 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

- Determine the possible genotypes of the parents.

  Parents could be I^AI^A or I^Ai.
- Determine the possible combinations of these genotypes.

  $I^AI^A \times I^AI^A$

  $I^AI^A \times I^Ai$

  $I^Ai \times I^Ai$
- The baby had genotype ii, so must have received an i allele from both parents.
- Draw a Punnett square to show the cross $I^Ai \times I^Ai$ and determine the expected frequency of O type offspring

		Parent 1 gametes	
		$\frac{1}{2}$ I^A	$\frac{1}{2}$ i
Parent 2 gametes	$\frac{1}{2}$ I^A	$\frac{1}{4}$ I^AI^A A type blood	$\frac{1}{4}$ I^Ai A type blood
	$\frac{1}{2}$ i	$\frac{1}{4}$ I^Ai A type blood	$\frac{1}{4}$ ii O type blood

Therefore, there is a probability or expected frequency of $\frac{1}{4}$ that the A type parents would have offspring with O type blood.

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SECTION REVIEW 10.1

REMEMBERING

1. Define 'purebreeding' also known as 'purebred'.
2. Define the P, F_1 and F_2 generations.
3. Briefly describe:
   - **a** autosomal dominance in inheritance
   - **b** sex-linked inheritance.

UNDERSTANDING

4. 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			

5. Distinguish between partial dominance and codominance.
6. 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 purebreeding parents – one white, one red – if:
   - **a** white is dominant to red
   - **b** the two alleles are partially dominant.
7. **a** Roan coat pattern is known to be codominantly inherited. Use a Punnett square and appropriate symbols to illustrate the cross between:
   - **i** a roan female (mare) and a white male (stallion)
   - **ii** a red stallion and a roan mare.

   b Is it necessary for the gender of the parents to be stated in part a? Explain.
8. Briefly explain:
   - **a** X-linked recessive
   - **b** X-linked dominant
   - **c** hemizygous.

APPLYING

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. Ichthyosis is an inherited condition characterised by scaly skin. The condition affects around 1 in 6000 males but female cases are almost unknown.
    - **a** What form of inheritance is indicated by the differences in ichthyosis occurrence among males and females?
    - **b** Using your answer to part a, from which parent would an affected male inherit the condition?
    - **c** What is the probability that the affected male would pass the scaly skin gene on to his sons? Explain your reasoning.

10.2 Polygenic inheritance

polygenic inheritance
transmission of characteristics controlled by two or more genes

continuous variation
the variation in characteristic caused by two or more genes; the range of different phenotypes is wide with small, smooth gradations between differences

In section 10.1, only cases of inheritance where a trait is controlled by the alleles of *one* gene were discussed. However, sometimes a single trait is controlled by alleles of two or more genes interacting with one another. A characteristic controlled by more than one gene is known as polygenic, and its transmission is called **polygenic inheritance**.

An example of polygenic inheritance in humans is height. Unlike pea plants, which are either tall or short, humans show a large range of heights, though a larger number of people have heights clustered around the mid-height, with fewer at the low and high height extremes. There is a smooth gradation across the range of heights. This can be seen with the large variation in heights when students line up for school photographs each year. In the last 40 years, many genes contributing to height have been identified by association with short stature (previously known as dwarfism) or overgrowth abnormalities. More recently, studies of the human genome have identified many more, with the total now exceeding 200 genes.

Clearly, height inheritance is complex; height is determined by many genes, most of which have just a modest effect. However, some genes have a great influence. For example, short stature can be caused by mutations that abolish the contribution of a single gene, such as the gene encoding the growth hormone, GH.

SYLLABUS LINK
Chapter 11 discusses hormonal control.

The condition of showing a range of phenotypes is called **continuous variation**. Traits that show continuous variation are controlled by two or more genes (**polygenes**). The greater the number of genes, and the greater the influence of environmental factors (e.g. nutrition, standard of medical care), the wider the expected distribution of phenotypes for height.

polygenes
genes for which different alleles have a small additive effect on a phenotype; many polygenes together contribute to continuous variation in phenotype

discontinuous variation
the variation in a characteristic caused by a single gene; shows two or just a few clearly distinct phenotypes

Discontinuous variation occurs when only one gene is involved and results in a small number of phenotypes, as in all the patterns of inheritance discussed in section 10.1.

Many phenotypes in humans are determined polygenically, including eye, skin and hair colour, and height and weight.

Figure 10.2.1 illustrates the large range in colour phenotypes for *Zea mays*, more commonly known as 'corn'. Basically, there are four different colours, three of which are yellow, red and purple. These three colours are produced by yellow pigments called carotenoids, and red and purple anthocyanine pigments. The fourth colour, white, results from lack of any pigments. The production or non-production of the different pigments is controlled by polygenes.

FIGURE 10.2.1 Corn cobs show a large range of colour phenotypes.

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SECTION REVIEW 10.2

REMEMBERING

1 Distinguish between inheritance through multiple alleles and inheritance through polygenes.

UNDERSTANDING

2 Explain why some phenotypes, such as human height, show continuous variation, yet others show discontinuous variation.

APPLYING

3 **a** The capacity to tolerate high salt concentrations varies continuously between different individuals of a population of salmonid fish.

Sketch a curve to approximate the shape a graph of salinity tolerance versus number of fish (in population) may have if the trait is determined by multiple genes.

b Draw a graph to show what you would expect if the trait is controlled by one gene with two alleles: an allele for saline intolerance and another for high tolerance, assuming high tolerance dominates intolerance, and equal proportions of these two alleles occur in the population.

CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1 Briefly define the following patterns of inheritance.

- **a** Autosomal dominance
- **b** Incomplete dominance
- **c** Codominance
- **d** Sex-linked
- **e** Multiple allelic
- **f** Polygenic

CATEGORY QUESTIONS

2 Consider the following types of inheritance.

- **i** Dominance of one allele over another
- **ii** Codominance
- **iii** X-linked
- **iv** Multiple alleles

- **a** Explain, using illustrated examples, how offspring may have a different genotype at a particular locus from either of their parents, for each of i–iv.
- **b** Comment on phenotypes of the offspring compared to those of the parents.

3 Distinguish between:

- **a** sex-linked and X-linked inheritance
- **b** X-linked recessive and X-linked dominant inheritance.

4 Explain how you would recognise phenotypes produced as a result of polygenic inheritance.

5 An individual with heterozygous genotype can be referred to as a 'carrier'. Briefly explain what this term means.

ELABORATION QUESTIONS

6 An autosomal allele R produces red coat colour in foxes and r produces silver-black coat colour.

By using Punnett squares, determine the expected frequencies for genotypes and phenotypes of the following matings.

- **a** Pure red fox and carrier red fox
- **b** Carrier red and silver-black
- **c** Pure red and silver-black

7 Radish shape can be long S^LS^L, round S^RS^R or oval S^LS^R. If long radishes are crossed with oval, and the resulting F_1 are allowed to cross randomly among themselves, determine the expected phenotypic frequencies in the F_2 generation.

8 Is it possible for a human male to be a carrier in X-linked type of inheritance? Explain.

9 Male chickens have two X chromosomes, females have one X and one Y, the opposite sex determination to that in humans. Barred feather pattern is due to a dominant allele, non-barred to a recessive allele of an X chromosome gene.

- **a** Choose suitable symbols to conventionally represent these alleles.
- **b** If a heterozygous barred male is crossed with a barred female, use a Punnett square to determine the expected frequencies of the offspring phenotypes and genders.

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10 Three tabby cat coat phenotypes exist, each purebreeding, and when matings occur between cats with two of these phenotypes, offspring always have one of three coat types. This indicates a case of multiple allelic inheritance. Abyssinian T^a dominates over mackerel T^m, which dominates over blotched T^b. Use this hierarchical dominance relationship and the symbols above to determine the expected phenotypic frequencies in the following purebreeding crosses:

- **a** Abyssinian × mackerel
- **b** mackerel × blotched
- **c** Abyssinian × blotched.

EVIDENCE QUESTIONS

11 One autosomal gene for eye colour has brown and blue alleles. A blue-eyed man whose parents were brown-eyed, married a brown-eyed woman whose father was blue-eyed and mother was brown-eyed. They have a blue-eyed child.

- **a** Is the brown or the blue allele dominant?
- **b** Justify your answer to part a by choosing appropriate symbols to represent the brown and blue alleles, and representing the described inheritance data in a suitable diagram that shows the genotype of each individual.

END-OF-CHAPTER EXAM

End-of-chapter test

1 With respect to an allele and a gene:

- **A** they are two different terms for the same entity.
- **B** an allele is one form of a gene.
- **C** a gene is one form of an allele.
- **D** alleles and genes alternate along a chromosome .

2 In the case of a recessive allele:

- **A** two copies of the allele are required for the phenotype to be observed.
- **B** only one copy of the allele is required for the phenotype to be observed.
- **C** only the recessive phenotype is ever observed if it is present in the genotype.
- **D** if two copies of the allele are present, the offspring will not survive.

3 An alternative term for partial dominance is:

- **A** almost dominant.
- **B** incomplete dominance.
- **C** codominant.
- **D** recessive.

4 An alternative description of X-linked inheritance could be an inheritance pattern in which the gene concerned:

- **A** is on one of the sex chromosomes.
- **B** is on the Y chromosome.
- **C** is on the X chromosome.
- **D** only occurs in the female.

5 Choose the correct word from the following list to match each definition.
heterozygous, homozygous, hemizygous.

- **a** Two copies of the same allele are present at a particular gene locus
- **b** There is only one copy of the gene in diploid organisms
- **c** Two different alleles are present at a particular gene locus

6 Briefly define each of the following types of inheritance patterns.

- **a** Sex-linked
- **b** Multiple alleles
- **c** Polygenic

7 Two black guinea pigs produced 29 black and 9 white offspring. Assuming this is a form of autosomal inheritance, assign appropriate allele symbols and propose the genotypes of the two black parents. Demonstrate the cross in a Punnett square showing genotypes of the offspring.

8 Yellow coat colour in guinea pigs is produced by genotype C^YC^Y, cream colour by C^YC^W and white by C^WC^W.

- **a** For a P cross of yellow and white guinea pigs, state the only genotype possible for the F_1 generation.
- **b** Use a Punnett square to illustrate a cross between these F_1 guinea pigs and determine the F_2 generation phenotypes and proportions of each.

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9 A human X-linked recessive gene (h) prolongs the time taken for blood to clot in a disease called haemophilia. Use Punnett squares and appropriate symbols to predict the expected frequencies of offspring phenotypes in the following crosses.

- **a** Carrier female × normal male
- **b** Haemophiliac female × normal male
- **c** Carrier female × haemophiliac male

10 Following are descriptions of the phenotypical make-up of some populations of species. For each, propose the pattern of inheritance that has produced the phenotypes, and justify your answers.

- **a** Three different phenotypes
- **b** Many different phenotypes in many different proportions
- **c** Phenotype proportions are different in the males of the population compared to the females
- **d** Only two different phenotypes with one in higher proportion to the other

11 BIOTECHNOLOGY

Introduction

Insulin is a protein that controls the amount of sugar in the bloodstream. Type 1 diabetes is a life-threatening disease that occurs when the pancreas fails to produce enough insulin. It is managed with insulin injections. Before 1980, this insulin was extracted from the pancreas glands of cattle, pigs and other farm animals. Although this generally worked well, it sometimes had unwanted side effects, such as stimulating an allergic reaction.

In a significant breakthrough, scientists were able to insert the gene for human insulin into a common bacterium, *Escherichia coli*. Once stimulated, the bacterium produced human insulin which, when purified, could be used to treat millions of diabetics. Today, human insulin continues to be mass-produced by this genetic modification process.

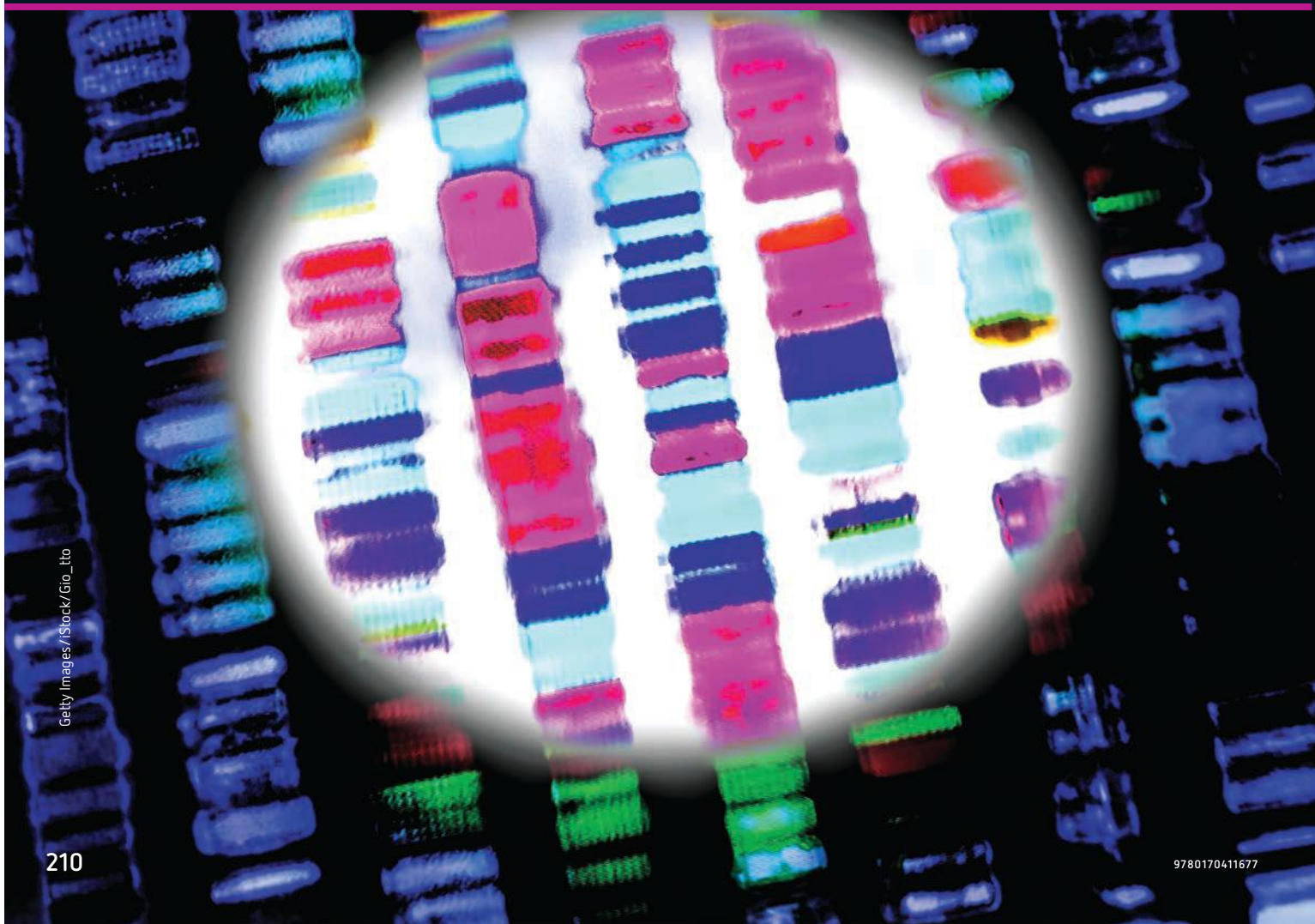
Stimulus questions

How can genes from different species be combined?

What procedures allow genes to be copied, visualised and compared?

How can individuals be identified at the molecular level?

In what way can biotechnology improve our lives?



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11.1 Making recombinant DNA

The term **biotechnology** describes the use of living things to make new products or systems. Early Egyptian and Babylonian civilisations used microorganisms to create 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.

biotechnology
the use of living organisms and biological systems and processes for human benefit

genetically modified organism (GMO)
an organism that has been modified by incorporating into its genome a piece of foreign DNA

Setting the scene: recombinant DNA

The technology that combines DNA from different sources to generate a modified DNA sequence is called **recombinant DNA technology**. One application of this technology is the generation of large numbers of copies of a specific gene, in a process called **gene cloning**. These genes can then be studied or used to genetically engineer animals such as goats and cows to create medically valuable proteins in their milk. Alternatively, cultures of recombinant microorganisms can generate pharmaceuticals such as human growth hormone and insulin.

A common method of producing recombinant DNA uses bacterial plasmids. A plasmid is a circular piece of DNA (Figure 11.1.1) found in bacteria, which reproduces independently of the bacterial chromosome (Figure 11.1.2). Plasmids are used as **vectors** to transport the gene of interest from an unrelated organism into bacterial cells. This technique was made possible after scientists learnt to cut and paste pieces of DNA from different genomes by using enzymes.

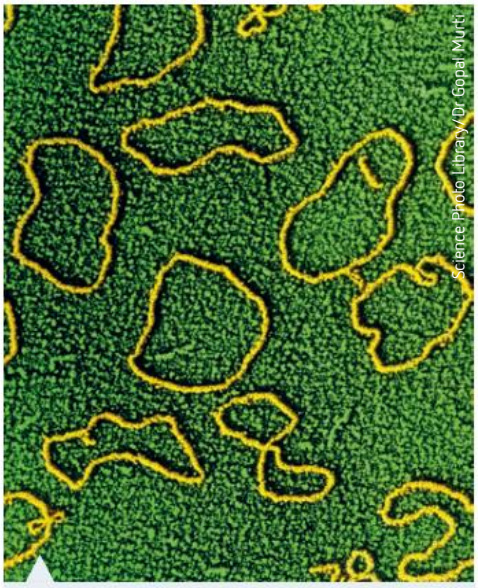

FIGURE 11.1.1 A transmission electron micrograph of bacterial plasmids from *Escherichia coli*.

11.1.1 Introduction to genetically modified organisms

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

gene cloning
the process of using plasmids and bacteria to make numerous identical copies of a gene

11.1.2 Recombinant DNA technology

vector
a vehicle used to transfer DNA sequences from one organism to another; a living organism that transmits pathogens from one host to another

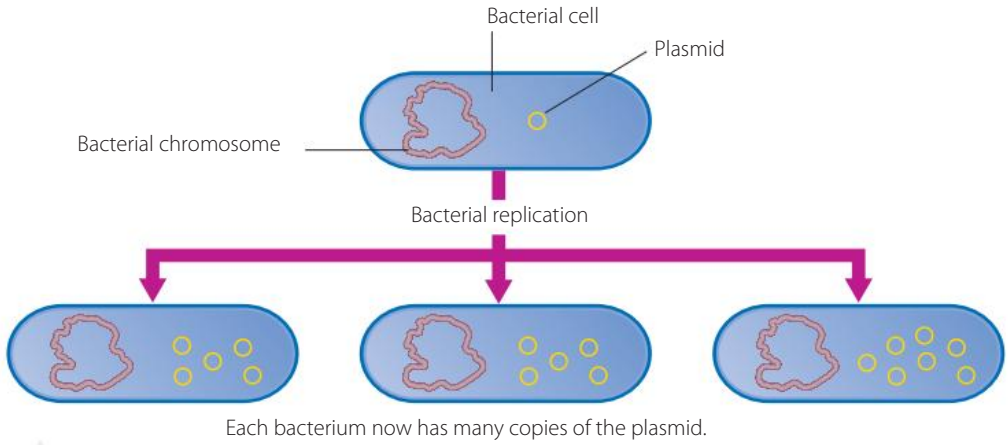

FIGURE 11.1.2 When bacteria replicate, bacterial plasmids reproduce independently of the bacterial chromosome.

Cutting and pasting DNA

DNA ligase
an enzyme used to catalyse the formation of a bond between two pieces of DNA

restriction enzyme
an enzyme that cuts DNA at a specific restriction site

restriction fragment
a short fragment of DNA generated after the cutting of a longer DNA fragment by a restriction enzyme

restriction site
a specific nucleotide sequence (usually 4–8 bp) that is recognised as a cleaving site for a restriction enzyme

sticky end
the end of a DNA fragment that is created after cleavage by a restriction enzyme that cuts DNA at different positions on each strand

blunt end
the end of a DNA fragment that is created after cleavage by a restriction enzyme that cuts DNA at the same position on both strands

All living cells use some version of a DNA-joining enzyme, **DNA ligase**, to join short strands of DNA during replication. The DNA ligase used to make recombinant DNA originated from *E. coli*. It forms a phosphodiester bond between the two fragments of DNA by joining the 3′-hydroxyl end of one nucleotide with the 5′-phosphate end of another nucleotide.

Another essential requirement in genetic engineering is the ability to cut DNA at specific sequences. The cutting tools used are **restriction enzymes**. Restriction enzymes occur naturally in bacteria, where they cut foreign DNA that enters from invading viruses. In preventing invasion by viruses, they are the immune system of bacteria.

Restriction enzymes are named according to the bacterial strain from which they are derived. The first restriction enzyme isolated was named *Eco*RI because it comes from *Escherichia coli* RY13 strain. Restriction enzymes cut DNA into smaller pieces, called **restriction fragments**, at specific base sequences, known as **restriction sites**. These restriction sites of between four and eight nucleotide base pairs (bp) are the reverse of their complementary sequence. As shown in Table 11.1.1, different restriction enzymes have different restriction sites. The cuts made by restriction enzymes may form overhanging steps, called **sticky ends**, which leave some nucleotides exposed (Figure 11.1.3a). Alternatively, they may produce **blunt ends** (Figure 11.1.3b), with no overlapping strands.

TABLE 11.1.1 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′

FIGURE 11.1.3 (**a**) Sticky ends produced by cutting DNA with the restriction enzyme EcoRI. (**b**) Blunt ends produced by cutting DNA with the restriction enzyme *Alu*I.

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Steps in making recombinant DNA

A number of steps are involved in making recombinant DNA (Figure 11.1.4).

1 Plasmids are extracted from bacteria by rupturing the cell membranes and cell walls. Similarly, the DNA of interest is isolated from the donor organism.

2 The same restriction enzyme is used to cut the plasmid DNA and the DNA of the gene to be inserted, to ensure they have complementary sticky ends.

3 The plasmid vectors and the gene of interest are mixed together and their sticky ends pair.

4 DNA ligase is used to join the two segments to form **recombinant plasmids**.

5 The recombinant plasmids are added to a bacterial culture, where they are taken up by some bacteria in a process called **transformation**. When the bacteria reproduce by dividing, the plasmid is also replicated. This generates numerous copies of the recombinant DNA.

recombinant plasmid
a plasmid with foreign DNA inserted into it

transformation
the process by which genetic material is taken up from the surroundings and incorporated into the genome

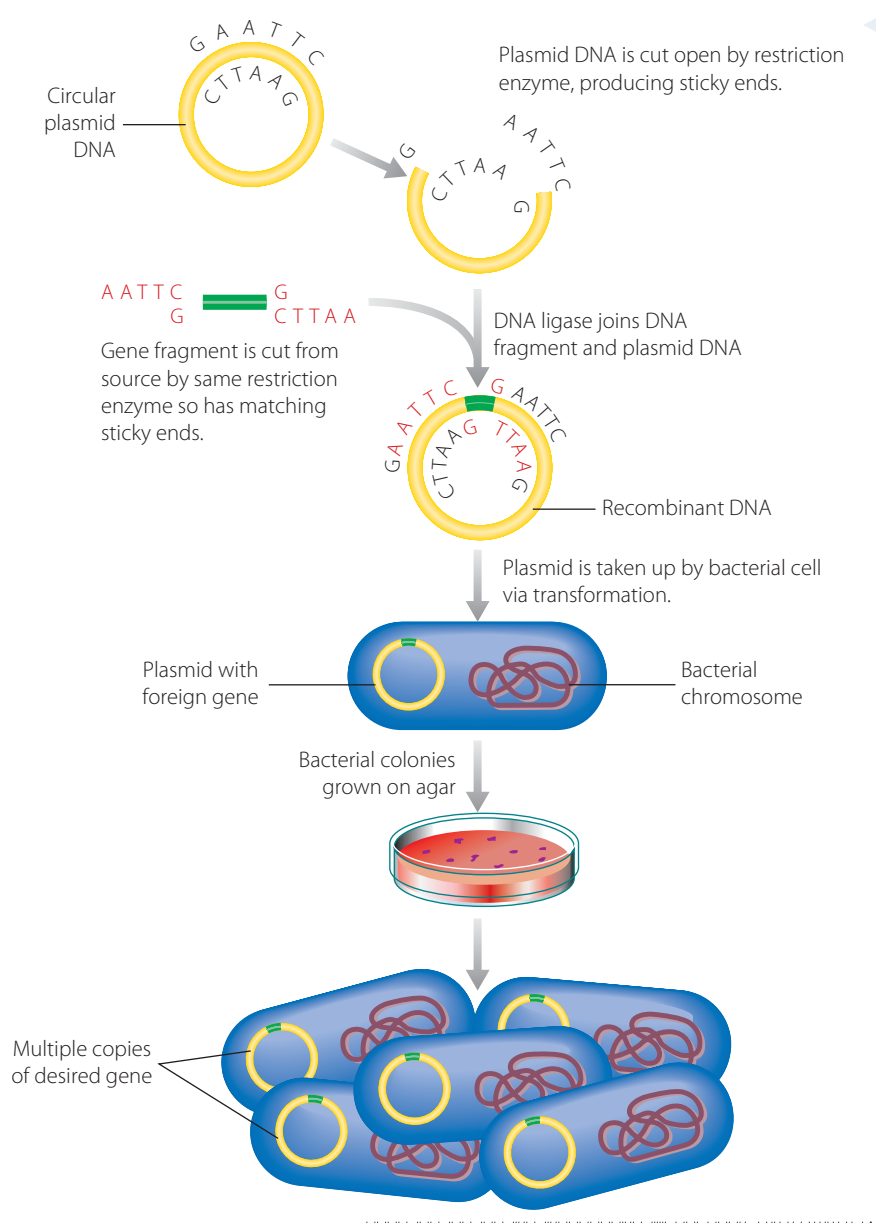

FIGURE 11.1.4 A foreign gene is inserted into plasmid DNA to produce a recombinant plasmid. This is introduced into bacteria, where it can make multiple copies of itself and the foreign gene.

Only a small percentage of the bacteria take up the recombinant plasmids and these transformed bacteria must be isolated from the rest of the colony. If the vector plasmid contains a gene for resistance to an antibiotic such as ampicillin, only transformed bacteria will be able to grow and multiply on a medium supplemented with ampicillin. Non-transformed bacteria will not grow because they are sensitive to the antibiotic (Figure 11.1.5). This process is called antibiotic selection and is an important component of many biotechnology techniques.

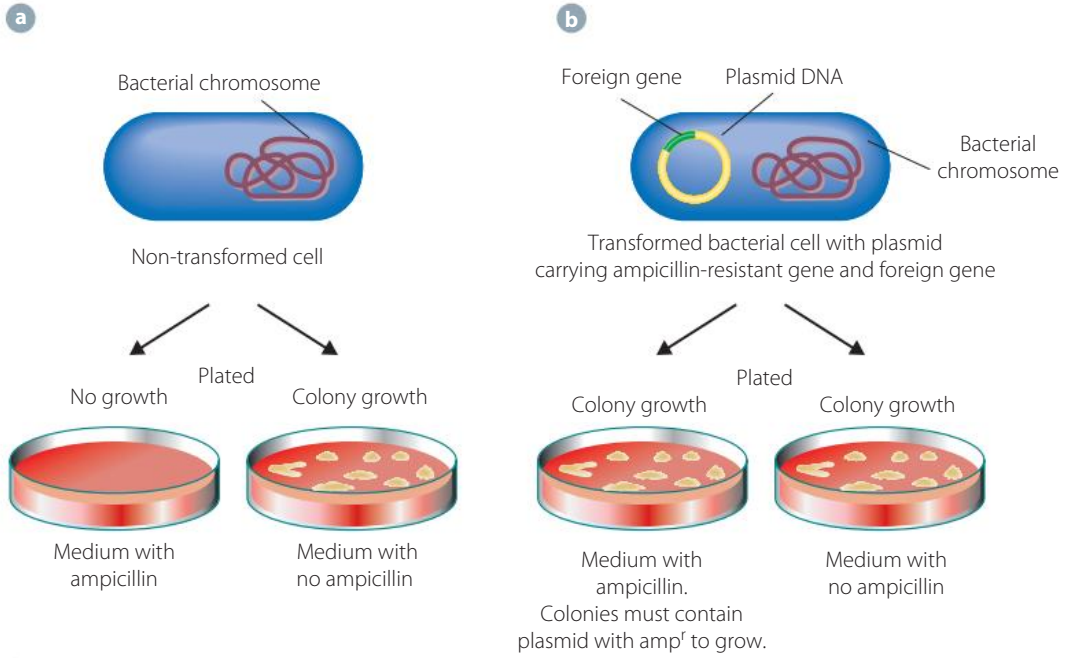

FIGURE 11.1.5 Antibiotic selection of transformed bacteria. (**a**) Non-transformed bacteria cannot grow on medium supplemented with ampicillin, but grow well on normal medium. (**b**) Transformed bacteria can grow equally well on either medium.

Once the bacteria with antibiotic resistance have been grown in culture, the plasmids can be isolated and the gene of interest studied. Alternatively, large quantities of useful proteins can be produced at low cost by culturing the transformed bacteria on an industrial scale.

SECTION REVIEW 11.1

REMEMBERING

1 **a** Define 'plasmid'.
   b Recall its use in biotechnology.
2 Define 'bacterial transformation'.
3 What is meant by gene cloning?
4 Name the two types of restriction enzymes.

UNDERSTANDING

5 When making a recombinant plasmid, clarify why it is important to cut the plasmid and the gene of interest with the same restriction enzyme.
6 Explain how it is that a foreign gene in a transformed bacterium can be used to produce proteins by the bacterial ribosomes.
7 Outline how bacteria transformed with a plasmid can be discriminated from bacteria that have not taken up the plasmid.

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APPLYING

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$^{\downarrow}$CGGA
AGGC$_{\uparrow}$GCCT

b A$^{\downarrow}$GGGCCT
TCCCGG$_{\uparrow}$A

c GC$^{\downarrow}$GGCCGC
CGCCGG$_{\uparrow}$CG

11.2 Polymerase chain reaction and gel electrophoresis

Biotechnology, like other areas of biology, has its own set of specialised tools used for specific purposes. These include techniques for amplifying, separating, viewing and analysing lengths of DNA.

Amplifying DNA: polymerase chain reaction

Usually only a small amount of DNA is available for analysis; for example, at a crime scene. A valuable tool in biotechnology is the **polymerase chain reaction (PCR)**. PCR is used to amplify, or make millions of copies of a specific sequence of DNA.

Today, PCR is an automated process that is carried out by a machine called a thermal cycler, which rapidly raises and lowers the temperature of the reaction. The technique makes use of the enzyme DNA polymerase, after which the method is named. The role of DNA polymerase is to catalyse the formation of new DNA molecules by joining together free nucleotides. One of the most commonly used DNA polymerases, called ***Taq* polymerase**, comes from the bacterium *Thermus aquaticus*, which lives in thermal springs. *Taq* polymerase is resistant to the high temperatures (around 95°C) used in the thermal cycler.

PCR can amplify a specific sequence of DNA because of its use of **primers**. Primers are short sequences (around 20 nucleotides) of single-stranded DNA, complementary to the nucleotide sequences at either end of the DNA section that is to be copied. These provide a starting point from which the DNA polymerase can add new DNA nucleotides. DNA polymerase can only extend a DNA strand from an existing nucleotide; it cannot create a new complementary strand without primers to extend from.

PCR in detail

To carry out PCR, you need:

- the DNA to be copied – called the template
- DNA polymerase
- a buffer solution that contains salts and other chemicals that help the polymerase to function
- a supply of the four nucleotides (i.e. A, T, C, G) from which to build the new DNA molecules
- two primers; the sequence of bases on the primers determines the DNA sequence that is amplified.

polymerase chain reaction (PCR)
a cyclical reaction in which DNA polymerase is used to copy a DNA template, making millions of copies of the same piece of DNA

11.2.1 Polymerase chain reaction

SYLLABUS LINK

Chapter 6 discusses the function of DNA polymerase in DNA replication.

***Taq* polymerase**
DNA polymerase from the bacterium *Thermus aquaticus*, which lives in hot thermal springs and is used in the polymerase chain reaction because it can withstand the high temperatures used in the process

primer
a single-stranded DNA molecule that acts as the start of the amplification process

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

annealing
in the polymerase chain reaction, a process of joining together separate strands of DNA as a result of hydrogen bonds pairing; occurs when the temperature is lowered

The three steps of PCR (Figure 11.2.1) are as follows.

1. **Denaturation**: The double-stranded DNA is heated to 95°C, breaking the hydrogen bonds between the bases, and thus causing the two strands to separate. This is sometimes called the melting stage.
2. **Annealing**: The temperature is reduced to 50–60°C, allowing the primers to anneal (join) to complementary sequences on opposite ends of each strand: either genomic DNA in the first cycle or PCR products generated during the previous cycle. The reduced temperature is necessary to allow base pairing and the formation of hydrogen bonds.
3. Extension: The temperature is raised to 72°C, the optimum temperature for the DNA polymerase used in PCR. Starting from the primers, new DNA strands are synthesised using DNA polymerase and the available nucleotides. At the end of this phase, there are two copies of the double-stranded DNA.

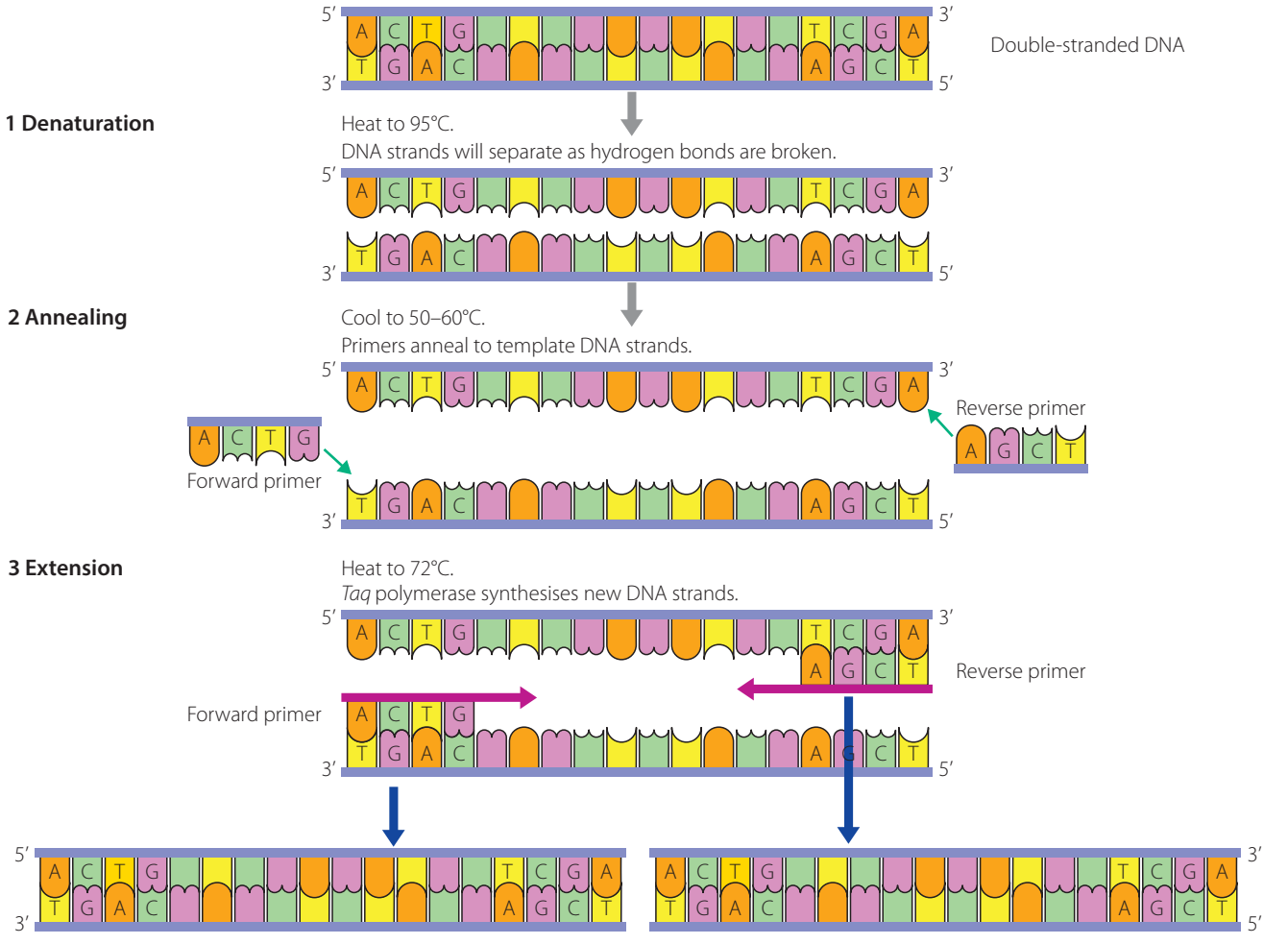

FIGURE 11.2.1 Amplifying DNA by using the polymerase chain reaction. The cycle is repeated many times.

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The processes of denaturation, annealing and extension constitute a single cycle. This cycle is repeated in an automated way (Figure 11.2.2), until there is enough DNA to work with. Each cycle doubles the number of DNA strands; therefore, in just 20 cycles more than one million copies of target DNA will be produced.

FIGURE 11.2.2 Thermal cyclers, in which the PCR is carried out as an automated process

Separating fragments of DNA by 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. Gel electrophoresis is used widely in biotechnology, particularly in forensics, molecular biology, genetics and microbiology. When diagnosing inherited medical disorders, the technique is critical for detecting genes associated with particular illnesses.

Fundamentals of the technique

Samples used for gel electrophoresis include fragments of DNA produced using a variety of restriction enzymes, as well as specific sequences of DNA selected and amplified by PCR. This use of PCR enables information to be recovered from very small or degraded starting samples. DNA has an overall negative charge due to the phosphate groups in its backbone. Electrophoresis makes use of this property to separate DNA fragments within an **agarose gel**. Once the agarose gel has been poured into a flat mould and cooled, DNA samples can be loaded into well-like indentations created as the gel sets (Figure 11.2.3).

gel electrophoresis
a technique that separates DNA fragments according to their size and charge

agarose gel
a gel matrix used for electrophoresis

The gel is placed in a tray filled with buffer solution, and positive and negative electrodes are attached at each end of the gel. When the electric current runs, the fragments move towards the positive electrode at the other end. The gel acts as a sponge through which the DNA strands move while under the influence of the electric current. Smaller fragments, which experience less resistance, migrate through the cross-linked gel matrix faster and further than the larger fragments.

FIGURE 11.2.3 A researcher injecting genetic material from coral into an agarose electrophoresis gel apparatus

DNA itself is not visible in the gel. To view the separated DNA fragments, **ethidium bromide** or another fluorescent DNA-binding dye is added to the agarose gel before it sets. The dye binds to DNA and fluoresces under ultraviolet light, 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.

ethidium bromide
a chemical that binds to double-stranded DNA and fluoresces pink when exposed to ultraviolet light; used to locate DNA in an agarose gel after electrophoresis

The position of bands on an agarose gel depends on the size of DNA fragments in each band; the smaller the fragments, the further they move in a given time. To determine the size of a particular segment of DNA, molecular biologists use **molecular size markers**. Molecular size markers are pieces of DNA of a known number of base pairs. They are used to determine the size of the DNA fragments in different bands by comparing their location along the gel. Figure 11.2.4 shows four markers in the calibration lane: 1700, 1000, 500 and 200 bp, respectively.

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

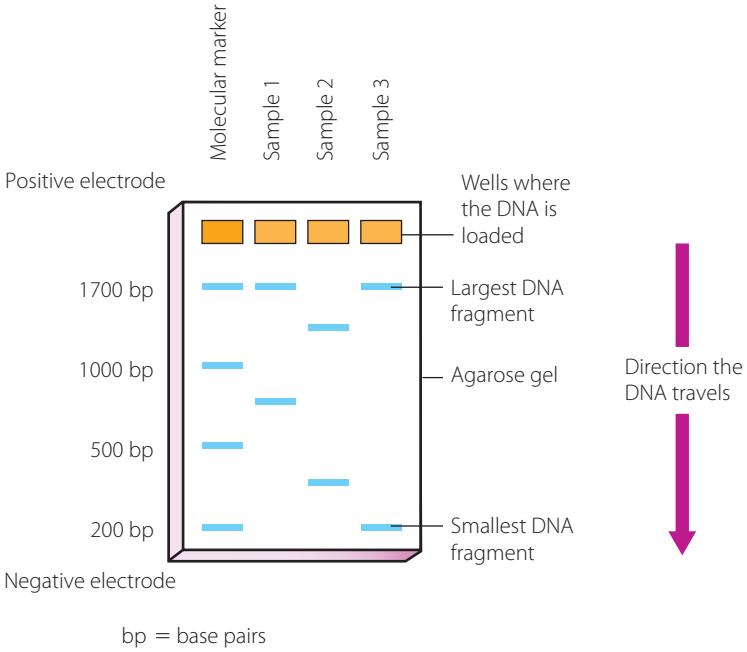

FIGURE 11.2.4 Molecular markers of known size are run alongside samples and allow estimation of the size of the DNA fragments migrating through the gel. (bp = base pairs)

SECTION REVIEW 11.2

REMEMBERING

1. State the components of 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.

UNDERSTANDING

4. Outline the three steps of PCR.
5. Explain the basis on which gel electrophoresis separates segments of DNA.
6. Describe how the size of a particular fragment of DNA, produced by gel electrophoresis can be determined.
7. Agarose gels can be made with different concentrations of agarose. If increasing the concentration of agarose results in tighter gel matrix, what would be the impact on migration speed?

APPLYING

8. If you start with five copies of a DNA region, how many copies will be produced if your sample goes through 10 cycles of PCR?
9. Look carefully at the gel in Figure 11.2.5. Match the size of fragments in lanes 1, 2, 3 and 4 to the sets of measurements presented below.
   - **a** 200, 250 and 900 bp
   - **b** 150, 400 and 600 bp
   - **c** 50, 450 and 650 bp
   - **d** 100, 100 and 450 bp

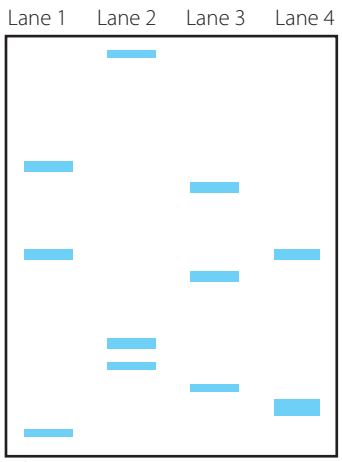

FIGURE 11.2.5 Gel electrophoresis

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11.3 DNA sequencing and DNA profiling

DNA sequencing and DNA profiling are important techniques that can provide data on the structure, function and interactions of a wide array of genes. They have revolutionised areas of study such as forensics and medical diagnosis, and have even shed light on the reproductive strategies of animals.

DNA sequencing to map species genomes

DNA sequencing can identify the exact nucleotide sequence of sections of DNA. This technique has helped us to understand that many genetic diseases result from simple mutations, such as single base substitutions or deletions. DNA sequencing is also used in medicine, agriculture, livestock and plant breeding, forensic identification, paternity testing, metagenomics and determining the origins and early history relationships of present-day humans.

DNA sequencing
a process of establishing the nucleotide sequence of a piece of DNA

The process of DNA sequencing

With the automation of DNA sequencing, large amounts of DNA can be sequenced in a very short time. To visualise them, the four nucleotides (T, A, G and C) are labelled with four different-coloured fluorescent dyes. As electrophoresis proceeds, a laser scans across the bottom of the gel, detecting the different dyes and consequently the base sequence. A computer then automatically analyses the information from the gel to read the base sequence.

A large number of faster and cheaper sequencing technologies are now available for use by biotechnologists. These methods are collectively called 'next generation sequencing' and they use whole genomic DNA as a template, resulting in much greater sequencing efficiency.

11.3.1 Genome map
11.3.2 DNA sequencing

Applications of DNA sequencing for medical diagnosis

In the field of medicine, technicians can sequence genes and sometimes full genomes from patients to determine if they are at risk of genetic diseases. DNA sequencing can be used to identify the particular type of cancer a patient has, enabling the doctor to make better choices for treatments.

The risk of developing cancer can be assessed by DNA sequencing. Female carriers of one or more mutations in breast cancer susceptibility gene 1 (BRCA1) or breast cancer susceptibility gene 2 (BRCA2) are at high risk of developing breast cancer and ovarian cancer, while male carriers are at increased risk of breast and prostate cancer. The proteins encoded by these genes play a role in repairing double-strand breaks in the DNA. A cell that has lost BRCA1 or BRCA2 activity is unable to repair this damage and can rapidly accumulate mutations, which eventually leads to cancer.

A blood test is now available to analyse the 20 000 nucleotides of the BRCA1 and BRCA2 genes. DNA sequencing is performed once the polymerase chain reaction has been used to amplify these genes. Any variation from the normal reference sequence is compared with an international database and assessed to determine if it is a pathogenic mutation or a benign variant. Molecular diagnosis of this type, before the onset of disease, is used to guide preventative treatment and alert family members of potential risks.

Applications of DNA sequencing in metagenomics

Metagenomics, also called environmental genomics, ecogenomics or community genomics, is the study of genetic material recovered directly from environmental samples. This field of study allows scientists to investigate microbial ecology at a much greater scale and level of detail than before.

metagenomics
the study of genetic material recovered directly from environmental samples

Currently, studies of lakes, rivers, soils, effluent and areas under remediation involve sampling followed by laboratory cultivation and identification of microorganisms. Metagenomics studies have revealed that the vast majority of microbial biodiversity has been missed by cultivation-based methods. Only a fraction of the microorganisms present in the sample can be grown successfully in the laboratory.

The methodology of metagenomics is based on PCR-directed DNA sequencing of some or all of the genomes of the microorganisms sampled from the area of interest.

Our understanding of the human gut flora has also been assisted by metagenomics. Patients with irritable bowel syndrome have been shown to exhibit 25% fewer genes and lower bacterial diversity than individuals without irritable bowel syndrome. This observation provides possible avenues for future research because it suggests that changes in the diversity of patients' gut biome may be associated with this condition.

The soils in which plants grow are densely inhabited by communities of microorganisms, with 1 gram of soil containing between 10^9 and 10^{10} microbes. Metagenomic sequencing of soil and water samples from agricultural settings is being used to explore the complex, but very important, interactions between these soil microbes and economically valuable plants.

DNA profiling

DNA profiling
a process that is able to identify natural variations that exist within an individual's genome, by using the polymerase chain reaction and gel electrophoresis

DNA profiling is a process used to compare the base sequence of two or more individuals to determine how similar or different they are. As an individual's DNA would be more similar to their parents' DNA than to that of an unrelated person, DNA profiling can be used to explore relatedness between individuals. It is also used in the fields of forensics to match individuals with biological samples from a crime scene.

The process of DNA profiling

short tandem repeats (STRs)
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

Short tandem repeats (STRs) are sections of non-coding DNA that are repeated many times. For example, the dinucleotide GA is repeated many times to form the short tandem repeat, GAGAGAGA. The repeat is present in all members of the population, but the number of the repeats varies between individuals (Figure 11.3.1). Each individual usually has two alleles for each STR, one from each homologous chromosome. DNA profiling identifies people according to differences in the length of their DNA repeats for a large number of individual STRs. Because every individual has their own unique number of repeats, this forms the basis of identification.

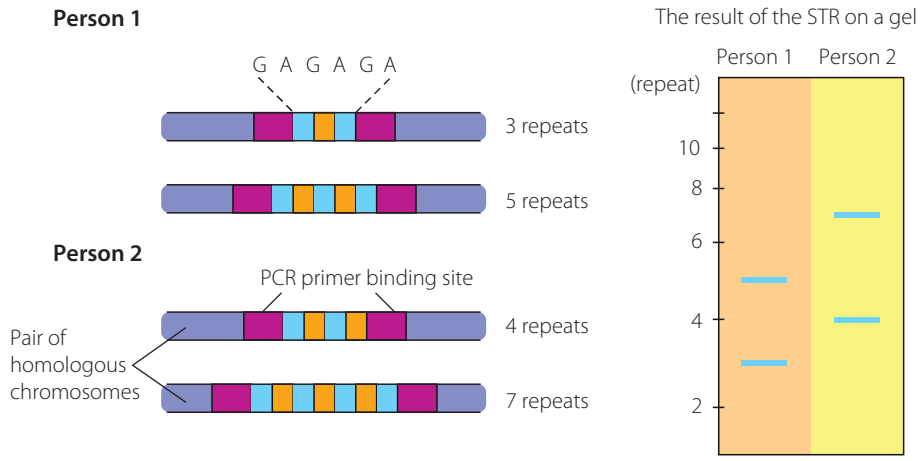

FIGURE 11.3.1 Short tandem repeats vary between individuals.

When constructing a DNA profile, a biotechnologist uses two techniques: PCR and gel electrophoresis. First, the DNA to be profiled is isolated. This DNA can come from any somatic body cell that contains a nucleus, including blood or cheek cells. PCR is used to amplify the DNA of up to

20 different STR regions in the sample. The amplified DNA repeat fragments are then separated by gel electrophoresis, which sorts the fragments according to their lengths. Smaller fragments have fewer repeats and migrate further on the gel than do alleles with more repeats.

Reading a DNA profile

As an individual inherits one homologous chromosome from each parent, their DNA profile will show one band from their mother and one band from their father. For example, in Figure 11.3.1, person 1 would have inherited thee repeats from one parent and five repeats from the other, while person 2 would have inherited four repeats from one and seven repeats from the other parent.

This means that comparing a person's profile with the DNA profiles of other individuals can determine who their parents are.

Non-criminal identification

DNA profiling can answer the question of paternity, maternity and other kinships quickly and accurately. This is valuable when reuniting parents and children separated during war, violence or natural disasters. It has also been used to settle paternity suits and child support litigation and can identify individuals killed in natural disasters, terror attacks and plane crashes.

Forensic applications

Very small quantities of DNA, isolated from blood, hair, skin cells or other biological evidence left at the scene of a crime can be analysed by DNA profiling and used to place a person at that crime scene. Similarly, DNA profiling can and does exonerate innocent people of crimes, sometimes after long periods of time. DNA profiling can also establish the identity of a homicide victim, either from DNA found as evidence or from the body itself.

Identification of plants and animals

Determining the genetic identity of individual animals and plants by DNA profiling has many applications. The technique can be used to measure and document the population structure and levels of genetic variation in a variety of natural populations. In the case of rare and endangered species, this information can better inform conservation management actions.

DNA profiling can be used to establish or confirm pedigrees of valuable animals such as race horses and stud cattle. In food animals, the technique can be used to trace meat to the source animal, while the profiles of plants can be verified to prevent counterfeiting of seeds and stock. Other tests developed directly from DNA profiling methods include non-invasive assays for sex determination.

Surprising reproductive strategies of animals

DNA profiling can be used to study paternity and the mating systems of birds, fish and marine and land mammals. In one such study, researchers found that three out of four superb fairy-wren (*Malurus cyaneus*) chicks are sired by a male other than their social fathers (Figure 11.3.2). This was surprising because females have never been seen copulating with males other than their partners. Concurrent multiple paternity has now been widely documented in virtually all vertebrate groups, including fish, mammals, birds and reptiles.

FIGURE 11.3.2 Paternity testing shows that superb fairy-wrens are actually promiscuous.

SECTION REVIEW 11.3

REMEMBERING

1 Recall the type of DNA sequence used for DNA profiling.

2 **a** Define 'metagenomics'.

b Describe two of its applications.

3 Describe the role of PCR in DNA profiling.

4 State how DNA sequencing can help identify mutations.

UNDERSTANDING

5 In the past, as few as 10 different STR regions were used in DNA profiling. Explain the advantage of using 20 different STRs.

6 Describe the role of the breast cancer susceptibility genes in the development of breast cancer.

7 Describe how short tandem repeats (STRs) are separated in DNA profiling.

APPLYING

8 Explain how DNA profiling can show that a man was not the father of a child.

9 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.

11.4 Current biotechnology techniques: examining data

transgenic organism an organism that has been modified by incorporating a piece of foreign DNA into its genome

Current biotechnology techniques include a range of processes for investigating and modifying DNA, genes and genomes of species. It is possible for scientists to use these techniques to switch genes on or off, remove genes and introduce genes from one species into another. For example, a US company created a genetically modified salmon that grows twice as fast as wild salmon. This was achieved by introducing a gene from a different fish species into the salmon genome to create a genetically modified organism (GMO) or **transgenic organism**.

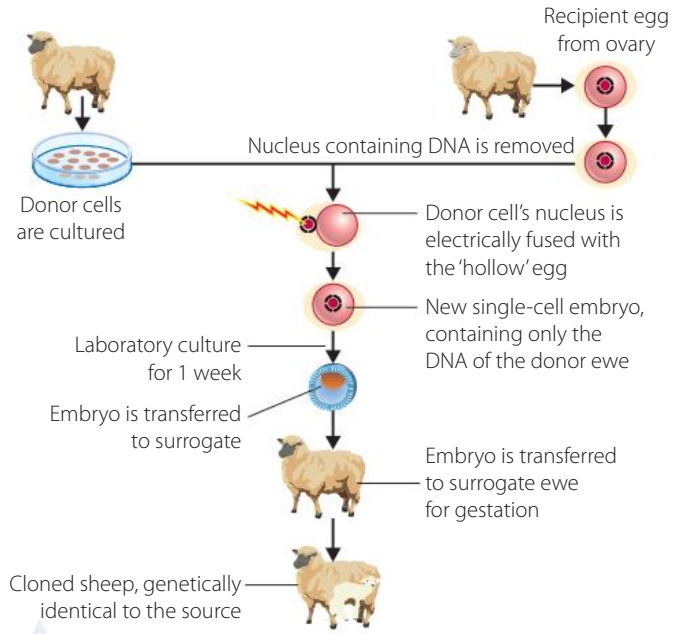

FIGURE 11.4.1 Cloning Dolly the sheep by nuclear transfer

Cloning Dolly the sheep

In 1997, a sheep called Dolly made headlines throughout the world for being the first mammal to be produced by cloning. The production of Dolly showed that genes in the nucleus of a mature differentiated mammalian body cell are still capable of recreating a whole individual.

Dolly was produced by somatic cell nuclear transfer (SCNT). In this technique, the nucleus from an adult body cell is transferred into an unfertilised egg cell. Once it has been stimulated to divide by an electric shock, the modified egg is implanted into a surrogate mother ewe (Figure 11.4.1).

How successful was the cloning of Dolly?

It took 277 attempts and 27 pregnancies to produce one Dolly. A few days after placing the modified eggs into the recipient ewes' oviducts, the researchers collected them to check their progress. Of the 277 put into ewes, only 247 were recovered. That means 11% of the modified eggs were lost in the first few days. Some may have been so difficult to find that they were overlooked; others may have died early and decomposed.

When the 247 recovered modified eggs were examined under the microscope, only 29 were undergoing cell division; 88% of the modified eggs transferred into ewes had not developed. The success rate of 12% for this important step suggests a significant difficulty in stimulating the modified egg to behave like a zygote.

The researchers then placed the remaining 29 developing embryos into 13 ewes, and only one, Dolly's mother, delivered a healthy lamb. One lamb from 277 eggs made by nuclear transfer means the total success rate was only 0.4%.

Dolly was mated and successfully reproduced on a number of occasions. Although her breed of sheep has a life expectancy of 10–12 years, Dolly was euthanised at 6.5 years, after developing lung disease. Scientists did not link her early death to the cloning process because that form of lung cancer, called sheep pulmonary adenomatosis, is a common disease of sheep, especially those kept inside. As well, other individuals in her flock died from the same disease. Extensive health screens carried out at the time failed to identify any abnormality with Dolly that would suggest premature ageing. Dolly had developed a mild arthritis, but this was thought to be because she spent much of her life on a hard floor, not the soft land where sheep normally graze.

SECTION REVIEW 11.4

REMEMBERING

1 State which step in cloning Dolly was the:
   - **a** most successful
   - **b** least successful.

2 Describe the method used to stimulate division in an unfertilised egg cell that has received a new nucleus.

3 Define 'transgenic organism'.

UNDERSTANDING

4 Describe the process of somatic cell nuclear transfer (SCNT).

APPLYING

5 Explain the characteristics of DNA that enables the DNA from one organism to be transcribed in a different organism.

CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1. What two biotechnology processes are used to carry out DNA profiling?
2. What happens during DNA profiling?
3. Which places on a genome are used to distinguish different individuals in DNA profiling?
4. Name two processes associated with making recombinant DNA.

CATEGORY QUESTIONS

5. What three processes are associated with PCR?
6. What equipment is associated with gel electrophoresis?
7. What applications are associated with PCR?

ELABORATION QUESTIONS

8. Predict how the DNA profiles of identical twins would differ from those of non-identical twins.
9. Predict how DNA profiling could be used to guide captive breeding programs of rare and endangered species to increase the genetic variation in the population.

EVIDENCE QUESTIONS

10. Provide evidence that supports your answer to Question 8.
11. By referring back to Question 9, describe the evidence that would demonstrate a successful captive breeding program for a rare and endangered species.

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END-OF-CHAPTER EXAM

End-of-chapter test

1 DNA profiling can be done with a very small sample. This is because:

A there is 2 metres of DNA in every body cell.

B segments of DNA code for specific polypeptide chains.

C the DNA sample can be amplified using recombinant DNA technology.

D the polymerase chain reaction can be used.

2 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 prepared and compared to that of the lost child. Figure 11.5.1 shows four possible mothers and one lost child. Which mother does the child belong to?

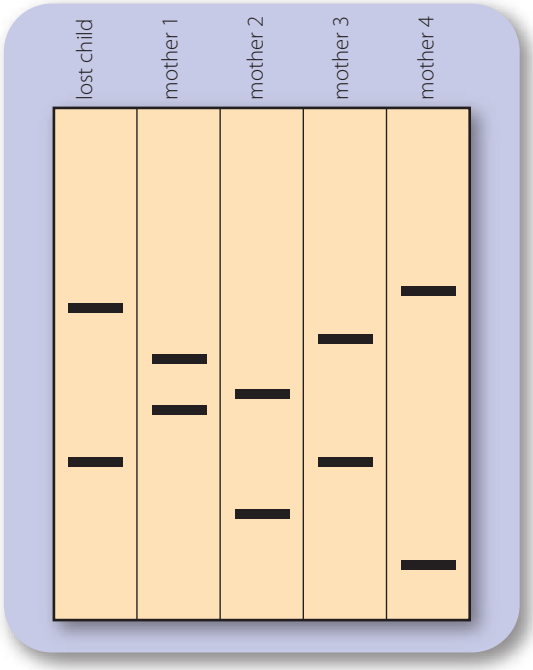

FIGURE 11.5.1 Identifying the possible mother of the 'lost child' by DNA profiling

A Mother 1

B Mother 2

C Mother 3

D Mother 4

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 not an example of:

A recombinant DNA technology.

B gene cloning.

C a transgenic animal.

D a genetically modified organism.

4 Choose the correct statement from the following.

A In electrophoresis, DNA moves from positive to negative, according to fragment size.

B DNA sequencing 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 Metagenomics has confirmed results from other ways of analysing microorganisms in the environment.

5 PCR involves all of the following except:

A increasing the temperature to 72ºC to break bonds between the double stranded DNA.

B extending the DNA using DNA polymerase.

C reducing the temperature to allow annealing of complementary bases.

D cycling between the following temperatures: 95ºC, 55ºC and 72ºC.

6 Which one of the following correctly describes a step in making recombinant bacteria?

A Cutting the DNA with DNA ligase

B Amplifying the DNA using PCR

C Transforming the bacteria with a specific plasmid

D Joining the DNA with a particular restriction enzyme

7 PCR is a useful technique in biotechnology.

a Explain why mammalian DNA polymerase is not used in PCR.

b Name and describe the role of three other requirements needed for PCR.

8 Describe two ways, other than in forensics, in which DNA profiling can be used to benefit society.

9 Dolly the sheep is said to have three mothers: the ewe that donated the nucleus from its 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.

10 The GloFish is a patented fluorescent zebra fish available in pet shops. It was produced in the laboratory from a jellyfish containing a green fluorescent protein. Name the factor that would have to be transferred from the cells of the jellyfish to the cells of the zebra fish to produce a GloFish.

11 Describe the importance of using primers in the polymerase chain reaction.

12 If person X has just witnessed another person being stabbed in the street and saw three men running from the scene, these men would immediately become suspects. DNA profiling can be used to help solve this crime because a knife was left beside the victim. Blood or cells could be taken from the knife, and DNA samples could be taken from the three men seen running from the scene. The victim's DNA as well as person X's DNA were also taken. Figure 11.5.1 shows the results of the DNA profiling.

a Explain why person X's DNA was also sampled.

b Who is the guilty person?

c Explain the reasoning behind your choice.

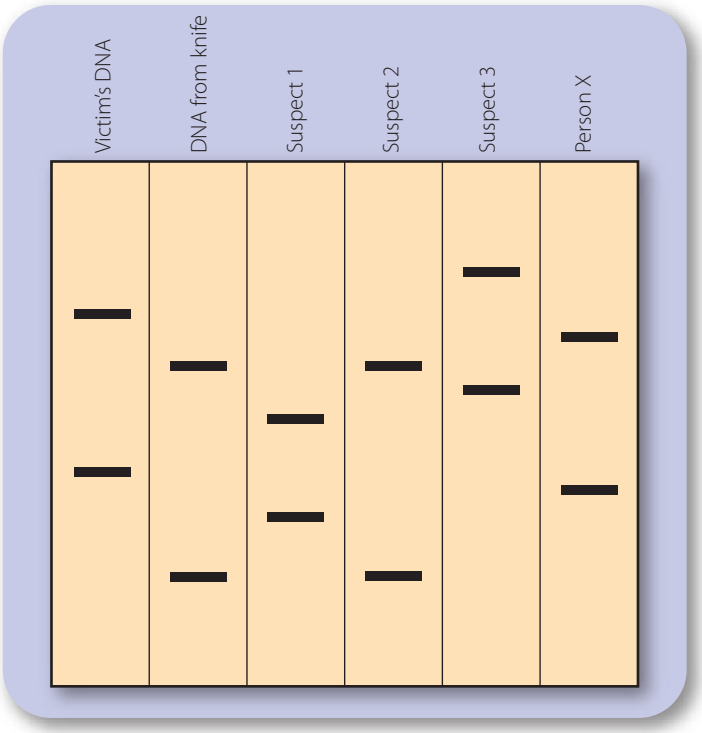

FIGURE 11.5.2 Identifying a criminal by DNA profiling

HEREDITY AND THE CONTINUITY OF LIFE

Alamy Stock Photo/Stocktrek Images, Inc./Roman Garcia Mora

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Topic 2: Continuity of life on Earth

All species that have ever lived are related by descent. The theory of evolution explains the mechanisms that cause species to change over time. The characteristics of a species may change through microevolution in a short time frame. These changes are caused by natural selection – some individuals in a population are better suited to the environment than others. Macroevolution is a result of major evolutionary changes over an extended time scale. As microevolutionary changes accumulate, new species of organisms arise.

SCIENCE AS A HUMAN ENDEAVOUR

Students should be given an opportunity to investigate the use of bioinformatics low-cost gene sequencing and the use of genetically modified organisms in agriculture and pharmaceuticals.

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12 EVOLUTION

Introduction

The diversity of life, estimated to include 8.7 million different species, is one of the most striking aspects of our planet. It is the result of evolution, the scientific explanation for the mechanisms that cause species to change over time. The contemporary view of evolution has come from more than 150 years of research and observations. Recently, emerging technologies such as the molecular analysis of DNA have been used to identify mechanisms that drive evolution and patterns within the process itself. Understanding the time scale of the history of Earth also helps our understanding of the evolution of life on Earth.

Stimulus questions

In what ways have the climate, conditions and structure of Earth changed over its lifetime?

What events have led to the variety of significant changes in life on Earth in the last 3.5 billion years?

How does comparing the DNA of different organisms contribute to our understanding of evolution?

Alamy Stock Photo / Bosiljka Zutich

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12.1 Evolution, microevolution and macroevolution

Research in the fields of genetics and earth sciences, as well as countless newly discovered species of living and fossil organisms, all provide evidence that builds on early ideas about evolution.

A brief history of evolutionary thought

In the late 1600s, Western civilisations believed in 'natural theology' – that every 'kind' of organism has essential, unalterable characteristics. As biological studies grew, naturalists began noticing variability within species. A growing interest in geology and fossils in the rocks (Figure 12.1.1) meant that scientists also began to discover the remains of animals very different in appearance from any living species (Figure 12.1.2). This introduced the idea of extinction, which challenged natural theology and posed the question: 'Where did these giant animals come from, and where did they go?'

12.1.1 Australia's fossil past

12.1.2 Fossils in Riversleigh, Queensland

FIGURE 12.1.1 This immaculately preserved fossil of the extinct fish *Ceratoichthys* is a rare example of a complete fossilised skeleton.

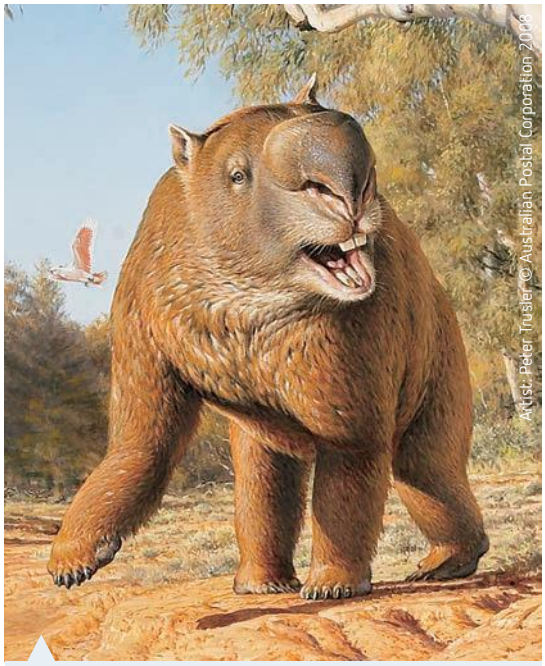

FIGURE 12.1.2 Remains of *Diprotodon optatum*, similar to a giant wombat, were found in Australia in the early 1800s.

Lamarck

Questions such as this prompted naturalist Jean-Baptiste Lamarck, in 1809, to devise what was essentially a theory of evolution. Lamarck suggested that organisms pass on to their offspring characteristics that they acquire during their lifetimes. He proposed that individual efforts during the lifetimes of organisms were the mechanism that drives adaptation. Although now discredited, this was the first, albeit flawed, theory that embraced evolution.

12.1.3 Early concepts of evolution: Jean - Baptiste Lamarck

Wallace and Darwin

In the 1850s, two naturalists, Alfred Russel Wallace and Charles Darwin, were studying and collecting forms of life in different parts of the world. By coincidence, their studies led them to propose a theory of evolution at the same time. Darwin referred to his theory as **descent with modification**, a term highlighting his proposition that all living organisms have descended from shared ancestors.

descent with modification
Darwin's terminology indicating that life today has descended and evolved from common ancestors that were generally different from their modern descendants

Photographer: Rodney Start, Museums Victoria. https://collections.museumvictoria.com.au/specimens/155837/ CC BY (Licensed as Attribution 4.0 International)

FIGURE 12.1.3 This is a reconstructed model of the bird-like dinosaur *Archaeopteryx*, an example of a transitional form between feathered dinosaurs and modern birds.

In 1861, two years after Darwin published his book *On the Origin of Species*, a fossil found in Germany provided evidence for evolution. It was the famous bird/dinosaur fossil *Archaeopteryx* (Figure 12.1.3), a transitional form that records an intermediate state between the organism's ancestral form (dinosaurs) and that of its descendants (birds).

Darwin wrote about his proposed mechanism of evolution in detail. He argued that individuals within a population show a range of variation in their characteristics. Those with characteristics most suited to their environment have an advantage, making them more likely to pass on these favourable alleles to the next generation. In this way, favourable alleles become more common in the next generation and the population becomes better suited to its environment. He called this process **natural selection**.

12.1.4 Charles Darwin
12.1.5 Alfred Wallace

natural selection
the process in which individuals with certain inheritable traits survive and reproduce more successfully than other individuals, leading to evolutionary change in the population

SYLLABUS LINK
Chapter 13 discusses the ideas of natural selection in more detail.

12.1.6 Natural selection

Evolution defined: evolution, microevolution and macroevolution

Scientists now distinguish between evolution, microevolution and macroevolution. The outcome of natural selection is a change in the frequency of various alleles within a population, a process called **microevolution**. Microevolution refers to any change in the gene pool of a population. An example is the acquisition of antibiotic resistance in a population of bacteria, after antibiotic exposure. It is important to note that in microevolution, while small variations in allele frequencies occur within a species or population, the descendant is classified in the same taxonomic group as the ancestor.

The concept of a change in allele frequency is also incorporated in the more general term **evolution**. However, evolution, unlike microevolution, may result in the formation of a new species.

In contrast, **macroevolution** is defined as the major evolutionary changes above the level of species and results in the divergence of taxonomic groups, in which the descendant is in a different taxonomic group from the ancestor. In macroevolution, a single species with adaptations that allow it to exploit new ecological roles eventually gives rise to a new group of organisms comprising many new species. An example of macroevolution is the formation of many new species from a single ancestral dinosaur that occurred over just a few million years, following a mass extinction event.

In essence, macroevolution and microevolution describe fundamentally identical processes on different time scales and macroevolution can be thought of as the compounded effects of microevolution.

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

evolution
the change in the genetic composition of a population during successive generations, which may result in the development of new species

macroevolution
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

SECTION REVIEW 12.1

REMEMBERING

1 Define:
   - **a** evolution
   - **b** microevolution
   - **c** macroevolution.
2 State the major difference between microevolution and macroevolution.
3 Describe Lamarck's contribution to the evolutionary debate.
4 Describe what is meant by descent with modification.

UNDERSTANDING

5 Explain the significance of a fossilised transitional form.
6 Explain why Lamarck is considered to have been both right and wrong about evolution.
7 Why is Darwin said to have explained evolution on two levels?

APPLYING

8 The polar bear is a member of the Ursidae family and has a common ancestor with the black and brown bear. State, with reasons, whether this information demonstrates microevolution or macroevolution.

12.2 An evolutionary timescale

12.2.1 History of life on Earth

Geologic time

Events in human lives are measured in hours, days, years and decades. In contrast, Earth was formed some 4.5 billion (4500 million) years ago and life has existed on Earth for approximately 3.5 billion (3500 million) years. To measure this enormous length of time, new time scales such as **periods**, **eras**, **epochs** and **eons** have been devised. These measurements are known as geologic time and are expressed in millions of years ago (**mya**).

period
a division of geologic time; periods and epochs together make up eras

era
a division of geologic time comprising periods and epochs

epoch
a division of geologic time that is shorter than a period and is marked by one or more significant events

eon
a division of geologic time that can be divided into periods, epochs and ages

mya
millions of years ago or simply millions of years (my), e.g. a fossil dated as being 5 million years old lived 5 mya

Changes to the surface of Earth: plate tectonics

Throughout its existence, Earth has undergone change, and it will continue to change in the future. According to the theory of **plate tectonics**, the seven major plates of Earth's crust float on the fluid mantle that lies over the core of Earth. This results in a process called **continental drift** in which the plates are constantly moving. For example, the plate on which Australia sits is moving north at about 5–7 cm each year.

Although this movement is slow, the immense time scales involved in the history of Earth are sufficient for vast physical changes to occur in Earth's surface. The tearing apart or collision of plates can induce earthquakes and volcanic activity, as well as causing continents to form and break up and mountains to be created and destroyed.

Geological evidence shows that 200 mya, the continental plates formed a single supercontinent known as Pangaea. Since then, Pangaea has broken up and the series of complex movements shown in Figure 12.2.1 (page 234) has resulted in the continents we know today.

plate tectonics
the theory that Earth's crust is divided into several plates that glide over the fluid mantle layer above the core

12.2.2 Plate tectonics

continental drift
the relative movement of Earth's continental landmasses that appear to drift or 'float' over Earth's mantle

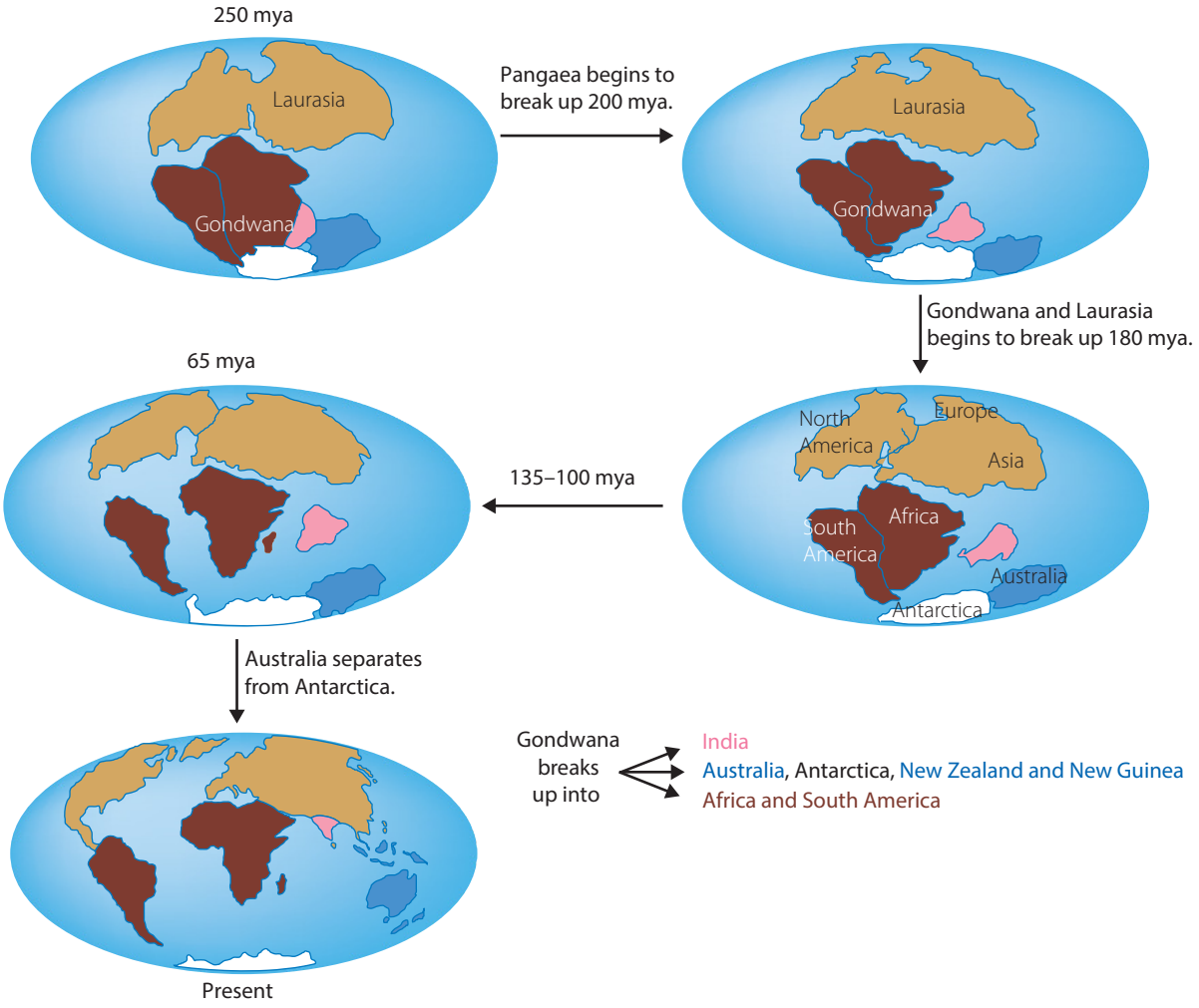

FIGURE 12.2.1 The breaking up of the supercontinent Pangaea to form the present-day continents

Changes in climate

Over the course of its history, Earth's climate has oscillated between hot, humid periods and cold, dry periods. Some of these changes were rapid and dramatic, causing major changes to sea levels and temperatures; others occurred more slowly over time. For much of the time, Earth was 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.

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Timescales of geological and biological events on Earth

Key events that have occurred so far in Earth's timeline are summarised in Table 12.2.1.

TABLE 12.2.1 Geologic timeline and key events

ERAS AND EONS	PERIODS (AND EPOCHS)	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 dominant
	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 dominant 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 dominant, rise of reptilian ancestors of mammals Third mass extinction: 96% of all species eliminated
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 dominant Cycads and conifers Flying reptiles (pterosaurs) *Archaeopteryx* (first dinosaur–bird fossil) dies and fossilises in Bavaria

ERAS AND EONS	PERIODS (AND EPOCHS)	mya	CONTINENTAL ASSOCIATIONS	ANIMALS AND PLANTS
	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
	– 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: formation of Great Barrier Reef begins

Changes in life on Earth

Life has flourished and dwindled throughout various stages of Earth's history, responding to the changes by either adapting or dying out. More than 90% of the organisms that have ever lived on Earth are extinct. Table 12.2.1 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% of species were wiped out.

evolutionary radiation
an increase in taxonomic diversity or morphological disparity

It is no coincidence that dinosaurs flourished after this mass extinction. 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 have evolved from a single ancestral form, have always followed mass extinctions.

SECTION REVIEW 12.2

REMEMBERING

1 Briefly describe changes to Earth caused by plate tectonics and continental drift.

2 Identify evidence in Figure 12.2.1 that supports the idea that Africa and South America were once connected.

UNDERSTANDING

3 Discuss how plate tectonics can cause earthquakes.

4 Discuss why episodes of evolutionary radiation followed mass extinctions.

5 Predict, giving reasons, how warmer and wetter global conditions might affect large land herbivore populations.

APPLYING

6 Refer to Table 12.2.1 to complete the following tasks.

- **a** Identify the era in which life first appeared.
- **b** List all periods in which dinosaurs existed.
- **c** Determine whether *Eucalyptus* species would be expected in Africa. Explain your reasoning.

7 Explain why the extinction of the dinosaurs 65 million years ago enabled mammals and birds to evolve rapidly during the Paleogene period.

12.3 Data interpretation: phylogenetic relationships

12.3.1 What is a phylogenetic relationship?

Phylogenetic relationships are in essence evolutionary relationships. **Phylogeny** seeks to reconstruct the evolutionary history of any given group of organisms.

phylogenetic relationship an evolutionary relationship that exists between a group of species, often expressed as a tree-like diagram

phylogeny evolutionary relationships that exist between species, often expressed as a tree-like diagram

Determining phylogenetic relationships

Phylogenetic relationships can be determined from data derived from a number of sources. Historically, data has come from body structures, comparative anatomy and fossilised structures, such as bones and teeth. More recently, in what is termed 'molecular phylogeny', DNA 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. In other instances, molecular investigations have successfully established phylogeny in groups that to date have eluded resolution and been intensively debated. In yet other situations, analysis of DNA data has revolutionised scientists' understanding of the path of evolution. However, in all cases the comparison of genomic features, such as the degree of similarity of DNA, provides strong evidence for the theory of evolution.

SYLLABUS LINK

Chapter 2 also discusses molecular phylogeny.

Displaying phylogenetic relationships

Phylogenetic relationships are often represented by a phylogenetic tree. A phylogenetic tree shows evolutionary relationships and the points at which lineages diverged. The root of the tree represents the ancestral lineage, and the tips of the branches represent the descendants of that ancestor. 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 – evolutionary events that occurred when populations became so different from other populations of the same species that they could no longer interbreed. This means that each node represents an ancestor common to all the species above that node.

SYLLABUS LINK

Chapter 2 discusses phylogenetic trees in more detail.

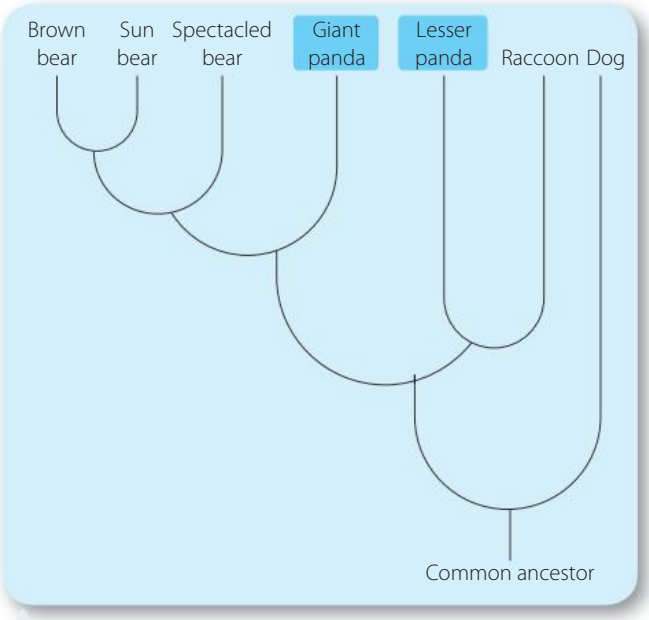

FIGURE 12.3.1 DNA analysis data was used to construct this phylogenetic tree, which shows that the giant pandas of Asia are related to bears and that the lesser pandas of Asia are more closely related to raccoons.

Panda phylogeny

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 phylogenetic tree in Figure 12.3.1. This shows that giant pandas and bears are closely related, but that lesser pandas are more closely related to raccoons than to giant pandas.

Primate phylogeny

A comparison of the degree of similarity of DNA between two species can also be expressed as a percentage. Table 12.3.1 shows a comparison of human DNA with DNA from other primates. This data confirms that our closest relative is the chimpanzee, with less than 3% of its DNA being different from human DNA. As the percentage similarity decreases, so does the closeness of our relationship with that species.

TABLE 12.3.1 Percentage similarity of human and primate DNA

PRIMATE	SIMILARITY WITH HUMAN DNA (%)
Human	100
Chimpanzee	97.6
Gibbon	94.7
Rhesus monkey	91.1
Capuchin	84.2

Comparative genomics

The mapping of the human genome in the Human Genome Project took 13 years and cost billions of dollars. Now, next generation sequencing methods are much more powerful and less expensive and the complete DNA sequences of many species of animals, plants and microorganisms are available for study by researchers.

The comparison of whole or large parts of genome sequences of different species or individuals is known as **comparative genomics**. 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 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 to align and to compare the complete genome sequences of different species. As this produces huge amounts of data to be stored and analysed in a logical and meaningful way, the scale of computation for this analysis is huge.

Only recently has it become possible to undertake these analyses, due to advancements in computer science, engineering and mathematics via bioinformatics. Bioinformatics is the digital storage, retrieval, organisation and analysis of biological (in this case, genomic) data. Bioinformatics has dramatically increased the size, accuracy and scope of data sets, such as those needed for comparative genomics.

Bioinformatics has provided significant advances in our knowledge of the entire genomes of organisms, and in turn this has revealed yet more evidence for the theory of evolution. When contrasting the base-pair composition of genes of seemingly unrelated organisms that code for comparable structures (for example, the code that provides instructions on how to build an eye), the composition of

SYLLABUS LINK
Chapter 8 also discusses the Human Genome Project.

SYLLABUS LINK
Chapter 2 also discusses comparative genomics.

12.3.2 All about the Human Genome Project

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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% similar to those responsible for building the eyes of octopus (Figure 12.3.2). Figure 12.3.3 shows the phylogenetic tree build using the molecular homologies of the eye-building *PAX* gene.

The similarities in sequence, function and abundance of these genes across organisms across a broad spectrum of phyla are yet another example of homology, in this case at a molecular level. This example shows that the identification of molecular homologies through comparative genomics can reveal the shared common ancestry of diverse species. As descendant lineages evolved, the gene was modified in a variety of ways in different lineages, giving rise to a diversity of eye-building genes seen in modern animals.

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Chapter 2 also discusses bioinformatics.

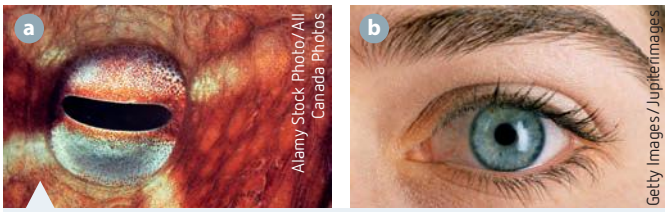

FIGURE 12.3.2 (**a**) Octopus eyes and (**b**) human eyes appear different but *PAX6* genes that code for 'building eyes' are more than 78% similar in the two groups.

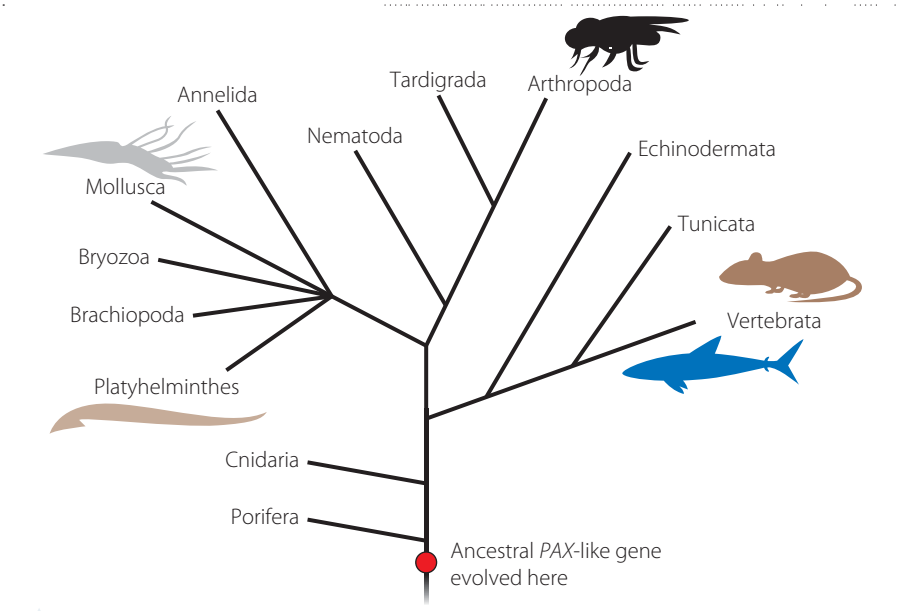

FIGURE 12.3.3 Comparative genomics has found shared 'eye-building' genes across all animals with eyes. From this, we can map a phylogenetic tree.

SECTION REVIEW 12.3

REMEMBERING

1 Recall what it means in terms of time to move from the root to the tips of a phylogenetic tree.
2 What is meant by 'phylogenetic relationships'?
3 Describe what the evolutionary history of a given group of organisms can tell about that group.

UNDERSTANDING

4 Interpret the meaning of a fork on the branch of a phylogenetic tree.
5 Describe bioinformatics and explain why it is important in comparative genomics.
6 Compare and contrast the meanings of molecular phylogeny and molecular homology.

APPLYING

7 Explain the process of comparative genomics and the value of this procedure.
8 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.

CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1. Name the people associated with the early ideas of evolution.
2. Describe one similarity and one difference between the theories of evolution proposed by Darwin and Lamarck.
3. What time period is associated with the publication of Darwin's theory of evolution?

CATEGORY QUESTIONS

4. What steps occur in comparative genomics?
5. What types of changes are associated with evolutionary radiation?
6. What consequences are associated with the category of mass extinction events?

ELABORATION QUESTIONS

7. Predict whether or not plate tectonics will cause changes in the positions of continents over the next 50 million years.
8. Predict the effect that glaciers and sheets of ice covering much of Earth would have on sea levels.
9. Explain the value of comparative genomics to determine evolutionary events.

EVIDENCE QUESTIONS

10. Provide evidence to support your answer to Question 7.
11. Explain the reasoning behind drawing phylogenetic trees.
12. Provide evidence to support your answer to Question 8.

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END-OF-CHAPTER EXAM

End-of-chapter test

1 Darwin's finches are a group of 15 species of birds that have very different beak form and function. The different species are believed 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 divergent evolution.

B microevolution.

C descent with modification.

D evolutionary radiation.

2 When Darwin proposed a mechanism for evolution, he coined the term 'natural selection'. Natural selection would not include the ability of an individual to:

A reproduce.

B find food.

C escape predators.

D adapt to its environment.

3 Which of the following statements best defines evolution?

A Individuals in the two populations having different appearances

B Change in genetic composition of a population from one generation to the next

C The close resemblance between parents and their offspring

D The difference between individuals in terms of survival

4 Choose the incorrect response. Plate tectonics:

A is caused by continental drift.

B commonly causes earthquakes.

C can lead to increased volcanic activity.

D may change the shape of coastlines.

5 Name the science of managing and analysing biological data by using advanced computing techniques.

6 Name the process of contrasting the entire hereditary information of organisms.

7 Explain how organisms originally fossilised on the sea floor came to be located high in the Himalayan mountains.

13 NATURAL SELECTION AND MICROEVOLUTION

Introduction

The peppered moth, *Biston betularia*, is widespread in the UK. Historically, the standard moth form, *typica*, was white, liberally speckled with black. During the 1800s, British cities and the countryside were transformed by the Industrial Revolution. Hundreds of coal-powered factories produced large quantities of airborne soot and other pollutants. By 1895, 95% of moths in industrial regions of the UK, such as Manchester, were black (form *carbonaria*). A well-known lepidopterist (someone who studies moths and butterflies), J.W. Tutt, proposed an evolutionary link between the Industrial Revolution and the moth population. Dark pigmentation was part of the natural, inheritable variation of the *B. betularia* population, but very rare. Blackening of tree trunks by soot presented a new environmental pressure for the moth population. The dark-coloured moths were better able to evade bird predation than the common white speckled form. Over time, black moths came to dominate the population.

Since 1950, when clean air legislation was passed, the situation has reversed. Once again, dark-coloured moths are suffering greater predation on the naturally white tree trunks, and their presence in the population is less common. Both dark and white forms continue to exist in the population.

Stimulus questions

- What are selection pressures and how do they act on gene pools?
- How does natural selection change allele frequencies?
- What effect does gene flow and genetic drift have on microevolutionary change?
- What are the main types of phenotypic selection?

Alamy Stock Photo/Stephanie Jackson - Australian wildlife collection

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13.1 Variation in populations

Individuals in any population express a range of different phenotypes; for example, the peppered moths (Figure 13.1.1). This is because members of a population have variation in genotypes that causes variation in their phenotypes. This genetic variation is **inheritable** – it can be passed to the next generation and under certain circumstances may give an individual an advantage in survival and reproduction compared to the rest of the population. In the case of the peppered moth, a mutation in genotype produced a dark-coloured form in this population. This dark phenotype conferred a survival advantage in the changed environment. On the other hand, the genotypic variation may also give a disadvantage or have no effect at all. Either way, genetic mutation introduces new alleles and, therefore, new variation into populations.

Variations in populations can be very small, but they are the basis of evolution.

inheritable
capable of being passed on to the next generation

13.1.1 Genetic variation

FIGURE 13.1.1 The peppered moth, *Biston betularia*, has (**a**) a white speckled *typica* form and (**b**) a dark *carbonaria* form.

Gene pools

Genes are the means of transmitting phenotypes from one generation to another. Many genes can exist in different forms as alleles, and the characteristics of individuals are determined by the alleles they inherit. Genetic mutations introduce new alleles into populations. It is this variation in alleles carried by different individuals that leads to most of the variation in a population. The total collection of alleles within a population is referred to as a **gene pool** (Figure 13.1.2). 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, so that they belong to the same gene pool.

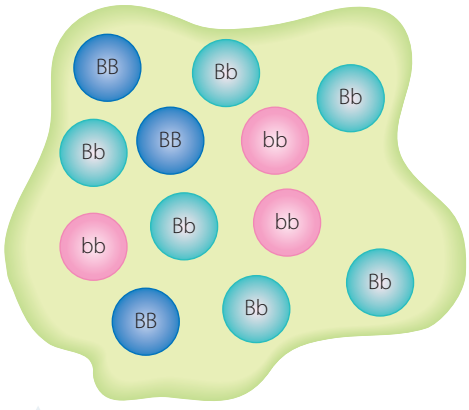

FIGURE 13.1.2 The sum total of all alleles found in a population is called the gene pool.

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

FIGURE 13.1.3 Bearded dragons have genes for a tail, scales and rudimentary teeth, but do not have genes for wings.

The range of variation possible in a population is restricted by the alleles available in its gene pool. For example, bearded dragons do not carry genes for wings or hard-shelled eggs or the enzymes required to synthesise chlorophyll or to digest cellulose. However, all bearded dragons carry genes for a tail, rudimentary teeth, scales and four legs (Figure 13.1.3). The many genes that have only one possible allele in a gene pool, and so do not contribute to any variation, are said to be 'fixed' in the population.

Scientists believe that approximately 80–85% of our 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% that can be drawn upon during evolutionary change.

Allele frequencies

genetic drift
a change in the gene pool of a population as a result of chance; usually occurs in small populations

bottleneck effect
when a catastrophic event or a period of adverse conditions drastically reduces the size of a population

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

Microevolution is a change in the frequency of alleles in a population. For variation to occur in phenotypes, more than one allele of a gene must exist. Phenotypes that vary because of genetic differences are termed 'genetic polymorphisms' (*poly* meaning 'multiple'; *morph* meaning 'form'). The frequency of polymorphic alleles is not usually constant and can be affected by:

- mutation of an allele
- immigration of individuals; that is, movement into the population
- emigration of individuals; that is, movement 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.

Other factors that can change an allele frequency are:

- **genetic drift**
- the **bottleneck effect**
- the **founder effect**.

These factors are discussed in more detail below.

The basis of evolutionary theory is that favourable traits become more common in each successive generation. Those members of a population that survive and reproduce in their habitat carry the traits most suitable for their circumstances, and so, over time, the population becomes more suited, or better adapted, to its habitat. But what happens when the habitat changes? In most cases where there is genetic variation in the population, some members will survive changes and pass on their genes. For example, some members of a locust population may be resistant to local pesticides. Those members would survive seasonal crop spraying and pass on their genes. If no members in the locust population possessed a genotype that resisted pesticides, the local locust population would not survive.

13.1.2 Allele frequencies and gene variation

13.1.3 Allele frequencies in worldwide populations

Such variation in the gene pool is essential. So, where do new alleles come from? The answer is that they generally come from old alleles through mutation. Mutations are rare and mostly produce harmful effects. In a large population, they are barely noticeable. But despite this they are essential to evolution because they are the ultimate source of variation within populations.

SYLLABUS LINK

Chapter 9 discusses the possible causes and effects of mutations on alleles.

Many mutations produce recessive alleles that can be masked by the effects of the original allele, which remains the dominant allele. We each may carry several hundred mutations, most of which will never be noticed, particularly as most of us will have children with partners who are not closely related.

Conversely, recessive alleles are an important source of variation within populations. This was the case with the peppered moth population. Before the Industrial Revolution, the dominant *carbonaria* forms

were extremely rare, and appear to have been maintained mainly through the occurrence of spontaneous mutations. However, during the Industrial Revolution, recessive alleles coding for the white (*typica*) trait were able to survive in the population at a low level. Only the extremely rare homozygous individuals experienced the selective pressure of increased predation. In this case, the population responded quickly to a changing environment. The evolution of sexual reproduction, with the random mixing and assortment of traits from one generation to the next through meiosis, has been very important in producing populations with variation.

The gene pool of a population is subject to many external influences. Gene pools are shaped by the movement of individuals and by environmental events that can sometimes rapidly and considerably change the composition of populations.

SYLLABUS LINK
Chapter 7 discusses how meiosis can cause variations in offspring.

Migration and gene flow

Populations, in a biological sense, are defined by their reproductive and genetic isolation. Few populations are completely isolated from each other and generally some migration takes place both into and out of the population. Gene flow may occur if the migrants breed. 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 13.1.4).

gene flow the transfer of alleles that results from emigration and immigration of individuals between populations

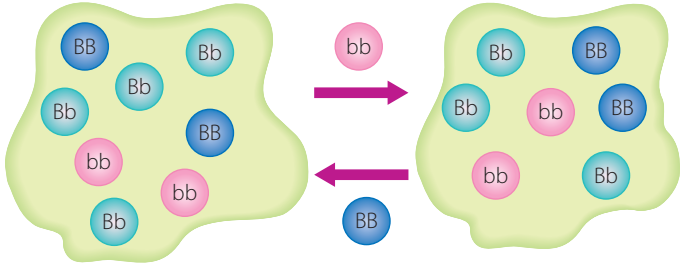

FIGURE 13.1.4 Gene flow is the transfer of alleles that results from emigration and immigration of individuals between populations.

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. They have largely been isolated for the last 50 000 years, except for some gene flow from Asia and New Guinea in the northern regions of Australia. Most Indigenous Australians do not possess the I^B allele of the ABO blood group that results in either the B or AB type blood. The I^B allele occurs at a frequency of up to 10% in European populations and up to 20% in Asian populations. The overall frequency of the I^B allele is increasing within the Indigenous Australian population as a result of migration of people from Asia and Europe into Australia and the genetic flow between these populations.

SYLLABUS LINK
Chapter 10 discusses the inheritance of the ABO blood group.

Genetic drift

The term 'genetic drift' applies generally to random changes in small populations. Every reproductive event involves chance. Each of us inherited half our alleles from our mother and half from our father. Which half of their alleles our respective parents passed on to us was a matter of chance. In large populations, this randomness in inheritance of alleles is not noticeable overall. But if a population is small, there is a chance that some alleles present in a parental group will not be passed on at all. These alleles may be permanently lost from the gene pool. Alleles may be easy to lose, but they are virtually impossible to replace.

Genetic drift can occur in a small population or when a large population is suddenly reduced (Figure 13.1.5, page 246). This can give rise to a bottleneck effect. When a small group of individuals migrates and establishes a population in a new location, the founder effect may occur.

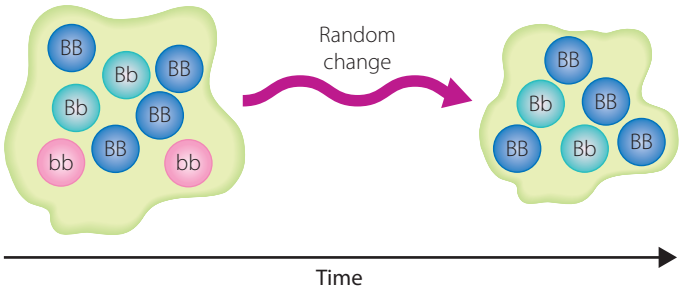

FIGURE 13.1.5 Chance events can cause the allele frequency in a population to change. This is known as genetic drift.

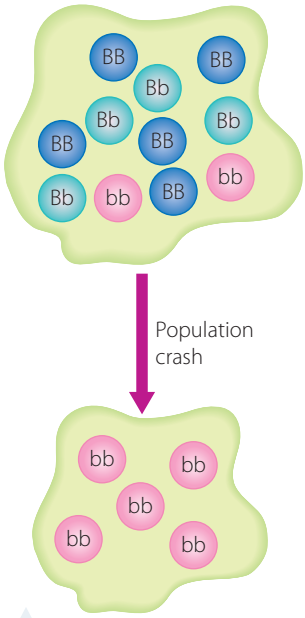

FIGURE 13.1.6 A catastrophic decrease in population size can result in a loss of some alleles from the gene pool. This is the bottleneck effect. Deleterious genes can be preserved by chance.

Bottleneck effect

Sometimes a catastrophic event or a period of adverse conditions drastically reduces the size of a population. In this scenario, certain alleles may be lost through chance. If some portion of the population survives the catastrophe, the original population gene pool cannot be recovered. The expanded population can only carry the alleles that existed in the population that survived the event. Therefore, the gene pool will now carry an indication of the bottleneck that occurred long after the population has recovered (Figure 13.1.6).

Cheetahs are an endangered species that have survived a drastic genetic bottleneck (Figure 13.1.7). Facing a declining population, the surviving parents mated with their own offspring, and the resulting generations were left with strikingly similar alleles. One of these is a mutated allele with negative effects on fertility. Typically, a male cheetah's sperm count is low and 70% of the sperm are abnormal. Other shared alleles result in lowered resistance to disease. Infections that are seldom life-threatening to other cat species can be lethal in cheetahs. There are only around 7000 cheetahs left in the world today.

FIGURE 13.1.7 Cheetahs survived a severe bottleneck that increased the frequency of some mutated alleles.

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Founder effect

The founder effect is a particular example of gene flow. A few individuals who move to a new area and become isolated from a larger population might not carry all the alleles that were present in the original population (Figure 13.1.8). 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.

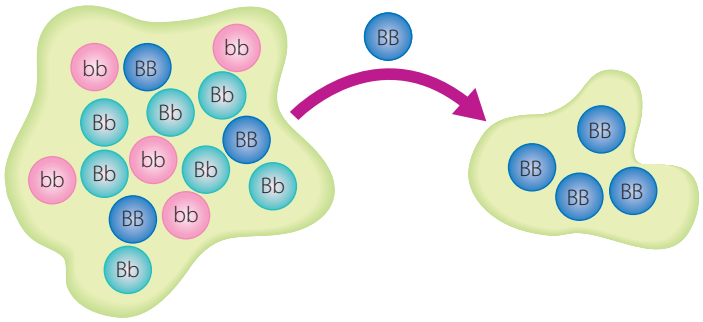

FIGURE 13.1.8 The founder effect occurs when a few individuals carry alleles to a new, isolated area and a new population is formed with different allele frequencies from the original population.

This effect has been observed in human populations when small groups of particular religious or ethnic backgrounds have settled somewhere new and mixed very little with other settlers. Around 200 people originally settled the Amish community of the USA and at least one of the settlers harboured a recessive allele for Ellis–van Creveld syndrome. This syndrome, symptoms of which include dwarfism, polydactyly (extra toes or fingers) (Figure 13.1.9) and sometimes a hole in the heart, has been common among Amish people of this region ever since.

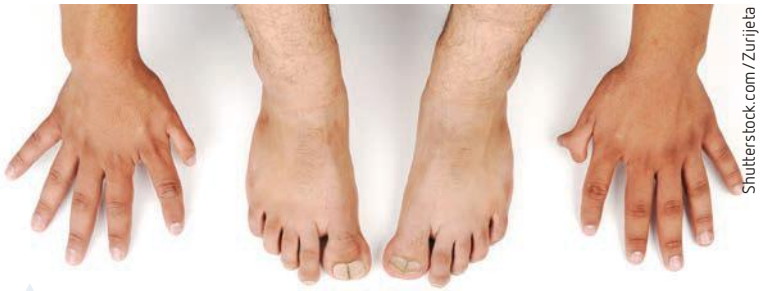

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FIGURE 13.1.9 Polydactyly is one of the symptoms of Ellis–van Creveld syndrome, which occurs at a higher than normal rate in Amish communities as a result of the founder effect.

SECTION REVIEW 13.1

REMEMBERING

1 Define:
   - **a** gene flow
   - **b** genetic drift.

2 Recall the relationship between genotype and phenotype.

UNDERSTANDING

3 Distinguish between a gene and an allele.

4 Outline why variations have to be inheritable for them to be relevant to evolutionary change.

5 Describe the mechanisms that can lead to changes in the gene pool of a population.

6 Outline how gene flow can affect allele frequency.

7 Mutations are rare and, in large populations, barely noticeable. Describe how mutations are still essential to evolutionary change.

ANALYSING

8 Construct a diagram that illustrates two examples of how deleterious recessive traits can survive in a population.

13.2 The process of natural selection

SYLLABUS LINK

Chapter 12 also discusses Darwin and Wallace and the ideas of descent with modification and natural selection.

13.2.1 Charles Darwin

13.2.2 Alfred Russel Wallace

In 1868, two publications were released simultaneously through the Royal Society in London. These papers were by Charles Darwin and Alfred Russel Wallace. Darwin and Wallace outlined their ideas on the evolution of life, what they referred to as 'descent with modification'. This term highlights the important idea that all life that exists today has descended from shared ancestors. Their proposed mechanism by which this happened was the process of natural selection, which has shaped nearly every feature of living things found in the world today. In this way, favourable traits are selected for and inherited, and become more common in subsequent generations.

The principle of natural selection leading to evolutionary change rests on a few propositions.

- Individuals differ from one another; that is, individuals within populations show variation.
- Many of these variations are caused by mutations in alleles and are inheritable.
- In general, more offspring are born than can survive to maturity and reproduce. Because of this, there is a struggle for existence and only some organisms can reproduce.
- Some individuals have traits that make them more suited than other individuals to their environment (**viability**), making them better able to reproduce and pass on their alleles to the next generation (**fecundity**).

viability
capability of living

fecundity
a measure of fertility; the capacity to reproduce

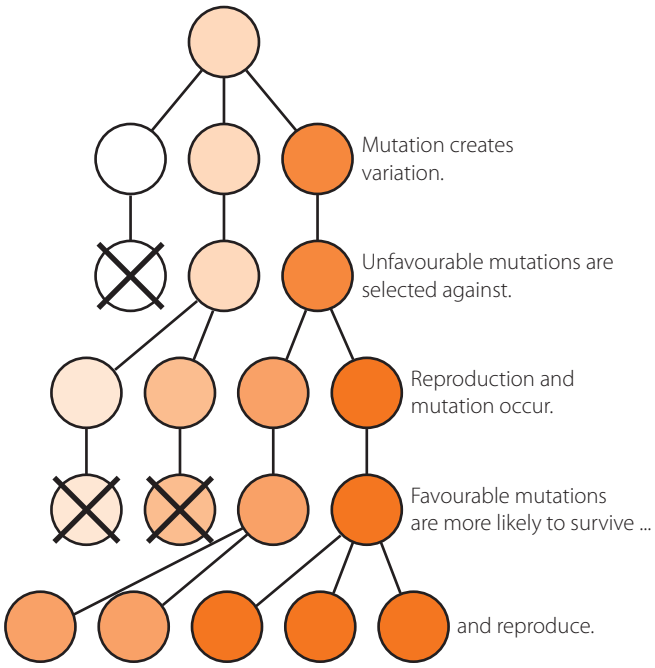

FIGURE 13.2.1 A diagrammatic representation of natural selection. In this example, the darker alleles confer an advantage over lighter alleles.

Natural selection acts on individuals to produce changes in whole populations over time (Figure 13.2.1). Natural selection acts on the phenotypes of individuals, so that some survive and reproduce while others do not. The capacity of an individual to survive and reproduce is sometimes referred to as its **fitness**. Natural selection is the only selection mechanism that can lead to **adaptive evolution**. This means that it is the only mechanism that leads to new populations, and the mechanism that produces species that are better adapted to their environment.

fitness
the capacity of an individual to survive and pass on viable offspring

adaptive evolution
changes in populations of organisms that make that population better adapted to its environment over time

Environmental factors vary from time to time and 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. Natural selection will only act on those phenotypes that are favourable where the individual lives and mates.

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. It is also important to understand that adaptive evolution will only occur if there is variation of heritable traits in a population for natural selection to act on.

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Selection pressures

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.

selection pressure
a factor that influences the survival of an individual within a population

INQUIRING FURTHER

Find and describe a situation that illustrates how each of the examples of selection pressures affects viability and fecundity of members in a population.

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 becoming larger or smaller due to selective pressures in a changing environment. As long as the environment of an organism is not changing, then the selective pressures will act against deleterious alleles that cause a departure from the optimal phenotype. This is referred to as **stabilising selection** (Figure 13.2.2).

stabilising selection
a form of selection that tends to advantage organisms similar to their parents; this usually occurs when the environment is very stable and unchanging and selects against extremes of phenotype

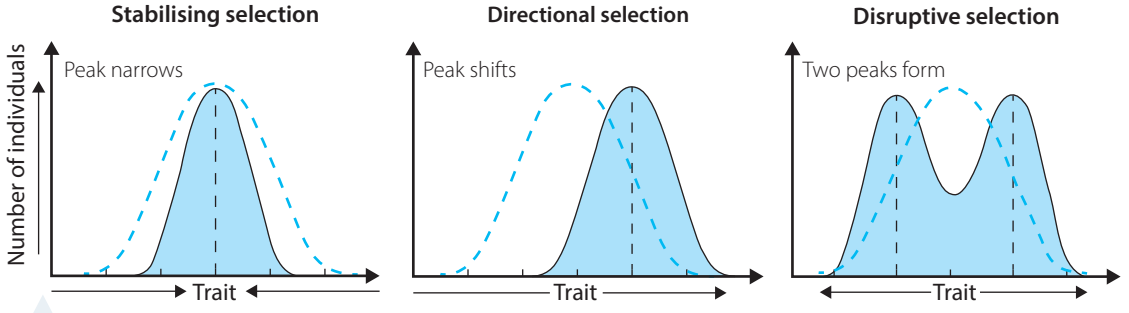

FIGURE 13.2.2 Selection can change the distribution of phenotypes (and therefore genotypes) in three different ways: stabilising selection – trait stabilises; directional selection – trait shifts in one direction; disruptive selection – extreme traits favoured. The original distribution of traits is shown with dotted lines in each graph.

Directional selection leads to a change in a trait over time. Changes in the environment lead to selective pressures favouring organisms with new or more extreme traits.

directional selection
a form of selection that selects against one of two extremes and leads to a change in a trait over time

A third mode of selection, called **disruptive selection**, operates in favour of extremes. For example, a drought may kill off a local species of shrub that produces medium-sized seeds. A species of seed-eating bird may experience disruptive selection in this situation, when there are only large seeds (or only small seeds) available to eat. Birds with intermediate-sized beaks would not be as well adapted for eating either the large or the small seeds and would be selected against.

disruptive selection
a form of selection that operates in favour of extremes and against intermediate forms

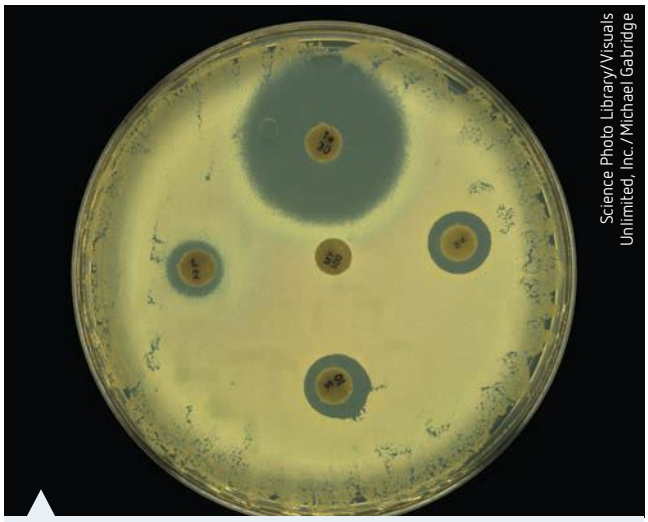

FIGURE 13.2.3 Golden Staph bacteria have increased resistance towards different traditional and newly introduced antibiotics.

Antibiotic resistance – an example of natural selection

In species that live in fast-changing environments, there is continual selection of individuals with favoured characteristics. This can be seen in species with short generation times, such as the bacteria *Staphylococcus aureus*. Usually, *Staphylococcus* infections are treated with a course of antibiotics. Some of these bacteria have a genetic predisposition that makes them resistant to the antibiotic. They survive and go on to reproduce offspring that are also resistant to the antibiotic. A broader range of antibiotics is then introduced to try to treat infections caused by the resistant bacteria. The over-use of antibiotics and failure by patients to complete courses of antibiotics lead to further selection of bacteria in a similar manner, over many generations. As a result, methicillin-resistant *S. aureus* (MRSA), also known as Golden Staph, has arisen. This means the *S. aureus* bacteria from 50 years ago are genetically different from the current Golden Staph bacteria. This change in a strain of organism over a short period of time is an example of microevolution.

INQUIRING FURTHER

Antibiotic resistance in Golden Staph is one example of natural selection. Bacteria are useful when researching and studying natural selection because some colonies of bacteria can produce several generations in one day, allowing researchers to quickly see the effects of various selection factors. There are many other examples of natural selection such as the beak size in the Galapagos finches, insecticide resistance in mosquitoes, virus resistance in rabbits and resistance and aversion to cane toads. Choose an example of natural selection and describe the process, including selection factors and changes in populations.

SCIENCE AS A HUMAN ENDEAVOUR

THE HUMAN STORY: ARE HUMANS STILL EVOLVING?

Population genetics is the study of allele frequencies in populations and how they change over time in response to various evolutionary processes. This area of study is also applied to the human population, which appears to be undergoing a major transition. Historically, there were many isolated small communities with distinct gene pools. Now, increased gene flow is leading to greater heterozygosity, which could have effects on health and survival.

Medical and genetic technologies interfere with the human evolutionary changes that might take place if we lacked these advances. Despite these technological advantages, several recently published research studies have found evidence of continued human evolution. University of Chicago scientists discovered that hundreds of our genes have undergone natural selection over the past 10 000 years. Genes for skin pigmentation, breaking down alcohol, and lactose tolerance are among the relatively recent changes. Findings from the University of Wisconsin reveal shrinking brain size and the University of Quebec discovered an island population with a genetic trend for early reproductive age.

Research natural selection for human genetic trends. Use the information to persuade a class member that humans are still evolving.

population genetics the study of allele frequencies in populations and how they change over time in response to various evolutionary processes

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SECTION REVIEW 13.2

REMEMBERING

1 Outline the meaning and give an example of natural selection.

2 List the four propositions that the principle of natural selection leading to evolutionary change rests on.

UNDERSTANDING

3 Describe how natural selection contributes to evolutionary change.

4 Identify the role of variation in evolutionary change.

APPLYING

5 A population of parrots in tropical Queensland has a darker range of feathers than parrots in other parts of Queensland. These parrots are more suited to the low light intensities of tropical rain forests.

- **a** Describe the type of phenotypic selection this represents and explain your answer.
- **b** Name the other two types of phenotypic selection.

6 Apply the definition of microevolution to discuss whether modern humans are still evolving.

13.3 Mandatory practical

ANALYSING GENOTYPIC AND PHENOTYPIC CHANGES

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 will 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 moths. The moth population has an inherited variation in colour – black, grey and white. Students will represent bird predators of the moth. Selection pressure will be determined by the background. Moths will be in 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) and a natural area with no covering.

Moth colour is determined by a pair of codominant alleles:

Black = C^BC^B

Grey = C^BC^W

White = C^WC^W

Aim

To analyse changes in genotypes in a gene pool when a hypothetical population of moths 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
- three A3 or poster-size pieces of cardboard – 1 black, 1 grey, 1 white
- dice

Procedure

1. The moth population at the beginning of this scenario consists of 10 black, 10 grey and 10 white. Record the genotypes (alleles) in Table 13.3.2. Record the phenotypes in Table 13.3.1. Breeding of a pair of moths results in one offspring. Determine the ratio of expected offspring by creating Punnett squares of the possible matings: black × black, black × grey, grey × grey, grey × white, white × white.
2. To represent random mating, mix the squares together then draw out 15 pairs. Add one offspring for each pair. The population now consists of 45 individuals.

   Use dice to choose the colour of the one offspring produced in each mating. If the expected ratio is 1:1, then numbers 1, 2 and 3 will be one colour and 4, 5, 6 will be the other colour when the dice is rolled. If the ratio is 1:2:1, then number 1 will be the first colour in the ratio, 2 and 3 will be the second colour in the ratio and 4 will be the third colour in the ratio. Roll again if numbers 5 or 6 come up.
3. In the first scenario, snow falls. Place the 45 squares randomly on the white cardboard. A predator (member of 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.
4. Count up the number of squares of each colour remaining and enter the phenotypes in Table 13.3.1 and genotypes in Table 13.3.2 for generation 2. The remaining squares make up the breeding population for the next generation.
5. Repeat steps 2–4, recording the genotypes for five generations.
6. In the second scenario, a coal station is established in the area and a layer of coal dust spreads over the ground. Repeat steps 1–5, using the black cardboard as the background.
7. In the third scenario, snow covers part of the coal dust area. Repeat steps 1–5, using both the white and black cardboard placed next to each other.
8. In the fourth scenario, the ground is not covered with either snow or coal dust. Repeat steps 1–5, using grey cardboard as the background.

Results

Draw up eight tables similar to Table 13.3.1 and Table 13.3.2, showing the phenotypes and genotypes of moths in each generation for the four scenarios.

TABLE 13.3.1 Phenotype frequencies in a moth population

SCENARIO:			
GENERATION	BLACK MOTHS	GREY MOTHS	WHITE MOTHS
1			
2			
3			
4			
5			

TABLE 13.3.2 Genotype frequencies in a moth gene pool

SCENARIO:			
GENERATION	BLACK ALLELES C^B	WHITE ALLELES C^W	TOTAL ALLELES
1			60
2			60
3			60
4			60
5			60

Discussion

1. Describe the genotypic changes in the gene pool for each of the four scenarios by calculating the percentage of C^B and C^W alleles in each generation and commenting on the trend.
2. Identify the alleles that are selected for and the alleles that are selected against in each scenario.
3. Describe the factor in each scenario that has brought about the genotypic changes and why.
4. Explain how a situation could arise where the percentage of C^B and C^W alleles are equal but only one phenotype is selected for. Identify in which scenario this happened.
5. Identify and explain which scenario is typical of:
   - **a** stabilising selection
   - **b** directional selection
   - **c** disruptive selection.
6. Compare the assumptions made in this activity to the real-life situation faced by a moth population.

Conclusion

Explain how different selective pressures affect the survival and reproduction of specific genotypes and phenotypes in a population.

CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1. What factors determine allele frequencies in a gene pool?
2. What is the mechanism that can lead to adaptive evolution?
3. What are environmental selection pressures?
4. What are the three main types of phenotypic selection?

CATEGORY QUESTIONS

5. How can gene pools be rapidly shaped by the movement of individuals?
6. How do selection pressures act on gene pools?
7. What are the types and consequences of gene flow in a population?
8. How is the development of antibiotic resistance an example of natural selection?

ELABORATION QUESTIONS

9. Why does natural selection change allele frequencies?
10. What effect does gene flow and genetic drift have on microevolutionary change?
11. What are the possible events that would lead to a change in a population's phenotype and gene pool allele frequency?

EVIDENCE QUESTIONS

12. What, if any, external sources did you use to support your answers to questions 9–11?
13. Explain your reasoning behind your answers to questions 9–11.
14. What other factors could affect microevolution?
15. How could your answers to questions 9–11 be improved?
16. What further evidence could be used to support your answers to questions 9–11?

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END-OF-CHAPTER EXAM

End-of-chapter test

1 Which of the following is true of gene pools?

A A gene pool includes half of the alleles for a trait within a population.

B New alleles can be introduced into a gene pool via mutations.

C Small gene pools are an advantage in a particular population.

D Alleles within a gene pool are all favourable.

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 migration.

B gene flow.

C genetic drift.

D emigration.

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 produce the largest number of viable offspring and therefore have the greatest influence on the next generation's phenotype.

B can out-run any competitors because they are physically healthy.

C are the most successful fighters, who regularly kill their opponents.

D live the longest due to being fit throughout their lives.

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 greater than 2.5 cm or less than 2.5 cm.

C greater than 2.5 cm.

D less than 2.5 cm.

5 Sockeye salmon migrate to the same river in which they were born to reproduce. In the Bristol Bay in Alaska, USA, it has been found that 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. This change in the salmon's behaviour is an example of:

A diversifying selection.

B disruptive selection.

C balancing selection.

D directional selection.

6 **a** Define 'genetic drift'.

b Draw a diagram to outline genetic drift.

7 Explain why mutations are vital to the process of evolutionary change.

8 Explain why adaptive evolution will only occur if there is variation of heritable traits in a population for natural selection to act on.

9 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 variation changed (Figure 13.4.1).

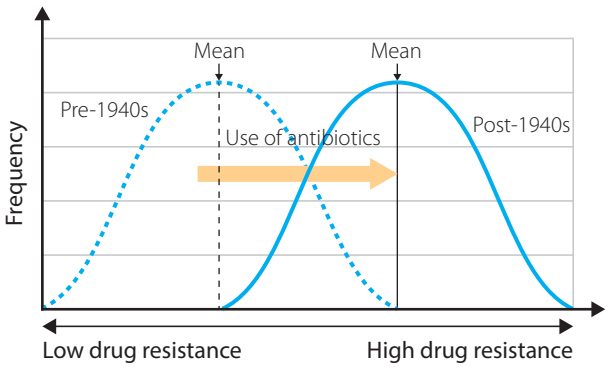

FIGURE 13.4.1 The range of antibiotic resistance in bacterial populations

a Name the selection pressure causing the change in antibiotic resistance.

b Name the type of phenotypic selection this represents.

c Outline the important steps that led to the increase in antibiotic-resistant bacteria after the 1940s.

10 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. These 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.

14 SPECIATION AND MACROEVOLUTION

Introduction

The Galapagos Islands lie 1000 km west of Ecuador (South America) in the Pacific Ocean. When Darwin visited them in 1835 during his famous voyage on the *Beagle*, he realised that these islands were geologically quite young. They were teeming with life but the animals and plants on the islands were of recent origin. Many of these appeared to be related to similar species on the South American mainland but were also clearly different from them. One of the most famous groups of animals on the Galapagos Islands is the giant tortoise (*Chelonoidis nigra*), whose ancestral species, the Chaco tortoise, still exists on the mainland. Darwin wondered how they had got to the islands, and how they had changed into a new species. He hypothesised that the tortoises on the islands originally came from the mainland population but had changed over time to become better suited to the environment of the Galapagos Islands.

Stimulus questions

How do new species form?

What are the patterns of diversification between species?

Why do species become extinct?

Alamy Stock Photo / Bluegreen Pictures / Andy Rouse

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14.1 The diversity of species

speciation
the evolution of one or more new species from an ancestral species

Before Darwin's theory of evolution by natural selection, there was a general belief that species were unchanging, that each species had been put on Earth in its current form and could not change over time. Indeed, our current understanding of evolution tells us that sometimes natural selection produces very little change.

In general, though, 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. 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. How this occurred was a key aspect of Darwin's theory. Darwin wondered how species arose only to disappear and be replaced by new animals and plants. This is known as **speciation**.

14.1.1 Understanding speciation
14.1.2 Speciation

FIGURE 14.1.1 (**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*), found in South America.

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 around 1.2 million species have been identified and classified so far. How new species have evolved in such large numbers is a key part of the theory of evolution.

There are three broad processes that work together in the evolution of this great diversity.

- Natural selection favours phenotypes that make the population better adapted to its environment. Populations change over time as their gene pools accumulate small changes in response to natural selection. This is microevolution.
- 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 the development of a collection of new species, or even genera, families or higher classification groups. This is macroevolution.

14.1.3 Evolution and natural selection
14.1.4 Natural selection
14.1.5 What is macroevolution?

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The emergence of new species through macroevolution results from an accumulation of microevolutionary changes over time.

Evolution is also marked by another powerful process: extinction. Most species that have ever evolved are now extinct. The broad sweep of evolution is exactly how Darwin imagined it: the constant appearance and disappearance of new species over vast periods of time.

A key idea required to make sense of these processes is the concept of what defines a species, and how a species can be identified in the present time and in the fossil record.

14.1.6 Mass extinction

Biological species concept

Species can be identified in a variety of ways. In 1940, Ernst Mayer 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 different species are unable to produce viable offspring under natural conditions. The biological species concept is the most widely used in evolutionary biology. It relates directly to the concept of a species as a genetically isolated group, which can only interbreed within itself. In this sense, a species is represented by a totally isolated gene pool.

SYLLABUS LINK
Chapters 1 and 2 discuss the definition of species.

The biological species model defines a species as a reproductively isolated group of organisms. These can be identified through consistent differences in morphological and physiological traits as well as genetic differences.

Sometimes, the only evidence that a species existed is in the fossil record. When dealing with fossils only, the morphological species concept can be applied. This concept identifies different species by their physical and physiological characteristics but is limited to what can be observed in the fossil record. For example, red and grey kangaroos are two of Australia's most recognised marsupials. Kangaroos are quite well represented in the fossil record. Twenty-five million years ago the ancestors of modern kangaroos lived in rainforests and fed on fruit (Figure 14.1.2). Kangaroos of today are connected to these distant ancestors through an unbroken line of descent.

FIGURE 14.1.2 Ancestral kangaroos 25 mya would have looked quite different from modern kangaroos but are connected with them through an unbroken line of descent.

SYLLABUS LINK
Chapter 2 also discusses the morphological species concept.

SECTION REVIEW 14.1

REMEMBERING

1. Define 'speciation'.
2. List three processes that work together in the evolution of new species.
3. Describe how microevolutionary changes contribute to macroevolution.

UNDERSTANDING

4. Relate the biological species concept to gene pools.
5. Differentiate between the morphological species concept and the biological species concept.

14.2 Mechanisms of isolation

Speciation occurs when a single population becomes two separate populations that are unable to interbreed because of changes that produce physical, biological or behavioural barriers. This separation, termed **reproductive isolation**, results in the gene pool of the original species being divided. Selection pressures act on the separated populations to cause microevolution, which can begin to change them in different ways. Over time, their allele frequencies may become so different that the individuals are no longer able to interbreed even if they are reunited, and we come to regard them as two distinct species.

reproductive isolation
the separation of populations that are unable to interbreed because of changes that produce physical, biological or behavioural barriers

The key to the formation of new species involves reproductive isolation combined with selection pressures, leading to a disruption of the flow of genes. For example, small species such as frogs can cover long distances given enough time. Thus, during a period of hundreds of thousands of years, frogs can 'pond hop' hundreds of kilometres, which means that they can colonise new habitats and exploit new breeding sites. It seems that Victorian frogs colonised Tasmania in this way during the succession of recent ice ages. They did not evolve into new species until the subpopulations became isolated, in this case by the rising sea waters of an interglacial period.

Reproductive isolating mechanisms

14.2.1 Reproductive isolation

Isolating mechanisms separate two groups and prevent them from producing fertile, viable offspring; that is, offspring that survive and can themselves reproduce (Figure 14.2.1). These mechanisms can operate before or after reproduction has occurred. Genetic isolation (where populations become so genetically different that they can no longer interbreed) can occur before or after physical isolation. In either case, once isolation has occurred, the two groups can acquire different phenotypes, as natural selection works on the members of the two groups so they become adapted to their new, different environments.

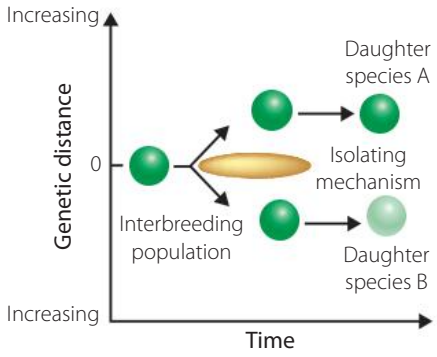

FIGURE 14.2.1 An isolating mechanism can prevent two subgroups of a species from breeding, until they are so genetically diverse that they form two new species. After a period of time they are no longer able to interbreed, even if the populations come back together.

Pre-reproductive isolating mechanisms

Some isolating mechanisms prevent organisms from being able to interact to reproduce. **Pre-reproductive isolating mechanisms** include:

pre-reproductive isolating mechanism
a mechanism that prevents organisms from being able to interact to reproduce

- geographical mechanisms: individuals are separated by geographic features, such as seas, mountains, distance or habitat
- temporal (time) mechanisms: individuals breed during different seasons of the year or times of the day
- behavioural mechanisms: individuals have different courtship patterns
- morphological mechanisms: individuals have different reproductive structures (e.g. genitalia of different size, shape or location), so that mating is physically impossible.

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Post-reproductive isolating mechanisms

If an individual from one species mates with an individual from another species, they will not produce fertile, viable offspring. It could be that the parents' chromosomes cannot line up successfully during meiosis, and no zygotes are formed.

Methods such as this are called **post-reproductive isolating mechanisms**. They do not prevent mating from occurring but they do prevent young from being produced. These genetic post-reproductive isolating mechanisms include:

post-reproductive isolating mechanism a mechanism that prevents fertilisation occurring or an embryo developing into viable offspring if fertilisation does occur

- gamete mortality: the gametes do not survive
- zygote mortality: the zygote forms but does not survive
- hybrid 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.

The hybrid offspring of a male donkey and female horse is a healthy and robust mule. The mule is sterile and unable to produce offspring. This is an example of post-reproductive hybrid sterility. In general, hybrid sterility acts as a post-reproductive isolating mechanism in animals but not in plants. Many plants can interbreed; for example, polyploidy, or multiple sets of chromosomes, is common in eucalypts. Species of coffee plants with 22, 44, 66 and 88 chromosomes are known; this suggests an ancestral plant with a haploid number of 11 and a diploid number of 22.

SECTION REVIEW 14.2

REMEMBERING

1. Name three types of barriers that separate populations, leading to speciation.
2. List and describe four pre-reproductive isolating mechanisms.

UNDERSTANDING

3. Describe how reproductive isolation results in speciation.
4. Distinguish between pre-reproductive isolating mechanisms and post-reproductive isolating mechanisms.

14.3 Modes of speciation

Gene flow between populations can be interrupted between populations of existing species. The populations may be geographically isolated by a physical barrier or sometimes species diverge without any physical or geographic isolation.

14.3.1 Allopatric speciation: the great divide

Allopatric speciation

In **allopatric speciation**, gene flow is disrupted as populations become physically separated through **geographic isolation**. The populations diverge. This may be because of different selection pressures on the two populations, or it may be due to other random processes such as genetic drift. The isolation may happen on a very small scale, such as when a river or stream changes course and divides a population of small animals that cannot cross it. On a somewhat larger scale, deserts may expand, cutting off populations that cannot live under desert conditions.

allopatric speciation the speciation that is due to physical or geographic isolation

geographic isolation when populations of the same species are separated by a type of physical barrier

Environmental disasters such as fire and earthquakes can separate populations. If gene flow between populations is no longer possible after the environmental disaster and environmental conditions exert different selection pressures, populations will diverge, resulting in the formation of new species.

SYLLABUS LINK

Chapter 13 discusses the process of genetic drift.

Allopatric speciation is the most common form of speciation and species can, in terms of evolutionary time scales, be easily and rapidly separated by:

- water, for terrestrial organisms
- land, for aquatic organisms
- mountains
- continental drift
- rising sea levels
- climate change.

The effectiveness of a geographic barrier as an isolating mechanism depends on the size and mobility of the individuals concerned. For example, small organisms may be easily transported across ocean barriers by being carried 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.

Islands display many examples of allopatric speciation. On the Galapagos Islands, 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. The two populations would have been physically isolated by the 1000 km of ocean between the islands and the South American mainland. There would have been no gene flow between the two populations. The islands were totally free from predators. Reduced predation changed the selective pressures acting on this cormorant population. There were still selection pressures for efficient movement underwater but there was less pressure for efficient flight. This led to a reduction in the size of the wings in the cormorant population, to a size and shape that was well suited to movement under water but which no longer allowed flight. This resulted in allopatric speciation (Figure 14.3.1).

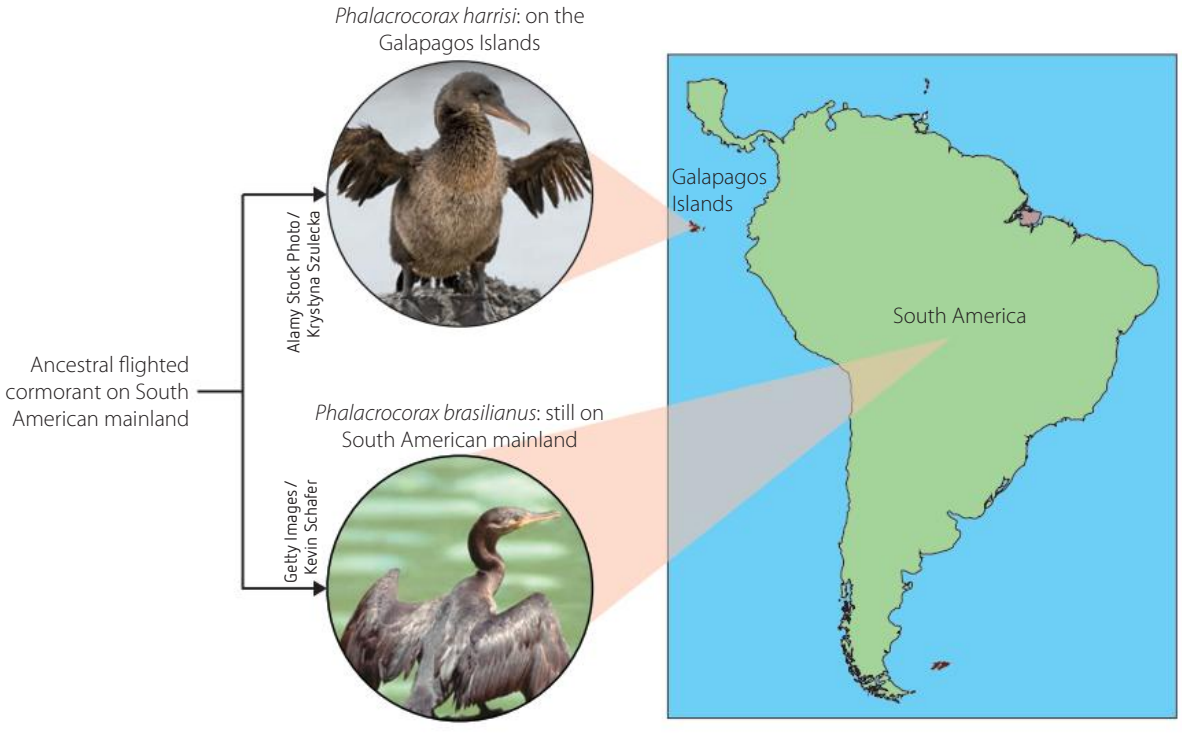

FIGURE 14.3.1 The flightless cormorant (*Phalacrocorax harrisi*) of the Galapagos Islands diverged from flighted cormorants on the mainland through allopatric speciation. *P. harrisi* is most closely related to cormorants such as the Neotropic Cormorant (*P. brasilianus*), which is widespread throughout tropical regions of South and North America.

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, which is now less well adapted to the new predation pressures because it cannot fly. The flightless cormorant is now recognised as an endangered species.

Habitat fragmentation

Since 1750, more than 20% of Australia's forests have been cleared for crops and grazing, with nearly 90% of the vegetation cleared in fertile areas of southeastern Australia. The loss of habitat caused by agriculture as well as other human activities, such as urban development, mining and pollution, has put pressure on populations. **Habitat fragmentation** is the process by which areas of a habitat are lost, resulting in division of a large continuous habitat into smaller, more isolated habitats. Gene flow between populations in the isolated habitats is prevented. Over time, subspecies will develop if selection pressures in the local areas become different. However, the geographic barrier created by habitat fragmentation often results in local populations with reduced fitness and an increased possibility of extinction.

SYLLABUS LINK
Chapter 5 also discusses habitat fragmentation.

wildlife corridor a small area of preserved wilderness designed to connect larger reserves; also known as a habitat or green corridor

Habitats may also become fragmented by natural processes. If a river floods or changes course, it may make it impossible for animals to cross it, isolating populations and preventing gene flow. During drought if the river dries up, leaving isolated bodies of water, aquatic animals will not be able to move between two different bodies of water. This, once again, prevents gene flow.

One possible way to overcome the problems of isolated habitats is to provide linking **wildlife corridors** (also known as habitat or green corridors) of natural landscape (Figure 14.3.2). These allow animals to move to new locations when resources become scarce, to facilitate seasonal migration and to permit interbreeding, ensuring that there is sufficient gene flow between different parts of the isolated populations.

FIGURE 14.3.2 Retaining green corridors assists wildlife conservation by providing a chance for species movement and gene flow.

14.3.2 Wildlife corridors

SCIENCE AS A HUMAN ENDEAVOUR

CONSERVATION RESERVES

One approach to protecting species in danger of extinction is to set up reserves where they are protected from human influence and predation. However, it can be difficult to determine how these should be set up and managed. How large do they need to be and what area do they need to cover? Is a single large reserve required or is it preferable to set up several smaller reserves? What population size of the endangered species is needed to ensure long-term survival?

The yellow-bellied glider, *Petaurus australis*, is a rare, nocturnal marsupial. Its range extends from southwestern Victoria up along the eastern coast of Australia to the rainforests north of Cairns. The federal government initiated a National Recovery Plan, which has identified a number of areas that need to be researched. These include understanding how the fragmentation of habitats currently suitable for the glider affect the dispersal of gliders between these areas, and how this affects the gene flow through the whole population.

Studies have shown that these gliders live in small social groupings occupying individual home ranges of 25–85 hectares. Also, individual habitats need to be able to accommodate at least 150 glider groups to be sustainable in the long-term. From these calculations, it was determined that a forest area of 10 000–35 000 hectares would be required to sustain such groups. This is a large area and could be used as a guide to provide minimum sizes for forest reserves along the east coast of Australia to allow for the conservation of many other plants and animals, which may be able to survive in a range of smaller areas.

Research the Australian Government's Wildlife Corridors Plan that aims to support Australia's biodiversity.

Sympatric speciation

sympatric speciation
the speciation that occurs without physical or geographic isolation

Allopatric speciation seems to be the main mechanism of producing new species throughout evolutionary history. But sometimes species diverge without any obvious physical or geographic isolation. **Sympatric speciation** refers to the evolution of two or more new species from a single population within the same place. How could new species arise without physical separation? Even though members of a population may have contact with each other, sympatric speciation may reduce gene flow. 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). The genetic separation may be due to the various pre-zygotic and post-zygotic processes (post-reproductive isolation).

14.3.3 Sympatric speciation

Sympatric speciation requires a reproductive barrier 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 isolated 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.

FIGURE 14.3.3 *Magicicada* is a periodical cicada endemic to northern USA.

There are not as many clear examples of this type of speciation but a few are quite striking, as in the case of *Magicicada* (Figure 14.3.3). Insects can have very precise timing systems that determine when mating occurs. Periodical cicadas have one of the longest insect life cycles known. In the USA there are several species of periodical cicadas (genus *Magicicada*). Recent studies have focused on several species; some that hatch out every 17 years and others that hatch every 13 years. It is possible that the unusually lengthy life cycle acts to prevent different populations interbreeding and producing offspring through temporal isolation.

Another example of a sympatric isolating mechanism can be seen in frogs (Figure 14.3.4). The mating calls of different frogs may sound very similar to us but to other frogs they sound vastly different. Frogs usually reproduce only with members of their own species so their call acts as a pre-reproductive behavioural isolating mechanism. In many cases, frogs have undergone speciation because their mating calls ensure that they mate only with their own species. If individuals from different species do mate, the tadpoles do not develop (post-reproductive behavioural isolating mechanism).

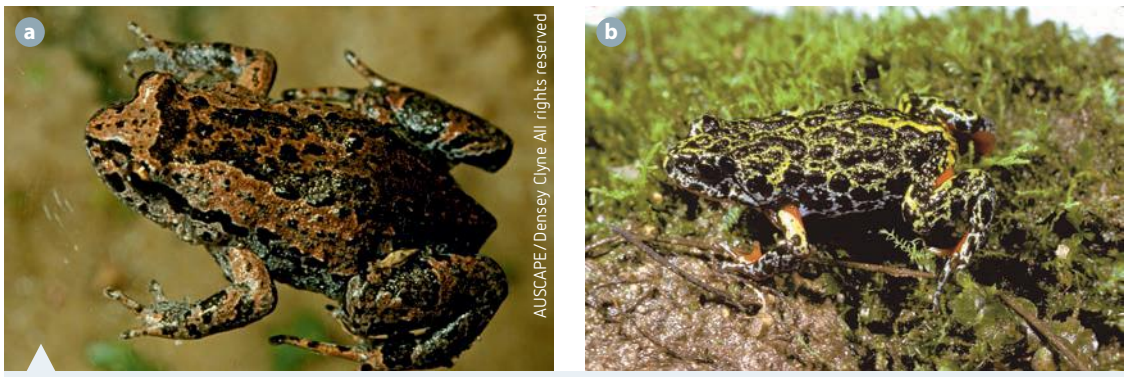

FIGURE 14.3.4 The two frogs (**a**) *Geocrina victoriana* and (**b**) *Pseudophryne semimarmorata* breed in the same habitat at the same time but do not interbreed because their mating calls do not occur at the same time.

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Parapatric speciation

Sometimes gene flow is not prevented within continuous populations yet reproductive isolation arises. In **parapatric speciation**, individuals are more likely to mate with individuals in their geographic area than with individuals in a different area.

parapatric speciation the speciation that occurs when populations are separated by an extreme change in habitat; populations may interbreed in bordering areas

This could arise if members of a population expanded into surrounding areas where conditions favoured a set of alleles different from the main population. Gene flow would still continue in the bordering areas but over time the populations would diverge to become better adapted to the different conditions in different areas of the environment. A hybrid zone would form where the two populations meet. Hybrids are often less fit than either population. In this case, unfit hybrids would reinforce reproductive barriers. The predicted conditions for parapatric speciation include spatial distance and patchy or changed habitats.

14.3.4 Parapatric speciation

Parapatric speciation sometimes happens when mining activities leave waste with high amounts of metals such as lead and zinc in parts of an environment. These metals are absorbed into the soil, preventing most plants from growing. Some grasses, such as *Anthoxanthum odoratum*, can tolerate the metals (Figure 14.3.5). These grasses are often found around mines. Neighbouring plants that do not live in contaminated soil are not tolerant to metals. There is some gene flow between the two types of plants in bordering areas, but metal-tolerant and non-tolerant populations flower at different times. The different flowering times result in a high amount of pre-zygotic genetic isolation.

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FIGURE 14.3.5 *Anthoxanthum odoratum* varieties can tolerate soils polluted with metals.

SECTION REVIEW 14.3

REMEMBERING

1. Explain 'allopatric speciation' and provide an example.
2. List at least four factors that can act as geographic barriers.
3. Outline how forest fragmentation can affect species diversity.

UNDERSTANDING

4. Describe how wildlife corridors are intended to maintain species diversity.
5. Describe the process of sympatric speciation and provide an example.

APPLYING

6. Explain the process of parapatric speciation and provide an example.
7. Allopatric speciation is more common than parapatric speciation. Explain why.

14.4 Patterns of evolution

Diversification of species over time can follow several different patterns. Selection pressures can have different effects on the ways in which species exposed to them evolve. Evolution gives rise to groups of organisms that become very different from each other. Evolution can also give rise to groups of organisms that are similar yet not related. Four patterns of evolution are identified: divergent, convergent, parallel and co-evolution. Three of these are shown in Figure 14.4.1.

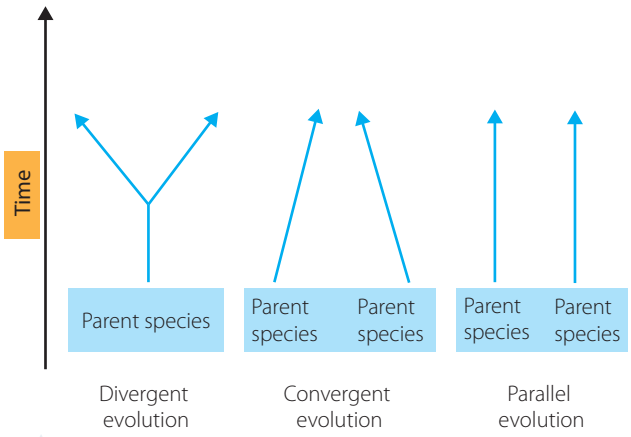

FIGURE 14.4.1 Three types of evolution: divergent, convergent and parallel evolution

Divergent evolution

Divergence is a pattern of evolution where differences between groups of organisms accumulate to a critical point that leads to speciation. This pattern is usually the result of the dispersal of a single species to different environments; that is, groups from the same species become isolated from each other. The isolation stops the gene flow between these separated populations. A group of organisms that has a recent common ancestor may evolve different adaptations in response to a range of environmental pressures.

As members of the population develop adaptations driven by mutations over successive generations, they may diverge enough to become new species.

divergent evolution
a process whereby related species evolve new traits over time, away from the common ancestor, to give rise to new species

For example, koalas (tree-dwelling herbivores), Tasmanian devils (ground-dwelling carnivores) and marsupial moles (dune-burrowing insectivores) are related because they have a common marsupial ancestor (Figure 14.4.2). However, they have quite different feeding structures that adapt them to different diets. These animals are an example of **divergent evolution** because they have evolved into separate species.

FIGURE 14.4.2 (**a**) Koalas, (**b**) Tasmanian devils and (**c**) marsupial moles evolved from a common ancestor. They are examples of the divergent evolution of marsupials.

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Convergent evolution

Convergent evolution is a pattern that occurs when unrelated organisms evolve similar adaptations in response to their environment. An example of convergent evolution is provided by anteaters. Many animals eat ants and 'white ants' or termites, and have developed similar structures even though they are not closely related.

convergent evolution
a process whereby unrelated organisms evolve similar adaptations in response to similar environmental pressures

Modern anteaters include echidnas, which are monotremes; numbats, which are marsupials; and aardvarks and pangolins, which are placentals (Figure 14.4.3). All of these species have an elongated snout that functions as a smelling and digging device; a long, extendible tongue that can extract ants from crevices; and powerful claws that are used for digging up ant and termite nests.

The different species of ant-eating mammals have a common ancestor, but not a recent one; they belong to different orders. They have developed ant-eating habits independently and coincidentally, rather than it being a legacy from their common ancestor. The results of convergent evolution often show up as adaptations of very different types of structures that solve a problem in a similar way.

FIGURE 14.4.3 Ant-eating mammals including: (**a**) echidnas (monotremes), (**b**) numbats (marsupials) and (**c**) pangolins (placentals) show convergent evolution with ant-eating structures.

Parallel evolution

Parallel evolution describes the pattern where species in the same environment evolve independently of each other and develop similar characteristics. The same degree of similarity is maintained. 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 14.4.4).

parallel evolution
a process whereby unrelated organisms evolve similar adaptations in response to the same environmental pressures

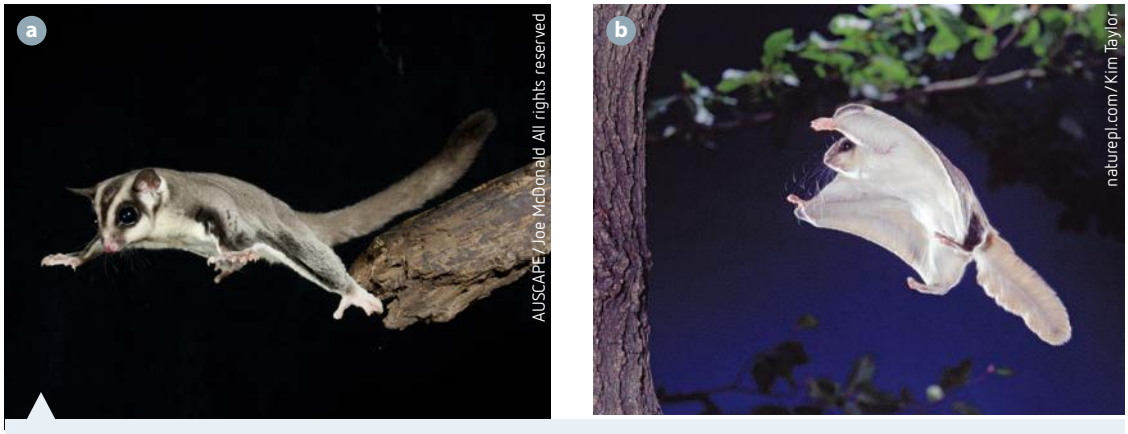

FIGURE 14.4.4 Parallel evolution of the (**a**) Australian sugar glider (*Petaurus breviceps*) and (**b**) North American flying squirrel (*Glaucomys volans*). Both have a membrane along either flank, attached to the forelegs and hind legs, allowing them to glide through the air.

Co-evolution

co-evolution
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 **co-evolution**.

In a predator–prey relationship, the activities of both predator and prey apply selection pressures. For example, if prey species become faster, this may select against individuals in the predatory species who are unable to move fast enough to capture the prey. In this case, only fast predatory individuals or those with adaptations allowing them to capture prey using other means will pass their genes to the next generation (Figure 14.4.5).

FIGURE 14.4.5 Predators have evolved hunting abilities to kill their prey and prey have evolved ways to protect themselves from predators.

SECTION REVIEW 14.4

REMEMBERING

1 Describe the four patterns of evolution: divergent, convergent, parallel and co-evolution.

UNDERSTANDING

2 During his famous voyage to the Galapagos Islands, Charles Darwin noticed different species of giant tortoises on different islands. The ancestral species is found on mainland Ecuador. Suggest the pattern of evolution involved and describe how new species of giant tortoises formed.

APPLYING

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 co-evolution.

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14.5 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 – the ultimate inability to reproduce – 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 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.

SYLLABUS LINK
Chapter 12 discusses mass extinctions.

All the species existing at a particular time are direct descendants of ancestral species and it will often be the case that an ancestral species is no longer present. In a sense, the ancestral species did not become extinct but became transformed into a different species over a long period of time. However, in other instances, species and entire groups of organisms have become extinct without leaving descendants. The high rate of current extinctions, caused by human activities, are real extinctions because they do not involve the transformation of existing species into new ones.

Low genetic diversity

Certain species are more prone to extinction than others. Rapid extinction events can lead to the loss of larger organisms rather than smaller ones. Large populations can be more resilient than small populations, probably because the population has a more diverse gene pool. That is, it holds a greater reserve of different alleles to draw on as the pressures from natural selection change.

SYLLABUS LINK
Chapter 13 describes the mechanism and consequences of a population bottleneck.

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 present, the species will become extinct.

SYLLABUS LINK
Chapter 5 explores the impact of reduced biodiversity on ecosystems.

The genetic diversity of the Tasmanian devil (*Sarcophilus harrisii*) (Figure 14.5.1) was drastically reduced when population numbers fell during an ice age about 20 000 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% 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.

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FIGURE 14.5.1 The Tasmanian devil (*Sarcophilus harrisii*) is facing extinction because of its low genetic diversity and new selection pressure.

INQUIRING FURTHER

Find out what is being done to save the Tasmanian devil (*Sarcophilus harrisii*) from extinction. Discuss whether these measures would have been effective in saving the extinct Tasmanian tiger (*Thylacinus cynocephalus*).

SECTION REVIEW 14.5

REMEMBERING

1 Explain how a population bottleneck can cause a species to become extinct.

UNDERSTANDING

2 Explain why small populations are more likely than larger populations to become extinct.

APPLYING

3 Explain the effect of a changed selection pressure on natural selection in a small population with low genetic diversity and inbreeding.

14.6 Mandatory practical

SPECIATION AND CONSERVATION

Introduction

The eastern barred bandicoot (*Perameles gunnii*) (Figure 14.6.1) was once common over a wide area of southwestern Victoria. Numbers were reduced dramatically in the 1900s and now the bandicoot is isolated to a small area, numbering less than 200. This resulted from a change in environmental conditions (e.g. clearing of woodlands, growing exotic pasture grasses, grazing by domestic stock, and introduction of rabbits and foxes), which severely reduced its available habitat in Victoria. However, there are still healthy numbers of the eastern barred bandicoot throughout most of Tasmania.

FIGURE 14.6.1 The eastern barred bandicoot (*Perameles gunnii*)

Conservation plans for the eastern barred bandicoot depend heavily on how populations are classified. A subspecies is a level of classification below species, referring to races of a species that are fairly permanently geographically isolated from each other and may in future diverge to become two different species. Because of the relatively healthy bandicoot populations in Tasmania, the bandicoot is not regarded as an endangered species. If the Victorian population were identified as a different species, or subspecies, then it could be recognised independently for conservation purposes.

A number of studies were conducted on the Victorian and Tasmanian populations in an attempt to protect the Victorian population. The bandicoots were trapped, small blood samples were taken and the animals were released immediately 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 found to be about 23%, and for those in Tasmania was 21.8% (Figure 14.6.2). The average percentage difference between the Hamilton and Tasmanian populations was 44.8%.

Further testing was done by mitochondrial DNA (MtDNA) restriction fragment length polymorphism (RFLP) analysis. This revealed a 0% nucleotide variation within the Tasmanian populations and a 1.1–1.7% variation for the Victorian populations. The percentage variation between the Victorian and Tasmanian populations was 2.3%. Variation of 2% is the average difference between subspecies of mammals.

There is no doubt that the two populations have diverged to some extent due to 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.

The biological species concept defines a species as a reproductive community of populations that occupies a specific niche in nature. The identification of species often uses data from genetic analysis. DNA fingerprinting is predominantly used to determine which groups are related (i.e. share a gene pool) and which are not. A species defined according to this concept would be the smallest group of organisms that share a common ancestor not shared by any other organism.

SYLLABUS LINK
Chapter 11 describes processes and applications of genetic technology.

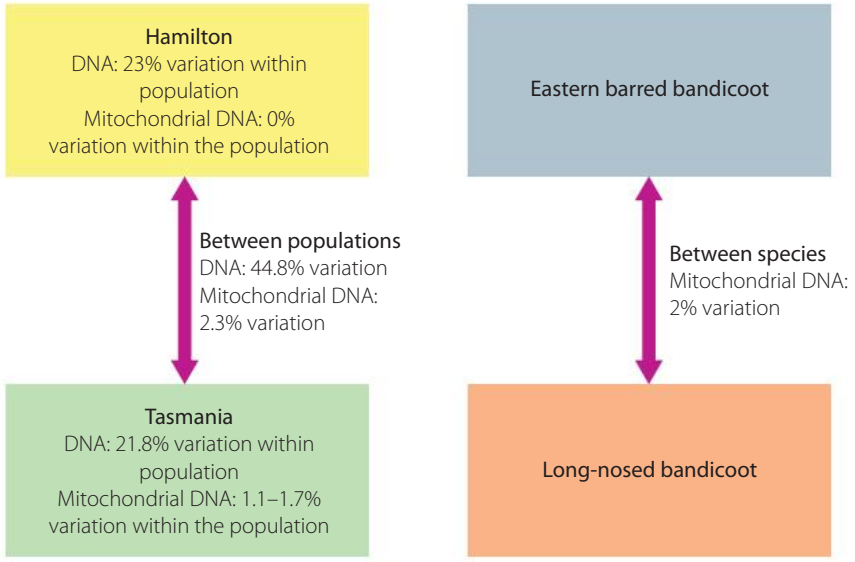

FIGURE 14.6.2 DNA variability in different populations of eastern barred bandicoots. A 2% variation is the average difference between subspecies and closely related species of mammals.

The Australian Government, through the Department of Sustainability, Environment, Water, Population and Communities, lists two subspecies of *P. 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.

Discussion

1. What species definition could be used to justify classifying the two populations as separate subspecies?
2. Does the recognition of two separate subspecies appear to be well accepted by the Australian Government at this stage?
3. What does the DNA evidence suggest about how the populations became separated? To what extent does this example illustrate the concept of allopatric speciation?
4. In your opinion, would the small genetic variability found in the eastern barred bandicoot populations affect their survival? Explain.
5. Explain why the identification of the two possible subspecies of bandicoot is important for their conservation.

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CHAPTER REVIEW QUESTIONS

DETAIL QUESTIONS

1 What is a biological species?
2 What are the mechanisms of reproductive isolation?
3 What are the modes of speciation?
4 What are the four patterns of diversification between species?
5 Why do species become extinct?

CATEGORY QUESTIONS

6 How does reproductive isolation lead to speciation?
7 How do natural disasters and habitat fragmentation contribute to geographic isolation?
8 How do sympatric, allopatric and parapatric speciation differ from each other?
9 Why do species resemble each other even though they are not related?
10 Why does reduced genetic biodiversity increase the risk of extinction?

ELABORATION QUESTIONS

11 How do new species form?
12 Why don't the number and type of species remain the same over long periods of time?
13 Why has the rate of species extinction rapidly increased in recent times?

EVIDENCE QUESTIONS

14 What, if any, external sources did you use to support your answers to questions 11–13?
15 Explain your reasoning behind your answers to questions 11–13.
16 What other factors could affect speciation?
17 How could your answers to questions 11–13 be improved?
18 What further evidence could be used to support your answers to questions 11–13?

END-OF-CHAPTER EXAM

End-of-chapter test

1 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:

A post-reproductive isolating mechanism.

B geographic isolating mechanism.

C temporal isolating mechanism.

D mechanical isolating mechanism.

2 Speciation occurs when a single population becomes two separate populations that do not interbreed. Which of the following occurs in allopatric speciation?

A Geographical isolation

B Temporal (time) isolation

C Behavioural isolation

D Morphological differences

3 Wildlife corridors are intended to:

A link conservation areas that have been isolated by human activities, allowing animals to move from one area to another.

B concentrate animals in smaller areas, minimising their impact on human activities, especially agriculture.

C increase the likelihood of inbreeding.

D allow animals to escape a wildfire in their normal habitat.

4 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.

5 What effects do isolating mechanisms have on a population?

6 In North America, species of fruit fly of the genus *Ragatosis* are confined to different species of apple trees and hawthorn bushes. Describe how this could lead to speciation.

7 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. Give a reason why.

8 Two species of plants are found growing in desert areas of Peru and Northern Africa. They are very similar in appearance.

a What pattern of evolution best describes the evolution of the two plant species.

b Explain how you reached your answer.

c Draw a diagram that represents this pattern of evolution.

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9 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.

a Name this mode of speciation.

b Give a reason why this is an example of geographic isolation.

c Explain the effect of geographic isolation on gene flow between the fish populations.

d Suggest whether the isolating mechanism for the fish speciation is pre-reproductive or post-reproductive. Explain your answer.

10 Define 'sympatric speciation'.

11 Explain how habitat fragmentation results in allopatric speciation.

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 co-evolution.

13 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 to extinction than large populations.

UNITS 3 & 4 PRACTICE EXAM

MULTIPLE-CHOICE QUESTIONS

QUESTION 1

The Simpson diversity index:

A measures the carrying capacity of a population.

B decreases when species richness increases.

C is a mathematical formula to explain interactions between species.

D is a quantitative measure of biodiversity.

QUESTION 2

Choose the correct answer.

A Cladistics relies on similarities in physical features.

B The Linnaean system of classification uses molecular sequences to classify organisms.

C Reproductive methods are used to infer evolutionary relatedness between groups of organisms.

D Phylogenetic trees show evolutionary relationships.

QUESTION 3

A conclusion that could be made from the competitive exclusion principle is that:

A no two ecologically similar species are able to coexist in the same community if they have one or more differences in their niche.

B two species with the same food habits tend to remain evenly balanced in numbers in the same region for a fairly long time.

C complete competitors cannot coexist.

D it is not possible to use experiments to observe changes that occur within an ecosystem.

QUESTION 4

A scientist was testing the work of one of her students who was studying a population of wallabies in a woodland. The scientist knew that the total population in the area was 500. When a random sample of 50 individuals was caught, each captured animal was marked and released. At a later date, a random sample of 30 animals was caught. If the student was carrying out the method correctly, the number of individuals expected to be marked would be:

A 3

B 6

C 10

D 83

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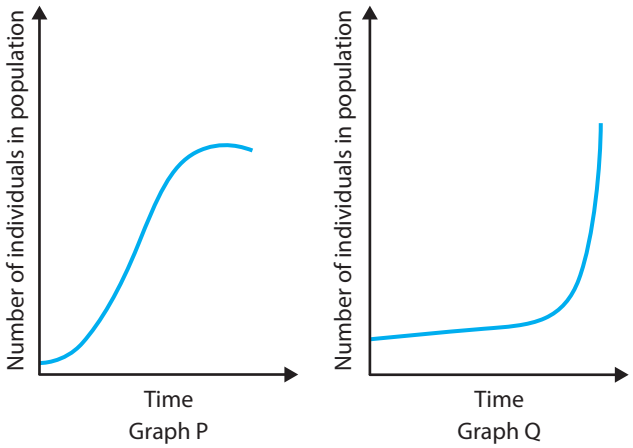
QUESTION 5

The graphs show the changes in numbers of individuals in two populations of plants, P and Q, over the same period.



The following is a valid conclusion consistent with the graphs.

A Members of population P are likely to produce more seeds than members of population Q over the same time interval.

B Members of population Q are more likely than population P to be slow growing.

C Population Q is K-selected and usually present in late succession.

D Population P is more likely than population Q to be found in an ecosystem during late succession.

QUESTION 6

DNA helicase:

A unwinds the double helix by breaking the hydrogen bonds between the nucleotides.

B binds histones to DNA.

C attaches free nucleotides to the unwound double helix.

D joins DNA single strands together according to the base-pairing rule.

QUESTION 7

Genes are expressed when:

A DNA is methylated.

B activating transcription factors are produced.

C micro RNA pairs with mRNA.

D DNA is packaged and coiled into chromatin.

QUESTION 8

Edward's syndrome is a disorder in which individuals have an extra copy of chromosome 18. They suffer mental retardation and congenital defects of all organs and typically die by the age of 6 months. Edward's syndrome is an example of:

A a frameshift mutation.

B monoploidy.

C aneuploidy from non-disjunction in meiosis.

D aneuploidy from mutations in mitosis.

QUESTION 9

The Cambrian explosion began around 542 million years ago and lasted for the next 20 million years. In this time, most major animal phyla appeared and the diversity of life began to resemble what it is today. This is an example of:

A macroevolution.
B allopatric speciation.
C stabilising selection.
D genetic drift.

QUESTION 10

Crocodile fossils that have been dated as 80 million years old still look like the crocodiles living today, so crocodiles are an example of 'living fossils'. Crocodiles have changed very little because:

A they are perfectly adapted and any changes would put them at risk of extinction.
B their habitat has changed very little so there has been minimal selection pressure.
C they are a top-order carnivore that is not eaten by other animals.
D there are no other species competing for their ecological niche.

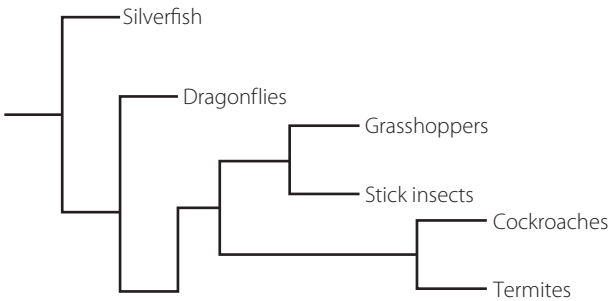
SHORT-ANSWER QUESTIONS

QUESTION 11

During a survey of an ecosystem, biologists find a group of insects that need to be classified.

a List three criteria scientists use to classify living organisms into species.

The insects were classified in the grasshopper group. The evolutionary history of grasshoppers was determined and is represented in the following diagram.



b Name the type of diagram that represents evolutionary history.
c Use the diagram to suggest which two organisms of grasshoppers, stick insects and cockroaches shared the most recent common ancestor.
d Decide whether silverfish or dragonflies are more closely related to grasshoppers, and give reasons why.
e During the ecosystem survey, biologists used stratified sampling. Explain the conditions in the ecosystem that indicated this was the best method for the survey.

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QUESTION 12

Plantation forests in Queensland produce up to 2.5 million cubic metres of logs annually. There are changes to the biotic and abiotic structure of the ecosystem in areas that have recently been logged.

a Describe the impact of logging. In your answer, include an explanation of biodiversity, ecological niche, carrying capacity and biomass.

b Biological succession occurs in the months following logging. Name the type of:

- **i** biological succession
- **ii** community immediately after logging
- **iii** community after a long period of time.

c Explain two methods biologists could use to monitor population growth rate and change in the area after logging.

d Leaf litter is drastically reduced after logging. Describe the effect this would have on local nitrogen cycling.

QUESTION 13

Cystic fibrosis is one of the most common inherited diseases in humans. It is caused by a mutation in the CFTR gene. The mutated allele is recessive. The DNA sequence for the normal CFTR allele is … ATCATCTTTGGTGTT … and the DNA sequence for the mutated allele is … ATCATTGGTGTT …

a Write the mRNA sequence for both the normal and mutated CFTR allele.

b Describe the mutation that has occurred.

Protein synthesis involves both transcription and translation. The mutation results in the loss of the amino acid phylalanine from the polypeptide chain.

c Name the compound that is formed as a consequence of transcription.

d Outline the steps that take place during:

- **i** transcription
- **ii** translation.

e DNA can be chemically modified at the transcription stage. Explain how the structure of the nucleosome modifies transcription.

f Explain why the type of mutation causes one amino acid to be deleted without affecting other amino acids in the CFTR protein.

g Explain how the polymerase chain reaction and DNA sequencing can be used to identify cystic fibrosis.

h Calculate the chance of two normal carrier parents having a child with cystic fibrosis. Explain your answer by using a Punnett square.

QUESTION 14

Egg size in birds is related to nest size. In some species of falcons, eggs laid in the hollows of trees are larger than eggs laid in stick nests or in cliff sites. It is thought that a genetically distinct population of birds may exist.

a Explain how natural selection has resulted in larger eggs being laid by falcons nesting in hollows of trees.

b Suggest how a genetically distinct population may lead to formation of a new species of falcons.

Populations of falcons may use the same tree for nesting sites, some using the hollows and some using stick nests, but there is very little gene flow. Sympatric speciation could provide an explanation of speciation in these two populations of falcons.

c Define 'sympatric speciation'.

d Explain one sympatric isolating mechanism that may have occurred in the falcons.

e The feather colour of falcons can be dark brown, light brown and white. Given that feather colour is under genetic control, explain how a single gene can determine the variety of colours.

f A new feather colour could be the result of a mutation. List two environmental influences that can greatly increase the mutation rate.

ANSWERS

CHAPTER 1: BIODIVERSITY

1.1 REVIEW

1 a Species: the lowest taxon in Linnaean classification; it is always italicised and combined with genus

b Ecosystem: a self-sustaining unit consisting of the interactions between the species in a community and the environment

2 Genetic diversity is the range of different genes within a species, species diversity is the range of different species in an ecosystem and ecosystem diversity is the range of different ecosystems in a particular location.

3 Student responses will vary but should focus on the different climate in Australia, which provided very different selection pressures for Australian organisms in their evolution.

4 Each species has a role to play in an ecosystem, with a balance of growth and predation, nutrition and mortality. Ecosystems with many different species are able to adapt to and absorb changes better than ecosystems with fewer species.

5 Student responses will vary but should include the effects of in-breeding, such as congenital health problems and susceptibility to disease, which contribute to short lifespans and low quality of life for the individual.

1.2 REVIEW

1 Species richness: the number of species present in an ecosystem

Relative species abundance: the number of individuals present for each species in an ecosystem

Percentage cover: the percentage of the quadrat that a species takes up

Percentage frequency: the percentage of quadrats that a species appears in

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

2 A 1 m × 1 m square frame is laid on the ground and everything inside the frame is sampled. Often several quadrats are averaged for more accurate data.

3 $D = 1 - \left(\frac{\sum n(n-1)}{N(N-1)} \right)$, where n is the number of individuals of each species and N is the total number of individuals at the site

4 Species richness is the number of species present in an ecosystem regardless of how populous each species is – a species with one individual is equal to a species with a million. Relative species abundance, however, is the number of individuals present for each species in an ecosystem, so a species with one individual is reported differently to a species with a million individuals.

5 0.552

Worked solution:

ORGANISM	NUMBER OF INDIVIDUALS (n)	$(n-1)$	$n(n-1)$
Flathead	36	35	1260
Australian bass	720	719	517 680
Garfish	934	933	871 422
Pearl perch	60	59	3540
Tailor	14	13	182
		$\Sigma n(n-1)$	1 394 084
Total individuals (N)	1764	1763	3 109 932
Simpson's diversity index	$D = 1 - \left(\frac{\sum n(n-1)}{N(N-1)} \right)$ $= 1 - \frac{1394084}{3109932}$ $= 0.552$		

6 Student responses will vary but should consider the benefits of standard indices, such as enhancing communication with a common language to discuss biodiversity, as well as the pitfalls, such as the prevalence of oversimplification.

1.3 REVIEW

1 a Spatial scale: how large an area an ecosystem covers

b Temporal scale: the time period over which an ecosystem is studied

2 Student responses will vary but may include nocturnal/diurnal animals or those that hibernate.

3 Student responses will vary but may include temperature across different latitudes or salinity across oceans rather than localised deltas.

4 Student responses should include sampling time (night vs day sampling), spatial scale (smaller section vs larger area) and number of quadrats taken (less vs more accurate averaged data).

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5 Student responses will vary. Example response:

SPATIAL DIFFERENTIATION	TEMPORAL DIFFERENTIATION
Micro-level The temperate rainforest has excellent biodiversity with dense habitation of birds, insects and animals.	Day Few diurnal animals, mainly birds and insects. As dusk falls, insect activity increases and nocturnal animals begin to replace diurnal birds.
Meso-level The Lamington National Park area has moderate biodiversity with areas of the park densely and richly inhabited, with other areas, such as the car parks and picnic areas, considerably less biodiverse.	Year Summer sees an influx of migratory birds from the southern climates and an increase in total individuals from new births. Winter sees a big decrease in insect species active.
Macro-level South-east Queensland has moderate biodiversity. Large areas are urbanised and have low biodiversity but there are patches of high biodiversity in a dozen national parks across the area.	Decade Forest is cut down to make way for urban spread. Ecosystem changes from temperate rainforest to urban with corresponding loss of biodiversity.

1.4 REVIEW

1 Limiting factors: aspects of the environment that restrict an organism's ability to live there

2 Biotic: predation, competition, lack of appropriate food sources, poor habitat access (e.g. tree-trunks)

Abiotic: temperature, rainfall, soil salinity, light levels, poor camouflage opportunities

3 Student responses should focus on our need for living space, since food is not an issue when it is shipped in anyway. They may include low supply of adequate housing, land zoning for farms and parks, and flood risks.

4 Student responses may focus on human culling when shark numbers rise or inadequate fish stocks to service both the human and shark populations.

5 Student responses will vary but should consider the increase in grass and seedling growth as well as increased access to water sources. The population will self-limit when the food sources dwindle again but humans are likely to intervene before then to protect green pasture for their livestock.

CHAPTER REVIEW QUESTIONS

1 Biodiversity: the full range of different living things in a particular area or region; it can be described at various levels, including the range of different species, genetic diversity or the diversity of ecosystems present in a larger area

2 Species richness, relative species abundance, percentage cover, percentage frequency and Simpson's diversity index

3 $D = 1 - \left(\frac{\sum n(n-1)}{N(N-1)} \right)$, where n is the number of individuals of each species and N is the total number of individuals at the site

4 Example: A riverbank in central Queensland will have considerably more biodiversity than the farmland that the river runs through, and the riverbank in the dry season will be less biodiverse than in the wet season.

5 Healthy biodiverse ecosystems should have many species of animal, fish, bird, insect and reptile. They should have a balanced triangle of trophic stages (producers, consumers and decomposers). No particular species is overabundant and the community is relatively stable over long periods of time.

6 The distribution of species is limited by their ability to access adequate food sources and habitats. They will be limited to areas where these factors are beneficial for their survival. The abundance of species is limited by the abundance of food, water and shelter in the areas with beneficial factors.

7 Student responses should include calculated D for each of three ecosystems and ranking them from smallest (least diverse) to largest (most diverse).

8 Student responses will vary widely but should be concisely summarised and clearly support their response.

9 Student responses will vary but should consider the dangers of oversimplification and that lack of context can reduce the meaningfulness of a single 'biodiversity score'.

END-OF-CHAPTER EXAM

1 C 2 D 3 A

4 Genetic diversity, species diversity and ecosystem diversity

5 A community of interconnected organisms and their interactions with their abiotic environment.

6 Reported diversity relies on sampling, which must be done at a specific time. Ecosystems change over the course of a day, a year and longer timescales, making it easy for sampling at different times to return different diversity measures.

7 Limiting factors restrict an organism's ability to live in an area, so by identifying and mitigating abiotic and biotic factors that are working against the success of a particular species in an area, the population can be rehabilitated.

8 Student responses will vary widely but should be concisely stated and clearly supported by evidence and more than one example.

9 Response:

SITE A				SITE B				SITE C			
SPECIES RICHNESS = 4				SPECIES RICHNESS = 3				SPECIES RICHNESS = 4			
	RELATIVE SPECIES ABUNDANCE	% COVER	% FREQUENCY		RELATIVE SPECIES ABUNDANCE	% COVER	% FREQUENCY		RELATIVE SPECIES ABUNDANCE	% COVER	% FREQUENCY
Green	8	8	19	Green	5	5	12	Green	1	1	4
Orange	15	1.5	15	Orange	17	2	17	Orange	23	2.5	25
Blue	17	1.5	9	Blue	unknown	6	12	Blue	33	4	36
Red	unknown	10	13	Red	0			Red	unknown	4	7
	SIMPSON'S DIVERSITY INDEX				SIMPSON'S DIVERSITY INDEX				SIMPSON'S DIVERSITY INDEX		
	n	$(n-1)$	$n(n-1)$		n	$(n-1)$	$n(n-1)$		n	$(n-1)$	$n(n-1)$
Green	8	7	56	Green	5	4	20	Green	1	0	0
Orange	15	14	210	Orange	17	16	272	Orange	23	22	506
Blue	17	16	272	Blue	6	5	30	Blue	33	32	1056
Red	10	9	90	Red	0	0	0	Red	4	3	12
		$\sum n(n-1)$	628			$\sum n(n-1)$	322			$\sum n(n-1)$	1 574
N	50	49	2450	N	28	27	756	N	61	60	3660
D	$D = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$ $= 1 - \frac{628}{2450}$ $= 0.744$			D	$D = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$ $= 1 - \frac{322}{756}$ $= 0.574$			D	$D = 1 - \left(\frac{\sum n(n-1)}{N(N-1)}\right)$ $= 1 - \frac{1574}{3660}$ $= 0.570$		

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Site A is considerably more biodiverse than sites B and C, which is clear by the even distribution of species. Site B is slightly more biodiverse than site C according to Simpson's diversity index, but both have mediocre biodiversity from the distribution of species in the images.

10 Student responses will vary widely but should consider the geographical isolation that caused considerably higher levels of speciation in Australia as well as the unique features that developed here in both flora and fauna to survive the Australian climate.

CHAPTER 2: CLASSIFICATION PROCESS

2.1 REVIEW

1 Taxonomy: a system of classification, particularly biological; or the study of these systems

2 Classifying organisms is beneficial in simplifying and condensing the vast diversity of life on Earth and visualising the relationships between groups of organisms.

3 Classification choices are not universal, which causes contention among the scientific community about the 'right' way and major similarities and differences are emphasised, while minor similarities and differences are ignored.

4 Student responses will vary but may focus on number of letters, vowels, consonants or syllables, language of origin, similar meanings, fuller or shorter names or gendered or neutral names.

2.2 REVIEW

1 Domain, kingdom, phylum, class, order, family, genus and species

2 Animalia includes animals, Plantae includes plants, Fungi includes mushrooms and yeasts, and Protista includes amoebae.

3 Physiological traits, reproductive methods and molecular sequences

4 Molecules such as proteins or DNA are sequenced and those sequences are compared. The number and nature of differences are used to rank relatedness.

5 Student responses will vary but may include the red panda, which was reclassified as its own family separate to the bears and raccoons that it is structurally similar to.

6 DNA evidence is considered superior evidence because DNA is passed directly from generation to generation, accumulating minor mutations along the way. Physical appearance is a by-product of DNA inheritance and can be similar even when DNA sequences are very different.

2.3 REVIEW

1 a Clade: a group comprising all of the descendants of a particular ancestor organism

b Common ancestor: a species of organism whose offspring diverged over time

2 Phylogenetic trees are oriented with the common ancestor at the bottom and branches upward. In this orientation, the passage of time moves from far in the past at the bottom towards the present at the top.

3 Student responses will vary but explanations should refer to the use of individuals rather than species and the use of two ancestors (mother and father) for describing relatedness.

4 The only clade that includes the bryophytes must include all of the other categories, because the bryophyte point of cladogenesis was at the earliest common ancestor in this diagram. Every possible clade includes the angiosperms because their point of cladogenesis is at the latest common ancestor, so all earlier ancestors will be common to the angiosperms as well.

2.4 REVIEW

1 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).

2 Cladograms organise species into clades that have a common ancestor. Since we have no proof of a common ancestor, scientists make logical deductions to determine the order of cladogenesis, which can be considered no more certain than a 'best guess'.

3 Plesiomorphic means similar to their parents. Most offspring of a species are similar to their parents because most DNA combinations from the parents will ensure this is so. Some offspring are occasionally apomorphic due to extensive or pivotal mutations in their DNA before or immediately after conception.

4 Student responses may vary but could consider that cladistics assumes that offspring will either be similar to their parents or different in only one way. It does not allow for the possibility that a single ancestor species could have produced multiple, very different offspring that formed multiple different species.

2.5 REVIEW

1 Present and absent

2 The nodes in a cladogram represent the most recent common ancestor species for all of the species that branch off from that node.

3 It is unlikely that seeds evolved twice in two separate organisms. Figure 2.5.2 describes a scenario where angiosperms developed seeds and ovaries while other offspring of the common ancestor remained plesiomorphic, and then later, gymnosperms developed seeds while other offspring of the plesiomorphic branch still did not. This is less likely than the scenario in Figure 2.5.1 where seeds evolved in the offspring of one common ancestor and then ovaries evolved in the offspring of the seeded ancestor.

4 Fungi and Animalia share the most recent common ancestor. These two groups diverged from a common ancestor that they shared with Plantae. This common ancestor diverged from Protista, and the four groups share a common ancestor that diverged from Archaea. All of these groups share a common ancestor that diverged from Bacteria.

5 Student responses will vary but 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.

PRACTICAL ACTIVITY 2.6.1

1 Molecular clock: a technique that uses the mutation rate in molecular sequences to deduce when two species last shared a common ancestor

2 Some species are not well dated from fossil records or geographic information and, in these cases, molecular clocks provide the best estimates for divergence.

3 $$\text{Base rate of mutation} = \frac{\left(\frac{\text{number of point differences}}{\text{number of residues analysed}}\right)}{\text{time since divergence}}$$

4 Base rate $= 10 \div 20 \div 1.5 \times 10^{9} = 3.3 \times 10^{-10}$

5 Estimated date of divergence $= 7 \div 50 \div 1.2 \times 10^{-8} = 1.16 \times 10^{7} = 11.6$ million years

6 Cytochrome c appears to have a base rate of mutation 100 times slower than DNA. This could be due to the differences in DNA sequences and protein sequences. Protein sequences are derived from three-letter codons of DNA, which could be why proteins mutate at a slower rate overall.

7 Student responses will vary but should indicate the estimated date is reasonable.

8 Limitations include: calculating the base rate of mutation for species from geographic or fossil record data, which is in itself, subject to error; relying on base rates from similar species rather than the actual species; and using only partial sections of the DNA or protein sequence for analysis when some sections will be highly conserved and others will be highly variable.

2.6 REVIEW

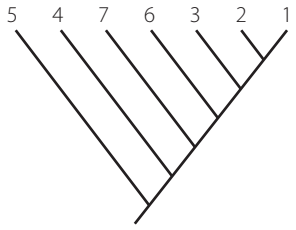
1 Comparative genomics: the study of DNA similarities across species

2 A neutral mutation is a change in DNA sequence that is of little consequence to survival and reproduction. Examples include eye colour, hair curliness and minor changes to proteins that do not affect the function or efficiency of the molecule.

3 Histones are central to the correct storage and transcription of DNA sequences. Histones are present in all eukaryotic cells and minor changes in their effectiveness would have drastic consequences for an organism. This means that organisms that have inherited mutations to the histone sequence are unlikely to survive beyond conception and thus, the only organisms that function properly must have the same correct histone sequence. Its vital role in life processes makes histones a good candidate for sequence conservation.

4 Cladistics assumes that two species will become increasingly more different as they get further from their point of divergence. The mutation rate estimates the number of differences accumulated per generation. 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 now and their point of cladogenesis.

5 Student responses will vary but should be similar to the following diagram.



2.7 REVIEW

1 Biological species concept: the definition of a species based on the capacity of individuals to interbreed

Morphological species concept: the definition of a species based on physical characteristics

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

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2 Morphological species concept

3 Examples are grolar bears, ligers and mules.

4 It is not possible to apply it to fossils of extinct organisms and fertile hybrids, the offspring of individuals from different species that can go on to have their own offspring, create issues when species is solely defined as interbreeding individuals.

5 The phylogenetic species concept requires scientists to reclassify all life into clades, based on genetic comparisons. Scientists have yet to genetically analyse our extant species, and cannot analyse our extinct species.

6 Student responses will vary but arguments should be clear, logical and well supported by evidence.

2.8 REVIEW

1 Hybrid: an organism resulting from the interbreeding of two different species

2 Mules are infertile hybrids; grolar bears are fertile.

3 Mules are infertile because their parents are a horse with 64 chromosomes (32 in the egg) and a donkey with 62 chromosomes (31 in the sperm). This pairing leaves mules with 63 chromosomes. Individuals with an odd number of chromosomes are often infertile due to the failure of meiosis to split the diploid cell evenly in half.

4 Student responses will vary but explanations could refer to nocturnalism or differences in mating calls and rituals.

5 In this example, bread wheat is fertile because it has six sets of chromosomes, which can be evenly divided by mitosis. Perhaps plant species tend to combine their whole $2n$ genome in hybrids, which would make them fertile.

PRACTICAL ACTIVITY 2.9.1

1 Specht's classification system relies on two factors, the size of the tallest vegetation present and the approximate area that the foliage of this vegetation covers.

2 Only identifying how tall the tallest vegetation was and how much land the foliage covered meant that ecologists no longer had to determine the most abundant species and identify it in order to name an ecosystem.

3 Open scrub

4 Open grassland or grassland depending on the student's determination of foliage cover as less than or more than 30%.

5 Student responses will vary but should consider the lack of detail in the photograph regarding the height of the canopy.

6 The foreground is closed sedgeland, the midground is shrubland and the background is likely to be some form of closed forest.

7 The foreground should be reasonably sure because of the detail in the image, while it is difficult to determine the height of the midground and the background is quite uncertain.

8 Student responses will vary but could consider the ease of determining the genus of the most common vegetation, the differences in ecological management required for forests with different types of trees or the better visual image that these more descriptive names provide.

2.9 REVIEW

1 Competition is struggling for the same resources, symbiosis is at least one organism benefiting from their interaction, predation is when an organism consumes another for food and disease is where one organism is directly harmed by the relationship.

2 Student responses will vary but may include competition within a species over mating females or nesting sites, and between two species over food sources.

3 Predator populations rely on prey populations. Shortly after prey increases, predators have more to eat and competition within the predator species relaxes. This means more predators will survive and their population increases. Shortly after the increase in predators, the prey species will experience greater levels of predation and so their population will fall as the predators eat them. This fall in prey populations will increase competition within the predator species and their population will fall as their food becomes scarce again.

4 Student responses will vary but could refer to myxomatosis in rabbits. This disease afflicted only rabbits and ensured the rabbit population remained under control despite their enormous reproductive rate. With fewer rabbits, other species were able to survive in the ecosystem alongside them.

5

2.10 REVIEW

1 Terrestrial examples include tundra, tropical rainforests and deserts. Aquatic examples include marine photic zones, freshwater rivers and swamps.

2 Rainfall, canopy cover and the concentration of various nutrients in the soil

3 The ecosystems in Australia are distributed according to climate and, in particular, rainfall patterns. The east coast of Australia has considerable rainfall and a moderate climate, which is very different from the central and western parts of Australia, which are characterised by a hot, dry climate. These climate variations are matched in vegetation patterns.

4 Student responses will vary but may include that rainfall supplies water to a plant but can also erode the soil around its roots.

5 Student responses will vary but could consider ways to cure or prevent *Chlamydia* infections or artificial fertilisation, ways to replenish eucalpyt forest and ways to safely cross between eucalypt pockets.

2.11 REVIEW

1 Stratified sampling: a statistical sampling technique that divides an area into strata for separate sampling

2 The quadrat method involves placing flat squares randomly around an area to count individuals within the square. The transect method involves laying a straight line through the area and counting individuals along the line.

3 Examples include ensuring the number of quadrats taken in each stratum is proportional to the size of the stratum; using random number generators to ensure random rather than equal spacing of quadrats; following strict counting criteria; and calibrating equipment.

4 Both of these methods require the sampler to sit with the area for a large period of time to count the individuals. Animals usually do not stay still in the vicinity of a human for long enough to be accurately counted. Also, many animals are too large to be accurately sampled with quadrats or transects.

5 a 1.3 individuals/m^2

b 7 individuals/m^2

c 2 individuals/m^2

6 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 odd data for the combination of species and ground coverage.

7 a 1.35 individuals/m^2

b 1.83 individuals/m^2

CHAPTER REVIEW QUESTIONS

1 Linnaean taxonomy is built upon a series of eight hierarchical taxa, with only a single Latin word to describe the various groups in each taxon.

2 Competition is struggling for the same resources, symbiosis is at least one organism benefiting from their interaction, predation is when an organism consumes another for food and disease is where one organism is directly harmed by the relationship.

3 Raymond Specht

4 Cladistics is different from Linnaean taxonomy in that it does not emphasise any hierarchy of taxa; instead, it emphasises the most recent common ancestor of a group of organisms and seeks to organise all life into interrelated clades. This is an improvement on Linnaean taxonomy because it is not restricted to dividing organisms by only eight degrees and it makes heavy use of genetic analysis, which is not a feature of Linnaean taxonomy.

5 Student responses will vary but should refer to the loss of reproductive ability as a key difference from fertile species. This should result in less competition for mating and young-rearing space, as well as less competition for food resources, since they have no offspring to feed.

6 Student responses will vary but should consider the benefits to understanding our environment and our place in it, including the ways that species and ecosystems work with and without our intervention.

7 Student responses will vary but should strive to be relatively accurate.

8 Student responses will vary widely but should be concisely summarised and clearly support their response.

9 Student responses will vary but should consider the time, space and equipment resources available to field ecologists.

END-OF-CHAPTER EXAM

1 B

2 A

3 D

4 A common ancestor is a species of organism whose offspring diverged over time.

5 a Yes

b Baboons, macaques, gibbons, chimpanzees and humans

c Chimpanzees

6 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

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relatedness. Species with greater similarity in their sequences will be more closely related.

7 Mutations are accumulated when DNA is copied for growth or reproduction. Organisms that grow larger or faster and those that have a higher reproductive rate (such as bacteria, which can have several generations in a matter of days) will have their DNA copied more frequently. This frequent DNA copying will accumulate mutations faster than organisms that grow and reproduce less frequently.

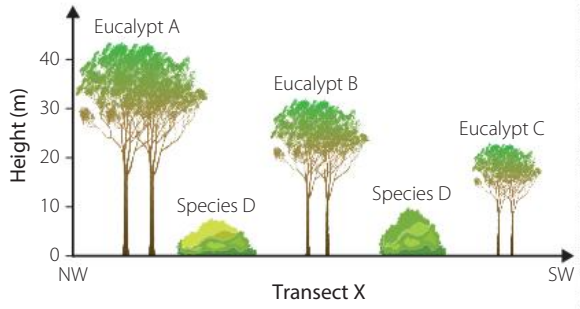
8 Student responses will vary but should consider the difficulty of finding a mate who is not directly related to them and the dangers involved in travel between population fragments. Koalas would be a common example.

9 Student responses should include the beginnings of scientific classification with Linnaeus, the development of Darwin's evolutionary theory that introduced comparative morphology to classification, and the development of genetic sequencing technologies that have supported the introduction of genetic classification and cladistics.

10 a Eucalypt species A

b 30–40%

c



d Tall woodland or tall open forest depending on answer to part b.

e Student responses will vary but should consider the risks of bias and sampling errors without multiple plots for verification.

CHAPTER 3: FUNCTIONING ECOSYSTEMS

3.1 REVIEW

1 Autotroph: an organism that can produce its own organic compounds from sunlight, water and carbon dioxide

Heterotroph: an organism that cannot convert sunlight to useful energy, and must consume other organisms for food

2 Autotrophs take in carbon dioxide and water from the environment and harness the light energy that falls on the chloroplasts to convert these reactants into the products glucose and oxygen. This glucose is used in cellular respiration to grow more cells, which increases biomass.

3 GPP is the total gross amount of chemical energy produced by an organism or group of organisms, while NPP is the net amount of chemical energy available for the next trophic level after the organism or group of organisms have used some for their own energy needs.

4 The Sun is the primary source of energy because all organisms either get their energy from the sun or from an organism that got its energy from the sun or from an organism that ate an organism that got its energy from the sun. Even geothermal energy is from the Sun, which warms the planet and pulls it gravitationally to induce flexing.

5 Student responses will vary but should consider benefits such as balancing the trophic levels and limitations such as the lack of species-specific information.

3.2 REVIEW

1 Energy transfers are not 100% efficient because energy is required at each level for moving, keeping warm and reproducing, and is lost in inedible portions of an organism and in body waste and heat radiation.

2 Percentage efficiency

$$= \frac{\text{net productivity of the organism}}{\text{net productivity of the previous trophic level}} \times 100$$

3 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.

4 Tertiary consumers are the most efficient at 50%, and the secondary consumers are the least efficient at 22.2%.

5 42 000 kJ − 50 kJ = 41 950 kJ

6 Producers 15%, primary consumers 19.8%, secondary consumers 20%, tertiary consumers 20%

7 $\frac{50}{42\,000} \times 100 = 0.1\%$

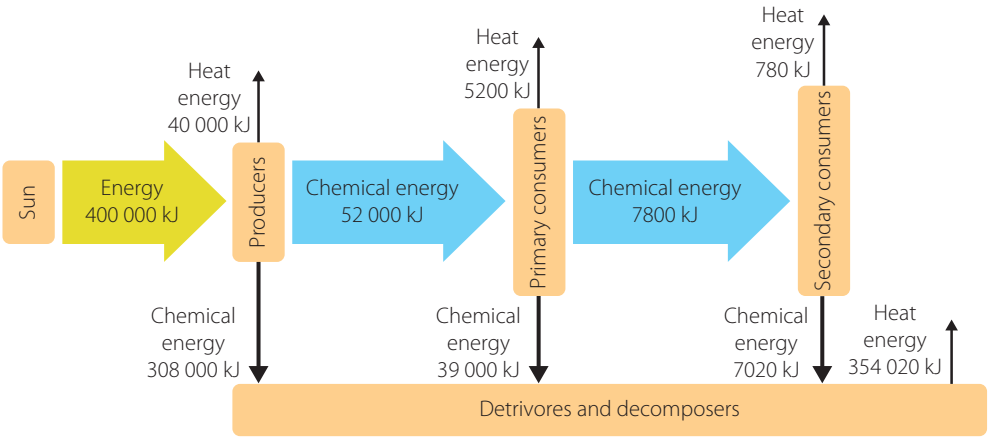
6 Student responses will vary widely but should consider the trophic level of each diet and the efficiency of energy used by eating from each trophic level.

3.3 REVIEW

1 Arrows show direction of energy flow; boxes represent trophic levels; heat energy is lost at each level and must add up to the chemical energy brought in by producers; and detritivores and decomposers are included as a subtrophic level.

2 Detritivores and decomposers process the wastes from each trophic level so that the energy in these wastes is released as heat and the nutrients are recycled into the soil.

3



4 a $\text{Percentage efficiency} = \frac{1609}{14146} \times 100 = 11.37\%$

b They have been included because organisms that leave the community take resources with them, which must be accounted for.

c 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).

5 Student responses will vary but should consider the small amount of energy available in carnivorous trophic levels.

3.4 REVIEW

1 Carbon, nitrogen, water and phosphorus

2 Photosynthesis converts atmospheric carbon dioxide into organic glucose, while respiration releases energy from glucose as it converts it back to atmospheric carbon dioxide.

3 If the nitrogen-fixing bacteria died, there would be limited means to trap atmospheric nitrogen in the soil, so the plants would not be able to use it. As the denitrifiers released nitrates into the atmosphere again, the stores of nitrogen in the soil would run out and plants would die off.

4 Two of the three main sinks for carbon out of the atmosphere are forest trees and fossil fuels. With these sinks being emptied for progress, the carbon has nowhere to go except the atmosphere and the remaining sink, the ocean.

5 In the first part, atmospheric nitrogen is taken into the soil as ammonia and nitrates by nitrogen-fixing bacteria and released by denitrifiers. Between these two organisms is the second part, where the ammonia and nitrates are taken up by plants, eaten by animals and returned to the soil in faeces and detritus.

6 Student responses will vary but should consider the likelihood of cloud cover and precipitation in various parts of the world, as well as the importance of continuous rainfall to the continuation of run-off, evaporation and cloud formation.

3.5 REVIEW

1 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; for example, the urban, diurnal, bin-feeding habits of crows.

2 The fundamental niche is the widest possible niche a species could ideally occupy without competitors, predators or parasites. The realised niche is the portion of the fundamental niche that the species actually occupies, given its restrictions.

3 By creatively using time and space, resource partitioning allows many unique ecological niches to exist in the same area. For example, a single tree can have fruit-feeding species living alongside leaf-eating species, both of which have a nocturnal and diurnal variation. On top of this, species that feed at the very top of the tree do not compete with species that feed at the bottom, despite having otherwise identical niches.

4 Student responses will vary but may consider that they feed during the day on anything they can get into, including food scraps and roadkill, usually are more active in the afternoon when the bins are full, congregate around schools and parks where waste is plentiful and spread out to nearby residential areas during school holidays.

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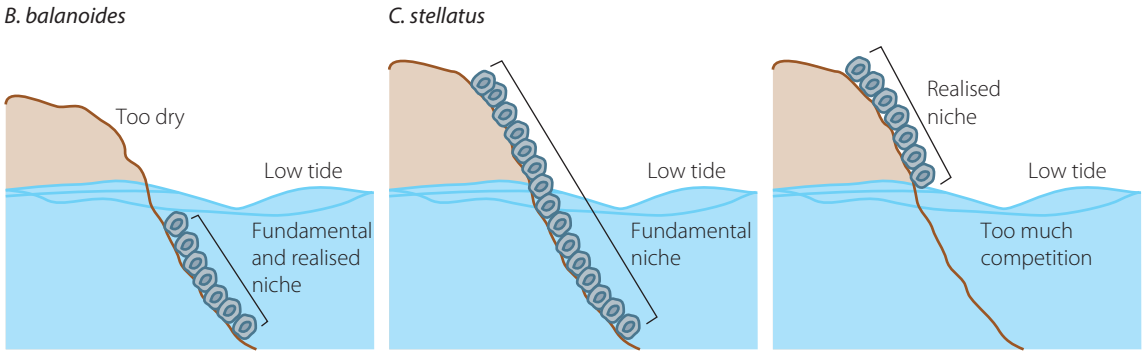
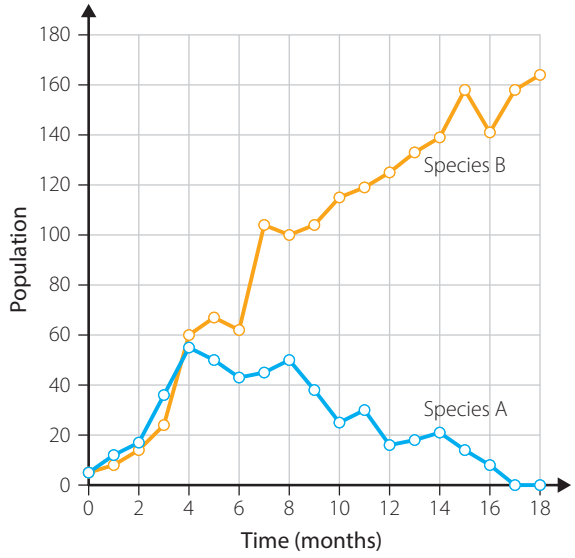
5



PRACTICAL ACTIVITY 3.6.1: DATA ANALYSIS

1



2 Species A

3 4 months

4 Species B

5 Species A began with a slight advantage and grew exponentially along the rock face. At 4 months, species A probably came into contact with species B and began competing for resources. Species A struggled to maintain its population as species B expanded over the next 4 months, until it could no longer compete and was driven to extinction by the competitive advantage of species B.

6 The biodiversity of the rock face in general will have fallen during the experiment, as species B grew at an exponential rate and may have displaced other species that were not recorded.

7 If species B were afflicted at 10 months, it is likely that species A may have recovered. If species B continued to experience reduced reproductive success, its competitive advantage may be nullified and it may be driven to extinction by the expansion of species A.

8 The competitive exclusion principle appears to be validated by this experiment, as the two species could only coexist for a limited time before the competitive advantage of species B over species A caused species A to be excluded from the rock face.

9 Student responses will vary but should consider that species B still has an advantage over species A, while species C, with its short maturation period, will reproduce quicker and thus, spread quicker than the other two species. It is likely that species C will exclude the other two species within the 18-month period.

3.6 REVIEW

1 Gause experimented by growing *P. aurelia* and *P. caudatum* separately and then together. He discovered that when grown separately, both species increased population exponentially until reaching the carrying capacity of the space. When grown together, *P. aurelia* grew quickly (though not as fast) and *P. caudatum* began to grow but was soon driven to extinction as *P. aurelia* out-competed it for food.

2 a Student responses will vary but should be a nocturnal, insectivorous animal, such as a possum, or a small nocturnal carnivore, such as a cat.

b Student responses will vary widely. Insectivorous animals that are not nocturnal include many birds, while nocturnal animals that are not insectivorous include owls and mice.

3 Feral cats are nocturnal carnivores that feed on sleeping native birds and animals, as well as competing for road-kill, lizards and frogs that many native animals use to supplement their diet during lean times.

4 Student responses will vary but should describe a reduced magpie population in the area with channel-billed cuckoos, as the magpie chicks are

more likely to die due to competition with the cuckoo chicks in the nest.

PRACTICAL ACTIVITY 3.7.1: DATA ANALYSIS

1 Amethystine python, whistling kite or rufous owl

2 Bennett's tree kangaroo and northern brown bandicoot

3 The nutrients in the soil come from decomposers, such as bacteria and fungi, and detritivores processing the fallen leaves and fruits into fertile soil.

4 The chances of a seed germinating on the forest floor are minimal. The canopy is thick and lets in minimal light for germination.

5 The black butcherbird eats only one species, the pied monarch, which is eaten by three other species so the lack of black butcherbirds would not impact them to a great extent. Black butcherbirds are also preyed on by only one species, the Amethystine python, but it also feeds on three other species and thus, would not be unduly affected by the loss of the black butcherbirds.

6 a Student responses will vary but could include the Queensland umbrella tree or southern cassowary.

b The Queensland umbrella tree is a keystone plant. The southern cassowary is a keystone link.

c Student responses will vary but should consider the service performed by the species and all other species it affects.

7 Saltwater crocodiles are top-level predators that eat large prey such as pythons and cassowaries. The effect of their introduction would be to limit the numbers of large animals in the rainforest, including cassowaries, which would reduce the seed dispersal service to rainforest trees as well as reducing the predation on other herbivores.

3.7 REVIEW

1 Keystone species: a plant or an animal that plays a unique and crucial role in the way an ecosystem functions

2 Purple sea stars prey on mussels in intertidal rock pools. Without the sea stars, the mussels overpopulate and outcompete other species in the pools, reducing biodiversity. The sea stars keep the mussel population under control to improve biodiversity in their community.

3 Narrow niches enable more unique niches in the same space, with the same resources. The more niches available, the more species are able to survive there, increasing biodiversity.

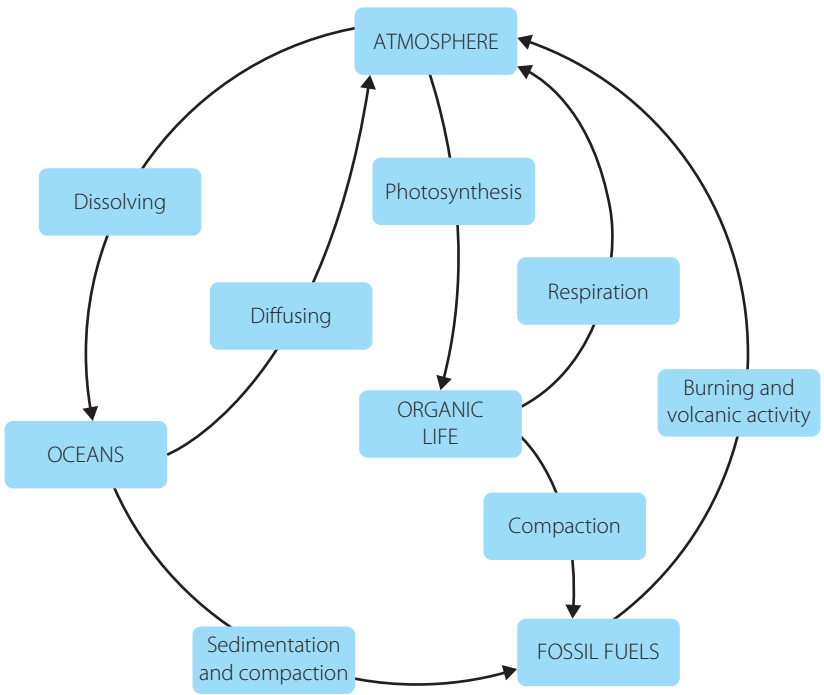
4 The two terms are similar in that both the dominant species and keystone species have large impacts on their communities. However, dominant species refers to the most abundant species in a community, regardless of its importance, while keystone species refers to a species whose interactions both directly and indirectly manage the biodiversity of the community.

5 Student responses will vary but should consider that seeds that are not dispersed are unlikely to germinate under the thick rainforest canopy of their parent tree, and that this would result in the shrinking of the rainforests and the rainforest animals' habitat.

6 Student responses will vary widely but should be concisely stated and clearly supported by evidence.

CHAPTER REVIEW QUESTIONS

1 a



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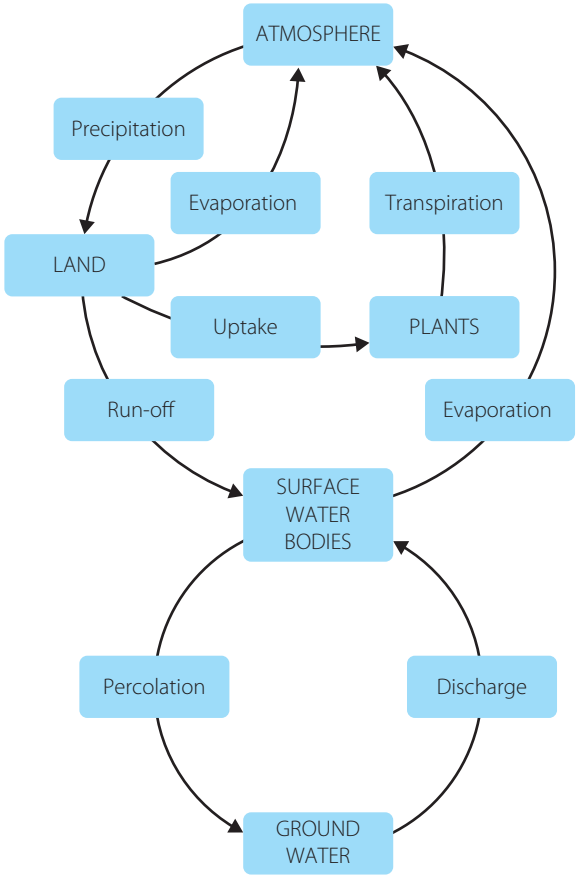
b



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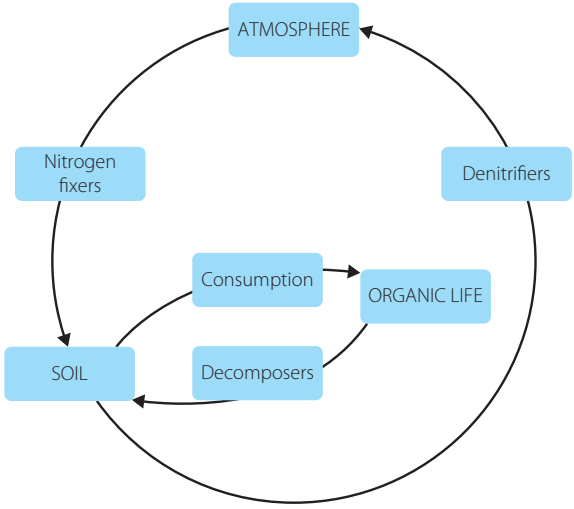
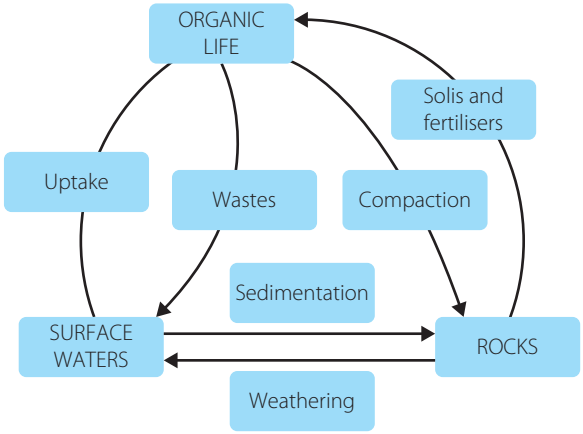


d



2 Phytoplankton $= \frac{60\,000}{2\,000\,000} \times 100 = 3\%$

Krill $= \frac{6000}{60\,000} \times 100 = 10\%$

Ice fish $= \frac{420}{6000} \times 100 = 7\%$

Adelie penguin $= \frac{63}{420} \times 100 = 15\%$

3 a 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

b For two species to occupy the same niche, they must occupy the same role and space within the ecosystem, including all of their biotic and abiotic interactions. Since both interactions and space are limited, the two species would compete for each aspect that they share, resulting in the species with a competitive advantage excluding the other species until they were no longer in competition for resources and space. The defeated species would occupy a separate niche, if possible, or it would fade to extinction.

4 The carbon and nitrogen cycles are similar in their inclusion of the atmosphere and their use within organic life. However, the nitrogen cycle requires specific organisms and events (such as nitrogen-fixing bacteria and lightning strikes) to transform atmospheric nitrogen into nitrates that are accessible for organic life, while in the carbon cycle, organic life can directly uptake and return carbon to the atmosphere. Also, while the atmosphere is the major sink for nitrogen, fossil fuels and the ocean are much larger carbon sinks than the atmosphere.

5 In general, keystone species directly or indirectly impact on the populations of a wide range of organisms in their community. Their removal is also often characterised by widespread destabilisation and loss of biodiversity.

6 Keystone species, particularly the keystone predators and prey, provide pressure and competition for other species in their ecosystem. This competition excludes species from roles and spaces that they would otherwise occupy, thus narrowing their realised niches from their fundamental niches.

7 Student responses will vary but should consider the average range of transfer efficiency for producers (less than 10%), and the ability of this rice species to produce biomass at least seven times faster, with the same space and light requirements, than generic rice. This could provide an enormous boost of basic food stock for humans.

8 Student responses will vary widely but should be concisely summarised and clearly support their response.

9 Student responses will vary widely but may consider the huge water requirements to support this level of photosynthesis, which would negatively impact our ability to provide water for other crops.

END-OF-CHAPTER EXAM

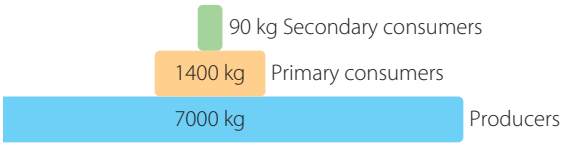
1 C

2 A

3 C

4 Student responses will vary widely but may resemble Figure 3.10.1.

5 Draw a biomass pyramid for an ecosystem with 7000 kg of sea grass, two 500 kg dugong, 400 kg of small fish and a 90 kg shark.



6 The ecosystem is well balanced because there is a very wide base of producers to support the higher trophic levels.

7 Student responses will vary widely but their choice of species should be clearly supported by the central importance of its role in its community.

8 Advantages include clarifying indirect effects of species in the community and ensuring that keystone species are given attention during conservation efforts. Disadvantages include unduly focusing on keystone species to the detriment of other species that have an important but not so wide-reaching role in the community.

9 Student responses will vary but should outline an intervention that will sequester atmospheric carbon into each of the other three major sinks, the ocean, the forests and the coal deposits.

10 Student responses will vary but should consider the biodiversity of an ecosystem as a measure of its health, and the positive impact of narrow niches on biodiversity.

CHAPTER 4: POPULATION ECOLOGY

4.1 REVIEW

1 Population: a group of individuals belonging to the same species living in a particular place at the same time

Carrying capacity: the maximum population size of a species that can be supported in a given environment

2 Examples include helping to understand how a vulnerable species is able to survive disturbances and determining how many individuals there are to sustain a viable population.

3 Biotic limiting factors include availability and abundance of foods, number of competitors, number of mates, number of predators and the number and variety of disease-causing organisms.

Examples could include availability of grass affecting the carrying capacity of kangaroos and introduction of the calicivirus and removal of rabbits affecting carrying capacity of sheep.

4 Abiotic limiting factors include availability of nutrients, shelter, refuge from predators, light, water and nesting sites.

An example could include an increase in carrying capacity of Sturt's desert pea after heavy rain.

5 Floods and fires are very quick changes. The carrying capacity would be drastically reduced very quickly.

4.2 REVIEW

1 Birth rate, immigration rate, death rate and emigration rate

2 Migration is the movement of individuals of a species from one place to another. Immigration is migration into an area and emigration is migration out of an area. Individuals immigrate 'to' and emigrate 'from'.

3 In an open ecosystem, population growth depends not only on birth and death rates but also on immigration and emigration whereas, in a closed ecosystem, growth depends only on birth and death rates.

4 Increasing

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5 Growth rate = (br + ir) − (dr + er)
= (1000 + 72) − (345 + 108)
= 1072 − 453
= 619 in 1000 or + 61.9%

6 Growth rate = (br + ir) − (dr + er)
= (59 + 105) − (86 + 40)
= 38 or 3.8%

7 Growth rate = (br + ir) − (dr + er)
= (150 + 59) − (29 + 30)
= 150 or 15%

INVESTIGATION 4.3.1

1 Student responses will vary.

2 Student responses will vary.

3 Some advantages of using the Lincoln index:

- It is accurate for mobile species in a defined area.
- Not all individuals need to be counted.
- Animals are unhurt when captured and released (although they may be stressed when captured).
- Extended analysis is possible if the population is sampled over a long period of time.

Some disadvantages of the Lincoln index:

- The chances of each individual being caught are not equal. This can lead to inaccuracy.
- Sometimes 'trap happy' individuals will be sampled over and over.
- The mark on the individual may disappear or the marked individuals may have moved away from the sample area or died.

4.3 REVIEW

1 $N = \frac{M \times n}{m}$

An estimate of the number of individuals in the total population equals the number of individuals caught, marked and released initially times the number of individuals caught on second sampling divided by the number of individuals recaptured which were marked.

2 Populations are distributed in three basic patterns:

- Random distribution: organisms are spaced unevenly, at random.
- Uniform distribution: organisms are evenly spaced.
- Clumped (grouped) distribution: a number of groups of organisms make up the population as a whole.

3 The abundance is the number of a species in a population, whereas distribution is the places in the ecosystem where individuals of the species are found.

4 Animals may be constantly on the move or too fast to count. Making direct observations and recording sightings might be possible but is time-consuming.

5 The Lincoln index is used to sample mobile species.

6 Total population = $\frac{30 \times 50}{10} = \frac{1500}{10} = 150$
individuals in the total population

7 Total population = $\frac{100 \times 200}{50} = \frac{20000}{50} = 400$
individuals in the total population

8 Step 1: Capture: turtles are caught randomly and in such a way that they are unhurt.

Step 2: Mark and release: each captured turtle is marked and returned to its habitat and left to mix with the unmarked individuals.

Step 3: Recapture: later, a random sample is taken and the number of marked individuals counted.

9 Drones are being used more frequently. Advantages include use of computer technology for identification and counting numbers and increasing data accuracy, particularly in places that may be inaccessible to humans on foot. Disadvantages include placing stress on animals.

4.4 REVIEW

1 S-shaped

2 Exponential population growth is continuous population growth occurring in an environment where resources are unlimited. When plotted on a graph it is a J-shaped curve. Logistic population growth occurs in an environment where resources are limited. It is an S-shaped curve when plotted on a graph.

3 Environmental resistance involves environmental factors that adversely affect populations. Biotic and abiotic limiting factors prevent a population from growing to a point beyond which the ecosystem is unable to sustain the number of individuals of a given species.

4 The exponential growth model assumes that resources remain abundant. This is not the case in the real world. As the population increases, each individual has access to fewer resources and population growth slows down.

5 The logged forest will experience exponential growth as the disturbed forest offers more opportunities for colonising species to grow without limiting factors. Logistic population growth would be found in the old-growth forest as the carrying capacity has been reached and an equilibrium is established.

MANDATORY PRACTICAL 4.5

1 Student responses will vary.

2 Using combined data is more accurate. For example, one site may not be typical of the area. If more sites are used, any difference in results will be considered and if one result for instance, is different to the other results, it could be discarded. Increasing the sample size improves reliability of results.

3 Student responses will vary.

CHAPTER REVIEW QUESTIONS

1 The carrying capacity of a population is the maximum population size of a species that can be supported in a given environment.

2 Factors that determine population growth rate are birth rate, death rate, immigration and emigration.

3 Exponential growth J-curve and logistic growth S-curve are two patterns of population growth.

4 Biotic and abiotic limiting factors affect the carrying capacity.

5 When limiting factors are favourable, for example when there is plentiful food, shelter and water, birth rates can increase and death rates will decrease. The abundance of resources and decreased competition allows for an increase in population numbers – an increase in the carrying capacity.

6 The population growth rate is calculated by adding the birth rate to the immigration rate and subtracting the death rate and emigration rate. Population growth rate = (birth rate + immigration rate) – (death rate + emigration rate).

7 Population size and distribution can be calculated by direct observations and sampling. This includes using the Lincoln index, satellite images, fish and plankton nets, aircraft traverses, GPS tracking and drones.

8 Populations increase exponentially when biotic and abiotic resources are abundant. Unstable and unpredictable ecosystems such as after a fire or land-clearing allow opportunistic species to move in and colonise as quickly as they can. They are able to reproduce rapidly and in relatively large numbers.

9 Populations do not continue to increase exponentially because resources are used. As populations increase, competition for resources such as food and space begins to take effect. The increased ability of disease-causing organisms and parasites to spread also increases deaths and possibly reduces breeding. The rate of population increase approaches zero as the population size nears the carrying capacity.

10 When biotic and abiotic resources are abundant, populations can expand rapidly. Depending on the changes in biotic and abiotic factors, population size can continue to increase or may decrease. The distribution of populations will also change if biotic and abiotic factors in the area change. Student answers should give examples of the effect of changes.

11 Making direct observations and recording sightings at particular intervals is often time-consuming and can sometimes be dangerous. Student answers should give examples.

12 Student responses will vary.

13 Student responses will vary.

14 Student responses will vary.

15 Student responses will vary.

16 Student responses will vary.

END-OF-CHAPTER EXAM

1 C

2 C

3 B

4 C

5 a Exponential population growth: growth of a population in an ideal, unlimited environment

b Logistic population growth: population growth that levels off as population size approaches carrying capacity

6 Biotic limiting factors are living components in an ecosystem that can determine the carrying capacity. Abiotic limiting factors are non-living components in an ecosystem that can determine the carrying capacity.

7 Resources would be distributed in a pattern that mirrors the population distribution pattern.

8 The mark may disappear; the marked individuals may have moved away from the sample area or died.

9 a Soil nutrients, water and amount of light

b Breeding sites and other penguins

c Water, sunlight, climatic conditions

10 a Carrying capacity would increase

b Carrying capacity would decrease

11 A population is increasing in size when the birth rate and immigration rate are higher than the death rate and emigration rate.

12 Step 1 Capture: beetles are caught randomly and in such a way that they are unhurt.

Step 2 Mark and release: each captured beetle is marked and returned to its habitat and left to mix with the unmarked individuals.

Step 3 Recapture: later, a random sample is taken and the number of marked individuals counted.

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13 a Widespread, heavy rain and plentiful food such as grain crops.

b Exponential population growth. J-shaped curve.

c Competition for resources such as food and space begins to take effect. Resources are used and the population begins to level or die off.

CHAPTER 5: CHANGING ECOSYSTEMS

5.1 REVIEW

1 The following factors may prevent a climax community from forming.

- Human events, such as forestry, cattle grazing, fires and land clearance
- Natural events, such as lightning strikes, lava flows and irregular flooding

2 Primary succession occurs when organisms colonise bare sites with no organisms inhabiting the affected area, whereas secondary succession deals with the changes in communities that are already established. In this instance, organisms recolonise recently disturbed communities.

3 Bare rock → lichens colonise rock, secreting acids which attack the rock's surface; dust accumulates in cracks in the rock → mosses grow → organic matter produced, resulting in simple soils → grasses and small herbaceous plants start to grow → small shrubs grow → larger trees grow → climax community is established.

4 a r-selected species would be seen in early stages of succession. They are often the first species to occupy unused resources and living space.

b K-selected species would be seen in later stages of succession.

5 The characteristic features of r-selected species make them successful in the early stages of succession. They generally are hardy and able to photosynthesise. They are able to fix nitrogen, have effective seed dispersal, rapid growth, and rapid reproduction. K-selected species live in more stable environments and outcompete other species around them. They live longer and grow slower than r-selected species making them better suited to the later stages of succession leading to a climax community.

5.2 REVIEW

1 Over the last 22 million years, there has been a major decrease in lush rainforests, an increase in fire-tolerant woody sclerophyll, a major increase in grassland and an increase in fire-sensitive woody sclerophyll (see Figure 5.2.3, page 110).

2 Models are built using data gathered and the interpretation of that data. Random sampling can be used to obtain data from the ecosystem.

3 The extensive biodiversity seen in the fossil record points to a climate that was very different to today's dry and hot habitat. Sedimentary rocks at the sites also indicate signs of a wetter climate. Scientists are using the characteristics of the grey limestone deposited between 25–15 mya. Early relatives of today's fauna were preserved in the lime-rich sediments of the wetlands that flourished at this time. This layer lies on top of older limestone without the fossil remnants and without sedimentation patterns characteristic of a wet climate.

4 Trapped gas bubbles and the presence or absence of traces of organisms in sampled ice cores reveal information about changes in temperature and relative concentrations of atmospheric gases.

5 In Australia, 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. Reduction in global temperatures and lower evaporation rates also affected the water cycle. Lower levels of atmospheric water meant lower rainfall. Some species were able to survive the last ice age by taking refuge in gullies and on mountain tops. These refuges became reservoirs of biodiversity. When the ice age was over, these species spread out and recolonised. Movement of species to other areas by means of exposed land links also helped to preserve Australia's biodiversity.

5.3 REVIEW

1 Land clearance causes a number of issues. If native vegetation is cleared in order to promote the growth of shallow-rooted crops, there is a risk that the water table will rise, bringing its often high salt content to the surface. Land clearance also affects the land's ability to hold its topsoil, leading to erosion and a reduction in soil formation. All of these factors lead to a decrease in biodiversity.

2 Responses will vary. Most land remediation revolves around some form of revegetation. In salt-affected areas, salt-tolerant plants are used in an effort to lower water tables and stabilise topsoil. Better drainage systems can be developed to halt short-term effects, while longer-term solutions such as widespread plantings in catchments can be put in place.

3 Removal of vegetation and the irrigation of pasture have both contributed to salination.

4 Early European settlers tried to impose their agricultural practices on Australian ecosystems that did not have the soil, water or climatic stability for it. These agricultural practices resulted in overgrazing. Clearing of bushland along with overgrazing led to denuding and erosion of areas, salt water springs appearing and some plants disappearing altogether.

5.4 MANDATORY PRACTICAL

As this is a first-hand investigation, student responses will vary.

CHAPTER REVIEW QUESTIONS

1 Lichens colonise bare rock, secreting acids, which attack the rock's surface. Dust accumulates in cracks in the rock allowing mosses to grow producing organic matter. Simple soils form, allowing grasses and small herbaceous plants to start to grow. Growth of small shrubs then growth of larger trees result in the establishment of a climax community.

2 Pioneer species are normally small and photosynthetic. They are hardy enough that they can live under extreme conditions and grow in poor soils with low nutrient levels. Pioneer species have effective seed dispersal, rapid growth and rapid reproduction. They are generally fast-growing and typical of r-selected species.

3 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.

4 Land clearing, urbanisation, habitat destruction and fragmentation, land practices leading to soil degradation and salination and growth of monocultures are some examples of human activity that reduce biodiversity.

5 Primary succession occurs when organisms colonise bare sites with no organisms inhabiting the affected area, whereas secondary succession deals with the changes in communities that are already established. In this instance, organisms recolonise recently disturbed communities.

6 Changes in types of species, population size and population distribution along with species interactions are examples of biotic ecological data that can be used to predict temporal and spatial successional changes. Abiotic data can include amount and quality of soil, rainfall and salinity.

7 Throughout much of Australia the first human inhabitants changed a regime of fire induced by lightning to fire induced by humans to manage and sustain the productivity of the land. In the process, the distribution and abundance of different species of plants changed to ones that became more fire-tolerant. This in turn produced changes in wildlife.

Student responses may include further examples of traditional and contemporary land management practices.

8 Agricultural practices of early European settlers resulted in overgrazing. Clearing of bushland along with overgrazing led to denuding and erosion of areas, saltwater springs appearing and some plants disappearing altogether.

9 If a catastrophic event such as a volcanic eruption or cyclone killed all living things the area would become denuded and result in bare sites with no organisms inhabiting them. The climax community would disappear. Pioneer species would subsequently move into the area. Depending on abiotic and biotic changes, the resulting climax community may be very different to the original one.

10 Habitat degradation has reduced biodiversity. Since 1750, more than 20% of Australia's forests have been cleared for crops and grazing, with nearly 90% of the vegetation cleared in the more fertile areas of southeastern Australia. Evidence of the loss of topsoil and the rise in salinity has reduced areas of natural vegetation leading to a reduction in biodiversity. Widespread monoculture farming practice often requires extensive use of fertilisers along with pesticides and herbicides that reduce the natural tendency of the community to diversify.

11 The rate of change to the environment from current agricultural practices has increased dramatically. Destruction of land habitats, the stripping of vegetation and the exploitation of wildlife have all contributed to the extinction of thousands of species. Urbanisation can cause rapid changes of large magnitude to an ecosystem. Local biodiversity is reduced and, even though new species may potentially move into an urban area, the ecosystem is changed for a very long time, often permanently. Loss of topsoil and salination due to current agricultural practices causes irreversible and significant change to the ecosystem.

12 Student responses will vary.

13 Student responses will vary.

14 Student responses will vary.

15 Student responses will vary.

16 Student responses will vary.

END-OF-CHAPTER EXAM

1 C

2 C

3 A

4 B

5 A

6 Primary succession

7 Any three of: pioneer species are hardy, are able to grow in poor quality soils with low nutrient levels,

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have the ability to fix nitrogen into the soil, are normally small and photosynthetic, have effective seed dispersal, rapid growth, and rapid reproduction and are generally fast-growing.

8 There is reduced recycling of matter and loss of biodiversity in an urban ecosystem compared with a natural ecosystem.

9 Rate of environmental change increased dramatically because European settlers imposed farming practices that did not suit the land.

10 Comparing present biota with those in the fossil record helps us to understand changes in living components of ecosystems over time. The layers and positions of sedimentary rocks in which fossils are embedded indicate the relative ages and relationships between organisms in past ecosystems.

11 It is likely that the orange and blue species are r-selected and the green and purple species are K-selected. Reasons include the fact that r-selected species are typically fast growing and are first to occupy a disturbed area. They increase rapidly but equally decline rapidly when competitive species move in. K-selected species are slow growing and live in more stable environments.

CHAPTER 6: DNA STRUCTURE AND REPLICATION

6.1 REVIEW

1 Nucleus, chloroplasts and mitochondria

2 DNA double helix and histone proteins

3 a Homologous: a pair of chromosomes that have the same size, shape and genes at the same locations

b Sister chromatid: one of the two identical copies of a single chromosome, formed by replication and connected by a centromere

c Endosymbiotic theory: a theory suggesting that mitochondria and chloroplasts arose from ancient prokaryotic cells that were ingested by another primitive prokaryotic host cell

d Centromere: waist-like constriction in a chromosome required for the movement of chromosomes in cell division

4 The DNA of both mitochondria and chloroplasts is similar to the single, circular chromosomes in prokaryotic cells.

5 Two number 21 chromosomes in humans are homologous, if they both carry genes for the same characteristics, although these genes may not be identical.

6

CHARACTERISTIC	PROKARYOTE CHROMOSOME	EUKARYOTE, NUCLEAR CHROMOSOMES
Similarity		
Genetic material	DNA	DNA
Types of nitrogenous bases	A, T, C, G	A, T, C, G
Difference		
Packaging material	Proteins	Histone proteins
Shape	Circular	Linear
Number	Single	Multiple, most are paired

7 A karyotype is a standard form used to display and analyse chromosomes. Photographic images of chromosomes are arranged into matched and ordered pairs. They can be matched as members of each pair share characteristic banding patterns. Chromosomes are ordered by length, from largest to smallest.

8 All human autosomes have a homologous pair, but the Y sex chromosome does not.

6.2 REVIEW

1 Maurice Wilkins, Ray Gosling, Alec Stokes, Rosalind Franklin, James Watson, Frances Crick

2 Nucleotide: a five-carbon sugar (deoxyribose in DNA, ribose in RNA), a negatively charged phosphate group and a nitrogen-containing base – A, G, C, or T in DNA or U in RNA.

3 A–T, G–C

4 Hydrogen bonds

5 DNA: CGGATAACGT

6 Differences: DNA vs RNA: deoxyribose vs ribose; T vs U; double stranded vs single stranded. Similarities, both contain: nucleotide subunits joined into long strands; nitrogenous bases.

7 DNA is made from two long strands of nucleotides, each made when a sugar group of one nucleotide binds to a phosphate group of the next nucleotide. The two strands are wound around each other to form a double helix with the nitrogenous bases of one strand linked to the bases of the second strand. Hydrogen bonds between the opposing pairs of nitrogenous bases hold the double helix together. A bonds with T, C bonds with G.

8 The name Gattaca is made up from the letters G, C, T and A that represent the four nitrogen bases in DNA.

6.3 REVIEW

1 Helicase unzips the DNA double helix by breaking the hydrogen bonds between the base pairs; DNA polymerase joins nucleotides together to form a new DNA strand.

2 Growth, repair, reproduction

3 The shapes of the bases on one strand form a mirror-image match to those on the other strand, such that they can easily bind together.

4 Helicase unzips and separates a small section of the double-stranded DNA by breaking the weak hydrogen bonds between the nucleotides, exposing nucleotide bases, in a continuous unwinding of the parental strands. Free nucleotides attach to the exposed bases T–A and G–C. DNA polymerase, joins the nucleotides to form a new complementary strand. Both strands act as templates for the production of new DNA strands.

5 Semiconservative replication means one strand is newly made and the other strand is from the original parent cell.

6 The mistake (T paired with C) that was made in the ninth base pair from the left, could have been made in two ways. Either a nucleotide carrying a C was wrongly matched with a T, or conversely, the original DNA had a C in that position and it was wrongly matched with a T.

After replication one of the double strands of DNA will have the correct base sequence and the other will contain one incorrect base pair. The cell receiving the latter may or may not produce a functional protein as a result of this mutation.

CHAPTER REVIEW QUESTIONS

1 DNA is found in the nucleus, chloroplasts and mitochondria of eukaryotes and the nucleoid region of the cytoplasm of prokaryotes.

2 Helicase unzips and separates a small section of the double-stranded DNA by breaking the weak hydrogen bonds between the nucleotides, exposing nucleotide bases, in a continuous unwinding of the parental strands. Both strands act as templates for the production of new DNA strands. Free nucleotides attach to the exposed bases T to A and G to C. DNA polymerase, joins the nucleotides to form a new complementary strand alongside each parent-derived strand.

3 DNA replication prepares a cell for cell division for growth, repair and reproduction.

4 DNA is involved in copying the genetic instructions for the next generation and for coding for the synthesis of proteins.

5 In eukaryotic cells, DNA is found in the nucleus, mitochondria and chloroplast.

6 The DNA in eukaryotic organelles codes for some of the proteins involved in the activity of that organelle.

7 If prokaryotes had not developed a nucleus, all organisms would probably be unicellular.

8 Without DNA helicase, the cell would not be able to replicate its DNA; therefore, it could not divide.

9 Without a nucleus, the DNA of prokaryotes would have probably remained in a circular form. This limits the size of the genome, which might prevent the organism becoming multicellular.

10 Having bases on the inside of the double helix allows specific pairing that suggests a possible copying mechanism for the DNA that would not apply if the bases stuck outwards from each nucleotide strand. Also there would be no reason for the complementary nucleotides (A-T, C-G) to be present in equal proportions (base-pairing rule), unless they were joined in the centre of the double helix.

11 The base-pairing rule says that in DNA, the amount of A equals the amount of T and C = G. The table shows that this is approximately true (within the experimental error expected at that time) for all bases pairs, e.g. in human sperm, A = 30% is roughly equal to T = 32%.

END-OF-CHAPTER EXAM

1 C

2 D

3 A

4 C

5 D

6 DNA helicase

7 Replication fork

8 Nucleotides are made up of a five-carbon sugar, a phosphate group and a nitrogenous base.

9 Homologous chromosomes: a pair of chromosomes that have the same size, shape and genes at the same locations

10 Not all homologous chromosomes are homologous because in many organisms one sex, usually the male, has a pair of sex chromosomes that differ in size, shape and the genes they carry.

CHAPTER 7: CELLULAR REPLICATION AND VARIATION

7.1 REVIEW

1 a A cell or organism that has a genome comprising two copies of each chromosome, represented by $2n$, is called diploid, whereas haploid (n) describes a cell or organism that has a genome that contains one copy of each chromosome, represented by n.

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b A gamete is a sex cell that combines with another sex cell at fertilisation to form a zygote, which is the first cell of a new individual. In humans, gametes are ova and sperm cells.

c Autosomes are chromosomes that are the same in both males and females of a species. Sex chromosomes are chromosomes that affect sexual traits.

2 a n equals 23, the haploid number.

b Somatic (body) cells are $2n$.

3 Cytokinesis is division of the cytoplasm, when half the cytoplasm and half the organelles separate to each daughter cell.

4 Oogenesis: cytokinesis in meiosis I and II is unequal producing single egg and small polar bodies that degenerate. At birth an ovary contains all the cells that will ever develop into eggs. A secondary oocyte is released each month after puberty. The break between beginning and end of meiosis I may be as long as 40 years

Spermatogenesis: each division produces four sperm. After puberty, sperm are produced continuously throughout a man's lifetime.

5 An allele is one of two or more different versions of the same gene (at the same locus) determined by small differences in the DNA sequence of the gene. For example, blue and brown are two alleles of the gene for eye colour.

6 Prophase I (cell is diploid – $2n$): chromatin threads shorten and thicken, spindle forms and is attached to centromere of each chromosome. Homologous chromosomes come to lie side by side and nuclear membrane breaks down.

Metaphase I: the homologous chromosomes line up across the equator.

Anaphase I: the maternal and paternal chromosomes of homologous pairs are pulled towards opposite poles of the cell by the spindle fibres. Sister chromatids remain attached at their centromeres, moving together towards the same pole.

Telophase I: spindle breaks down, cell starts to split across its middle, and nuclear envelopes form around the two new nuclei. Division of cytoplasm, completes meiosis I. The two resulting cells are each haploid – n.

7 Males determine the sex of their offspring, so Henry VIII was wrong to blame his wives for not producing any sons. All eggs carry one X chromosome; 50% of his sperm would have also carried an X chromosome, which would produce a girl, and 50% of his sperm would have carried a Y chromosome, which would produce a boy.

8 In meiosis, chromosomes exchange segments of genetic material with one another in a process called crossing over. This recombination scrambles lengths of maternal and paternal genes and rearranges the combinations of alleles on the homologous chromosomes. This produces new combinations of genes, which increase genetic diversity in offspring.

9 If from a human, the karyotype would have 22 pairs of chromosomes and two sex chromosomes. A female would have two X chromosomes and a male would have an X and a Y chromosome.

7.2 REVIEW

1 Metaphase I

2 2^{23} or 8 388 608 possible combinations

3 Independent assortment is the process by which paternal and maternal chromosomes of each homologous pair behave independently of the other homologous pairs, as they separate in meiosis. The original maternal and paternal chromosomes are distributed randomly to the gametes instead of moving as a predefined set.

4 Random fertilisation means that any sperm can fertilise any egg.

5 Independent assortment shuffles existing alleles into different combinations in the sex cells, greatly increasing genetic variation in the offspring.

6 In bees, there would be much more variation in eggs than in sperm. As sperm are produced by mitosis, they would be identical. In eggs, which are produced during meiosis, crossing over rearranges the combinations of alleles on the homologous chromosomes and independent assortment shuffles existing alleles into different combinations in the eggs. Both processes greatly increase genetic variation between the eggs.

CHAPTER REVIEW QUESTIONS

1 Nucleus

2 In the ovaries of females, the primary oocytes begin meiosis during embryonic development, before a woman is born. They remain in prophase I until the female matures sexually. Then a primary oocyte completes meiosis I each month to form a secondary oocyte that is released from the ovary. The second meiotic division, which produces a haploid ovum (egg), occurs only if a sperm fertilises the egg. Meiosis stops occurring after the woman enters menopause, at around the age of 50 years old. By contrast, males produce sperm by meiosis after becoming sexually mature and continue throughout the rest of their lives.

3 The purpose of meiosis is the production of sperm in males and ova in females.

4 DNA and histone proteins

5 Meiosis and fertilisation

6 Sexual reproduction would not be possible in a haploid organism because meiosis cannot occur without homologous pairs of chromosomes.

7 Meiosis would stop in this cell culture, because if the spindle could not contract, the chromosomes would not be able to move to the poles.

8 This statement is incorrect because every cell contains identical genetic material, which comprises one set of chromosomes from the mother and a second set from the father.

9 Crossing over, independent assortment and random fertilisation are the processes that produce genetic variation among offspring. These processes only occur in sexual reproduction.

END-OF-CHAPTER EXAM

1 C

2 B

3 B

4 a Cell B could be in any one of: prophase I, metaphase I or anaphase I.

b Cell B would contain 32 chromatids.

5 Karyotype

6 The sequence of DNA would not be exactly the same in all members of the koala species because different individuals would have slightly different genes for characteristics such as coat colour and body size, and males and females would have some different genes.

7 Only cells from the testes or ovary undergo meiosis so they would not necessarily be dead just because they have not undergone meiosis.

CHAPTER 8: GENE EXPRESSION

8.1 REVIEW

1 A genome consists of all the DNA in a cell or an organism, including genes, which are segments of DNA that code for the protein production.

2 a Genomics: the study of genomes of different species

b Bioinformatics: the science of managing and analysing huge amounts of complex biological data using advanced computing techniques.

3 The Human Genome Project was mapping the human genome, i.e. determining the complete sequence of over three thousand million nucleotide bases in human DNA

8.2 REVIEW

1 a Specific examples listed in text: haemoglobin carries oxygen (and some carbon dioxide) in blood; keratin is a fibrous protein in protective tissues, such as hair, skin and nails; actin and myosin proteins are components of muscle cells that allow them to contract for movement of body structures; a myriad of different proteins are required for structural, functional and regulatory roles in cells and thus whole organisms (see part b also).

b Every chemical reaction in every cell is regulated by enzymes. Without enzymes, reactions would not occur at a rate fast enough to maintain cellular functions.

c mRNA is a single-stranded molecule produced against a DNA template in the nucleus, with triplet codes complementary to those of the DNA template. It moves out of nucleus to ribosomes in the cytoplasm where amino acids are assembled in order according to mRNA codon sequence.

2 Proteins are made up of one to many polypeptide chains which are composed of a series of amino acids joined by peptide bonds.

3 a transcription: formation of mRNA molecule against DNA template strand; translation: mRNA molecule 'read/translated' by ribosome to form chain of amino acids in order specified by mRNA codons

b The RNA transcribed directly from the DNA is called pre-mRNA. It is then modified to make mature mRNA, which moves out to the cytoplasm. Modifications involve addition of a methylated cap and a poly-A tail and removal of the introns.

4 The segment of a DNA strand that is used as a template for transcription of a pre-mRNA strand is called a gene, and this gene contains both exons and introns, as does the transcribed pre-mRNA molecule; before this mRNA moves out of the nucleus to the cytoplasm, the introns are removed, leaving only the exons to code for amino acids in what is then called mature mRNA.

5 a When exons from the same mRNA molecule are spliced together in different arrangements, varied forms of the mature mRNA are created and are translated into different versions of polypeptides. Therefore, variations in expressed proteins are generated by this alternative splicing.

b Particular tissue types in multicellular organisms contain uniquely different versions of proteins suited to each tissue type, yet all have been encoded by the same gene. Alternative splicing such as this occurs in the processing of 95% of human genes.

6 a i AUG

ii UAA, UAG, UGA

b i UCG AUA GCU CAG UUU

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ii TCG ATA GCT CAG TTT

iii Serine, isoleucine, alanine, glutamine, phenylalanine

8.3 REVIEW

1 Central dogma of molecular biology: one-way sequence of information transfer where DNA acts as a template for its own replication, and also as a template for the production of mRNA; newly formed mRNA is modified to become mature mRNA, before the mature mRNA moves out to the cytoplasm to act as template for translation into amino acid chain.

2 a i Coding DNA sequences are transcribed into mRNA and then translated into polypeptides, components of proteins.

ii Non-coding DNA may be transcribed into RNA but is not translated into proteins.

b Non-coding DNA includes genes for non-coding RNA (e.g. rRNA-ribosomal RNA and tRNA-transfer RNA), regulatory DNA and introns, and centromeres and telomeres.

3 Non-coding DNA may be transcribed into RNA other than mRNA that results in polypeptide and protein production (see part 2b) or there may be DNA sequences that are never transcribed into RNA, some of which have other functions, such as centromeres and telomeres, and some perhaps no function.

4 They both serve particular functions in protein synthesis: tRNA carries particular amino acids to the mRNA at the ribosomes for translation into specific polypeptides, and thus proteins; and rRNA combines with proteins to form ribosomes to carry out translation of mRNA.

5 Centromeres hold duplicated chromosomes (sister chromatids) together, and are the site of attachment for spindle fibres to move chromosomes in cell division. Telomeres are extensions of DNA at the ends of chromosomes that act to prolong the life of chromosomes. At each replication of a DNA molecule, some of the repeating segments making up the telomeres are lost, but the coding sections are preserved. Introns regulate gene expression, including by alternative splicing to increase variety of proteins produced from single gene.

8.4 REVIEW

1 Those genes that are 'switched on' or expressed produce only the polypeptides (and thus proteins) that are necessary for the functioning of that particular cell type at that particular time, so that cell energy is not wasted in producing unnecessary polypeptides, which could potentially interfere with the functioning of the required proteins.

2 a Gene expression: gene is transcribed into mRNA and translated into a polypeptide, or into functional RNA

b Gene regulation: various processes that enable a gene to be expressed (or not) in specific cells at specific times and at specific rates

3 a Housekeeping gene: gene that encodes a polypeptide as part of a protein required to maintain essential and ongoing cellular processes

b Production of enzymes for essential chemical reactions such as those in cellular respiration, photosynthesis and other synthesis reactions for essential biomolecules or their breakdown.

4 Genes are routinely inactive/switched off, unless the particular protein/polypeptides they code for are required in that particular cell at that particular time, and then would need to be switched on by regulatory substances.

8.5 REVIEW

1 a Chromatin: in eukaryotic organisms, DNA exists in combination with a protein called histone.

b Nucleosome: structural unit of chromatin where DNA strand is looped twice around a spherical-shaped core of eight histone protein molecules.

c Histone: protein around which DNA winds in nucleosome of eukaryotic organisms

d Regulatory protein: protein that binds to DNA to switch a gene on or off

e Epigenetics: the study of chemical modifications to gene function that are not due to a change in the DNA sequences

2 In chromatin, the DNA molecule is tightly coiled around histone proteins in units called nucleosomes, and it is not possible for RNA polymerase enzyme to access the DNA for production of mRNA to occur.

3 If a cold pad is fixed to the Himalayan rabbit's back, where white fur normally grows, and is kept cold and left in position for a certain period of time, black hair begins to grow beneath the pad. In cold weather, this happens naturally at the extremities, where body temperature is lower. Black hair is an adaptation to cold conditions as black colour absorbs more heat than white.

4 Transcription

5 Some nucleotide bases in DNA have a methyl chemical group attached; DNA is 'methylated'. Genes are switched off when methylation occurs, due to the methyl group projecting out from the DNA and blocking the RNA polymerase enzyme from binding to DNA to transcribe it into mRNA.

X-inactivation in female tortoiseshell cats (Figure 8.5.2, page 163) occurs due to methylation of one of the two X chromosomes in cells of the early

embryo. As a result, some cells have only the black fur colour allele active on that one X chromosome, and others have only the orange active.

All cells descended from these original embryonic cells then occur in a 'patch' where only either the black or orange allele is expressed, producing the characteristic black and orange 'patchwork' coat pattern.

6 When the agouti gene is expressed, phenotypic results include hairshaft with yellow coloured banding and disadvantageous features including obesity, and a higher risk of cancer and diabetes. If pregnant mice are given a diet high in methyl groups, they give birth to a higher proportion of mice with plain brown fur, and normal weight. The agouti gene is methylated, and thus switched off. When methylation is low, the agouti gene has a high expression of its protein product, producing yellow mice, with the previously described characteristics harmful to their health.

7 a mRNA is prevented from being translated into a polypeptide at the ribosome by: (i) attachment of protein(s) to the mRNA strand that block(s) the process of tRNA 'delivering' amino acids to form polypeptide chain; or (ii) another type of RNA called microRNA (miRNA), which has a codon sequence complementary to mRNA, base-pairs with the mRNA, and thus blocks the tRNA molecules being attracted to the complementary mRNA codons to deliver amino acids. miRNA are short segments, around 20 nucleotides in length, transcribed from non-coding DNA in the nucleus.

b i Similarity: the proteins described in part a(i) that bind to mRNA act just like the protein 'transcription factors' that bind to regions of DNA near to coding genes and prevent transcription of the DNA by blocking access of RNA polymerase enzyme.

ii Differences: at translation for part a (i) it is 'delivery' of amino acids by tRNA to mRNA that is blocked, rather than blocking RNA polymerase from DNA in transcription; and in (ii) miRNA blocks translation of mRNA by bonding with it to form double stranded RNA at the ribosomes, rather than a protein acting as a barrier.

8.6 REVIEW

1 Morphology: shape and form of an organism or its body part

2 A homeobox gene codes for a protein that regulates morphology in a developing embryo; there are only quite a small number of these genes, also known as 'toolkit genes', with each being expressed precisely in specific parts of the embryo.

3 Several maternal-effect proteins diffuse across the egg, creating varying concentration gradients at various positions in the egg. These combinations of different protein gradients at different positions are maintained as the zygote divides to form the embryo and affect non-coding regions adjacent to genes to either activate or repress gene expression. In this way, different genes are expressed in different positions to produce the various positional development of embryonic structures.

4 a SRY gene (sex-determining region of the Y chromosome)

b SRY protein

c SRY protein is a regulatory protein that activates the genes responsible for testes development. As the testes develop, they produce hormones, including testosterone, that steer the embryo towards the differentiation of male features, ultimately including formation of the penis and other components of the male reproductive system.

CHAPTER REVIEW QUESTIONS

1 A small segment of DNA; specific sequence of nucleotides in a genome containing the code for a protein molecule or one of its parts, or for a functioning RNA molecule, such as rRNA or tRNA

2 The process of information in a gene being transcribed into mRNA and translated into a protein, or one of its parts: a polypeptide; or transcribed into functional RNA (tRNA, rRNA) necessary for protein synthesis

3 Various processes that enable a gene to be expressed (or not) in specific cells at specific times and at suitable rates of protein production

4 Polypeptides and functional RNA required for protein synthesis

5 a Coding DNA is transcribed into mRNA and then translated into polypeptides, which combine to form proteins; non-coding DNA does not code for polypeptides

b
- Genes producing introns: for gene regulation (switching genes on or off)
- DNA transcribed into functional RNA, including rRNA – folded molecule of RNA that combines with proteins to form ribosomes – and tRNA – RNA molecules that pick up amino acids from cytoplasm and carry them to ribosomes to pair up with specific mRNA codons
- Centromeres: waist-like constrictions in chromosomes holding chromatids together after DNA replication and points of attachment of spindle fibres for the movement of chromosomes during cell division

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- Telomeres: hundreds to thousands of repeated short DNA sequences at the ends of chromosomes to help maintain the coding DNA sections considering that short lengths of chromosomes are lost with each replication of DNA

6 (1) Transcription: a single-stranded mRNA molecule is generated from the single template strand of the 'unwound' DNA double helix, as a result of complementary pairing/bonding between nitrogen bases (adenine on DNA strand with uracil on RNA; thymine on DNA with adenine on RNA), and between cytosine and guanine. RNA polymerase enzyme bonds the RNA nucleotides together into a single strand molecule called pre-mRNA.

(2) Modification of pre-mRNA in nucleus: methylated cap added at one end of pre-mRNA strand and poly-A tail to other end; sections of RNA called introns are removed (introns are regions of base sequences that don't code for polypeptide production), and remaining sections called exons are spliced back together to form mature mRNA which then moves out into cytoplasm.

(3) Attachment of one to many ribosomes to mRNA, in cytoplasm

(4) Translation: each ribosome moves along mRNA until it comes to an AUG start codon, the signal to begin the process of assembling amino acids into the polypeptide chain specific to the particular nucleotide sequence in the mRNA; tRNA molecules during translation carry amino acids to the ribosome for assembly into the polypeptide chain, where peptide bonds connect them to each other.

7
- At transcription: chemical modification (e.g. acetylation) of histone proteins in chromatin to 'unwrap' and expose DNA; direct chemical modification of DNA; transcription factors (regulatory proteins) produced by genes other than those they are regulating; environmental influence, including epigenetic effects: chemical modifications that can be passed on to offspring without alteration of the base sequencing in genes
- At modification of pre-mRNA to mature mRNA in the nucleus
- At translation: mRNA-binding proteins can attach to the mRNA and block ribosomes from being able to translate it; a type of RNA called microRNA (miRNA) can base-pair with mRNA to block translation
- Regulation can also occur after translation

8 DNA, expression and regulation (non-coding DNA produces regulatory proteins); mRNA, expression; tRNA, expression; rRNA, expression; miRNA, regulation

9 Himalayan rabbits exposed to cold conditions for a certain period of time develop black hair instead of white at body extremities, and those not exposed to such conditions retain white hair. Pregnant mice carrying the agouti allele for hair colour produce lower proportion of offspring expressing agouti allele if they're fed a diet high in the methyl chemical group compared to those fed a diet low in methyl chemicals.

10 After publication of the human gene sequence, estimates of the number of protein coding genes were reduced by 80% of original 100 000 estimate.

There are many examples other than the proposed one-way sequence of information transfer (DNA transcription followed by mRNA translation), e.g. retroviruses, as in human immunodeficiency virus (HIV), using the enzyme reverse transcriptase to produce DNA from the RNA genome.

Only a tiny fraction of the genome results in polypeptide production.

Chemical modification of DNA can affect the expression of genes.

Genes work together in networks.

11 Single or double stranded; tyrosine (T) nitrogen base or uracil (U) base; recovered from nucleus or cytoplasm

12 a 100 codons – one for each amino acid (not counting start and stop codons)

b 300 bases – 3 for each codon

c 63 adenine bases in template pair with 63 thymine bases in non-template

d No, only know there would be 237 non-thymine bases (adenine, cytosine and guanine) in the non-template strand

13 Student responses will vary.

Possible interpretation of analogy: *house plans* for carpenter to 'read' = DNA base sequence code carrying instructions to be passed on to ribosomes by mRNA transcribed from DNA; *timber* represents 'building blocks put together' to make kitchen = amino acids comprising polypeptide chain manufactured during translation at the ribosomes; *hammer* is tool to help construct kitchen from timber = mRNA, ribosome and/or tRNA are necessary in polypeptide assembly from amino acids; *nails* holding timber together = peptide bonds holding amino acids together after translation.

14 Explanations are within answers of Question 13.

15 a 100 codons – one for each amino acid

b 400 bases – 4 for each codon

16 Explanations are within answers of Question 15.

END-OF-CHAPTER EXAM

1 A

2 B

3 C

4 D

5 C

6 a Gene expression is the process in which gene codes direct the production of RNA – mRNA codes for the production of a polypeptide, or rRNA or tRNA, which are functional RNA molecules needed for polypeptide production

b Gene regulation includes several processes to activate or repress gene expression in particular cells at particular times and at particular rates of protein production.

7 Answers in *italics*:

DNA	NON-TEMPLATE STRAND	*T*	*G*	*G*	*C*	*A*	*C*	*G*	*G*	*A*	T	C	A
	TEMPLATE STRAND	*A*	*C*	*C*	G	*T*	*G*	*C*	*C*	*T*	*A*	*G*	*T*
mRNA CODON		*U*	*G*	*G*	*C*	A	C	*G*	*G*	*A*	*U*	*C*	*A*
tRNA ANTICODON		*A*	*C*	*C*	*G*	*U*	*G*	C	C	U	*A*	*G*	*U*
AMINO ACID		Tryptophan			*Histidine*			*Glycine*			*Serine*		

8 Polypeptide, rRNA, amino acids, ribosome, division

9 a Both exons and introns are transcribed into pre-mRNA, but introns are removed and exons joined back together, in a process called splicing, before the mature mRNA leaves the nucleus.

b When exons from the same RNA segments are spliced together differently, alternative forms of the mRNA are created, and are then translated into different versions of the polypeptides, and thus different final proteins. Introns direct this alternative splicing.

In this way, particular tissue types in multicellular organisms contain uniquely different versions of proteins that have all been encoded by the same gene. Alternative splicing such as this occurs in the processing of 95% of human genes.

10 The addition of acetyl chemical groups, 'histone acetylation', to specific amino acids in the histone protein tails results in a loosening of the association of the histones with DNA, so that transcription of the exposed DNA can occur; thus the gene is 'switched on'/can be expressed. Conversely, the addition of methyl groups, 'histone methylation', results in gene inactivation, due to attraction between the methylated histones and DNA, that block transcription.

11 a Female tortoiseshell cat

b Transcription of the inactivated gene would not occur

12 Translation

13 Two possible answers are:

- Himalayan rabbit body parts exposed to cold conditions for a certain period of time develop black hair to replace white, at extremities, and those not exposed to such conditions retain white hair.
- Pregnant mice carrying the agouti allele for hair colour produce lower proportion of offspring expressing agouti allele (phenotypic features yellow hair, overweight and prone to obesity, diabetes and cancer) if they're fed a diet high in the methyl chemical group, compared to those fed a diet low in methyl chemicals.

14 The distinctive localised expression of homeobox genes in the embryo to direct development is accomplished due to specific proteins formed in the egg before fertilisation: maternal-effect proteins. These proteins diffuse across the egg, forming concentration gradients that convey positional information in the egg. The concentration gradients are preserved during the early rounds of cell divisions in the zygote, after fertilisation, so that positional information is retained by later generations of daughter cells in the developing embryo. The maternal-effect proteins interact with non-coding DNA regions immediately adjacent to the homeobox genes to either activate or repress gene expression. The pattern of expression of the homeobox genes, and thus development of body structures, ultimately reflects the concentrations of the positional proteins within the developing embryo as it undergoes cell division.

CHAPTER 9: MUTATIONS

9.1 REVIEW

1 Intraspecific variation: differences between characteristics of individuals within the same species

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2 Mutation: a change in a gene or chromosome relative to original; may also refer to process of generating change

3 The non-dividing S (synthesis) phase of the cell cycle, specifically when DNA is being replicated; and cell division

4 a Point mutation: a mutation that affects a single base-pair position within a gene

b Phase shift mutation: a mutation caused by the insertion or deletion of one or more nucleotides (but not for three or a multiple of three); therefore starting point for the reading of triplet code sequences for amino acids to be included in synthesised polypeptide chain is shifted away from original position; resulting in all the codons 'downstream' of the mutation being affected.

5 a A mutagen is an agent that causes changes in DNA sequences, increasing the rate of mutations above natural background level

b Mutagen: a chemical mutagen is a molecular substance that would not normally be present in a natural environment (Table 9.1.2, page 175); a physical mutagen is non-molecular ionising radiation, such as high-frequency ultraviolet light (UV light), and certainly even higher energy radiation, such as X-rays, gamma rays and nuclear radiation

6 In a DNA sequence, substitution occurs when a single nucleotide with one nitrogen base type is swapped for a nucleotide with a different nitrogen base; insertion occurs when one or more nucleotides are added in to sequence; a deletion occurs when one or more nucleotides are left out.

7 Referring to Question 4b, it is seen that in a frameshift mutation the consequence for the polypeptide or protein produced is that the amino acid sequence beyond the location of the mutation is most probably completely different from that in the polypeptide that would have originally been produced. Therefore, the protein coded for would be unlikely to be functional. However, for a substitution mutation, with only one nucleotide affected within one codon, effects may range from nothing (where the altered codon may still code for the same amino acid to be added to polypeptide), to the greatest effect where one whole amino acid is substituted for another one in the polypeptide, with consequences dependent on how different the chemical properties of the two amino acids are.

8 a Chemical

b Physical

c Radiotherapy is also known as radiation therapy: physical

9.2 REVIEW

1 From longest (numbered one) to shortest

2 a Aneuploidy: a cell or an organism has an unconventional variation in chromosome number due to loss or addition of one or small number of chromosomes

b Cell division, either mitosis or meiosis

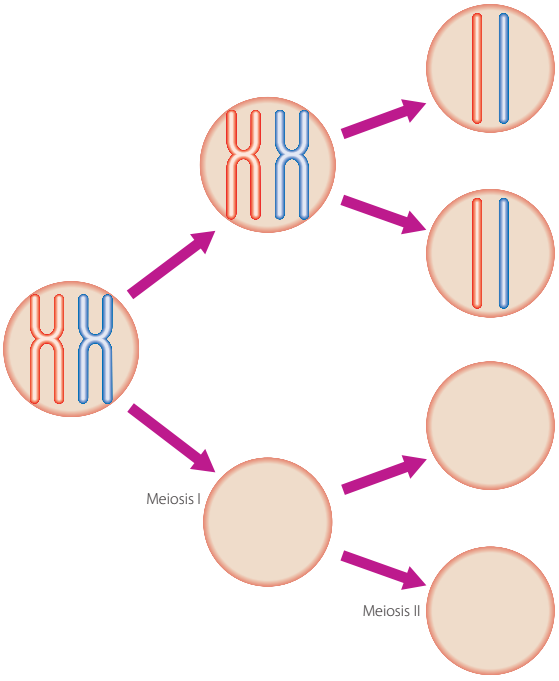
3 Non-disjunction: an error during anaphase in meiosis or mitosis where homologous partner chromosomes or sister chromatids fail to separate to opposite poles

4 a In monosomy, somatic cells contain only one copy of a particular chromosome. In trisomy, they contain three copies of a particular chromosome.

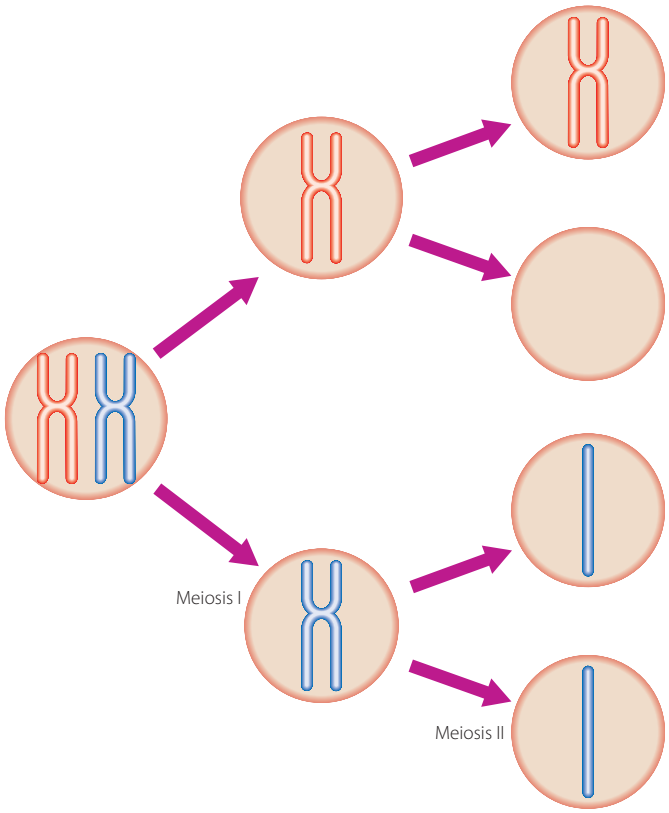
b Down syndrome, also known as trisomy 21, Patau syndrome (trisomy 13) or Edward syndrome (trisomy 18)

5 Metaphase I of meiosis, when each (double) chromosome is beside its homologous partner

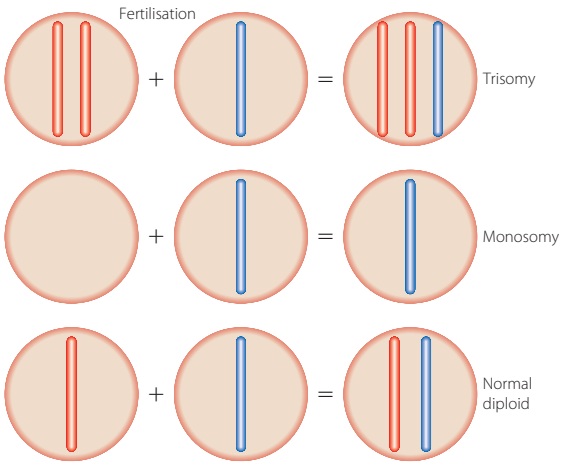
6 a i Non-disjunction at meiosis I produces equal number of gametes with two and no chromosomes instead of all with one chromosome.



ii Non-disjunction at meiosis II produces one gamete with two chromosomes, one gamete with no chromosome and two normal haploid gametes with one chromosome.



b See diagram: top: two chromosome aneuploid gamete + normal haploid gamete = trisomic aneuploid zygote; middle: aneuploid gamete with no chromosome + normal haploid gamete = monosomic aneuploid zygote; bottom: two normal haploid gametes produce normal diploid zygote.



7 In abnormal diploid cells: aneuploid cells could be $2n + 1$, for one extra chromosome and $2n - 1$ for one missing chromosome; or $2n + 2$, $2n - 2$ for two extra or missing chromosomes.

In abnormal haploid cells: aneuploid cells could be $n + 1$, $n - 1$ for one extra or one missing chromosome, or $n + 2$, $n - 2$ for two extra or missing chromosomes.

8

GENETIC ABNORMALITY	SEX CHROMOSOME COMBINATION/S	MALE OR FEMALE?	PHENOTYPIC ABNORMALITIES
Klinefelter syndrome	XXY	Male	Very small genitals, infertile, may develop breasts
Turner syndrome	XO	Female	Infertile, shorter than normal height, webbed neck

9 No. Trisomy is a condition in which three copies of just one chromosome occurs instead of two copies, as in Down syndrome, where there are three copies of chromosome 21. Triploidy is a condition in which there are three copies of every chromosome; extremely rare.

9.3 REVIEW

1 a Apoptosis: programmed series of events that lead to natural cell death as a result of dismantling of the internal contents of the cell by various enzymes

b Allele: one of different versions of the same gene determined by small differences in DNA nucleotide sequences of the gene

c Genotype: a particular combination of paired alleles for a particular gene that determines a characteristic

d Phenotype: a form of observable structural or functional characteristic determined by genotype

e Variation: differences in phenotypes of individuals within a species resulting from their unique genotypes inherited from parents

2 A germ-line cell is a cell line in eukaryotic organisms from which sex cells are produced. A somatic cell is a body cell that will not pass its genes onto next generation.

3 Variation can occur within the following types of features of individuals: morphological (form or shape); biochemical (metabolism – the sum of

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all chemical reactions occurring); physiological (structures and functions); behavioural (set of actions performed in response to environment).

4 The size to which an organism grows depends on quality and quantity of nutrition available to individual, regardless of their genotype.

5 Mitosis is cell division that produces two diploid daughter cells from diploid parent cell; carried out by somatic cells. Meiosis is division of diploid germline cells that produces four haploid gametes (sex cells).

6 Mutations in somatic cells occur only in that affected cell and the daughter cells produced from that cell, and are not passed on to the next generation. Mutations in gametes have the potential to be inherited or passed on to the next and all future generations.

7 Variation in the characteristics (phenotype) of each individual in a species is largely determined by the unique paired combinations of alleles in its coding genes, that is, its genotype. These alleles arise via mutation. Mutations in coding genes cause changes in proteins produced. Occasionally gene mutations lead to the generation of a new allele (alternative of the gene) that benefits the survival of the organism, and perhaps of the species in the long term. A *beneficial* mutation could improve the function of the original protein, or it could eliminate a protein that may have been harmful to the organism in some circumstances.

8 Student responses will vary.

CHAPTER REVIEW QUESTIONS

1 a Spontaneous mutation: a mutation occurring in the absence of exposure to mutagens

b Point mutation: a mutation that affects a single base-pair position within a gene

c Frameshift mutation: a mutation caused by the insertion or deletion of one or more nucleotides (but not for a multiple of three nucleotides) that alters a series of amino acids in a polypeptide from the mutation point on the gene of the DNA onwards

d Whole chromosome mutation: a mutation that affects whole (or large segments of) chromosomes; severe consequences due to so many genes being affected; occurs during cell divisions: meiosis and mitosis, when chromosomes do not separate as they should

e Mutagen: a chemical or physical agent that causes/increases the rate of mutations

2 Karyotype: a display of all the paired chromosomes of an organism or a cell; arranged and numbered in order from 1 (largest) to smallest.

3 a Aneuploidy: where cells have unconventional chromosome number (other than $2n$ in diploid body cells and other than n in haploid gamete cells) due to loss or addition of one or small number of chromosomes

b Non-disjunction: a failure of homologous partner chromosomes in meiosis I, or sister chromatids in meiosis II or mitosis, to separate into different daughter cells

4 Somatic cells are all diploid cells of an organism's body other than cells that produce gametes. Germ-line cells are diploid cells that carry out meiosis to produce haploid gametes (eggs and sperm)

5 During the non-dividing S (synthesis) phase of the cell cycle, specifically when DNA is being replicated; and during cell division

6 Original sequence: GTACATGGC

a GTA*ATGGC: any base other than C substituted at * to change codons to GTA *AT GGC (one codon changed – one, at most, amino acid changed in polypeptide)

b GTA*CATGGC: any base additionally inserted at * to change codons GTA *CA TGG C_ _ (and therefore change all amino acids coded for from * in polypeptide)

c GTA*ATGGC: C removed at * to change codons to GTA ATG GC_ (and therefore change all amino acids coded for from * in polypeptide)

7 Cell division phase – mitosis or meiosis

8 a For example:

- addition and/or removal of bases in DNA
- disruption of packing of DNA by molecule slipping between nitrogen base
- cross-link formed between adenine and guanine to block DNA repair
- nucleotide substitution
- prevention of spindle formation in mitosis and so chromosome number doubled.

b For example:

- affect the chemical structure of the nitrogen bases, e.g. fusing adjacent thymine or cytosine bases in the DNA sequence
- deletion of adenine and guanine bases, creating gaps in the double helix
- cause double-strand breaks in chromosomes.

9 Length of chromosome 'arms'; banding pattern

10 Mutations in germ-line cells can potentially be passed on from generation to generation, but those in somatic cells cannot.

11 See Figure 9.1.2 (page 174) for a frameshift mutation that changes several amino acids in resulting

polypeptide, but substitution only changes one amino acid, at the most.

12 A chromosome contains multiple genes.

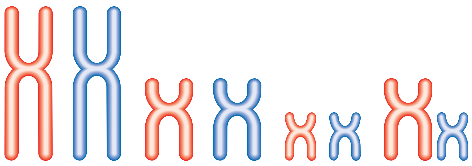
13 Trisomy: 'tri' means three and refers to three copies of chromosome(s); 21 refers to chromosome number 21

14 a Monoploid: only one copy of each chromosome in cells

b Triploid: three copies of each chromosome in cells

c Polyploid: four or more copies of each chromosome in cells

15



16 For an embryo to receive three copies of chromosome 13, one gamete from either mother or father, either egg or sperm, must have had two copies of chromosome 13 due to non-disjunction occurring at meiosis in the production of the gamete, while the other gamete had one copy of chromosome 13. Make sure your diagram illustrates this. (Just show chromosome 13 in your gametes and zygote.)

17 Identify the chromosome pair with an extra part of another chromosome attached. Examine all other chromosome pairs in karyotype, looking for a second pair of non-matching chromosomes, specifically a pair where one chromosome is *shorter* than its homologous partner. If such a chromosome pair is found, compare the difference in length of the shorter chromosome arm to the longer, and determine if that length difference is comparable with the length of the additional chromosomal material attached to the chromosome, which is the subject of this question. If it is, you have identified from which chromosome the extra material originated.

END-OF-CHAPTER EXAM

1 B

2 C

3 D

4 C

5 D

6 Aneuploidy; somatic; XX; X; aneuploid; $2n+1$

7 Different alleles produce phenotypic variation due to the different sequence of amino acids in the polypeptides and thus proteins coded for by the alleles. These different proteins may have many and various effects on phenotype, depending on their function, for example:

- producing a faster metabolic rate in an animal due to an 'improvement' in an enzyme that catalyses the digestion of certain organic molecules in food
- a protein pigment molecule may be altered due to a mutation in the allele and thus a change in amino acids that produce a different pigment colour to the original one, and in this way a different fur colour may be introduced into a population of mammals.

8 Morphological: a dachshund dog has a very long body shape phenotypically unique among other breeds of domestic dogs.

Biochemical: the speed and efficiency of digestion reactions in different dog breeds vary so that some take longer to digest fats in their diet that contain a large quantity of energy, and so are more lethargic after eating than others that have more efficient lipase enzymes to release energy for use from fat more quickly.

Physiological: domestic dogs are descended from wolves, but have shorter muzzles and smaller teeth. There is a lot of variation between jaw and muzzle length among different dog breeds, which is related to the abilities they have for particular types of hunting that they have been selectively bred for.

Behaviour: temperaments or aspects of behaviour vary greatly among different dog breeds, with retrievers, for instance, being very energetic, obedient, vocal and are submissive enough to hand over the prey they retrieve to their handler.

9 It is possible to enhance the feather colour in domestic birds by feeding them capsicum. Likewise in nature, birds that have different diets can show variation in feather colour even if their genotypes are the same for this characteristic.

10 a X-rays are a type of high-energy radiation that is known to cause mutations or increase the mutation rate, and repeated exposure to radiation can damage the body's cells, which can increase the risk of cancer developing.

b Radiation is a mutagen and in high doses can cause mutations (changes in the rapidly growing cells of the foetus). However, it is unlikely that mutations would occur at the levels of radiation that may be used in diagnostics, but it is to be avoided due to the cumulative effect of radiation over your lifetime.

11 This is the unmutated sequence on the template strand of DNA: CCC CCA CCC ACC

Therefore, the unmutated mRNA strand would be GGG GGU GGG UGG, coding for the following

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amino acid sequence in the polypeptide: glycine, glycine, glycine, tryptophan.

i For insertion of A at *, DNA template sequence would change to: CCA CCC ACC CAC C_ _

Therefore, the mRNA strand would be GGU GGG UGG GUG G_ _, coding for amino acid sequence glycine, glycine, tryptophan, valine, and producing a change in one of the four amino acids compared to that in original polypeptide, just for this particular DNA segment.

ii For deletion of the second C, the DNA sequence would be CCC CAC CCA CC_. The transcripted mRNA would be GGG GUG GGU GG, producing the amino acid sequence glycine, valine, glycine, proline – a change of two amino acids of the four in the original polypeptide, just for this particular DNA segment.

The second mutation, ii, would potentially produce the greatest chemical differences in the polypeptide produced, though codons in whole gene would really have to be considered for a definitive answer.

CHAPTER 10: INHERITANCE

10.1 REVIEW

1 When purebreeding/purebred individuals breed among themselves, they always produce offspring like the parents with regards to the gene being studied. Individuals are homozygous for this gene.

2 The P or parental generation refers to two individual organisms that represent the start of a breeding experiment. Their offspring are the F_1 (first filial) generation and the F_2 (second filial) generation are the offspring of the F_1 generation. F_2 represents the second generation produced from a cross between the original two parents (P generation).

3 a In autosomal dominance inheritance, the gene for characteristic is on an autosome (non-sex chromosome) and only one allele of the two at the gene locus is required for characteristic to show; allele for characteristic is dominant

b In sex-linked inheritance, the gene for a characteristic is on a sex chromosome.

4

	POSSIBLE GENOTYPE	HOMOZYGOUS OR HETEROZYGOUS	DOMINANT OR RECESSIVE PHENOTYPE
1	TT	Homozygous	Dominant
2	Tt	Heterozygous	Dominant
3	tt	Homozygous	Recessive

5 Partial/incomplete dominance: heterozygous individual has phenotype intermediate to those of corresponding homozygous individuals

Codominance: both alleles of heterozygous individual are fully expressed in phenotype

6 a Symbols: W white, w red

P cross: WW × ww

For F_1 offspring of purebreeding white and red P generation:

		WHITE PARENT GAMETES
		ALL W
RED PARENT GAMETES	ALL w	All Ww white

F_1 genotype ratio: all heterozygous Ww

F_1 phenotype ratio: all white flowers

F_1 cross: Ww × Ww:

		F_1 PARENT 1 GAMETES	
		$\frac{1}{2}$ W	$\frac{1}{2}$ w
F_1 PARENT 2 GAMETES	$\frac{1}{2}$ W	$\frac{1}{4}$ WW white	$\frac{1}{4}$ Ww white
	$\frac{1}{2}$ w	$\frac{1}{4}$ Ww white	$\frac{1}{4}$ ww red

From this Punnett square, it is expected that $\frac{3}{4}$ of the F_2 generation would be white.

F_2 genotype ratio: WW: Ww : ww = 1 : 2 : 1

$$= \frac{1}{4} : \frac{1}{2} : \frac{1}{4}$$

F_2 phenotype ratio: white : red = 3 : 1

b Symbols: C^W white, C^R red

P cross: $C^WC^W \times C^RC^R$:

		WHITE PARENT GAMETES
		ALL C^W
RED PARENT GAMETES	ALL C^R	All C^WC^R pink

F_1 genotype ratio: all C^WC^R

F_1 phenotype ratio: all pink flowers

F_1 cross: $C^WC^R \times C^WC^R$:

		F_1 PARENT 1 GAMETES	
		$\frac{1}{2}$ C^W	$\frac{1}{2}$ C^R
F_1 PARENT 2 GAMETES	$\frac{1}{2}$ C^W	$\frac{1}{4}$ C^WC^W white	$\frac{1}{4}$ C^WC^R pink
	$\frac{1}{2}$ C^R	$\frac{1}{4}$ C^WC^R pink	$\frac{1}{4}$ C^RC^R red

F_2 genotype ratio: $C^WC^W : C^WC^R : C^RC^R = 1 : 2 : 1$

$$= \frac{1}{4} : \frac{1}{2} : \frac{1}{4}$$

F_2 phenotype ratio: white : pink : red = 1 : 2 : 1

7a i Symbols: C^W white, C^R red

P cross: $C^WC^R \times C^WC^W$

Punnett square for F_1 offspring:

		PARENT 1: ROAN MARE GAMETES	
		$\frac{1}{2}$ C^W	$\frac{1}{2}$ C^R
PARENT 2: WHITE STALLION GAMETES	ALL C^W	$\frac{1}{2}$ C^WC^W white	$\frac{1}{2}$ C^WC^R roan

F_1 genotype ratio: $C^WC^W : C^WC^R = 1 : 1$

$$= \frac{1}{2} : \frac{1}{2}$$

F_1 phenotype ratio: white : roan = 1 : 1

$$= \frac{1}{2} : \frac{1}{2}$$

Note: Offspring ratios would be the same for roan stallion and white mare, i.e. ratios do not differ between the sexes.

ii P cross: $C^RC^R \times C^WC^R$

Punnett square for F_1 offspring:

		PARENT 1: RED STALLION GAMETES
		ALL C^R
PARENT 2: ROAN MARE GAMETES	$\frac{1}{2}$ C^W	$\frac{1}{2}$ C^WC^R roan
	$\frac{1}{2}$ C^R	$\frac{1}{2}$ C^RC^R red

F_1 genotype ratio: $C^WC^R : C^RC^R = 1 : 1$

$$= \frac{1}{2} : \frac{1}{2}$$

F_1 phenotype ratio: roan : red = 1 : 1

$$= \frac{1}{2} : \frac{1}{2}$$

Note: Offspring ratios would be the same for roan stallion and red mare, i.e. ratios do not differ between the sexes.

b Not necessary to state gender of parents: inherited on autosomal gene.

8 a Inheritance pattern: recessive allele on X chromosome

b Inheritance pattern: dominant allele on X chromosome

c Only one allele for the characteristic, as with X and Y chromosomes: there are non-matching alleles at every locus on both

9 P: red × cream

F_1: all cream

Assume autosomal gene, with cream allele dominant: C cream allele, c red allele

P cross: cc × CC

F_1 cross: Cc × Cc

Punnett square for F_2 offspring from heterozygous $F_1 \times F_1$ generation:

		PARENT 1 GAMETES	
		$\frac{1}{2}$ C	$\frac{1}{2}$ c
PARENT 2 GAMETES	$\frac{1}{2}$ C	$\frac{1}{4}$ CC cream	$\frac{1}{4}$ Cc cream
	$\frac{1}{2}$ c	$\frac{1}{4}$ Cc cream	$\frac{1}{4}$ cc red

F_2 genotype ratio: CC: Cc : cc = 1 : 2 : 1

$$= \frac{1}{4} : \frac{1}{2} : \frac{1}{4}$$

F_2 phenotype ratio: cream : red = 3 : 1

10 a X-linked recessive

b Affected male must have inherited ichthyosis allele from mother on her X chromosome

c Scaly skin allele is on X chromosome, and father passes Y chromosome onto sons. Therefore, probability = 0.

10.2 REVIEW

1 Multiple alleles: three or more alleles for one gene

Polygenes: more than one gene controls phenotype of a characteristic

2 Continuous variation: variation in characteristic caused by two or more genes; some genes contribute more than others to characteristic; therefore range of different phenotypes is wide with small, smooth gradations between differences

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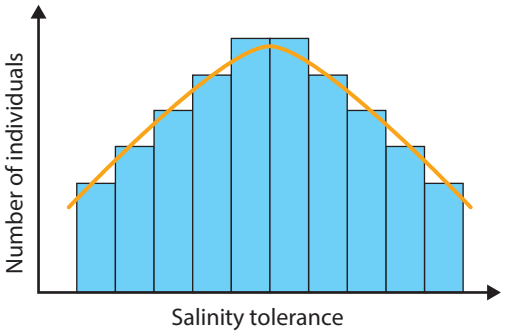
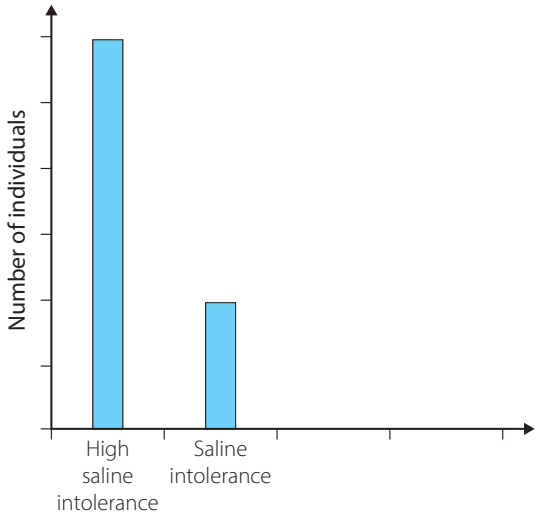
Discontinuous variation: variation in characteristic caused by single gene; shows two or just a few clearly distinct phenotypes

3 a



b



CHAPTER REVIEW QUESTIONS

1 a Autosomal dominance: dominant allele on autosomal (non-sex) chromosome produces characteristic

b Incomplete dominance: heterozygous individual has phenotype intermediate to those of corresponding homozygous individuals

c Codominance: both alleles of heterozygous individual are fully expressed in phenotype

d Sex-linked: gene for characteristic is on a sex chromosome

e Multiple allelic: three or more alleles exist for a particular gene

f Polygenic: two or more genes control phenotype of characteristic

2 i a P: AA × aa; F_1: Aa – offspring has heterozygous genotype; both parents homozygous

b Offspring has same phenotype as AA parent

ii a P: $C^RC^R \times C^WC^W$; F_1: $C^R C^W$ – offspring has heterozygous genotype; both parents homozygous

b Offspring has phenotype different from both parents, intermediate between parent phenotypes

iii a P: $X^A X^a \times X^A Y$; F_1: $X^a Y$ – offspring has genotype different from both parents

b Offspring has recessive phenotype, both parents have dominant phenotype

iv a P: $I^AI^i \times I^BI^i$; F_1: I^AI^B (ABO blood group gene) – offspring has genotype different to both parents

b Offspring has phenotype different to both parents, phenotype of both parents is expressed

3 a Allele on sex chromosome (X or Y); allele on X chromosome

b Recessive allele on X chromosome; dominant allele on X chromosome

4 Continuous range of more than 3 (usually many) phenotypes

5 'Carries' the recessive allele in heterozygous genotype, but it is not expressed due to presence of dominant allele; can pass on recessive allele to offspring

6 Symbols: R red coat, r silver-black coat

a P: RR × Rr

		PARENT 1: RR
		ALL R
PARENT 2: Rr	$\frac{1}{2}$ r	$\frac{1}{2}$ Rr
	$\frac{1}{2}$ R	$\frac{1}{2}$ RR

F_1 Genotype: $\frac{1}{2}$ RR : $\frac{1}{2}$ Rr

F_1 Phenotype: all red

b P: Rr × rr

		PARENT 1: Rr	
		$\frac{1}{2}$ R	$\frac{1}{2}$ r
PARENT 2: Rr	ALL r	$\frac{1}{2}$ Rr	$\frac{1}{2}$ rr

Genotype: all Rr

Phenotype: all red

c P: RR × rr

	PARENT 1: RR
	ALL R
PARENT 2: rr	ALL r: All Rr

F_1: Genotype: $\frac{1}{2}$ Rr : $\frac{1}{2}$ rr

F_1: Phenotype: $\frac{1}{2}$ red : $\frac{1}{2}$ silver-black

7 P: $S^LS^L \times S^LS^R$

F_1: $\frac{1}{2}$ S^LS^L : $\frac{1}{2}$ S^LS^R

F_1 possible crosses: (i) $S^LS^R \times S^LS^R$, (ii) $S^LS^L \times S^LS^L$, (iii) $S^LS^L \times S^LS^R$

(i) F_1 cross $S^LS^R \times S^LS^R$

	PARENT 1: S^LS^R GAMETES	
	$\frac{1}{2}$ S^L	$\frac{1}{2}$ S^R
PARENT 2: S^LS^R GAMETES		
$\frac{1}{2}$ S^L	$\frac{1}{4}$ S^LS^L	$\frac{1}{4}$ S^LS^R
$\frac{1}{2}$ S^R	$\frac{1}{4}$ S^LS^R	$\frac{1}{4}$ S^RS^R

F_2 1 long : 2 oval :1 round

(ii) F_1 cross $S^LS^L \times S^LS^L$

	PARENT 1: S^LS^L GAMETES	
	$\frac{1}{2}$ S^L	$\frac{1}{2}$ S^L
PARENT 2: S^LS^L GAMETES		
$\frac{1}{2}$ S^L	$\frac{1}{4}$ S^LS^L	$\frac{1}{4}$ S^LS^L
$\frac{1}{2}$ S^L	$\frac{1}{4}$ S^LS^L	$\frac{1}{4}$ S^LS^L

F_2 : all long radish

(iii) F_1 cross $S^LS^L \times S^LS^R$

	PARENT 1: S^LS^L GAMETES	
	$\frac{1}{2}$ S^L	$\frac{1}{2}$ S^L
PARENT 2: S^LS^R GAMETES		
$\frac{1}{2}$ S^L	$\frac{1}{4}$ S^LS^L	$\frac{1}{4}$ S^LS^L
$\frac{1}{2}$ S^R	$\frac{1}{4}$ S^LS^R	$\frac{1}{4}$ S^LS^R

F_2: 2 long : 2 oval

Overall expected phenotypic frequencies in F_2: 7 long : 4 oval :1 round = $\frac{7}{12}$ long : $\frac{4}{12}$ oval : $\frac{1}{12}$ round

8 No. Male only has one X allele and even if it is recessive, it is not masked as in an autosomal recessive allele in a heterozygote carrier.

9 a Symbols: X^B barred, X^b non-barred, XY female, XX male

b X^BX^b male × X^BY female

	MALE X^BX^b GAMETES	
	$\frac{1}{2}$ X^B	$\frac{1}{2}$ X^b
FEMALE X^BY GAMETES		
$\frac{1}{2}$ X^B	$\frac{1}{4}$ X^BX^B male	$\frac{1}{4}$ X^BX^b male
$\frac{1}{2}$ Y	$\frac{1}{4}$ X^BY female	$\frac{1}{4}$ X^bY female

F_1 expected frequencies: $\frac{1}{4}$ barred female : $\frac{1}{4}$ non-barred females : $\frac{1}{2}$ barred males

10 $T^a > T^m > T^b$

a P: $T^aT^a \times T^mT^m$; F_1 expected F_1 frequencies: all T^aT^m, all Abyssinian

b P: $T^mT^m \times T^bT^b$; F_1 expected F_1 frequencies: all T^mT^b, all mackerel

c P: $T^aT^a \times T^bT^b$; F_1 expected F_1 frequencies: all T^aT^b, all Abyssinian

11 a Brown eye colour is dominant.

b Symbols: B brown eyes, b blue eyes

P of male F_1: brown-eyed man: Bb × brown-eyed woman: Bb P of female F_1: blue-eyed man: bb × (BB/Bb woman)

F_1: blue-eyed son (bb) × brown-eyed daughter (Bb)

F_2: blue-eyed grandchild (bb)

END-OF-CHAPTER EXAM

1 B

2 A

3 B

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4 C

5 a Homozygous

b Hemizygous

c Heterozygous

6 a Sex-linked: gene is on one of the sex chromosomes

b Multiple alleles: there are three or more alleles for the one gene;

c Polygenic: two or more genes are involved in determining phenotype

7 F_1 phenotypic ratio is approximately $3:1 = \frac{3}{4}:\frac{1}{4}$

Three times more black than white guinea pigs indicate black is dominant to white. To produce recessive white offspring, both parent black guinea pigs must be heterozygous.

Symbols: B black, b white

P cross: Bb × Bb

		PARENT 1: Bb GAMETES	
		$\frac{1}{2}$ B	$\frac{1}{2}$ b
PARENT 2: Bb GAMETES	$\frac{1}{2}$ B	$\frac{1}{4}$ BB black	$\frac{1}{4}$ Bb black
	$\frac{1}{2}$ b	$\frac{1}{4}$ Bb black	$\frac{1}{4}$ bb white

8 a F_1: must be all C^YC^W

b F_1 cross: $C^YC^W \times C^YC^W$

		C^YC^W GAMETES	
		$\frac{1}{2}$ C^Y	$\frac{1}{2}$ C^W
C^YC^W GAMETES	$\frac{1}{2}$ C^Y	$\frac{1}{4}$ C^YC^Y yellow	$\frac{1}{4}$ C^YC^W cream
	$\frac{1}{2}$ C^W	$\frac{1}{4}$ C^YC^W cream	$\frac{1}{4}$ C^WC^W white

F_2 phenotype proportions: $\frac{1}{4}$ yellow: $\frac{1}{2}$ cream: $\frac{1}{4}$ white

9 Symbols: X^h haemophilia, X^H normal blood clotting

a Carrier female × normal male

Cross $X^HX^h \times X^HY$

		X^HX^h GAMETES	
		$\frac{1}{2}$ X^H	$\frac{1}{2}$ X^h
X^HY GAMETES	$\frac{1}{2}$ X^H	$\frac{1}{4}$ X^HX^H normal female	$\frac{1}{4}$ X^HX^h normal carrier female
	$\frac{1}{2}$ Y	$\frac{1}{4}$ X^HY normal male	$\frac{1}{4}$ X^hY haemophiliac male

Expected phenotypic frequencies: $\frac{1}{4}$ normal males : $\frac{1}{4}$ haemophiliac males : $\frac{1}{2}$ normal females

b Haemophiliac female × normal male

Cross $X^hX^h \times X^HY$

		X^hX^h GAMETES	
		$\frac{1}{2}$ X^h	$\frac{1}{2}$ X^h
X^HY GAMETES	$\frac{1}{2}$ X^H	$\frac{1}{4}$ X^HX^h	$\frac{1}{4}$ X^HX^h
	$\frac{1}{2}$ Y	$\frac{1}{4}$ X^hY haemophiliac. male	$\frac{1}{4}$ X^hY haemophiliac. male

Expected phenotypic frequencies:

$\frac{1}{2}$ haemophiliac males : $\frac{1}{2}$ normal female carriers

c Carrier female × haemophiliac male

Cross $X^HX^h \times X^hY$

		X^HX^h GAMETES	
		$\frac{1}{2}$ X^H	$\frac{1}{2}$ X^h
X^hY GAMETES	$\frac{1}{2}$ X^h	$\frac{1}{4}$ X^HX^h normal carrier female	$\frac{1}{4}$ X^hX^h haemophiliac female
	$\frac{1}{2}$ Y	$\frac{1}{4}$ X^HY normal male	$\frac{1}{4}$ X^hY haemophiliac. male

Expected phenotypic frequencies:

$\frac{1}{4}$ normal males : $\frac{1}{4}$ haemophiliac males : $\frac{1}{4}$ normal carrier females : $\frac{1}{4}$ haemophiliac females

10 a Either incomplete dominance (partial dominance) or codominance. One allele must not dominate or mask the other allele's effect, so that the heterozygote is either intermediate between

the two homozygous phenotypes, or shows both characteristics of the homozygous phenotypes. Would need more information to decide between these two.

b Polygenic inheritance; several genes in combination determine the phenotype, with some genes having a greater effect than others producing not only a variety of phenotypes but also a variety of proportions of those phenotypes

c Sex-linked inheritance; different proportions for different genders means gene producing phenotype must occur on a sex chromosome, more likely the X chromosome

d Autosomal dominance; only two phenotypes means that heterozygote must show phenotype the same as the homozygous dominant genotype does

CHAPTER 11: BIOTECHNOLOGY

11.1 REVIEW

1 a Plasmids: small circular pieces of DNA, found in bacteria, that can replicate independently of the cell's chromosomes

b Plasmids are used as vectors to carry a gene of interest into a host cell.

2 Bacterial transformation: when bacteria take up genetic material from their surroundings and incorporate it into their genome

3 Gene cloning is the process of using plasmids and bacteria to make numerous identical copies of a gene

4 Restriction enzymes may produce sticky ends (e.g. *Eco*RI) or blunt ends (e.g. *Alu*I).

5 When making a recombinant plasmid, it is important to cut the plasmid and the gene of interest with the same restriction enzyme so that they have complementary sticky ends that can be joined with DNA ligase.

6 The DNA in all organisms has the same genetic code, so genes from one organism can be used to make proteins in any other organism.

7 To discriminate between transformed and untransformed bacteria, the vector plasmid must contain a gene for resistance to a specific antibiotic. The bacteria are then cultured on a medium supplemented with that antibiotic and only transformed bacteria will be able to grow.

8 a Blunt ends

b Sticky ends

c Sticky ends

11.2 REVIEW

1 The components of a PCR reaction are: the DNA to be copied (template), DNA polymerase, buffer solution that contains salts and other chemicals that help the polymerase to function, a supply of the four nucleotides (i.e. A, T, C, G) from which to build the new DNA molecules and two primers.

2 The sequence of bases on the primers are complementary to base sequences at the start and end of the DNA sequence to be copied; therefore, the primers determine the section of DNA sequence that is amplified.

3 Lowering the temperature to 50–60°C during the annealing phase of PCR allows base pairing and the formation of hydrogen bonds between the primers and the DNA to be copied.

4
- Denaturation, when the double-stranded DNA is heated to 95°C, breaking the hydrogen bonds between the bases, and causing the two strands to separate.
- Annealing, when the temperature is reduced to 50–60°C, to allow the primers to join (anneal) to complementary sequences on opposite ends of each strand.
- Extension, when the temperature is raised to 72°C, to allow DNA polymerase to synthesise new DNA strands.

5 Gel electrophoresis separates segments of DNA on the basis of their size and charge. Smaller fragments, with a greater positive charge move further than larger, less charged fragments.

6 The size of a particular fragment of DNA produced by gel electrophoresis can be determined by its position on the gel in relation to molecular size markers.

7 Increasing the concentration of agarose to make a tighter gel matrix would decrease the speed of migration.

8 After 10 cycles of PCR there would be 2560 copies: 5, 10, 20, 40, 80, 160, 320, 640, 1280, 2560

9 a Lane 2: 200, 250 and 900 bp

b Lane 3: 150, 400 and 600 bp

c Lane 1: 50, 450 and 650 bp

d Lane 4: 100, 100 and 450 bp

11.3 REVIEW

1 Short tandem repeats (STRs) are sections of non-coding DNA used for DNA profiling.

2 a Metagenomics: the study of genetic material recovered directly from environmental samples

b Metagenomics has been used to study the gut flora of patients with irritable bowel syndrome

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and the important interactions between soil microbes and economically valuable plants.

3 PCR is used select and to amplify the DNA of up to 20 different STR regions in a sample for DNA profiling.

4 Once a gene has been sequenced, it will be compared with a normal reference sequence to identify any changes (mutations).

5 The greater the number of STR regions used in DNA profiling, the less likely that a match will be due to chance, instead of it being from the same person.

6 The proteins encoded by the BRCA1 or BRCA2 genes play a role in repairing double-strand breaks in the DNA. As a cell that has lost BRCA1 or BRCA2 activity is unable to repair this damage, it can rapidly accumulate mutations which eventually lead to cancer.

7 Short tandem repeats (STRs) are separated in DNA profiling because gel electrophoresis sorts the fragments according to their lengths. Smaller fragments have fewer repeats and migrate further on the gel than do alleles with more repeats.

8 As an individual inherits one homologous chromosome from each parent, their DNA profile will show one band from their mother and one band from their father. If the man is not the father, few of his bands on his DNA profile will match those of the child.

9 A match between the DNA profiles of a tissue sample at the scene of a crime and a suspect is not necessarily good evidence for a conviction. Being at the crime scene is not evidence that the person actually committed the crime and the tissue may have come to the crime scene either before or after the crime. DNA evidence must be supported with other kinds of evidence like motive and opportunity.

11.4 REVIEW

1 a The most successful process in cloning Dolly was placing the modified eggs into the recipient ewes' oviducts as it had an 89% success rate (247 out of 277).

b The least successful process in cloning Dolly was that 88% of the modified eggs transferred into ewes did not develop.

2 Division in an unfertilised egg cell that has received a new nucleus is stimulated by an electric shock.

3 Transgenic organism: an organism that has been modified by incorporating into its genome a piece of foreign DNA

4 In somatic cell nuclear transfer (SCNT), the nucleus from an adult body cell is transferred into an unfertilised egg cell, whose nucleus has been removed. After being stimulated to divide by an electric shock, the modified egg is implanted into a surrogate mother ewe.

5 DNA from one organism can be transcribed in a different organism because the genetic code is the same in all organisms.

CHAPTER REVIEW QUESTIONS

1 Polymerase chain reaction (PCR) and gel electrophoresis

2 Segments of DNA called short tandem repeats (STRs) are separated according to their size.

3 Short tandem repeats (STRs), which are sections of non-coding DNA where bases are repeated many times

4 Cutting DNA with restriction enzymes and joining the DNA with DNA ligase

5
- Denaturation in which the double-stranded DNA is heated to 95°C to break the hydrogen bonds between the bases thus causing the two strands to separate.
- Annealing in which the temperature is reduced to 50–60°C, to allow the primers to join (anneal) by the formation of hydrogen bonds to complementary sequences on opposite ends of each strand.
- Extension when the temperature is raised to 72°C, so that DNA polymerase can synthesise new DNA strands starting from the primers.

6 In gel electrophoresis, an agarose gel is placed in a tray filled with buffer solution, and positive and negative electrodes are attached at each end of the gel to produce an electric current through the gel.

7 PCR is used to amplify, or make millions of copies of a specific sequence of DNA. It is common that only a small amount of DNA is available for analysis for example, at a crime scene, but techniques like DNA profiling require large numbers of copies of the DNA of interest. Because it uses primers that match the DNA of interest, PCR is able to accurately select particular parts of the genome to copy.

8 The DNA profiles of identical twins would be identical; those from non-identical twins would be similar but not identical.

9 Inbreeding, which leads to low genetic diversity, often occurs in captive breeding programs of rare and endangered species. Increased genetic variation, which enables organisms to tolerate a variety of environmental conditions, is more likely to result from breeding between individuals with greater genetic diversity. The diversity between individuals can be measured by genetic profiling.

10 Non-identical twins arise from two eggs, each fertilised by a different sperm. This situation would give rise to some genetic variation as a result of

meiosis and random fertilisation. By contrast, identical twins arise when a fertilised egg divides and the resulting cells separate and develop into two separate individuals, which will have identical genes as they both arose from the same egg and the same sperm.

11 The evidence that demonstrates a successful captive breeding program for a rare and endangered species would be increased variation as measured by DNA profiling as well as larger numbers of offspring surviving to adulthood and reproducing offspring themselves.

END-OF-CHAPTER EXAM

1 D

2 C

3 B

4 B

5 A

6 C

7 a Mammalian DNA polymerase is not used in PCR because it would be denatured during the PCR process. This is because to denature the double-stranded DNA at the start of a cycle, the temperature of the solution must be raised to 95°C. This temperature can only be withstood by DNA polymerase from bacteria living in thermal springs called *Taq* polymerase.

b Any three of:

- the template DNA which is the DNA to be copied.
- a buffer solution that contains salts and other chemicals that help the polymerase to function
- a supply of the four nucleotides (A, T, C, G) from which the new DNA molecules are built.
- two primers that are short sequences (around 20 nucleotides) of single-stranded DNA, complementary to the nucleotide sequences at either end of the DNA section that is to be copied. The sequence of bases on the primers determines the DNA sequence that is amplified.

8 Student responses may vary, and could include:

- answering questions of paternity, maternity and other kinships quickly
- identifying individuals killed in natural disasters, terror attacks and plane crashes
- establishing or confirming pedigrees in valuable animals such as race horses and stud cattle
- tracing meat to the source animal
- using profiles of plants to prevent counterfeiting of seeds and stock
- non-invasive assays for sex determination.

9 Dolly the sheep's DNA profile would match the profile of the ewe that donated the nucleus from its mammary gland for the nuclear transfer.

10 The gene for the green fluorescent protein would have to be transferred from the cells of the jellyfish to the cells of the zebra fish to produce a GloFish.

11 PCR uses two primers that are short sequences (around 20 nucleotides) of single-stranded DNA. These provide a starting point from which the DNA polymerase can add new DNA nucleotides. DNA polymerase can only extend a DNA strand from an existing nucleotide; it cannot create a new complementary strand without primers to extend from. As the primers are complementary to the nucleotide sequences at either end of the DNA section that is to be copied, the sequence of bases on the primers determines the DNA sequence that is amplified, ensuring PCR amplifies a highly specific segment of DNA.

12 a Person X's DNA was also sampled to ensure that he or she is not actually the criminal.

b The guilty person is suspect 2.

c Suspect 2 is likely to be the guilty person because their DNA profile matches the DNA profile taken from the knife.

CHAPTER 12: EVOLUTION

12.1 REVIEW

1 a Evolution: process of gradual change in the gene pool of a population during successive generations, which may result in the development of new species

b Microevolution: any change in the frequency of alleles within a population

c Macroevolution: major evolutionary changes above the level of species, resulting in the descendant being in a different taxonomic group to the ancestor

2 Although macroevolution and microevolution describe identical processes, they occur on different time scales. In macroevolution, the compounded effects of microevolution over time result in the divergence of taxonomic groups.

3 Lamarck proposed that when organisms acquired characteristics during their lifetimes, they would pass these on to their offspring. For example, a giraffe stretching to obtain leaves high up in a tree would stretch its neck and this longer neck would be passed on to its offspring.

4 Descent with modification was Darwin's terminology for indicating that life today descended

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and evolved from common ancestors that were generally different to their modern descendants.

5 Fossilised transitional forms show traits common to both an ancestral group and its derived descendant group, providing evidence for evolution. For example, *Archaeopteryx* is a bird–dinosaur fossil that shows an intermediate state between the ancestral form of a dinosaur and its descendants which are birds.

6 Before Lamarck's time, it was generally believed that organisms on Earth remained unchanged over time. Lamarck correctly recognised that older fossils were less like living organisms than more recent fossils, concluding that evolutionary change is continually occurring. He incorrectly proposed that the mechanism for evolution was the inheritance of acquired characteristics. It is now known that characteristics acquired during an organism's lifetime are not passed on to its offspring.

7 Darwin's idea of descent with modification described his observations that life today has descended and evolved from common ancestors that were generally different from their modern descendants. He also described the mechanism of evolution, which he called natural selection. He argued that individuals within a population show a range of variation in their characteristics. Those with characteristics most suited to their environment have an advantage, making them more likely to pass these favourable alleles to the next generation. In this way, favourable alleles become more common in the next generation and the population becomes better suited to its environment.

8 The observation that the polar bear shares a common ancestor with two other species of bears, the black and brown bear, demonstrates macroevolution. This is because by definition macroevolution describes major evolutionary changes above the level of species, resulting in the descendant being in a different taxonomic group to the ancestor.

12.2 REVIEW

1 Geological evidence shows that in the past, the continental plates formed a single supercontinent known as Pangaea. Beginning 225 mya, Pangaea broke up into two landmasses: the northern continent Laurasia and the southern continent Gondwana. Around 180 mya, these two land masses themselves broke up, with Laurasia giving rise to North America, Asia and Europe. Gondwana broke into three parts, India, South America and Africa, and Australia, Antarctica, New Zealand and New Guinea. Initially, New Zealand and New Guinea split off, then finally, Australia broke free from Antarctica and began moving northward.

2 Evidence in Figure 12.2.1 that supports the idea that Africa and South America were once connected is that the eastern coast of South America is an almost perfect fit with the western coast of Africa.

3 Tectonic plates are in constant movement, either tearing apart or colliding. Either of these types of movement may result in earthquakes.

4 Evolutionary radiation occurs when many new species evolve from a single ancestral form. This always follows mass extinctions, because the destruction of many species means that major competitors are wiped out. As a result, survivors will no longer have to compete for food and water, so their populations can increase significantly. They will also have access to new and different habitats which will give rise to a variety of selective pressures likely to lead to speciation.

5 Warmer and wetter global conditions are likely to encourage plant growth which might result in the evolution of new species of plants. This will favour large land herbivores, whose populations could increase, as they will have access to a greater amount and variety of plant food. New species of herbivores are also likely to evolve because of these different selective pressures.

6 a Precambrian era

b Carboniferous, Permian, Jurassic and Cretaceous periods

c *Eucalyptus* species would not be expected in Africa because the first eucalypts evolved around 40 mya and Africa and Australia separated long before that in the Cretaceous, more than 65 mya.

7 The extinction of the dinosaurs 65 million years ago, enabled mammals and birds to evolve rapidly during the Paleogene period, because with the destruction of so many species, major competitors were wiped out, and survivors had access to new habitats and no longer had to compete for food and water.

12.3 REVIEW

1 Moving from the root to the tips of a phylogenetic tree means moving forward in time.

2 Phylogenetic relationships are evolutionary relationships. A study of phylogeny tries to reconstruct the evolutionary history of any given group of organisms.

3 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. 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.

4 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.

5 Bioinformatics is an interdisciplinary field combining computer science, biology, mathematics, and engineering. It is responsible for the digital storage, retrieval, organisation and analysis of biological (usually genomic) data. Comparative genomics has dramatically increased the size, accuracy and scope of data sets that need to be analysed, making bioinformatics an indispensable tool in this area of study.

6 Molecular phylogeny is the study of evolutionary relationships using DNA data, the assumption being that the closer the relationship between two organisms, the greater the similarities between their DNA. Molecular homology is shared biomolecular elements, for example amino acid sequences in proteins or base sequences in DNA. This means that molecular homology is one type of evidence used when studying molecular phylogeny.

7 Comparative genomics is the comparison of the entire 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.

8 A comparison of the degree of similarity of DNA between two species can be expressed as a percentage. For example, a comparison of human DNA with DNA from other primates shows that less than 3% of the DNA of the chimpanzee differs from human DNA, whereas around 9% of the DNA of a Rhesus monkey differs from human DNA. The more time two species have been reproductively separated, the more differences they will accumulate in their DNA. Therefore, as the percentage difference in their DNA increases, so the closeness of the relationship between those species decreases. This means that humans are more closely related to chimps than to Rhesus monkeys.

CHAPTER REVIEW QUESTIONS

1 Jean-Baptiste Lamarck, Alfred Russel Wallace and Charles Darwin

2 Similarity: both theories recognised that older fossils are less like living organisms than more recent fossils and concluded that evolutionary change is continually occurring.

Difference: how they explained the mechanism for evolution. Lamarck proposed that when organisms acquired characteristics during their lifetimes, they would pass these on to their offspring. In contrast, Darwin called his mechanism of evolution 'natural selection', in which he said that individuals within a population show a range of variation in their characteristics. Those with characteristics most suited to their environment would have an advantage, making them more likely to survive and pass on these favourable alleles to the next generation. Favourable alleles would then become more common in the next generation and the population would become better suited to its environment.

3 Although Darwin's theory of evolution was published in 1859, he had been working on the theory since returning, in 1836, to England from his voyage around the world on the *Beagle* and he discussed his theory with colleagues as early as 1838.

4 Comparative genomics is the comparison of the entire hereditary information of organisms as encoded in their DNA. First, segments of the genomes of the species to be compared must have their base sequences determined, using next generation sequencing machines that work much faster than previous techniques. Next, sequence alignment techniques are used to identify similarities and differences in DNA from the different sources. Several powerful alignment algorithms have been developed to align and to compare the complete genome sequences of different species. As this produces huge amounts of data to be stored and analysed in a logical and meaningful way, the scale of computation for this analysis is huge and requires the expertise of bioinformatics specialists.

5 Evolutionary radiation occurs when many new species evolve from a single ancestral form. This often occurs with access to new and different habitats which give rise to a variety of selective pressures likely to lead to speciation. For example, the evolutionary radiation of plants after their ancestral green alga colonised land gave rise to a huge variety of forms ranging from mosses, ferns, trees as well as thousands of species of flowering plants.

6 Evolutionary radiation, when many new species evolve from a single ancestral form, is always a consequence of mass extinctions. This is because the destruction of many species means that major competitors are wiped out and survivors will no longer have to compete for food and water. This will lead to an increase in population numbers. These survivors will also have access to new and different

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habitats, which will give rise to a variety of selective pressures likely to lead to speciation.

7 Plate tectonics will cause significant changes in the positions of continents over the next 50 million years.

8 The formation of new glaciers and sheets of ice covering much of Earth would reduce sea levels.

9 In comparative genomics, researchers use a variety of tools to compare the complete genome sequences of different species in order to pinpoint regions of similarity and difference. This enables the drawing of phylogenetic trees that demonstrate the evolutionary events that occurred to give rise to these related organisms. In addition, the identification of molecular homologies via comparative genomics can reveal the shared common ancestry of diverse species.

10 Evidence that plate tectonics will cause significant changes in the positions of continents over the next 50 million years, is that the plates have moved significant distances in the last 50 million years and there is no reason to think that they will stop moving.

11 Drawing a phylogenetic tree demonstrates evolutionary relationships of related organisms and the points at which lineages have diverged. The root of the tree represents the ancestral lineage, and the tips of the branches represent the descendants of that ancestor. 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, when populations became so different from other populations of the same species that they could no longer interbreed. This means that each node represents an ancestor common to all the species above that node.

12 Evidence that the formation of new glaciers and sheets of ice covering much of Earth would reduce sea levels comes from the past as during previous ice ages sea levels dropped. This is because water remaining on the continents as ice and glaciers reduces the amount of water entering the sea and so reduces sea volumes.

END-OF-CHAPTER EXAM

1 B

2 D

3 B

4 A

5 Bioinformatics

6 Comparative genomics

7 The major plates of Earth's crust are in constant movement, floating on the fluid mantle that lies over the core of Earth. Colliding plates can create major mountain ranges when sections of continents crush together, forcing soft rocks upwards. The Himalayas, which were once seafloor sediments containing marine fossils, were thrust upwards when the plate carrying India collided with the Asian plate.

CHAPTER 13: NATURAL SELECTION AND MICROEVOLUTION

13.1 REVIEW

1 a Gene flow: the transfer of alleles that results from emigration and immigration of individuals between populations

b Genetic drift: random changes in genetic frequency in small populations. Each of us inherited half our alleles from our mother and half from our father, and which of these alleles were passed on was a matter of chance. In a small population there is a chance that some alleles present in a parental group will not be passed on at all, and these alleles may be permanently lost from the gene pool.

2 A genotype is the specific combination of alleles belonging to an individual or cell. A phenotype is the actual form taken by a specific feature in a particular individual.

3 An allele is one of different versions of the same gene (at the same locus).

4 Variations that can be passed to the next generation may give an individual an advantage in survival and reproduction compared to the rest of the population. Evolution theory is based on individuals with the alleles best suited to their environment surviving, reproducing and passing their alleles on to future generations.

5 The gene pool of a population may be changed by chance in recombination and mating, migration, the bottleneck and founder effects, and differential selection of phenotypes of individuals in a population.

6 Gene flow is the exchange of alleles of genes between individuals. Gene flow can take place between populations. Immigrants may add new alleles to the gene pool and emigrants may completely remove some alleles or significantly change the frequency of others.

7 Genetic mutation introduces new alleles and, therefore, new variation into populations. Genetic mutations can be advantageous, disadvantageous, or make no difference at all, but they are the main source of variation in a population.

8 Students' diagrams will vary. They could include an example of the founder effect.

13.2 REVIEW

1 Natural selection is a process that occurs in natural systems whereby certain members of a species

that are more suited to the habitat are more likely to reproduce and pass on their alleles to the next generation. For example, in Britain's forests before the Industrial Revolution, the white speckled form of the peppered moth was naturally selected for. After the Industrial Revolution, the dark form of the moth was naturally selected for.

2 Proposition 1: Individuals differ from one another; that is, individuals within populations show variation.

Proposition 2: Many of these variations are caused by mutations in alleles and are inheritable.

Proposition 3: In general, more offspring are born than can survive to maturity and reproduce. Because of this, there is a struggle for existence and only some organisms can reproduce.

Proposition 4: Some individuals have traits that make them more suited to their environment than others (viability), making them better able to reproduce and pass on their alleles to the next generation (fecundity).

3 Natural selection pressures act on traits in the population, resulting in some traits becoming more common as others became less so. This results in changes to the gene pool. Natural selection is the mechanism of evolution.

4 The advantageous variations in traits are naturally selected for their suitability to the environment. Over time, natural selection of the advantageous variations changes populations, resulting in evolution.

5 a This example represents directional selection as one extreme variant is favoured more than others in the distribution.

b The other two types are stabilising and disruptive selection.

6 Microevolution describes a change in the gene pool of a single population over a short time. Historically there were many isolated small human communities with distinct gene pools. Now, increased gene flow is leading to greater heterozygosity, causing changes in the gene pool.

13.3 MANDATORY PRACTICAL

1 Student results will vary but should follow this trend.

First scenario: C^W alleles will become more frequent.

Second scenario: C^B alleles will become more frequent.

Third scenario: C^B and C^W alleles will be even.

Fourth scenario: C^B and C^W alleles will be even.

2 First scenario: C^W alleles selected for, C^B alleles selected against.

Second scenario: C^B alleles selected for, C^W alleles selected against.

Third scenario: C^B and C^W alleles will be selected for or against depending on the background.

Fourth scenario: C^B and C^W alleles will be selected for when together in the grey moth.

3 The colour of the environment or background cardboard has caused the changes. Those moths most visible will be predated at a greater rate than those who are less visible.

4 Grey moths were selected for in scenario four. As these moths have the genotype C^B and C^W, there are equal numbers of each allele.

5 a The fourth scenario is typical of stabilising selection because the extreme variants from the population have been removed and the intermediate types have been preserved.

b The first and second scenarios are typical of directional selection because the variants are at one extreme in the population.

c The third scenario is typical of disruptive selection because variants at both ends of the population are favoured.

6 Answers could include: the number of offspring for each mating pair and in different generations will vary; it is unlikely there would be exactly half males and half females in any one generation; the predation rate would change from generation to generation; other environmental factors would affect predation, survival and reproduction rates.

Conclusion

Variation exists within a population. A change in environmental conditions acting on the population occurs. One phenotype within the population has a selective advantage over the other. The phenotype selected for will survive to reproduce and pass on their alleles to the next generation.

CHAPTER REVIEW QUESTIONS

1 Mutation of an allele, immigration and emigration of individuals and the reproduction rate of various individuals in the population

2 Natural selection is the only selection mechanism that can lead to adaptive evolution. This means that it is the only mechanism that leads to new populations, and the mechanism that produces species that are better adapted to their environment.

3 Factors that influence the viability and fecundity of an individual, a population or a species. They act on traits in the population, resulting in some traits becoming more common as others became less common.

4 Stabilising selection, directional selection and disruptive selection

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5 Immigrants may add new alleles to a gene pool and emigrants may remove alleles during gene flow. If a population crashes in a bottleneck effect only some of the original population gene pool may survive, causing changes in the gene pool. In the founder effect a few individuals isolated from a larger population might not carry all the alleles that were present in the original population.

6 Selection pressures act on traits in the population. Individuals with advantageous traits in the population are selected for, and produce more offspring than those with disadvantageous traits. More advantageous alleles are therefore passed on to the next generation increasing their percentage in the gene pool.

7 Gene flow allows alleles to move between populations. If the population is small, chance events may lead to loss of alleles from the population. The term 'genetic drift' applies generally to random changes in small populations. The 'bottleneck effect' is a term that refers to a situation where only a small number of the original population survive an event. The gene pool of the surviving population contains only some of the original alleles. The founder effect results in a loss of alleles in the gene pool of an isolated population that has formed when some members of the parental population move to a new area.

8 There is genetic variation in the original bacterial population to antibiotics. Those bacteria more resistant will survive and produce more offspring when exposed to antibiotics (the selection pressure) than those bacteria with less resistance. The gene pool of the following generations will have a greater percentage of antibiotic resistant alleles.

9 Natural selection occurs when a selection pressure favours one trait over another. The traits selected for and against must be inherited for natural selection to occur. Allele frequencies change in populations as individuals with the inherited traits produce more or less offspring.

10 Microevolution is a change in the frequency of alleles in a population. Gene flow adds or removes alleles from a population and genetic drift generally reduces the variety of alleles.

11 Changes include mutation of an allele, immigration and emigration of individuals, reproduction rates of various individuals, gene flow, genetic drift, the bottleneck effect and the founder effect.

12 Student responses will vary.

13 Student responses will vary.

14 Student responses will vary.

15 Student responses will vary.

16 Student responses will vary.

END-OF-CHAPTER EXAM

1 B

2 C

3 A

4 A

5 D

6 a Genetic drift: a change in the gene pool of a population as a result of chance. It usually occurs in small populations.

b Refer to Figure 13.1.5, page 246.

7 Mutations are the ultimate source of variation within a population. They result in new alleles. Evolutionary change depends on variation.

8 Natural selection acts on genetic differences among individuals within a population. Without such differences, allele frequencies could not change over time and hence the population could not evolve.

9 a Use of antibiotics

b Directional selection

c Antibiotic resistant bacteria existed in the population before the development of antibiotics.

When antibiotics are introduced, non-resistant bacteria are killed.

Resistant bacteria survive to reproduce and pass on the allele for resistance.

Over generations, the proportion of antibiotic resistant bacteria increases.

10 a Black rabbits would be found in the dark rocks and white rabbits in the white rocks. There would be very few grey rabbits.

b Disruptive selection

c Rabbits with black fur would be able to hide from predators amongst the black rocks and the white furred rabbits would be able to hide in the white rocks, but the grey furred rabbits would stand out in both of the habitats and thus would not survive.

CHAPTER 14: SPECIATION AND MACROEVOLUTION

14.1 REVIEW

1 Speciation: the evolution of one or more new species from an ancestral species

2 Natural selection, speciation and macroevolution

3 The emergence of new species through macroevolution results from an accumulation of microevolutionary changes over time.

4 According to the biological species concept, species are groups of actual, or potentially, interbreeding natural populations that are reproductively isolated from other such populations. According to this model individuals from different species are unable

to produce viable offspring under natural conditions. A biological species is represented by a totally isolated gene pool.

5 The morphological species concept identifies different species based on their physical and physiological characteristics but is limited to what can be observed in the fossil record. The biological species model defines a species as a reproductively isolated group of organisms. These can be identified through consistent differences in morphological and physiological traits as well as genetic differences.

14.2 REVIEW

1 Physical, biological and behavioural barriers

2
- Geographical mechanisms: individuals are separated by geographic features, such as seas, mountains, distance or habitat.
- Temporal (time) mechanisms: individuals breed during different seasons of the year or times of the day.
- Behavioural mechanisms: individuals have different courtship patterns.
- Morphological mechanisms: individuals have different reproductive structures – that is, genitalia of different size, shape or location – so that mating is physically impossible.

3 When populations become isolated and are unable to interbreed and the selection pressures on each population are different, the gene pool of each population changes. Over time their allele frequencies may become so different that the individuals are no longer able to interbreed even if they are reunited.

4 Pre-reproductive isolating mechanisms prevent organisms from being able to interact to reproduce. Post-reproductive isolating mechanisms do not prevent mating from occurring but they do prevent young from being produced.

14.3 REVIEW

1 Allopatric speciation takes place when organisms that could interbreed do not do so because their ranges do not overlap owing to geographic isolation. One example is the flightless cormorant of the Galapagos Islands.

2 Geographic barriers physically prevent individuals of a species from associating to breed. Geographic isolating mechanisms include large bodies of water such as seas, mountain ranges and changes to habitat owing to land clearing and desertification.

3 Forest fragmentation isolates small groups of organisms from a particular species. The lack of gene flow throughout the whole population causes lack of species diversity.

4 Wildlife corridors, also known as habitat or green corridors of natural landscape, allow animals to move to new locations when resources become scarce, to facilitate seasonal migration and to permit interbreeding, ensuring that there is sufficient gene flow between different parts of the isolated populations.

5 Sympatric speciation refers to the evolution of two or more new species from a single population within the same place. It requires a reproductive barrier 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 isolated 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. Examples could include the case of *Magicicada* cicadas and mating calls of frogs.

6 In parapatric speciation individuals are more likely to mate with individuals in their geographic area rather than individuals in a different area. Gene flow would still continue in the bordering areas but over time the populations would diverge to become better adapted to the different conditions in different areas of the environment. Examples could include grasses growing in contaminated soil.

7 New species form in allopatric speciation while populations are geographically separated from each other. No gene flow occurs. Some gene flow is possible during parapatric speciation so formation of new species is more unlikely.

14.4 REVIEW

1 Divergent evolution is a process whereby related species evolve new adaptations over time, away from the common ancestor, to give rise to new species.

Convergent evolution is a process whereby unrelated organisms evolve similar adaptations in response to similar environmental pressures.

Parallel evolution is a process whereby unrelated organisms evolve similar adaptations in response to the same environmental pressures.

Co-evolution is a process whereby an evolutionary change in one species influences the evolution of another species.

2 The giant tortoises showed divergent evolution. As time passed, the different populations adapted to their own unique island habitats. 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

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pressure on the parasite population. If the parasite species become more harmful and kill the host for instance, 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.

14.5 REVIEW

1 After a population bottleneck, the surviving population are 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. It holds a greater reserve of different alleles to draw on as the pressures from natural selection change. Small populations are unlikely to carry all the alleles that were present in the original population. 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 present, the species will become extinct.

14.6 MANDATORY PRACTICAL

1 The definition of species that would lead to a conclusion that the two populations should be considered as two subspecies is the biological species concept (a species is a reproductive community of populations that occupies a specific niche in nature). They would not be considered different species because they would still be able to reproduce fertile offspring if they were to mate. The two populations are fairly permanently geographically isolated from each other and may in future diverge to become two different species. This is the definition of subspecies.

2 The Australian Government has recognised and listed them as subspecies.

3 Data indicates separation of the two populations around 270 000–620 000 years ago. This would be when mainland Australia and Tasmania separated. Allopatric speciation occurs due to physical or geographic isolation. This is illustrated in the two populations of Eastern barred bandicoots that have diverged to some extent due to geographical isolation.

4 The small genetic variability found in the population would reduce the survival chances of the population. With less variability, should a change in selection pressures take place, there is a smaller chance that a possible genetic variation that might assist individuals to survive (and reproduce) would be passed on in their genes to the next generation.

5 Subspecies of the bandicoot are still able to interbreed and produce fertile offspring. By breeding the subspecies together, the diversity in the gene pool will increase. This improves the Victorian population's chances of surviving in its environment.

CHAPTER REVIEW QUESTIONS

1 A biological species is a group of actual, or potentially, interbreeding natural populations that are reproductively isolated from other such populations. According to this model, individuals from different species are unable to produce viable offspring under natural conditions. A biological species is a genetically isolated group, which can only interbreed within itself.

2 Pre-reproductive isolating mechanisms include geographical, temporal, behavioural and morphological mechanisms. Post-reproductive isolating mechanisms include gamete mortality, zygote mortality and hybrid sterility.

3 Allopatric, sympatric and parapatric speciation are modes of speciation.

4 Divergent evolution, convergent evolution, parallel evolution and co-evolution are patterns of diversification between species.

5 When changes in the environment make the habitat so unsuitable that all members of the species die, the species becomes extinct.

6 When populations are reproductively isolated and different selection pressures act on the separated populations, microevolution occurs. Over time, allele frequencies of the isolated populations become so different that the individuals are no longer able to interbreed even if they are reunited, and speciation results.

7 Habitat fragmentation results in division of a large continuous habitat into smaller, more isolated habitats. Gene flow between populations in the isolated habitats is prevented. Over time, subspecies will develop if selection pressures in the local areas become different. Natural disasters such as a river flooding or changing course, may make it impossible for animals to cross it, isolating populations and preventing gene flow. During drought if the river dries up, leaving isolated bodies of water, aquatic animals will not be able to move between two different bodies of water. This, once again, prevents gene flow.

8 In allopatric speciation, gene flow is disrupted as populations become physically separated through geographic isolation. In sympatric speciation, species diverge without any obvious physical or

geographic isolation. A reproductive barrier that isolates members of a population from the rest of the population in the same area is required. Parapatric speciation occurs without physical or geographic isolation. Populations are separated by an extreme change in habitat and it is possible for interbreeding to occur between populations in bordering areas.

9 Species can resemble each other even though they are not related through convergent evolution. Unrelated organisms evolve similar adaptations in response to environments that are similar.

10 If a population with reduced genetic biodiversity is exposed to a changed selection pressure, there is less chance of there being alleles that suit the selection pressure. If no individuals in the species have the genetic variation present for survival, the species will become extinct.

11 New species form when single populations are separated and are no longer able to interbreed and gene flow is prevented. Different selection pressures act on the different populations. Populations change over time as their gene pools accumulate small changes in response to their environment. Eventually a population accumulates so many changes that the individuals are no longer able to interbreed even if they are reunited and a new species can be identified.

12 Environments change over time. For example the earth's climate has been warmer or colder than now, areas have been exposed to more or less rainfall. Many other environmental conditions have changed over long periods of time. Changing environmental selection factors have favoured some phenotypes over others, resulting in changes to the number and type of species.

13 Human overpopulation and activities, for example modern agricultural practices, urbanisation, habitat loss, introduced species, and global warming have had huge impacts on the environment. As selection pressures change rapidly, many species are not able to survive and adapt resulting in a very high rate of species extinction.

14 Student responses will vary.

15 Student responses will vary.

16 Student responses will vary.

17 Student responses will vary.

18 Student responses will vary.

END-OF-CHAPTER EXAM

1 C

2 A

3 A

4 D

5 Isolating mechanisms prevent individuals within a population from breeding. They reduce the alleles in the gene pool involved so that the range of available phenotypes is restricted.

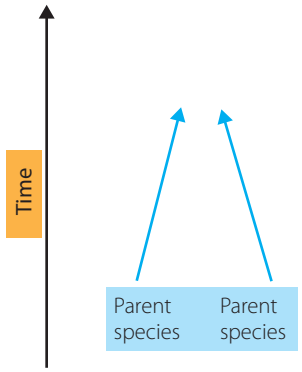
6 Speciation requires variation and isolation. If fruit flies become dependent on a particular variety of apple (or hawthorn) that flowers and fruits at a specific time of the year, they may become isolated from each other and not interbreed.

7 The isolation in Tasmania has not been long enough for speciation to occur or the selection pressures in Tasmania are similar to mainland Australia.

8 a Convergent evolution

b The species are not closely related. The desert environment exerts similar selective pressures. Species adapt similarly to the selective pressure, becoming similar in appearance.

c



Convergent evolution

9 a Allopatric speciation

b Individuals from one population are separated from another population by a geographic barrier. In this case, distance is the geographic barrier.

c Isolated populations cannot meet to mate therefore there is no gene flow between populations.

d Pre-reproductive. The isolated groups are prevented from breeding. If it was post-reproductive isolation, mating would not be prevented from occurring but young are prevented from being produced.

10 Sympatric speciation: speciation that occurs without physical or geographic isolation

11 Habitat fragmentation is the process by which areas of a habitat are lost, resulting in division of a large continuous habitat into smaller, more isolated habitats. Gene flow between populations in the isolated habitats is prevented. Over time, new species will develop if selection pressures in the local areas become different.

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12 The flower shape selects for insects with long tongues that can pick up pollen on their body. If this doesn't happen, flowers are less fit in an evolutionary sense. So flowers with longer tubes would be selected for. If an insect had a short tongue, they wouldn't be able to reach the nectar and would be at a selective disadvantage. An evolutionary change in one species has affected evolution in the other species.

13 a Genetic diversity is reduced.

b Selection pressures such as human predation and loss of habitat through land clearing for agriculture affected all individuals in the species.

c Large populations generally have a more diverse gene pool that has a greater number of different alleles to draw on as the pressures from natural selection change. Low genetic diversity and inbreeding in small populations reduces the chance of alleles suiting a selective pressure being present in the population.

BIOLOGY UNITS 3 & 4 PRACTICE EXAM

MULTIPLE-CHOICE QUESTIONS

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

SHORT-ANSWER QUESTIONS

11 a Physical features, reproductive methods and molecular sequences

b Cladogram

c Grasshoppers and stick insects shared a common ancestor more recently than they did with cockroaches.

d Dragonflies are more closely related to grasshoppers because they shared a common ancestor more recently than silverfish and grasshoppers.

e Stratified sampling is used when the ecosystem comprises a wide variety of subsections and habitats. When the abiotic and biotic factors vary widely across an ecosystem, stratified sampling can ensure that the data reflects a more accurate portrayal of the area.

12 a Biodiversity would decrease because the number of ecological niches would be greatly reduced. The carrying capacity would also be reduced because there are, for example, fewer producers (biotic factors) and more exposure to the sun (abiotic factors). Productivity is drastically reduced, so biomass is reduced.

b i Secondary succession

ii Pioneer community

iii Climax community

c Two of:

- direct observation; for example, with satellite images and video capture, GPS tracking and drones
- sampling; for example, through quadrats, transects and stratified sampling
- Lincoln index, using the capture–recapture measure.

d Plants rely on nitrogen-fixing bacteria to convert elemental nitrogen into ions that they can absorb. Animals absorb nitrogen from the nitrates in plants. Nitrogen-fixing bacteria and denitrifying bacteria in soil and leaf litter absorb nitrogen from the atmosphere and release it back to the atmosphere. After logging, there will be much less leaf litter and hence less available nitrogen available for plants and animals.

13 a Normal: ... UAGUAGAAACCACAA ...

Mutated: ... UAGUAACCACAA ...

b There has been a deletion of three base pairs – CTT has been deleted.

c Messenger RNA

d i Double-stranded DNA unwinds and one strand acts as the template for transcription.

Complementary nucleotide subunits move to pair with those in the template strand.

RNA polymerase joins the complementary nucleotides together to form messenger RNA.

d ii Messenger RNA moves to ribosomes and the codons are read.

Transfer RNAs with complementary anticodons carry specific amino acids to codons in mRNA.

Amino acids link together to form a polypeptide chain.

e DNA is packaged with histone proteins to form the DNA–protein complex referred to as chromatin. The most fundamental unit of chromatin is the nucleosome. When DNA is packaged and coiled into chromatin, the genes within the DNA are not available for expression because they are wrapped and coiled tightly into a very condensed structure. RNA polymerase cannot access the DNA in the chromatin to begin transcription of the mRNA molecule from the DNA template strand. In essence, such genes are 'switched off' and the corresponding polypeptides are not made.

f The mutation in CFTR is the deletion of three nucleotides. This triplet codes for one amino acid. All other codons are

translated into amino acids the same as in the normal CFTR allele.

g Polymerase chain reaction amplifies a section of the DNA containing the CFTR gene from a person's blood sample to make more than one million copies. The gene is then sequenced by a gene-sequencing machine, which determines the order of base pairs. The results identify if the gene contains the normal or mutated allele.

h If C represents the normal CFTR allele and c represents the mutated CFTR allele, normal carrier parents are both Cc.

	C	c
C	CC	Cc
c	Cc	cc

Three-quarters of offspring would be expected to be normal (CC and Cc) and one-quarter would be expected to be cc and develop cystic fibrosis.

14 a There was genetic variability determining egg size within the original population. Within tree-hollow nesting sites, those falcons laying larger eggs produced more offspring than those laying smaller eggs. Over time, more of the population was laying larger eggs.

b Natural selection favours phenotypes that make the population better adapted to its environment. Populations change over time as their gene pools accumulate small changes in response to natural selection (microevolution). Eventually a population accumulates so many changes that a new species can be identified. This process can lead to speciation.

c Speciation that occurs without physical or geographic isolation.

d One of:

- behavioural isolation – falcons choose mates with different nesting patterns
- temporal isolation – falcons mate at different times due to availability of nesting sites
- pre- and post-zygotic reproductive isolation – so many changes to gene pools have occurred that falcons can no longer produce viable offspring.

e Two possible answers: It may be a case of two alleles that have a codominance or incomplete dominance relationship *or* there could be a single gene with more than two alleles.

f Chemical mutagens and physical mutagens

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GLOSSARY

A

abiotic factors the non-living components of an ecosystem, including the physical landscape, minerals and weather conditions

adaptive evolution changes in populations of organisms that make that population better adapted to its environment over time

agarose gel a gel matrix used for electrophoresis

allele one of different versions of the same gene (at the same locus) determined by small differences in the DNA sequence of the gene

allopatric speciation the speciation that is due to physical or geographic isolation

amino acid a simple organic compound that contains both amino ($-NH_2$) and carboxyl ($-COOH$) groups and combine to make proteins

amino acid binding site the site of attachment of an amino acid to a tRNA molecule

anaerobic in the absence of oxygen

aneuploidy a genome variant having unconventional chromosome number due to loss or addition of one or a small number of chromosomes

annealing in the polymerase chain reaction, a process of joining together separate strands of DNA as a result of hydrogen bonds pairing; occurs when the temperature is lowered

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

apomorphic having a characteristic or trait unique to a particular group of organisms that is different from their evolutionary relatives, e.g. snakes, in class Reptilia, have no legs

apoptosis a programmed series of events that lead to natural cell death when the internal contents of the cell are dismantled by various enzymes

aquatic of water

arboreal mostly tree-dwelling

asexual reproduction a form of reproduction in which offspring are produced from a single parent

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, such as genus and species or first name and surname

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

bioinformatics the digital storage, retrieval, organisation and analysis of biological data (e.g. genomic); it is especially important in genomics research because of the large amount of complex data this research generates

biological species concept the definition of a species based on the capacity of individuals to interbreed

biomass the total mass of living matter in an ecosystem

biomass pyramid a pyramid diagram that shows the relative proportions of each trophic level in an ecosystem

biota the living organisms in a region

biotechnology the use of living organisms and biological systems and processes for human benefit

biotic factors the living components of an ecosystem, including animals, plants and bacteria

bivalent visible bodies in a cell during prophase I of meiosis, which are made up of two homologous chromosomes joined together

blunt end the end of a DNA fragment that is created after cleavage by a restriction enzyme that cuts DNA at the same position on both strands

bottleneck effect when a catastrophic event or a period of adverse conditions drastically reduces the size of a population

C

capture–mark–recapture an ecological surveying technique used to measure animal populations, in which individual animals are captured, marked and released; after a time, the population is re-sampled and the number of marked animals caught gives an indication of population size

carrier a non-affected, heterozygous organism carrying an allele for a recessive phenotype; organism may transmit recessive allele to its offspring

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

cellular respiration the process of releasing chemical energy from the bonds of glucose molecules

centromere the waist-like constriction in a chromosome required for the movement of chromosomes during cell division

character matrix a table of characteristics used for classification

chiasmata the point of contact between homologous chromosomes during prophase I of meiosis

chromatid a daughter strand of a duplicated chromosome that is joined to a sister chromatid by a centromere

chromatin a complex of proteins and DNA in eukaryotic chromosomes

chromosome a structure composed of DNA and protein that contains along its length linear arrays of genes carrying genetic information; prokaryotes have one circular chromosome whereas eukaryotes have a number of linear chromosomes

clade a group comprising all of 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 where the community has become relatively stable, e.g. old-growth forests and rainforests

clumped (grouped) distribution a measurement of distribution in which individuals are grouped together when biotic and/or abiotic factors are favourable; can be social (e.g. schools of fish) or clumping of vegetation

coding DNA the small part of DNA used as a template for mRNA synthesis and thus for polypeptide synthesis; also known as a gene

codominant when both alleles of heterozygous individual are fully expressed in phenotype

codon a series of three adjacent nucleotide bases in DNA and mRNA; each codon specifies a particular amino acid to be added when a polypeptide is assembled; start and stop codons also occur

co-evolution a process whereby an evolutionary change in one species influences the evolution of another species

common ancestor a species of organism whose offspring diverged over time

comparative genomics the study of DNA similarities across species

competition a species interaction in which two or more individuals (whether the same species or not) 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 on nucleotides that bind to each other (e.g. A–T and C–G)

congenital present at birth; may or may not be inherited genetically

conserved sequence a DNA or protein sequence that is preserved across species due to optimal function

consumer an organism that eats other organisms for nutrition

continental drift the relative movement of Earth's continental landmasses that appear to drift or 'float' over Earth's mantle

continuous variation the variation in characteristic 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

D

daughter cell either of the two cells formed when a cell undergoes cell division

decomposer an organism, such as a fungus, that grows on and absorbs nutrients from dead tissues

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

deoxyribonucleic acid (DNA) an information molecule that is the universal basis of an organism's genetic material; it contains instructions, written in a chemical code, for the production of proteins by the cell

descent with modification Darwin's terminology indicating that life today has descended and evolved from common ancestors that were generally different from their modern descendants

detritivore an organism, such as a worm, that consumes detritus, the dead tissues of once-living organisms

dichotomous having two branches, two opposing aspects

diploid (2*n*) describes a cell or organism that has a genome comprising two copies of each chromosome, represented by 2*n*

direct observation a method used to measure abundance, e.g. recording sightings at particular intervals; can be time-consuming and dangerous

directional selection a form of selection that selects against one of two extremes and leads to a change in a trait over time

discontinuous variation the variation in a characteristic caused by a single gene; shows two or just a few clearly distinct phenotypes

disjunction the moving apart of homologous chromosomes during anaphase of meiosis

disruptive selection a form of selection that operates in favour of extremes and against intermediate forms

diurnal active during the daylight hours

divergent evolution a process whereby related species evolve 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 an enzyme that helps the two strands of the DNA double helix unwind and separate

DNA ligase an enzyme used to catalyse the formation of a bond between two pieces of DNA

DNA polymerase an enzyme capable of making exact copies of fragments of DNA

DNA profiling a process that is able to identify natural variations that exist within an individual's genome, by using the polymerase chain reaction and gel electrophoresis

DNA sequencing a process of establishing the nucleotide sequence of a piece of DNA

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

dominant the phenotype expressed when at least one copy of its dominant allele occurs in genotype

double-strand break a mutation involving breaks in both of the sugar–phosphate backbones at the same nucleotide pair, resulting in the complete breakage of a chromosome

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

ecosystem a self-sustaining unit consisting of the interactions between the species in the community and the environment

ectothermic when the internal body temperature of an organism 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 prokaryote cells that were ingested by other prokaryote host cells

endothermic when the internal body temperature of an organism is regulated and maintained higher than the temperature of the surroundings

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

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eon a division of geologic time that can be divided into periods, epochs and ages

epigenetics the study of chemical modifications to gene function that are not due to a change in the DNA sequences

epoch a division of geologic time that is shorter than a period and is marked by one or more significant events

era a division of geologic time comprising periods and epochs

ethidium bromide a chemical that binds to double-stranded DNA and fluoresces pink when exposed to ultraviolet light; used to locate DNA in an agarose gel after electrophoresis

eukaryote a complex type of cell with a nucleus and membrane-bound organelles; a member of domain Eukarya

eutherian (placental) a mammal that gives birth to fully developed, or very near fully developed, live young, e.g. dog

eutrophication the increased concentration of nutrients, such as phosphates and nitrates, in a waterway that promotes algal bloom

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, pre-mRNA or mRNA that codes for a polypeptide

exponential population growth the growth of a population in an ideal, unlimited environment

extant currently in existence, not extinct

F

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

fecundity a measure of fertility; the capacity to reproduce

first filial generation (F_1) the first generation of offspring produced from a cross between two parents (P)

fitness the capacity of an individual to survive and pass on 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 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

frequency histogram a specialised column graph illustrating frequencies or proportions on vertical axis of different items (genotypes and phenotypes) on horizontal axis

fundamental niche the widest potential niche that a species could ideally 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 unit of heredity that transmits information from one generation to the next; a segment of DNA that codes for polypeptide

gene cloning the process of using plasmids and bacteria to make numerous identical copies of a gene

gene expression the process in which information encoded in genes directs the production of RNA molecules (mRNA, tRNA and rRNA) for polypeptide and thus protein synthesis

gene flow the transfer of alleles that results from emigration and immigration of individuals between populations

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 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 into its genome a piece of foreign DNA

genome all genetic material contained in an organism or a cell, including DNA existing as chromosomes within the nucleus, and DNA in mitochondria and chloroplasts (if present)

genotype the alleles present in the cells of an organism

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-line the cell line in eukaryotic organisms from which sex cells are produced

Gondwana the southern supercontinent formed after the break up of Pangaea; it included what is now Antarctica, India, Africa, Australia and South America

gross primary productivity (GPP) the total organic matter produced annually in an area by photosynthesis

H

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 (*n*) describes a cell or organism that has a genome that contains one copy of each chromosome, represented by *n*

hemizygous a gene that occurs only as single copy in diploid organism or cell

heredity study of inheritance; genetic transmission of characteristics from one generation to another

heterotroph (consumer) an organism that cannot convert sunlight to useful energy, and must consume other organisms for food

heterozygous a genotype with two different alleles for single gene locus

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

histone a protein that DNA winds around in eukaryotic cells

homeobox gene a gene of a group that code for proteins that regulate body formation and patterning in the developing embryo

homologous a pair of chromosomes that have the same size, shape and genes at the same locations

homozygous a genotype with two identical alleles for single gene locus; purebreeding

host an organism that is infected with a pathogen or parasite

housekeeping gene a gene that encodes a polypeptide as part of a protein (often an enzyme) required to maintain basic cellular processes

humus the dark brown organic matter in soil, derived from decomposed plant and animal remains

hybrid an organism resulting from the interbreeding of two different species

I

immigration the movement of individuals of a species into a place

incomplete dominance when a heterozygous individual has a phenotype intermediate to those of corresponding homozygous individuals

indel a collective term for mutations caused by insertions and/or deletions

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

inheritable capable of being passed on to the next generation

interphase the stage between nuclear divisions

intraspecific variation differences between characteristics or phenotypes of individuals of same species

intron a section of DNA or pre-mRNA that does not code for a polypeptide; is removed (spliced) from pre-mRNA to form mature mRNA molecule

ion an atom or group of atoms that has either lost or gained valence shell electrons, acquiring a net positive or negative charge

ionising radiation radiation that is strong enough to break chemical bonds in molecules, and remove tightly bound electrons from the orbits of individual atoms, causing atoms to become charged or ionised

K

K-selected species a slow-growing, long-lived species typical of those in a climax community

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

Laurasia the northern supercontinent formed after the break up of Pangaea; it included what is now North America, Europe, Asia, Greenland and Iceland

limiting factor an aspect of the environment that restricts an organism's ability to live there

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

locus the position a gene occupies in a chromosome

logistic population growth the population growth that levels off as population size approaches carrying capacity

M

macro-level ecosystem a large area of land or water (typically a whole continent or ocean) and its inhabitants

macroevolution 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

marine saltwater

marsupial a mammal that gives birth to undeveloped live young, who complete their development in their mother's pouch, e.g. kangaroo

maternal inheritance inheritance only from mothers; any trait that is encoded by organelle DNA is contributed by the female

mature mRNA a modified pre-mRNA molecule with introns removed; ready to move out of nucleus to cytoplasm

megafauna large animals

meiosis a two-phase type of cellular division in which the chromosome number of a cell is halved to the haploid number; meiosis is the basis of gamete formation in animals and spore formation in plants

meso-level ecosystem a medium-sized area of land or water (typically a single-named location, such as a desert or lake) and its inhabitants

messenger RNA (mRNA) a ribonucleic acid molecule formed in the nucleus during gene transcription; has nitrogen base sequence complementary to DNA template segment; travels to cytoplasm where ribosomes attach

metagenomics the study of genetic material recovered directly from environmental samples

micro-level ecosystem a small area of land or water (typically a single biome, such as temperate rainforest) and its inhabitants

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

microRNA (miRNA) a small non-coding segment of RNA that plays a role in regulating gene expression at the post-transcription level

migration the movement of individuals of a species from one place to another

mitosis a type of nuclear division that produces daughter cells with the same chromosomal content as the parent cells; the basis for growth and repair in multicellular individuals, and for asexual reproduction in many eukaryotic species

molecular homology the identification of shared biomolecular elements – generally genes – used to test the relationships between organisms, which can demonstrate common ancestry

molecular phylogeny the study of evolutionary relationships using comparative genomics

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 plant species over a wide area for a large number of consecutive years

monohybrid cross only one characteristic with contrasting phenotypes is considered

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monosomy when somatic cells contain only one copy of a particular chromosome pair

monotreme a mammal that does not give birth to live young, but lays eggs, e.g. platypus

morphological species concept the definition of a species based on physical characteristics

morphology the shape and form of an organism or its part

mutagen any agent capable of inducing mutation

mutation a change in a gene or a chromosome relative to original; may also refer to process of generating change

mutation rate the estimated number of base pair changes per nucleotide site per generation of a population

mya millions of years ago or simply millions of years (my); e.g. a fossil dated as being 5 million years old lived 5 mya

N

natural selection the process in which individuals with certain inheritable traits survive and reproduce more successfully than other individuals, leading to evolutionary change in the population

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

niche a specialised position or role

nitrogen-fixing bacteria bacteria that absorb elemental nitrogen (N_2) from the atmosphere and convert it to nitrates (NO_3^-) or ammonium (NH_4^+)

node a point in a diagram where lines branch or intersect

nodule a small swelling or lump

non-coding DNA all DNA sequences within the genome that are not found within mRNA-coding exons, i.e. do not code for polypeptides

non-disjunction the failure of homologous partner chromosomes in meiotic cell division or sister chromatids in mitotic cell division to separate to opposite poles

non-renewable a resource that exists in limited supply and cannot be replaced if it is used up within normal human timescales

non-template strand the DNA strand complementary to template strand; does not form the pattern for the synthesis of complementary polynucleotide

nucleoid the region within a prokaryotic cell that contains the genetic material

nucleosome basic structural unit of chromatin comprising DNA strand wrapped around a group of 8 histone molecules

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, 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

oogenesis the process in the ovary that results in the production of female gametes

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

P

palaeontologist a scientist who studies palaeontology, the science of the forms of life that existed over the course of Earth's history (e.g. the study of fossils)

Pangaea the supercontinent consisting of all of Earth's land masses; it existed from the Permian through the Jurassic period before breaking up during the late Triassic period

parallel evolution a process whereby unrelated organisms 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 in cell division the DNA of the original cell

parental generation (P) two individual organisms originally crossed in breeding experiment; their offspring are the F_1 generation

partial dominance an alternative term to incomplete dominance

pathogen an organism that causes disease, resulting in damage or death, such as a bacterium or virus

peptide bond the bond that forms between adjacent amino acid monomers

percentage cover the percentage of the quadrat that a species takes up

percentage frequency the percentage of quadrats in which a species appears

period a division of geologic time; periods and epochs together make up eras

photic zone the first 200 m of ocean depth

photosynthesis the process of converting light energy into chemical energy held in the bonds of glucose molecules

photosynthetic efficiency how well a producer converts light energy into the chemical energy of carbohydrates

phylogenetic relationship an evolutionary relationship that exists between a group of species, often expressed as a tree-like diagram

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

phylogenetic tree a branching diagram showing evolutionary relationships

phylogeny evolutionary relationships that exist between species, often expressed as a tree-like diagram

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

pioneer plant a plant capable of invading bare sites, such as a newly exposed soil surface

plasmid a small circular piece of DNA, found in bacteria, which can replicate independently of a cell's chromosomes; plasmids carry antibiotic resistance markers

plate tectonics the theory that Earth's crust is divided into several plates that glide over the fluid mantle layer above the core

plesiomorphic having characteristics or traits that are common among their evolutionary relatives but are not unique to their clade; e.g. members of class Reptilia usually have legs as do many organisms not in class Reptilia

point mutation a mutation that affects a single base-pair position within a gene

polar body a very small cell produced during oogenesis, containing a nucleus, but very little cytoplasm

polygenes genes for which different alleles have a small additive effect on a phenotype; many polygenes together contribute to continuous variation in phenotype

polygenic inheritance 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 template, 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 belonging to the same species living in a particular place at the same time

population genetics the study of allele frequencies in populations and how they change over time in response to various evolutionary processes

post-reproductive isolating mechanism a mechanism that prevents fertilisation occurring or an embryo developing into viable offspring if fertilisation does occur

pre-mRNA an unmodified 'immature' mRNA molecule that contains introns

pre-reproductive isolating mechanism a mechanism that prevents organisms from being able to interact to reproduce

predation a species interaction in which one species kills and eats another

prey an organism that is hunted by another organism for food

primary succession the colonisation of plants in a barren place

primer a single-stranded DNA molecule that acts as the start of the amplification process

producer an organism, such as a plant, that converts energy to sugars

prokaryote a simple type of cell that lacks a nucleus and membrane-bound organelles; a member of domains Archaea or Bacteria

Punnett square a grid used to graphically illustrate and predict the outcome of a genetic cross

purebreeding when crossed with each other, offspring all have parental phenotype

Q

quadrat a 1 m × 1 m square frame that is placed over a location to provide a boundary for sampling in ecology

R

r-selected species a fast-growing and reproducing organism, often the first to occupy unused resources and living space

r/K selection a form of mathematical classification based on the number of offspring a species produces and the level of parental involvement required to care for them

random distribution a measurement of distribution in which organisms are spaced irregularly

realised niche the actual niche that a species occupies, given the restrictions placed on it by interactions with other species

recessive the phenotype only expressed if both copies of its recessive allele occur in 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

regulatory protein a protein that binds to DNA to switch a gene on or off

relative species abundance the number of individuals present for each species in an ecosystem

replication fork the junction between the unwound single strands of DNA and the intact double helix during replication

reproductive isolation the separation of populations that are unable to interbreed because of changes that produce physical, biological or behavioural barriers

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 fragment a short fragment of DNA generated after the cutting of a longer DNA fragment by a restriction enzyme

restriction site a specific nucleotide sequence (usually 4–8 bp) that is recognised as a cleaving site for a restriction enzyme

ribonucleic acid (RNA) a molecule consisting of a single strand of nucleotides; it plays an essential role in protein synthesis (as messenger RNA and transfer RNA) and as a structural component of ribosomes

ribosomal RNA (rRNA) a folded molecule of RNA that combines with proteins to form ribosomes; formed in nucleolus of eukaryotic cells

ribosome organelle where polypeptide synthesis occurs in all cells; locks onto mRNA molecule and moves along it to translate its code and link amino acids; formed in nucleolus

S

salination increased salt concentration

sample a small group of organisms selected from the total population; is representative of the whole population

second filial generation (F_2) the offspring of F_1 generation; second generation produced from original cross between two parents (P)

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

sessile fixed or non-moving, as in a species that remains fixed in one place for its lifespan

sex chromosome a chromosome that affects sexual traits; sex chromosomes are different in male and female individuals of the same species, one sex having homologous sex chromosomes, the other sex having a dissimilar set

sex-linked a gene located on sex chromosome

sexual reproduction a form of reproduction in which offspring are produced from two parents

short tandem repeats (STRs) 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

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

single nucleotide polymorphism (SNP) a nucleotide difference that occurs at one given position in the gene

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 a body cell that will not pass its genes onto next generation

spatial scale how much area a studied ecosystem covers

spatio-temporal relating to space and time

speciation the evolution of one or more new species from an ancestral species

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

species richness the number of species present in an ecosystem

spermatogenesis the continuous production of sperm cells in the testis

spontaneous mutation a mutation occurring in the absence of exposure to mutagens

stabilising selection a form of selection that tends to advantage organisms similar to their parents; this usually occurs when the environment is very stable and unchanging and selects against extremes of phenotype

start codon the first codon of an mRNA transcript translated by a ribosome; signals ribosome to start translating mRNA

sticky end the end of a DNA fragment that is created after cleavage by a restriction enzyme that cuts DNA at different positions on each strand

stop codon the codon that discontinues the synthesis of the polypeptide chain

stratified sampling a statistical sampling technique that divides an area into strata for separate sampling

stratum a layer or subsection of a whole

substitution mutation a mutation in which 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 physical or geographic isolation

synapsis the pairing of homologous chromosomes

T

***Taq* polymerase** DNA polymerase from the bacterium *Thermus aquaticus*, which lives in hot thermal springs and is 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 hundreds to thousands of repeated short DNA sequences at the ends of chromosomes to help maintain them; short lengths lost with each replication of DNA

template strand the DNA strand that serves as pattern for making complementary polynucleotide

temporal scale the time period over which an ecosystem is studied

terrestrial of land

trait heritable characteristic; phenotype

transcription the formation of an mRNA molecule against the template strand of 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 repressed

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

transfer RNA (tRNA) an RNA molecule that picks up a particular amino acid from the cytoplasm and then pairs with a specific mRNA codon to deliver the amino acid to the growing polypeptide chain

transform to change from one type to another

transformation the process by which genetic material is taken up from the surroundings and incorporated into the genome

transgenic organism an organism that has been modified by incorporating a piece of foreign DNA into its genome

translation the joining of amino acids in a specific order, according to information in mRNA 'read' by ribosome, to form polypeptide

trisomy when somatic cells contain three copies of a particular chromosome

trophic level a level in the food chain of an ecosystem based on feeding relationships

U

uniform (continuous) distribution a measurement of distribution in which organisms are evenly spaced

V

vector a vehicle used to transfer DNA sequences from one organism to another; a living organism that transmits pathogens from one host to another

viability capability of living

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 cause salinity levels in the soil to rise

wildlife corridor a small area of preserved wilderness designed to connect larger reserves; also known as a habitat or green corridor

X

X-linked dominant a phenotype that is determined by a dominant allele on X chromosome

X-linked recessive a phenotype that is determined by a recessive allele on X chromosome

Z

zygote the first cell of a new individual, which is formed by fusion of a sperm and ovum at fertilisation

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