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QCE | BIOLOGY UNITS 3&4

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Second Edition 2026

ISBN 978-1-99-101436-8

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First Printing

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Although every care has been taken, Aboriginal and Torres Strait Islander people should be aware that this title may contain images of deceased persons.

The external weblinks (URLs) referenced in this book were correct at the time of publishing. However, due to the dynamic nature of the internet, some addresses may have changed, or cease to exist. While BIOZONE regrets any inconvenience that this may cause readers, no responsibility for any such changes or unforeseeable errors can be accepted by BIOZONE.

Acknowledgements

BIOZONE wishes to thank and acknowledge the team for their efforts and contributions to the production of this title.

Cover Photograph

Photo: Adobe Stock - Sergey Skleznev

Latticed butterflyfish (*Chaetodon rafflesii*), also known as Raffles' coralfish

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QCE BIOLOGY UNITS 3&4

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CODING Activity is marked: ☐ to be done ☑ when completed ● Practical Investigation

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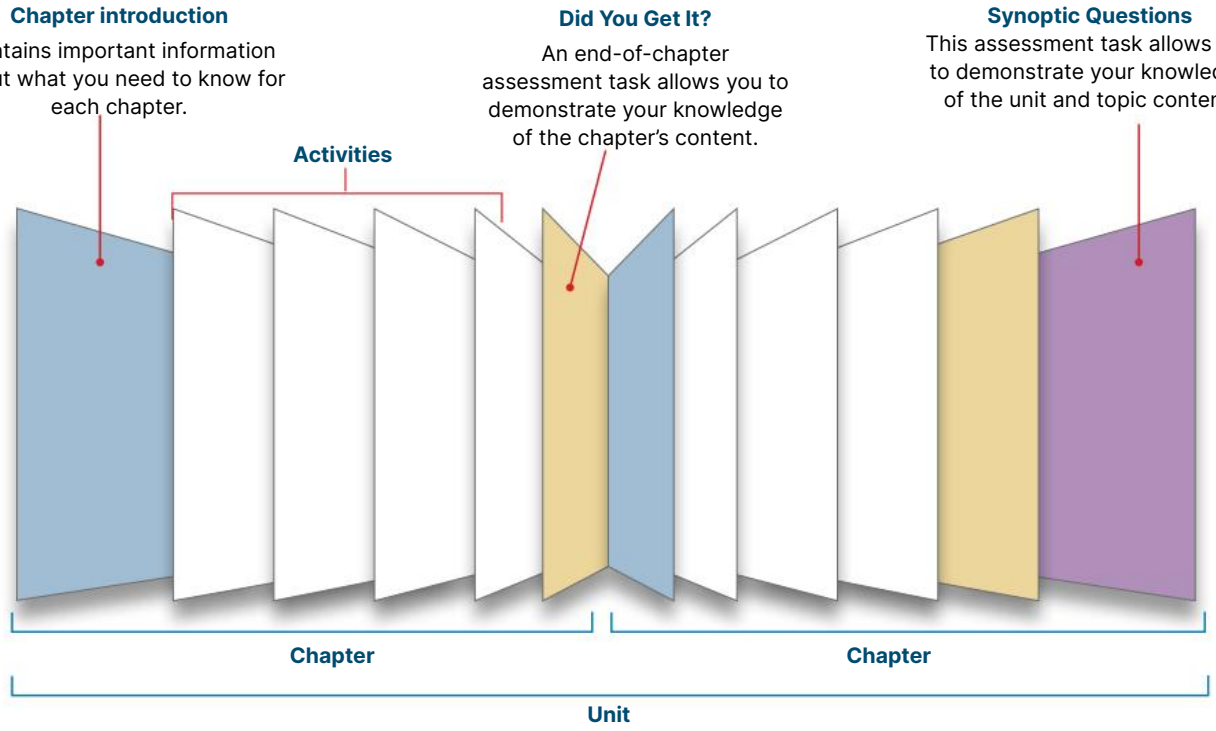
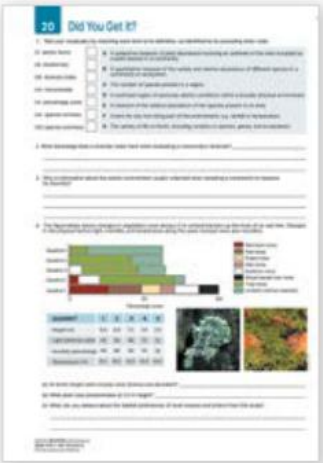
CODING Activity is marked: ☐ to be done ☑ when completed ● Practical Investigation

Using This Worktext

This edition of Biology for QCE Units 3&4 has been specifically written for the Queensland (QCE) Biology general senior syllabus (2025 version). The next few pages provide information about this resource and how to make best use of it.

Structure of a Unit and Chapter





Introduction

- Provides important key concepts for the chapter.
- Includes important key terms (vocab) for the chapter.
- Provides a checklist of unit objectives for the chapter.
- Activities with SHE, SU, and SI components are identified.

Activities

- The KEY IDEA provides the focus for the activity.
- Annotated diagrams and photographs help you understand the content.
- Answering the questions helps you consolidate your understanding of the content.
- Use the material to revise for tests and exams.

Chapter test

- End-of-chapter assessment tasks test your understanding of the biological terms and concepts covered within the chapter.
- Reviewing the answers can help you study for tests and exams.

Synoptic questions

- Synoptic questions conclude each unit and topic of study covered in the book.
- Use them to see how well you understand the content.
- Reviewing the answers can help you study for tests and exams.

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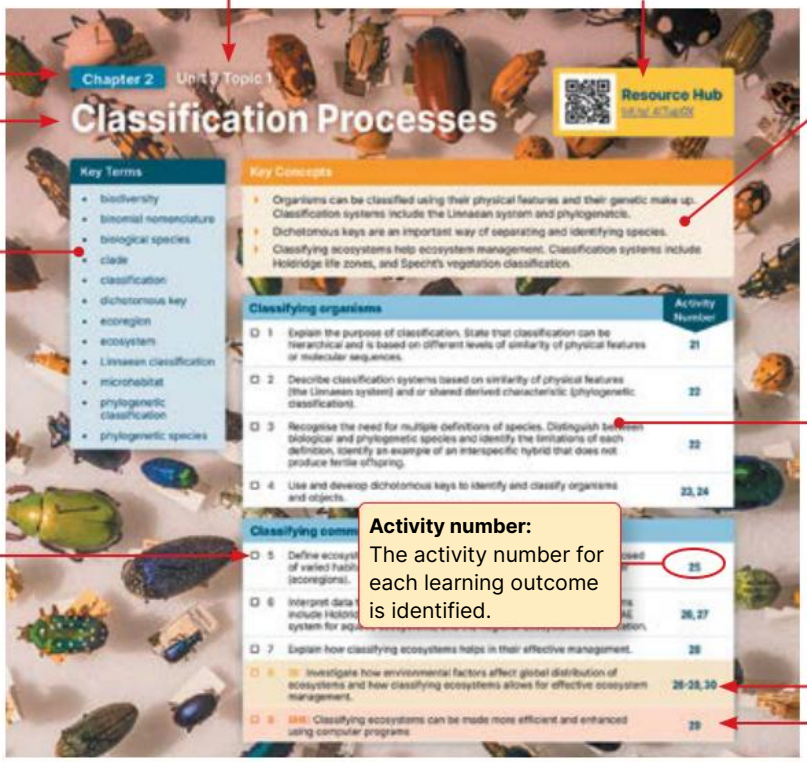
Chapter introductions

The chapter introductions contain useful information about what you need to know for QCE Biology. They identify key concepts and learning outcomes (what you need to know), important vocabulary, and provide a quick link to supporting resources on BIOZONE's **Resource Hub**. The key features of the chapter introductions are explained below.

The section of the worktext you are in is identified for easy navigation.

QR codes and bitly tags allow you to quickly navigate to helpful content (e.g. videos and models) on BIOZONE's **Resource Hub.**

Chapter number and chapter title are identified for quick navigation.



Key terms
Important vocabulary you should understand and use in your course. Definitions are provided in the glossary at the back of the book.

Check boxes
Use the check boxes to keep a record of which activities you need to complete and tick them off as you work through them.

Key concepts
These are the important key ideas for the chapter. Make sure you understand the concepts summarised here.

Learning outcomes
These provide a point by point summary of what you need to know or do by the end of the chapter.

Component coding
Colour panels and codes identify where Science as a Human Endeavour (SHE) or Science Inquiry (SI), occur in the chapter.

Structure of the activity pages

Activities make up most of the worktext. Be sure to interact with all the elements on the page so you don't miss any valuable information. As you work through the material, answer the questions and complete the tasks provided. Inputting your answers will form a record of work which helps you remember what you have learned. It can also be used for revision at a later date.

Key Idea:
This provides a focus for the activity and can be used as a summary take-home point of the activity.

Activity number:
Identifies the activity number to help you navigate between activities.

Introductory paragraph:
This provides background or introductory information to the topic.

More information about the topic is provided through explanatory text, images, diagrams, case studies, and data.

QR codes:
These provide a quick link to interactive 3D models.

Activity based questions:
Answering the questions helps reinforce your learning. Use your answers to review for tests and other assessments.

Tab system:
Page tabs identify where components of the syllabus are embedded in an activity (see more on page viii). The grey tab indicates there is support material available on the **BIOZONE Resource Hub**.

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Understanding the tab system

A simple tab system identifies where key Science as a Human Endeavour (SHE), Science Understandings (SU), and Science Inquiry (SI) are integrated into an activity.

Science as a human endeavour (SHE): This indicates an activity contains a SHE component, and promotes appreciation of the nature and development of science and its use and influence on society.

Resource Hub: The grey Resource Hub tab indicates there is material to support this activity on **BIOZONE's Resource Hub** (see page x for more information).

Syllabus objectives (left to right):
Investigate phenomena
Evaluate conclusions, claims, and processes
Interpret evidence
Analyse data
Apply understanding
Describe ideas and findings

Science Inquiry: This tab indicates an activity contains material to support the science inquiry components of the syllabus.

Science understanding: This tab indicates an activity covers a science understanding component.

The glossary: helping you build your science vocabulary

Building your science vocabulary is important to help you understand ideas and communicate information about what you know. Your BIOZONE worktext has several tools to help you with this. They are explained below.

Key terms: chapter introduction
Each chapter introduction has a list of key terms. These are important words and they are defined in the glossary at the back of the book. Try to use these terms as you communicate with your classmates and teacher.

Key terms: activities
You may notice that some words in an activity are written in **blue bold**. This is because they are key terms. If you are unsure of their meaning, they are defined in the glossary at the back of the worktext.

Glossary
A glossary of key terms is located at the back of this worktext. Use the glossary to find definitions for key terms and improve your understanding of what the terms mean.

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Mathematical skills

Developing and using skills in numeracy are an important component of the QCE Biology syllabus. You should be able to use a variety of mathematical skills in a wide range of situations and see their relevance in scientific inquiry and real world applications. Many of the basic skills you need are first explained in the *"Basic Skills"* chapter in QCE Biology Units 1&2. Refer back to that chapter at any time to review the skills covered there. These include:

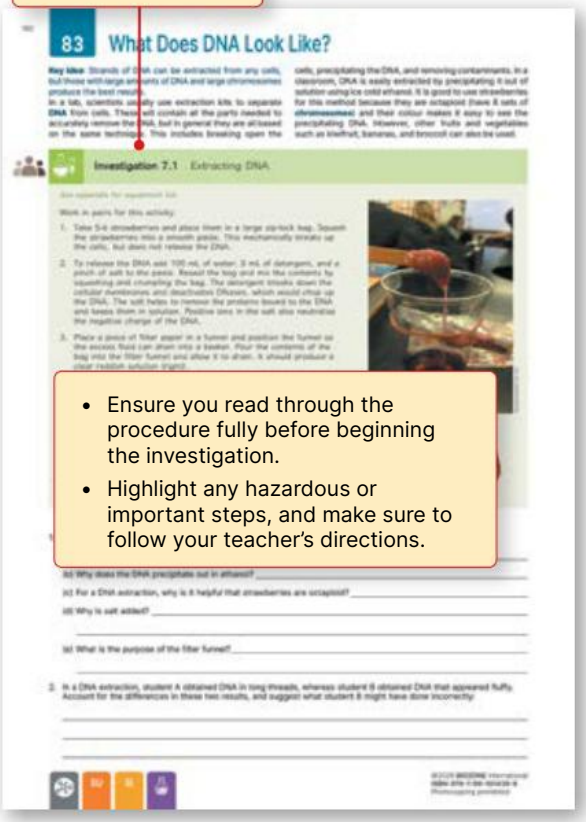
- Graphing
- Ratio and proportion
- Converting units
- Using the correct scientific notation
- Significant figures
- The reliability of data
- Basic statistical tests

Your BIOZONE QCE Biology workbooks provide many opportunities to practise and develop mathematical skills before you sit the data test. By completing activities, practicals, and synoptic questions you can practise and develop confidence in numeracy. Tasks include measuring and recording data, using formulae, interpreting graphical and numerical information, and using mathematical equations to justify answers.

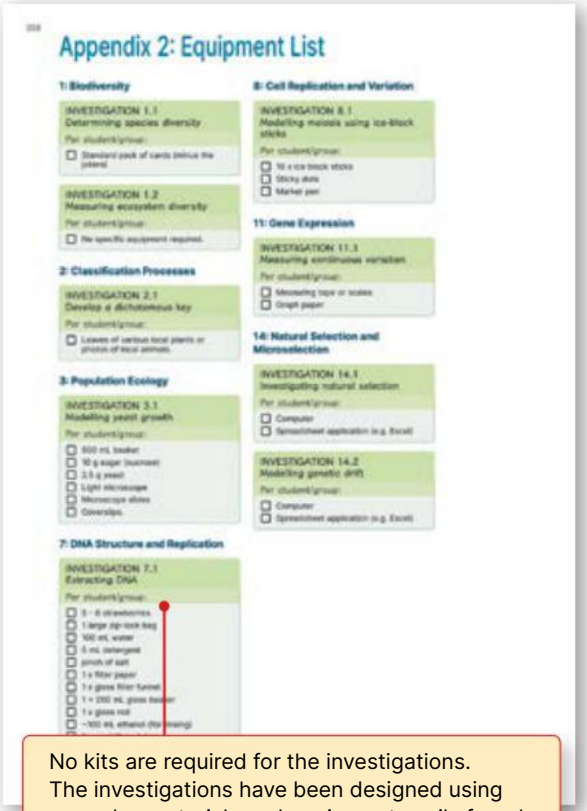
Practical investigations

Practical investigations form an important component of the QCE Biology syllabus. Practical work provides opportunity for inquiry and investigation and allows you to develop your manipulative skills. Practicals encourage the use of 21st century skills (collaboration and teamwork, communication, critical thinking) and provide opportunities to apply your skills in literacy and numeracy. An equipment list at the back of this worktext details the equipment needed to carry out the practical investigations.

Each investigation is clearly numbered sequentially through the chapter.



- Ensure you read through the procedure fully before beginning the investigation.
- Highlight any hazardous or important steps, and make sure to follow your teacher's directions.



No kits are required for the investigations. The investigations have been designed using everyday materials and equipment easily found in most high school laboratories.

A list of the equipment and reagents required for each investigation is provided in Appendix 2.

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Using BIOZONE's Resource Hub

- Many activities have interesting resources, such as videos and 3D models, to help you understand the content. A grey tab (right) on the activity page indicates there is support on the BIOZONE **Resource Hub** for the activity.
- Navigate to the Resource Hub either by bookmarking the link below, or by using the bitly tag or QR code found on each chapter introduction (below, right).

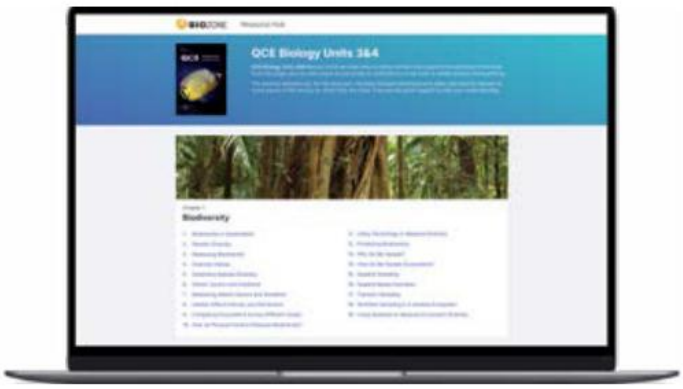
Step 1: Navigate to the BIOZONE **Resource Hub**

www.BIOZONEhub.com

Step 2: Enter this code in the box displayed.

QCE12-2-4368

Step 3: Bookmark this page.

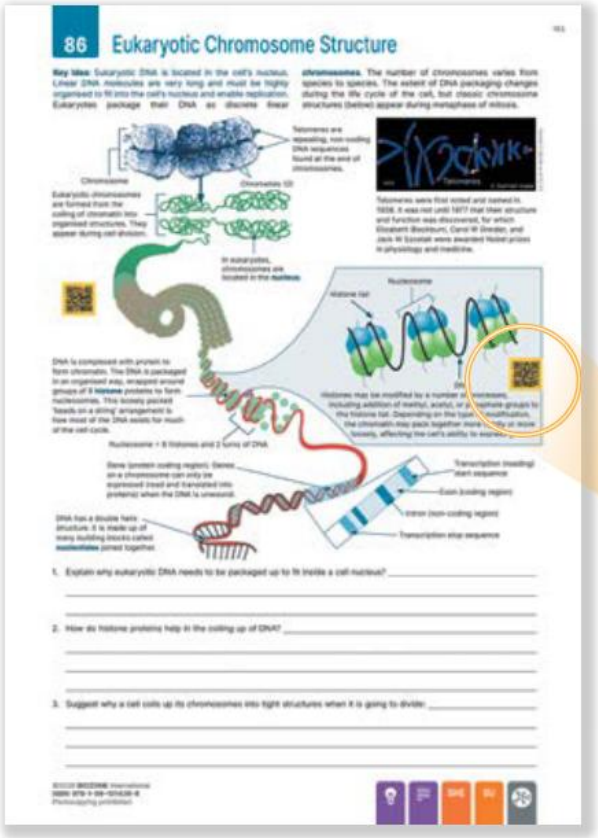


https://bit.ly/3Hol55s

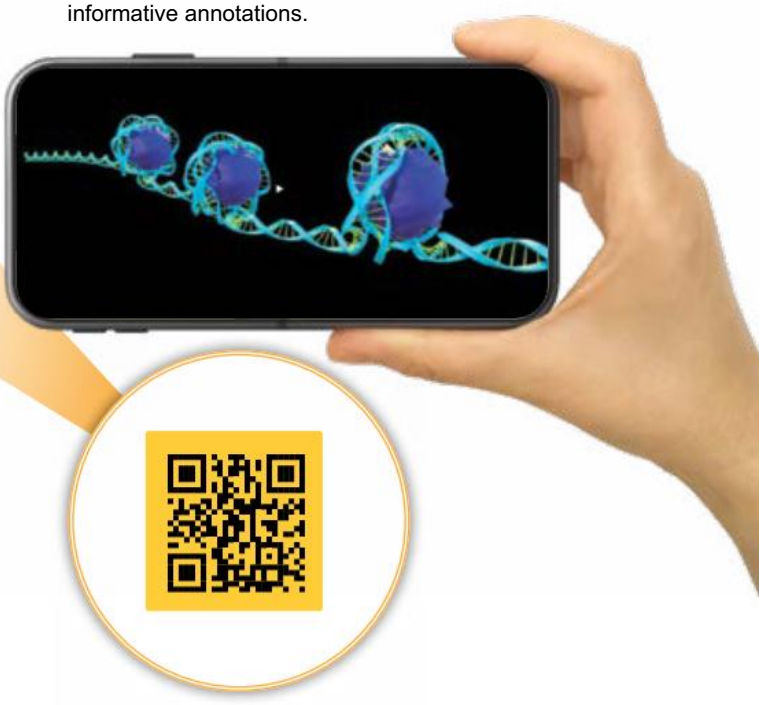
Use this bitly tag or QR code to directly access the BIOZONE Resource Hub.

Using the QR codes on activity pages

Some activities have QR codes on the pages (below). These link directly to informative and engaging 3D models. If your school does not let you use your phone in class, you can still access the models and data sets through the **Resource Hub**. Follow the steps above to access the resources through the **Resource Hub**.



Scan the **QR codes** on the activity pages. These link directly to informative and engaging 3D models. All models can be rotated and zoomed, and some contain informative annotations.



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Chapter 1 Topic 3 Unit 1

Biodiversity

Resource Hub
bit.ly/43aYPEI

Key Terms

- abiotic (physical) factor
- abundance
- biodiversity
- biotic factor
- data logger
- density
- distribution
- diversity index
- environmental gradient
- microclimate
- percentage cover
- percentage frequency
- quadrat
- remote sensing
- sample
- satellite tracking
- Simpson's diversity index
- species evenness
- species richness
- transect

Key Concepts

- Biodiversity includes the variety of life on Earth, including genetic, species, and ecosystem diversity.
- Biodiversity can be described using concepts including species richness, and diversity indices such as Simpson's Diversity Index. Sampling techniques include transects, quadrats, and mark and recapture.
- Ecosystems and biodiversity can be affected by abiotic factors including humidity, light, temperature and windspeed.

What is biodiversity and how do we measure it?		Activity Number
☐ 1	Describe the different aspects of biodiversity and give your own evaluation of Queensland's biodiversity, including where biodiversity is threatened.	1
☐ 2	Explain why it is important to maintain biodiversity. Describe the many and varied reasons for maintaining biodiversity, including the benefits provided by diverse ecosystems (e.g. ecosystem services such as nutrient cycling, water purification, and climate regulation).	1
☐ 3	Describe the different aspects of genetic diversity including measurement of genetic diversity and the effect of genetic diversity on the health of a species.	2
☐ 4	Determine species diversity using measures such as percentage cover and percentage frequency (for plants) and species richness (number of species) and species evenness (relative abundance). Demonstrate the use of Simpson's diversity index (D), which incorporates species richness and evenness, to quantify biodiversity. State what the index tells you about the community you are studying.	3-5, 19
☐ 5	Explain what is meant by a physical (abiotic) factor. Explain how abiotic factors can influence the distribution and abundance of species, e.g. by creating environmental gradients and microclimates.	6, 8, 9
☐ 6	Use appropriate technology and equipment to measure abiotic factors in the classroom and in the field using samples collected in the field.	7, 11
☐ 7	Describe the process of stratified sampling in terms of: • purpose (what can sampling tell us?) • site selection (how do we choose where to sample?) • sampling technique (quadrats or transects?) • minimising bias (size and number of samples, random sampling, counting criteria) • methods of data presentation and analysis (tables, graphs, descriptive statistics)	13-18

Investigating biodiversity		
☐ 8	SI: Investigate factors affecting species distribution and/or abundance.	3-5, 8, 19
☐ 9	SI: Investigate species composition along environmental gradients,	6, 7, 9, 13-18
☐ 10	SI: Use the process of stratified sampling to: • investigate changes to abiotic factors in different strata • investigate changes to community composition in different strata • infer species interactions within and between strata • classify an ecosystem.	13-18
☐ 11	SI: Compare species diversity in spatially separate ecosystems of the same classification.	19

1 Biodiversity in Queensland

Key Idea: Biodiversity is the sum of all biotic variation from the level of genes to ecosystems.

Biodiversity is defined as the sum of all biological variation, including genetic, species, and ecosystem variation. Species diversity refers to the number of species (**species richness**). Genetic diversity describes the diversity of genes within a species. Ecosystem diversity (which includes habitat diversity) refers to the variation present in the ecosystems of a region. An ecosystem is a community of living organisms and the physical (non-living) components of their environment. Total biodiversity is threatened by the loss of just one of these components. Biodiversity contributes to the functioning and stability of ecosystems. High diversity ecosystems tend to be stable (constant in character over time) and resilient (able to resist and recover from disturbances). Reducing biodiversity tends to also reduce ecosystem stability and resilience.

Queensland's biodiversity

- Queensland is Australia's most naturally diverse state. Queensland has 13 terrestrial and 14 marine bioregions (a region defined by characteristics of its natural environment).
- The 27 bioregions support more than 1000 ecosystem types, including rainforests, savannas, rangelands, the dry tropics, wetlands, and coastal land.
- Queensland is home to 70% of Australia's mammals, 80% of its native birds and more than 50% of its native reptiles, frogs, and plant species.
- Five world heritage listed areas are located in Queensland. These include the wet tropics, the Great Barrier Reef (below) and Fraser Island (the largest sand island on Earth).

Why is biodiversity important?

Maintaining Australia's biodiversity is important for many reasons:

- **Ecosystem stability**: Evidence from both experimental and natural systems indicates that the most diverse ecosystems are generally the most stable. This is most probably because the complex network of species interactions buffers the ecosystem against change. Maintaining biodiversity is critical to maintaining key ecological functions such as nutrient cycling, water purification, and climate regulation.
- **Species interactions**: Ecosystems include many interdependent species (e.g. flowering plants and pollinators, hosts and parasites). The loss of even one species can alter ecosystem dynamics, especially if the species is a keystone species (a species with a pivotal role in ecosystem functioning, e.g. in nutrient cycling or as a top predator).
- **Culture**: biodiversity is also closely linked to culture, especially for indigenous (native) people. For the aboriginal and Torres Strait Islanders, it is important to conserve not only biological diversity but also biocultural diversity (the people, knowledge, stories, songs, and traditions of a region).
- **Tourism and economics**: more than 28 million tourists visited Queensland in 2024, many to enjoy nature-based activities such as visiting the national parks and the Great Barrier Reef, whale-watching, and hiking. Tourism contributes billions of dollars to Queensland's economy, creating jobs and income streams for local populations. Many other industries (e.g. seafood) rely on the productivity of natural ecosystems to sustain them (again contributing to the economy).
- **Biodiscovery**: Biodiscovery involves collecting samples of native biological materials (e.g. plants, fungi, sponges) to test for compounds that may have commercial uses (e.g. pharmaceuticals and insecticides). The higher the biodiversity, the more likely it is that something useful will be found.

1. In your own words define biodiversity: _____

2. Summarise why maintaining biodiversity is important to Queensland: _____

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The rainforests of the Wet Tropics bioregion and shrublands of the Brigalow Belt bioregion are described below. Human activity has affected the biodiversity of both these biologically distinctive regions to different degrees.

High biodiversity: Wet tropics of Queensland

Killerscene Public Domain

Wet Tropics bioregion of Queensland stretches along the north-east Queensland portion of the Great Dividing Range and covers an area of around 8,940 km². It is a significant region of biodiversity, with many different types of vegetative communities, several World Heritage sites, and a rich variety of plants and animals. Many of the species are endemic (found nowhere else) and many are endangered (at high risk of extinction in the wild).

- The region contains 2800 plant species, 700 of which are endemic.
- The area provides a living record of plant evolution, with the highest concentration of primitive flowering plants in the world.
- 676 species of mammals, birds, reptiles and amphibians, many of which are endemic and/or endangered.

Preserving the Wet Tropics rainforests (mainly from the expansion of the sugarcane industry) is key to preserving the biodiversity and functioning of the wet tropics ecosystems.

Reduced biodiversity: Brigalow Belt

Ethel Aardvark cc3.0

The Brigalow Belt bioregion is named after the Brigalow (*Acacia harpophylla*) which once dominated this bioregion. The band of acacia woodland and shrubland runs from Townsville into New South Wales. This unique region is home to many endemic species, and is now considered a biodiversity hotspot (a biogeographic region that is both a significant reservoir of biodiversity and is threatened with destruction).

Around 90% of the original brigalow has been cleared to make way for agriculture, coal mining and coal seam gas extraction, leaving highly fragmented patches. Combined with the introduction of new species (e.g. pasture grass), this means many endemic species are endangered or threatened. Extinctions have already occurred (e.g. paradise parrot) and 17 others are seriously threatened (meaning critically endangered, endangered, or vulnerable). The biodiversity (and therefore functioning) of the Brigalow Belt has already been lowered and will continue to reduce without intervention and protection.

3. (a) Look around your everyday environment and find examples of high and low biodiversity areas. Describe them below:

i) High biodiversity: _____

_____

ii) Low biodiversity: _____

_____

(b) Can you locate an area that might be at risk of declining biodiversity? Why is it at risk? _____

_____

_____

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2 Genetic Diversity

Key Idea: Genetic diversity is important in maintaining healthy species populations.

The vast majority of the genetic material in two unrelated individuals in a species is identical. It must be or else they are unlikely to be the same species. However, a small fraction of the genetic material varies between individuals (about 0.1% in humans compared to about 1% difference between humans and chimpanzees). This tiny variation results in the differences between individuals of the same species (e.g. eye colour, differences in height, body shape, or behaviour). These variations allow a species to adapt to changes in the environment, such as changes in food availability or the ability of the immune system to react to a disease. As a result, maintaining genetic diversity is extremely important for the long term survival of a species. Many endangered species have low genetic diversity.

What is diversity?

Biological diversity consists of three main parts:

Genetic diversity is the total number of genetic characteristics in a species. Genetic diversity is an important consideration in studies of biodiversity because species with high genetic diversity are less susceptible to disease and inbreeding depression (reduced breeding success as a result of inbreeding).

Example: Eastern grey kangaroos have a high level of genetic diversity due to their abundance, wide **distribution**, and gene flow between populations.

Species diversity is the number of different species (**species richness**) that are represented in a given community and their relative abundance (**species evenness**). High species diversity is associated with stable ecosystems and a large number of **biotic** interactions.

Example: The Raja Ampat Islands in Indonesia are considered the centre of marine biodiversity. The region is home to 75% of all known species of hard corals.

Habitat diversity describes the number of different habitats provided by a particular region. Habitat diversity is often described as heterogeneity and is associated with species diversity. More heterogeneous environments can support a larger number of species with different habitat needs.

Example: The tropical climate of the Raja Ampat Islands provides an enormous range of marine and terrestrial habitats. It is also relatively undisturbed by humans.

Genetic diversity affects ecosystems

Genetic diversity is important in determining how well an ecosystem functions. Important components include:

- Fitness (survival and reproductive success) of individuals
- Long term viability and adaptability of populations
- Evolution of new species or traits
- Community structure and stability
- Genetic diversity affects how members of the same species behave (e.g. some may be more aggressive or less curious). This in turn affects how they interact with other organisms and so with the ecosystem as a whole.
- The millions of interactions from genetically diverse organisms ultimately affect how stable and resilient the ecosystem is.

1. What percentage of DNA is variable between any two humans? _____

2. What is genetic diversity? _____

_____

3. Why is it advantageous for a population to have high genetic diversity? _____

_____

_____

4. Why would the functioning of an ecosystem be affected by genetic diversity? _____

_____

_____

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Measuring diversity

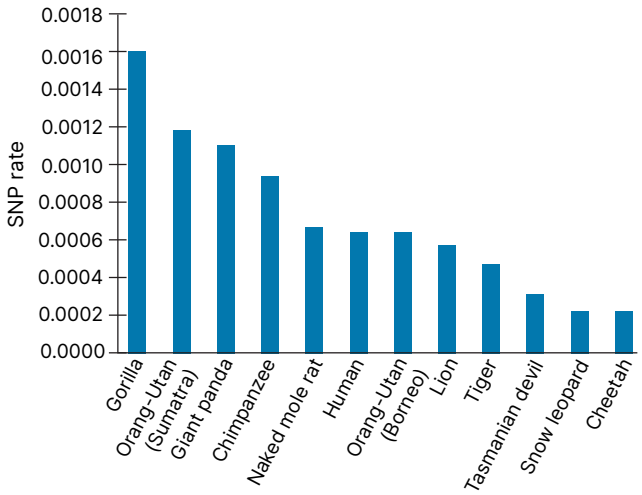
There are various ways to measure the genetic diversity of populations and individuals. The most common way is to measure the diversity of single nucleotide polymorphisms. (SNPs). SNPs are variations in single DNA bases.

- SNPs behave just like alleles, i.e. individuals can be heterozygous or homozygous for an SNP. The proportion of heterozygous SNPs in individuals can therefore give a measure of the genetic variation in the population.
- A second measure is the heterozygous SNP rate. This is the number of heterozygous SNPs divided by the size of the genome. A high heterozygous SNP rate indicates a high degree of variation.

Jss367 cc 4.0

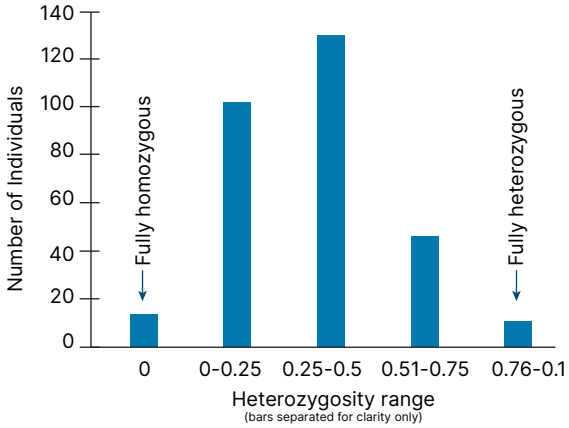
The regent honeyeater has high genetic diversity despite being critically endangered. The populations are highly mobile and this maintains gene flow.

Mammalian genetic diversity



Source: The tiger genome and comparative analysis with lion and snow leopard genomes. Yun Sung Cho et al www.nature.com/naturecommunications

Tasmanian devil SNP heterozygosity



Development of a SNP-based assay for measuring genetic diversity in the Tasmanian devil insurance population. Wright et al. BMC Genomics (2015) 16:791

Degree of diversity

Different species have different amounts of genetic variation. These differences are the result of the species' biology and their evolutionary histories. Genetic diversity declines when populations suffer a near extinction, and species with small populations (e.g. Tasmanian devils) often do have lower genetic diversity than those with large populations. However, this is not always the case. In fact, there is no clear correlation between population size and genetic diversity. Western lowland gorillas, for example, have a much higher genetic diversity than humans.

Diversity in Tasmanian devils

Tasmanian devils have a particularly low genetic diversity. This is especially so in the MHC (Major Histocompatibility Complex) genes. This group of genes codes for the cell surface proteins responsible for immune recognition of self and non-self. Low allelic diversity means that tissue from one devil is recognised by another individual's immune system as "self" and is not attacked. This has led to an infectious cancer spreading among devils because cancerous tissue transferred among individuals in fights is not recognised by the recipient's immune system as foreign.

5. (a) What might cause some species to have lower genetic diversity than others: _____

(b) How might gene flow (individuals moving between populations and sub-populations) account for higher than expected genetic diversity in some endangered species (e.g. regent honeyeater)?

6. (a) What is one negative effect of low genetic diversity in Tasmanian devils? _____

(b) Describe the heterozygosity range in Tasmanian devils: _____

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3 Measuring Diversity

Key Idea: There are a number of ways to measure diversity. Some are suited only to plant communities, while others can be used to assess the diversity of both plants and animals in a community or ecosystem.

When sampling an ecosystem, a researcher must decide where and how to **sample**. The choice depends a lot on the questions being asked and the types of organisms being studied. Sampling grids (**quadrats**) are often used to define a sample area (right) or sample points can be selected to indicate where samples should be taken and recorded. Ecological sampling collects data about where organisms are found and how they are distributed. **Abiotic factors** are frequently measured at the same time. This information can be used to answer questions about the **biodiversity** of a community or ecosystem and serve as a baseline to measure changes in time or space.

Measuring diversity in plant populations

Two commonly used methods to sample plant communities are **percentage frequency** and **percentage cover**. Percentage frequency is a measure of the number of times a plant species is present within a given number of samples. Percentage cover measures how much space a species occupies in that area. Identifying individual plants in communities where plants overlap can be difficult, so percentage cover is often used to evaluate these communities. However, overlapping plant parts can result in summed estimates of percentage cover being greater than 100%. Note that percentage cover is not a suitable method for most animal communities.

Percentage frequency

A student sampled a local area using ten 1 m x 1 m quadrat grids to determine the percentage frequency of the plants in the sample area.

If a species was present within a grid, they marked it with a tick. If the species was not found, an X was recorded. Their results are recorded in Table 1.

Table 1. Recorded frequency of five species of plants.

Species	Quadrat number										Total	Percentage frequency
	1	2	3	4	5	6	7	8	9	10		
Species A	X	X	X	✓	✓	✓	✓	✓	✓	✓	*7/10*	*70%*
Species B	X	X	X	X	✓	✓	✓	X	X	X		
Species C	✓	X	✓	✓	X	X	X	X	X	X		
Species D	X	X	X	X	✓	X	✓	✓	✓	✓		
Species E	X	X	X	X	✓	✓	✓	✓	X	X		

Percentage cover

The student divided a 1 m x 1 m grid into 100 smaller grids. At each intersect on the grid they placed a pin (right). If the pin touched a plant, the plant species was listed and every individual touch (hit) was recorded (Table 2).

The percentage cover is calculated by the formula:

Percentage cover = (Hits (touches) ÷ total sampling points) x 100

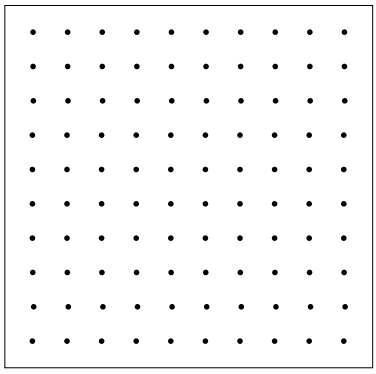

Table 2. Percentage cover of five species of plants.

Species	Number of hits	Percentage cover
Species A	*34*	*34%*
Species B	*9*	
Species C	*15*	
Species D	*17*	
Species E	*19*	

1. Complete the calculations for percentage frequency in Table 1 and % cover in Table 2.

2. How is it possible that species B and C have the same % frequency but species B has a much smaller % cover value?

3. Study the diagrams at the top of the next page.

   (a) Estimate the percentage cover of the large plant in the top right corner of the quadrat: _____

   (b) Calculate the % cover of the same plant in the point quadrat. How does this compare with the estimate?

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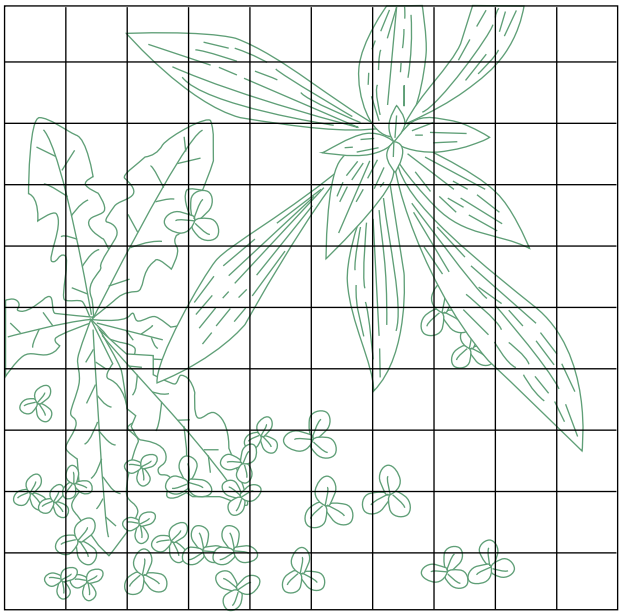
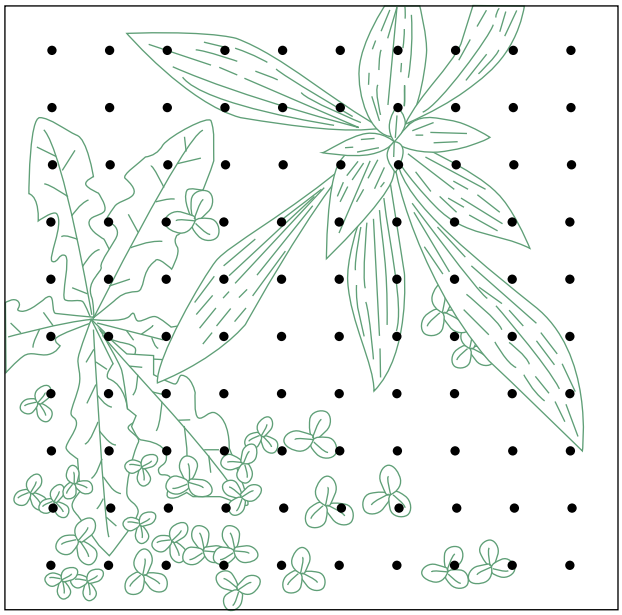
Quadrat divided into 100 smaller squares



Point quadrat

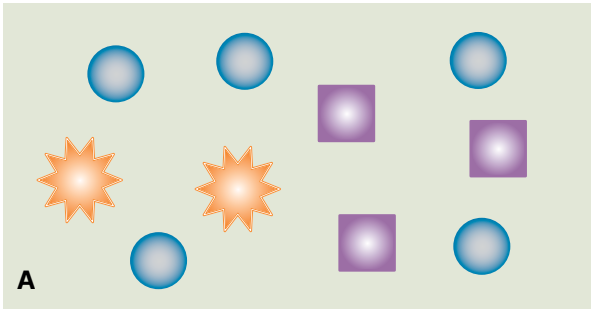


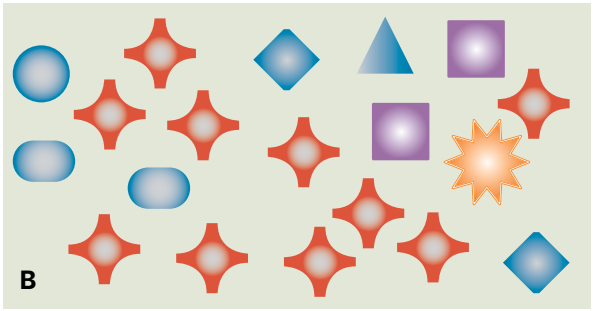
Measuring diversity in animal populations

Because the species in a community are so varied, it is necessary to use several measures to describe them to prevent skewed interpretation of the community structure. One measure of biodiversity is to count all the species present (**species richness**). Species richness (S) is directly related to the number of species in a sampled area. It is a crude measure of the sameness (homogeneity) of a community but it does not give any information about the relative abundance of particular species and so is relatively meaningless by itself. For example, a sample area with populations of 500 of species A and 3 of species B has the same species richness as a sample area with populations of 200 species A and 300 species B. Both have a species richness of 2.

Species evenness is a measure of the proportion of each species in an area (the relative abundance). Species evenness is highest when the proportions of all species are the same and decreases as the proportions of species become less similar. As a general rule, communities with low species richness and low species evenness are also communities with low diversity.

4. The diagrams below represent two ecosystems (A and B). Each shape represents a different species. Describe in words the species richness and species evenness of ecosystem A and B:





A _____

B _____

5. Students used quadrats to sample three sites in a stream. They recorded the species found and number of individuals per m^2 at each site. Their results are shown in Table 3.

(a) Calculate the species richness at each site: _____

_____

(b) Rank the sites in terms of species evenness: _____

_____

(c) Which is the most abundant species in the stream? _____

_____

(d) Which site has the lowest species diversity? _____

Table 3. Sample of freshwater stream invertebrates

Common name	Site 1 (no. m^{-2})	Site 2 (no. m^{-2})	Site 3 (no. m^{-2})
Freshwater shrimp	20	67	5
Freshwater mite	15	0	0
Flat mayfly	21	23	0
Bighead stonefly	18	12	2
Blackfly	40	78	100
Bloodworm	22	21	43

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4 Diversity Indices

Key Idea: Diversity indices incorporate both species richness and relative abundance, so are a good measure of diversity.

A **diversity index**, like Simpson's index of diversity, is a mathematical measure of species diversity in a community. It takes into account the number of species present as well as their relative abundance. Diversity indices can also be used to assess the health of an ecosystem. A change in species composition can indicate changes in an ecosystem's status (e.g. in response to pollution or climate change). Certain 'sensitive' species are associated only with specific conditions (e.g. clean, cold water). The presence (or absence) of these indicator species tells us about the health of an ecosystem.

Photos: Stephen Moore

Using diversity indices and the role of indicator species

To be properly interpreted, indices are often evaluated with reference to earlier measurement or a standard ecosystem measure. The images above show **samples** from two streams: a high diversity community with a large number of invertebrate species (left) and a low diversity community (right) with fewer species in large numbers. These images also show typical stream indicator species. The left photograph shows a stonefly (1) and an alderfly larva (2). These species (and mayfly larvae) are typical of high water quality. The right photograph shows a dominance of snails (3) which are tolerant of a wide range of conditions, including degraded environments.

Simpson's index of diversity

Simpson's Diversity Index (below) produces values ranging between 0 and almost 1. There are other variants of this index, but the more limited range of values provided by this calculation makes it more easily interpreted. No single index offers the "best" measure of diversity; each is chosen on the basis of suitability to different situations.

Simpson's Diversity Index (D) is easily calculated using the simple formula below. Communities with a wide range of species produce a higher score than communities dominated by larger numbers of only a few species.

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

D = Simpson's diversity index
N = Total number of individuals (of all species) in the sample
n = Number of individuals of each species in the sample

Example of species diversity in a stream

The example below describes the results from a survey of stream invertebrates. It is not necessary to know the species to calculate a diversity index as long as the different species can be distinguished. For the example below, Simpson's Diversity Index using $D = 1 - (\sum n(n-1) \div N(N-1))$ is:

	Species	n	n(n–1)
A	Backswimmer	12	132
B	Stonefly larva	7	42
C	Silver water beetle	2	2
D	Caddisfly larva	6	30
E	Water spider	5	20
F	Mayfly larva	8	56
	$N(N-1) = 40 \times 39 = 1560$	$\sum n = N = 40$	$\sum n(n-1) = 282$
	$\sum n(n-1) \div N(N-1) = 282 \div 1560 =$		0.18
	D = 1 – 0.18 =		**0.82**

1. Why might it be useful to have baseline data (prior knowledge of a system) before interpreting a diversity index?

2. (a) How might you monitor the recovery of a stream ecosystem following an ecological restoration project?

(b) What role could indicator species play in the monitoring programme?

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Comparing the biodiversity of ecosystems

In a field study, students used **quadrats** to sample the invertebrate animals in the leaf litter of two different areas, a rainforest fringe and a eucalypt plantation. They found 8 species and recorded the numbers of each species present at each site. The results are presented in the tables and images below. The invertebrates are not drawn to scale.

Species	Number of animals (n)	n(n–1)
Species 1	35	
Species 2	14	
Species 3	13	
Species 4	12	
Species 5	8	
Species 6	6	
Species 7	6	
Species 8	4	
N(N–1) =	**N = 98**	∑n(n–1) =
∑n(n–1) ÷ N(N–1) =		D =

Fir0002 CC3.0

Species	Number of animals (n)	n(n–1)
Species 1	74	
Species 2	20	
Species 3	3	
Species 4	3	
Species 5	1	
Species 6	0	
Species 7	0	
Species 8	0	
N(N–1) =	**N = 101**	∑n(n–1) =
∑n(n–1) ÷ N(N–1) =		D =

Species 1 Mite | Species 2 Ant | Species 3 Earwig | Species 4 Woodlice | Species 5 Centipede | Species 6 Longhorn beetle | Species 7 Small beetle | Species 8 Pseudoscorpion

3. Write a hypothesis for this investigation: _____

_____

_____

4. (a) Complete the two tables above by calculating the values for ∑n(n–1) and N(N–1) for the student's two sampling sites:

   (b) Calculate the Simpson's diversity index for site 1: _____

   (c) Calculate the Simpson's diversity index for site 2: _____

   (d) Compare the diversity of the two sites. Which site appears to be where conservation efforts are being carried out?

   _____

   _____

   _____

5. (a) Species richness is a measure of the number of different species in an area. Which of the two areas sampled above has the greatest species richness?

   _____

   (b) Why would measuring species richness be less informative than measuring species diversity? _____

   _____

   _____

   _____

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5 Determining Species Diversity

Investigation 1.1 Determining species diversity

See appendix for equipment list.

A pack of playing cards can be used as a model community to investigate species diversity.

In this practical exercise you will work in pairs or small groups to investigate diversity in three different 'communities' of playing cards. The playing cards represent the 'species' and you will measure diversity using Simpson's diversity index (D). You can apply the knowledge gained in this activity to a real population if you wish.

1. Divide the class into pairs or small groups. Each pair or group will need one pack of 52 standard playing cards (Jokers removed).
2. The cards represent nine different species (see table 1 below).
3. You will use your pack of cards to create and sample three different communities. One sample will be drawn from a community that is the entire pack of cards, one sample will be drawn from a community that has 7 face cards removed, and one sample will be drawn from a community that has all face cards and one suit removed.

Table 1. Description of card species

Species 1: All face cards (jacks, queens, kings) 	**Species 2**: Clubs (odd numbered) 	**Species 3**: Clubs (even numbered) 
Species 4: Diamonds (odd numbered) 	**Species 5**: Diamonds (even numbered) 	**Species 6**: Hearts (odd numbered) 
Species 7: Hearts (even numbered) 	**Species 8**: Spades (odd numbered) 	**Species 9**: Spades (even numbered) 

1. (a) Predict which community will show the highest diversity and explain why: _____

_____

(b) Predict which community will show the lowest diversity and explain why: _____

_____

4. Community 1: Shuffle the pack of cards and count out 26 cards (this is your sample). Note how many of each species (1-9) you have in your sample and record it in record sheet 1. Complete the table to calculate the Simpson Diversity Index.
5. Community 2: Remove seven face cards from the pack of 52 cards. Shuffle the cards and count out 26 cards into a pile. Record how many of each species you have in your sample in record sheet 2. Complete the table to calculate the Simpson Diversity Index.
6. Community 3: Remove all of the face cards and one of the suits (e.g. all the clubs) from the pack of 52 cards. Shuffle the cards and count out 26 cards into a pile (this is your sample). Shuffle the cards and count out 26 cards into a pile. Record how many of each species you have in your sample in record sheet 3. Complete the table to calculate the Simpson Diversity Index.

2. Students decided to repeat the experiment described above but used two packs of cards instead of one. Explain the advantage of this over using a single pack of cards:

_____

_____

_____

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Record sheet 1: Community 1- all cards					
Species		**Tally**	**Total (n)**	**n-1**	**n(n-1)**
Species 1: Face cards					
Species 2: Clubs (odds)					
Species 3: Clubs (evens)					
Species 4: Diamonds (odds)					
Species 5: Diamonds (evens)					
Species 6: Hearts (odds)					
Species 7: Hearts (evens)					
Species 8: Spades (odds)					
Species 9: Spades (evens)					
N = N(N–1) =			∑n =		∑n(n–1) =
∑n(n–1)÷ N(N–1) =				D =	

Record sheet 2: Community 2 - seven face cards removed					
Species		**Tally**	**Total (n)**	**n-1**	**n(n-1)**
Species 1: Face cards					
Species 2: Clubs (odds)					
Species 3: Clubs (evens)					
Species 4: Diamonds (odds)					
Species 5: Diamonds (evens)					
Species 6: Hearts (odds)					
Species 7: Hearts (evens)					
Species 8: Spades (odds)					
Species 9: Spades (evens)					
N = N(N–1) =			∑n =		∑n(n–1) =
∑n(n–1)÷ N(N–1) =				D =	

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Record sheet 3: Community 3 - all of the face cards plus one entire suit removed					
Species		**Tally**	**Total (n)**	**n-1**	**n(n-1)**
Species 1: Face cards					
Species 2: Clubs (odds)					
Species 3: Clubs (evens)					
Species 4: Diamonds (odds)					
Species 5: Diamonds (evens)					
Species 6: Hearts (odds)					
Species 7: Hearts (evens)					
Species 8: Spades (odds)					
Species 9: Spades (evens)					
N = N(N–1) =			∑n =		∑n(n–1) =
∑n(n–1)÷ N(N–1) =				D =	

3. (a) Compare the diversity of the three communities: _____

(b) Do the results match your predictions about which community would have the highest and lowest diversity? _____

(c) If not, what could be the reason for the differences? _____

4. How does the number of species present in a community affect Simpson's diversity index?

5. How could you check that your results were reliable indicators of species diversity?

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6 Abiotic Factors and Gradients

Key Idea: Spatial variations in abiotic (physical) factors within an ecosystem can determine species distribution.

Abiotic factors are the non-living, physical components of an ecosystem. They include water, light, temperature, humidity, and soil chemistry. Organisms have a range for the abiotic conditions they can tolerate (e.g. -2°-36°C) and a narrower range that is most favourable to their growth, survival, and reproduction (e.g. 4°-28°C). Gradients in abiotic factors, which occur in almost all environments, are therefore important in determining the distribution and limits of species. **Environmental gradients** are not necessarily uniform, and local topography and aspect can result in restricted areas called **microclimates**. Species can exploit these small areas to persist in what is an apparently unsuitable environment.

Abiotic factors in a stratified forest environment

In forests, environmental gradients arise as a result of vertical distance from the ground. Light quantity and quality, wind speed, humidity, and temperature all change gradually from the canopy to the forest floor. These changes are associated with a vertically layered (stratified) community in which different plant species occupy different vertical positions in the forest according to their tolerances. The diagram shows how light, wind, and humidity vary from canopy to floor and how some abiotic conditions may affect the plant community.

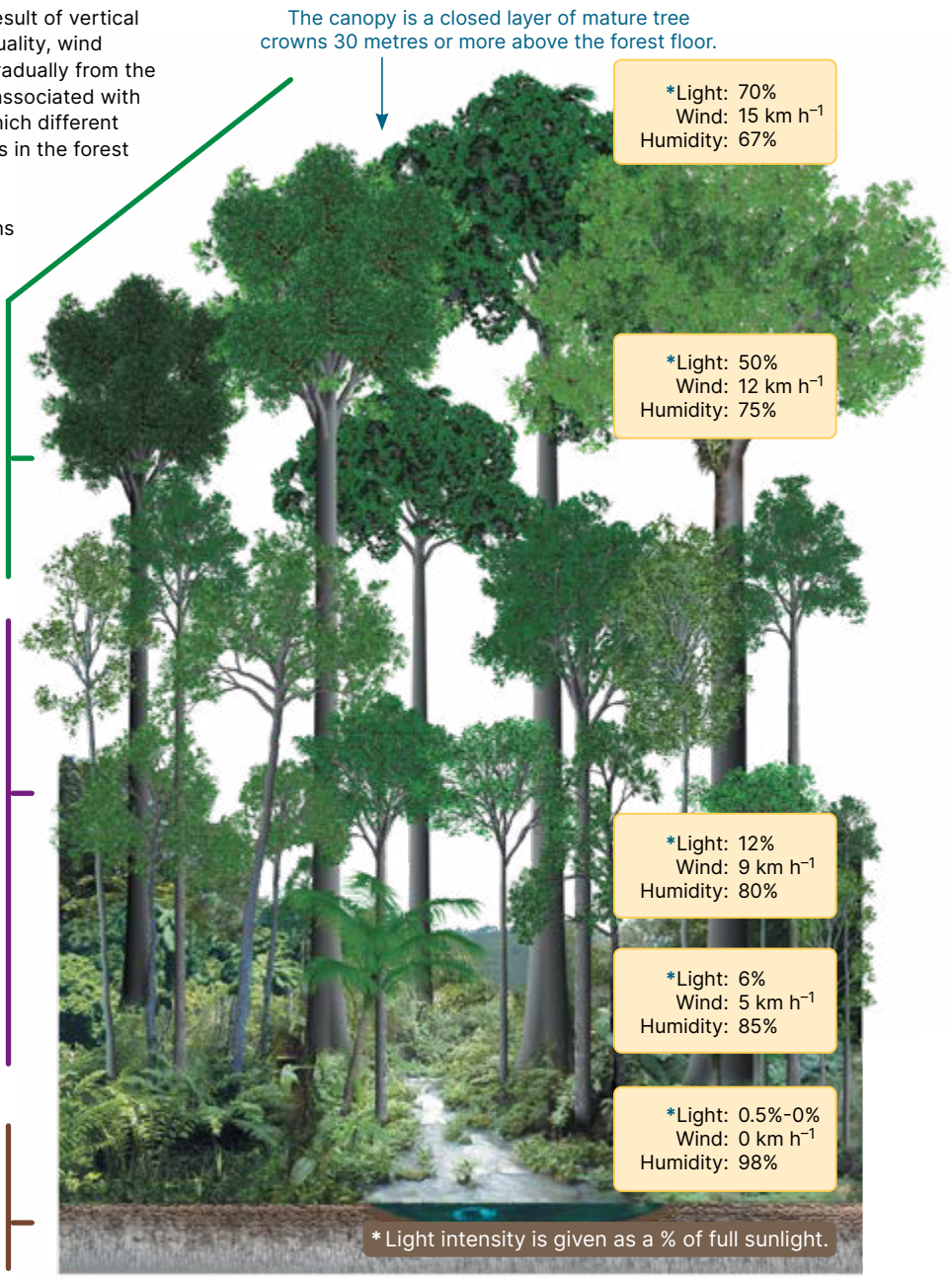
The canopy intercepts most of the incoming light and it is also exposed to the highest wind intensities. The uppermost leaves of canopy tree species are often small and waxy to minimise water losses in the windy, high light environment. Some young canopy species will only make it to canopy height if a gap is created by a wind fall of a larger tree. Epiphytes (perching plants) such as orchids and bromeliads create microhabitats within this layer, contributing to high diversity.

Plants found in the understorey are the young saplings of the canopy trees and those adapted to lower light levels and reduced wind intensities. Water losses from the leaves here are low, so leaves are broad and dark to maximise light capture for photosynthesis. Shrubs, which require high light, are generally absent from pristine tropical rainforest although deciduous temperate forest can have a rich shrub layer.

Water is critical for the survival of subtropical rainforests in Australia. Many rainforest species depend on high soil moisture and high annual precipitation (as rain, snow, cloud, and fog). Rainfall through the winter dry season is particularly crucial.

Very little, if any, light reaches the forest floor, so plant growth here is restricted to a few low-light adapted species (e.g. mosses).

Many rainforest soils are leached and nutrient poor. Soil pH also affects nutrient availability.



1. Explain how environmental gradients and stratification in a rainforest community contribute to diversity:

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7 Measuring Abiotic Factors and Gradients

Key Idea: Measuring abiotic factors provides information about the physical environment, which can be correlated with patterns of species distribution.

Abiotic factors can be measured in a way which provides quantitative (numerical) data about an environment or **sample**. Measurements can be taken manually using specialised equipment, but data can also be collected using a **data logger** (right). Data loggers are electronic devices that automatically record data over time. There are several advantages to using a data logger:

- Recordings have a high degree of precision and accuracy. Calibration of data loggers is factory-set so the accuracy is known.
- Data loggers can be left for extended periods without the need for monitoring.
- Data loggers can be programmed to take readings over a long period of time (e.g. hourly readings every day) or many readings in a short period of time.
- They can be used when there is a safety risk involved (e.g. extreme temperatures).
- Data collected can be downloaded to a computer so that the data can be accessed and analysed.

Pasco

A data logger can be fitted with specific probes to gather and record physical measurements (e.g. wind speed, pH, humidity, temperature).

How are abiotic factors measured?

Each abiotic factor is measured using a dedicated device (e.g. oxygen meter) or a specific probe fitted to a base data logger. Many modern meters measure several variables at once (e.g. light, moisture, and pH). Temperature is an almost universal measurement in ecosystem studies but the data collected needs to be appropriate to the sample. For example, measures of turbidity (the degree to which the water loses its transparency) can only be made in water. Some examples of abiotic measurements are provided below.

pH is the measure of how acidic or basic something is. Living organisms have very specific tolerance ranges for pH in either soil or water, so pH is an important environmental measure. In the field, pH is measured using meters, like the one above. In the lab you could use a pH meter or pH indicators (e.g. pH test paper).

USGS public domain

Turbidity (cloudiness of a fluid) is caused by suspended particles. Field measurements are made using a secchi disc (above). The disc is lowered into the water and the depth at which is no longer visible is recorded. Lab samples are generally measured using a turbidity meter. Some species may find it hard to hunt prey in highly turbid waters.

Victor 'rdfr' Morozov CC3.0

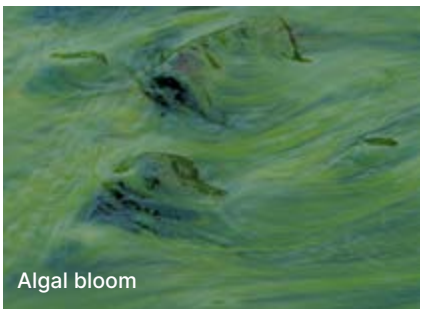
Salinity, the dissolved inorganic salt content of water or soil, is measured by passing an electric current between two electrodes. The conductivity is influenced by the concentration and composition of dissolved salts. Organisms have specific salinity preferences although many intertidal and estuarine organisms are tolerant of wide fluctuations.

Tim Keegan cc 2.0

Menindee ponds on the Murray-Darling River system

Dissolved oxygen (DO) meters and sensors measure the amount of dissolved oxygen in water. DO decreases when temperatures increase or if organic matter in the water column increases. Many native fish species (e.g. bony bream, Murray cod) are highly susceptible to oxygen depletion. High temperatures in the summer of 2018-2019 resulted in massive fish kills in the Menindee lakes on the Murray-Darling River system, NSW.

Carbonates are chemical compounds containing the carbonate ion, CO_3^{2-}. In natural waters, a dynamic equilibrium exists with CO_3^{2-}, bicarbonate, CO_2, and carbonic acid. Increased CO_2 (which dissolves in the water from the atmosphere) shifts the equilibrium towards more H^+ and CO_3^{2-}, decreasing pH and making it more difficult for shell building organisms, such as corals to build and maintain their shells.



Algal bloom

Nitrogen compounds have many negative environmental effects. For example an excess of nitrogen in water bodies, commonly from fertiliser runoff can result in algal blooms (above). These blooms are often toxic. Nutrient enrichment (eutrophication) leads to other physical changes (e.g. lower DO and increased turbidity) and affects species survival, **distribution**, and dispersal. Nitrogen levels are tested using laboratory tests.

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Planning your sampling

Careful thought must go into deciding how to carry out abiotic sampling in order to obtain useful data. Things to consider include:

- Have you thought about and identified potential safety issues? How will you reduce any risk to yourself and your peers?
- Make sure that you can use the equipment properly *before* you start analysing your samples.
- Will you take measurements in the field or collect samples and analyse them in the laboratory? How do you decide?
- If you are collecting samples, how will you label them? How will you make sure the samples do not deteriorate before you analyse them?
- What physical factors will you measure?
- What equipment will you need?
- How will you decide where to carry out the measurements?
- How many samples or measurements will you take?
- Over what duration will you collect data?

Pasco

Where should you carry out your abiotic measurements?

Where you test your samples depends on the abiotic factors you are measuring and the equipment available to you. Some abiotic measurements can only be carried out in the field, or are best carried out in the field because the samples will deteriorate or change over time. Other measurements can only be carried out in the laboratory because special equipment (e.g. titration) is needed for the analysis. Some abiotic factors can be measured in the field *or* in the laboratory.

1. Some commonly measured abiotic factors are listed below. Decide where you think these abiotic factors should be measured, and sort them into the boxes below:

   pH, dissolved oxygen, temperature, light, nitrogen nutrients, wind speed, salinity, carbonates, turbidity, humidity.

Field only	*Laboratory or field*	*Laboratory only*

2. (a) As a class, choose a site for taking samples (for example soil samples from the school grounds or water samples from a nearby pond or stream). Each student or group should take samples as close as possible to each other. Record the sample type and collection location here:

   _____

   (b) Now decide what abiotic factors you can measure for each sample and list them here. The types of tests you choose will depend on the type of equipment that you have available:

   _____

   _____

   _____

   _____

   _____

   (c) How many times will you test each sample? _____

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(d) In small groups carry out the sampling and measurement. Depending on the equipment available, each group may not be able to measure all of the abiotic factors. Record your results in the space below:

(e) Share your results with the class (e.g. on a shared electronic document). Summarise the class results below:

3. Two groups of students measured pH in the same soil sample but obtained very different results. What could have caused these differences?

4. Explain why it is important that you know how to use the equipment before you analyse any samples:

5. Why do you think abiotic factors are usually measured when biotic samples are taken? _____

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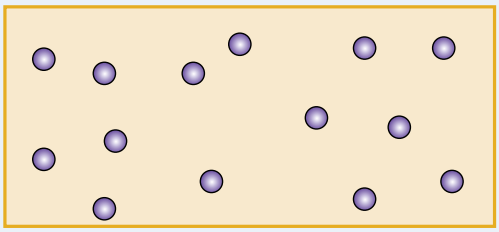
8 Habitat Affects Density and Distribution

Key Idea: Population density is the number of organisms of one species in a specified area. Distribution describes how the organisms are distributed relative to each other.

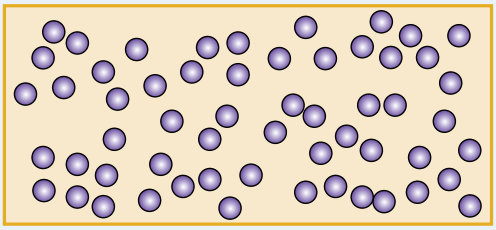
A population is defined as all the members of the same species in a particular geographical area (and therefore capable of interbreeding). Populations have characteristics, such as **density**, **distribution**, and age structure, not shown by individuals. Population density is the number of individuals per unit area or volume. The way the individuals are spaced in the physical environment is called the population distribution.

Low density



In low density populations, individuals are spaced well apart. There are only a few individuals per unit area or volume (e.g. highly territorial, solitary mammal species).

High density



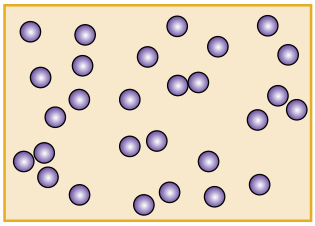
In high density populations, individuals are crowded together. There are many individuals per unit area or volume (e.g. colonial organisms, such as many corals).

Michael J Fromholtz cc 4.0

Quolls are mostly solitary, meeting up solely for mating.

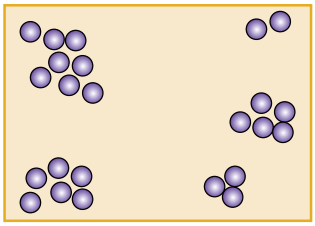
Termites form well organised, high density colonies.

Random distribution



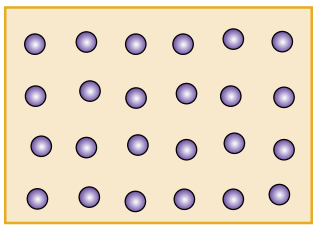
A random distribution describes an irregular spacing between individuals. The presence of one individual does not directly affect the location of any other. Random distributions are uncommon in animals but are often seen in plants.

Clumped distribution



Clumped distributions occur when individuals are grouped in patches (often around resources). The presence of one individual increases the chance of finding another close by. Such distributions occur in herding and social species.

Uniform distribution



Regular distribution patterns occur when individuals are evenly spaced within the area. The presence of one individual decreases the probability of finding another individual very close by. The gannets above are also at a high density.

1. (a) How could the distribution of resources lead to organisms having a clumped distribution pattern?

   _____

   _____

   (b) How could a group social behaviour lead to organisms having a clumped distribution pattern?

   _____

   _____

2. What type of behaviour might encourage a uniform distribution of an animal species? _____

   _____

3. What type of environment would encourage uniform distribution? _____

4. Describe an example of each of the following types of distribution pattern:

   (a) Clumped: _____

   (b) Random (more or less): _____

   (c) Uniform (more or less): _____

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9 Comparing Ecosystems Across Different Scales

Key Idea: Both biotic and abiotic factors determine species distribution and abundance. Their combined effects result in measurable changes in communities over time and distance.

Species **distribution** is affected by interactions amongst other living organisms (**biotic factors**) and the physical (**abiotic factors**) in their environment. Scientists determine the effect of these factors by observing how communities change over time (temporal scales) or over space and distance (spatial scales). In this activity you will look at case studies to see how communities vary over time and distance.

Biotic factors and community change over time

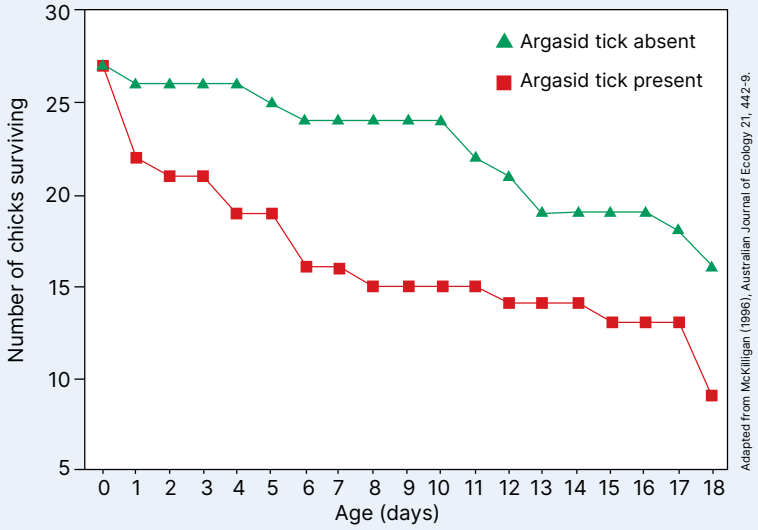
Species rarely exist in isolation, they are always interacting with other species (their biotic environment). These interactions influence the number of each species present and community composition (relative abundance of different species). Some important interspecific interactions (interactions between different species) are described below:

- Predation: One species, the predator, kills another species (the prey) and eats it.
- Interspecific competition: Members of different species attempt to acquire the same limited resources (e.g. food, space) (competition between members of the same species is called intraspecific competition).
- Symbiosis: Symbioses involve two or more species living closely together. In many cases, the symbiosis is obligate, meaning neither species can survive on its own. Important examples include:
  - Mutualism, in which both species benefit from the relationship, e.g. a ruminant and its rumen microorganisms.
  - Parasitism: One species (parasite) depends on a host for its survival. The host is harmed but not usually killed.
  - Disease results from infection with a disease-causing organism (pathogen). The relationship is essentially parasitic.

Parasitic infections affect the health of the host species. In animals, the parasite consumes tissue, often blood, and can reduce the nutrients available to the host for growth and reproduction. In severe cases, the parasites weaken their host, making them more vulnerable to predators and disease.

A three year study of cattle egrets (*Bubulcus ibis*) in south-east Queensland found that chick survival is negatively affected by the presence of the parasitic argasid tick (*Argas robertsi*). During the 1991-92 breeding season, cattle egret chicks were divided into two groups of 27. One group of chicks had their nest treated with a pesticide to kill the argasid tick, the other group were untreated. Their survival was monitored over 18 days and the results are presented in the graph (right).

Survival of cattle egret chicks with and without the argasid tick present during the 1991-92 breeding season



1. (a) Study the graph above of the cattle egret chick survival. Compare the survival rates of the infected and non-infected chicks:

_____

_____

_____

_____

_____

(b) In some breeding seasons, the numbers of argasid tick present are quite low and in others their numbers are very high. How do you think these changes would affect the population of cattle egrets?

_____

_____

_____


Cattle egret (*Bubulcus ibis*)

Stig Nygaard CC2.0

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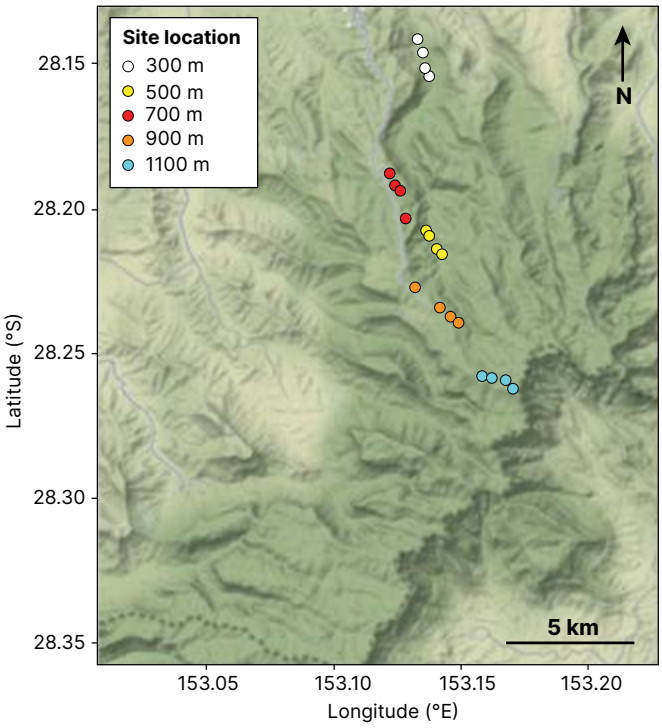
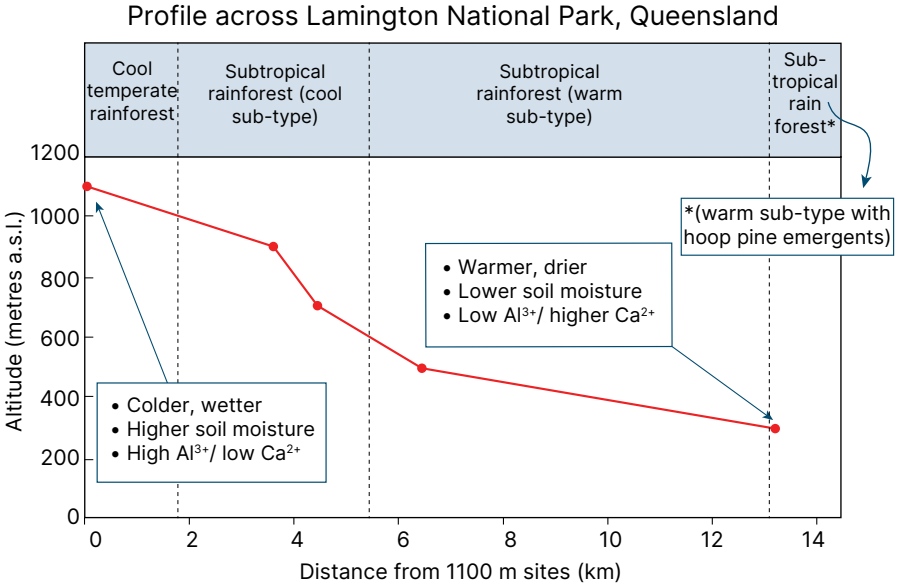
Abiotic factors and community change over distance

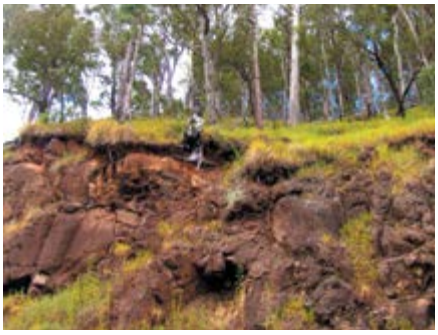
- As you have seen earlier, abiotic factors vary along spatial gradients to produce **environmental gradients**. Each species in an environment has a range of abiotic conditions most suitable to its survival and reproduction, so environmental gradients are important determinants in patterns of species distribution.
- This principle is especially well shown when we look at altitudinal gradients. As altitude increases, abiotic conditions change and so too does the dominant vegetation. This leads to a phenomenon called altitudinal zonation, with zones of distinct vegetation type associated with a particular suite of altitude dependent abiotic conditions.
- A large research group from a number of institutions, including Griffith University, Qld, studied aspects of **biodiversity** and physical environment in Lamington National Park, south-east Queensland on the Qld/NSW border 110 km south of Brisbane. The ongoing research is part of an international research programme examining forest diversity. They set up 20 permanent plots over an altitudinal range of 300 m to 1100 m above sea level (a.s.l). This activity looks at some aspects of that research (see **BIOZONE's resource hub** for sources) and allows you to explore spatial and temporal changes in ecosystems.
- The map, right, shows the site locations. Note that the 700 m altitude sites are offset. This is because of 1) the terrain and 2) necessary access to sites.
- Some of the findings of two different studies are reported here. Laidlaw et. al. examined floral species diversity at each of the 20 sites, while Strong et. al. logged physical data over a period of 333 days.
- The aims of the studies were to track changes in environmental factors and to provide a baseline for evaluating the impacts of climate change.
- Lamington NP is located on the flanks of a basaltic shield volcano. The acidic soils are derived from weathered basalts. Four rainforest types were surveyed, and 12 distinct species assemblages were recognised, each specific to their site conditions. Lamington National Park is considered a biodiversity hotspot and includes many endemic species and several Gondwanan relicts (e.g. Antarctic beech).
- A profile generated from the latitude-longitude data is shown below with some summary data on and below the diagram. Much of the park consists of Complex Notophyll Vine Forest (CNVF). The distribution of the rainforest types is correlated with features of topography, climate, and soil properties.





Malcolm Jacobson cc 3.0

Elabana Falls, located at 844 m altitude is one of many waterfalls within the forest.



Johncatsoulis Public Domain

The weathered volcanic soils of Lamington National Park are acidic and those at high altitudes are leached of nutrients.

	300 m	500 m	700 m	900 m	1100 m
Species richness	135	147	138	108	80
Mean pH	6.4	6.0	5.4	4.6	4.3
Mean soil organic matter (%)	12.05	15.85	14.95	21.50	27.18
Mean soil moisture (%)	22.52	26.24	26.76	33.55	44.37

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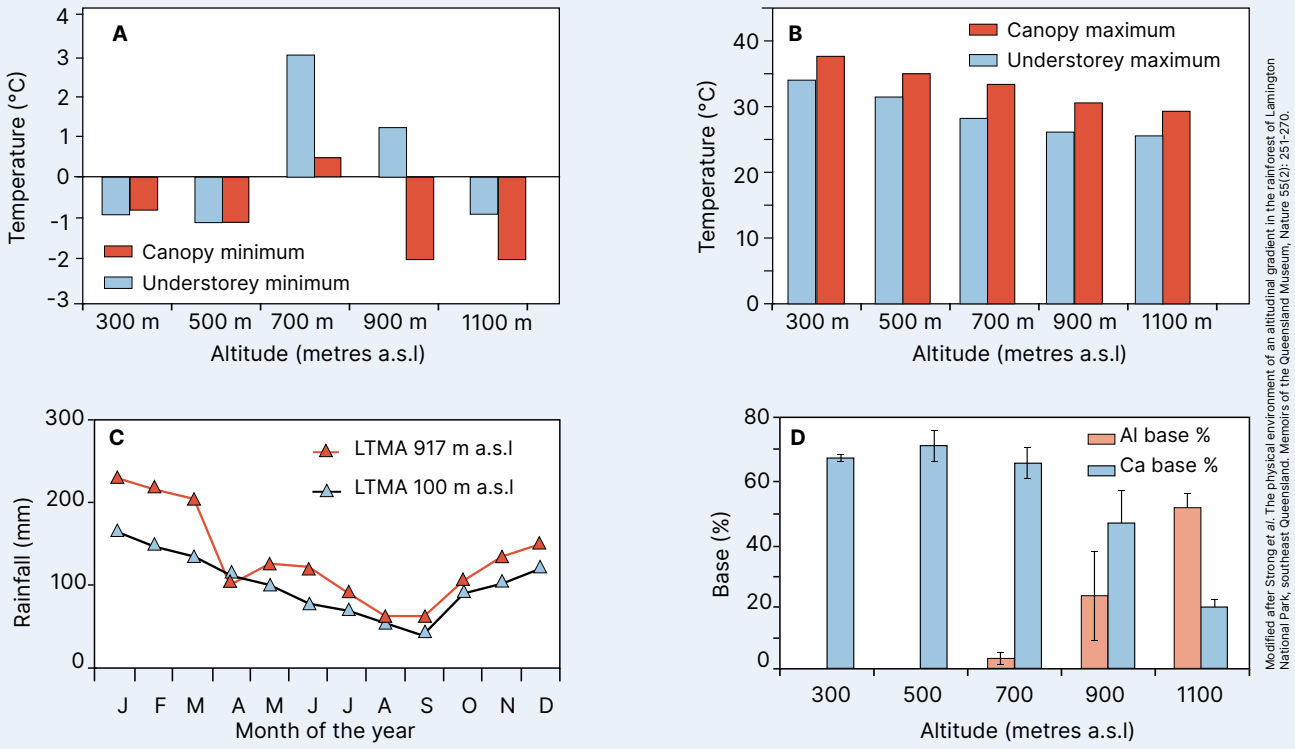
Trends in some of the abiotic factors determining rainforest type at different altitudes, Lamington National Park, south-east Queensland



Modified after Strong *et al.* The physical environment of an altitudinal gradient in the rainforest of Lamington National Park, southeast Queensland. Memoirs of the Queensland Museum, Nature 55(2): 251-270.

Descriptions: Plots A & B (top) show minimum and maximum temperatures recorded in the canopy and understorey across 5 altitudes July 2007 - August 2008. Plot C (bottom left) shows the monthly average rainfall over three years (2006-2008) recorded at permanent weather stations at two altitudes in Lamington National Park. Plot D (bottom right) shows change in Al and Ca in the top soils across 5 altitudes. Base (%) describes the percentage of the soil exchange sites occupied by the named cation. At low pH, Al^{3+} (just referred to as Al) dominates and is toxic to many plant species.

2. Answer the following with reference to plots A and B above:

   (a) What was the trend in the maximum temperature in the understorey and canopy between 300 m and 1100 m a.s.l?:

   _____

   (b) Which region of the forest (canopy or understorey) experienced the coldest temperatures overall? Why might this be?

   _____

   _____

   (c) The minimum temperatures experienced by canopy and understorey at 700 m do not show the same trend as the other altitudes. What factors might have contributed to this difference? How could you find out?

   _____

   _____

3. Rain gauge failures at the sampling sites meant that rainfall data from nearby stations was used instead.

   (a) Describe the trend in monthly average rainfall in Lamington National Park (plot C above): _____

   _____

   _____

   (b) How does the rainfall differ between 917 m and 100 m? (plot C above): _____

   _____

4. (a) Looking at the table opposite, describe the trends in soil pH and soil moisture from 300 m to 1100 m:

   _____

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Bangalow palms are recorded at most altitudes in Lamington National Park as part of an assemblage of more generalist rainforest species that can survive under a range of conditions.

Moran's Falls is close to the 900 m sampling sites. The vegetation here requires a largely uniform rainfall distribution with a summer peak and regular contact with cloud and fog, as shown above.

Lady aly's cc 3.0

Antarctic beech is a Gondwanan relict (pre-dates the break-up of Gondwana). It is part of a species assemblage found only above 1000 m. Plants are adapted to low pH, nutrient-poor, waterlogged soils, cold wet conditions and occasional frost and snow.

There are 20 distinct ecosystems in Lamington National Park reflecting the many different **microclimates** created by differences in slope and aspect as well as in altitude. Some of these micro-climates may shrink or shift their distribution as the climate warms.

(b) How do you think the trends you described in (a) might account for the increase observed in soil organic matter from 300 m to 1100 m?

(c) What happens to species richness as you move from 300 m to 1100 m? How might you explain this trend in terms of the changes in abiotic conditions?

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5. The increase in aluminium ions with altitude is related to low pH because soluble aluminium levels increase as a consequence of increasing acidity. High aluminium is toxic for many plants. Looking at plot D on page 17, what does this tell you about the species that can and cannot live at or above 900 m? How can you relate this to species richness at higher altitudes?

6. (a) How does the data from the research summarised here provide evidence for the characteristics of different ecosystems being determined by spatial and temporal differences in abiotic factors:

   (b) Explain how a warming climate might put some of these characteristic ecosystems at risk. Which would be most threatened?

7. Using your knowledge of abiotic factors and environmental gradients, work in small groups to discuss how environmental gradients contribute to the diversity of ecosystems found in Queensland. Summarise your discussion below:

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10 How Do Physical Factors Influence Biodiversity?

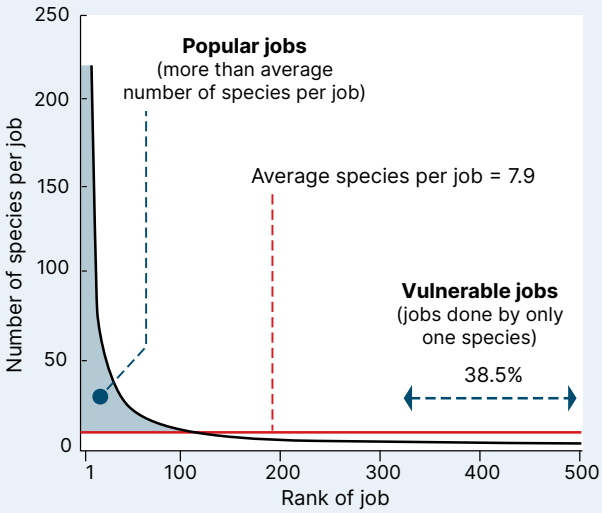
Key Idea: Changes in abiotic factors can have marked effects on the diversity of vulnerable ecosystems.

High species diversity generally buffers ecosystems against environmental change because the large number of species present creates functional redundancy in ecosystem processes such as nutrient recycling (meaning many species can do the same job). However, some biologically diverse systems are more vulnerable than others to physical changes in the environment, usually because they are heavily dependent sensitive key species. The Great Barrier Reef, which is built by corals, is one such example. Reef building tropical corals are very sensitive to changes in temperature and ocean pH. Changes in **abiotic** conditions can therefore have a significant impact on reef diversity and functioning.

- On the Great Barrier Reef, some functional roles (ecosystem 'jobs') are carried out by numerous species, but most jobs are performed by only a few species and almost 40% are carried out by only one species. That makes these functional roles very vulnerable. If that one species is lost, the role is no longer performed, and ecosystem function is compromised.
- The graph, right, shows the number of fish species carrying out jobs in the Indo-Pacific region, which includes the Great Barrier Reef.

The Great Barrier Reef is:

- A world heritage site.
- The largest living structure on Earth (2300 km long) and visible from space.
- Home to at least 9000 species.
- Made up of 2500 individual reefs and 900 islands.



Changing environments and the long term health of the Great Barrier Reef

In recent decades, scientists have become concerned about how the physical changes associated with global warming are affecting **biodiversity** on the Great Barrier Reef.

- Corals are colonial marine invertebrates. The reef structure itself is formed of colonies of coral polyps held together by calcium carbonate. Some trap their own food, but most rely on the presence of symbiotic algae living within the coral structure. These algae supply the coral with 90% of its energy (as sugars, glycerol, and amino acids).
- When coral becomes stressed (e.g. due to changes in temperature), the algae are expelled from the coral. This is called coral bleaching (because the coral becomes very pale). Bleached coral is not dead, and it can reacquire new algal symbionts. However, it is not healthy and more vulnerable to further environmental stress.
- Different stressors can cause coral bleaching including changes in ocean temperature, increased pollution, exposure to too much sunlight, and extreme low tides.
- Several coral bleaching events associated with increased water temperature have affected the Great Barrier Reef in recent decades, with major bleaching events occurring in 1998, 2002, 2016, 2017, 2020, 2022, and 2024. The 2024 bleaching event coincided with the highest sea surface temperatures experienced since 1900 (0.19°C higher than the previous record in 2017). An estimated 79% of the all reefs in the Great Barrier Reef experienced some level of bleaching, with 49% showing >30% of coral cover bleached and 39% showing >60% of coral cover bleached.
- Much of the marine ecosystem along the reef's north coast has become barren and skeletal with little hope of recovery. Such large-scale changes to reef structure affect biodiversity and the **distribution** of species dependent on reef habitat.

Toby Hudson, cc 3.0

Coral diversity, Flynn Reef, Great Barrier Reef, near Cairns, Qld.

Acropora, cc 3.0

Staghorn corals (above), are especially sensitive to bleaching. Here, bleached coral sits next to healthy coral.

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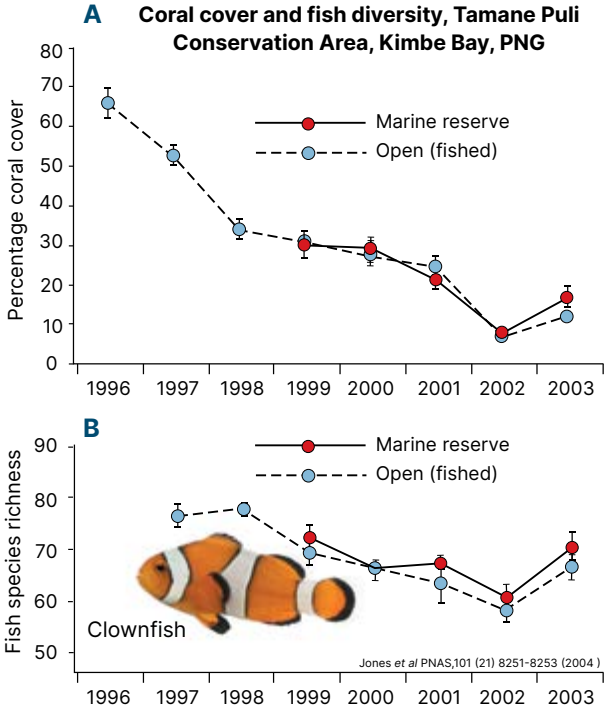
How does temperature affect reef biodiversity?

Thousands of species shelter, find food, reproduce, and raise their young in coral reefs. When irreversible coral bleaching occurs the coral dies and begins to break down. Any species reliant on the coral now become vulnerable themselves. For example, with no coral to hide in, prey species will be found and eaten by predators more easily, there is no where safe to raise young, and fewer places to find food. Every time a species is removed from the food chain other species become vulnerable.

Many species are directly affected by an increase in ocean temperature. Many biological processes in fish are moderated by water temperature. As a result, growth, reproduction, swimming ability, and behaviour can be negatively affected when ocean temperatures fall outside specific ranges.

Protection of marine habitats within marine reserves may not protect against decline in the diversity of reef communities. An eight year study in Papua New Guinea found fish diversity declined with percentage coral decline regardless of protection status.

Graphs right: (A) declining mean cover of branching corals 1996 - 2003 (Kimbe Reef). Coral cover was estimated from annual surveys of eight reefs, four within a marine protected area and four open to fishing. (B) Change in mean fish **species richness** for four reef families between 1997 and 2003 for the four marine reserves and four fished reefs. Bars = standard errors in both (A) and (B).




The conspicuous angelfish

Clownfish and marine angelfish (above) are just one of more than 20 species-rich families associated with coral reefs, and directly or indirectly dependent on them for food or habitat. All the species in some genera (e.g. the coral crouchers) depend completely on corals.


Loggerhead turtle

Six of the world's seven marine turtles, including the vulnerable loggerhead are found on the Great Barrier Reef. Turtle sex is determined by the temperature at which the eggs are incubated, so a warming climate is also likely to alter the sex ratio of turtle populations.

1. Working in groups, use the information on this page and your own research to evaluate the evidence for the link between increasing sea surface temperatures, coral bleaching, and changes to the biodiversity of reef ecosystems. Why are coral reefs so vulnerable to climate change and why do marine protected areas not necessarily help in stopping biodiversity declines. Summarise your findings as points below, along with any supporting evidence.

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11 Using Technology to Measure Diversity

Key Idea: Technology provides a way to monitor populations or measure diversity in ecosystems that are not easily monitored by traditional sampling methods.

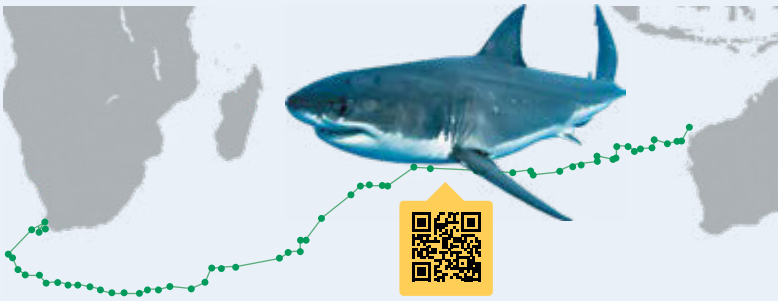
It is not always possible or practical to directly measure diversity within an ecosystem by traditional count methods. For example, some ecosystems are too large or too difficult to access, or the populations being studied may be too difficult or dangerous to monitor. In these instances, technology provides a useful way to measure, analyse, and monitor changes in **biodiversity**. A number of techniques can be used to help monitor diversity (below). Some techniques are well established, while others are relatively new.

Electronic tracking

Radio-tracking and **satellite tracking** can be used to obtain real time, accurate information about where an animal spends its time. The methods are non-invasive, so the animals are not harmed. It provides information about dispersal, **distribution**, habitat use, and competitive relationships.

Satellite transmitters can be used to study migratory movements of large animals and marine species (right), which are difficult to track because of the large distances involved.

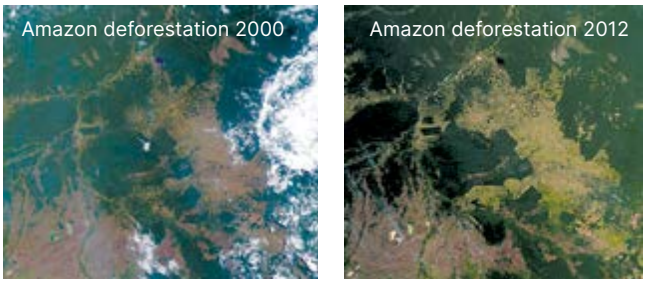
Radio-tracking is useful for studying threatened species. The information gathered can be used to manage an endangered species effectively.



During 2002 and 2003, a number of great white sharks were radio-tagged in South African waters. The data recovered showed the first ever recorded intercontinental migration by a great white. A female shark known as P12, swam 11,000 km from South Africa to Australia in 99 days with a minimum speed just under 5 km per hour. Within 9 months she had returned to South African waters, completing a round trip of more than 20,000 km.

From Bonfil et al 2005.

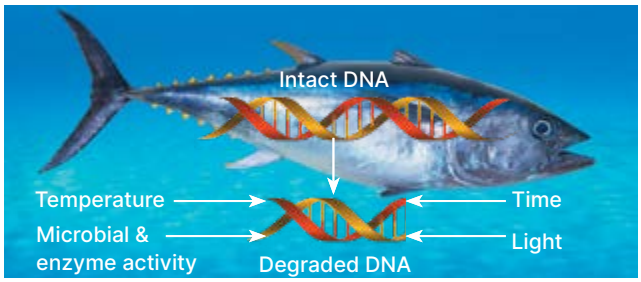
Remote sensing



Photos: NASA Earth Space Laboratory

Remote sensing involves collecting information from a distance (e.g. satellite imagery or aircraft sensor technologies). Data can be collected from dangerous or inaccessible areas, and large areas can be studied. Some remote sensors detect the energy that is reflected from Earth, whereas others collect photographic images. A common use is to monitor how land use and vegetation type are changing over time. The extent of deforestation (the removal of forest) is often measured in this way. The data can be used to help in the management and conservation of biodiversity and natural resources. For example, priority can be given to conservation in areas of high diversity. The technology can also be applied to the oceans. Data (e.g. currents, temperatures) can be used to manage ocean resources. The images above record increase in deforestation (pale areas) in the Amazon over 12 years.

Environmental DNA (eDNA)



Molecular techniques provide another way to assess diversity. Environmental DNA (eDNA) involves collecting DNA from environmental samples (e.g. soil, water, air) rather than directly from an organism. The rationale is that an organism leaves its DNA in their environment (e.g. via shed skin), so their DNA can be collected and quantified as a measure of diversity. This is achieved by comparing the collected DNA against a database to identify which species are present. It is also possible to quantify species abundance. The advantages of eDNA analysis is that large areas can be studied and the technique is fast and cheap to run. However, being relatively new, only a few comparative studies have been made to validate its reliability and there are some difficulties. Detecting low abundance species is not always reliable and DNA degrades over time due to environmental factors (above) making it harder to analyse.

1. Form a group of three. Each person should choose one of the three examples above and research how the technology can be used to measure diversity. Your research should include how the technology is used, any benefits or problems associated with its use, and how reliable it is. Summarise your findings below and share them with your group:

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12 Protecting Biodiversity

Key Idea: Agreements to protect biodiversity aim to reduce species losses, often through setting conservation targets.

Each species performs an important role within its ecosystem. As species disappear, their roles may no longer be performed and ecosystem functioning will suffer. Over time, species loss could cause irreversible change to the planet. A number of formal agreements and action plans are in place to protect global biodiversity or manage species conservation. Many agreements set biodiversity targets aimed at reducing biodiversity loss and ensuring that progress towards biodiversity goals is maintained. These targets may be regional, national or international. International conventions, such as the World Heritage Convention and the Convention on Biological Diversity (below) are particularly important for the protection of species that cross national boundaries (e.g. migrating birds or whales).

The World Heritage Convention

- The World Heritage Convention (WHC) aims to promote the protection of heritage around the world which has been identified as having outstanding universal value. These can be natural areas or cultural sites.
- Australia was one of the first countries to sign up to the WHC which came into force in 1974.
- The WHC links the concepts of nature conservation and the preservation of cultural properties into a single document. It does this by recognising the way in which people interact with nature, and the important need to keep the two balanced.
- A committee elected from the 187 member countries meets annually to update and manage the administration of the convention. For example they may provide help to countries to meet their WHC obligations, or update the list of sites recognised under the convention.
- Australia has several sites covered by the WHC. These include the Sydney Opera House, the Great Barrier Reef, the wet tropics of Queensland, and Fraser Island (below). None of the sites in Australia are on the list of world heritage sites in danger.

The Convention on Biological Diversity

- The Convention on Biological Diversity (CBD) has 196 parties (members) and was established in 1992.
- The CBD is legally binding. Countries that join it must obey its rules.
- It covers all ecosystems, species, and genetic resources.
- The Convention has three main goals. These are:
  - The conservation of biological diversity.
  - The sustainable use of the Earth's resources.
  - Fair and equitable sharing of benefits arising from genetic resources.
- The CBD has been modified to keep up with evolving issues and advancements. There have been two important additions. These are:
  - The Cartagena Protocol on Biosafety (2003).This aims to account for advances in biotechnology (which occur very rapidly). It addresses technology development and transfer, sharing of benefits resulting from technology (e.g. discovery of new compounds) and addressing biosafety issues.
  - The Global Strategy for Plant Conservation (1999) which aims to slow the rate of plant extinctions.

Fraser Island (K'gari), the largest sand island on Earth

1. Why do you think it is important to have international conventions to conserve biodiversity? _____

2. Several Queensland sites are identified in the WHC. Select an example and explain why it is included in the WHC:

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3. Two significant modifications have been made to the CBD, one is the Cartagena Protocol on Biosafety. Using this example, explain why it is important that international conventions are regularly updated:

Why set biodiversity targets?

A target provides a measurable way to see how well a set goal or objective is progressing. When applied to biodiversity, targets are set to reduce (or ultimately stop) the loss of biodiversity by an agreed amount within a set time frame. The targets are regularly assessed to see if the goal will be met on time. Interventions and changes can be applied if the steps required to meet the targets are falling behind schedule. Some specific biodiversity targets relating to the CBD include:

- The Global Strategy for Plant Conservation (GSPC). This recognises the important role plants play on Earth, acknowledging that without plants, there is no life. The initial aim of this target was to slow the pace of plant extinction by 2010. However, the original GSPC targets were not achieved and the project was updated and now has a 2020 time frame.
- Aichi biodiversity targets. These are a group of 20 biodiversity targets and are included as part of the CBD strategies. The Aichi targets are categorised under four strategic goals (diagram below).
- Each country then sets their own national targets linked to the international targets. This approach means that countries are able to identify and address their own biodiversity issues while achieving the overall international targets. In Australia, these consist of the 10 national targets that are part of Australia's Biodiversity Conservation Strategy (ABCS). Queensland-specific goals include the Great Barrier Reef plan, pest eradication to stop invasive species harming Queensland's native species (e.g. the protection of native turtles being eaten by wild pigs), and management of the Lake Eyre Basin.

Strategic Goal A:
Address the underlying causes of biodiversity loss by including actions related to conservation and sustainable use at every stage of development.

Strategic Goal B:
Reduce the direct pressures on biodiversity and promote sustainable use.

Strategic Goal C:
To improve the status of biodiversity by safeguarding ecosystems, species, and genetic diversity.

Strategic Goal D:
Enhance the benefits to all from biodiversity and ecosystem services.

The Lake Eyre drainage basin has an area of 1,200,000 km^2 and covers 1/6 of Australia, including much of inland Queensland (right). Identified as a priority in the ABCS, the Australian and Queensland governments have adopted policies "to maintain the ecological integrity and natural function of in-stream and floodplain ecosystems of the Lake Eyre Basin and ensure that other activities do not threaten these environmental values".

4. In groups or individually, research the Lake Eyre Basin:
   - Explain why its natural value is being protected.
   - What targets and actions exist to deliver the ABCS goal stated above? Summarise their progress.
   - Explain the role of regional (state) government and national government in this process.
   - Explain how projects such as this are linked to achieving the goals set out in international biodiversity agreements.

   Attach your work to this page.

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13 Why Do We Sample?

Key Idea: Sampling an ecosystem provides information about its composition and structure, its health, and the likelihood it will be able to resist change.

Take a look outside. Could you count every individual organism in the ecosystem you see? Could you reliably plot their location? Most likely not, because there are too many individuals and not enough time or resources to count them all. To get around these problems, researchers **sample** the ecosystem. Sampling involves choosing a smaller area that represents the ecosystem and counting the organisms in that area. The information gathered from the sample is used to draw conclusions about that ecosystem. But how well does the sample represent the community? You will see in the next few activities that there are ways to design sampling to make it as representative of the ecosystem as possible.

What can sampling tell us?

Stephen Moore

Community composition
Sampling reveals which species are present in an ecosystem and helps to build a picture of community structure or identify species of particular interest. For example, are there endangered species, or introduced, or pest species present?

Marc tarlock cc 2.0

Species interactions
Sample data can be used to construct models of species interactions (e.g. food webs or ecological pyramids). The information can be used to predict the effect of a change in community structure (e.g. decrease in one species).

Species distribution
How is a particular species distributed in the ecosystem and does this change over time (e.g. seasonally). Sample data can tell us about the geographical range of the species and how might this be affected by environmental change.

BH

Species abundance
Sampling reveals information about species **abundance**, i.e. how many of a particular species are present at the location. Species abundance is one measure for estimating biodiversity as well as ecosystem health and stability. The presence or absence of certain species can be used to indicate ecosystem health.

High diversity ecosystem

Ecosystem stability
Data can be used to predict how likely it is that an ecosystem will remain unchanged in its characteristics. We know that low diversity systems are more likely to be negatively affected by disturbance than high diversity systems. The presence or absence of key indicator species are also used to monitor ecosystem changes.

Northern hairy-nosed wombat

Eva Hejda cc2.0

Conservation management
Sampling provides a way to evaluate the success of conservation management strategies. For example, are the numbers of a threatened or endangered species increasing or decreasing? How are the numbers of an invasive species changing? If no progress is made towards conservation goals, the plan can be altered.

1. Suggest why it is important to select a sampling area that is a true representation of the area you are sampling?

_____

_____

_____

2. Why must scientists sample an ecosystem or population instead of studying it in its entirety? _____

_____

_____

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14 How Do We Sample Ecosystems?

Key Idea: Sampling should provide data that are unbiased and accurate. Choice of sampling method and design should be based on suitability to the populations being sampled, the environment, and the time and resources available.

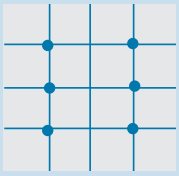
Most practical exercises in ecology involve collecting data about the **distribution** and **abundance** of one or more species in a community. Most studies also measure the physical factors in the environment as these may help to explain the patterns of distribution and abundance observed. There are many sampling options (below), each appropriate to different environments or organisms and with advantages and drawbacks. You must take several factors into account when sampling to make sure the data you collect accurately and impartially represents the ecosystem being investigated.

Sampling designs and techniques

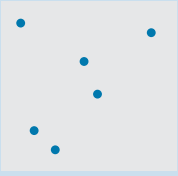
Point sampling

Individual points are chosen using a grid reference or random numbers applied to a map grid. The organisms at each point are recorded. Point sampling is often used to collect data about vegetation distribution.

Pros: Point sampling is efficient if time is limited. It is a good method for determining species abundance and community composition.
Cons: May miss organisms in low abundance.



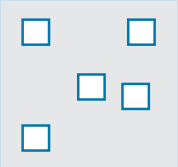
Systematic (grid)



Random

Area sampling using quadrats

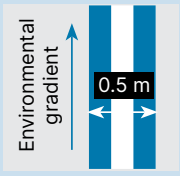
A quadrat provides a known unit area of sample (e.g. 1 m^2). Quadrats are placed randomly or in a grid pattern on the sample area. The presence and abundance of organisms in each square is noted. Quadrat sampling is appropriate for plants and slow moving animals and can be used to evaluate community composition.



Line and belt transects

In a line **transect**, a tape or rope marks the line. The species occurring on the line are recorded (all along the line or at regular points). Lines can be chosen randomly (right) or may follow an **environmental gradient**. **Pros**: Low environmental impact and good for assessing the presence/absence of plant species. **Cons**: Rare species may be missed.

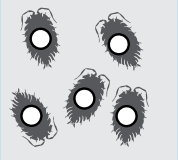
In a belt transect, quadrats are used to sample the plants and/or animals at regular intervals along a measured strip. **Pros**: Provide a lot of information on abundance and distribution as well as presence/absence. **Cons**: Can be time consuming to carry out properly.



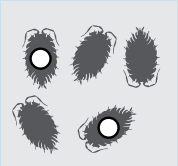
Mark and recapture sampling

1. Animals are captured, marked, and then released back into the population (right).

2. After a suitable time to allow the marked animals to remix with the population, the population is resampled. The number of marked animals recaptured in a second sample is recorded as a proportion of the total. **Pros**: Useful for highly mobile species which are otherwise difficult to record. **Cons**: Time consuming to do well.



1: All marked.



2: Proportion recaptured

Sampling considerations

- Random sampling methods should be used to avoid bias in the data. In random sampling, every possible **sample** of a given size has the same chance of selection.
- The methods used to sample communities and their populations must be appropriate to the ecosystem being investigated. Communities in which the populations are at low **density** and have a random or clumped distribution will require a different sampling strategy to those where the populations are uniformly distributed and at higher density.
- The sample size (e.g. the number of **quadrats**) must be large enough to provide data to enable us to make inferences about aspects of the whole population.

1. Name a sampling technique that would be appropriate for determining:

   (a) Percentage cover of a plant species in pasture:

   _____

   _____

   (b) Change in community composition from low to high altitude on a mountain:

   _____

   _____

   (c) Association of plant species with particular soil types in a nature reserve:

   _____

   _____

   (d) Determining the population size of a fish in a lake:

   _____

   _____

2. What are the benefits of collecting information about the physical environment when sampling populations?

   _____

   _____

   _____

   _____

   _____

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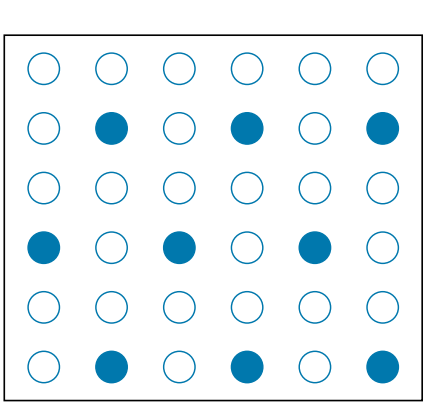
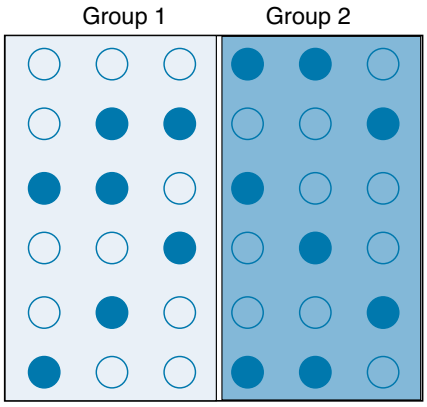
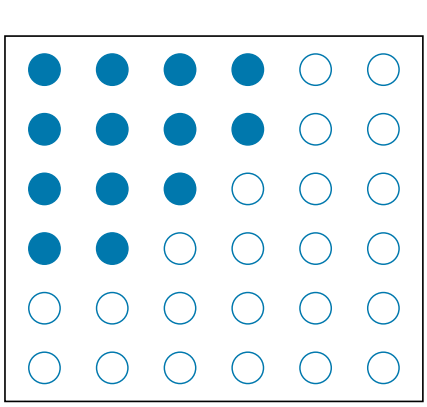
Sampling strategies

In most ecological studies, it is not possible to measure or count all the members of a population. Instead, information is obtained through sampling in a manner that provides a fair (unbiased) representation of the organisms present and their distribution. This is usually achieved through random sampling. Sometimes researchers collect information by non-random sampling, a process that does not give all the individuals in the population an equal chance of being selected. While faster and cheaper to carry out than random sampling, non-random sampling may not give a true representation of the population.







Systematic sampling

Samples from a larger population are selected according to a random starting point and a fixed, periodic sampling interval. For the example above, the sampling period is every fourth individual. Systematic sampling is a random sampling method, provided the periodic interval is determined beforehand and the starting point is random.

Example: Selecting individuals from a patient list.

Stratified sampling

In stratified sampling the population is divided into subgroups (strata) before sampling. Samples are then taken from a stratum in proportion to its representation in the total population. The strata should be mutually exclusive, and individuals must be assigned to only one stratum. Random or systematic sampling is then applied within each stratum.

Example: Dividing the population into males and females.

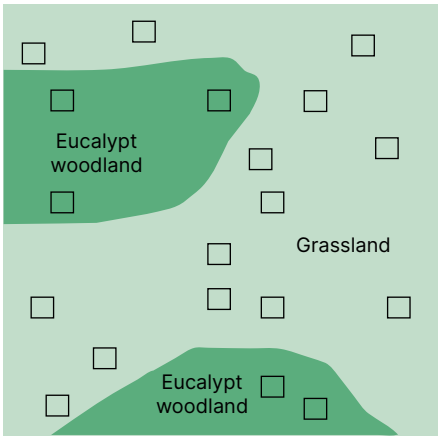
Opportunistic sampling

A non-random sampling technique in which subjects are selected because they are easily accessible to the researcher. Opportunistic sampling excludes a large proportion of the population and is usually not representative of the population. It is sometimes used in pilot studies to gather data quickly and with little cost.

Example: Selecting 13 people at a cafe where you are having lunch.

Stratified sampling in ecology

- Many study areas are not uniform. Instead, they include a variety of distinct habitats, especially if the study site is large. In stratified sampling, the various habitats are sampled separately in proportion to their representation in the total area. This ensures that the sampling fairly represents the entire habitat.
- The sample area is usually divided into groups (strata) based on biophysical features (e.g. landform, soil type, elevation etc) and then by vegetative structure (e.g. forest, woodland, grassland etc).
- Proportional sampling is an essential feature of stratified sampling. For example, the ecosystem on the right contained 30% eucalypt woodland and 70% grass. The researcher decided to place 20 random quadrat samples in total. To ensure proportional sampling, they placed six quadrats in the eucalypt woodland and 14 in the grass.



3. A student wants to investigate the incidence of asthma in their school. Describe how they might select samples from the school population using:

(a) Systematic sampling: _____

_____

(b) Stratified sampling: _____

_____

(c) Opportunistic sampling: _____

_____

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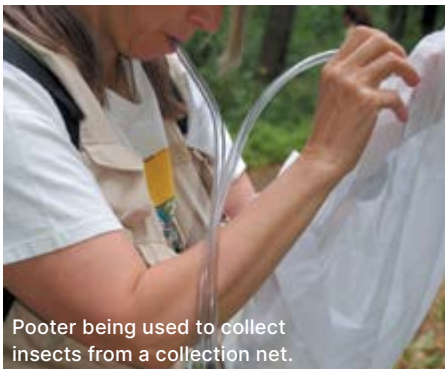
Reducing sampling bias

Bias refers to the selection for or against one particular group. It has the potential to dramatically influence the findings of an investigation and is often a result of non-random sampling, so that certain individuals are under- or over-represented relative to others in the population. Bias can also occur when counts and identification are not accurate, e.g. when only larger (adult) invertebrates from a sample are correctly identified and recorded. Sampling bias can be reduced by:

- **Large sample size**: The sample size (number of samples) should be large enough to accurately reflect the population as a whole. However, the number of samples taken is often determined by the resources and time available.
- **Random sampling**: This ensures that all organisms have an equal chance of being selected. Some sample sites may be very difficult and expensive to access. It can be tempting to not sample them, and sample the easily accessible sites, but their exclusion can bias results.
- **Appropriate collection methods and apparatus:** Failure to select the right sampling technique could mean that some organisms are not recorded at all, so the results are not a true reflection of the population. This type of bias tends to be systematic, e.g. when the wrong net size is chosen to sample a lake community.



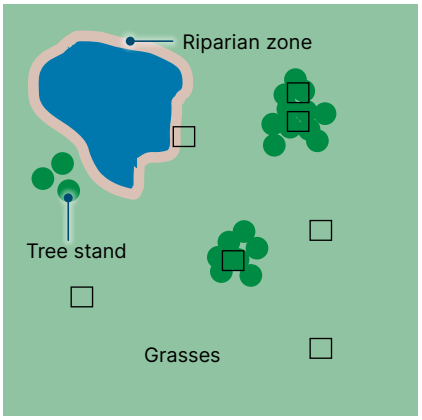
Pooter being used to collect insects from a collection net.

Fritz Geller-Grimm CC3.0

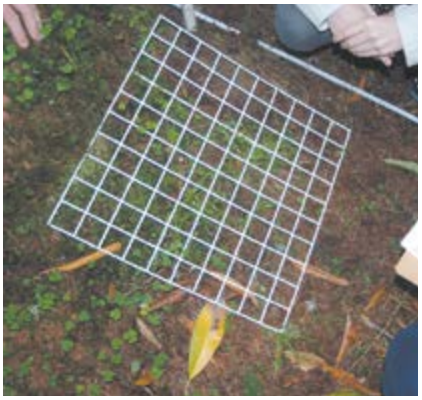
Quadrats are excellent for collecting data on plants but are not so useful for highly mobile species. Researchers use a variety of collection methods, including pooters (aspirators) to collect insects and other mobile species.

4. Explain when stratified sampling would be used in ecological sampling: _____

5. Study the diagram on the right which shows three strata. Identify two errors the researcher has made with their sampling design:



6. Mike, Georgia, and Sam were sent out to randomly sample near a stand of trees along the school fence line. Their instructions were to record the number of plant and animals species present using quadrat sampling (right). The area that they were sampling was quite uniform except for around one tree near a slowly leaking tap, which was quite damp and looked to have different plant species present. During their sampling they found a range of different plants, some very slow moving animals, and some very fast moving animals (e.g. ants).



   (a) Do you think the students should have included the damp area in their sampling? Why or why not?

   (b) The students noticed that some animals moved very quickly and were difficult to count. Describe the limitations of a quadrat for fast moving animals, and explain how it could bias the results:

   (c) Suggest a technique they could use to collect information on mobile species: _____

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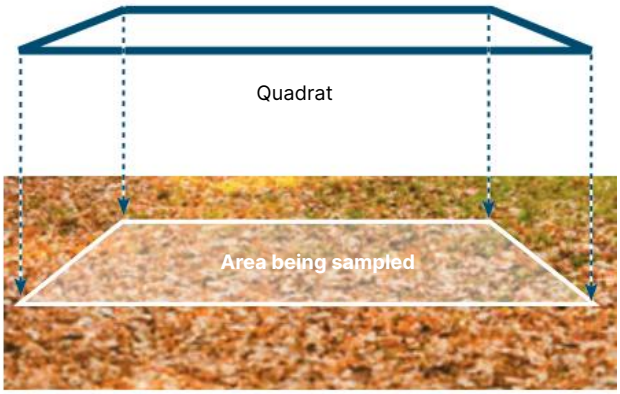
15 Quadrat Sampling

Key Idea: Quadrat sampling involves a series of random placements of a frame of known size over an area of habitat to assess the abundance or diversity of organisms.

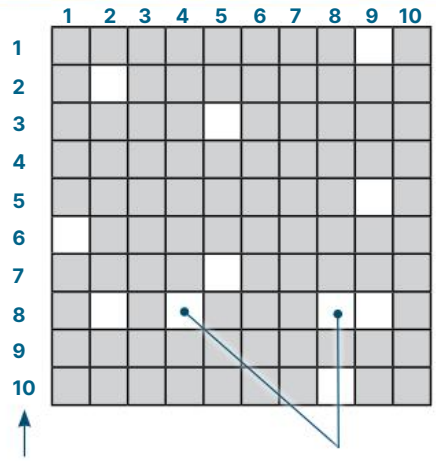
Quadrat sampling is a method by which organisms in a certain proportion (**sample**) of the habitat are counted directly. It is used when the organisms are too numerous to count in total. It can be used to estimate population **abundance** (number), **density**, frequency of occurrence, and **distribution**. Quadrats may be used without a **transect** when studying a relatively uniform habitat. In this case, the quadrat positions are chosen randomly using a random number table. The general procedure is to count all the individuals (or estimate their **percentage cover**) in a number of quadrats of known size and to use this information to work out the abundance or percentage cover value for the whole area.



$$\text{Estimated average density} = \frac{\text{Total number of individuals counted}}{\text{Number of quadrats X area of each quadrat}}$$

Guidelines for quadrat use:

1. The area of each quadrat must be known. Quadrats should be the same shape, but not necessarily square.
2. Enough quadrat samples must be taken to provide results that are representative of the total population.
3. The population of each quadrat must be known. Species must be distinguishable from each other, even if they have to be identified at a later date. It has to be decided beforehand what the count procedure will be and how organisms over the quadrat boundary will be counted.
4. The size of the quadrat should be appropriate to the organisms and habitat, e.g. a large size quadrat for trees.
5. The quadrats must be representative of the whole area. This is usually achieved by random sampling (right).

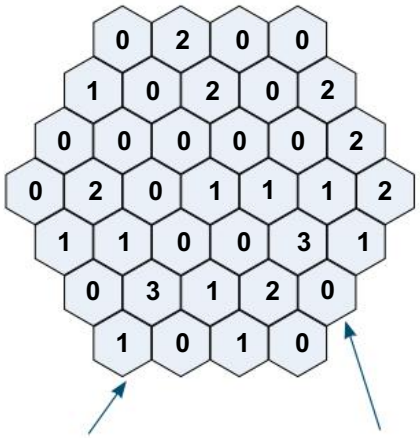


The area to be sampled is divided up into a grid pattern with indexed coordinates

Quadrats are applied to the predetermined grid on a random basis. This can be achieved by using a random number table.

Sampling a centipede population

A researcher by the name of Lloyd (1967) sampled centipedes in Wytham Woods, near Oxford in England. A total of 37 hexagon–shaped quadrats were used, each with a diameter of 30 cm (see diagram on right). These were arranged in a pattern so that they were all touching each other. Use the data in the diagram to answer the following questions.



Each quadrat was a hexagon with a diameter of 30 cm and an area of 0.08 square meters.

The number in each hexagon indicates how many centipedes were caught in that quadrat.

1. Determine the average number of centipedes captured per quadrat:

2. Calculate the estimated average density of centipedes per square metre (remember that each quadrat is 0.08 square metres in area):

3. Looking at the data for individual quadrats, describe in general terms the distribution of the centipedes in the sample area:

4. Describe one factor that might account for the distribution pattern.

Centipede

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16 Quadrat-Based Estimates

Key Idea: The size and number of quadrats used to sample a community must be sufficient to be representative of that community without taking an excessively long time to use.

The simplest description of a community is a list of the species present. This does not provide information about the relative **abundance** of the species, although this can be estimated using abundance scales (e.g. ACFOR). **Quadrats** can provide quantitative information about a community. The size of the quadrat and the number of **samples** taken must represent the community as fairly as possible.

What size quadrat?

Quadrats are usually square, and cover 0.25 m^2 (0.5 m x 0.5 m) or 1 m^2, but they can be of any size or shape, even a single point. The quadrats used to sample plant communities are often 0.25 m^2. This size is ideal for low-growing vegetation, but quadrat size needs to be adjusted to habitat type. The quadrat must be large enough to be representative of the community, but not so large as to take a very long time to use.

A quadrat covering an area of 0.25 m^2 is suitable for most low growing plant communities, such as this alpine meadow, fields, and grasslands.

Very large quadrats (e.g. 10 × 10 m) may be marked out for communities with taller vegetation. For densely forested environments, **transects** are often better.

Small quadrats (0.01 m^2 or 100 mm x 100 mm) are appropriate for lichens and mosses on rock faces and tree trunks.

How many quadrats?

As well as deciding on a suitable quadrat size, the other consideration is how many quadrats to take (the sample size). In species-poor or very homogeneous habitats, a small number of quadrats will be sufficient. In species-rich or heterogeneous habitats, more quadrats will be needed to ensure that all species are represented adequately.

Determining the number of quadrats needed

- Plot the cumulative number of species recorded (on the y axis) against the number of quadrats already taken (on the x axis).
- The point at which the curve levels off indicates the suitable number of quadrats required.

Fewer quadrats are needed in species-poor or relatively uniform habitats, such as this woodland.

Describing vegetation

Density (number of individuals per unit area) is a useful measure of abundance for animal populations, but can be problematic in plant communities where it can be difficult to determine where one plant ends and another begins. For this reason, plant abundance is often assessed using **percentage cover**. Here, the percentage of each quadrat covered by each species is recorded, either as a numerical value or using an abundance scale such as the ACFOR scale.

The ACFOR abundance scale

A = Abundant (30% +)

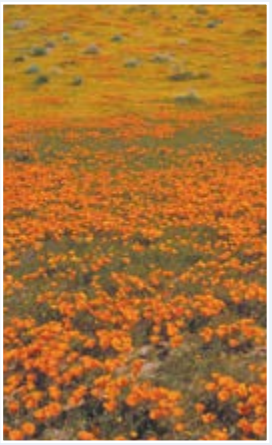
C = Common (20-29%)

F = Frequent (10-19%)

O = Occasional (5-9%)

R = Rare (1-4%)

The ACFOR scale could be used to assess the abundance of species in this wildflower meadow. Abundance scales are subjective, but it is not difficult to determine which abundance category each species falls into.



1. Describe one difference between the methods used to assess species abundance in plant and in animal communities:

   _____

2. What is the main consideration when determining appropriate quadrat size? _____

3. What is the main consideration when determining number of quadrats? _____

4. Explain two main disadvantages of using the ACFOR abundance scale to record information about a plant community:

   (a) _____

   (b) _____

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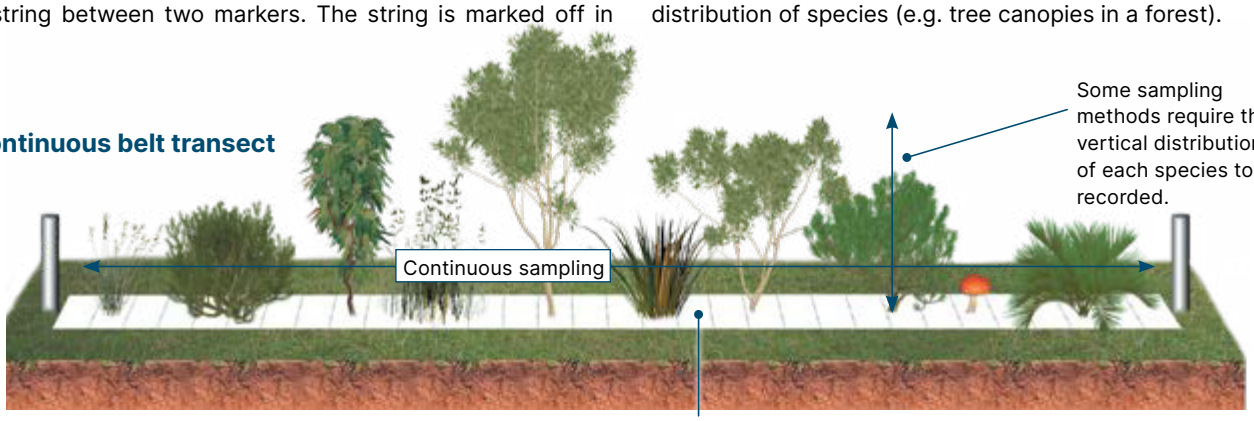
17 Transect Sampling

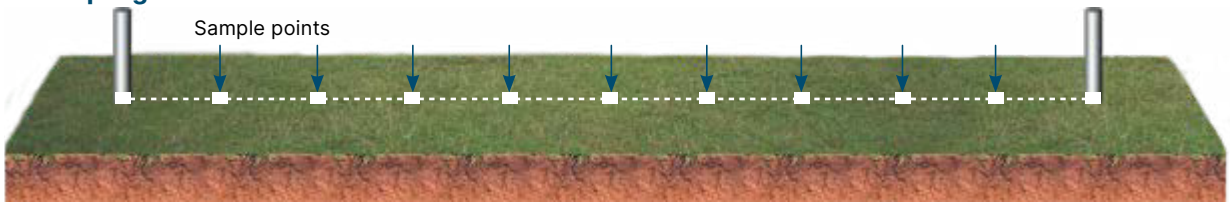
Key Idea: Transect sampling is useful for providing information about species distribution along an environmental gradient.

A **transect** is a line placed across a community of organisms. Transects provide information on the **distribution** of species in the community. They are particularly valuable when the transect records community composition along an **environmental gradient** (e.g. up a mountain or across a seashore). The usual practice for small transects is to stretch a string between two markers. The string is marked off in measured distance intervals and the species at each marked point are noted. The sampling points along the transect may also be used for the siting of **quadrats**, so that changes in **density** and community composition can be recorded. Belt transects are essentially a form of continuous quadrat sampling. They provide more information on community composition but can be difficult to carry out. Some transects provide information on the vertical, as well as horizontal, distribution of species (e.g. tree canopies in a forest).

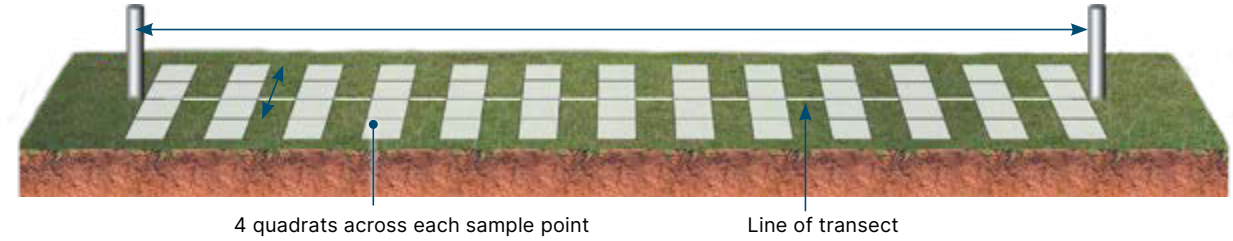
Continuous belt transect



Point sampling



Interrupted belt transect



1. Belt transect sampling uses quadrats placed along a line at marked intervals. In contrast, point sampling transects record only the species that are touched or covered by the line at the marked points.

   (a) Describe one disadvantage of belt transects: _____

   _____

   (b) Why might line transects give an unrealistic sample of the community in question? _____

   _____

   _____

   (c) How do belt transects overcome this problem? _____

   _____

   (d) When would it not be appropriate to use transects to sample a community? _____

   _____

2. How could you test whether or not a transect sampling interval was sufficient to accurately sample a community?

   _____

   _____

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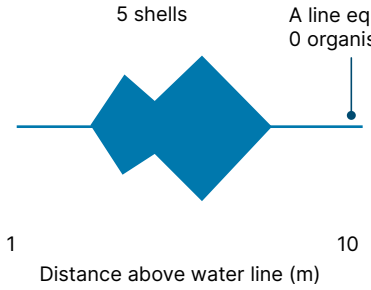
A kite graph is a good way to show the distribution of organisms sampled using a belt transect. Data may be expressed as **abundance** or percentage cover along an environmental gradient. Several species can be shown together on the same plot so that the distributions can be easily compared.

3. The data in the table, below right, were collected from a rocky shore field trip. Four common species of barnacle were sampled in a continuous belt transect from the low water mark, to a height of 10 m above that level. The number of each of the four species in a 1 m^2 quadrat was recorded.
   Plot a kite graph of the data for all four species on the graph paper below. Be sure to choose a scale that takes account of the maximum number found at any one point and allows you to include all the species on the one plot. Include the scale on the diagram so that the number at each point on the kite can be calculated.

An example of a kite graph



Distribution of 4 common barnacle species on a rocky shore

	Barnacle species			
Height above low water (m)	Plicate barnacle	Columnar barnacle	Brown barnacle	Sheet barnacle
0	0	0	0	65
1	10	0	0	12
2	32	0	0	0
3	55	0	0	0
4	100	18	0	0
5	50	124	0	0
6	30	69	2	0
7	0	40	11	0
8	0	0	47	0
9	0	0	59	0
10	0	0	65	0

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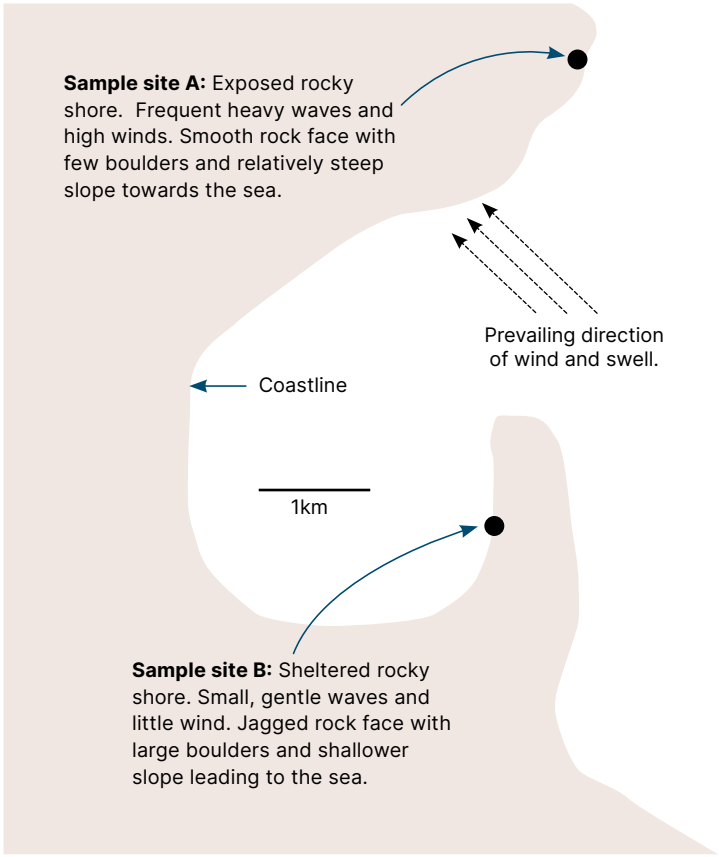
18 Stratified Sampling in a Variable Ecosystem

Key Idea: Stratified sampling of a rocky shore ecosystem can highlight differences between different regions.

Stratified sampling can be used to investigate the physical and **biotic** differences between regions in the same ecosystem.

In a rocky shore ecosystem, the type of organisms found and their **distribution** can vary depending on the physical attributes of the shoreline and the amount of wave exposure received. These differences can be quantified.



The aim

To investigate the differences in the **abundance** of intertidal animals on an exposed rocky shore and a sheltered rocky shore.

Background

The composition of rocky shore communities is strongly influenced by the shore's physical environment. Animals that cling to rocks must keep their hold on the substrate while being subjected to intense wave action and currents. However, the constant wave action brings high levels of nutrients and oxygen. Communities on sheltered rocky shores, although encountering less physical stress, may face lower nutrient and oxygen levels.

To investigate differences in the abundance of intertidal animals, students laid out eight 1 m^2 **quadrats** at regular intervals along one tidal zone at each of two separate but nearby sites of roughly the same area: 1) a rocky shore exposed to wind and heavy wave action and 2) a rocky shore with very little heavy wave action. The animals were counted and their numbers in each quadrat recorded.

Rocky shore animals

The oyster borer is carnivorous and preys on barnacles such as the brown barnacle and the plicate barnacle. Numbers of oyster borers may be lower when there are fewer barnacles as prey.

The columnar barnacle is found around the high to mid tide level but can extend lower in suitable areas. It is uncommon on soft substrates and prefers moderately exposed shorelines.

The plicate and brown barnacles can be found together on exposed rocky shores. On more sheltered shores, the columnar barnacle is more prevalent.

The rock oyster often grows on steeply sloped or vertical surfaces and tends to flourish in harbours, as settlement on rocks is inhibited by even moderate wave action.

Limpets are found throughout rocky shores, although the ornate limpet has a slight preference to exposed shores.

The black nerite (snail) is widespread on rocky shores and extends across most tidal zones. It is more common on exposed sites.

All photos: C. Pilditch except where indicated

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1. During the field study, students counted the number of animals in each quadrat and recorded them in a logbook (below). Complete the table below the raw data with the total number of each species at each site, the mean number of animals per quadrat, and the median and mode for each set of samples per species. Remember, in this case, there can be no 'part animals' so you will need to round your values to the nearest whole number:

Field data logbook

Count per quadrat. Quadrats 1 m^2

Site A	1	2	3	4	5	6	7	8
Brown barnacle	39	38	37	21	40	56	36	41
Oyster borer	6	7	4	3	7	8	9	2
Columnar barnacle	6	8	14	10	9	12	8	11
Plicate barnacle	50	52	46	45	56	15	68	54
Ornate limpet	9	7	8	10	6	7	6	10
Radiate limpet	5	6	4	8	6	7	5	6
Black nerite	7	7	6	8	4	6	8	9
Site B								
Brown barnacle	7	6	7	5	8	5	7	7
Oyster borer	2	3	1	3	2	2	1	1
Columnar barnacle	56	57	58	55	60	47	58	36
Plicate barnacle	11	11	13	10	14	9	9	8
Rock oyster	7	8	8	6	2	4	8	6
Ornate limpet	7	8	5	6	5	7	9	3
Radiate limpet	13	14	11	10	14	12	9	13
Black nerite	6	5	3	1	4	5	2	3

		Brown barnacle	Oyster borer	Columnar barnacle	Plicate barnacle	Rock oyster	Ornate limpet	Radiate limpet	Black nerite
Site A	Total number of animals								
	Mean number of animals per m^2								
	Median value								
	Modal value								
Site B	Total number of animals								
	Mean number of animals per m^2								
	Median value								
	Modal value								

2. Why was a stratified sampling design chosen to investigate the animal diversity of this rocky shore ecosystem?

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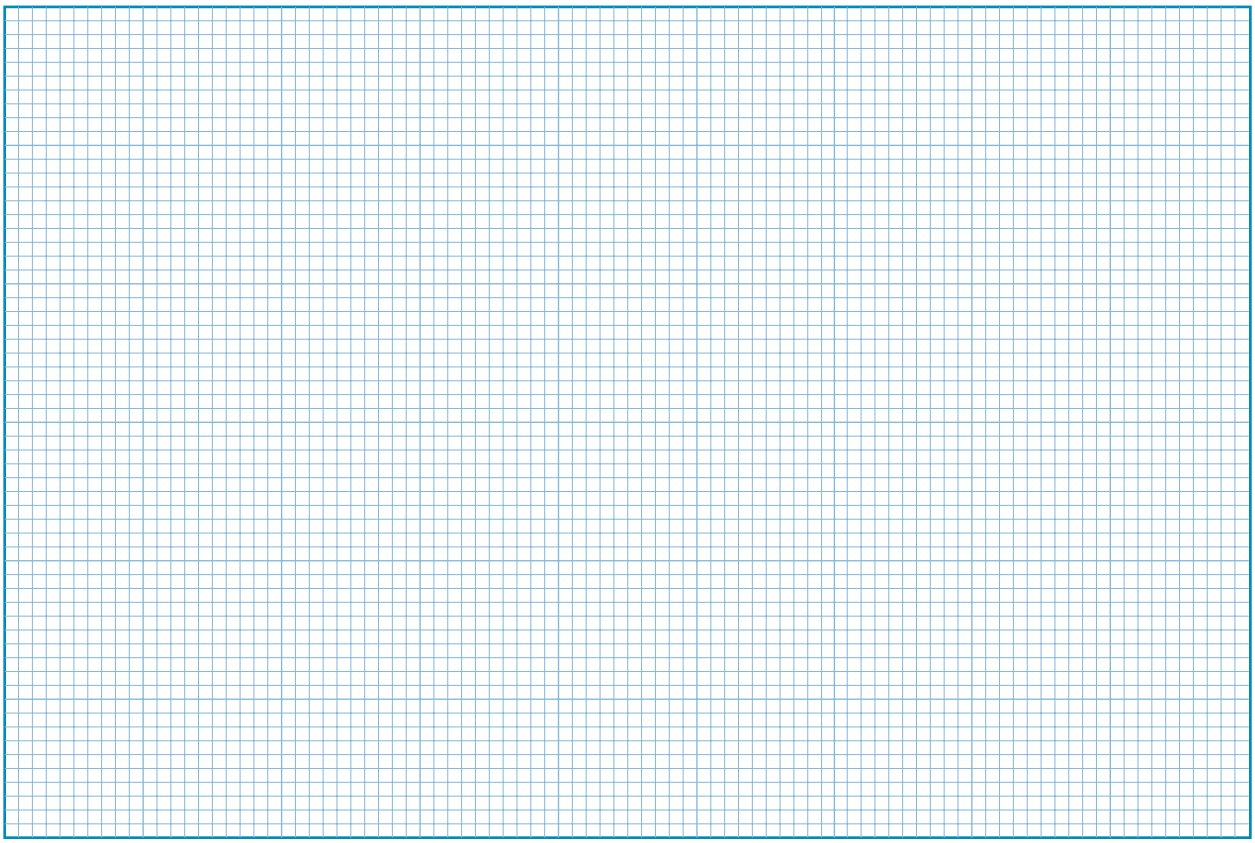
3. Use the grid below to draw a column graph of the mean number of species per 1 m2 at each sample site. Remember to include a title, correctly labelled axes, and a key.



4. (a) Compare the mean, median, and modal values at each site: _____

   (b) What does this tell you about the distribution of the data: _____

5. (a) Which species was entirely absent from site A? _____

   (b) Suggest why this might be the case: _____

   _____

6. (a) Explain why more brown barnacles and plicate barnacles were found at site A: _____

   _____

   (b) Explain why more oyster borers were found at site A: _____

   _____

   _____

7. (a) Comment on the numbers of limpets at each site: _____

   _____

   (b) What does this suggest to you about their biology: _____

   _____

8. Did stratified sampling provide more information about this ecosystem than if only one area had been sampled? Explain:

   _____

   _____

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19 Using Quadrats to Measure Ecosystem Diversity

Key Idea: Events that disturb forests, such as fire, can affect the species diversity of the forest.

In this practical you will demonstrate how quadrat sampling can be used to quantify the diversity of plants in a forest community. Here you will examine two plots of wet sclerophyll forest based on plots from Tasmania, one that has been undisturbed for many decades and the other that has been affected by fire.

Investigation 1.2 Measuring ecosystem diversity

See appendix for equipment list.

Setting up the sampling grid

1. Mark out a grid pattern
   Use a ruler to mark out the sample areas into grids of 6 squares by 6 squares. This will split the area up into 36 squares that can be used as quadrats.

2. Number the axes of the grid
   Only a small proportion of the possible quadrat positions will be sampled. It is necessary to select the quadrats in a random manner. It is not sufficient to simply guess or choose your own on a 'gut feeling'. The best way to choose the quadrats randomly is to create a numbering system for the grid pattern and then select the quadrats from a random number table. Starting at the top left hand corner, number the columns and rows from 1 to 6 on each axis.

Quadrat sampling (random counts)

3. Choose quadrats randomly: To select the position of quadrats randomly, use random numbers from a random number table. The random numbers are used as an index to the grid coordinates. Select one of the columns of random numbers (A-D) from the table opposite to obtain the coordinates for placing your sample of 6 quadrats.

4. Decide on the counting criteria: Before you count the individuals of each species, the criteria for counting need to be established. You must decide before sampling begins as to what to do about individuals that are only partly inside the quadrat. Possible answers include:

(a) Only counting individuals that are completely inside the quadrat.

(b) Counting individuals with any part of the body (e.g. the main stem and root mass) inside the quadrat.

(c) Allowing for 'half individuals' (e.g. 3.5 plants).

(d) Counting an individual that is inside the quadrat by half or more as one complete individual.

You will need to think about the merits and problems of the suggestions above and any other factors that could cause problems with your counting

5. Carry out the sampling for the undisturbed forest: Examine each selected quadrat and count the number of individuals of each species present. Record your data in the spaces provided in the table, right.

6. Repeat your sampling for the disturbed forest.

7. Calculate a diversity index for each ecosystem.

Table of random numbers

A		B		C		D	
2	6	4	6	5	4	4	6
3	3	6	4	6	4	1	2
2	5	1	3	2	1	5	3
5	6	4	2	5	2	6	2
4	2	2	3	2	5	3	6
4	4	6	2	3	6	2	4

The table above has been adapted from a table of random numbers from a statistics book. Use this table to select quadrats randomly from the grid above. Choose one of the columns (A to D) and use the numbers in that column as x, y coordinates for grid. The first digit refers to the column number and the second digit refers to the row number. To locate each of the 10 quadrats, find where the row and column intersect, as shown below:

Example: 5 2 refers to the 5th column and the 2nd row

Random quadrat count:

	Disturbed	Undisturbed
Acacia		
Atherosperma		
Eucalyptus 1		
Eucalyptus 2		
Leptospermum		
Monotoca		
Nematolepis		
Nothofagus		
Olearia		
Pittosporum		
Phyllocladus		
Total individuals		

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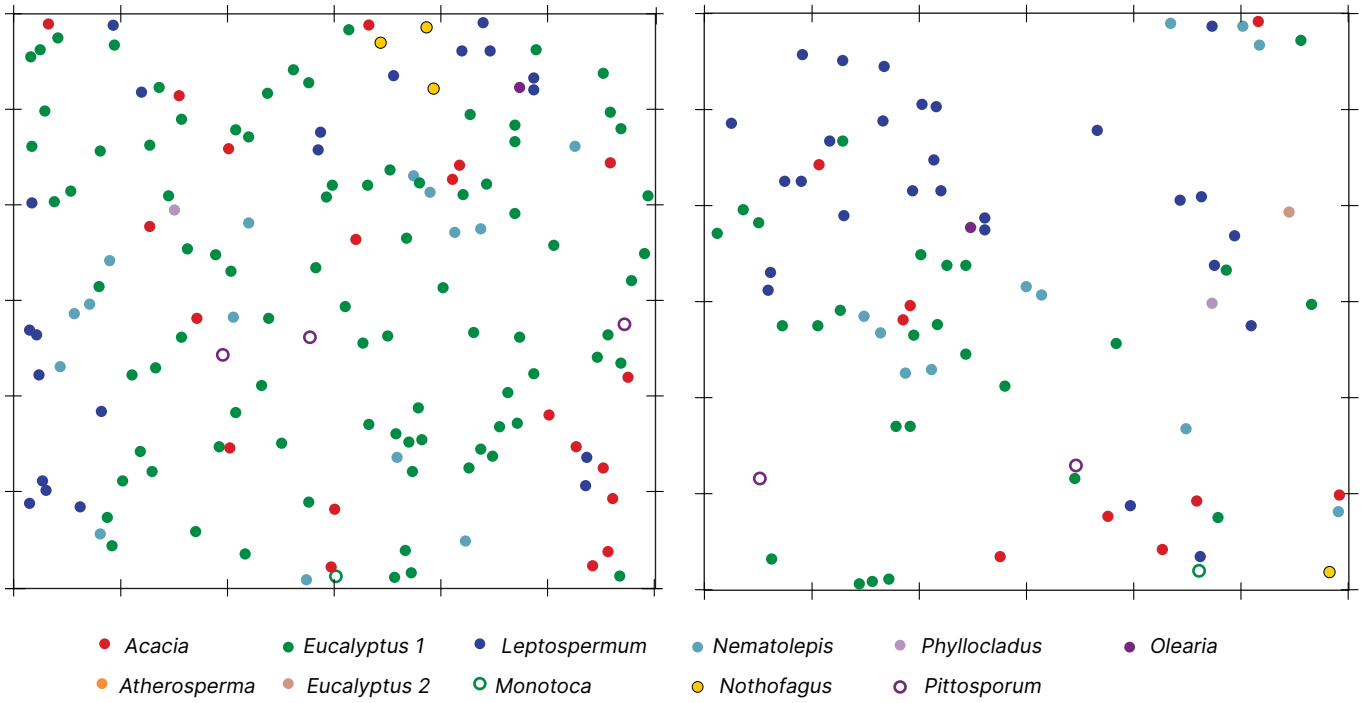
Undisturbed wet sclerophyll forest

Disturbed (by fire) wet sclerophyll forest



1. Recall the calculation of Simpson's diversity index you learned about earlier in chapter 1. D = 1 - ((∑n(n−1)) ÷ (N(N−1))) Use the space below to calculate the diversity for each of the sampling areas.

2. (a) Simpson's index diversity results for undisturbed ecosystem: _____

   (b) Simpson's index diversity results for fire disturbed ecosystem: _____

3. The disturbed ecosystem actually had a higher biodiversity (D(undisturbed area) = 0.63, D(fire disturbed area) = 0.75. Can you explain why?

   _____

   _____

   _____

4. Compare the diversity calculations you obtained to these known indexes, was you result close or far away, why?

   _____

   _____

5. As an extension activity, try using systematic quadrat sampling or using a line transect to compare the results these techniques produce compared to random sampling.

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20 Did You Get It?

1. Test your vocabulary by matching each term to its definition, as identified by its preceding letter code.

(i) abiotic factor ☐
(ii) biodiversity ☐
(iii) diversity index ☐
(iv) microclimate ☐
(v) percentage cover ☐
(vi) species richness ☐
(vii) species evenness ☐

A A subjective measure of plant abundance involving an estimate of the area occupied by a plant species in a community.

B A quantitative measure of the variety and relative abundance of different species in a community or ecosystem.

C The number of species present in a region.

D A restricted region of particular abiotic conditions within a broader physical environment.

E A measure of the relative abundance of the species present in an area.

F A term for any non-living part of the environment, e.g. rainfall or temperature.

G The variety of life on Earth, including variation in species, genes, and ecosystems.

2. What advantage does a diversity index have when evaluating a community's diversity? _____

_____

_____

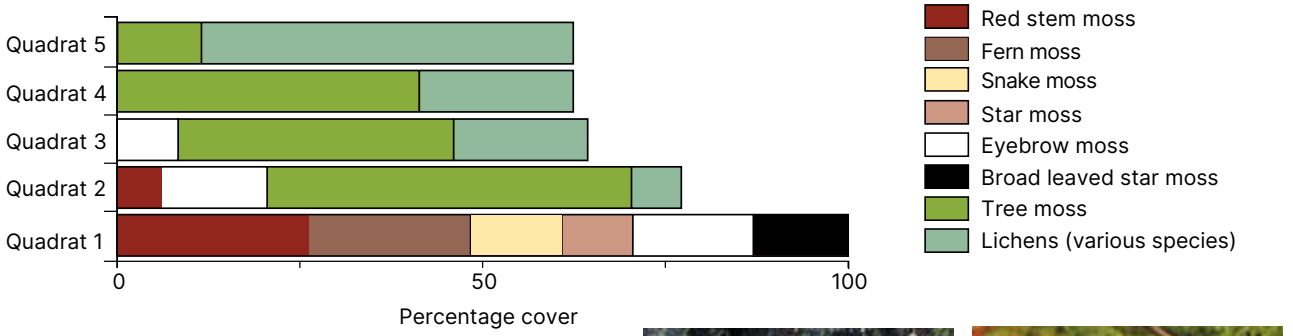
3. Why is information about the abiotic environment usually collected when sampling a community to measure its diversity?

_____

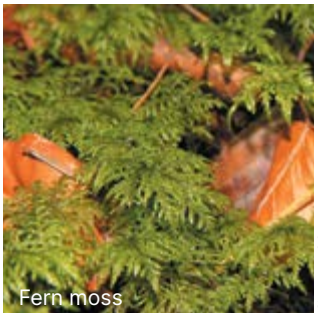
_____

_____

4. The figure below shows changes in vegetation cover along a 2 m vertical transect up the trunk of an oak tree. Changes in the physical factors light, humidity, and temperature along the same transect were also recorded.



QUADRAT	1	2	3	4	5
Height (m)	0.4	0.8	1.2	1.6	2.0
Light (arbitrary units)	40	56	68	72	72
Humidity (percentage	99	88	80	76	78
Temperature (°C)	12.1	12.2	13.0	14.3	14.2



Chmee cc 3.0

(a) At which height were mosses most diverse and abundant? _____

(b) What plant type predominates at 2.0 m height? _____

(c) What can you deduce about the habitat preferences of most mosses and lichens from this study?

_____

_____

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Chapter 2 Unit 3 Topic 1

Classification Processes

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Key Terms

- biodiversity
- binomial nomenclature
- biological species
- clade
- classification
- dichotomous key
- ecoregion
- ecosystem
- Linnaean classification
- microhabitat
- phylogenetic classification
- phylogenetic species

Key Concepts

- Organisms can be classified using their physical features and their genetic make up. Classification systems include the Linnaean system and phylogenetics.
- Dichotomous keys are an important way of separating and identifying species.
- Classifying ecosystems help ecosystem management. Classification systems include Holdridge life zones, and Specht's vegetation classification.

Classifying organisms		Activity Number
☐ 1	Explain the purpose of classification. State that classification can be hierarchical and is based on different levels of similarity of physical features or molecular sequences.	21
☐ 2	Describe classification systems based on similarity of physical features (the Linnaean system) and or shared derived characteristic (phylogenetic classification).	22
☐ 3	Recognise the need for multiple definitions of species. Distinguish between biological and phylogenetic species and identify the limitations of each definition. Identify an example of an interspecific hybrid that does not produce fertile offspring.	22
☐ 4	Use and develop dichotomous keys to identify and classify organisms and objects.	23, 24

Classifying communities and ecosystems		
☐ 5	Define ecosystem. Using examples, explain that ecosystems are composed of varied habitats from the very small (microhabitats) to the much larger (ecoregions).	25
☐ 6	Interpret data to classify and name an ecosystem. Classification systems include Holdridge life zones, Specht's vegetation classification, the ANAE system for aquatic ecosystems, and the Regional Ecosystems classification.	26, 27
☐ 7	Explain how classifying ecosystems helps in their effective management.	28
☐ 8	**SI:** Investigate how environmental factors affect global distribution of ecosystems and how classifying ecosystems allows for effective ecosystem management.	26-28, 30
☐ 9	**SHE:** Classifying ecosystems can be made more efficient and enhanced using computer programs	29

21 Classifying Organisms

Key Idea: The classification of biodiversity into groups, or taxa, is constantly being updated in light of new information. Various classification systems exist, each based on different methods and with different advantages and disadvantages.

The **classification** of Earth's **biodiversity** into formal groups is called **taxonomy**. As with all science, taxonomic approaches are constantly changing as new information is discovered. Early classification systems were based on physical appearance. The increasing use of molecular analysis as a taxonomic tool has since led to the reclassification of many taxa, including birds, reptiles, many plants, and primates. Recognising three domains of life, based on genetic analyses, is an early example of this. Increasing use of molecular tools has provided new insights into how we group organisms.

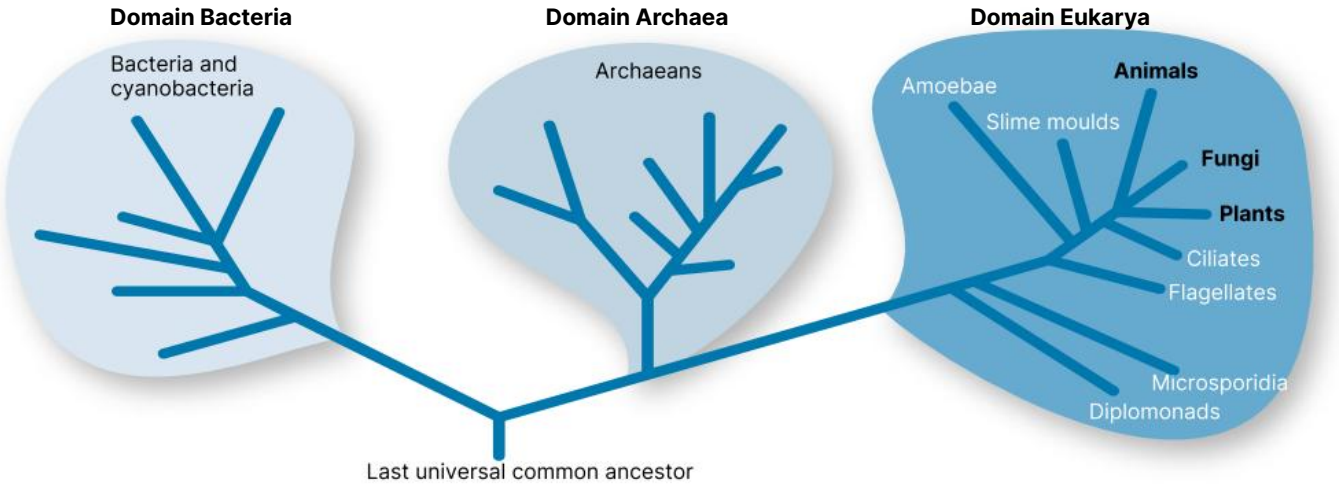
A changing view of classification

- Before DNA sequencing, taxonomists divided life into five kingdoms, classifying organisms based mainly on visible characteristics (**morphology**). The five kingdom system places all prokaryotes in one kingdom, with protists, fungi, plants, and animals being the other four.
- This system conflicted with new molecular evidence and did not fairly represent the diversity or evolutionary history of the prokaryotic organisms or unicellular eukaryotes.

A new view of the world

- In 1996, scientists deciphered the full DNA sequence of the thermophilic bacterium *Methanococcus jannaschii*. The data supported the hypothesis of three major evolutionary lineages and gave rise to a modified six kingdom classification.
- This was further revised to the current three domain system (below), which more properly represents the evolutionary relationships of life on Earth.

Whittaker 1969	Woese *et al.* 1977	Woese *et al.* 1990
Five kingdoms	**Six kingdoms**	**Three domains**
Monera	Eubacteria	Bacteria
	Archaebacteria	Archaea
Protista	Protista	Eukarya
Fungi	Fungi	
Plantae	Plantae	
Animalia	Animalia	

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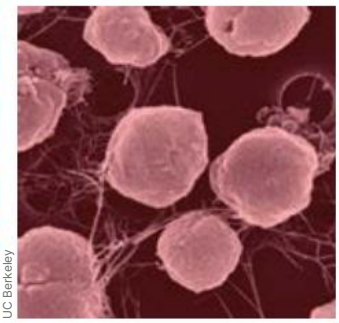
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Domain Bacteria
Lack a distinct nucleus and cell organelles. Present in most of Earth's habitats and vital to its ecology. Includes well-known pathogens, many harmless and beneficial species, and the cyanobacteria (photosynthetic bacteria containing the pigments chlorophyll a and phycocyanin).

Domain Archaea
Methanococcus jannaschii was the first archaean genome to be sequenced. The sequencing identified many genes unique to Archaea and provided strong evidence for three evolutionary lineages. Although archaeans may resemble bacteria, they possess several metabolic pathways that are more similar to eukaryotes. Other aspects of their structure and metabolism, such as their membrane lipids and respiratory pathways, are unique. Although once regarded as organisms of extreme environments such as volcanic springs, archaeans are now known to be widespread, including in the ocean and soil.

Domain Eukarya
Complex cell structure with organelles and nucleus. The three domain classification recognises the diversity and different evolutionary paths of the unicellular eukaryotes (formerly Protista), which have little in common with each other. The fungi, animals, and plants form the remaining lineages.

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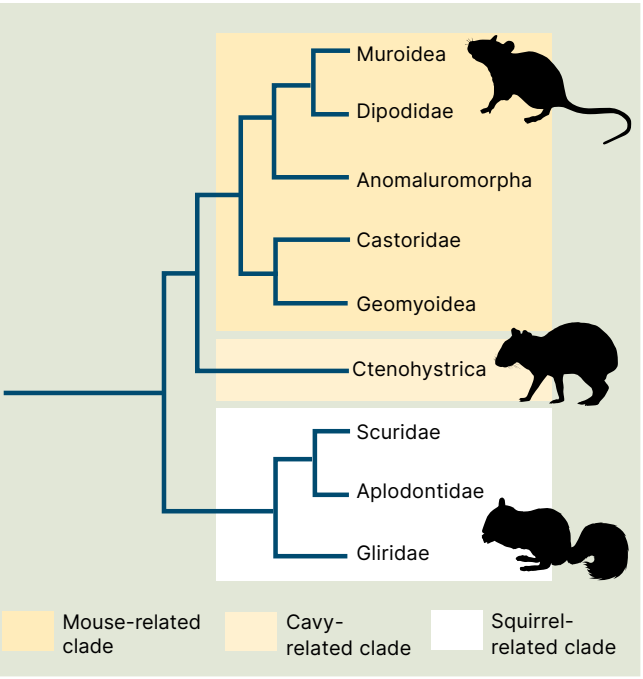
Traditional classification

Based on the **Linnaean classification** (after Linnaeaus), organisms are grouped into taxonomic ranks (levels) on the basis of similarities in physical features (morphology). The scheme is hierarchical. Each taxonomic rank progressively 'sorts' the organisms until the final rank, the species, which includes organisms of just one type. A group within a taxonomic rank is called a taxon (pl. taxa) and is defined by a type, which is often a specimen. Species are named using **binomial nomenclature** by genus and species (italicised). One difficulty with traditional taxonomy is that ranks are not equivalent for different types of organisms. What's more, unrelated species can be grouped together simply because they look alike. Historically, this resulted in many newly discovered organisms in the New World being misclassified into Old World taxa.

Phylogenetic classification

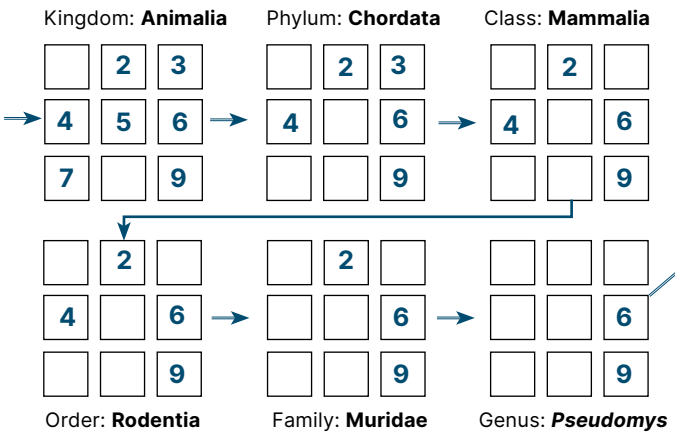
Phylogenetic classification ties names to **clades**, so it is often called cladistic. A clade is taxonomic group that consists of an ancestor and all its descendants (they are monophyletic). The characteristics used for assigning organisms to a clade can be morphological or molecular (DNA or proteins). Molecular data is useful because species that appear similar can be easily distinguished. Phylogenetic classification schemes do not rely on taxonomic rank in the same way as traditional schemes. Using cladistics, many of the taxa with which we are familiar (such as reptiles) do not exist because they do not meet the classification criteria (they are not monophyletic). However, some familiar taxa, e.g. rodents, are clades because the taxon consists of a common ancestor and all its descendants. The rodent clade (below) corresponds to the order Rodentia.

Taxonomic rank	Taxon
Kingdom	Animalia
Phylum	Chordata
Class	Mammalia
Order	Rodentia
Family	Muridae
Genus	*Pseudomys* (Australian mice)
Species	*P. australis* (Plains mouse)



The example below shows how as we move through the taxonomic ranks, the organisms we are grouping become more exclusive based on the characteristics of the group. In this case, we are looking at the classification of the plains mouse *Pseudomys australis*.

Domain: **Eukarya**



Species:
Pseudomys australis

Credits: (2) Central rock rat, Michael Barritt & Karen May, cc 2.0 (6) Plains mouse, Tim Bawden cc 2.0 (9) Inland sandy mouse, Christopher Watson cc 3.0

1. What is the purpose of a classification system? _____

2. Using the example of the three domains system, explain how the use of molecular data (e.g. DNA sequencing) has led to a more accurate representation of the diversity of life on Earth:

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Naming organisms

Many organisms have common names that people use in everyday language. However, common names change from place to place and language to language. Common names may also apply to more than one organism, which causes confusion when people from different parts of the world are referring to particular organisms. For example, the mountain lion, cougar, puma, catamount, and panther are all names given to the same animal, *Puma concolor*. To solve this problem, each species is given a two part (binomial) name, called the scientific name, that is unique to that species. It was pioneered in 1753 by Carl Linnaeus.

Names and meanings

Scientifically, every species is given a classification that reflects its known lineage, i.e. its evolutionary history. The last two (and most specific) parts of that lineage are the genus and species names. Together, these are called the scientific name, and every species has its own that is specific to it. The term given to this two-part naming system is binomial nomenclature. When typed, the name is always *italicised*. If handwritten, it should be underlined. The genus name is always written with a capital letter, but the species name is not.

Scientific names are normally based on Latin and sometimes Greek. The name often, but not always, describes the organism. For example, *Hippopotamus amphibius* is derived from Greek - hippos meaning horse and potamos meaning river, giving 'river horse'. *Amphibius* meaning two lives - *Hippopotamus amphibius* lives both in the water and out of it.

In 2011, researchers from San Francisco State University discovered a sponge-like mushroom growing in the Malaysian rainforest. They named it *Spongiforma squarepantsii* after the cartoon character SpongeBob SquarePants.

Rangifer tarandus is known as the caribou in North America, but as the reindeer in Europe. The scientific name is unambiguous.

Tom Bruns

3. (a) What is the two part naming system for classifying organisms called? _____

   (b) What are the two parts of the name? _____

4. Give three reasons why the classification of organisms is important:

   (a) _____

   (b) _____

   (c) _____

5. Describe what is wrong with the way each of the following scientific names is written:

   (a) Ceratotherium simum: _____

   (b) *Canis Lupus*: _____

6. The table below shows part of the classification for humans using the eight major levels of classification. For this question you may need to do a little research to complete the classification:

   (a) Complete the list of the taxonomic ranks on the left hand side of the table below:

   (b) Complete the classification for humans (*Homo sapiens*) on the right hand side of the table below.

	Taxonomic rank	Human classification
1.		
2.		
3.		
4.		
5.		
6.		
7.	*Family*	*Hominidae*
8.		

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Classification of the red kangaroo

Below is the classification scheme for the red kangaroo. Only one of each group is subdivided in this chart showing the levels that can be used in classifying an organism. Not all possible subdivisions (e.g. sub-order) have been shown here. The only natural category is the species, often separated into races, or sub-species, which generally differ in appearance.

The classification below follows that in "The Australian Museum Complete Book of Australian Mammals" R. Strahan (Ed.) 1983. Cornstalk Publishing. ISBN 0 207 14454 0. It differs from many classifications in raising the marsupials to a sub-class (rather than an order) and dividing the sub-class into the orders Polyprotodonta and Diprotodonta.

Kingdom:	**Animalia** Animals; one of 5 kingdoms	
Phylum:	**Chordata** Animals with a notochord (supporting rod of cells along the upper surface) *Sea squirts, salps, lancelets, and vertebrates*	23 other phyla
Sub-phylum:	**Vertebrata** Animals with backbones *Fish, amphibians, reptiles, birds, mammals*	
Class:	**Mammalia** Animals that suckle their young on milk from mammary glands *Placentals, marsupials, monotremes*	
Sub-class:	**Metatheria or Marsupialia** Mammals whose young develop for some time in the female's reproductive tract and then migrate to a pouch. Marsupials	
Order:	**Diprotodonta** Herbivorous marsupials *Possums, rat kangaroos, honey possums, cuscuses and bushtails, koala, pygmy possums, wombats, gliders, kangaroos, wallabies*	
Superfamily:	**Macropodoidea** Possess extremely long and powerful hindlegs *Potoroos, bettongs, rat-kangaroos, kangaroos, wallabies*	
Family:	**Macropodidae** Kangaroo and wallaby family with 50 species of kangaroos, *wallabies, rock-wallabies, nailtail wallabies, forest wallabies, tree kangaroos, pademelons, quokka, swamp wallabies*	
Genus:	**Macropus** Ground-dwelling kangaroos and wallabies consisting of 14 species in this genus: red kangaroo, eastern grey, western grey kangaroo, wallaroo, several species of wallaby	10 other genera
Species:	**rufus** Red kangaroo	13 other species

Red kangaroo
Macropus rufus

Description: One of the largest living marsupials and powerfully built. Colouration varies, often regionally; red to blue-grey above, and distinctly white below. Females are usually blue-grey and are often called blue-fliers. In some regions of Australia, both sexes are reddish-brown.

Synonyms: plains kangaroo, marloo, blue-flier (female).

Subspecies: Several subspecies have been described but their validity is not well established.

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22 What is a Species?

Key Idea: How we define species has implications for classification but also for conservation.

There are two ways by which we can define species. The first is based on the ability to successfully interbreed (a **biological species**) and the second is based on shared evolutionary history (a **phylogenetic species**). Both methods of defining species have their merits and their problems. However we define a species, being able to recognise the true diversity of organisms has implications for conservation because you cannot protect what you cannot recognise.

	Biological species concept	Phylogenetic species concept
Definition	A group of organisms that can interbreed to produce fertile offspring.	The smallest group of organisms that share a common ancestor and can be distinguished by a unique set of morphological and/or genetic traits.
Criteria	Reproductive isolation. Cannot successfully interbreed with other species.	Must be distinguishable from other such groups. Does not rely on reproductive isolation.
Works well for...	Sexually reproducing organisms.	Asexual organisms. Detecting recent divergences.
Difficulties	Difficult to apply to asexual organisms. Difficult to apply to extinct organisms.	Can require enough genomic diversity to evaluate (enough loci to analyse). Can result in a proliferation of species.

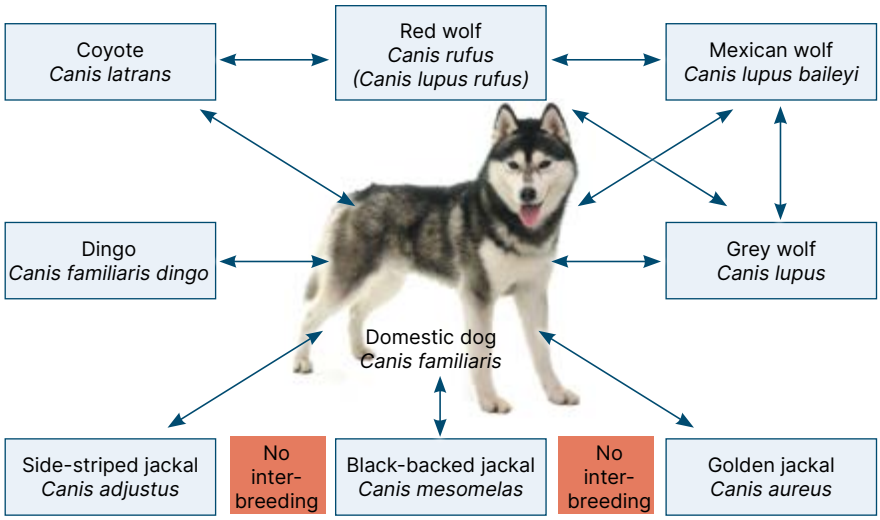
Donkey (Equus africanus asinus)

Horse (Equus ferus caballus)

Horses and donkeys are true species despite the fact that they can produce viable offspring. A mule is the hybrid offspring of a male donkey and female horse, but mules are sterile (infertile).

Biological species and the problem with hybrids

- The species of the genus *Canis* illustrate problems with a species concept defined by successful interbreeding.
- The domesticated dog is able to breed with other members of the same genus to produce fertile hybrids. Red wolves, grey wolves, Mexican wolves, and coyotes are all capable of interbreeding to produce fertile hybrids. The taxonomic status of the red wolf is debated as its original lineage was as a grey wold-coyote hybrid. Red and Mexican wolves are very rare and now extinct in the wild.
- By contrast, the ranges of the three distinct species of jackal overlap in the savanna of Eastern Africa. These animals are highly territorial, but they ignore members of the other jackal species and no interbreeding takes place.



1. (a) Explain what you understand by the term species: _____

_____

_____

(b) Why is it important to be able to define species and also to recognise them: _____

_____

(c) Identify an interspecific hybrid that does not produce fertile offspring: _____

(d) Suggest how interbreeding may have been a factor in the decline of the red wolf, Mexican wolf, and dingo:

_____

_____

_____

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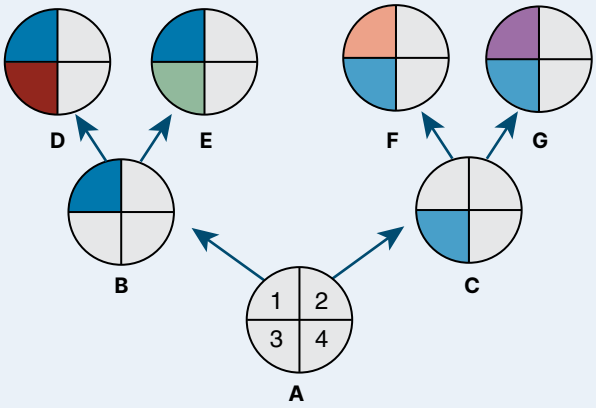
The phylogenetic species concept (PSC)

- Phylogenetic species are defined on the basis of their evolutionary history. A species is defined as the smallest group of organisms that all share a derived character state. A shared derived character is one that evolved in the lineage's ancestor and is present in all its descendants.
- The principles of defining a phylogenetic species are illustrated right. The derived characters are identified by colours. Although the primitive character unites all 4 species, the branching of the tree is based on characters derived from the ancestral ones. These may be morphological, especially for higher taxonomic ranks, or biochemical (e.g. DNA differences).
- If large numbers of characters are included in the analysis, it is easy to see how this method results in a proliferation of species that may or may not be meaningful. Under the phylogenetic species model, there are no subspecies. Either a population is a phylogenetic species or it is not taxonomically distinguishable.



Species B and C are related to species A as they share three of four characters with it. However they only share two characters with each other. D and E share characteristics with B, while F and G share characteristics with C.

Tree sparrows (*P. montanus*) are ~10% smaller than the similar house sparrow but the two species hybridise freely.

House sparrows (*P. domesticus*) are widespread with many intermediate "subspecies" of unknown status.

True sparrows all belong to the genus *Passer*. There are a large number of species distinguished by size, song, and plumage. Many populations are not good biological species because they hybridise freely to produce fertile offspring. Many birds are like this and may be best described using the phylogenetic species model.

Remember that all sexually reproducing organisms are genetically variable, so scientists must determine what level of variation is acceptable within a species before a new species **classification** is made. If such boundaries were not set, every molecular variation observed would result in the classification of a new species.

African forest elephant
Loxodonta cyclotis

African bush elephant
Loxodonta africana

Molecular analysis can aid conservation

Molecular studies have been important in identifying **cryptic species**, i.e. two or more distinct species disguised under one species name.

The African bush elephant and the African forest elephant were once considered subspecies, but recent genetic analysis has confirmed they are separate species, which diverged from each other 2-7 million years ago. Analysis of morphological differences, including skull anatomy, supports this. The finding has been important in making sure populations of both species are conserved.

2. (a) Explain how species are assigned under the PSC: _____

_____

(b) Describe one problem with the use of the PSC: _____

_____

(c) Describe situations where the use of the PSC might be more appropriate than the BSC: _____

_____

_____

3. Suggest how genetic techniques could be used to determine the likely phylogeny of several related phylogenetic species:

_____

_____

_____

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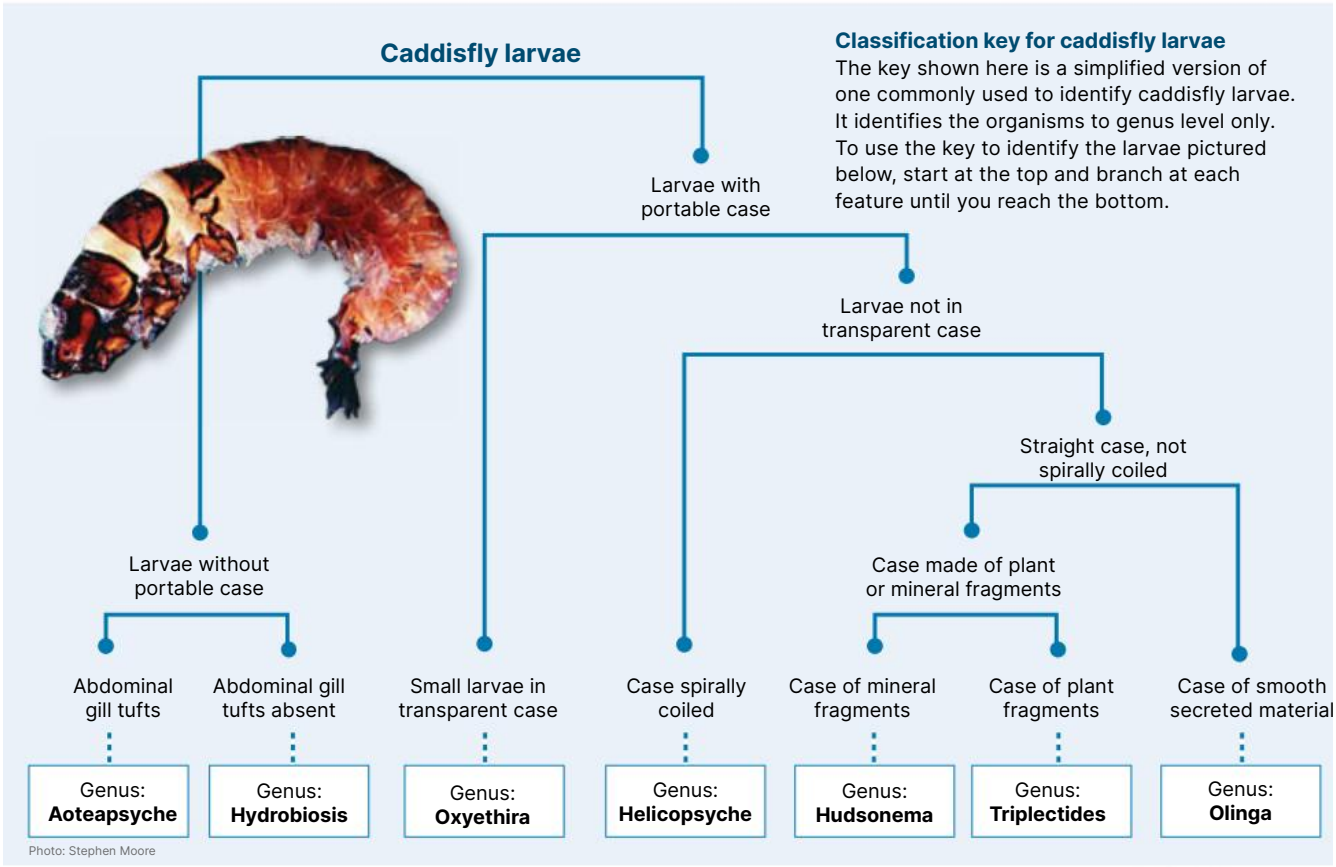
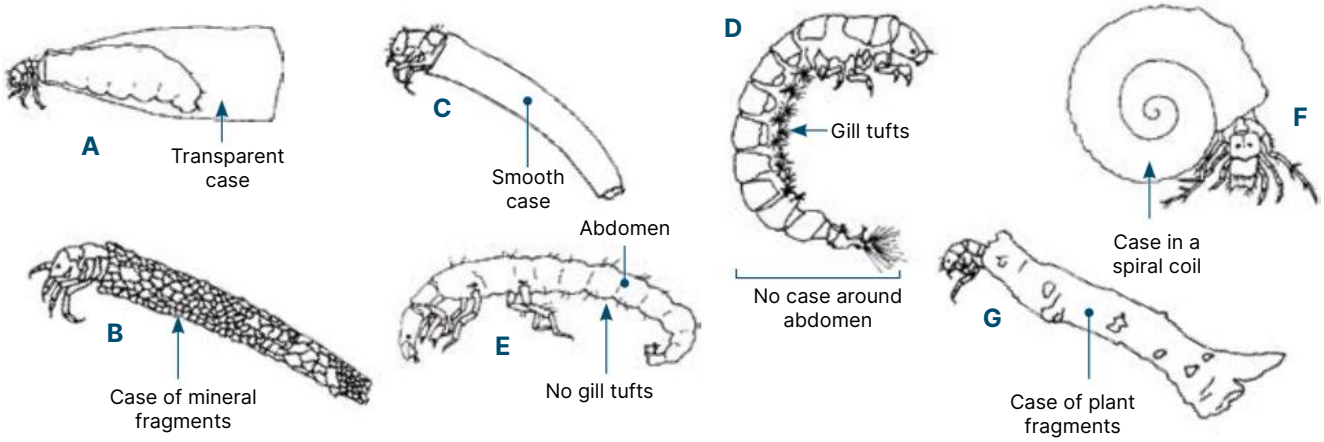
23 Using Dichotomous Keys

Key Idea: Classification keys are used to identify an organism based on its distinguishing features and assign it to a species.

An organism's **classification** should include a clear, unambiguous description, an accurate diagram, and its unique name, denoted by the genus and species. Classification keys are used to identify an organism and assign it to the correct species (assuming that the organism has already been formally classified and is included in the key). Typically, keys involve a series of linked steps. At each step, a choice is made between two features (**dichotomous key**). Each alternative leads to another question until an identification is made. If the organism cannot be identified, it may be a new species or the key may need revision. This activity describes two examples of dichotomous keys. The first describes features for identifying the larvae of genera within the order Trichoptera (caddisflies). The second is a key to the identification of aquatic insect orders.





1. Describe the main feature used to distinguish the genera in the key above: _____

_____

2. Use the key above to assign each of the caddisfly larvae (A-G) to its correct genus:

A: _____ D: _____ G: _____

B: _____ E: _____

C: _____ F: _____

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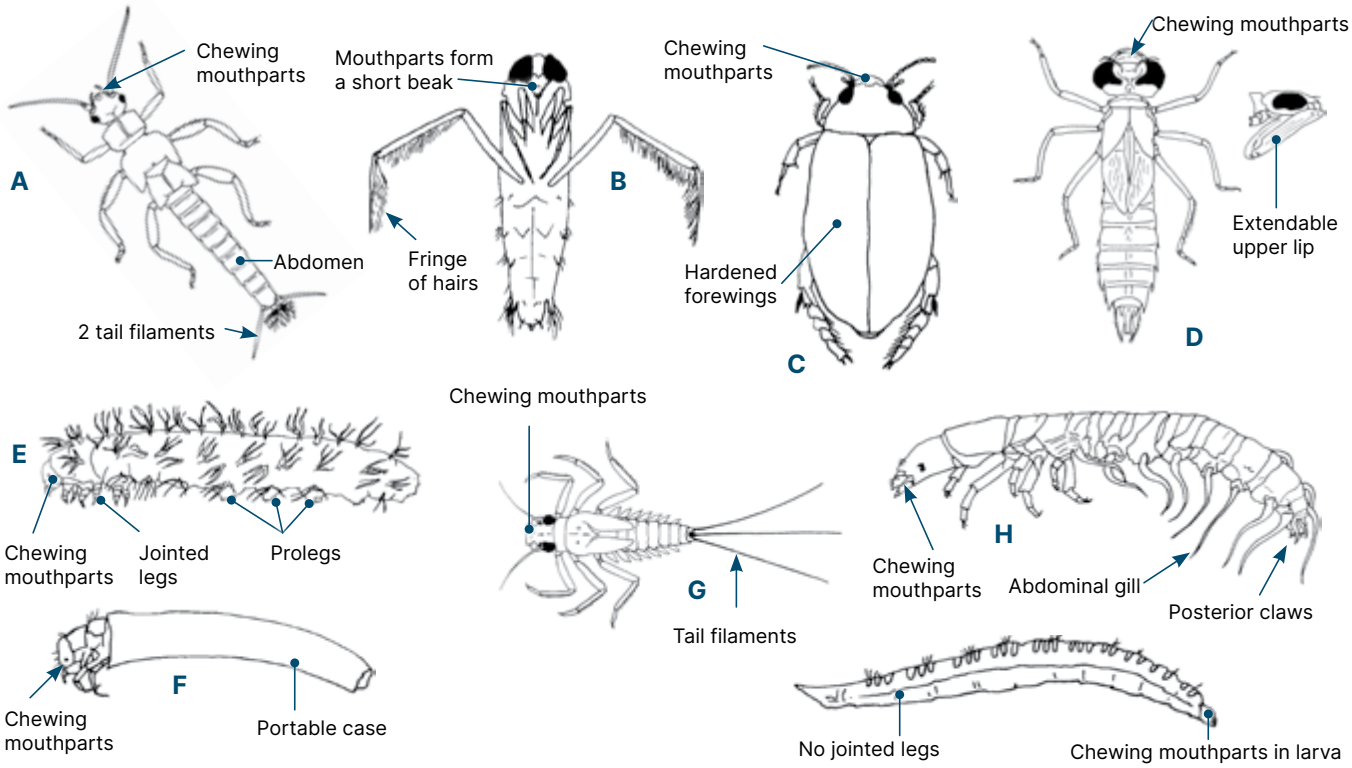

3. Use the simplified key to identify each of the orders (by order or common name) of aquatic insects (A-I) pictured above:

(a) Order of insect A: _____

(b) Order of insect B: _____

(c) Order of insect C: _____

(d) Order of insect D: _____

(e) Order of insect E: _____

(f) Order of insect F: _____

(g) Order of insect G: _____

(h) Order of insect H: _____

(i) Order of insect I: _____

Key to Orders of Aquatic Insects		
1	Insects with chewing mouthparts; forewings are hardened and meet along the midline of the body when at rest (they may cover the entire abdomen or be reduced in length).	**Coleoptera** (beetles)
	Mouthparts piercing or sucking and form a pointed cone. With chewing mouthparts, but without hardened forewings.	*Go to 2* *Go to 3*
2	Mouthparts form a short, pointed beak; legs fringed for swimming or long and spaced for suspension on water.	**Hemiptera** (bugs)
	Mouthparts do not form a beak; legs (if present) not fringed or long, or spaced apart.	*Go to 3*
3	Prominent upper lip (labium) extendable, forming a food capturing structure longer than the head.	**Odonata** (dragonflies & damselflies)
	Without a prominent, extendable labium	*Go to 4*
4	Abdomen terminating in three tail filaments which may be long and thin, or with fringes of hairs.	**Ephemeroptera** (mayflies)
	Without three tail filaments	*Go to 5*
5	Abdomen terminating in two tail filaments	**Plecoptera** (stoneflies)
	Without long tail filaments	*Go to 6*
6	With three pairs of jointed legs on thorax	*Go to 7*
	Without jointed, thoracic legs (although non-segmented prolegs or false legs may be present).	**Diptera** (true flies)
7	Abdomen with pairs of non-segmented prolegs bearing rows of fine hooks.	**Lepidoptera** (moths and butterflies)
	Without pairs of abdominal prolegs	*Go to 8*
8	With eight pairs of finger-like abdominal gills; abdomen with two pairs of posterior claws.	**Megaloptera** (dobsonflies)
	Either, without paired, abdominal gills, or, if such gills are present, without posterior claws.	*Go to 9*
9	Abdomen with a pair of posterior prolegs bearing claws with subsidiary hooks; sometimes a portable case.	**Trichoptera** (caddisflies)

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24 Making a Classification Key

Key Idea: A dichotomous classification key can be designed for all groups of organisms.

When designing a **dichotomous key**, it is important to remember that it must be based on easily distinguishable structures, including their presence or absence. Descriptions such as 'lives in water,' are not useful as this cannot be determined by simply looking at physical structures and requires some knowledge of the organism's habitat. Ideally, a key should be designed so that, at each step, the user can make a choice based on the structures they are able to see, count, and measure, e.g. 'three hairs present at end of abdomen', or 'leaves are compound'. In this activity, you will design your own dichotomous key to separate local plant or animal species.

Investigation 2.1 Develop a dichotomous key

See appendix for equipment list.

1. You are to develop a dichotomous key to distinguish between local species. These may be animal or plant species. You should have at least 10 species to distinguish. They do not need to be closely related.
2. For animal species, select several which you can easily observe and work with; photographs may serve provided they provide enough details. For plant species, select matching parts of the plants that will give the best variation in structure, e.g. leaf or flower structure.
3. Your key should be usable by someone else to identify any of the species in the list without them having to ask you questions.
4. Your key can be either a list (as on page 50) or a branched diagram (as on page 49).
5. Use the space below to produce your key:

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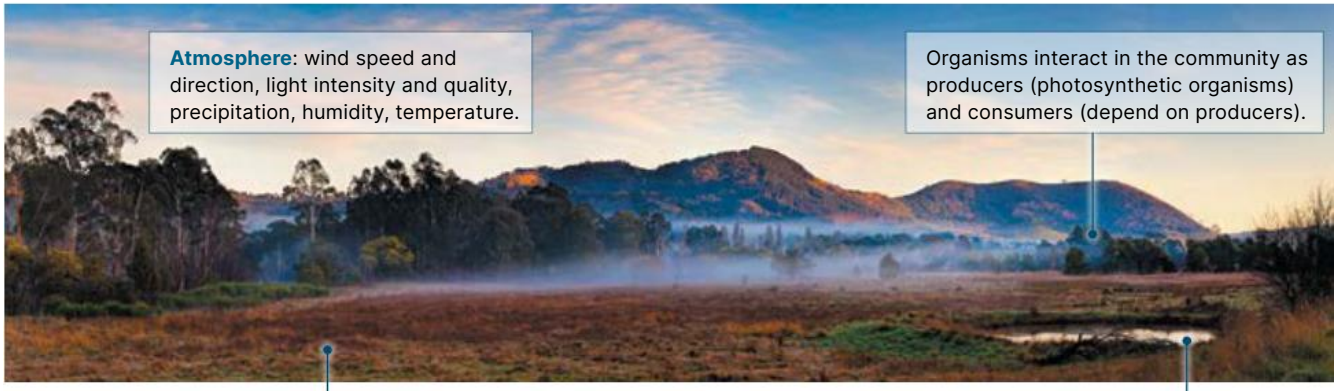
25 Ecosystems Include Varied Habitats

Key Idea: An ecosystem is a community of living organisms and the abiotic components of their environment, interacting as a system. Ecosystems include varied habitats.

An **ecosystem** is a community of living organisms and the physical (non-living) components of their environment. The community (living component of the ecosystem) is in turn made up of a number of populations (organisms of the same species living in the same geographical area). The abiotic and biotic components of an ecosystem determine its characteristic features and help us to define it and distinguish it from other ecosystems. Within larger ecosystems we can often recognise and classify different habitats.

Physical environment: abiotic factors

Community: biotic factors



Atmosphere: wind speed and direction, light intensity and quality, precipitation, humidity, temperature.

Organisms interact in the community as producers (photosynthetic organisms) and consumers (depend on producers).

Soil: nutrient availability, moisture and pH, composition, temperature.

Water: pH, salinity, dissolved oxygen, dissolved nutrients, temperature.

1. (a) Distinguish between a community and an ecosystem: _____

_____

_____

(b) Distinguish between biotic and abiotic factors: _____

_____

_____

2. For each aspect of a rainforest (a-d), assign one the following descriptors: population, community, ecosystem, abiotic factor:

(a) All the green tree frogs present: _____ (c) All the organisms present: _____

(b) The entire rainforest: _____ (d) The humidity: _____

Ecosystems and the scale of habitats

- Ecosystems can include a variety of habitats on different scales from the very small (**microhabitat**) to the much larger (**ecoregion**).

Bottletree scrub of the Queensland Brigalow belt

Ecoregions are a WWF **classification** for geographically distinct plant and animal communities. Australia has 40 terrestrial ecoregions, including the Queensland tropical rainforests and the Brigalow tropical savanna (above).

Melburnian CC 3.0

Microhabitats are small areas within a larger surrounding habitat. The bottletree (flower above), which is an emergent tree in the Brigalow, is itself a microhabitat, being the host plant for orange mistletoe, the pale cotton stainer bug, and the kurrajong leaf roller.

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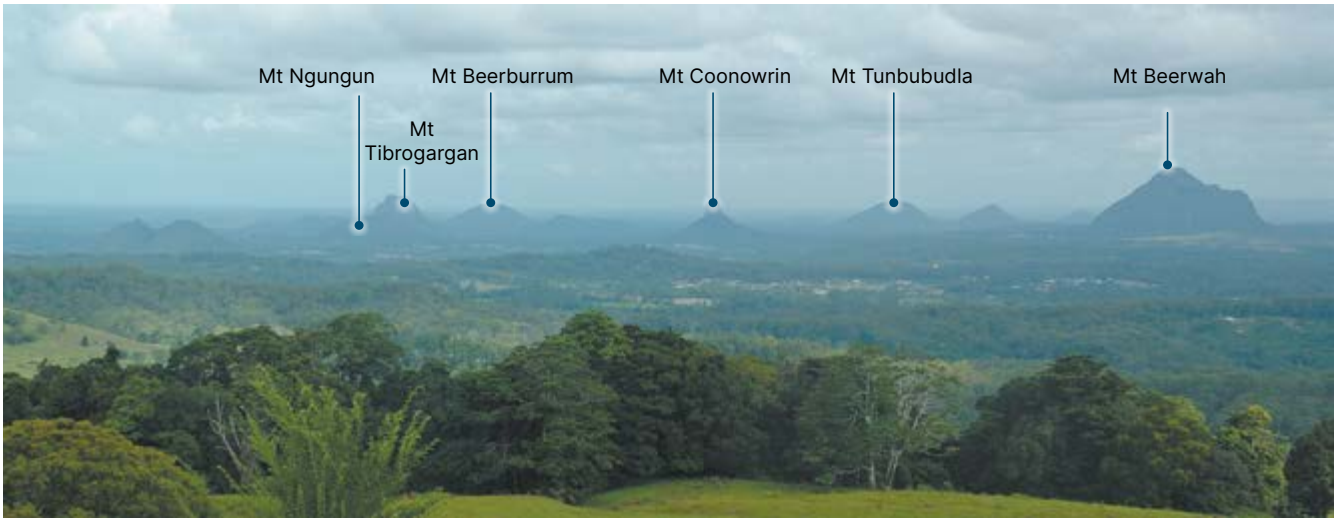

Bidgee cc 3.0

The **Glass House Mountains** are a group of thirteen hills in Glass House Mountains National Park, Sunshine Coast region, Queensland. The protected area covers 11 of the 16 Glass House Mountains as well as an 11 hectare area called Blue Gum Creek, which supports populations of the endangered swamp stringbark and provides habitat for several vulnerable frog species.

The cores of the extinct volcanoes rise from a flat plain, providing a diverse topography of ridges, scree slopes, outcrops, and gullies. These support a variety of vegetation types, from montane heath, shrubland, open woodland, and isolated patches of rainforest on some peaks (e.g. Mount Beerburrum). Each peak supports a characteristic assemblage of plant and animal species, many of which are rare, threatened, or vulnerable.

3. Divide the class into groups of two or three. Each group of students should choose from Blue Gum Creek or one of the peaks in the Glass House Mountains National Park and research its characteristic features, including topography, vegetation, and animal species. Include notes on species that are rare or threatened, or endemic to the region.

   Choose from: Blue Gum Creek, Mt Beerburrum, Mt Beerwah, Mt Coochin, Mt Coonowrin (Crookneck), Mt Elimbah, Mt Ngungun, Mt Tibberoowuccum, Mt Tibrogargan, Mt Tunbubudla, Mt Miketeebumulgrai, Wild Horse Mountain.

   Summarise your findings as notes below and report back to the class. How many different distinctive habitats are present in the National Park? How important is it for conservation that these habitats are recognised?

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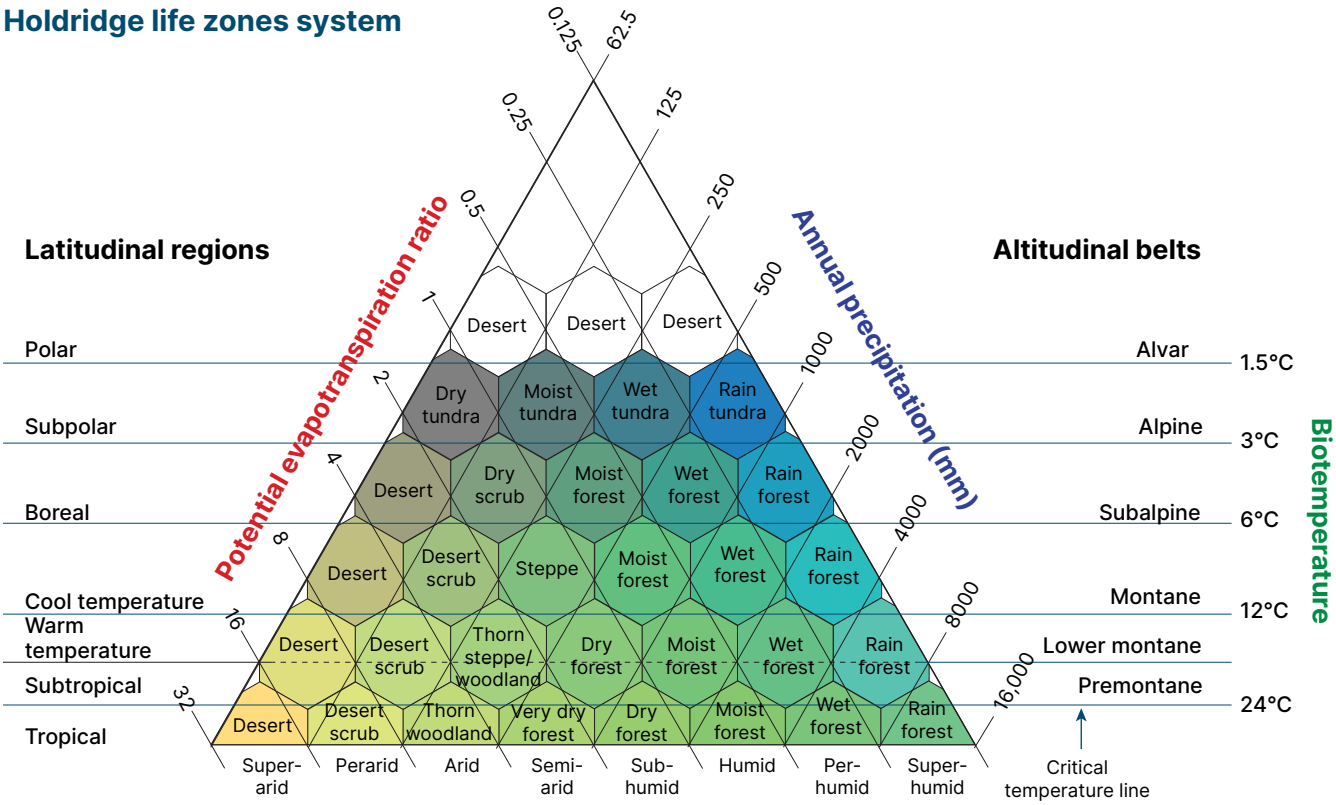
26 Classifying Australia's Ecosystems

Key Idea: Systems for classifying ecosystems are based on vegetation type, which is broadly linked to trends in major abiotic factors such as precipitation and temperature.

The ability to classify **ecosystems** allows us to recognise them and determine their extent. Broad **classifications** for ecosystem types can be applied globally (e.g. the Holdridge life zone classification scheme) or on a regional basis. Australia has a number of different classification schemes for its terrestrial and aquatic ecosystems. Different schemes offer different levels of resolution in terms of their ability to identify the characteristics of different regional environments. Other countries have their own schemes. Australia has highly variable climatic, topographical, and edaphic (soil) factors influencing vegetation type and distribution.

Holdridge life zones system



The Holdridge life zones system, developed in 1947, is a bioclimatic scheme for classifying land areas. It is similar to the Whittaker biome diagram, but whereas Whittaker uses mean annual temperature and precipitation as the key indicators of the environment (2 factors), Holdridge life zones consider temperature, precipitation, and potential evapotranspiration (3 factors). It has lately been used to help understand the effect of climate change on ecosystems.

Biotemperature is based on the length of the growing season and temperature. Plants often become dormant above 30°C and below 0°C so areas where these temperatures are common are almost always deserts (either hot or cold).

Evapotranspiration in tropical rainforests is low due to trees blocking wind, light, and heat from reaching the ground. Foliage collects moisture and returns it to the ground often faster than it is being transpired, producing a very wet environment.

Where evapotranspiration, precipitation, and temperatures are all moderate, dry ecosystems tend to predominate. These can be either dry forests, such as along much of the east of Australia, or dry grasslands, such as the savannah in Africa.

1. Identify the life zones that have:

   (a) a potential evapotranspiration ratio of 1, annual precipitation of 1000 mm and a biotemperature of about 20°C:

   _____

   (b) a potential evapotranspiration ratio of 3, annual precipitation of 200 mm and a biotemperature of about 10°C:

   _____

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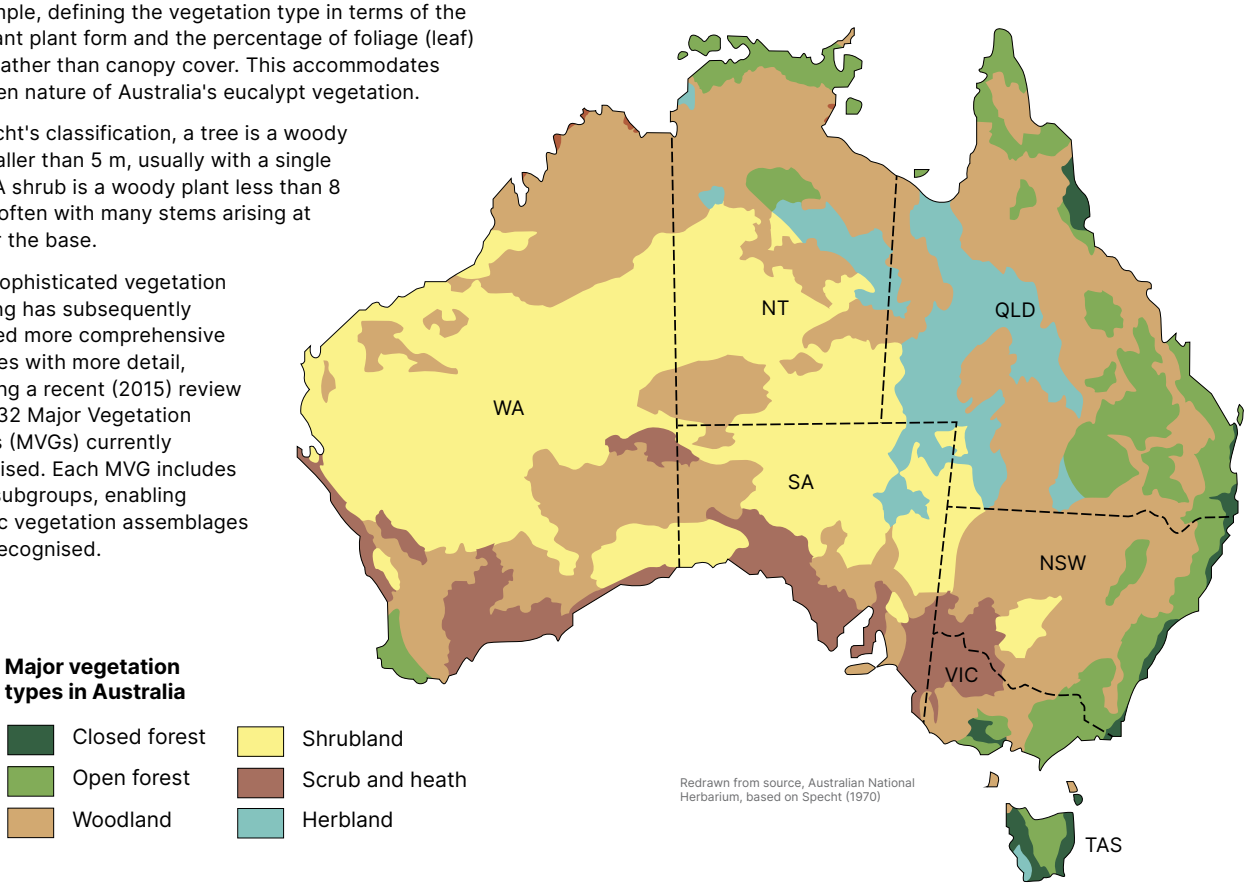
Terrestrial vegetation based schemes

Australia's distinctive and diverse ecosystems are not easily accommodated within the classifications devised for the Northern Hemisphere. Specht's system (1970) for defining the structural forms of Australia's vegetation is one of the most widely recognised. It is simple, defining the vegetation type in terms of the dominant plant form and the percentage of foliage (leaf) cover rather than canopy cover. This accommodates the open nature of Australia's eucalypt vegetation.

In Specht's classification, a tree is a woody plant taller than 5 m, usually with a single stem. A shrub is a woody plant less than 8 m tall, often with many stems arising at or near the base.

More sophisticated vegetation mapping has subsequently provided more comprehensive schemes with more detail, including a recent (2015) review of the 32 Major Vegetation Groups (MVGs) currently recognised. Each MVG includes many subgroups, enabling specific vegetation assemblages to be recognised.



	Percentage foliage cover of tallest plant layer			
Form and height of tallest stratum	**Dense (70-100%)**	**Mid-dense (30-70%)**	**Sparse (10-30%)**	**Very sparse (<10%)**
Trees > 30 m	Tall closed-forest	Tall open-forest	Tall woodland	Tall open-woodland
Trees 10-30 m	Closed-forest	Open-forest	Woodland	Open-woodland
Trees 5-10 m	Low closed-forest	Low open-forest	Low woodland	Low open-woodland
Shrubs 2-8 m	Closed-scrub	Open-scrub	Tall shrubland	Tall open-shrubland
Shrubs 0-2 m	Closed-heath	Open-heath	Low shrubland	Low open-shrubland

2. Using Specht's scheme, give a broad description of the ecosystem (vegetation) types for the following Australian states. The first has been completed for you:

(a) Tasmania: *Approximately 50% open forest with the remaining vegetation mostly closed forest towards the west and east coasts. Some isolated pockets of coastal herbland and woodland to the west.*

(b) NSW: _____

(c) Queensland: _____

(d) Northern Territory: _____

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What about aquatic ecosystems?

We have seen how Australia's terrestrial ecosystems can be classified according to dominant vegetation. But how do we classify aquatic ecosystems? These ecosystems present special challenges because their defining characteristics are always obvious.

- The Australian National Aquatic Ecosystem (**ANAE**) Classification Framework was developed to provide a broad-scale scheme based on biological and geophysical attributes. It is semi-hierarchical, designed to capture broad spatial patterns and ecological diversity (recognising that detailed biological data is often patchy or sparse).
- ANAE provides a nationally consistent flexible framework for recognising and classifying different aquatic ecosystems and habitats including rivers, floodplains, lakes, inland wetlands, estuaries and subterranean ecosystems. The scheme can be integrated with other classification schemes or used as a tool on its own to identify manage aquatic ecosystems more effectively.
- At each level, the scheme draws on information from National databases on climate, soil type, landform, vegetation, and hydrology. The semi-hierarchical nature of the scheme provides increasing detail. For example, climate may be coastal, arid, semi-arid etc., topography might be floodplain habitats, e.g. water type may be brackish, saline, freshwater etc. If freshwater, that might be flowing, standing, permanent, seasonal etc.
- Codes are often used to identify the ecosystem type, e.g. for a lacustrine (lake) system, a dune lake is DL.

ANAE structure										
Level 1	**Regional scale** (Attributes: hydrology, climate, landform)									
Level 2	**Landscape scale** (Attributes: water influence, landform, topography, climate)									
Level 3	Class	**Surface water**						**Subterranean**			
	System	Marine	Estuarine	Lacustrine (lakes)	Palustrine (inland marsh)	Riverine	Floodplain	Fractured	Porous sedimentary rock	Unconsolidated	Cave/karst
	Habitat	**Pool of attributes to determine aquatic habitats** (e.g. water type, vegetation, substrate, porosity, water source)									

Lake Wabby, Fraser Is. Qld. is a small freshwater lake created by a natural spring being blocked by a sandmass. Unlike most of Fraser Island's other lakes, which are too acidic, it supports a fish community.

3. The categories of Specht's scheme give a broad description of the ecosystem (vegetation) types for Australia:

   (a) In what way are the broad categories of Specht's scheme useful in describing the ecosystems of Australia?

   (b) In what ways do you think this classification scheme is deficient, or at least not very helpful in planning strategies for ecosystem management at the local level?

4. Explain how the structure of the ANAE framework provides the detail to distinguish different types of aquatic ecosystem:

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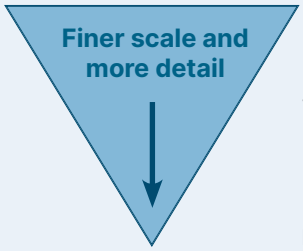
27 Classifying Queensland's Terrestrial Ecosystems

Key Idea: Bioregions are large, geographically distinct areas with common geological and ecological characteristics.

Australia's terrestrial landscapes are classified into 89 large geographically distinct bioregions based on common climate, geology, landform, native vegetation and species information. These bioregions are defined in the Interim Biogeographic Regionalisation for Australia (the IBRA), which is the planning framework for Australia's National Reserves System (NRS) and was developed to help identify areas of conservation priority. Each bioregion includes many regional **ecosystems**. Australia's marine parks are marine protected areas within Australia's waters. They include the Coral Sea Marine Park (the Great Barrier Reef) and the North Marine Parks Network off the coast of Northern Territory and Queensland.



Geographic extent	Name	Number in Australia
	Biogeographical realm (ecozone)	1
	Terrestrial ecoregion	7
	IBRA region (bioregion)	89
	IBRA subregion	419
	Regional ecosystem	**1000s**

Queensland recognises 13 bioregions. Within these are thousands of regional ecosystems, identified by characteristics of their land zone and vegetation type.

Regional ecosystems are classified by a three-number code, which identifies (1) the **bioregion** (e.g. Brigalow Belt), then (2) the **land zone** (e.g. clay plain), then (3) the **vegetation type** (shrubby, open forest).

The information is available on a searchable database, which also provides fields for **biodiversity** status (e.g. threatened).


Regional ecosystem code: 11.3.3

Ethel Aardvark cc 3.0


Regional ecosystem code: 12.1.3

BoundaryRider cc 3.0


Regional ecosystem code: 8.2.1

Ethel Aardvark cc 3.0

1. Using **BIOZONE's Resource Hub,** click on the Queensland Government's page "Search regional ecosystem descriptions". Start by clicking on the Bioregion, then find the regional ecosystem description for each of the images shown above. Briefly describe the ecosystem, including defining species, biodiversity status, and any notes of special interest:

   (a) RE code 11.3.3: _____

   _____

   (b) RE code 12.1.3: _____

   _____

   (c) RE code 8.2.1: _____

   _____

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Regional ecosystem code: 3.5.3

Paste cc 3.0


Regional ecosystem code: 10.3.13

Wittylama cc 3.0


Regional ecosystem code: 4.3.21

Mark Marathon cc 3.0

(d) RE code 3.5.3: _____

_____

(e) RE code 10.3.13: _____

_____

(f) RE code 4.3.21: _____

_____

2. Now that you are familiar with how to use the regional ecosystem framework to describe ecosystems, locate a distinctive ecosystem in your area (or one that you have visited). Try to classify it using the regional ecosystem framework and give it a code. If you need help, you can use the menu to request a list of species for a specified region. What are the features of your ecosystem? What is its conservation status? Can you easily distinguish it from other ecosystems? Write your summary of your ecosystem below. You can attach a photograph if you wish:

_____

_____

_____

_____

_____

_____

_____

_____

_____

_____

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28 Classification Aids Ecosystem Management

Key Idea: Being able to identify and classify specific ecosystems allows us to manage them more effectively, monitor changes, and create better options for conservation. As with the **classification** of plant and animal taxa, we have seen how classifying **ecosystems** allows us to recognise and record diversity. Queensland supports a diverse range of regional ecosystems, but many of them are now remnant and threatened by urban expansion and climate changes. Recognising the ecosystem diversity that exists makes it possible to protect and manage that diversity so that the unique characteristics of a region are not lost. Here, we will examine one example of how the establishment of a habitat corridor has enabled a valuable area of connected green spaces to be managed as a collective entity.

The Flinders Karawatha Corridor (the corridor) is a forested passage between Boonah and Karawatha Forest Reserve in Brisbane City. Covering 56,350 ha, it is the largest remaining area of intact lowland eucalypt forest in South East Queensland (SEQ) and provides habitat for wildlife and allows the movement of populations through a range of distinctive habitats. The corridor includes a number of protected areas under either state or local council ownership and laws.

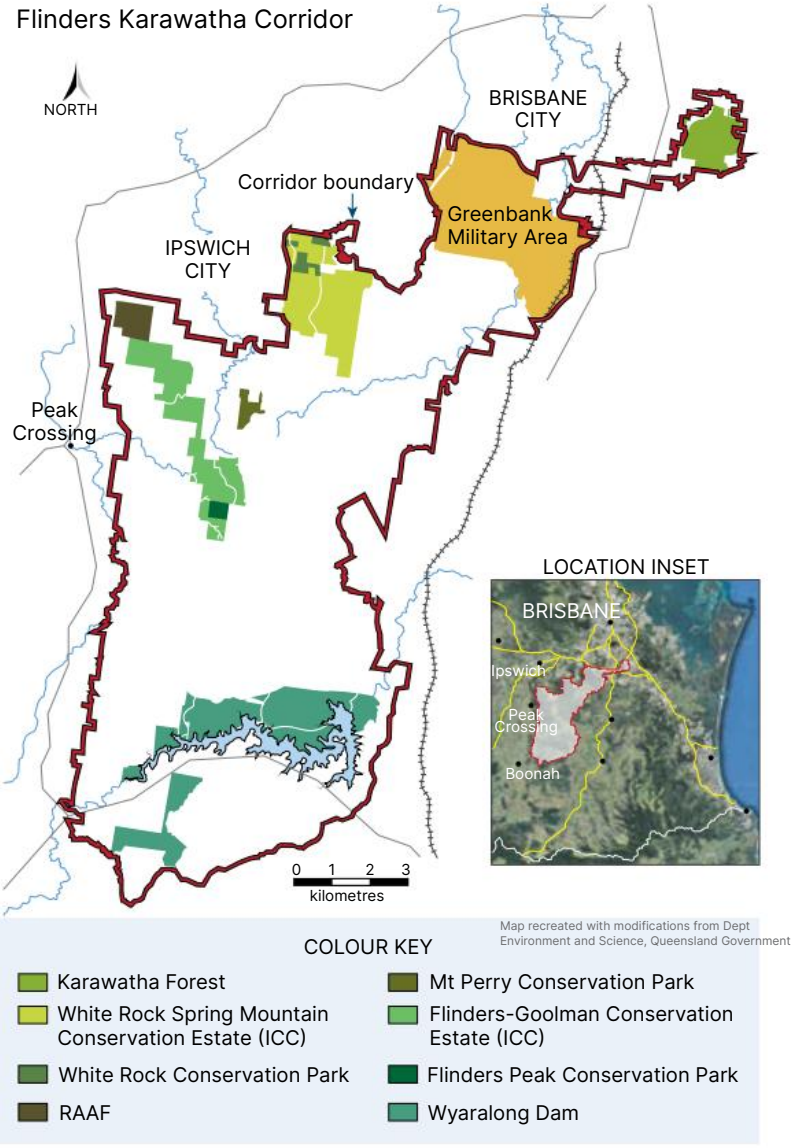
From 2011, the Queensland Government, in partnership with local government and other stakeholders developed the Flinders Karawatha Corridor Management Strategy. This 5-year management plan (released in 2014) identified actions to maintain and enhance the environmental, recreational and cultural heritage values of the corridor. The focus of the management strategy is the long term sustainability of the corridor's values and its implementation has involved commitment from the Queensland Government, local councils, landowners and the public. It has been assessed as a State-significant region because of its relatively large size, high value for wildlife refugia, SEQ endemism, and species richness.

Landowner participation is voluntary but there are financial incentives for landowners to participate in programmes such as the Nature Assist programme and the Koala Nature Refuge programme.

An analysis of regional ecosystems (RE) was crucial to assessing the corridor's environmental values. 27 REs occur in the corridor, and 16 have a **biodiversity** status of "endangered" or "of concern". 16 REs have special value and include:

- habitat for 36 threatened and 22 near threatened plant species.
- habitat for threatened animal species.
- wetland habitat for plants and animals
- habitat for species with restricted or separated distributions.
- habitat for cool subtropical species at the limits of their climatic range.

Flinders Karawatha Corridor



Map recreated with modifications from Dept Environment and Science, Queensland Government

Biodiversity of the Flinders Karawatha Corridor


Swamp paperbark (*Melaleuca irbyana*)

Murray Fagg, cc 3.0 au

The swamp paperbark is endemic to NSW and Queensland. Its distribution is very limited and it is listed as endangered under state legislation. Other rare plants include the Flinder's plum and Lloyd's native olive.


Regent honeyeater (*Anthochaera phrygia*)

Incandescent, cc 3.0

The regent honeyeater is a critically endangered species endemic to south-east Australia. It is considered a flagship species - a species chosen to support the conservation of biodiversity in a given region.

Murray Fagg, cc 3.0 au

The swift parrot (*Lathamus discolor*) is a critically endangered species that depends on connected areas of forest to make its migration north from its breeding grounds in Tasmania. Fewer than 2000 remain in the wild.

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Management actions and responsibilities for the Flinders Karawatha Corridor

Different agencies or partners have responsibility for different actions within the corridor's management strategy. Actions are defined under the general areas of: biodiversity; waterways and wetlands; rural land use; cultural heritage; recreation; infrastructure; and reporting, research, and monitoring. Each area has its own overall objective and key actions to achieve this.

Illaweena Lagoon, Karawatha Forest

Shiftchange, Public Domain

Wetlands provide important habitat for organisms, especially as climate changes. They improve water quality by trapping sediment and excess nutrients but need to managed to control pests and weeds and preserve the riparian vegetation.

Compton Road land bridge

Lyle Radford, cc 2.0

This fauna overpass links Karawatha forest to the northern Kuraby bushland. The passageway also included two fauna underpasses, three rope ladders, and a line of glider poles. Managing infrastructure such as this is an important part of the strategy.

Picnic area and boat ramp, Wyaralong Dam

Shiftchange, Public Domain

Providing amenities for recreation and sight-seeing amenities is an important part of the corridor's management strategy. Sustainable nature-based recreation contributes to the local economy and landowners can also benefit from tourism opportunities.

1. To be successful, an ecosystem management strategy requires an impartial, accurate assessment of the ecosystems present and their environmental values **and** the input of all parties with an interest in the region. Briefly explain why both of these things are important:

2. (a) Divide the class into seven groups. Each group should be assigned one of the general areas within the management strategy: 1) biodiversity 2) waterways and wetlands 3) rural land use 4) cultural heritage 5) recreation 6) infrastructure 7) reporting, research, and monitoring. Using the information provided via **BIOZONE's Resource Hub** for this activity find out about the objectives and required actions of the area you have been assigned. Summarise your findings as a presentation or brief report, including why you think each action is important.

   (b) As a class, discuss how all the different areas contribute to the sustainable management of the Flinders Karawatha Corridor and why its sustainable management is important. Capture your discussion as a mind map on a whiteboard. Photograph the finished map and attach it to this page.

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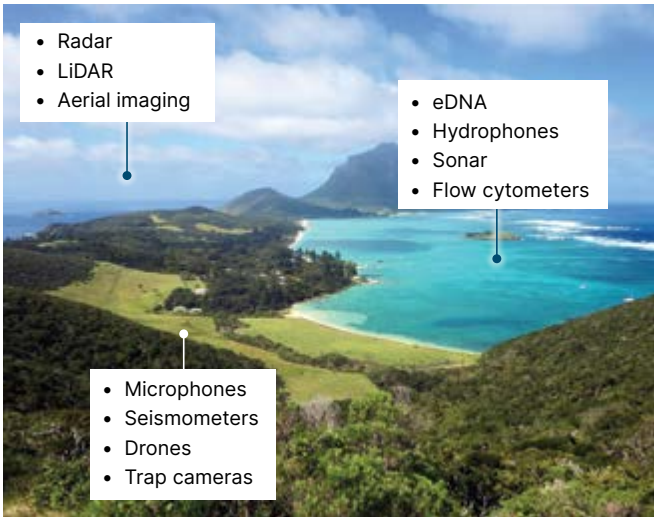
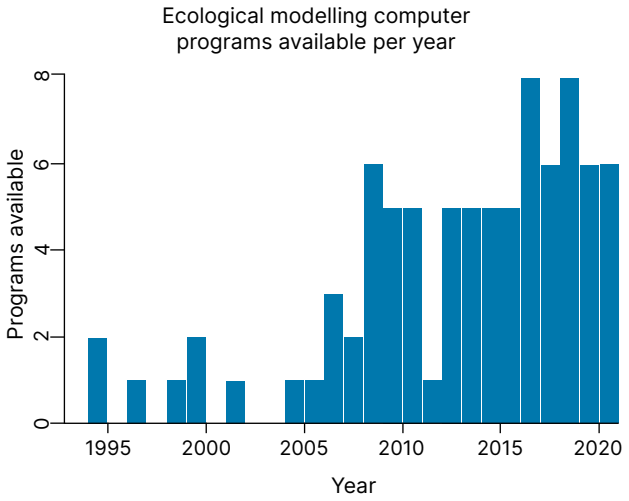
29 Computing Ecosystems

Key Idea: The amount of ecological data available needs a large amount of computing to analyse and understand.

Traditional methods of gathering ecological data can be difficult and time consuming. Landing a team of ecologists in a particular area and keeping them supplied can be logistically difficult, let alone the difficultly in actually gathering data from animals that don't want to be found, or plants spread over vast areas of land. Often, the data gathered is then so detailed or diverse that making sense of it requires large amounts of computing power. In the last few decades the use of computer software, and ever more commonly AI programs, to analyse ecological data have led to much better understanding of the extent of various **ecosystems** and how they behave. It is now possible for computer programs to scan thousands of aerial or satellite photographs or radar or thermal images of land and assign areas to an ecosystem type. This makes gathering data faster and more efficient which can then help making decisions to do with ecosystem management faster, simpler, and more targeted, producing better environmental outcomes.



The technology available to ecologists to help monitor ecosystems means that not only can data be gathered almost continuously, but vast amounts of data are gathered. Huge amounts of computing power are needed to process this data but it provides accurate information, allowing better decision making.



Emmanuel Paradis. A review of computer tools for prediction of ecosystems and populations: We need more open-source software. Environmental Modelling and Software, 2020.

As computing power and integration have increased, the number of computer programs available to analysise data have also increased. The graph above shows the number of computer programs available online that are specifically designed to predict ecosystem type and future behaviour.

Using programs to classify ecosystems

The spreadsheet on the right uses a very simple formula to match the abundance of plants in a hypothetical area to a specific ecosystem type. The spreadsheet can be downloaded from the **BIOZONE Resource Hub**. Data can be input into cells B2 to B6, the result is output in cell D2. Use the spreadsheet to answer the questions below.

Programs used to analyse real world situations are obviously much more complex than this but even a simple program like this, once written, can significantly reduced the time required to analyse data and produce useful results.

	A	B	C	D
1	**Plant species**	**Abundance (number/m2)**		**Ecosystem type**
2	a	12		ECO1
3	b	14		
4	c	3		
5	d	2		
6	e	3		
7				
8				

1. Explain how continuous monitoring of ecosystems helps to understand ecosystem behaviour:

2. Explain how AI systems help classify ecosystems more efficiently:

3. Use the spreadsheet to identify the ecosystem based on the plant abundance:

   (a) Plant A: 12, plant B: 10, plant C: 34, plant D: 1, plant E: 10: _____

   (b) Plant A: 1, plant B: 2, plant C: 12, plant D: 1, plant E: 4: _____

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30 Classifying An Ecosystem Using Primary Data

Key Idea: The collection of biotic and abiotic data can be used to classify an ecosystem.

In this activity you will use your understanding about ecosystem classification and sampling techniques to design a sampling investigation to obtain data that will allow you to classify a specific **ecosystem**.

1. Identify the area you are going to sample. Record:

   (a) The name of the area (if the area has a name e.g. Fred Rohlf Park): _____

   (b) The latitude and longitude of the area (using GPS or a mapping program): _____

   (c) The land zone, e.g. coastal dune, tidal flat, floodplain: _____

2. Identify the major vegetation strata within the area you are going to sample. This could be done using satellite images to generally identify patches of trees or grass etc. Draw a general map below to show where the vegetation types are located within the area. If there is an environmental gradient, e.g. increase in altitude, record it here.

3. (a) Calculate the general percentages of each vegetation type in your area using the map you drew (e.g. 40% grass, 50% trees, 10% shrubs).

   _____

   _____

   (b) Why is this calculation important? _____

   _____

4. How will you sample your area? Will you use quadrats or transects? How many will you use? How big will any quadrats need to be? How will you chose to place them in the sample area? What abiotic data will you need to collect? Record you methods in the space below and justify your choice:

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5. Collect your data. Create a results table in the space below to summarise your data.

6. You will need to analyse your data so that you can classify the ecosystem type. Using the regional ecosystem framework (see Activity 27) what code will you give your sample area? Use the website in the **BIOZONE Resource Hub** to request a species list for your area, using the latitude and longitude information you recorded earlier.

   (a) How would you classify your sample area? Give reasons for your choice: _____

   (b) Does the species list you obtained match the one you compiled from your sampling? Explain: _____

   (c) Use the regional ecosystem framework website to obtain the actual code for you sample area. How closely does it match your description or coding?

7. Compare your results to others in your class who have sampled the same area. Did they obtain similar result to you? Explain any differences in data and classification:

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31 Did You Get It?

1. (a) Define a biological species: _____

_____

_____

(b) Define a phylogenetic species: _____

_____

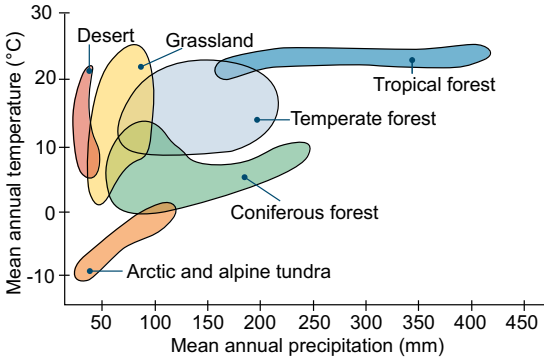
_____

2. Place the taxanomic ranks in order of most general to most specific: *Species*, *Phylum*, *Kingdom*, *Class*, *Family*, *Genus*, *Order*.

_____

3. Produce a dichotomous key in a list form to separate the items below:

4. Ecosystems can be classified by rainfall and temperature (after Whittaker) as in the diagram below:



(a) Which ecosystem has the greatest rainfall per year?

_____

(b) Which ecosystem has the lowest annual temperature?

_____

(c) What is the temperature range of grassland?

_____

5. Why is classifying ecosystems a useful process? _____

_____

_____

_____

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Chapter 3 Unit 3 Topic 1

Population Ecology

Resource Hub
bit.ly/4k5wOUV

Key Terms

- abiotic (physical) factor
- biotic factor
- birth rate
- carrying capacity
- death rate
- density dependent factor
- density independent factor
- emigration
- exponential growth
- immigration
- limiting factor
- Lincoln index
- logistic growth
- mortality
- natality
- population

Key Concepts

- Carrying capacity is the maximum number of organisms an environment can support indefinitely, determined by the most limiting factor.
- Changes in limiting factors, such as food supply or water availability, can alter the carrying capacity over time, affecting population size.
- Population growth may be modelled as exponential or logistic. Outcomes of these models can be determined using computer software.

Carrying capacity and limiting factors		Activity Number
☐ 1	Define the term carrying capacity. Explain how limiting factors determine the carrying capacity of the environment. Discuss how changes in limiting factors can alter carrying capacity over time. State what might cause changes in limiting factors.	31
☐ 2	Identify biotic and abiotic limiting factors in the environment. State that abiotic factors are density independent whereas biotic factors are density dependent. Describe how both types of factors may operate to create the fluctuations we see in natural populations.	31
☐ 3	Describe how population size increases through births and immigration and declines through deaths and emigration. Express this relationship mathematically and use it to calculate population growth rate and change.	32
☐ 4	Describe an example of how a biotic factor, e.g. level of available food/ prey, can regulate population growth and size. Describe how predator-prey relationships result in cycles of population growth in both predator and prey populations.	33
☐ 5	Describe an example of how an abiotic factor, e.g. rainfall, can regulate population growth and size over the long term. Describe which abiotic factors are particularly important in the Australian environment and how they operate.	34
☐ 6	Use the Lincoln Index (N = M x n ÷ m) to estimate population size from primary and/or secondary data.	35

Exponential and logistic growth		
☐ 7	Distinguish between exponential and logistic growth and describe the characteristic features of each. Analyse population growth data to determine the growth pattern exhibited (J shaped exponential or S shaped logistic).	36
☐ 8	Use a computer model to develop an understanding of how population size affects populations growth rate in a logistic model with a predetermined carrying capacity.	36
☐ 9	Measure a population of microorganisms in a closed system (e.g. petri dish) to observe carrying capacity.	37, 38
☐ 10	Use a computer simulation to model continuous density-independent (exponential) and density-dependent (logistic) population growth. Explain the effect of changing r (biotic potential or intrinsic rate of increase). Describe what happens if you introduce a lag into the logistic model and explain why introducing a lag makes the model more realistic.	39

32 Factors Affecting Population Size

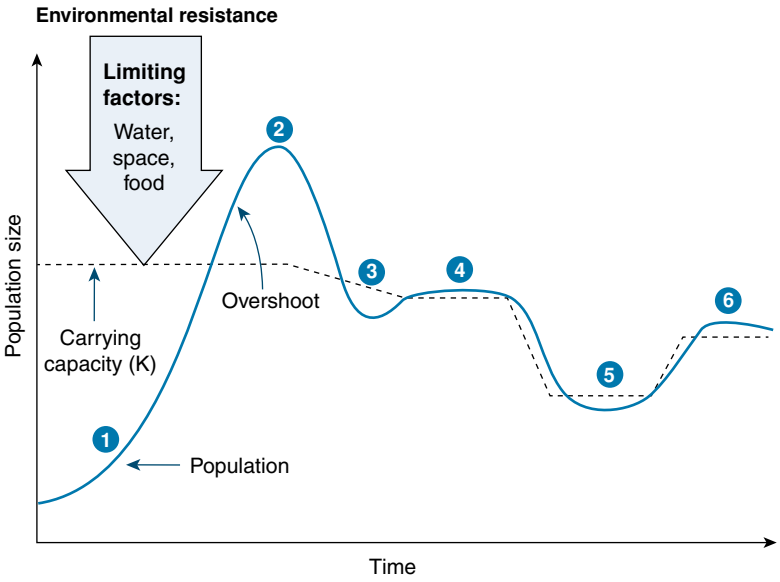
Key Idea: Carrying capacity is the maximum number of organisms a particular environment can support indefinitely.

An ecosystem's **carrying capacity**, i.e. the size of **population** that the available resources can sustain indefinitely, is limited by the ecosystem's resources. Factors affecting carrying capacity (population limiting factors) can be **biotic** (e.g. food supply) or **abiotic** (e.g. water, climate, and available space). The carrying capacity is determined by the most limiting factor and can change over time (e.g. as a result of environmental changes). Below carrying capacity, population size increases because resources are not limiting. As the population approaches its carrying capacity (or exceeds it) resources become limiting and environmental resistance increases, decreasing population growth.

Limiting factors

Limiting factors are factors limiting the growth, abundance, or distribution of an organism or a population. The effect of limiting factors and the type of factor that is limiting may change over time. The graph, right, shows how the carrying capacity of a forest environment varies based on changes to the biotic and abiotic limiting factors:

1. A population moves into the forest and rapidly increases in numbers due to abundant resources.
2. The population overshoots the carrying capacity.
3. Large numbers damage the environment and food becomes limiting. The carrying capacity falls.
4. The population becomes stable at the new carrying capacity.
5. The forest experiences a drought and the carrying capacity is reduced as a result.
6. The drought breaks and the carrying capacity rises but is less than before because of habitat damage during the drought.



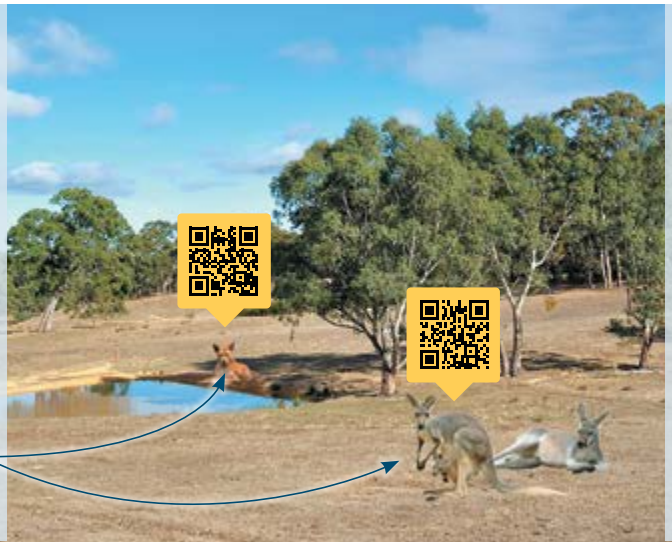
Limitations to population growth are either density-dependent or density-independent

Density dependent factors
The effect of these on population size is influenced by population density. They are most important at high population densities.

- Tend to be **biotic factors**.
- They generally regulate population size by decreasing **birth rates** and increasing **death rates**. Usually self regulating (negative feedback).

Examples:
Biotic interactions such as:

- Competition and predation
- Parasitism and disease



Density independent factors
The effect of these on population size does not depend on population density. Their action is independent of population density.

- Tend to be **abiotic factors**.
- They generally regulate population size by increasing death rates and can lead to sudden changes in population size.

Examples:
Natural disasters such as:

- Bushfires, droughts, floods
- Volcanic eruptions, earthquakes

1. What is carrying capacity? _____

_____

2. How can changes in limiting factors alter carrying capacity? _____

_____

_____

3. What limiting factors have changed at points 3, 5, and 6 in the graph above, and how have they changed?

(a) 3: _____

(b) 5: _____

(c) 6: _____

SU

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33 Calculating Change in Population Size

Key Idea: Population size increases through births or immigration and decreases through deaths and emigration.

Populations are dynamic and the number of individuals in a population may fluctuate considerably over time. Populations gain individuals through births or **immigration**, and lose individuals through deaths and **emigration**. For a population in equilibrium, these factors balance out and there is no net change in the population abundance. When losses exceed gains, the population declines. When gains exceed losses, the population increases.

Births, deaths, immigration (movements into the population) and emigration (movements out of the population) are events that determine the population size. Population growth depends on the number of individuals added to the population from births and immigration, minus the number lost through deaths and emigration. This is expressed as:

Population growth =

Births – Deaths + Immigration – Emigration

(B) (D) (I) (E)

The difference between immigration and emigration gives **net migration**. Ecologists usually measure the rate of these events. These rates are influenced by environmental factors (see below) and by the characteristics of the organisms themselves. Rates in population studies are commonly expressed in one of two ways:

- **Numbers per unit time**, e.g. 20,150 live births per year. The **birth rate** is termed the **natality**, whereas the **death rate** is the **mortality**.
- **Per capita rate** (number per head of population), e.g. 122 live births per 1000 individuals per year (12.2%).

Limiting factors

Limiting factors affect population growth and abundance. Availability of food, predation pressure, or available habitat are all population limiting factors operating to different degrees at different times.

The human population is estimated to peak at around 10 billion by 2050 as a result of multiple factors, including falling birth rates. Humans have the technology and production efficiency to solve many resource problems and so might appear exempt from limiting factors, but declining availability of water and land for food production is likely to constrain population growth, at least regionally.

1. Define the following terms used to describe changes in population numbers:

   (a) Death rate (mortality): _____

   (b) Birth rate (natality): _____

   (c) Net migration rate: _____

2. Explain how the concept of limiting factors applies to population biology: _____

   _____

   _____

3. Using the terms, B, D, I, and E (above), construct equations to express the following:

   (a) A population in equilibrium: _____

   (b) A declining population: _____

   (c) An increasing population: _____

4. A population started with a total number of 100 individuals. Over the following year, population data were collected. Calculate birth rates, death rates, net migration rate, and rate of population change for the data below (as percentages):

   (a) Births = 14: Birth rate = _____ (b) Net migration = +2: Net migration rate = _____

   (c) Deaths = 20: Death rate = _____ (d) Rate of population change = _____

   (e) State whether the population is increasing or declining: _____

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34 Predation and Population Cycles

Key Idea: Predator and prey populations frequently show regular population cycles. The predator cycle is often based on the population cycle of the prey species.

It was once thought that predators regulated the **population** numbers of their prey. However, we now know that this is not usually the case. Prey species are more likely to be regulated by other factors such as the availability of food. However, predator population cycles are often regulated by the availability of prey, especially when there is little opportunity for switching to alternative prey species.

A case study in predator-prey numbers

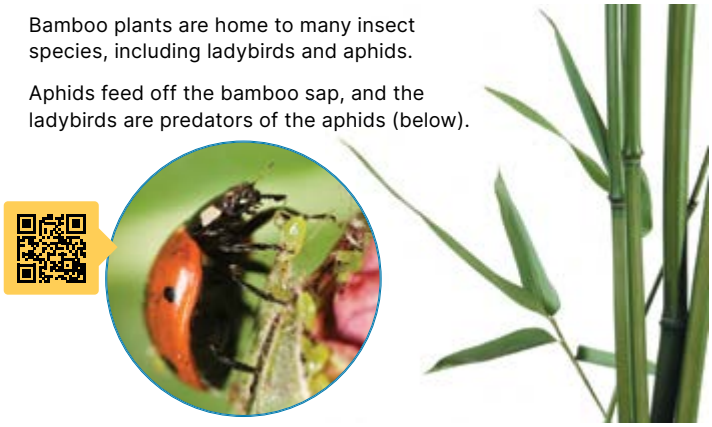
In some areas of Northeast India, a number of woolly aphid species colonise and feed off bamboo plants. The aphids can damage the bamboo so much that it is no longer able to be used by the local people for construction and the production of textiles.

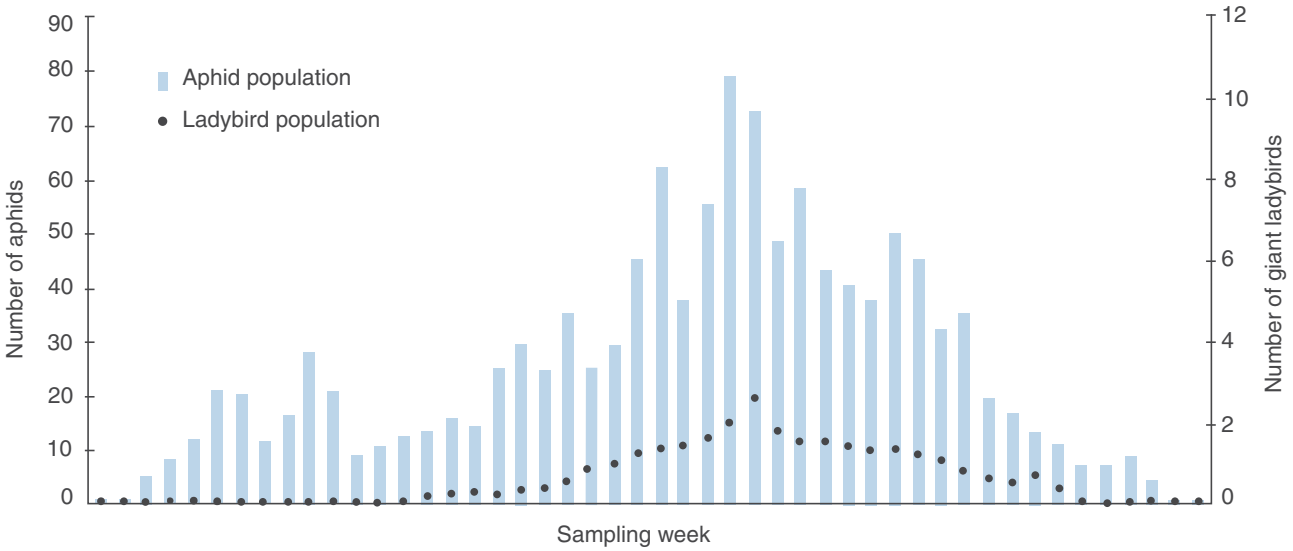
Giant ladybird beetles (*Anisolemnia dilatata)* feed exclusively on the woolly aphids of bamboo plants. There is some interest in using them as biological control agents to reduce woolly aphid numbers, and limit the damage woolly aphids do to bamboo plants.

The graph below shows the relationship between the giant ladybird beetle and the woolly aphid when grown in controlled laboratory conditions.

Bamboo plants are home to many insect species, including ladybirds and aphids.

Aphids feed off the bamboo sap, and the ladybirds are predators of the aphids (below).





Source: Majumder & Agarwala (2013) World Journal of Zoology 8 (1): 55–61

1. (a) On the graph above, mark (using different coloured pens) where the peak numbers of woolly aphids and giant ladybirds occurs:

   (b) Do the peak numbers for both species occur at the same time? _____

   (c) Why do you think this is? _____

2. (a) What is the response of the ladybird population when their prey decline? _____

   (b) What feature of the ladybird's response to prey suggests it would be a good choice to control woolly aphids?

   (c) Can you think of any other factors that could affect the numbers of ladybirds and aphids? _____

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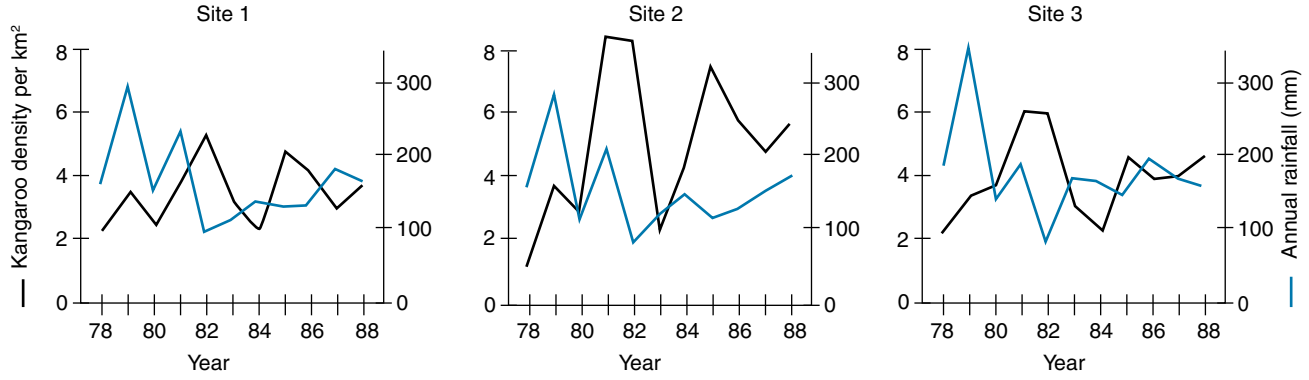
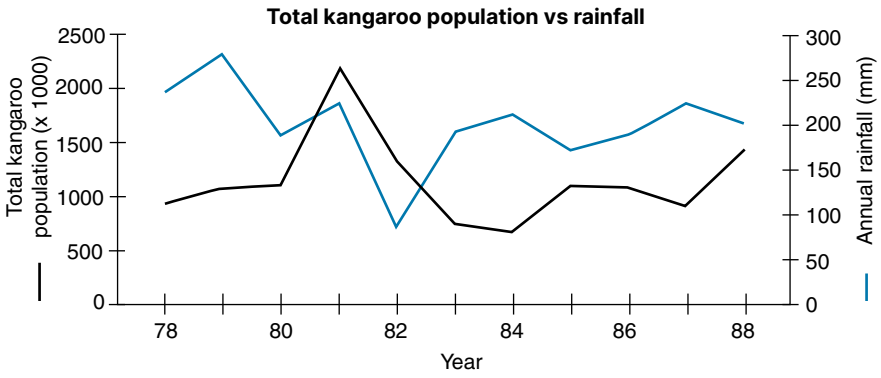
35 Abiotic Factors and Population Size

Key Idea: Abiotic factors can affect population size.

Abiotic factors such as rainfall and temperature can play an important role in the size of **population** an area can support. For example, rainfall is needed for plant growth and so to support grazers of that plant material. Low rainfall reduces plant growth and biomass and available water for animals, so it would be expected that it would also reduce animal population sizes. The study below was conducted from 1978 to 1988 on the relationship between population sizes of red kangaroos and rainfall in South Australian pastoral zones.

Kangaroo population density and rainfall





Aerial surveys (1978-1988) were made of red kangaroo populations in South Australia. Rainfall was also recorded. The plots show the results of three of the areas surveyed.

1. How might rainfall affect the size of an population of:

   (a) Animal grazers? Explain: _____

   _____

   (b) Predators dependent on those grazers? Explain: _____

   _____

2. (a) Would you expect the effect of reduced rainfall to be seen immediately? _____

   (b) Explain why: _____

   _____

   _____

   _____

3. Why do you think the survey above used kangaroo density instead of population numbers in each site?

   _____

   _____

4. Is there any pattern in the way kangaroo density and total kangaroo population fluctuate over the time of the survey?

   _____

   _____

   _____

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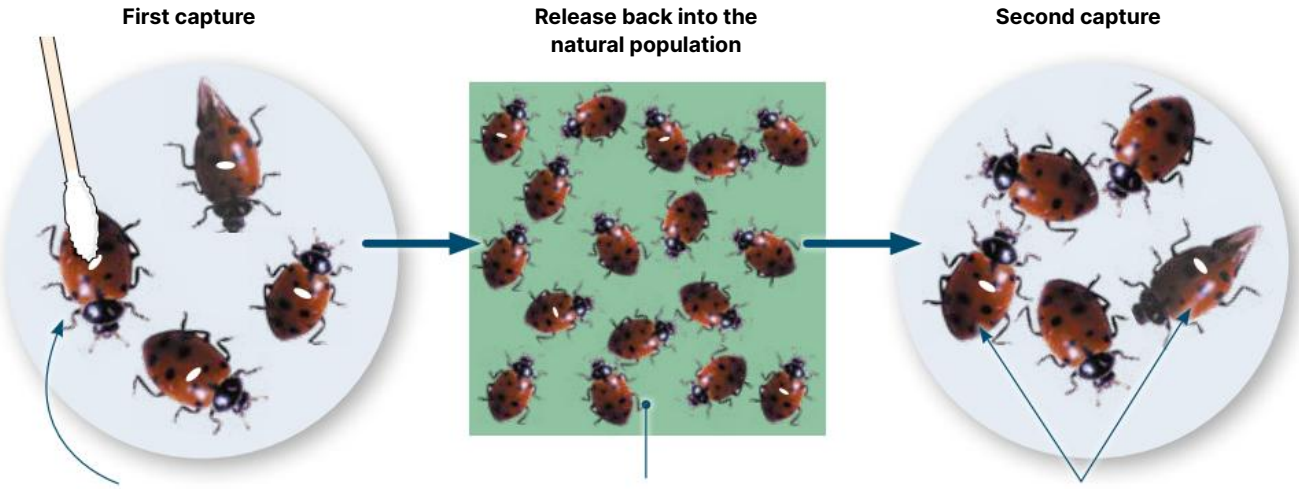
36 Estimating Population Size

Key Idea: Mark and recapture sampling enables estimates of the population size of highly mobile organisms.

The mark and recapture method of estimating **population** size is used in the study of animal populations in which the individuals are highly mobile. It is of no value where animals do not move or move very little. The number of animals caught in each sample must be large enough to be valid. The technique is outlined in the diagram below. The population of a surveyed area can be estimated using the **Lincoln Index**, a statistical measure of population size.



In the first capture, a random sample of animals from the population is selected. Each selected animal is marked in a distinctive way.

The marked animals from the first capture are released back into the natural population and left for a period of time to mix with the unmarked individuals.

Only a proportion of the second capture sample will have animals that were marked in the previous capture.

The Lincoln Index

$$\text{Total population (N)} = \frac{\text{Number in 1st sample (all marked) (M)} \times \text{Number in 2nd sample (n)}}{\text{Number of marked individuals recaptured in 2nd sample (m)}}$$

Steps in the mark and recapture technique:

1. Sample the population by capturing as many individuals as possible and practical. Capture technique will depend on the animal.
2. Mark the captured animals to distinguish them from unmarked animals.
3. Return the marked animals to their habitat and leave them for an extended period to allow them to redistribute themselves in the population.
4. Sample the population again (the sample must be large enough to provide valid data but the sample size can be different to the first).
5. Determine the numbers of marked to unmarked animals in the second sample. Use the equation above to estimate the population size.

1. For this exercise you will need several boxes of matches and a pen. Work in a group of 2-3 students to 'sample' the population of matches in the full box by using the mark and recapture method. Each match will represent one animal.

   (a) Take out 10 matches from the box and mark them on 4 sides with a pen so that you will be able to recognise them from the other unmarked matches later.
   (b) Return the marked matches to the box and shake the box to mix the matches.
   (c) Take a sample of 20 matches from the same box and record the number of marked matches and unmarked matches.
   (d) Determine the total population size by using the equation above.
   (e) Repeat the sampling 4 more times (steps b–d above) and record your results:

	Sample 1	Sample 2	Sample 3	Sample 4	Sample 5
Estimated population					

   (f) Count the actual number of matches in the matchbox: _____

   (g) Compare the actual number to your estimates and state by how much it differs: _____

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Researchers at New Zealand's University of Waikato used mark and recapture to obtain estimates of population number and biomass of four fish species and one hybrid in one of the campus lakes. Fish were sampled using electrofishing (right), which temporarily stuns the fish so that they can be netted. Biomass estimates for each species were calculated from mean mass of all fish sampled in the recapture.

Fish were marked with a fin clip (tagging carries a higher risk of infection at the tagging site). Resampling period was 7 weeks (22 January 2014-14 March 2014). The purpose of recapture was to remove pest species (all species except shortfin eels).

Each of the campus lakes is isolated with no inflow or outflow.

Results are presented in the table below:

Electrofishing, campus lakes, University of Waikato NZ

Prof. Brendan Hicks, UOW

Species	Number originally marked (M)	Number caught in recapture (n)	Number of marked recaptures (m)	Population estimate (N = M x n / m)	Mean fish mass (g)	Biomass (kg)	Lake area (ha)	Biomass by area (kg per ha)
Goldfish	32	104	14		365		0.69	
Koi carp-goldfish hybrids	6	9	3		1020		0.69	
Koi carp	9	35	2		114		0.69	
Catfish	7	33	2		303		0.69	
Shortfin eels	45	12	1		189		0.69	

2. (a) Complete the columns in the table above for population estimate, biomass, and biomass by area (kg per hectare).

   (b) What is the significance of the lake being isolated in terms of the reliability of the mark-recapture estimates?

   _____

   _____

   (c) Why is it useful to make biomass estimates for the fish in this lake, especially when the pest fish are being removed:

   _____

   _____

3. Describe some of the problems with the mark and recapture method if the second sampling is:

   (a) Left too long a time before being repeated: _____

   _____

   _____

   (b) Too soon after the first sampling: _____

   _____

   _____

4. Describe two important assumptions in this sampling method that would cause the method to fail if they were not true:

   (a) _____

   _____

   (b) _____

   _____

5. Some types of animal would be unsuitable for this method of population estimation (i.e. would not work).

   (a) Name an animal for which this method of sampling would not be effective: _____

   (b) Explain your answer above: _____

   _____

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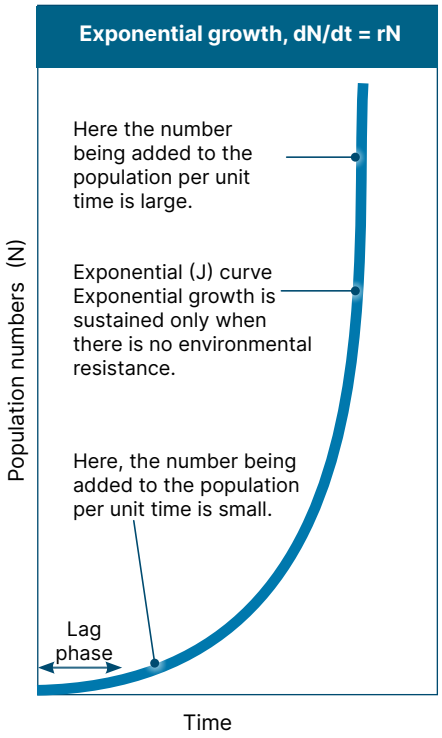
37 Patterns of Population Growth

Key Idea: Populations typically show either exponential or logistic growth. The maximum sustainable population size is limited by the environment's carrying capacity.

Population growth is the change in a population's numbers over time (dN/dt or ΔN/Δt). It is regulated by the **carrying capacity** (K), which is the maximum number the environment can sustain. Population growth falls into two main types: exponential or logistic. Both can be defined mathematically. In these mathematical models, the per capita (or intrinsic) growth rate is denoted by a lower case *r*, determined by the per capita births minus deaths, i.e. (B-D)/N. **Exponential growth** occurs when resources are essentially unlimited. **Logistic growth** begins exponentially, but slows as the **population** approaches environmental carrying capacity.

Exponential growth occurs when the population growth rate is not affected by the population size, N. In this case, the population growth rate is simply r (the maximum per capita rate of increase) multiplied by N so that dN/dt = rN. On a graph, exponential growth is characterized by a J shaped curve. A lag phase occurs early in population growth due to low population numbers.

In nature, exponential growth is observed in two circumstances: (1) a few individuals begin a new population in a new habitat with plenty of resources, (2) a natural disaster reduces the population to a few survivors, and the population recovers from a low base.



The human population is currently in an exponential phase of growth. In ancient times, the human population remained relatively stable, but low. It was not until the end of the Middle Ages and the beginning of the Renaissance that the population began to grow. The Industrial Revolution increased living standards and population with it. Antibiotics and the Green Revolution sparked the current rapid increase in the human population.

The kangaroo population in Australia (all kangaroos) fluctuates wildly over cycles lasting many years. In 1984, the total kangaroo population was estimated at 16 million. In 2015, it reached over 50 million. Droughts cause rapid collapse of the population, but it can recover almost as quickly afterwards. The data below shows the population increase after the last collapse of the population in 2003-2004.

Total kangaroo population (millions)	
Year	Population
2006	23.6
2007	24.0
2008	25.8
2009	27.0
2010	25.0
2011	34.3
2012	40.0
2013	53.0
2014	50.0

1. Produce a line graph of the kangaroo population on the grid above:
2. Around which year(s) did explosive exponential growth begin in the kangaroo population? _____
3. Use the data to calculate the approximate doubling time of the kangaroo population: _____
4. Why did the human population only begin its rapid increase after the Renaissance? _____

_____

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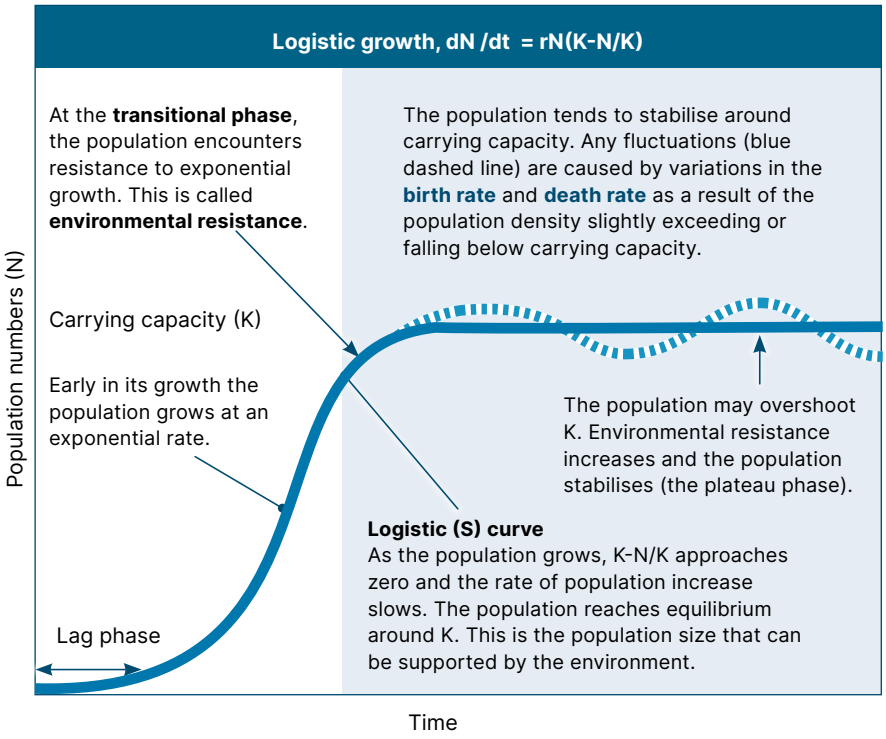
In nature, the population growth of most organisms follows a logistic growth curve. When entering a new environment, a founding population will enter a period of exponential growth. The maximum size of population that the environment can support is called the carrying capacity (K). As the population nears K and the resources become limiting, population growth slows.

Under the logistic growth model, dN/dt = rN is multiplied by the proportion of K that is left unfilled or unused. As the population increases, the proportion of K available decreases and individuals find it difficult to find or utilise space and resources. The rate of population increase therefore slows as population size approaches carrying capacity.

Occasionally a population's growth rate may not slow as it approaches K. This usually occurs in rapidly breeding organisms when there is a time lag between the depression in resources and the population response. In this case, the population overshoots K and then declines again as it responds to low resource availability. In time, populations usually stabilise around K.



Logistic growth curve on a spreadsheet.

Plotting a logistic growth curve on a spreadsheet can help in understanding the effect of population size on the population growth rate and how the logistic equation describes this. For a hypothetical population of 2, r is 0.15 and K 100. The following formulae can be entered into the spreadsheet:

	A	B	C	D	E	F	G
1	r	t (period)	N	K	K-N/K	dN/dt	
2	0.15	0	2	100	=($D$2-C2)/$D$2	=$A$2*C2*E2	
3		=B2+1	=C2+F2				
4							
5							
6							
7							
8							

Population at t_1 = population at t_0 + dN/dt (the amount of population change over 1 time period)

The cells can then be filled down. The first three steps have been filled here. Fill the cells down to about 60 time periods, then plot t vs N.

	A	B	C	D	E	F	G
1	r	t (period)	N	K	K-N/K	dN/dt	
2	0.15	0	2.00	100	0.98	0.29	
3		1	2.29		0.98	0.34	
4		2	2.63		0.97	0.38	
5		3	3.01				
6							
7							

5. Why don't populations continue to increase exponentially in an environment? _____

_____

6. How does carrying capacity act to slow the rate of population growth? _____

_____

_____

7. Describe and explain the phases of the logistic growth curve: _____

_____

_____

_____

8. (a) Around which time period does the curve on the spreadsheet above begin to flatten out? _____

(b) Describe how dN/dt changes over time: _____

_____

(c) What is the general shape of the logistic curve: _____

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38 Microbial Growth

Key Idea: Bacterial growth can be measured over time using a spectrophotometer. A plot of microbial growth in a closed system shows a characteristic growth curve.

Bacteria divide and increase their cell numbers by binary fission. Some bacterial species divide rapidly (every 20 minutes) while others can take days to divide. The increase in cell numbers can be measured in the laboratory with a spectrophotometer as an increase in culture turbidity (below). When in a closed system, microbial growth is described by a characteristic growth curve.

The aim

To investigate the growth rate of *E.coli* in two different liquid cultures, a minimal growth medium and a nutrient enriched complex growth medium.

The method

Using aseptic technique, the students added 0.2 mL of a pre-prepared *E.coli* culture to two test tubes. One test tube contained 5.0 mL of a minimal growth medium and the second contained 5.0 mL of a complex medium. Both samples were immediately mixed, and 0.2 mL samples removed from each and added to a cuvette. The absorbance of the sample was measured using a spectrophotometer at 660 nm. This was the 'time zero' reading. The test tubes were covered with parafilm, and placed in a 37°C water bath. Every 30 minutes, the test tubes were lightly shaken and 0.2 mL samples were taken from each so the absorbance could be measured. The results are presented in the table (right).

A spectrophotometer (left) is an instrument used to measure transmittance of a solution and so can be used to quantify bacterial growth where an increase in cell numbers results in an increase in turbidity.

In this experiment, students measured the absorbance of the solution. Absorbance measures the amount of light absorbed by the sample. Often, transmission (the amount of light that passes through a sample) is used to measure cell growth.

All bacteria should be treated as pathogenic and strict hygiene practices should be followed. These include wearing gloves, using aseptic techniques, not consuming food or drink in the laboratory, washing all surfaces with disinfectant afterwards, and hand washing.

Results

	Absorbance at 660 nm	
Incubation time / min	**Minimal medium**	**Complex medium**
0	0.021	0.014
30	0.022	0.015
60	0.025	0.019
90	0.034	0.033
120	0.051	0.065
150	0.078	0.124
180	0.118	0.238
210	0.179	0.460
240	0.273	0.698
270	0.420	0.910
300	0.598	1.070

1. Why is it important to follow strict hygiene precautions when working with bacteria?

_____

_____

_____

2. (a) On the grid (right) plot the results for *E.coli* growth on the two media:

(b) What is the absorbance measuring? _____

_____

(c) Describe the effect of the complex medium on *E.coli* growth:

_____

_____

_____

(d) What do you think might account for the difference in *E.coli* growth between the two media? _____

_____

_____

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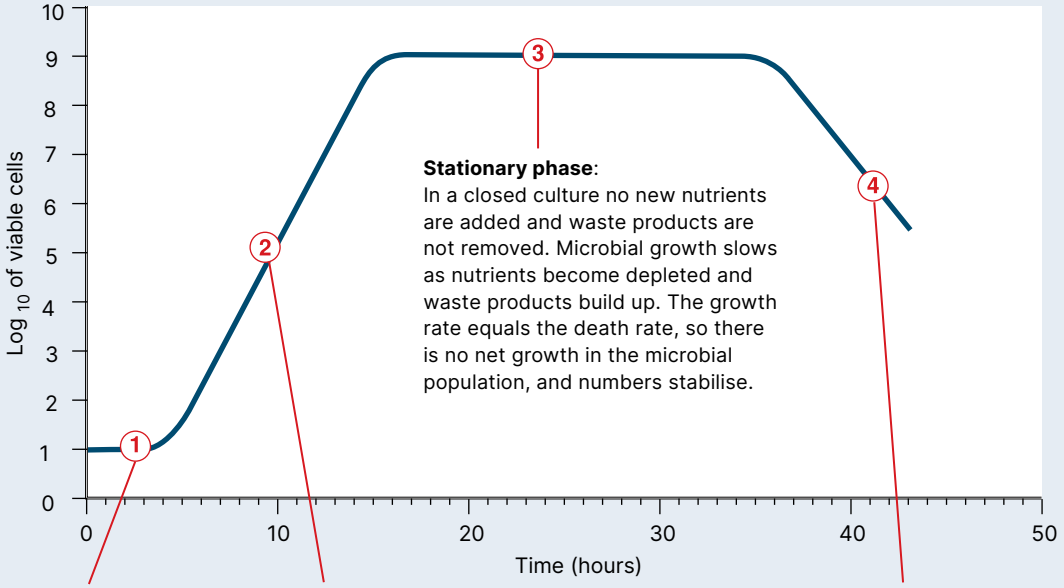
- When a **population** reaches the **carrying capacity** of an environment its growth rate slows to zero as deaths and **emigration** equal births and **immigration**. This reduction in growth is partially because resources are being replaced at the same rate they are being used, and there are no spare resources available to support further population increase. This is typical of an open system.
- In a closed system (such as a test tube or petri dish), resources are not replenished and there is no emigration or immigration. The population is therefore regulated only by birth and deaths and the rate of resource use. In such an environment, microbial populations exhibit a very specific pattern of growth consisting of four discrete phases (lag, log, stationary, and death phases).
- In the stationary phase, growth rate equals **death rate**. In this way, the stationary phase resembles the carrying capacity of an open environment. However, being a closed system, resources are not replenished and the population declines (deaths outnumber the production of new cells). A typical growth curve is shown below.

Typical microbial growth curve (closed system petri dish)



Lag phase:
Cells increase in size and synthesise enzymes, but there is little or no cell division. Cell numbers are relatively constant.

Log phase
The phase of **exponential growth**. In conditions optimal for microbial growth, the cells begin multiplying at an exponential rate, due to high metabolic activity and cellular reproduction. Cells are most vulnerable to adverse conditions and anti-microbial agents.

Death phase:
Microbial numbers decrease as the death rate exceeds growth rate. This is the result of a lack of essential nutrients and build up of toxic metabolites.

3. Why is there an initial lag in the growth of a microorganism placed into a new culture? _____

4. (a) Identify the phase where growth is fastest: _____

   (b) Explain why this growth rate cannot be maintained in a closed system: _____

   (c) How could the experimenters have maintained the population in the log phase? _____

5. What causes the death phase? _____

6. (a) What is the "carrying capacity" of the petri dish environment above? _____

   (b) What is the difference between the stationary phase and carrying capacity: _____

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39 Modelling Microbial Growth

Key Idea: Population growth can be studied using an organism that reproduces quickly in laboratory conditions.

Yeasts are unicellular fungi commonly used in baking and brewing. Yeast can reproduce rapidly in warm environments by asexual reproduction. New cells bud off old cells. A small **population** of cells can quickly lead to a large population. In this practical, you will make a yeast solution and count and record the population growth over time.

Investigation 3.1 Modelling yeast growth

See appendix for equipment list.

1. You will model the population growth of yeast cells over the course of 2-3 days (depending on lab time).
2. To a 500 mL beaker, add a tablespoon (about 10g) of sugar to 300 mL of tap water at room temperature. Stir until the sugar is dissolved.
3. Add 2.5g (about half a teaspoon) of baker's yeast and stir gently.
4. Using a pipette, remove 1 drop of the solution from the middle of the beaker.
5. Place the drop on a microscope slide and cover with a coverslip.
6. Focus the microscope on low power (10x) and then on high power (40x).
7. Count the number of yeast cells you can see and record. Carefully move the view to another section of the slide and again count and record the number of cells you can see. Do this two more times. Calculate and record the average number of cells. In a logbook, create a table for recording the time and average number of yeast cells counted. Make sure you record the amount of time (in hours) elapsed since the experiment started every time you count the number of yeast cells.
8. Cover the beaker with a petri dish or similar to prevent anything further entering the dish. It does not need to be air tight. Place the beaker in a dark place where the temperature is relatively stable (the temperature will not rise above about 40°C or fall below 15°C).
9. After 1 hour (earlier if the lesson is shorter), repeat steps 4-7. Stir the yeast solution gently to ensure the cells are evenly dispersed before taking a sample.
10. Repeat sampling and counting as often as possible over the course of three days. Every 2-3 hours is best.
11. If there are too many cells to count, you can dilute your sample in the following way. Remove one drop of yeast solution and place in a test tube. Add one drop of distilled water and mix. Remove one drop and place on the microscope for counting. This has diluted the solution by half, so make sure you multiply your counts by two (if you dilute by three times, multiply your counts by three, etc).
12. Once you have gathered your data, use a spreadsheet, e.g. Excel, to graph the average cell count vs time. Produce a linear and a logarithmic plot of the data. Print them out and attach to this page.

1. How did the yeast population develop over the time of the experiment? Was there exponential or logistic growth?

2. Explain the population growth you saw:

3. How might the population growth have differed if the sugar in the original solution was increased?

4. How might the population growth have differed if the sugar in the solution was replenished every day of the experiment?

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40 Modelling Population Growth

Key Idea: Computer programs can be used to model population growth. This activity uses Populus 6.0.

Population growth can be simulated using spreadsheets or computer programs. This activity uses Populus 6.0, a Javascript program, which will run on Mac or Windows platforms. It models continuous and discrete population growth as well as the effects of competition. In this activity you will model continuous density-independent (exponential) and density-dependent (logistic) growth. Using Populus, you can also model discrete growth, which uses λ instead of *r*, where λ is the discrete-time per capita growth rate. Discrete models are used for organisms with a discrete breeding season (e.g. annual plants and insects that breed once a year) because population growth occurs in 'steps' only within a discrete time period (not continuously) and there is no population growth outside those times.

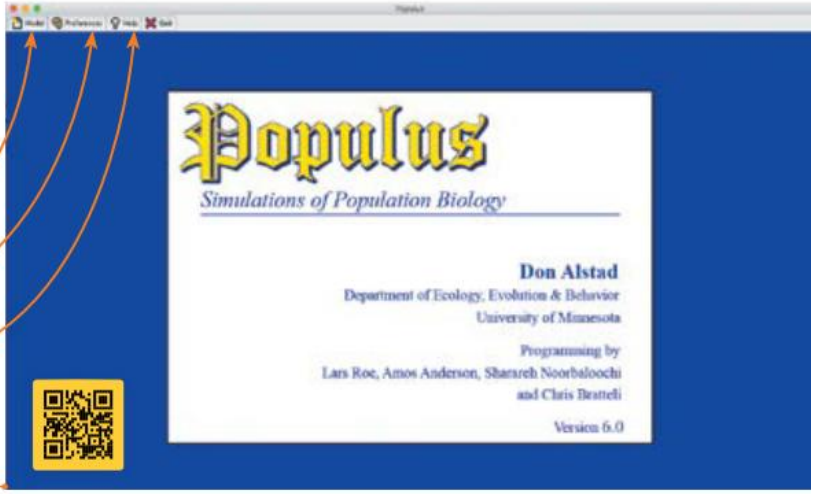
Populus is shareware. Download it free using the QR code on this page (right). Read the download instructions carefully. You may have to install Java.

You can also download via **BIOZONE's Resource Hub**.

The opening screen looks like this.

- **Model** allows you to choose which type of simulation you want to run.
- **Preferences** lets you to load saved files and save new ones.
- **Help** loads a comprehensive PDF file covering all aspects of the program.

If it fills the entire screen, grab the lower corner and resize it with the mouse.

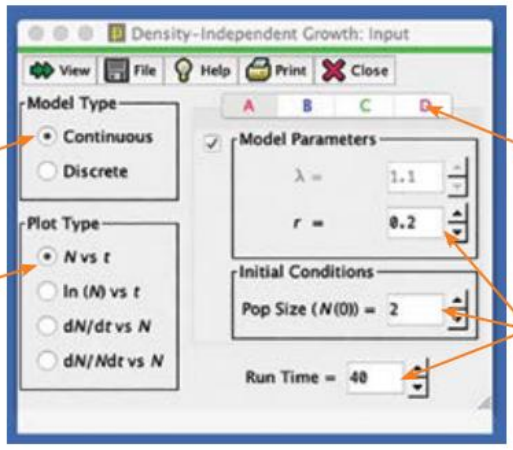


Density independent growth

- Click on the Model in the menu bar
- Select Single-Species Dynamics
- Then choose **Density-Independent** Growth

Set the model type to continuous (as in continuous growth). This produces a single line in the output window. Discrete produces a series of points (as in discrete bursts of growth).

Set plot type to N vs t. This models population vs time.



Up to four populations can be displayed on the one graph, using A, B, C, and D. Make sure the check box is ticked.

Set r to 0.2 and population size N to 2. Set run time 40. Click View to see the graph.

Questions 1-4 refer to density independent growth

1. What is the shape of the graph produced? _____

2. Describe what happens to the shape of the graph when:

   (a) *r* is increased to 0.4: _____

   _____

   (b) Population size is increased to 20: _____

   _____

   (c) Population size is increased to 20 but *r* is reduced to -0.2: _____

   _____

3. Set the parameters back to N = 2 and *r* = 0.2. Set the plot type to dN/dt vs N and view the plot. Describe the shape of the graph and explain what it means:

   _____

   _____

4. What is the value of *r* if the population doubles over one time period? _____

SAVE AND PRINT ALL YOUR SIMULATIONS AND ATTACH THEM TO THIS PAGE

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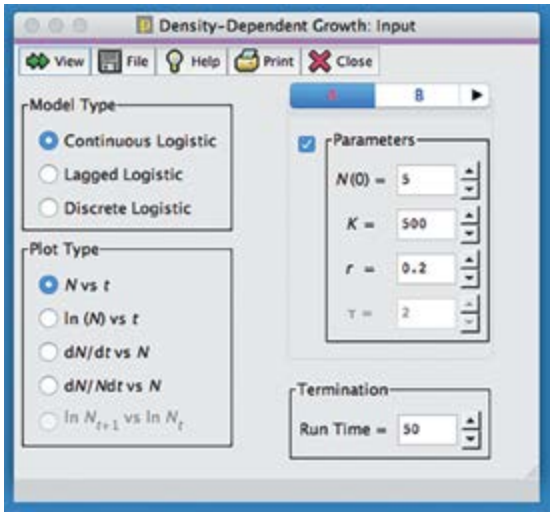
Density dependent growth

- Click on the Model in the menu bar
- Then select Single-Species Dynamics
- Then select **Density-Dependent Growth**

- As before set the model type to continuous.
- Produce a plot for N = 5, K = 500, r = 0.2, and t to 50.



Questions 5-9 refer to density dependent growth

5. Describe what happens to the shape of the graph when:

   (a) r is increased to 0.4: _____

   _____

   (b) Population size is increased to 50: _____

   _____

   (c) Reset the parameters and plot a graph of dN/dt vs N. Describe the shape of this graph and explain what it means:

   _____

   _____

   _____

6. The standard logistic growth curve assumes the effect of the population size immediately affects the population growth rate. Now set the graph type to Lagged Logistic. This introduces a time lag between the population size and its effect on growth rate. Set the parameters to N = 5, K = 500, r = 0.2, and t to 50. Set the time lag T to 4 and view the graph. What is the effect of the time lag on population growth?

   _____

   _____

   _____

7. (a) Now set r to 0.5 and t to 150. Describe the shape of the graph: _____

   _____

   (b) What kind of species (r-selected or K-selected) would show this type of growth? _____

8. (a) Keep T at 4 and set r to 0.2 view the graph. Describe the shape of the graph now: _____

   _____

   (b) What kind of species (r-selected or K-selected) would show this type of growth? _____

9. Keeping r at 0.2, vary T between 1 and 10. How does increasing the lag affect how the population oscillates around K?

   _____

   _____

   _____

   _____

   _____

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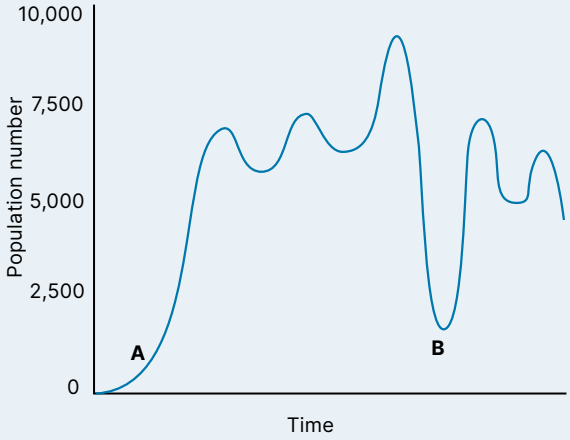
41 Did You Get It?

1. Study the graph of population growth for a hypothetical population below and answer the following questions:



(a) Estimate the carrying capacity of the environment:

_____

(b) What happened at point **A**?_____

_____

(c) What happened at point **B**? _____

_____

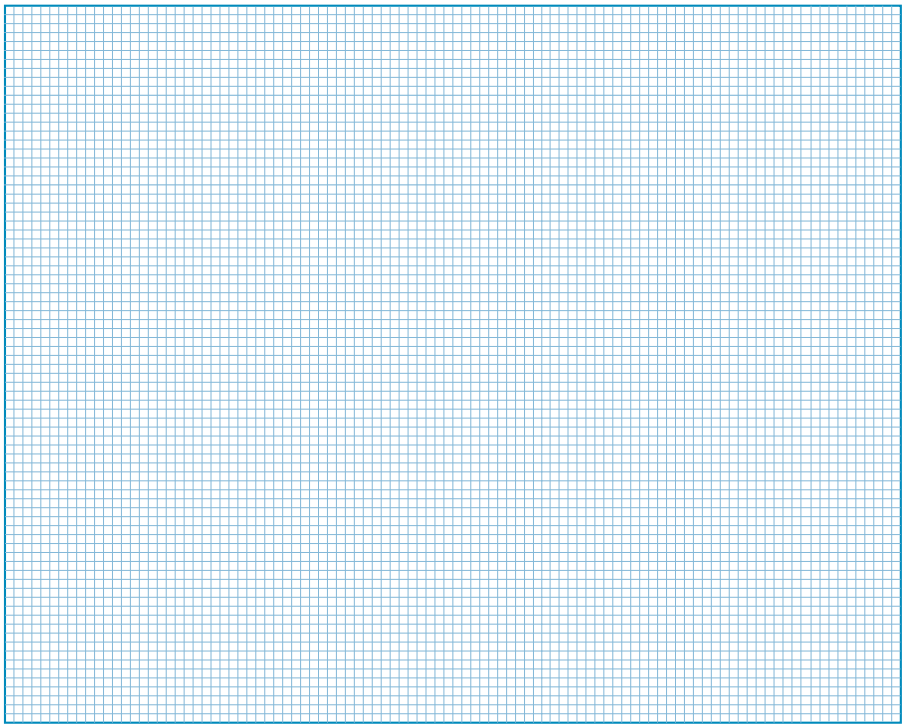
(d) What factors may have caused this?

_____

_____

2. (a) The global human population has grown rapidly since the discovery of antibiotics and advancements in food production. It is estimated that the human population will peak between 8.1 and 11 billion sometime around 2050, but there is little evidence of population growth slowing down. The data below shows the human population since 1850. Graph the data and comment on the shape of the curve:

Year	Population (billions)
1850	1.26
1900	1.65
1910	1.75
1920	1.86
1930	2.07
1940	2.30
1950	2.52
1960	3.01
1970	3.68
1980	4.44
1990	5.31
2000	6.12
2010	6.93
2018	7.60



_____

(b) What is the doubling time of the human population? _____

(c) The global human population shows almost perfect exponential growth since 1900 (R^2 value = 0.98) and follows the equation dN/dt = rN. Estimating our maximum population is difficult because humans tend to keep resetting K, the carrying capacity of our environment. Describe one way humans have done this and how this affects K:

_____

_____

_____

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42 Synoptic Questions: Unit 3, Topic 1

1. Use Specht's vegetation classification below to classify each of the Australian ecosystems pictured below. Describe the abiotic factors you would expect to be important in each system and how they might influence the vegetation:

	Percentage foliage cover of tallest plant layer			
Form and height of tallest stratum	**Dense (70-100%)**	**Mid-dense (30-70%)**	**Sparse (10-30%)**	**Very sparse (<10%)**
Trees > 30 m	Tall closed-forest	Tall open-forest	Tall woodland	Tall open-woodland
Trees 10-30 m	Closed-forest	Open-forest	Woodland	Open-woodland
Trees 5-10 m	Low closed-forest	Low open-forest	Low woodland	Low open-woodland
Shrubs 2-8 m	Closed-scrub	Open-scrub	Tall shrubland	Tall open-shrubland
Shrubs 0-2 m	Closed-heath	Open-heath	Low shrubland	Low open-shrubland

(a)

(b)

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2. The photo below shows a community of barnacles. What is the diversity of this community? What is the most expedient way of finding the number of species and individuals in the photo. Describe a method to find the biodiversity of this community.

3. Identify the two types of growth curve A and B below and give an example of the type of organism associated with each.

A: _____

B: _____

4. A group of students wanted find the population of fish in a small pond. In the first sample 10 fish were caught and tagged. The fish were released back into the pond. A week later the students carried out another sampling round. 15 fish were caught, 5 of which were marked. What is the population of fish in the pond?

5. A woodland population of birds is noted to be 95. Over the next 5 years chicks hatched and raised were recorded as 10, 12, 14, 9, 8 and deaths were recorded as 9, 12, 10, 16, 7. Net migration was recorded as +5 individuals over the 5 years. What is the average population growth rate per year?

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Chapter 4 Unit 3 Topic 2

Functioning Ecosystems

Resource Hub
bit.ly/3SfqxtB

Key Terms

- autotroph
- biomass
- carbon cycle
- cellular respiration
- competition
- competitive exclusion principle
- consumer (heterotroph)
- ecological niche
- ecological pyramid
- flagship species
- food chain
- food web
- gross primary production
- herbivore
- heterotroph
- hydrologic cycle
- interspecific competition
- keystone species
- net primary production
- nitrogen cycle
- omnivore
- photosynthesis
- predator
- producer (=autotroph)
- saprotroph (=decomposer)
- secondary production
- trophic level
- umbrella species

Key Concepts

- Energy from the Sun is stored through photosynthesis in the chemical bonds of carbon based molecules and is released by cellular respiration into the ecosystem via food chains.
- Matter is conserved and cycled through ecosystems via nutrient cycles including the hydrologic, carbon, and nitrogen cycles.
- Every species occupies an ecological niche. Species interactions impact niche breadth.
- Keystone species play critical roles in maintaining the health of an ecosystem.

Energy transfers and nutrient cycling in ecosystems		Activity Number
☐ 1	Sequence and explain the transfer and transformation of energy from the Sun into biomass as it flows through the biotic components of an ecosystem. Include reference to the role of photosynthesis and cellular respiration and how they interact in the cycling of carbon.	43, 44, 55
☐ 2	Describe energy transfer through ecosystems in food chains, food webs, or energy flow diagrams. Identify trophic levels including producers, primary consumers, and secondary and subsequent consumers. What limits the number of links in a food chain?	44, 46, 50
☐ 3	Analyse data and calculate energy transfers through ecosystems to include: • loss of energy through radiation, reflection, and absorption, • efficiencies of energy transfer from one trophic level to another, • biomass at successive trophic levels	46-51
☐ 4	Explain the shapes of ecological pyramids of number, biomass, and energy for different ecosystems. Use your knowledge of the efficiency of energy transfers to explain why pyramids of energy are never inverted.	45
☐ 5	Define the terms gross primary production, net primary production, and secondary production. Analyse data to determine trophic efficiency. Explain how productivity and efficiency are increased in managed monoculture (as opposed to natural) systems.	51, 52
☐ 6	Describe the transfer and transformation of matter as it cycles through ecosystems. Consider the cycling of carbon, nitrogen, and water. Include reference to the role of microorganisms in transformations.	53-56

Niche, competition, and keystone species		
☐ 7	Define niche in terms of an organism's functional role including its habitat, tolerance range, feeding relationships, and biotic interactions. Distinguish between the fundamental and realised niche of a species and explain how niche breadth is affected by competition.	57, 58
☐ 8	Explain what is meant by the competitive exclusion principle and what it means for the distribution of species with overlapping niches	57, 58
☐ 9	Analyse data to identify species occupying an ecological niche. Explain how species with similar resource requirements avoid direct competition through niche partitioning (e.g. in eucalypt woodland and coral reefs).	59-60
☐ 10	Explain species interactions including predation, competition, mutualism, commensalism and parasitism.	61
☐ 11	Using examples, explain the role of keystone species in the stability of community structure and function.	62
☐ 12	Analyse data from an Australian ecosystem to identify a keystone species and predict the outcomes of removing the species from an ecosystem.	63
☐ 13	**SI:** Investigate the competitive exclusion principle as displayed in vertical zonation of birds feeding in trees in a eucalypt forests.	59
☐ 14	**SI:** Investigate the effectiveness of conservation of single key species on ecosystem conservation.	64
☐ 15	**SHE:** Suggest why conserving keystone species might be a better conservation strategy than other strategies (such as conservation of flagship species).	64

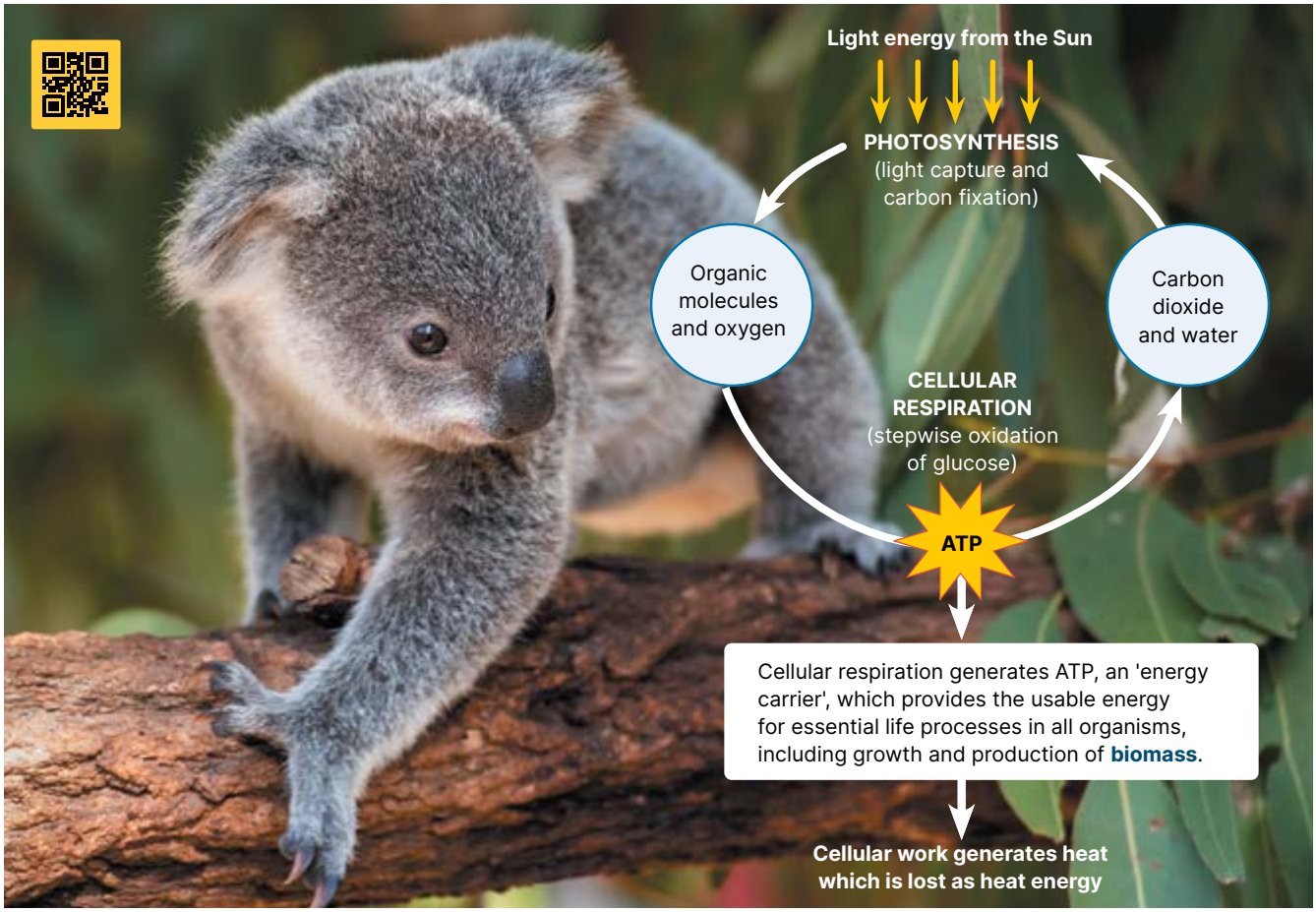
43 Energy in Ecosystems

Key Idea: Photosynthesis and cellular respiration provide most of the energy needed for life processes on Earth.

As matter and energy move through the biotic and abiotic environments on Earth, chemical elements are combined and recombined in different ways. Each transformation results in storage of energy and its dissipation into the environment as heat. Matter and energy are conserved at each transformation. The dissipation of energy as heat means that it is lost from the system, so ecosystems must receive a constant input of energy from an outside source to maintain their function. For most ecosystems on Earth, this source of energy is the Sun.

Where does the energy for life processes come from?

- **Photosynthesis** and **cellular respiration** provide most of the usable energy for life's essential processes such as metabolism and growth. Green plants and other photosynthetic organisms can fix atmospheric carbon using sunlight energy to produce their own food. We therefore call them **producers**. All other organisms rely on producers for their energy, so we call them **consumers**.
- A few systems (such as deep sea vents) rely on chemosynthetic organisms as producers. In chemosynthesis, bacteria produce food using chemicals as the energy source, rather than sunlight. However, these systems are not common.
  - The products of photosynthesis (glucose and oxygen) are used as the starting products in cellular respiration.
  - The waste products of cellular respiration (carbon dioxide and water) are used as the starting materials for photosynthesis.
  - Photosynthesis and cellular respiration are both central processes in the cycling of carbon.



1. Why do ecosystems need a constant input of energy from an external source? _____

_____

2. How do photosynthesis and cellular respiration interact to cycle matter through an ecosystem? _____

_____

_____

_____

_____

3. What is the role of ATP in biological systems? _____

_____

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44 Food Chains

Key Idea: A food chain is a model to illustrate the feeding relationships between organisms.

Organisms in ecosystems interact by way of their feeding (trophic) relationships. These interactions can be shown in a **food chain**, which is a simple model to illustrate how energy, in the form of food, passes from one organism to the next. Each organism in the chain is a food source for the next. The levels of a food chain are called **trophic levels**. An organism is assigned to a trophic level based on its position in the food chain. Organisms may occupy different trophic levels in different food chains or during different stages of their life. Arrows link the organisms in a food chain. The direction of the arrow shows the flow of energy through the trophic levels. Most food chains begin with a **producer**, which is eaten by a primary **consumer** (**herbivore**). Higher level consumers (carnivores and **omnivores**) eat other consumers.

Eucalypt woodland

Producers (**autotrophs**), e.g. plants, algae, and autotrophic bacteria, make their own food from simple inorganic substances, often by **photosynthesis** using energy from the sun. Inorganic nutrients are obtained from the abiotic environment, such as the soil and atmosphere.

Gang gang cockatoo

Consumers (**heterotrophs**), e.g. animals, get their energy from other organisms. Consumers are ranked according to the trophic level they occupy, i.e. 1st order, 2nd order, and classified according to diet, e.g. carnivores eat animal tissue, omnivores eat plant and animal tissue.

Millipede

Marshal Hedin CC 2.0

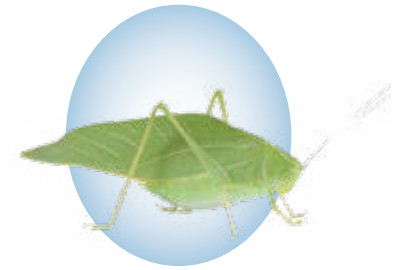
Detritivores and **saprotrophs** (decomposers) are consumers that obtain nutrients from dead organic matter (DOM). Detritivores, e.g. earthworms, millipedes, ingest DOM whereas saprotrophs (fungi, soil bacteria) secrete enzymes to digest DOM extracellularly and absorb the nutrients released.

The diagram below represents the basic elements of a food chain.

Respiration

Producers

Trophic level: 1



Primary consumers
Herbivores
Trophic level: 2

Secondary consumers
Omnivores & carnivores
Trophic level: 3

Tertiary consumers
Omnivores & carnivores
Trophic level: 4

Detritivores and saprotrophs

1. (a) What is the original energy source for this food chain? _____

   (b) Draw arrows on the diagram above to show how the energy flows through the organisms in the food chain. Label each arrow with the process involved in the energy transfer. Draw arrows to show how energy is lost by respiration.

2. Describe how the following obtain their energy:

   (a) Producers: _____

   (b) Consumers: _____

   (c) Detritivores: _____

   (d) Saprotrophs: _____

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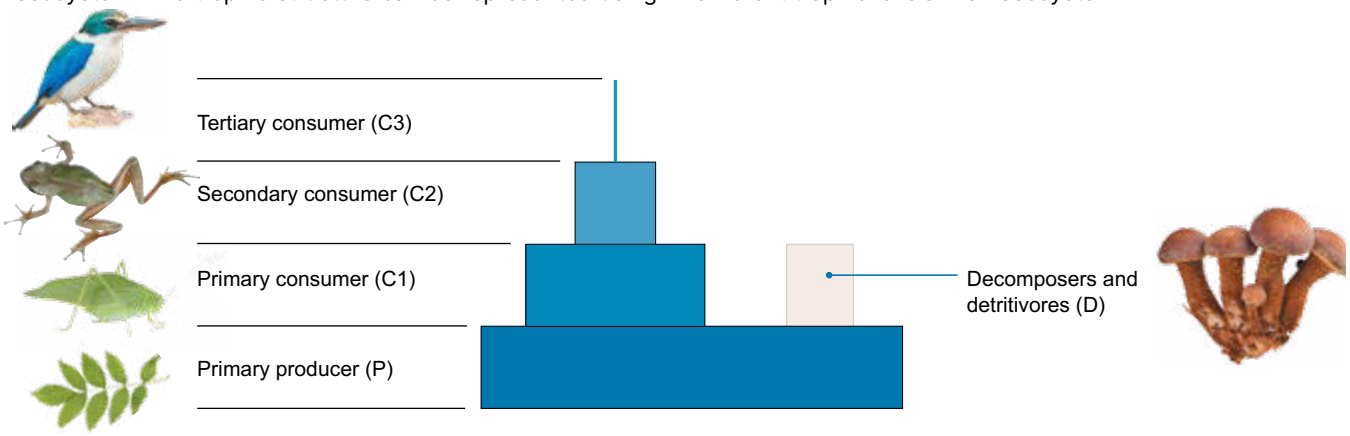
45 Ecological Pyramids

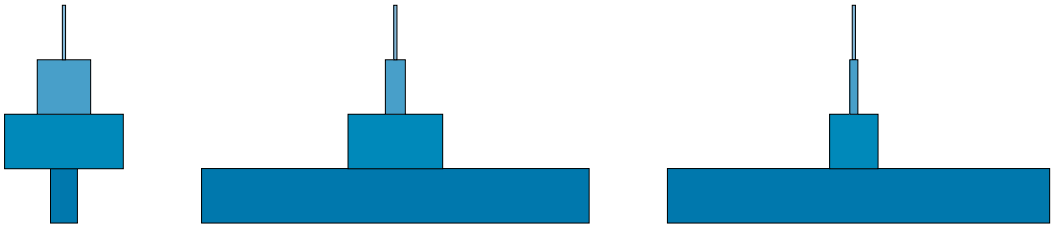
Key Idea: Ecological pyramids provide a quantitative representation of the trophic structure of an ecosystem. They can show number, energy, or biomass.

Ecological pyramids are graphical models showing the quantitative differences between **trophic levels** in an ecosystem. The trophic structure can be represented using energy, **biomass**, or numbers of organisms at each trophic level. The first trophic level is placed at the bottom of the pyramid and subsequent trophic levels are stacked on top in their 'feeding sequence'. Ecological pyramids provide a convenient quantitative model for the relationship between different trophic levels in an ecosystem.



- The generalised ecological pyramid pictured above shows a conventional pyramid shape, with a large number (or biomass) of **producers** forming the base for an increasingly smaller number (or biomass) of **consumers**.
- Decomposers are placed at the level of the primary consumers and off to the side. They may obtain energy from many different trophic levels and so do not fit into the conventional pyramid structure.
- For any particular ecosystem at any one time (e.g. the forest ecosystem below), the shape of this typical pyramid can vary greatly depending on whether the trophic relationships are expressed as numbers, biomass, or energy.

C3 Weasels
C2 Birds
C1 Insects
P Trees



Numbers in a forest community

Pyramids of numbers display the number of individual organisms at each trophic level. Pyramids of numbers can be a pyramid shape or they can sometimes be inverted (above) if a small number of large organisms (e.g. trees) support the next trophic level.

Biomass in a forest community

Biomass pyramids measure the mass of biological material at each trophic level. Water content of organisms varies, so 'dry mass' is often used. Organism size is taken into account, allowing meaningful comparisons of different trophic levels.

Energy in a forest community

Pyramids of energy are often very similar to biomass pyramids. The energy content at each trophic level is generally comparable to the biomass (i.e. similar amounts of dry biomass tend to have about the same energy content).

1. How do ecological pyramids provide a quantitative model of trophic structure in an ecosystem?

2. What is the advantage of using a biomass or energy pyramid rather than a pyramid of numbers to express the relationship between different trophic levels?

3. Explain why a pyramid of numbers can be inverted but a pyramid of energy can never be :

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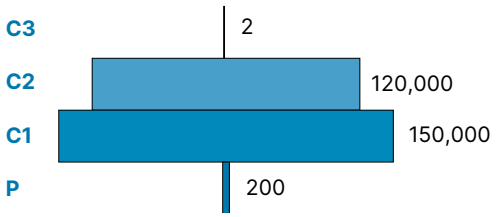
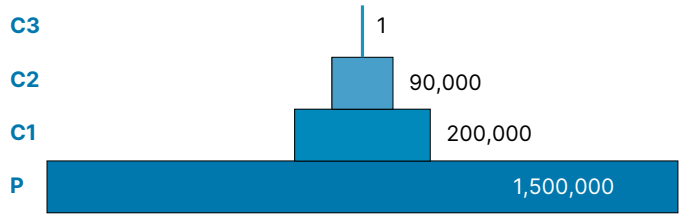


Pyramid of numbers: forest community

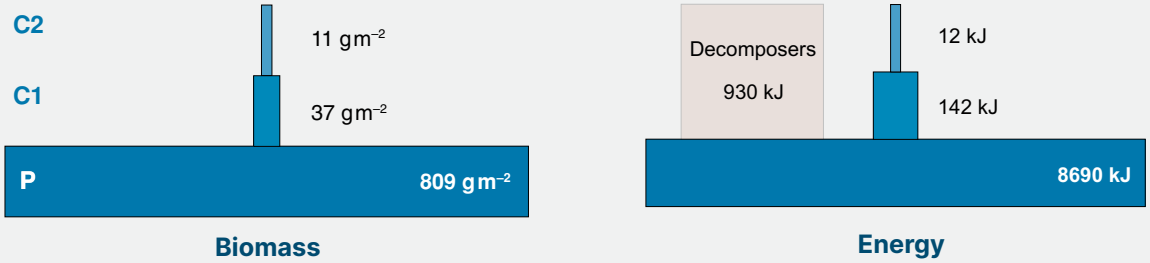
In a forest community, a few producers may support a large number of consumers. This is due to the large size of the producers: large trees can support many individual consumer organisms. The example above shows the numbers at each trophic level for an oak forest in England, in an area of 10 m^2.



Pyramid of numbers: grassland community

In a grassland community, a large number of (small) producers support a much smaller number of consumers. Grass plants can support only a few individual **consumer** organisms and take time to recover from grazing pressure. The example above shows the numbers at each trophic level for a derelict grassland area (10 m^2) in Michigan, United States.

Pyramids for a plankton community



- The two pyramids shown here relate to the same plankton community. The pyramids of biomass and energy are virtually identical.
- A large biomass of producers supports a smaller biomass of consumers. The energy at each trophic level is reduced with each progressive stage in the **food chain**. As a general rule, a maximum of 10% of the energy is passed on to the next level in the food chain. The remaining energy is lost due to respiration, waste, and heat.

4. Determine the energy transfer between trophic levels in the plankton community example in the above diagram:

   (a) Between producers and the primary consumers: _____

   (b) Between the primary consumers and the secondary consumers: _____

   (c) Why is the amount of energy transferred from the producer level to primary consumers considerably less than the approximate 10% that commonly occurs in many other communities?

   _____

   _____

   (d) After the producers, which trophic group has the greatest energy content? _____

   (e) Give a likely explanation why this is the case: _____

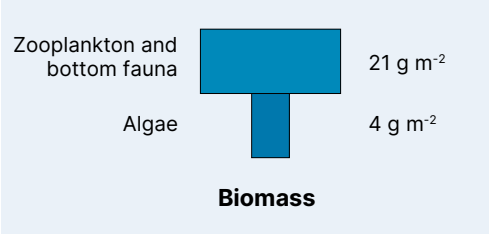
   _____

   _____

   _____

An unusual biomass pyramid

The biomass pyramids of some ecosystems appear rather unusual, with an inverted shape. The first trophic level has a lower biomass than the second level. What this pyramid does not show is the rate at which the producers (algae) are reproducing in order to support the larger biomass of consumers.



5. Give a possible explanation of how a small biomass of producers (algae) can support a larger biomass of consumers (zooplankton):

   _____

   _____

   _____

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46 Food Webs

Key Idea: A food web shows how the food chains of a community are interconnected. The complexity of a food web depends on the number of organisms, food chains, and trophic levels present.

In any community, no species exists independently of others. All organisms, dead or alive, are potential sources of food for other organisms. Within a community, there are hundreds of feeding relationships, and most species participate in several **food chains**. The different food chains in an ecosystem tend to form **food webs**, a complex series of interactions showing the feeding relationships between the organisms in an ecosystem. A food web model (below) can be used to show the trophic linkages between different organisms in a community and can be applied to any ecosystem.

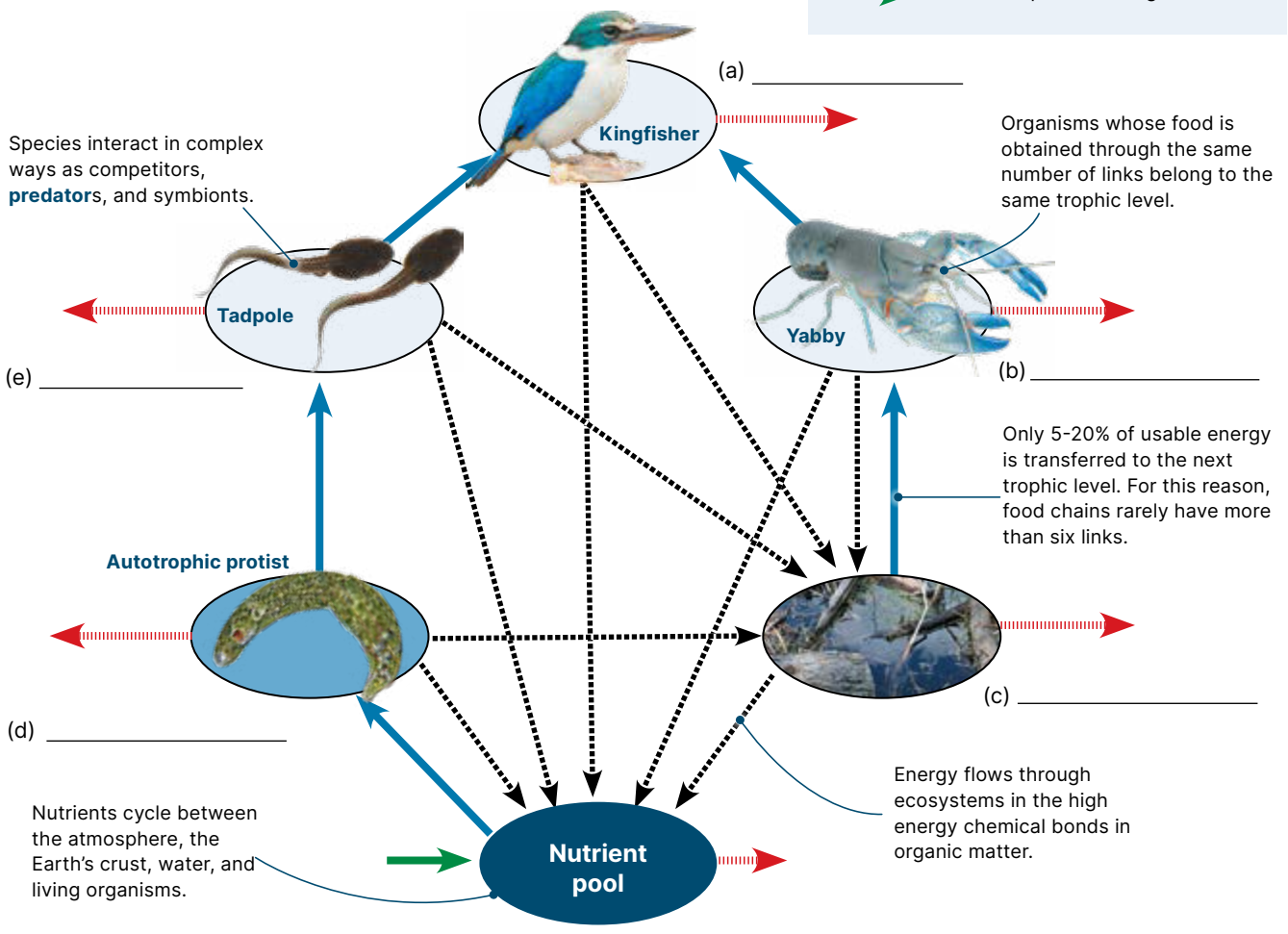
The complexity of food webs varies

The complexity of feeding relationships in a community contributes to its structure and specific features. A simple community, like those that establish on bare soil after a landslide, will have a simpler web of feeding relationships than a mature forest.

Key to food web (below)

- Flow of nutrients from the living components to detritus or the nutrient pool.
- Consumer–resource interactions.
- Losses of energy/**biomass** from the system.
- External input of limiting nutrients.

A simple food web



1. (a) - (e) Complete the food web above by adding the labels: carnivore, herbivore, autotroph, detritus, detritivore.
2. Why would a newly established community have a much simpler food web than a more established mature community?

_____

_____

3. In what way are different communities and different ecosystems linked? _____

_____

_____

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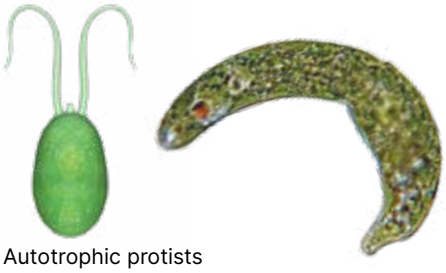
47 Constructing a Food Web

Key Idea: The many food chains in a community can be organised into food webs to show the feeding interactions.

A **food web** depicts the interconnected **food chains** in an ecosystem. For the lake community below, the organisms can be assembled into a food web to illustrate their trophic interactions. Remember that species are assigned to **trophic levels** on the basis of what they eat, with the first trophic level (the **producers**), ultimately supporting all other levels. **Consumers** are ranked according to the trophic level they occupy, although some may feed at several different trophic levels. For this example, the detritus that settles to the lake bottom (accumulated dead organic matter) has been omitted, but it provides a rich source of nutrients for many organisms, including yabbies and ducks.

Feeding requirements of lake organisms

Daphnia (*Daphnia* spp.)
Small freshwater crustacean that forms part of the zooplankton. It feeds on planktonic algae by filtering them from the water with its limbs.



Autotrophic protists
e.g. *Chlamydomonas* (left), *Euglena* (right)
Microscopic, autotrophic protists. Two of many species that form the phytoplankton.

Mallard duck (*Anas platyrhynchos*)
Feed mostly on water plants. Sifts fallen seed, aquatic plants and small animals from the muddy margins of the lake.

Yabby (*Cherax destructor*)
These freshwater crayfish filter water to extract zooplankton (*Daphnia*), feed on macrophytes, and stir up detritus to scavenge from it.

Macrophytes (various species)
A variety of flowering aquatic plants are adapted for being submerged, free-floating, or growing at the lake margin.

Kingfisher (*Alcedo*)
Although not restricted to the lake community, kingfishers feed on small fish, yabbies, and tadpoles.

Diving beetle (*Dytiscus*)
Diving beetles (adults and larvae) feed on aquatic insect larvae and adult insects blown into the lake community.

NSW Dept Primary Industries

Brown trout (*Salmo trutta*)
Feed on zooplankton, freshwater crayfish, aquatic insect larvae, and insects blown into the water from the surrounding area.

Tadpole (immature frog, *Litoria* spp.)
Feed on algae and very small zooplankton. Adult frogs feed on terrestrial (land dwelling) invertebrates.

Silver perch (*Bidyanus bidyanus*)
Omnivorous, feeding on a range of invertebrates, including crustaceans, aquatic insects, and molluscs, but also some vegetation.

Mosquito larva (*Culex* spp.)
The larvae of most mosquito species, e.g. *Culex*, feed on planktonic algae and small protozoans before passing through a pupal stage and undergoing metamorphosis into adult mosquitoes.

Humans (*Homo sapiens*)
Humans most commonly exploit the lake community food sources by taking trout and yabbies. Traditionally, aboriginal populations have fed on yabbies and fish.

Pelican
(*Pelecanus conspicillatus*)
Pelicans feed on fish of varying sizes, including smaller trout and silver perch.

Platypus (*Ornithorhynchus anatinus*)
A nocturnal mammal that feeds on small vertebrates and invertebrates such as insects, molluscs, and worms.

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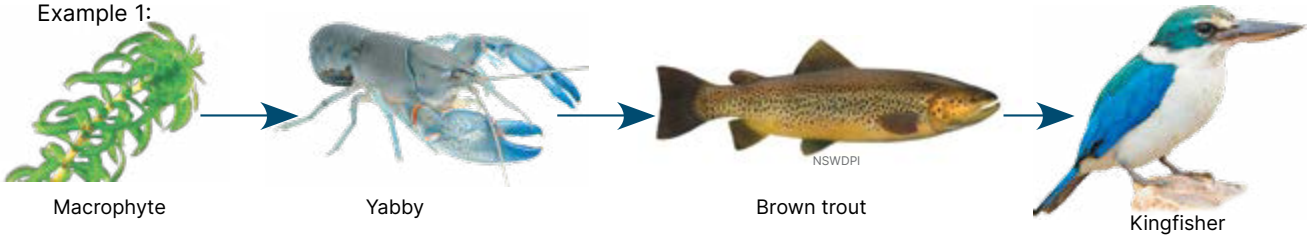
1. From the information provided for the lake food web components on the previous page, construct ten different food chains (using their names only) to show the feeding relationships between the organisms. Some food chains may be shorter than others and most species will appear in more than one food chain.
An example has been completed for you.

Example 1:



Macrophyte → Yabby → Brown trout → Kingfisher

(a) _____

(b) _____

(c) _____

(d) _____

(e) _____

(f) _____

(g) _____

(h) _____

(i) _____

(j) _____

2. (a) Use the food chains that you have created above to help you to draw up a complete food web for this community. Use only the supplied information to draw arrows showing the flow of energy between species. (NOTE: Only energy from (not to) the detritus is required)

(b) Label each species with the following codes to indicate its trophic group: Indicate:
- Diet type: **P** = Producer, **H** = Herbivore, **C** = Carnivore, **O** = Omnivore (Note: based on the information given).
- Position in the food chain as a consumer (1st, 2nd, 3rd, 4th order consumer): **1–4** (does not include producers).

Example: Mosquito larva is **H1**

Trophic level 5	Kingfisher	Pelican	Humans		Detritus
Trophic level 4	Trout	Silver perch		Platypus	
Trophic level 3	Tadpole	Diving beetle	Yabby	Duck	
Trophic level 2	*Daphnia*	Mosquito larva			
Trophic level 1	Autotrophic protists			Macrophytes	

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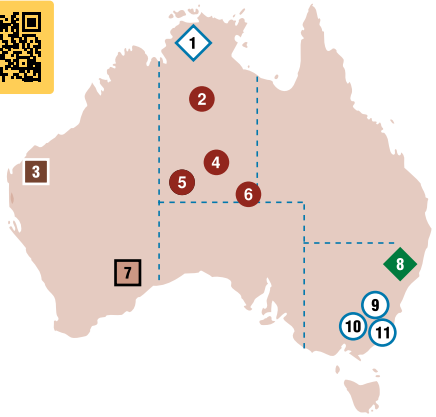
48 Dingo Food Webs

Key Idea: The habitats and trophic interactions of dingoes vary regionally, depending on the community composition.

Dingoes are widespread in Australia as top **predators**. Dingoes are members of different communities in different parts of Australia, and the **food webs** they are part of also vary regionally. Samples taken from six different locations (below) show how the prey taken by dingoes varies from one location to another.

RA

Despite the immense range of potential prey species across Australia, only ten species formed almost 80% of a dingo's diet. Dingoes are specialists, rather than generalists, with respect to dietary intake.



Location of sampling sites

1 Kakadu National Park
2 Barkley Tableland
3 Fortesque River
4 Harts Ranges
5 Eldunda
6 Simpson Desert
7 Nullarbor Plain
8 George's Creek Nature Reserve
9 Kosciusko National Park
10 Victorian Highlands
11 Nadgee Nature Reserve

The table below shows the diet of dingoes in six major Australian habitats. The numbers represent the percentage of stomachs or faeces that contained each prey species. A total of 12,802 stomachs and faeces were sampled over a 20 year period (1966-1986).

Wet-dry tropics North Australia	6722 faeces
Dusky rat	33.8
Magpie goose	32.5
Agile wallaby	15.1
Northern ringtailed possum	9.7
Grass species	7.1
Feral water buffalo	5.8
Feral pig	3.5
Unidentified matter	2.6
Antilopine wallaroo	1.8
Northern brown bandicoot	1.4
Feral cattle	1.3
Bird (undetermined species)	0.7
Insect (undetermined species)	0.7
Beetle	0.4

Arid & semi-arid central Australia	1480 stomachs
Rabbit	37.9
Cattle	23.3
Long-haired rat	17.6
Red kangaroo	10.2
Central netted dragon	7.8
Small mammal (undetermined sp.)	3.8
House mouse	3.6
Grasshopper	2.7
Bearded dragon	2.2
Zebra finch	2.1
Bird (undetermined species)	2.0
Feral cat	1.8
Galah	1.8
Budgerigar	1.5

Arid south-west Australia	131 faeces/ stomachs
Rabbit	63.4
Red kangaroo	32.1
Cattle	7.6
Red fox	3.8
Little crow	2.3
Bobtail skink	1.5
Feral cat	1.5
Centipede/millipede	0.8
Dingo	0.8
Grasshopper	0.8

Semi-arid north-west Australia	413 faeces/ stomachs
Red kangaroo/euro	80.6
Cattle	11.4
Sheep	8.0
Bird (undetermined species)	5.6
Reptile (undetermined species)	3.4
Insects (undetermined species)	2.9
Echidna	2.2
Dingo	1.7
Feral cat	0.5
Bat (undetermined species)	0.2
Fish (undetermined species)	0.2
Red fox	0.2
Rothschild's rock wallaby	0.2

Cool coastal mountains SE Australia	2063 faeces/ stomachs
Swamp wallaby	17.9
Wallaby (undetermined spp.)	15.8
Wombat	15.0
Animal remains (unidentified)	11.5
Rabbit	10.5
Common ringtail possum	8.0
Waterbird (undetermined sp.)	7.7
Red-neck wallaby	5.3
Possum (undetermined species)	5.1
Rat (undetermined species)	5.0
Little penguin	4.4
Fish (undetermined species)	3.7
Mutton bird	3.6
Echidna	3.3

Humid coastal mountains E Australia	1993 faeces
Swamp wallaby	30.5
Bush rat	12.2
Red-necked wallaby	11.1
Brushtail possums	6.9
Bandicoots (long-nosed, Southern brown)	6.8
Rabbit	6.4
Antichinuses (brown, dusky)	5.8
Parma wallaby	4.6
Common ringtail possum	4.4
Ring-necked pademelon	3.8
Echidna	3.5
Long-nosed potoroo	1.7
Greater glider	1.5

Adapted from: Corbett, L. 1995. The dingo in Australia and Asia, Appendix C: pp. 183-186. University of NSW Press

1. Sites 3 and 7 (above) yielded a small number of prey species in the samples taken. Suggest the likely reason for this:

2. Name three prey species taken by dingoes in the 'Cool coastal mountains, SE Australia' (sites 9, 10, and 11) that are restricted to that type of environment (i.e. not represented in the prey taken at other sites):

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3. What evidence is there from the data that dingoes engage in cannibalism? _____

_____

4. Which general kind of prey makes up most of the dingoes' diet? _____

5. At some sample sites, the dingoes' prey included domesticated animals.

   (a) Which prey items represent domesticated animals? _____

   (b) What kind of environmental conditions have encouraged dingoes to make these animals part of their diet?

   _____

6. (a) Which of the sample sites has the least reliable data for indicating the diet of dingoes in its area?

   _____

   (b) Explain your choice: _____

   _____

7. In this study, the diet of dingoes was determined by the sampling methods of examining large numbers of stomach contents and faeces.

   (a) Explain which of these two methods should prove the most reliable for positive identification of prey species:

   _____

   (b) Suggest two reasons why the researchers did not simply follow the dingoes and watch what they ate as a way of gathering dietary information on the dingoes:

   Reason 1: _____

   Reason 2: _____

8. Using the data on the previous page, choose one of the 'regional ecotypes' (e.g. wet-dry tropics, north Australia) and produce a food web in the space below. Use only the first **five positively identified** prey species (in most cases, do not include unidentified species). This activity will require you to carry out some research into what the prey species eat.

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49 Earth's Energy Budget

Key Idea: The Sun is the ultimate source of energy on Earth. Not all of the energy reaching Earth is retained. Some is radiated back into space.

The Sun ultimately provides all the energy required to power all life on Earth. The Sun produces tremendous amounts of energy (174 petawatts (PW) or 174 quadrillion joules per second). To put this in context, the world's most powerful lasers can produce power of 1.25 PW and only keep this up for one picosecond (1×10^{-12} seconds). Not all of the solar radiation reaching Earth is retained. Factors such as albedo and vegetation cover determine how much solar radiation is retained and how much is radiated back into space.

Energy is not evenly distributed on Earth

The energy from the Sun is not distributed evenly about the globe. Because the Earth is spherical, the poles receive less energy per square kilometre than the equator. The Earth's angle of rotation further influences the uneven distribution of the energy received.

Below the Arctic and Antarctic circles, the Earth receives only about 40% of the solar energy that is received at the equator. Ice has high albedo (it reflects a lot of light).

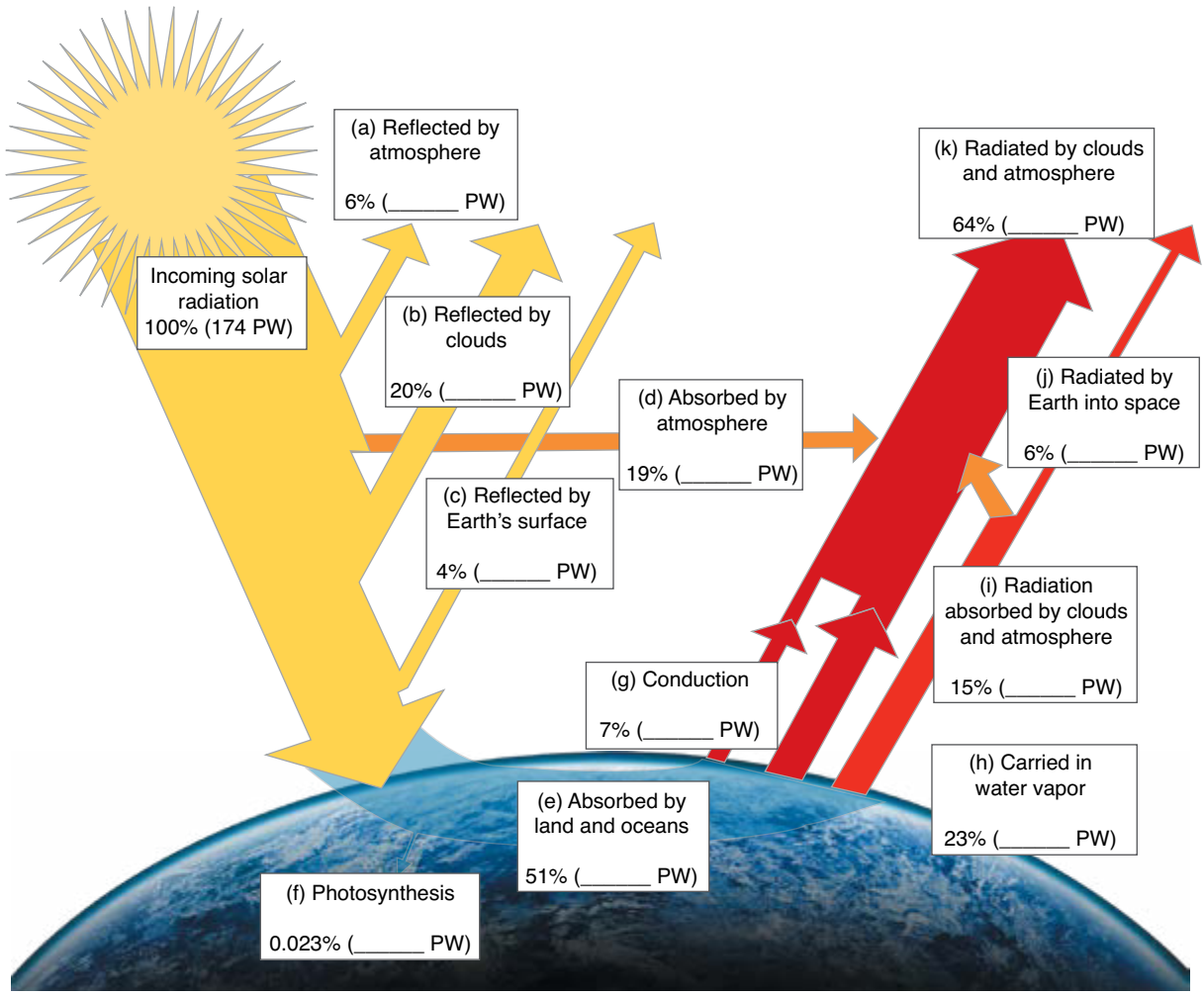
The tropics receive the full amount of sunlight and energy available. This causes heating, which carries water into the air, creating a hot, wet climate.

NASA

Differential heating between the tropics and poles drives air currents from the tropics towards the poles. This is because air rises at the equator and falls at the poles.

The diagram below represents a model of the Earth's energy budget. A large amount of incoming solar radiation is absorbed by the atmosphere or reflected off clouds or the Earth's surface. About 51% of the incoming solar radiation is absorbed by the Earth's surface. A small amount of this 51% (0.023%) is used by **photosynthesis** in plants to build organic molecules. The rest drives atmospheric winds and ocean circulation and is eventually radiated back into space.

1. Use the information provided to complete the calculations on the diagram below:



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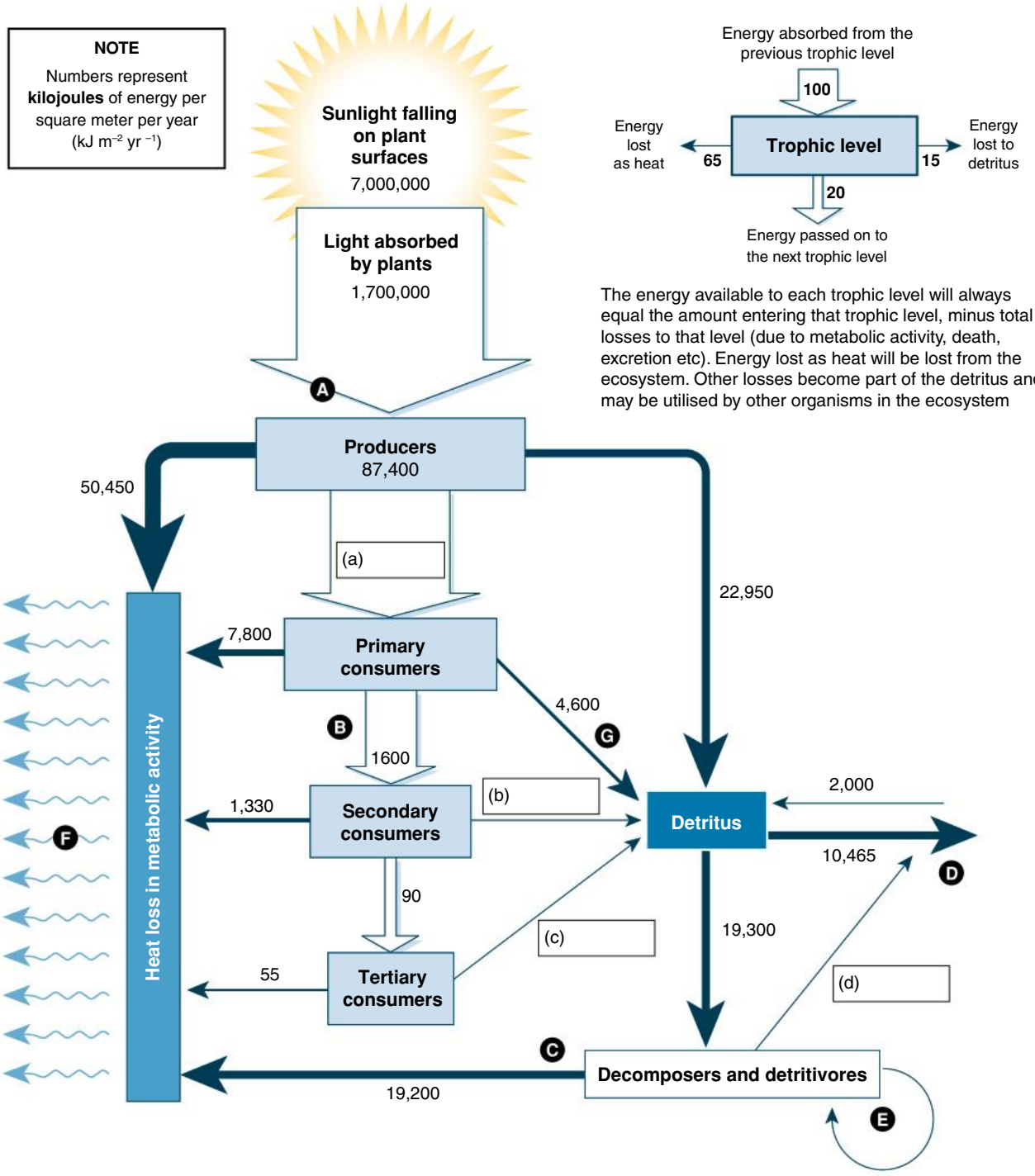
50 Quantifying Energy Flow in an Ecosystem

Key Idea: Chemical energy in the bonds of molecules flows through an ecosystem between trophic levels. Only 5-20% of energy is transferred from one trophic level to the next.

Energy cannot be created or destroyed, only transformed from one form (e.g. light energy) to another (e.g. chemical energy in the bonds of molecules). This means that the flow of energy through an ecosystem can be measured. Each time energy is transferred from one **trophic level** to the next (e.g. by eating), some energy is given out as heat to the environment, usually during **cellular respiration**. Living organisms cannot convert heat to other forms of energy, so the amount of energy available to one trophic level is always less than the amount at the previous level. Potentially, we can account for the transfer of energy from its input (as solar radiation) to its release as heat from organisms, because energy is conserved. The percentage of energy transferred from one trophic level to the next is the trophic efficiency. It varies between 5% and 20% and measures the efficiency of energy transfer. An average figure of 10% trophic efficiency is often used. This is called the ten percent rule.

Energy flow through an ecosystem



The energy available to each trophic level will always equal the amount entering that trophic level, minus total losses to that level (due to metabolic activity, death, excretion etc). Energy lost as heat will be lost from the ecosystem. Other losses become part of the detritus and may be utilised by other organisms in the ecosystem

1. Study the diagram above illustrating energy flow through a hypothetical ecosystem. Use the example at the top of the page as a guide to calculate the missing values (a)–(d) in the diagram. Note that the sum of the energy inputs always equals the sum of the energy outputs. Place your answers in the spaces provided on the diagram.

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2. What is the original source of energy for this ecosystem? _____

3. Identify the processes occurring at the points labelled A – G on the diagram:

   A. _____ E. _____

   B. _____ F. _____

   C. _____ G. _____

   D. _____

4. (a) Calculate the percentage of light energy falling on the plants that is absorbed at point **A**:

   Light absorbed by plants ÷ sunlight falling on plant surfaces x 100 = _____

   (b) What happens to the light energy that is not absorbed? _____

   _____

5. (a) Calculate the percentage of light energy absorbed that is actually converted (fixed) into producer energy:

   Producers ÷ light absorbed by plants x 100 = _____

   (b) How much light energy is absorbed but not fixed: _____

   (c) Account for the difference between the amount of energy absorbed and the amount actually fixed by producers:

   _____

   _____

6. Of the total amount of energy fixed by producers in this ecosystem (at point **A**) calculate:

   (a) The total amount that ended up as metabolic waste heat (in kJ): _____

   (b) The percentage of the energy fixed that ended up as waste heat: _____

7. (a) State the groups for which detritus is an energy source: _____

   (b) How could detritus be removed or added to an ecosystem? _____

   _____

8. Under certain conditions, decomposition rates can be very low or even zero, allowing detritus to accumulate:

   (a) From your knowledge of biological processes, what conditions might slow decomposition rates?

   _____

   (b) What are the consequences of this lack of decomposer activity to the energy flow? _____

   _____

   (c) Add an additional arrow to the diagram on the previous page to illustrate your answer.

   (d) Describe three examples of materials that have resulted from a lack of decomposer activity on detrital material:

   _____

   _____

   _____

9. The ten percent rule states that the total energy content of a trophic level in an ecosystem is only about one-tenth (or 10%) that of the preceding level. For each of the trophic levels in the diagram on the preceding page, determine the amount of energy passed on to the next trophic level as a percentage:

   (a) Producer to primary consumer: _____

   (b) Primary consumer to secondary consumer: _____

   (c) Secondary consumer to tertiary consumer: _____

   (d) Which of these transfers is the most efficient? _____

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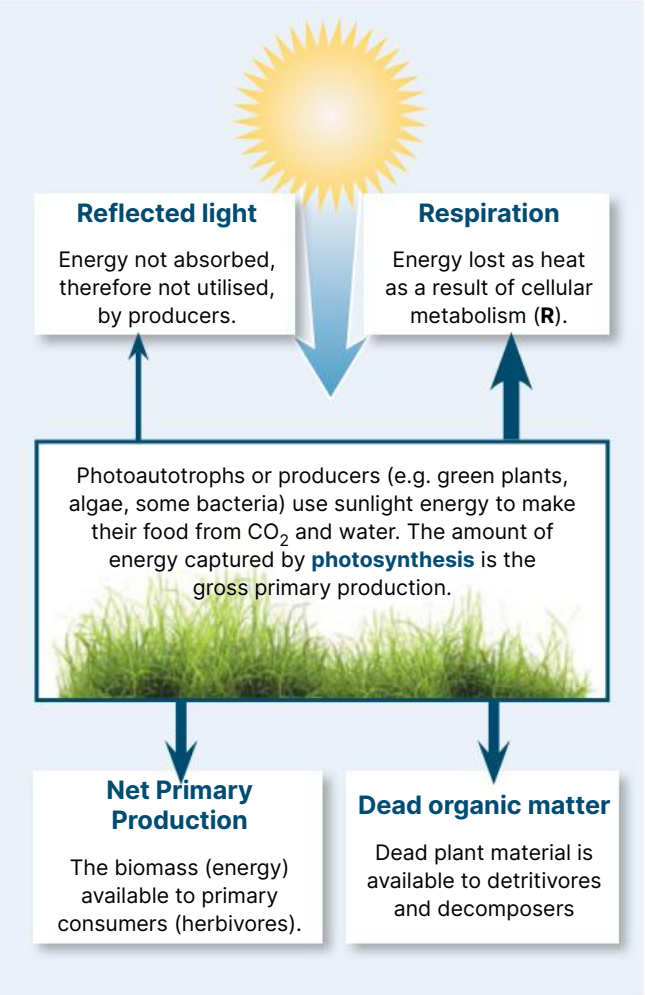
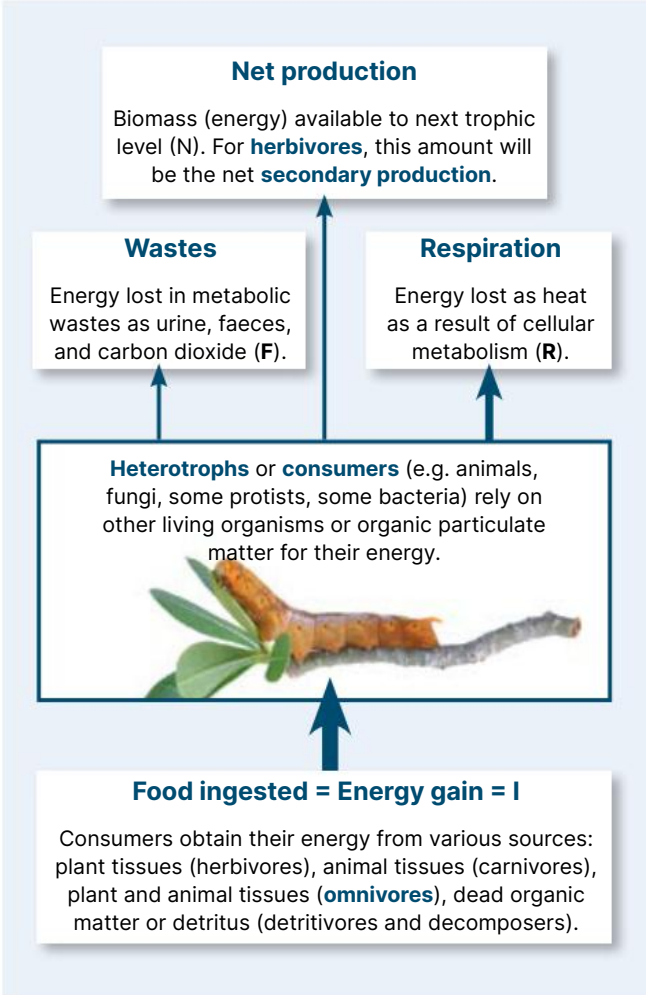
51 Productivity and Efficiency

Key Idea: The total amount of energy captured by photosynthesis is the gross primary production. Net primary production is the amount of energy available to herbivores after losses to respiration. The amount of biomass production is called the net primary productivity.

The **gross primary production** (GPP) of any ecosystem will depend on the capacity of the **producers** to capture light energy and fix carbon in organic compounds. The **net primary production** (NPP) is then determined by how much of the GPP goes into plant **biomass**, after the respiratory needs of the producers are met. This will be the amount available to the next **trophic level**.





1. (a) Explain the difference between gross and net primary production: _____

_____

_____

_____

(b) Write a simple word equation to show how NPP is derived from GPP: _____

_____

2. (a) Describe how energy may be lost from organisms in the form of:

(i) Wastes: _____

_____

(ii) Respiration: _____

_____

(b) Identify another process that prevents energy being available to producers: _____

_____

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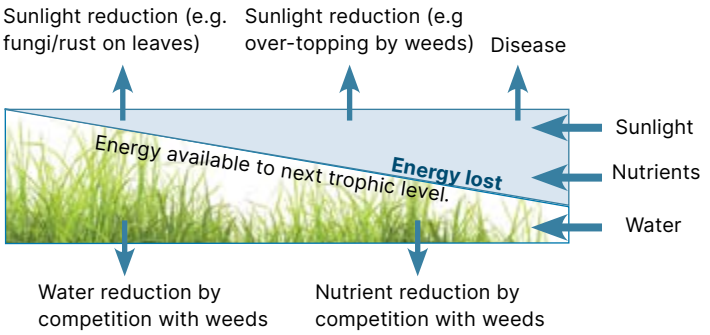
Productivity of ecosystems

- The energy entering ecosystems is fixed by producers at a rate that depends on limiting factors such as temperature and the availability of light, water, and nutrients such as nitrogen.
- This energy is converted to biomass by anabolic reactions. The rate of biomass production (net primary productivity), is the biomass produced per area per unit time.
- Recall that the trophic (ecological) efficiency refers to the efficiency of energy transfer from one trophic level to the next. The trophic efficiencies of **herbivores** vary widely, depending on how much of the producer biomass is consumed and assimilated (incorporated into new biomass). In some natural ecosystems this can be surprisingly high.
- Humans intervene in natural energy flows by simplifying systems and reducing the number of transfers occurring between trophic levels.

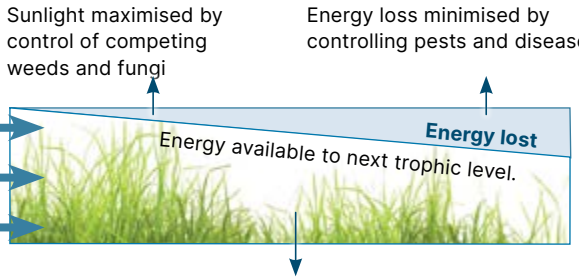
Agriculture and productivity

Increasing net productivity in agriculture (increasing yield) is a matter of manipulating and maximising energy flow through a reduced number of trophic levels. On a farm, the simplest way to increase the net primary productivity is to produce a monoculture (single crop). Monocultures reduce **competition** between the desirable crop and weed species, allowing crops to put more energy into biomass. Other agricultural practices designed to increase productivity in crops include fertiliser (e.g. nitrogen) application, pest (herbivore) control, and spraying to reduce disease. Higher productivity in feed-crops also allows greater secondary productivity (e.g. in livestock). Here, similar agricultural practices make sure the energy from feed-crops is efficiently assimilated by livestock.

1 Natural vegetation system



2 Managed monoculture system



3. (a) Compare the energy loss between the natural system and the monoculture system above: _____

_____

(b) Explain why managed monocultures can be more productive than a natural grassland: _____

_____

_____

_____

_____

(c) How is this higher productivity achieved? _____

_____

_____

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52 Investigating Trophic Efficiencies

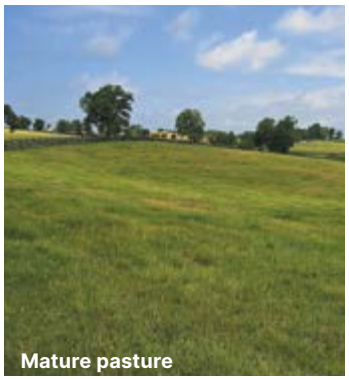
Key Idea: The efficiency of energy transfers in ecosystems can be quantified if we know the amount of energy entering and leaving the different trophic levels.

The **gross primary production** of any ecosystem will be determined by the efficiency with which solar energy is captured by **photosynthesis**. The efficiency of subsequent energy transfers will determine the amount of energy available to **consumers**. In this activity, you will calculate energy and **biomass** transfers in real and experimental systems. This will help you understand how energy transfers through **food chains** are quantified. You may wish to repeat part or all of the *B. rapa* experiment described as a practical.

Production vs productivity: what's the difference?

Strictly speaking, the primary production of an ecosystem is distinct from its productivity, which is the amount of production per unit time (a rate). However because values for production (accumulated biomass) are usually given for a certain period of time in order to be meaningful, the two terms are often used interchangeably.


Corn field


Mature pasture

1. The energy budgets of two agricultural systems (4000 m^2 area) were measured over a growing season of 100 days. The results are tabulated right.

	Corn field	Mature pasture
	kJ x 10^6	kJ x 10^6
Incident solar radiation	8548	1971
Plant utilisation		
Net primary production (NPP)	105.8	20.7
Respiration (R)	32.2	3.7
Gross primary production (GPP)	138.0	24.4

(a) For each system, calculate the percentage efficiency of energy utilisation (how much incident solar radiation is captured by photosynthesis):

Corn: _____

Mature pasture: _____

(b) For each system, calculate the percentage losses to respiration:

Corn: _____

Mature pasture: _____

(c) For each system, calculate the percentage efficiency of NPP:

Corn: _____

Mature pasture: _____

(d) Which system has the greatest efficiency of energy transfer to biomass? _____

Estimating NPP in *Brassica rapa*

Background

Brassica rapa (right) is a fast growing brassica species, which can complete its life cycle in as little as 40 days if growth conditions are favourable. A class of students wished to estimate the gross and net primary productivity of a crop of these plants using wet and dry mass measurements made at three intervals over 21 days.

The method

- Seven groups of three students each grew 60 *B. rapa* plants in plant trays under controlled conditions. On day 7, each group made a random selection of 10 plants and removed them, with roots intact. The 10 plants were washed, blotted dry, and then weighed collectively (giving wet mass).
- The 10 plants were placed in a ceramic drying bowl and placed in a drying oven at 200°C for 24 hours, then weighed (giving dry mass).
- On day 14 and again on day 21, the procedure was repeated with a further 10 plants (randomly selected).
- The full results for group 1 are presented in Table 1 on the next page. You will complete the calculation columns.

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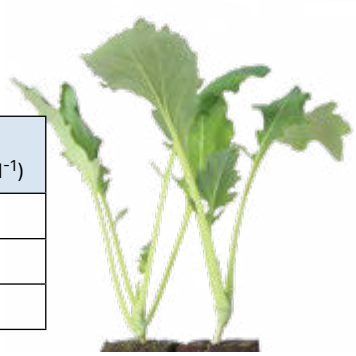


Table 1: Group 1's results for growth of 10 *B. rapa* plants over 21 days

Age in days	Wet mass of 10 plants (g)	Dry mass of 10 plants (g)	Percent biomass	Energy in 10 plants (kJ)	Energy per plant (kJ)	NPP (kJ plant^{-1} d^{-1})
7	19.6	4.2				
14	38.4	9.3				
21	55.2	15.5				

2. Calculate percent biomass using the equation: % biomass = dry mass ÷ wet mass x 100. Enter the values in Table 1.

3. Each gram of dry biomass is equivalent to 18.2 kJ of energy. Calculate the amount of energy per 10 plants and per plant for plants at 7, 14, and 21 days. Enter the values in Table 1.

4. Calculate the Net Primary Productivity per plant, i.e. the amount of energy stored as biomass per day (kJ plant^{-1} d^{-1}). Enter the values in Table 1. We are using per plant in this exercise as we do not have a unit area of harvest.

5. The other 6 groups of students completed the same procedure and, at the end of the 21 days, the groups compared their results for NPP. The results are presented in Table 2, below.

   Transfer group 1's NPP results from Table 1 to complete the table of results and calculate the mean NPP for *B. rapa*.

Table 2: Class results for NPP of *B. rapa* over 21 days

Time in days (d)	Group NPP (kJ plant^{-1} d^{-1})							
	1	2	3	4	5	6	7	Mean NPP
7		1.05	1.05	1.13	1.09	1.13	1.09	
14		1.17	1.21	1.25	1.21	1.25	1.17	
21		1.30	1.34	1.30	1.34	1.38	1.34	

6. On the grid (right), plot the class mean NPP vs time.

7. (a) What is happening to the NPP over time?

   _____

   _____

   (b) Explain why this is happening: _____

   _____

   _____

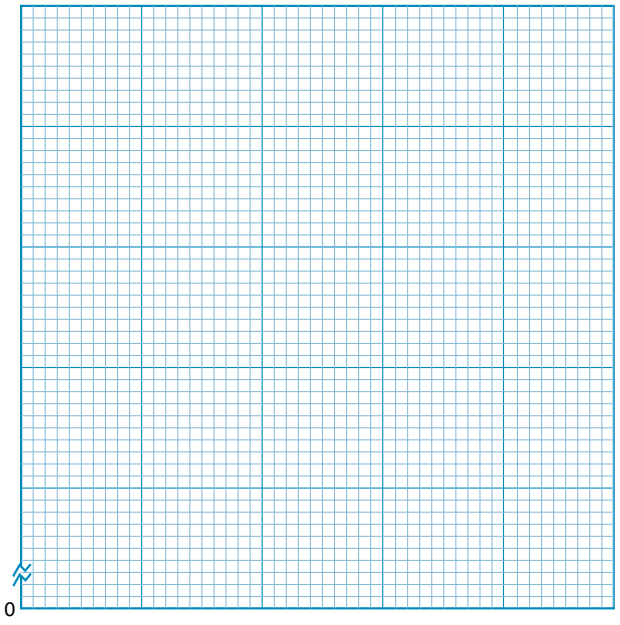
   _____

   _____

   _____

   _____

   _____



8. What would you need to know to determine the gross primary productivity of *B. rapa*?

   _____

   _____

9. Net production in consumers (N), or secondary production, can be expressed as N = I – (F+R). Red meat contains approximately 700 kJ per 100 grams. If N = 20% of the energy gain (I), how much energy is lost as F and R?

   _____

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Calculating energy flow from producers to primary consumers

Secondary production is the generation of primary **consumer** (heterotrophic) biomass in a system. In this experiment, students determined the net secondary production and respiratory losses using 12 day old cabbage white larvae feeding on Brussels sprouts. Of the NPP from the Brussels sprouts that is consumed by the larvae, some will be used in **cellular respiration**, some will be available to secondary consumers (the net secondary production) and some will be lost as egested waste products (frass).

The method

- The wet mass of ten, 12 day old larvae, and approximately 30 g Brussels sprouts was accurately measured and recorded.
- The larvae and Brussels sprouts were placed into an aerated container. After three days the container was disassembled and the wet mass of the Brussels sprouts, larvae, and frass was individually measured and recorded.
- The Brussels sprouts, larvae and frass were placed in separate containers and placed in a drying oven and their dry mass was recorded.

Cabbage white caterpillar (larva)

Note: We assume the % biomass of Brussels sprouts and caterpillars on day 1 is the same as the calculated value from day 3.

Table 3: Brussels sprouts

	Day 1	Day 3	
Wet mass of Brussels sprouts	30 g	11 g	g consumed =
Dry mass of Brussels sprouts	_	2.2 g	
Plant proportion biomass (dry/wet)			
Plant energy consumed (wet mass x proportion biomass x 18.2 kJ)			kJ consumed per 10 larvae =
Plant energy consumed ÷ no. of larvae			kJ consumed per larva **(I)** =

Table 4: Caterpillars (larvae)

	Day 1	Day 3	
Wet mass of 10 larvae	0.3 g	1.8 g	g gained =
Wet mass per larva			g gained per larva =
Dry mass of 10 larvae	_	0.27 g	
Larva proportion biomass (dry/wet)			
Energy production per larva (wet mass x proportion biomass x 23.0 kJ)			kJ gained per larva **(S)** =

Table 5: Frass

	Day 3
Dry mass frass from 10 larvae	0.5 g
Frass energy (waste) = frass dry mass x 19.87 kJ	
Energy from frass from 1 larva **(F)**	

10. Complete the calculations in tables 3-5 above.

11. (a) Write the net secondary production per larva value here: _____

    (b) Write the equation to calculate the percentage efficiency of energy transfer from producers to consumers (use the notation provided) and calculate the value here:

    _____

    (c) Is this value roughly what you would expect? Explain: _____

    _____

    _____

12. (a) Write the equation to calculate respiratory losses per larva (use the notation provided): _____

    (b) Calculate the respiratory losses per larva here: _____

13. Why can't we measure the actual dry biomass of Brussels sprouts and larvae on day 1? _____

    _____

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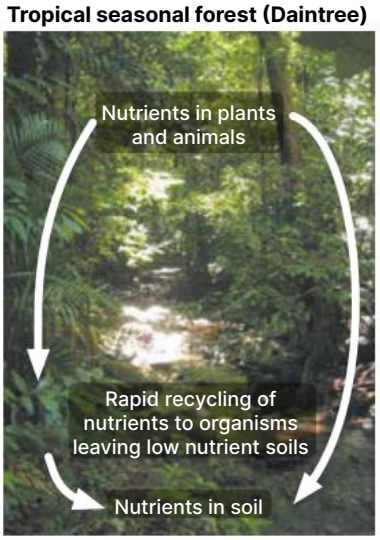
53 Nutrient Cycles

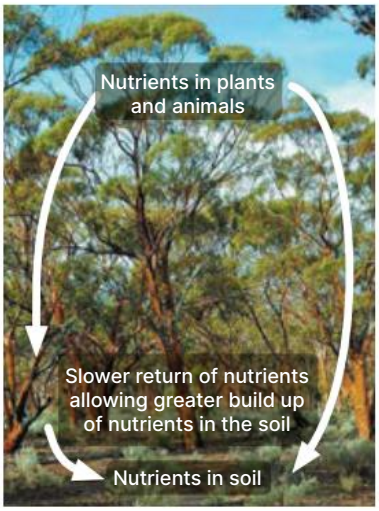
Key Idea: Matter cycles through the biotic and abiotic compartments of Earth's ecosystems. These cycles are called nutrient cycles or biogeochemical cycles.

Nutrient cycles move and transfer chemical elements (e.g. carbon, hydrogen, nitrogen, and oxygen) through an ecosystem. Because these elements are part of many essential nutrients, their cycling is called a nutrient cycle, or a biogeochemical cycle. The term biogeochemical means that biological, geological, and chemical processes are involved in nutrient cycling. In a nutrient cycle, the nutrient passes through the biotic (living) and abiotic (physical) components of an ecosystem (see diagram below). Recall that energy drives the cycling of matter within and between systems. Matter is conserved throughout all these transformations, although it may pass from one ecosystem to another.

Tropical seasonal forest (Daintree)

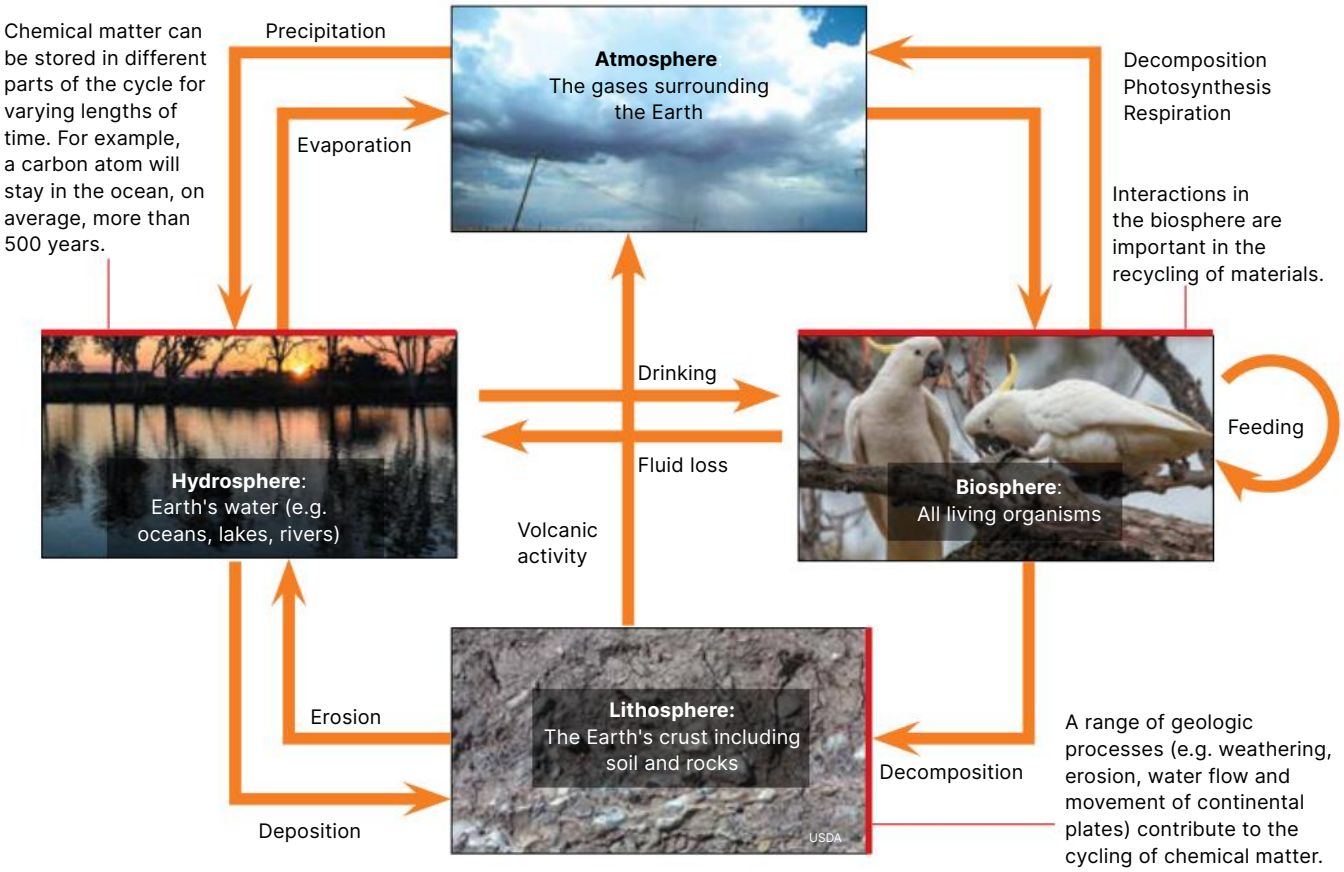


Temperate woodland SW Australia



Rates of nutrient cycling vary depending on temperature and vegetation type. In tropical rainforests, recycling is rapid so nutrient storage in the soil is low. In temperate woodlands, recycling rates are lower and soil nutrient levels are higher.

Processes in a generalised biogeochemical cycle



1. What is a nutrient cycle? _____

_____

_____

2. Why do you think it is important that matter is cycled through an ecosystem? _____

_____

_____

_____

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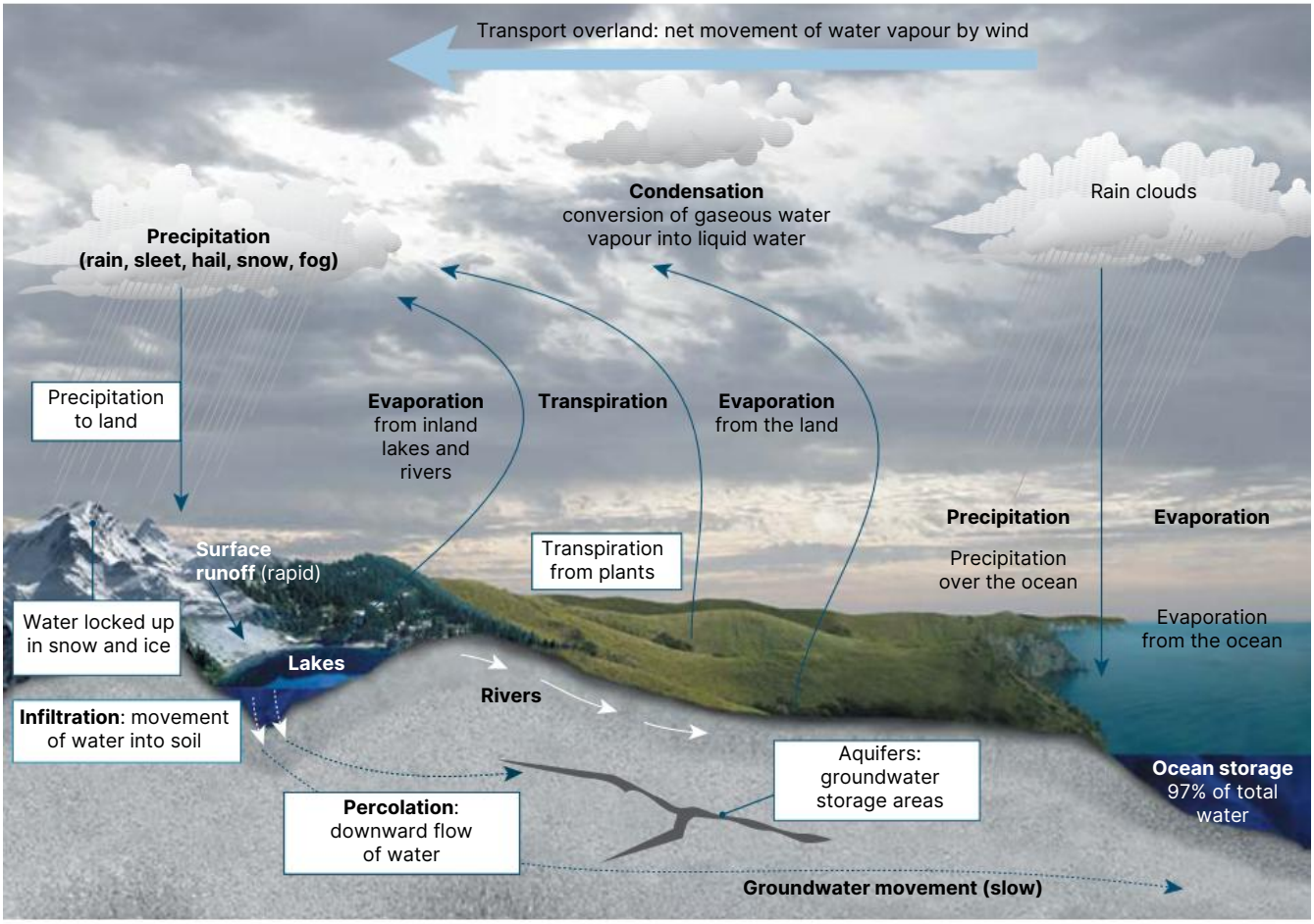
54 The Water Cycle

Key Idea: The water cycle results from the cycling of water from the oceans to the land and back.

The water cycle (**hydrologic cycle**), collects, purifies, and distributes the Earth's fixed supply of water. Besides replenishing inland water supplies, rainwater causes erosion and is a major medium for transporting dissolved nutrients within and among ecosystems. On a global scale, evaporation (conversion of water to gaseous water vapour) exceeds precipitation (rain, snow) over the oceans. This results in a net movement of water vapour (carried by winds) over the land. On land, precipitation exceeds evaporation. Some of this precipitation becomes locked up in snow and ice but most forms surface and groundwater systems that flow back to the sea, completing the major part of the cycle. Over the sea, most of the water vapour is due to evaporation alone. However on land, about 90% of the vapour results from plant transpiration. Animals (particularly humans) intervene in the cycle by utilising the resource for their own needs.



1. Identify two ways in which water returns to the oceans from the land:

   (a) _____ (b) _____

2. Describe three ways in which humans may intervene in the water cycle, and the effects of these interventions:

   (a) _____

   _____

   (b) _____

   _____

   (c) _____

   _____

3. Identify the main reservoir for water on Earth: _____

4. Identify the main reservoirs for fresh water: _____

5. Describe the important role of plants in the cycling of water through ecosystems: _____

   _____

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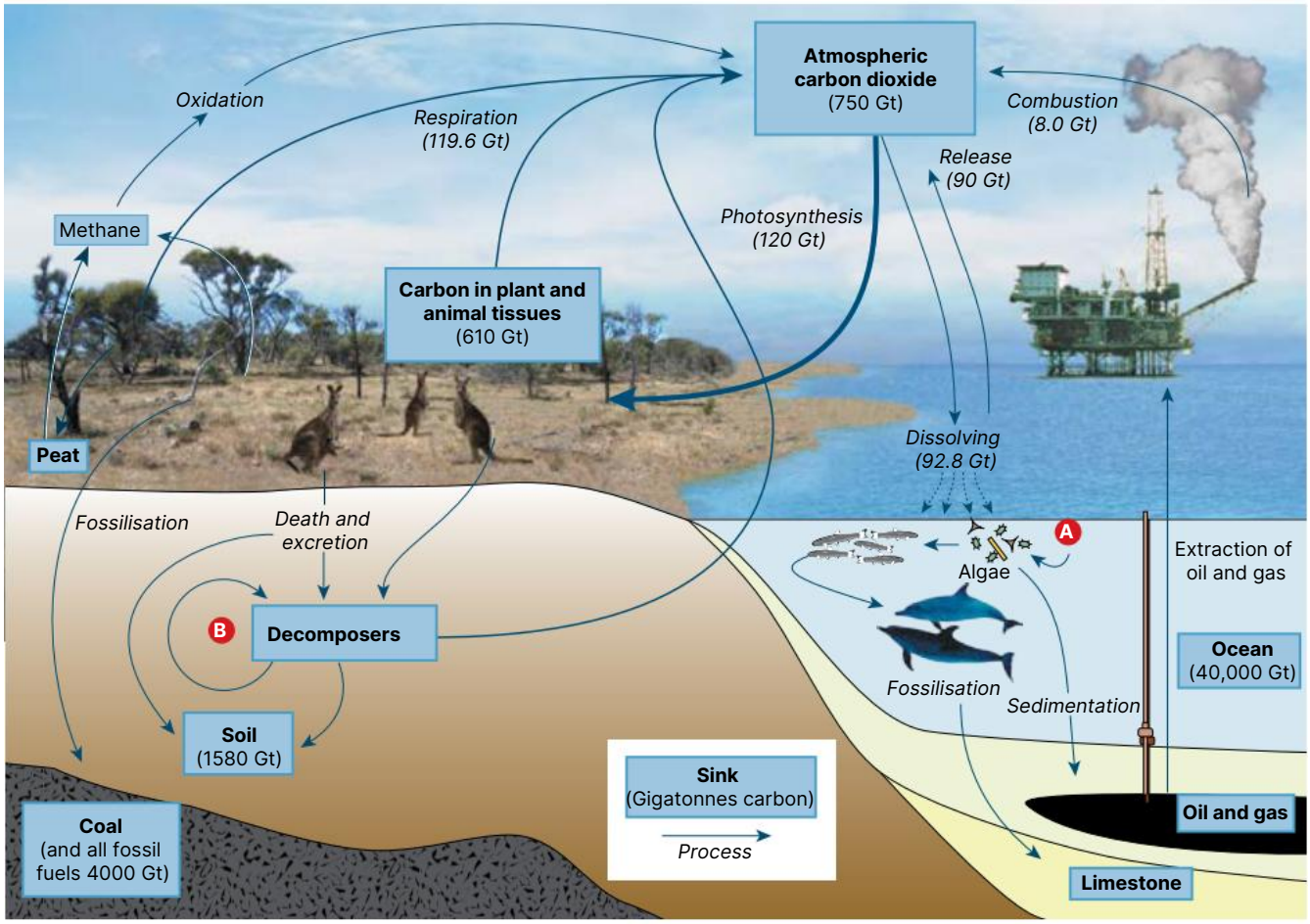
55 The Carbon Cycle

Key Idea: The continued availability of carbon in ecosystems depends on carbon cycling through the abiotic and biotic components of an ecosystem.

Carbon is an essential element of life and is incorporated into the organic molecules that make up living organisms. Large quantities of carbon are stored in sinks, which include the atmosphere as carbon dioxide gas (CO_2), the ocean as carbonate and bicarbonate, and rocks such as coal and limestone. Carbon cycles between the biotic and abiotic environment. Carbon dioxide is converted by **autotrophs** into carbohydrates via **photosynthesis** and returned to the atmosphere as CO_2 through respiration (fluxes). These fluxes can be measured. Some of the sinks and processes involved in the **carbon cycle**, together with the carbon fluxes, are shown below. Humans intervene in the carbon cycle through activities such as combustion and deforestation.



1. Add arrows and labels to the diagram above to show:
   (a) Dissolving of limestone by acid rain
   (b) Release of carbon from the marine food chain
   (c) Mining and burning of coal
   (d) Burning of plant material.

2. (a) Name the processes that release carbon into the atmosphere: _____

   _____

   (b) In what form is the carbon released? _____

3. Name the four geological reservoirs (sinks), in the diagram above, that can act as a source of carbon:

   (a) _____ (c) _____

   (b) _____ (d) _____

4. (a) Identify the process carried out by algae at point **A**: _____

   (b) Identify the process carried out by decomposers at **B**: _____

5. What would be the effect on carbon cycling if there were no decomposers present in an ecosystem? _____

   _____

   _____

   _____

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Termite mound

Termites: These insects play an important role in nutrient recycling. A symbiotic relationship with protozoa and bacteria in their guts allows termites to break down the cellulose of woody tissues in trees. They fulfil a vital role in breaking down the plant debris in tropical ecosystems.


Dung beetle

Dung beetles: Beetles play a major role in the decomposition of animal dung. Some beetles merely eat the dung, but true dung beetles, such as the scarabs and *Geotrupes*, bury the dung and lay their eggs in it to provide food for the beetle grubs during their development.


Fungus on tree trunk

Fungi: Together with saprotrophic bacteria, fungi have a crucial role in breaking down dead organic matter in forests. Mycorrhizal fungi have a mutualistic relationship with the roots of higher plants. This relationship allows the exchange of essential nutrients between the fungus and the plant.

6. Describe the biological origin of the following geological deposits:

   (a) Coal: _____

   (b) Oil: _____

   (c) Limestone: _____

7. Explain the role of each of the following organisms in the carbon cycle:

   (a) Dung beetles: _____

   _____

   _____

   (b) Termites: _____

   _____

   _____

   (c) Fungi: _____

   _____

   _____

8. Bushfires are an important part of Australia's ecology. How do you think fire might contribute to nutrient recycling:

   _____

   _____

   _____

9. In natural circumstances, accumulated reserves of carbon such as peat, coal and oil represent a sink or natural diversion from the cycle. Eventually, the carbon in these sinks returns to the cycle through the action of geological processes which return deposits to the surface for oxidation.

   (a) What is the effect of human activity on the amount of carbon stored in sinks? _____

   _____

   _____

   (b) Describe two global effects of this activity: _____

   _____

   _____

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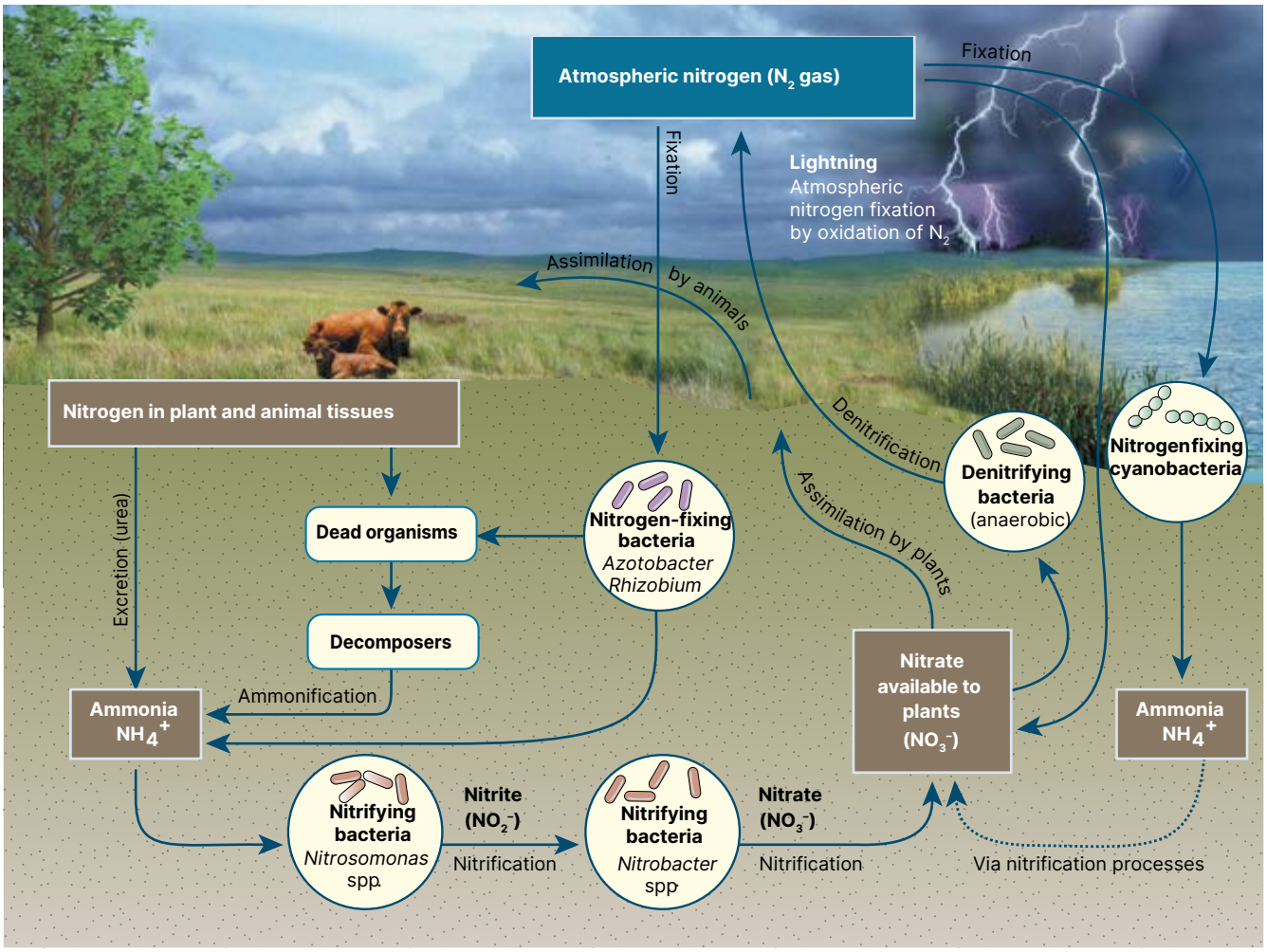
56 The Nitrogen Cycle

Key Idea: Nitrogen gas is converted to nitrates which are taken up by plants. Heterotrophs obtain their nitrogen by feeding off other organisms.

Nitrogen is an essential component of proteins and nucleic acids and required by all living things. The Earth's atmosphere is about 80% nitrogen gas (N_2), but molecular nitrogen is so stable that it is only rarely available directly to organisms and is often in short supply in biological systems. Bacteria transfer nitrogen between the biotic and abiotic environments. Some bacteria can fix atmospheric nitrogen, while others convert ammonia to nitrate, making it available to plants. Lightning discharges also cause the oxidation of nitrogen gas to nitrate. Nitrogen-fixing bacteria are found free in the soil (*Azotobacter*) and in symbioses with some plants in root nodules (*Rhizobium*). Denitrifying bacteria reverse this activity and return fixed nitrogen to the atmosphere. Humans intervene in the **nitrogen cycle** by applying nitrogen fertilisers to the land. Overuse of these can pollute water supplies.



1. Describe five instances in the nitrogen cycle where bacterial action is important. Include the name of each of the processes and the changes to the form of nitrogen involved:

(a) _____

_____

(b) _____

_____

(c) _____

_____

(d) _____

_____

(e) _____

_____

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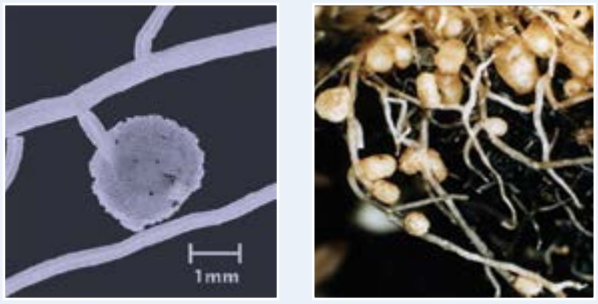
Nitrogen fixation in root nodules

Root nodules are a root symbiosis between a higher plant and a bacterium. The bacteria fix atmospheric nitrogen and are extremely important to the nutrition of many plants, including the economically important legume family. Root nodules are extensions of the root tissue caused by entry of a bacterium. In legumes, this bacterium is *Rhizobium*. Other bacterial genera are involved in the root nodule symbioses in non-legumes.

The bacteria in these symbioses live in the nodule where they fix atmospheric nitrogen and provide the plant with most, or all, of its nitrogen requirements. In return, they have access to a rich supply of carbohydrate. The fixation of atmospheric nitrogen to ammonia occurs within the nodule, using the enzyme nitrogenase. Nitrogenase is inhibited by oxygen and the nodule provides a low O_2 environment in which fixation can occur.



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Two examples of legume nodules caused by *Rhizobium*. The images above show the size of a single nodule (left), and the nodules forming clusters around the roots of *Acacia* (right).

Human intervention in the nitrogen cycle

The largest interventions in the nitrogen cycle by humans occur through farming and effluent discharges. Other interventions include burning, which releases nitrogen oxides into the atmosphere, and irrigation and land clearance, which leach nitrate ions from the soil.

Farmers apply organic nitrogen fertilisers to their land in the form of green crops and manures, replacing the nitrogen lost through cropping and harvest. Until the 1950s, atmospheric nitrogen could not be made available to plants except through microbial nitrogen fixation (left). However, during WW II, Fritz Haber developed the Haber process, combining nitrogen and hydrogen gas to form gaseous ammonia. The ammonia is converted into ammonium salts and sold as inorganic fertiliser. This process, although energy expensive, made inorganic nitrogen fertilisers readily available and revolutionised farming practices and crop yields.

Two examples of human intervention in the nitrogen cycle. The photographs above show the aerial application of a commercial fertiliser (left), and the harvesting of an agricultural crop (right).

2. Identify three processes that fix atmospheric nitrogen:

   (a) _____ (b) _____ (c) _____

3. What process releases nitrogen gas into the atmosphere? _____

4. What is the primary reservoir for nitrogen? _____

5. What form of nitrogen is most readily available to most plants? _____

6. Name one essential organic compound that plants need nitrogen for: _____

7. How do animals acquire the nitrogen they need? _____

   _____

8. Why might farmers plough a crop of legumes into the ground rather than harvest it? _____

   _____

9. Describe five ways in which humans may intervene in the nitrogen cycle and the effects of these interventions:

   (a) _____

   _____

   (b) _____

   _____

   (c) _____

   _____

   (d) _____

   _____

   (e) _____

   _____

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57 Ecological Niche

Key Idea: An organism's niche describes its functional role within its environment.

The **ecological niche** describes the functional role of an organism in an ecosystem, including its habitat and all its interactions with the environment. It includes how the species responds to the distribution of resources and how it alters those resources for other species. The full range of environmental conditions under which an organism can exist describes its fundamental niche. As a result of interactions with other organisms, species usually occupy a realised niche that is narrower than this. Central to the niche concept is the idea that two species with exactly the same niche cannot coexist, because they would compete for the same resources and one would exclude the other. This is **Gause's competitive exclusion principle**. More often, species compete for only some of the same resources.

The physical conditions influence the habitat. A factor may be well suited to the organism, or present it with problems to be overcome.

Physical conditions

- Substrate
- Humidity
- Sunlight
- Altitude
- Aspect
- Salinity
- pH
- Exposure
- Temperature
- Depth

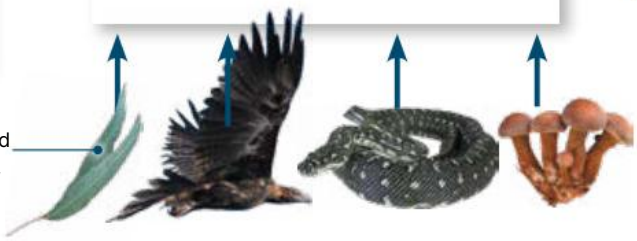
Adaptations enable the organism to exploit the resources of the habitat. The adaptations take the form of structural, physiological and behavioural features of the organism.

Adaptations for:

- Locomotion
- Activity (day/night)
- Tolerance to physical conditions
- Predator avoidance
- Self defence
- Defence of range
- Reproduction
- Feeding

Resources offered by the habitat

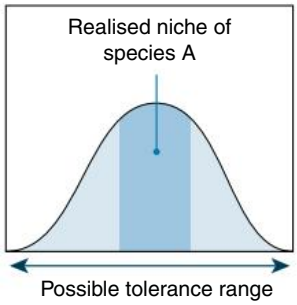
- Food sources • Shelter • Mating sites
- Nesting sites • Predator avoidance



Resource availability is affected by the presence of other organisms and interactions with them: competition, predation, parasitism, and disease.

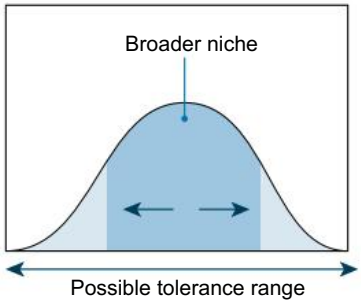
The habitat provides opportunities and resources for the organism. The organism may or may not have the adaptations to exploit them fully.

The realised niche



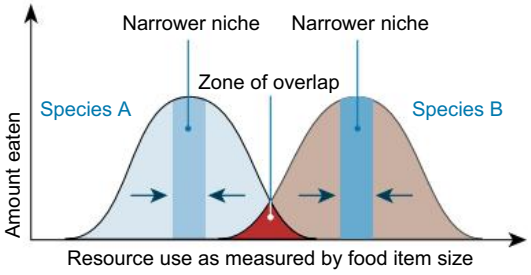
The tolerance range represents the **fundamental niche** of a species. The **realised niche** of a species is narrower than this because of **competition** with other species.

Intraspecific competition



Individuals of the same species exploit the same resources so competition is intense. Individuals must use resources at the extremes of their tolerance range and the realised niche expands.

Interspecific competition



When two (or more) species compete for some of the same resources, their resource use curves will overlap and competition will be intense in this zone. Selection will favour niche specialisation so that one or both species occupy a narrower niche.

1. (a) In what way could the realised niche be regarded as flexible? _____

_____

_____

(b) What factors might further constrain the extent of the realised niche? _____

_____

_____

2. Contrast the effects of interspecific competition and intraspecific competition on niche breadth: _____

_____

_____

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58 Interspecific Competition

Key Idea: Interspecific competition is competition between individuals of different species. It can affect species distribution.

Competition occurs when two or more organisms attempt to access the same limited resource (e.g. food or space). **Interspecific competition** (i.e. competition between members of different species) may force organisms to occupy a more restricted niche than would be available to them in the absence of competition. To avoid direct competition, naturally coexisting species have evolved slightly different niche requirements, even if many of their resource needs are much the same. However, when a foreign species is introduced to the range of a native species with very similar ecological requirements, one (usually the native) may be outcompeted and decline in numbers (the **competitive exclusion principle**).

Gliders in Australia

Gliders are small, nocturnal possum-like marsupials that live most of their life in tree canopies. Seven species of glider are found in Australia, and six of these are found in Queensland. In Australia, gliders of the genus *Petaurus* occupy very similar niches. All are nocturnal, require tree hollows for nesting, and feed on insects, nectar, pollen, honeydew, and plant sap.

Squirrel glider: The squirrel glider is distributed from Victoria to northern Queensland, but is not found on the Cape York Peninsula. Squirrel gliders have a limited habitat range, and are restricted to dry eucalypt forests and woodlands. Squirrel gliders live in family groups of 2-10 individuals and weigh 200-260 g.

Sugar glider: The distribution of the sugar glider is broader than the squirrel glider. It inhabits the eastern and northern coasts of Australia, New Guinea, and the surrounding islands. The sugar glider is found in a wide range of habitats including drier coastal eucalypt forests and woodlands to wetter rainforest habitats. Sugar gliders live in family groups of 2-10 individuals and weigh 95-160 g.


Squirrel glider


Sugar glider

Investigating niche overlap and coexistence in gliders

In large areas of eastern Australia, the distribution of sugar gliders and squirrel gliders overlap. Researchers looked at historical and recent data (below) to see how the two species were ecologically separated where their distribution overlapped.

Table 1. Occurrence of glider species in rainforest and other forest.

	Forest type	
	Rainforest	Other
Historical data		
Sugar glider	77%	23%
Squirrel glider	17%	83%
Recent data		
Sugar glider	64%	36%
Squirrel glider	7%	93%

Table 2. Frequency of glider species at different elevations.

	Records in elevation class			% of records that were rainforest at:	
	< 80 m	80-300 m	> 300 m	< 80 m	> 80 m
Historical data					
Sugar glider	77%	0%	23%	70%	100%
Squirrel glider	85%	12%	3%	14%	33%
Recent data					
Sugar glider	71%	0%	29%	50%	75%
Squirrel glider	85%	13%	2%	6%	13%

Data: Rowston, C & Catterall, C.P. (2004) Habitat segregation, competition and selective deforestation: effects on the conservation status of two similar *Petaurus* gliders. Conservation of Australia's forest fauna http://hdl.handle.net/10072/416

1. Study table 1. What do you notice about the type of forest each species is found in? _____

2. The majority of both species are found below 80 m (Table 2). How do they avoid competition with each other?

3. Suggest why the niche of the sugar glider is more restricted when both species inhabit the same area:

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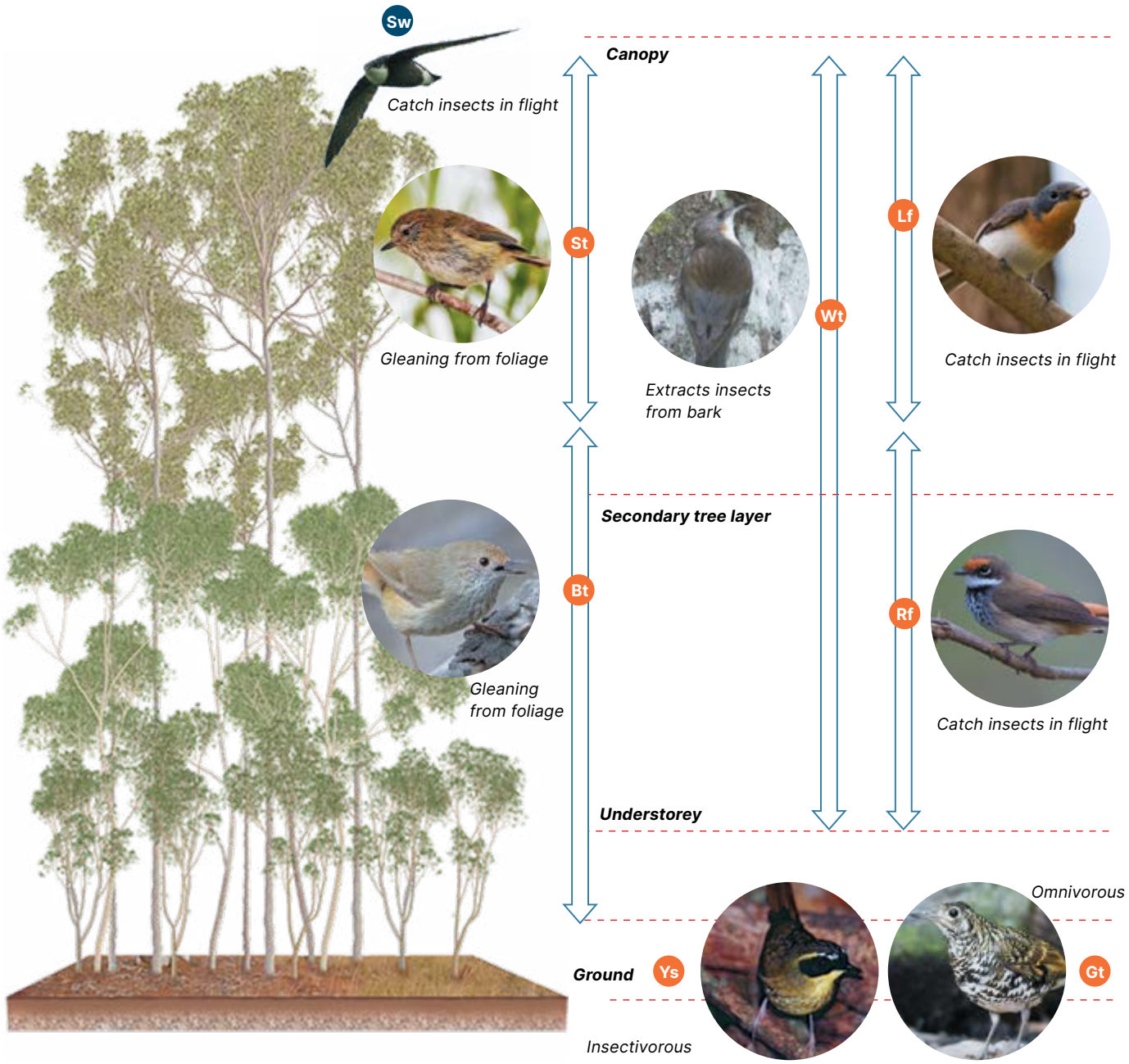
59 Competition and Species Distribution

Key Idea: Interspecific competition is reduced when different species exploit slightly different resources.

Competition is most intense between members of the same species because their habitat and resource requirements are identical. **Interspecific competition** is usually less intense, although many species exploit at least some of the same resources. Different species with similar ecological requirements may reduce direct competition by exploiting the resources within different microhabitats or by exploiting the same resources at different times of the day or year.



Adapted from: Recher et al., 1986. A Natural Legacy: Ecology in Australia. Maxwell Macmillan Publishing Australia.

Reducing competition in a eucalypt forest

The diagram above illustrates how a layered forest structure provides the opportunities and resources for species with similar foraging niches to coexist. Different layers of the forest allow insectivorous birds to specialise in foraging at different heights and in different ways. The similar sized striated and brown thornbills feed at different heights, as do the leaden flycatcher and the rufous fantail. Adaptations reflect their feeding specialisations. The ground-dwelling yellow-throated scrubwren and the larger ground thrush have robust legs and feet, while the white-throated treecreeper has long toes and large curved claws, specialising in removing insects from the bark. The swifts are extremely agile fliers capable of catching insects on the wing.

Key to bird species

- Rf Rufous fantail — PHOTO: Greg Miles cc 2.0
- Lf Leaden flycatcher — PHOTO: Jim Bendon cc 2.0
- Bt Brown thornbill — PHOTO: JJ Harrison cc 3.0
- Gt Ground thrush — PHOTO: JJ Harrison cc 3.0
- Sw Spine-tailed swift — PHOTO: Ron Knight cc 2.0
- Wt White-throated treecreeper — PHOTO: Lip Kee cc 2.0
- St Striated thornbill — PHOTO: JJ Harrison cc 3.0
- Ys Yellow-throated scrubwren — PHOTO: Bernard Dupont cc 2.0

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1. Describe two ways in which species can avoid directly competing for the same resources in their habitat:

   (a) _____

   _____

   (b) _____

   _____

2. How do the insectivorous birds in the secondary tree layer of the forest avoid direct competition for the same resources?

   _____

   _____

   _____

   _____

3. The yellow-throated scrubwren (Ys) and ground thrush (Gt) are both ground feeders. Explain why both species are able to inhabit the ground layer in eucalypt forest:

   _____

   _____

   _____

   _____

4. In forests where shrubs are absent or sparse, only the striated thornbill (St) is present. In shrub habitats with few trees there are few striated thornbills and the brown thornbills (Bt) are common. Suggest why this is the case:

   _____

   _____

   _____

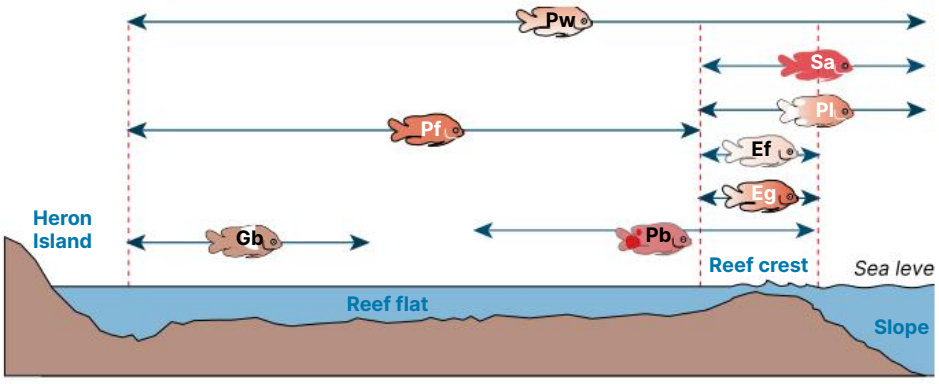
   _____

   _____

5. The diagram below shows the distribution of ecologically similar damselfish over a coral reef at Heron Island, Queensland, Australia. The habitat and resource requirements of these species overlap considerably.

Key to damselfish species

Pw	*Pomacentrus wardi*
Pf	*Pomacentrus flavicauda*
Pb	*Pomacentrus bankanensis*
Sa	*Stegastes apicalis*
Pl	*Plectroglyphidodon lacrymatus*
Ef	*Eupomacentrus fasciolatus*
Eg	*Eupomacentrus gascoynei*
Gb	*Glyphidodontops biocellatus*



How might the damselfish on the reef at Heron Island (above) reduce competition? _____

_____

_____

_____

_____

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60 Identifying Species in a Eucalypt Forest

Key Idea: Leaf litter communities can be used to assess biodiversity. Many different species are found in leaf litter, but some are more common than others.

Many different species are found in the leaf litter and in surface soil under trees. Decomposers such as bacteria and fungi have essential roles in breaking down organic matter, recycling nutrients, and making minerals available to plants. Larger organisms, through activities such as burrowing and digging, also contribute to decomposition and improved soil structure. The biodiversity of invertebrate communities can provide valuable reference information to monitor ecosystem change and the effect of management practices.

Common invertebrates found in leaf litter

Leaf litter provides habitat to a wide range of invertebrates. While many are too small to be observed with the naked eye, it is possible to identify and count many of the larger species (> 1 mm). These invertebrates generally fall into two categories: the mesofauna (100 µm -10 mm), and the macrofauna (10 mm - 10 cm). The table below will help you identify some of the common invertebrates you may find during your own investigations.

With wings	May have wings	Usually wingless	Appears wingless but wings are hidden	Winged or wingless. Broad flat body
 **Hard wing covers** BEETLES Over 30,000 different species in Australia. Some are specific to eucalyptus stands. Depending on species they eat other insects, plant material, fungi, or dead animal matter.	 **Membranous wings** BUGS A very diverse group found in a wide range of different habitats and with varied diets. Their defining feature is a 'beak' with modified mouthparts forming a piercing stylet.	 **Narrow waist** ANTS Large number of species and found in most terrestrial ecosystems. Diverse feeding habits (will eat earwigs). Prey to a number of other invertebrates (e.g. pseudoscorpion).	 **Tail nippers** EARWIGS Flat, flexible body, short, rarely used wings. Common under bark and plant debris. Omnivorous and mostly nocturnal. Prey to frogs, lizards, spiders, mantids, ants, and birds.	 **Spiky legs** COCKROACHES Native cockroaches are found in leaf litter, bark, or rotting wood. Most eat pollen, bark and leaf material. Prey for lizards, birds and some invertebrates.
Seems to have more than 6 legs	Six legs, very small (1 mm long or less)	Six slender legs, small (1-10 mm long)	Six legs but not insects wingless, <6 mm long	Eight legs. Body divided into two parts
 **4-10 false legs** CATERPILLARS The larvae of butterflies and moths. Many species overwinter in the soil surface or leaf litter as larvae or pupae. Eat leaf material. Eaten by predatory beetles birds, and wasps.	 **Very small and slender** THRIPS Many species transition from pupa to adult in soil and leaf litter. Common food sources for leaf-litter dwelling species are fungi found in leaf litter or on dead branches, supplemented by pollen.	 **Often long wings** BOOKLICE (BARKFLY) Mainly found on plants, but sometimes found in leaf litter. Booklice feed on lichens, algae, plant spores, and dead plant and insect material. Prefer moist environments.	 **Have a folded tail-like furcula for jumping** SPRINGTAILS Important detritivores. Abundant in soil and leaf litter, especially after rain (prefer moist conditions). Omnivorous, mainly eating bacteria and fungi, and dead organic matter.	 **Obvious fangs** SPIDERS Arachnids. A number of different species may occupy leaf litter. Most species are predatory, feeding on invertebrates, including other spiders. Some are web builders, others run down prey.
Eight legs. 'Head" is actually just mouthparts	Eight legs, 2-8 mm, and long pincers	14 legs, flattened body, antennae	Many legs, one pair of legs per body segment	Many legs, two pairs of legs per body segment
 **Small size, simple unsegmented body** MITES Common arachnids throughout Australia. Often large numbers in soil and leaf litter where they are important detritivores, feeding on dead organic matter. Food for predatory invertebrates.	 **Flat pear-shaped body** PSEUDOSCORPIONS Also called false scorpions. Long pincers may be different colour to the body. Found in many habitats, mainly under leaf litter, bark and rocks. They are **predators** and feed on small invertebrates (e.g. ants, mites beetles, booklice).	 **Body segmented** WOODLICE (SLATERS) Crustaceans restricted to moist conditions (they easily dry out and die in dry conditions). Mainly active at night when dehydration risk is low. Often grouped together in the day. Feed on dead plant matter. Preyed on by woodlouse spiders.	 **Body flattened** CENTIPEDES Size ranges from a few mm to more than 10 cm. Fast moving nocturnal carnivores, with poison pincers. They prey mainly on invertebrates, including spiders. Found in a variety of habitats, mostly under rocks, logs, leaf litter and tree bark.	 **Body rounded** MILLIPEDES More common in milder climates. They prefer moist conditions, being generally absent from dry habitats. Their absence is used as an indicator of environmental water stress. Slow moving detritivores eating dead plant material.

Insect hexapods | Non-insect hexapods | Arachnids | Crustaceans | Myriapods

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The soil and leaf litter under trees in a *Eucalyptus pilularis* forest in NSW was sampled for invertebrates. Abundance of the mesofauna and macrofauna found is provided in the table below.

Organism	Abundance (number per m^2)
Mites (Mi)	130
Spiders (Sp)	6
Pseudoscorpions (Ps)	9
Centipedes (Ce)	18
Beetles (Be)	18
Springtails (St)	48
Earwigs (Ew)	1
Cockroaches (Co)	1
Millipedes (Ml)	2
Ants (An)	3
Bugs (Bu)	24
Woodlice (Wo)	13
Caterpillars (Ca)	8
Booklice (Bo)	1
Thrips (Th)	24
TOTAL	**296**

Data: Hurditch, W.J. (1981). From Recher, H.E ed) *et.al.* (1992) A Natural Legacy Ecology in Australia.

1. Graph the species abundance on the grid above. Use the letter codes provided in the table to identify each organism:

2. (a) Identify the most abundant species found: _____

   (b) What percentage of the total organisms does it make up? _____

   (c) Describe their importance in this habitat: _____

   _____

   _____

3. One measure of environmental stress is lack of soil moisture. What litter invertebrates would be useful indicators of environmental stress and why?

   _____

   _____

   _____

4. (a) Identify an organism that you might not find easily if you sample during day time: _____

   (b) Could this affect your biodiversity assessment? Explain? _____

   _____

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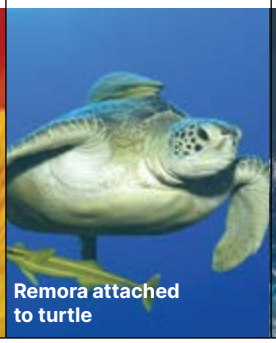
61 Species Interactions

Key Idea: Every species interacts with others. The interactions usually, but not always, benefit at least one of the species.

Species interact with other species. The nature and outcome of these interactions structures communities and leads to interdependence. Interactions range from those that are beneficial to all parties, to those where only one species benefits. In a relationship involving exploitation, one party benefits at the expense of another. Sometimes, neither party benefits from the interaction. Such interactions include amensalism (below) or **competition**, a relationship in which two parties (which may be the same or different species) directly or indirectly contest the same resource (e.g. food).

Type of interaction between species				
Mutualism	Commensalism	Amensalism	Exploitation	
			Predation	Parasitism
A ⇄ B Benefits Benefits	A → B Benefits Unharmed	A → B Unaffected Harmed	A → B Benefits Harmed	A → B Benefits Harmed
Both species benefit from the association. **Examples**: Tick bird on zebra removes parasites and alerts zebra to danger, while tick bird gains access to food. Flowering plants and their insect pollinators have a mutualistic relationship. Flowers are pollinated and the insect gains food (below).	One species benefits and the other is unaffected by the association. **Examples**: Remora are fish with special sucker organs to attach to other marine animals such as sharks or turtles. The remora saves energy by hitching a ride on the other animal, and the shark or turtle is unharmed.	One species incidentally harms the second species but does not obtain any benefit from the interaction. **Examples**: Algal blooms can lead to the death of fish and other aquatic organisms by depleting the water of oxygen or producing toxins. However, the algae do not benefit from the deaths of the fish.	**Predator** kills the prey outright and eats it. **Examples**: Lion preying on wildebeest or praying mantis (below) consuming insect prey. The adaptations of predators and prey are the result of their close ecological relationship throughout their evolution: predators have adaptations to capture prey and prey have adaptations to avoid capture.	The parasite lives in or on the host, taking (usually all) its nutrition from it. The host is harmed but usually not killed. **Examples**: Pork tapeworm in a pig's gut. Some plants (e.g. mistletoes) are semi-parasitic (hemi-parasites). They photosynthesise but rob the host plant of nutrients and water.
 Honeybee and flower	 Remora attached to turtle	 Algal bloom	 Mantid eats cricket	 Pork tapeworm

1. Summarise your knowledge of species interactions by completing the following, entering a (+), (–), or (0) for each species, and writing a brief description of each relationship.
   Codes: (+): species benefits, (–): species is harmed, (0): species is unaffected.

Interaction	Species		Description of relationship
	A	B	
(a) Mutualism			
(b) Commensalism			
(c) Amensalism			
(d) Parasitism			
(e) Predation			
(f) Competition			

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Examples of interactions between different species are illustrated below. For each example, identify the type of interaction, and explain how each species in the relationship is affected.

JJ Harrison cc 3.0

2. The honeyeaters are a diverse family of small to medium-sized nectar-feeding birds common in Australia. Many Australian plant species, including proteas and myrtles, are pollinated by honeyeaters.

   (a) Identify this type of interaction: _____

   (b) Describe how each species is affected (benefits/harmed/no effect):

   _____

   _____

3. The squat anemone shrimp, also known as the sexy shrimp, lives among the tentacles of sea anemones, where it gains protection and scavenges scraps of food from the anemone. The anemone is apparently neither harmed nor benefitted by the shrimp's presence.

   (a) Identify this type of interaction: _____

   (b) Describe how each species is affected (benefits/harmed/no effect):

   _____

   _____

Marc Tarlock cc 2.0

4. Dingoes will kill and scavenge a range of species. In groups of two or more, they can attack and kill large animals, such as kangaroos, but will also scavenge carrion, such as this dingo with a fish on Fraser Island.

   (a) Identify this type of interaction: _____

   (b) Describe how each species is affected (benefits/harmed/no effect):

   _____

   _____

   _____

5. The Australian paralysis tick, Ixodes holocyclus, lives attached to the skin of mammalian hosts, commonly bandicoots, koalas, possums, and kangaroos, where it sucks body fluids and causes irritation. Most native species are immune to the tick's toxins but it can cause paralysis in susceptible species.

   (a) Identify this type of interaction: _____

   (b) Describe how each species is affected (benefits/harmed/no effect):

   _____

   _____

   _____

6. Large herbivores expose insects in the vegetation as they graze. The cattle egret, which is widespread in tropical and subtropical regions, follows the herbivores as they graze, feeding on the disturbed insects when the herbivore moves away.

   (a) Identify this type of interaction: _____

   (b) Describe how each species is affected (benefits/harmed/no effect):

   _____

   _____

   _____

7. Explain the similarities and differences between a predator and a parasite:

   _____

   _____

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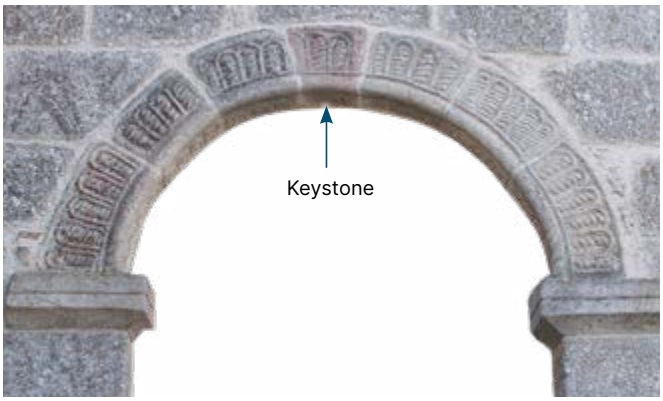
62 Keystone Species

Key Idea: All organisms within an ecosystem contribute to its structure and functioning, but keystone species have a disproportionate effect on ecosystem processes.

Although every species has a role in ecosystem function, some have a disproportionate effect on ecosystem processes and stability (how unchanging the ecosystem is over time). These species are called **keystone species** and they are important because they play a pivotal role in the way the ecosystem works, e.g. as top predators or by recycling nutrients. The loss of a keystone species can have a large and rapid impact on the structure and function of an ecosystem, changing the balance of relationships and leading to instability. This has important implications for ecosystem management because many keystone species are endangered.

Why are keystone species important?

A keystone species is one that plays a unique and crucial role in the way an ecosystem functions. Often, but not always, keystone species are top **predators**. The role of the keystone species varies from ecosystem to ecosystem, but the loss of a keystone species from any ecosystem has a domino effect, and a large number of species can be affected. This can lead to can rapid ecosystem change or the collapse of the ecosystem completely.



The term keystone species comes from the analogy of the keystone in a true arch (above). An archway is supported by a series of stones, the central one being the keystone. If the keystone is removed the arch collapses.

Ochre starfish: Paine removed these in his study to see what the effect would have on the rocky shore community.

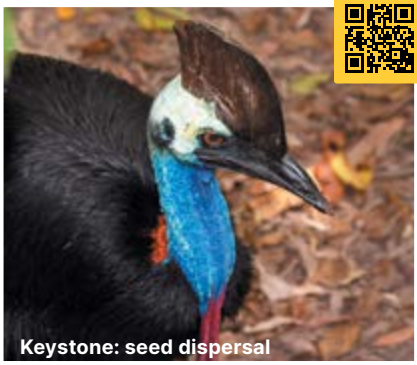
Keystone species in action

The idea of the keystone species was first hypothesised in 1969 by Robert Paine. He studied an area of rocky seashore, noting that diversity seemed to be correlated with the number of predators (ochre starfish) present (i.e. diversity declined as the number of predators declined).

To test this he removed the starfish from an 8 m by 2 m area of seashore. Initially, the barnacle population increased rapidly before collapsing and being replaced by mussels and gooseneck barnacles. Eventually the mussels crowded out the gooseneck barnacles and the algae that covered the rocks. Limpets that fed on the algae were lost and the number of species present in the study area dropped from 15 to 8.

Keystone: predator

The humphead wrasse is a protected reef fish. It is large, long lived and slow breeding species and an opportunistic predator of a wide range of invertebrates. It is a keystone species because it preys on crown-of-thorns starfish and keeps the populations of this coral predator in check. It is also considered an **umbrella species** because its protection benefits a large number of other species.



Keystone: seed dispersal

istockphotos.com

The endangered southern cassowary is a keystone species in Australia's wet tropics. They are obligate fruit eaters, and their gut passes seeds, unharmed, into a pile of manure. More than 200 plant species depend on the cassowary to disperse their seeds, yet their populations are all declining. Their loss would also mean the loss of an ecological role.

Keystone: critical food source

Gnangarra cc 2.5

All species of banksias produce large amounts of nectar, and are a vital component of **food chains** in the Australian bush. In the Avon Wheatbelt region of Western Australia, the acorn banksia is the sole source of nectar for honeyeaters at certain times of the year. The loss of this plant species would also result in the loss of honeyeaters from the region.

1. Why are keystone species so important to ecosystem function? _____

_____

_____

_____

_____

SU

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Australian keystone species

Many sharks are top predators and are keystone species in the waters around Australia. One shark species inhabiting Shark Bay (WA) is the tiger shark. It doesn't even have to kill its prey to exert an effect on ecosystem structure. The presence of the tiger shark causes marine **herbivores** such as green turtles and dugongs to avoid the area or to spend less time grazing because they are looking out for the sharks. As a result, the seagrass meadows thrive and support many more species than would be possible if they were grazed intensively by herbivores. As a result, biodiversity in Shark Bay is high. Fishing is the main threat to tiger sharks as they hunted for their flesh, fins, and skin. Finning, although largely banned in Australian waters, still continues illegally.

Marjorie Lundgren cc3.0

Cockatoo grass (*Alloteropsis semialata*) is found through tropical savannas in northern and north eastern Australia. Cockatoo grass is an early developer in the wet season, providing a food source to many animal species before other plant species are available. Cockatoo grass is considered to be a keystone species because at certain times of the year it is the only food source available for two endangered species, the golden-shouldered parrot and the Northern bettong, a small marsupial. Young cockatoo grass is a preferred food source cattle and pigs, so it is easily overgrazed, leaving little for the wild species that rely on it. Conservation efforts are made to protect stands of cockatoo grass in some areas.

Andrew Mercer cc 4.0

The grey-headed flying fox (*Pteropus poliocephalus*) is found in a variety of habitats along the east coast of Australia, including Victoria. The grey-headed flying fox feeds on the fruit and nectar of over 180 species of trees, including Australian natives *Eucalyptus*, *Banksia*, palms, and myrtles. It will fly up to 50 km each night looking for food and this allows it to fulfill an important ecological role by dispersing the pollen and seeds of a wide range of plants. Its role is especially important in the subtropical rainforests as it is the only mammalian species to consume nectar and fruit in these regions. The species is under threat from the loss of foraging and roosting habitat and control measures by horticulturists to prevent crop losses.

2. For each species below, summarise the features of its ecology that contribute to its position as a keystone species:

(a) Acorn banksia: _____

_____

_____

(b) Southern cassowary: _____

_____

_____

(c) Humphead wrasse: _____

_____

_____

(d) Tiger shark: _____

_____

_____

(e) Cockatoo grass: _____

_____

_____

(f) Grey-headed flying fox: _____

_____

_____

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63 The Effect of Keystone Species

Key Idea: When mulgara were excluded from a fenced area, the number of smaller dasyurid species present reduced.

Two species of mulgara (*Dasycercus* genus) are found in Australia, the brush-tailed mulgara and the crest-tailed mulgara. Mulgara are nocturnal marsupials belonging to the family Dasyuridae, which includes the Tasmanian devil and the quolls. Both mulgara species are small (30 cm long from head to tail) and weigh up to 190 g.

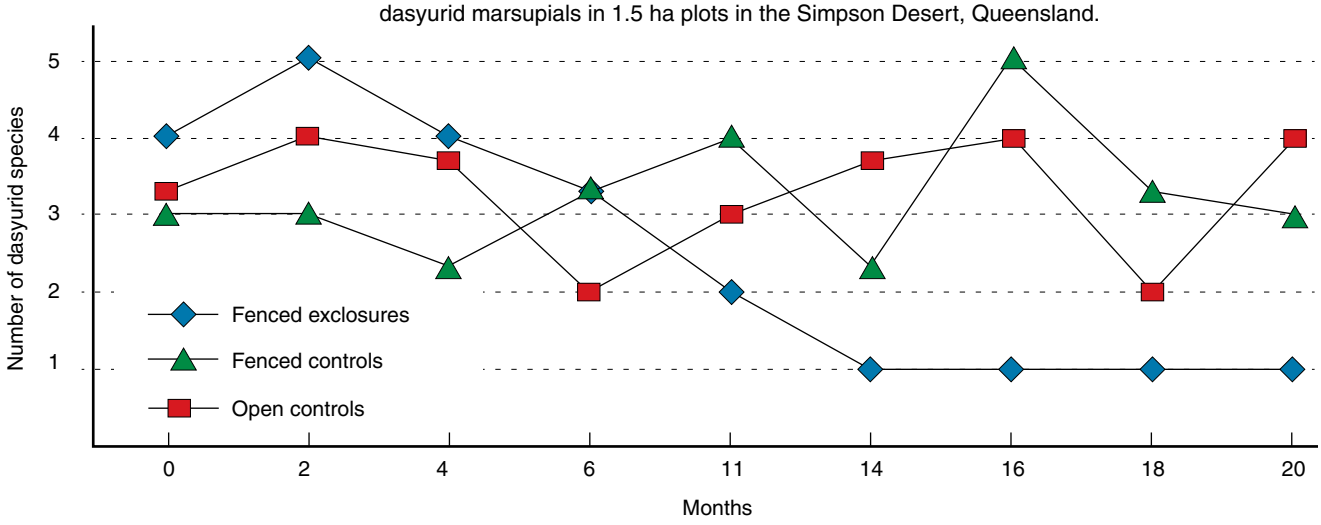
Mulgaras live in arid central Australia, and burrow 50 cm under the surface to avoid the heat. While the brush-tailed mulgara has an extensive range through the middle of Australia, the crest-tailed mulgara is found only in a small part of the Simpson Desert within Queensland's borders.


Crest-tailed mulgara

Bobby Tamayo CC 4.0

The effect of the crest-tailed mulgara (*Dasycercus cristicauda*) as a **keystone species** was tested by excluding them from a 1.5 ha plot of land. Fenced exclosures were established 10 months after sampling began. All dasyurid species (except mulgara) could access the site. Fenced controls and open controls were established at the same time. All dasyurid species (including mulgara) could access these plots. The results are shown in the graph below.

Effects of crest-tailed mulgara (*Dasycercus cristicauda*) on the number of smaller dasyurid marsupials in 1.5 ha plots in the Simpson Desert, Queensland.



Data source: Dickman in Attiwill, P. and Wilson. B (2003) Ecology: An Australian Perspective.

1. Describe what happens to species numbers after the fences were established (at 10 months) for each of the following:

   (a) Fenced exclosures: _____

   (b) Fenced controls: _____

   (c) Open controls: _____

2. Describe the difference in species numbers between the fenced exclosure and the:

   (a) Fenced control: _____

   (b) Open control: _____

3. (a) Based on the data presented above, do you think the crest-tailed mulgara acts as a keystone species? _____

   (b) Explain your answer: _____

   _____

   _____

   _____

4. Why do you think the researchers included a fenced control and open control? _____

   _____

   _____

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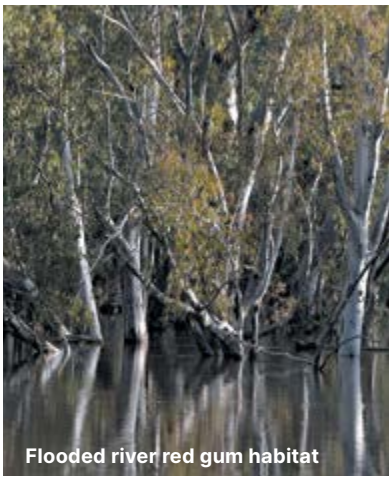
64 Keystone Species and Conservation

Key Idea: The river red gum is a keystone species in the Murray Darling Basin. A reduction in its numbers due to reduced flooding events and increased harvesting has altered the ecology of the Murray Darling Basin.

Increasing demand on water resources in the Murray-Darling Basin (MDB) has resulted in wide-spread dieback of floodplain forests. This has been observed in the river red gum (*Eucalyptus camaldulensis*). The river red gum is the dominant floodplain tree in the southern MDB and is a **keystone species**. Their loss alters biodiversity in the region.



Flooded river red gum habitat

MargaretRDonald CC 4.0

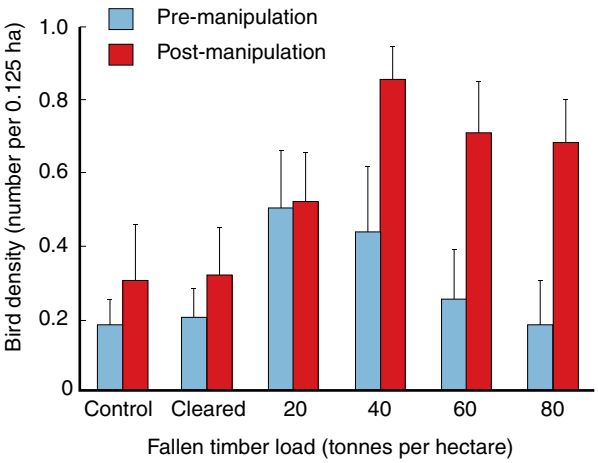
Importance of the river red gum

- *Eucalyptus camaldulensis* is commonly found along Australian waterways and has the widest natural distribution of Australian eucalyptus species. In its natural habitat, the species is subject to regular flooding. Regular flood events recharge the soil with water.
- River red gums provide habitat for many species. For example:
  - Fallen trees produce "snags" in the water course. The snags provide breeding sites for blackfish during the flooding season. Aquatic birds feed off fish in the snags.
  - Hollows in trees create habitats for many species including the superb parrot, a threatened species. Birds, bats, and carpet pythons are also found in hollows.
  - The gum's dense foliage provides species with shade and shelter from the sun.
- River red gums contribute nutrients and energy to the ecosystem through leaf and insect fall. This is especially important in areas with low nutrient levels.
- The trees have an important role in flood mitigation and slow silt runoff.
- Unlike species that are chosen as **flagship species**, river red gums are not cute or charismatic. However, their conservation has many benefits because of the large number of species that depend on them either directly or indirectly.

Changes to the woodlands

Over the last century, higher water demands (extraction and damming) have changed the flow characteristics along the MDB. Tree dieback has occurred as a result, and large changes to the vegetation structure and composition have been observed. Dieback is likely to continue with predicted climate changes (reduced precipitation and increased temperatures). Human management of the river red gum forests has also contributed to community change. Typically, the natural forest structure consists of large spreading trees with mixed aged trees between. Harvesting has resulted in mostly even-aged tree stands with "straight poles", and few stands of spreading trees. A higher percentage of fallen trees occur in natural forests compared to managed forests, and this likely affects forest fauna. Small mammals and birds prefer the spreading canopy and higher loads of fallen trees because they provide increased cover, shelter from **predators**, and more invertebrate food sources. Natural forests also contain more hollows than managed forest. The graph (right) shows how manipulating the load of fallen timber affects the density of brown treecreepers, a near threatened species. A near threatened species is one that may be threatened with extinction in the near future.

Effect of fallen timber on brown treecreeper density (mean ± SE)



DATA: Mac Nally, R., *et.al.* (2011) Dynamics of Murray-Darling floodplain forests under multiple water stressors – the past, present and future of an Australian icon. Water Resources Research, 47, W00G05.

1. Study the post manipulation data (above). Explain the effect of fallen timber load on brown treecreeper density:

2. Explain what continued loss of river red gum could mean for the survival of the brown treecreeper:

3. Flagship species are chosen to raise public support for biodiversity conservation in a region. They are usually charismatic animals but they are not always keystone species. Why might the conservation of a keystone species such as river red gum be more effective as a conservation strategy than use of flagship species?

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65 Did You Get It?

1. Test your vocabulary by matching each term to its definition, as identified by its preceding letter code.

(i) consumer	
(ii) ecological niche	
(ii) food chain	
(iii) food web	
(iv) interspecific competition	
(iv) keystone species	
(v) trophic level	

A A sequence of steps describing how an organism derives energy from the ones before it.

B Any of the feeding levels that energy passes through in an ecosystem.

C An organism that obtains its carbon and energy from other organisms.

D A complex series of interactions showing the feeding relationships between organisms in an ecosystem.

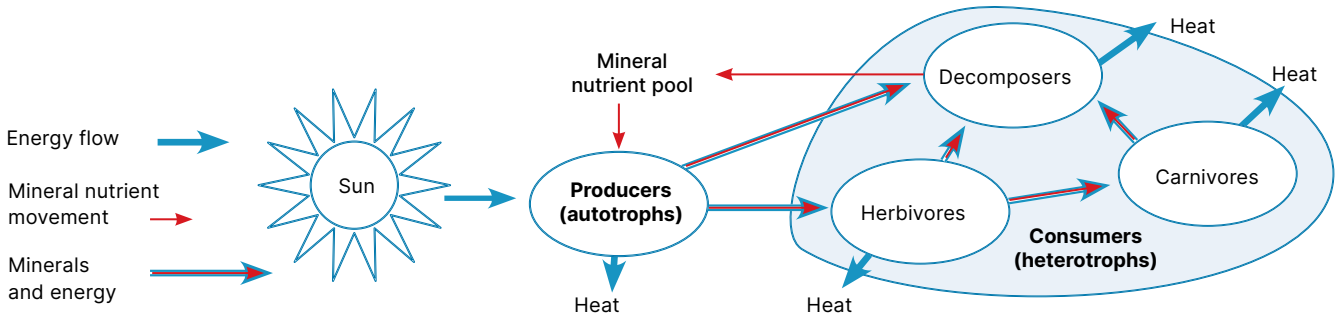
E A species that has a disproportionate effect on an ecosystem's characteristics because of their pivotal role in some aspect of ecosystem functioning.

F The relationship of a species with all the biotic and abiotic factors affecting it. A species' functional role in an ecosystem.

G Competition for resources between different species.

2. The following observations were made about the feeding relationships in an Australian rural ecosystem. Use the information to construct a food web diagram in the space below.
Honey-eater birds feed on the nectar and pollen of native shrubs. These shrubs are also eaten by insects and wallabies. Grass is eaten by insects, rabbits, and wallabies, while mice feed on the grass seeds. Frogs eat insects, while dingoes prey on rabbits and wallabies. Kookaburras hunt snakes and frogs. The snakes feed on frogs and mice and take the eggs and chicks from honey-eater nests.

3. The schematic below shows the movement of energy and minerals from producers to consumers.



(a) How are the movements of minerals and energy different? _____

_____

_____

(b) What process is responsible for losses of energy from the system? _____

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Chapter 5 Unit 3 Topic 2

Changing Ecosystems

Resource Hub
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Key Terms

- biodiversity
- biosphere
- climax community
- ecological succession
- ecosystem
- fossil record
- K-selected
- pioneer species
- primary succession
- r-selected
- secondary succession

Key Concepts

- Ecological succession is the change in the species structure of an ecological community over time and includes primary succession (on bare land) and secondary succession (on previously occupied land).
- Human activities such as exploitation, pollution, and habitat destruction significantly affect community structure and ecosystem functioning. Examples include overfishing, plastic pollution, and deforestation.
- Integrating traditional ecological knowledge with modern science can enhance conservation practices and ecosystem management.

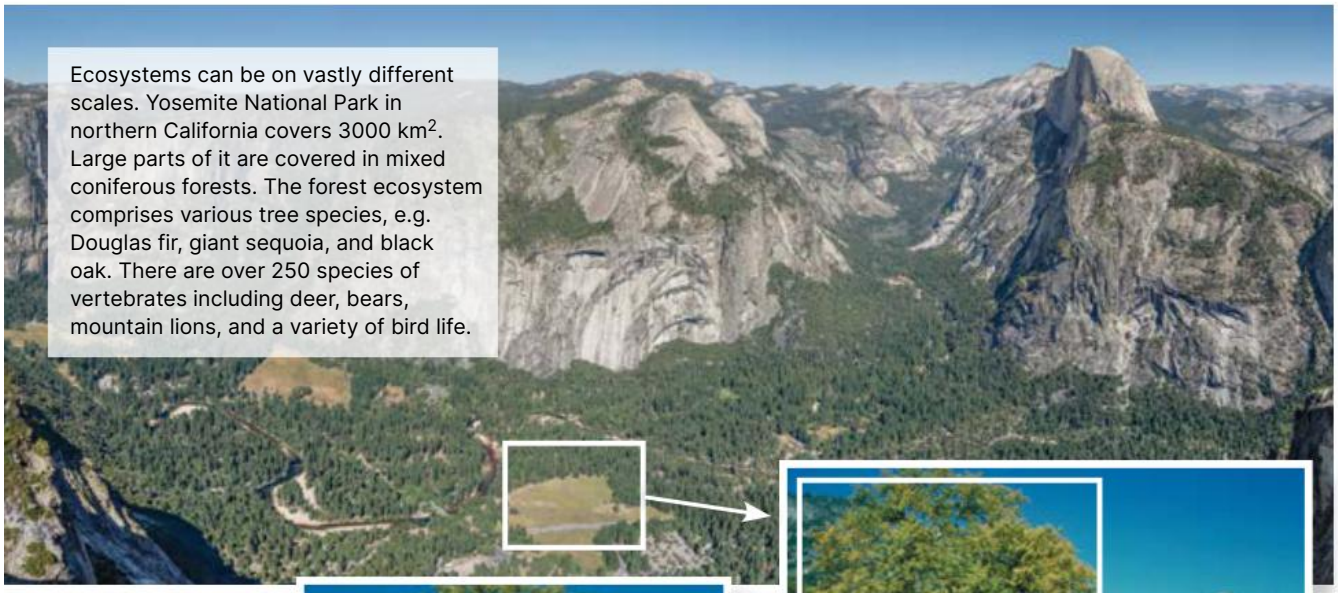
Ecological change		Activity Number
☐ 1	Explain how the scale of an ecosystem can be defined by boundaries. Describe how ecosystems and change can be defined by both time and area covered (scale).	66, 67
☐ 2	Explain what is meant by ecological succession and describe in general terms how the environment changes from one seral community (sere) to the next. Include reference to pioneer and climax communities and the types of species that make up these communities in different types of successions.	68
☐ 3	Analyse ecological data to explain or predict temporal and spatial successional changes, e.g. in a newly erupted island such as Surtsey or in a eucalypt forest after disturbance. Describe which factors are important in the colonisation (primary succession) or regeneration (secondary succession) of a habitat.	66-68, 70
☐ 4	Distinguish between primary and secondary succession, identifying the characteristic features of each type. Compare the time course for each type of succession and explain why secondary successions typically proceed more rapidly than primary successions.	68, 69
☐ 5	Describe features of pioneer species and explain how these make them effective colonisers. Identify typical pioneers in primary and secondary successions. Describe the role pioneer species have in creating an environment that will support the later communities, considering soil formation, moisture retention, shade, and moderation of environmental extremes.	68, 69
☐ 6	Distinguish between r-selected and K-selected species and describe features correlated with each type. Predict what type of selection (and species) would dominate in an early successional community and in a climax community.	71
☐ 7	Predict the impact of human activity on biodiversity and the magnitude, duration, and rate of environmental change, including exploitation and pollution. Compare exploited environments to protected environments, e.g. marine parks.	75, 76

Interpreting the past and predicting the future		
☐ 8	Explain how the carrying capacity of an ecosystem is affected by changes to biotic and abiotic factors, including climatic events.	74
☐ 9	**SHE/SI:** Analyse data from the fossil record to interpret past ecosystems, including changes to their biotic and abiotic components. Explain how information from fossils and their living representatives can be used to infer what past environments were like.	72, 73
☐ 10	**SHE/SI:** Explain how indigenous knowledge can be used to complement conservation practices and manage natural ecosystems more effectively.	77

66 Scales of Ecosystems

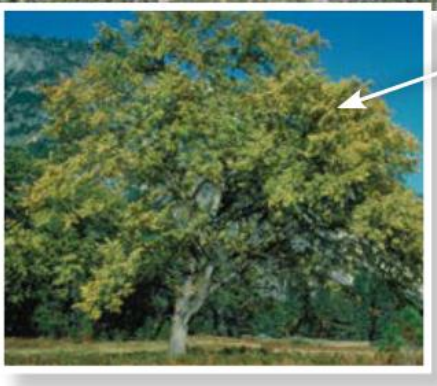
Key Idea: Ecosystems have no fixed boundaries and so can vary in size.

Ecosystems can be any size. The only limit is the size determined by the human observer. For example, a tree can be thought of as an ecosystem if we ignore the individual comings and goings of animals and look at the system as a whole. However, the tree may be part of a larger ecosystem, a forest, which again is part of a larger biome, and so on until we encompass the entire **biosphere**: the narrow belt around the Earth containing all living organisms.



Ecosystems can be on vastly different scales. Yosemite National Park in northern California covers 3000 km^2. Large parts of it are covered in mixed coniferous forests. The forest ecosystem comprises various tree species, e.g. Douglas fir, giant sequoia, and black oak. There are over 250 species of vertebrates including deer, bears, mountain lions, and a variety of bird life.

Tuxyso / Wikimedia Commons / CC-BY-SA-3.0



The ecosystem of a tree can be quite varied. The tree provides energy and materials for insects and other invertebrates that live on or in it. Bacteria and fungi decompose leaves and dead material on the tree or in the soil. The tree provides roosts for birds and fruit or seeds as a food source.

Within the forested areas, there are clearings that consist of grasses and scrub with the occasional isolated tree. These areas provide good grazing for deer and open hunting areas for owls.

Tidal rock pools are micro-ecosystems. Each one is slightly different from the next, with different species assemblages and **abiotic factors**. The ocean in the background is an ecosystem on a vastly larger scale.

Animals can be ecosystems in the same way as trees. All animals carry populations of microbes in their gut or on their bodies. Invertebrates, such as lice, may live in the fur and spend their entire lifecycle there.

Seasonal rainforest, Queensland, Australia

The many biomes around the Earth are, in part, produced its wind patterns. Tropical regions are found around the equator, deserts and temperate regions at higher latitudes, and cold deserts at the poles.

1. Describe the borders that would define each of the three Yosemite ecosystems described above:

(a) _____

_____

(b) _____

_____

(c) _____

_____

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67 The Scale of Environmental Change

Key Idea: Environmental changes occur on many scales.

Environmental changes come from three sources: the **biosphere** itself, geological forces (crustal movements and plate tectonics), and cosmic forces (the movement of the Moon around the Earth, and the Earth and planets around the Sun). All three forces can cause cycles, steady states, and trends (directional changes) in the environment. Environmental trends such as climate cooling cause long term changes in communities. Some short-term cycles may also influence patterns of behaviour and growth in many species, regulating internal, cyclical behaviour patterns, called biological rhythms.

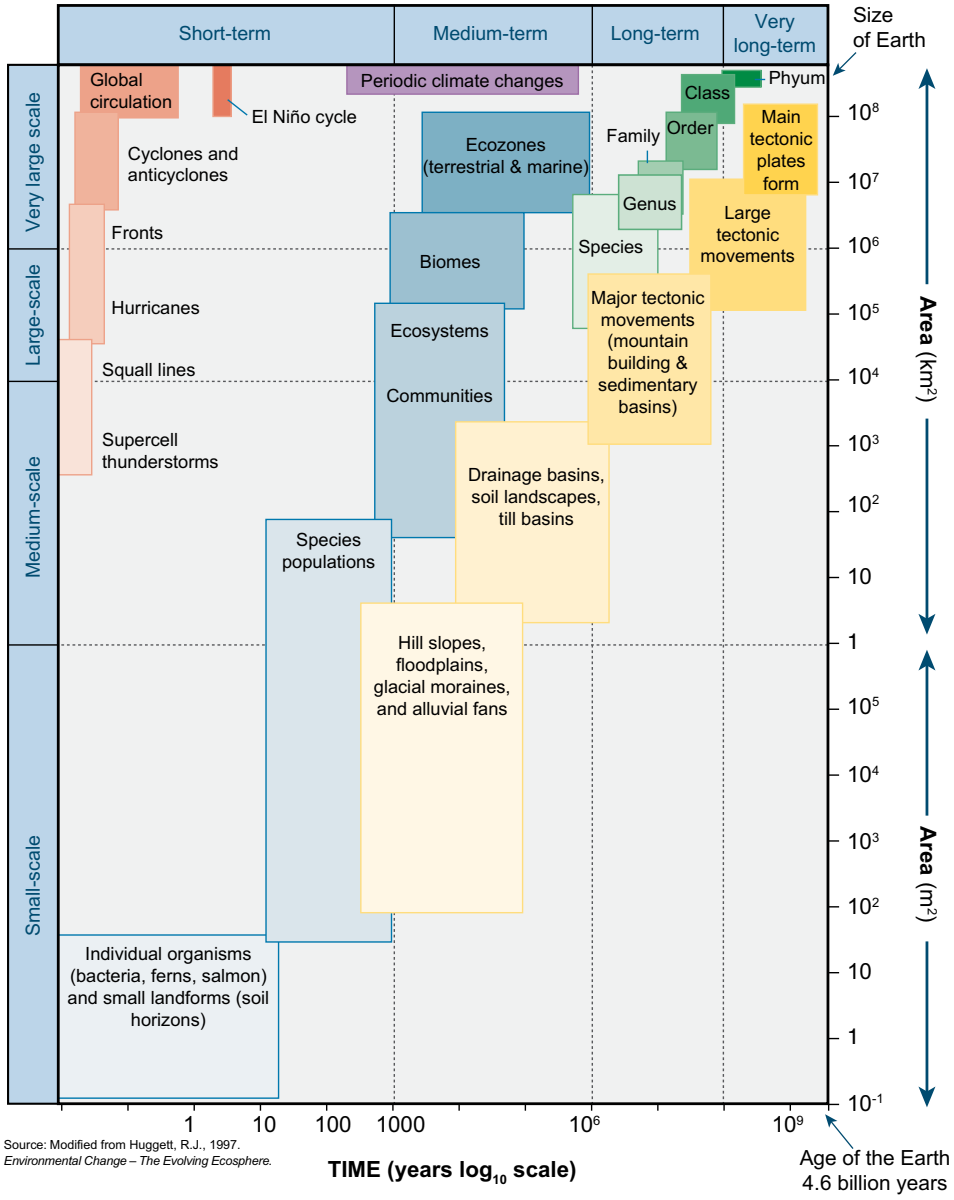
Climatic change during the last 2-3 million years has involved cycles of glacial and interglacial conditions. These cycles are largely the result of an interplay between astronomical cycles and atmospheric CO_2 concentrations.

Volcanic eruptions may have a large effect on local biological communities. They may also cause prolonged changes to regional and global weather, e.g. Mount Pinatubo eruption, 1991.

Some weather patterns are responsible for subtle changes to ecosystems, such as the gradual onset of a drought. They may also provide large scale and forceful changes, such as those caused by hurricanes or cyclones.

Time scale and geographic extent of environmental change

(X axis = time scale, Y axis = geographic extent)



Source: Modified from Huggett, R.J., 1997. *Environmental Change – The Evolving Ecosphere.*

1. Periodic, long term changes in the Earth's orbit, a change in the Sun's heat output, and continental drift may have been the cause of cycles of climate change in the distant past. These climate changes involved a cooling of the Earth.

   (a) Identify the term referring to these periods of global cooling: _____

   (b) Describe two changes to the landscape that occurred during this period: _____

2. Identify the main causes of environmental change: _____

   _____

3. Identify the scale of the following ecological or geographical changes:

   (a) Supercell thunderstorm: _____

   (b) Biome: _____

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68 Primary Succession

Key Idea: Primary succession occurs in a region where there is no pre-existing vegetation or soil.

Ecological succession (often just called succession) is a natural process of progressive change in an ecological community. It occurs as a result of the dynamic interactions between biotic and abiotic factors over time. Earlier communities modify the physical environment, making it more favourable for the species that make up later communities. Over time, a succession may result in a stable **climax community**. When succession occurs in a region where there is no pre-existing vegetation or soil it is called **primary succession**.

The composition of the community changes with time

Lower diversity → *Higher diversity*

Past seral community

Some species in the past seral community did not tolerate the changes in the environment.

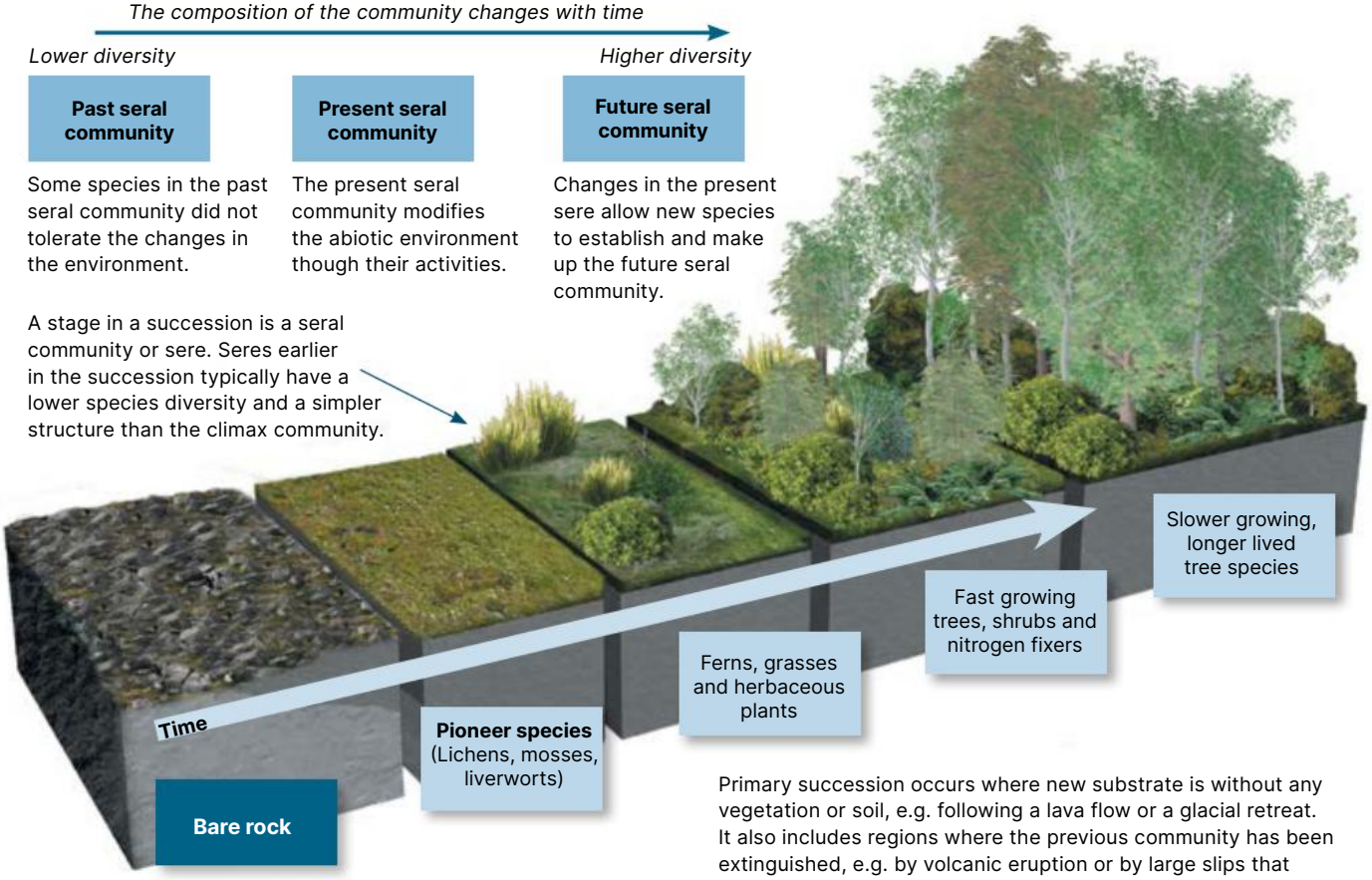
Present seral community

The present seral community modifies the abiotic environment though their activities.

Future seral community

Changes in the present sere allow new species to establish and make up the future seral community.

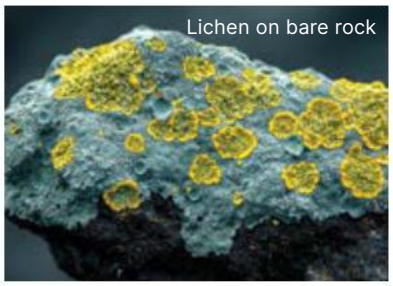
A stage in a succession is a seral community or sere. Seres earlier in the succession typically have a lower species diversity and a simpler structure than the climax community.



Primary succession occurs where new substrate is without any vegetation or soil, e.g. following a lava flow or a glacial retreat. It also includes regions where the previous community has been extinguished, e.g. by volcanic eruption or by large slips that expose bedrock. The time period for recolonisation of the area and the composition of the final community depend on the local environment. Recovery is quicker when vegetation is close.

Features of pioneer species

The earliest **pioneer species** are microorganisms (e.g. cyanobacteria) and simple photosynthetic plants and algae. They are able to survive on exposed substrates lacking in nutrients and make their own food using sunlight energy. Even at this simple level, ecological associations are important. Lichens, which are important pioneers, are a symbiosis between fungi and algae. Associations between mosses and cyanobacteria (which can fix atmospheric nitrogen) are also important. Pioneers begin the process of soil formation by breaking down the substrate and adding organic matter through their own death and decay. Their growth thus creates more favourable environment for vascular plant growth.



Lichens will help create an environment in which small vascular plants are able to establish and grow.

Associations between mosses and cyanobacteria provides mosses with nitrogen.

Bob Blaylock CC 4.0

1. Describe situations in which a primary succession is likely to occur: _____

2. (a) Identify pioneers during the colonisation of bare rock: _____

   (b) Describe two important roles of the species that are early colonisers of bare slopes: _____

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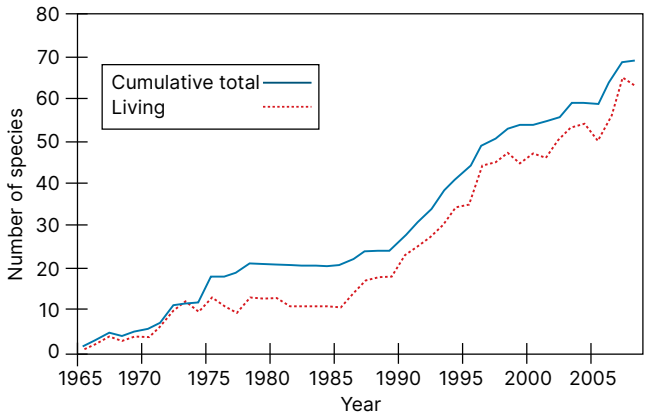
Surtsey: A case study in primary succession

Surtsey Island is a volcanic island lying 33 km off the southern coast of Iceland. The island was formed over four years from 1963 to 1967 when a submarine volcano 130 m below the ocean surface built up an island that initially reached 174 m above sea level and covered 2.7 km^2. Erosion has since reduced the island to around 150 m above sea level and 1.4 km^2.

As an entirely new island, Surtsey was able to provide researchers with an ideal environment to study primary succession in detail. The colonisation of the island by plants and animals has been recorded since the island's formation. The first vascular plant there (sea rocket) was discovered in 1965, two years before the eruptions on the island ended. Since then, 69 plant species have colonised the island and there are a number of established seabird colonies.

Number of vascular plant species found on Surtsey




Janke

Sea rocket


Daderot

H. peploides

The first stage of colonisation on Surtsey was dominated by shore plants colonising the northern shores, brought by ocean currents. The most successful of these was *Honckenya peploides,* which established on tephra sand and gravel flats. It set seed in 1971 and subsequently spread across the island. This initial colonisation by shore plants was followed by a lag phase with few new colonisers. A number of new plant species arrived after a gull colony became established at the southern end of the island.


Rasbak

P. annua


Mikrolit

S. phylicifolia

Populations of plants within or near the gull colony expanded rapidly to about 3 ha, while populations outside the colony remained low but stable. Grasses such as *Poa annua* formed extensive patches of vegetation. After this rapid increase in plant diversity, the arrival of new colonisers again slowed. A third wave of colonisers began to establish following this slower phase and soil organic matter increased markedly. The first bushy plants established in 1998, with the arrival of willow, *Salix phylicifolia*.

3. Explain why Surtsey provided ideal conditions for studying primary succession: _____

4. Explain why the first colonising plants established in the north of the island, but later colonisers established in the south.

5. There are three distinct phases on Surtsey where species richness increased rapidly.

   (a) Label on the graph the three phases of increase in species richness on Surtsey.

   (b) Label the two lag phases where species richness increased slowly.

6. A gull colony established on the island in 1985. What was the effect of this on the number of plant species on the island?

7. Why is the living number of plant species on the island less than the cumulative number colonising the island?

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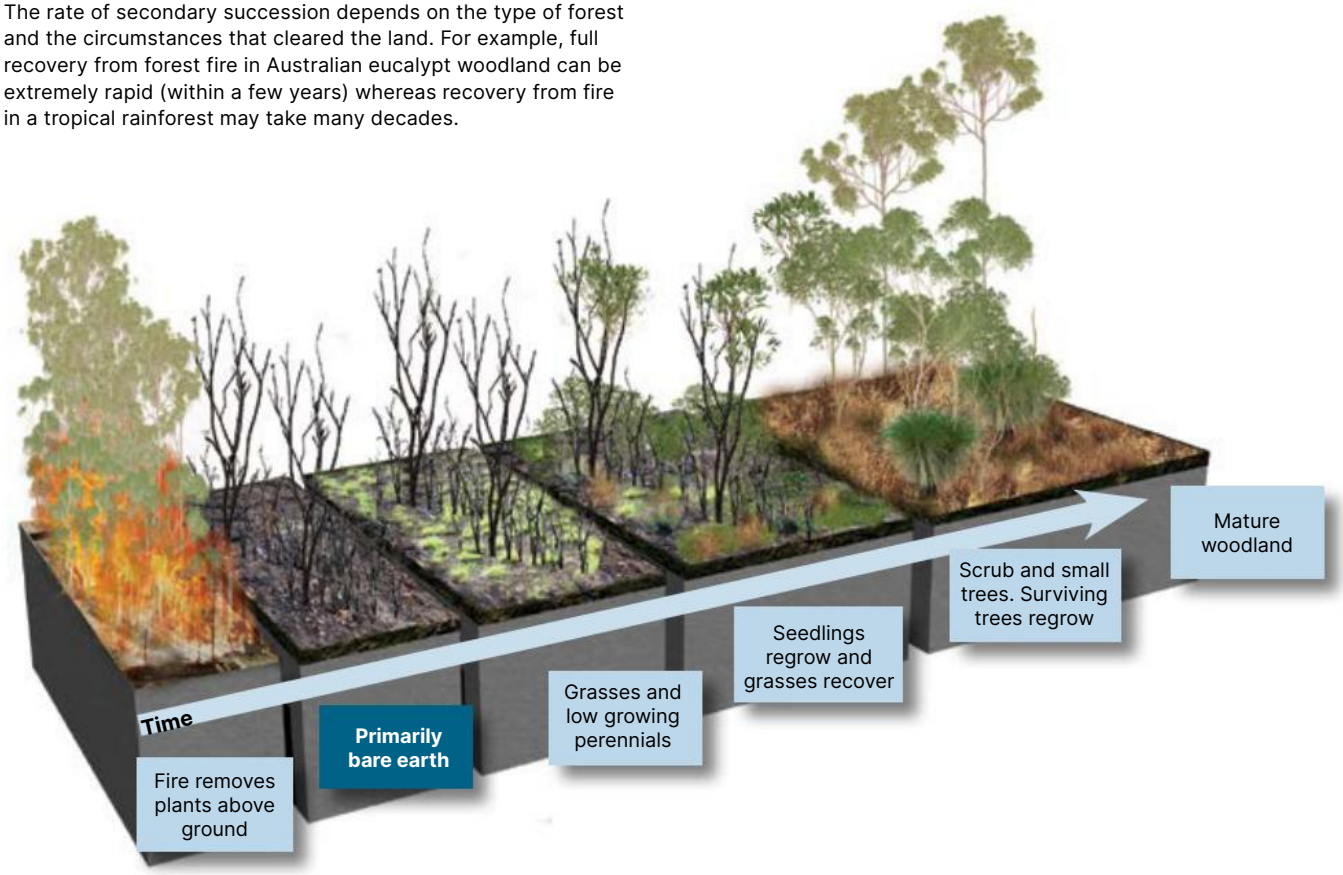
69 Secondary Succession

Key Idea: Secondary succession occurs when a previously vegetated area is cleared, leaving behind soil and seeds.

Secondary succession occurs when land is cleared of vegetation (e.g. after a fire). Soil and seed stocks are not lost and root stocks are often undamaged. As a result, the succession tends to proceed more rapidly than is the case with **primary succession**, although the time scale depends on the species involved, soil composition, and climate. Secondary succession may occur over a wide area (as after a forest fire), or in smaller areas where single trees have fallen (leaving a gap to be filled) or abandoned farmland has been left to regenerate.

The rate of secondary succession depends on the type of forest and the circumstances that cleared the land. For example, full recovery from forest fire in Australian eucalypt woodland can be extremely rapid (within a few years) whereas recovery from fire in a tropical rainforest may take many decades.



The progression of a succession depends on many factors. The rate of growth of the various plants involved is important. Plants in some climax communities grow to full height within decades (e.g. eucalypt forests) while in other communities (e.g. cold boreal forests) recovery may take many decades or even centuries.

The intensity of the clearance of the land and community can play a role in secondary succession. Low intensity fire may remove smaller grasses and low lying plants while leaving the larger trees relatively intact, whereas high intensity fires may completely remove all vegetation. Clear felling tends to affect larger trees more than undergrowth.

Succession can be suspended by frequency disturbances, so that "climax" communities never develop. Many Australian species respond to frequent fires by rapid regeneration. The nitrogen-fixing, fast growing and fire tolerant acacias are an important pioneer tree species in Australia, dominating many landscapes.

1. (a) Why does a secondary succession proceed more rapidly than a primary succession? _____

_____

_____

(b) Name an important pioneer in secondary successions in Australia: _____

SU

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70 Predicting Successional Changes

Key Idea: The nature of secondary succession depends on the original community and the nature of the disturbance.

Succession is affected by the plants that invade or grow after a clearance or occurrence of new land. There have been numerous studies on succession. Most are begun straight after a patch of land has been cleared or created. The data they provide has allowed ecologists to build up detailed models on how succession progresses in different environments and after different kinds of disturbances.

Forest fires are common in Australia and forests have evolved to survive them. In many cases, the forest can regrow within a few years, obtaining maximum recovery in a few decades (below).

The number and diversity of fire adapted species present after a fire will influence **secondary succession** growth patterns. Regeneration may come from vegetative reproduction or seed growth.

A succession sequence in a eucalypt forest may include the appearance of low herbs and bryophytes for the first 12 months. The following seedling stage is dominated mainly by eucalypt and acacia seedlings, but other shrubs, bracken, and tree ferns may also be present.

Daniel Cleaveley cc3.0

1. Bush fires (above) are more common in some types of forest (e.g. dry sclerophyll forests) than cool, temperate forests. Fire adapted vegetation types in Queensland include eucalypt forests, woodlands, paperbark forests, grasslands, and heathlands.

RA

2. Bush fires are a common occurrence in Australia. Some occur naturally (e.g. start from a lightning storm) while others are set by humans either intentionally or unintentionally. Many plant species have evolved to survive the effects of bush fires (e.g. the grass tree), while others, such as many species of Eucalyptus, need fires in order to survive and reproduce. Several months after a fire, trees can be seen regenerating from the base (above).

Many factors affect forest regeneration after a fire including the composition of the forest, the type and duration of the fire, and whether large trees are destroyed leaving gaps in the canopy.

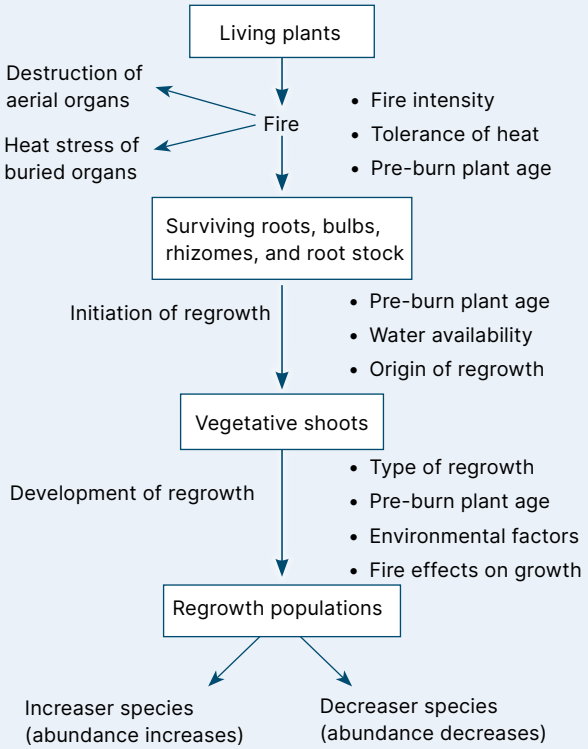
3. During regeneration, competition between species is intense. Acacias are early pioneers in secondary successions, seeding prolifically. Fast growing *Eucalyptus* species begin to dominate as they overtop smaller tree species.

Ethel Aardvark cc 3.0

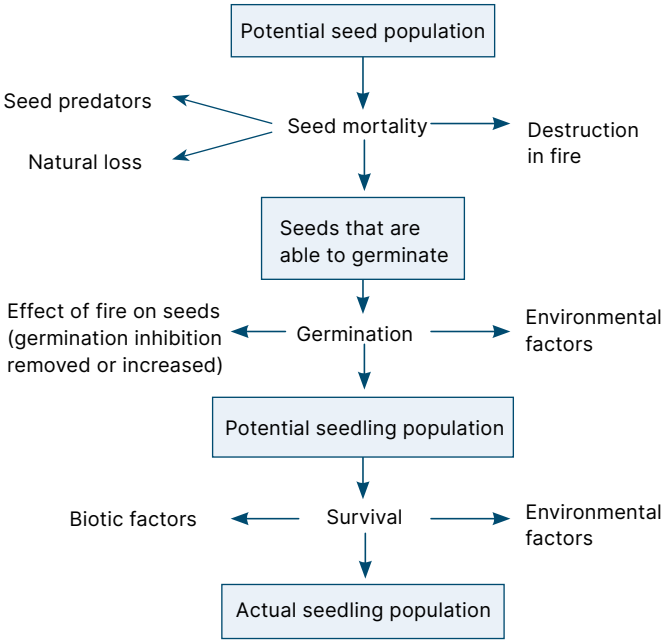
The bimblebox is found associated with acacia species in semi-arid woodlands.

The diagrams below show how various factors affect the recovery of forests after fire:

Factors affecting regeneration by vegetative means



Factors affecting regeneration by residual seeds



Modified from Vegetation succession after fire in sclerophyll woodland communities in south-eastern Australia Rosemary W. Prudie & R.O. Slayter, Australian Journal of Ecology (1976), I, 223-236

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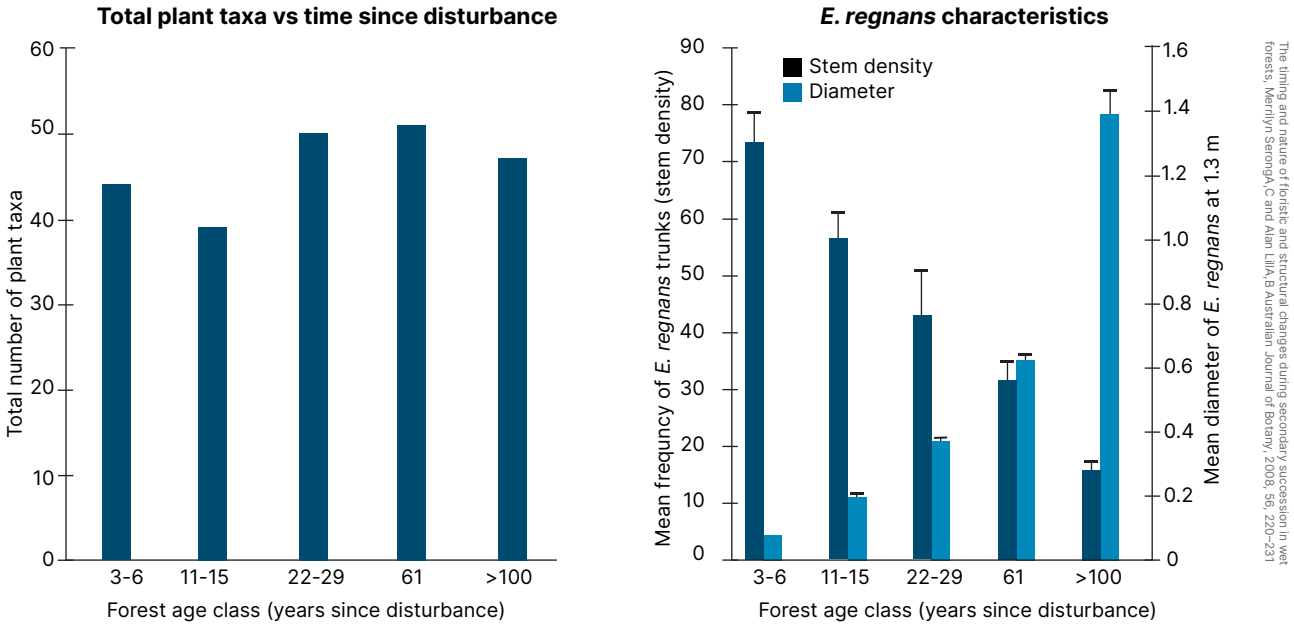
The recovery of forests can be measured by measuring similar forests of different times since disturbance. The results of a 2008 study of Australian mountain ash (*Eucalyptus regnans*) forest in Victoria are shown below:



The timing and nature of floristic and structural changes during secondary succession in wet forests, Merrilyn SerongA,C and Alan LillA,B Australian Journal of Botany, 2008, 56, 220–231

1. Explain why succession from cleared agricultural land would follow a different course than succession after a forest fire:

2. Why would the age of a stand of trees affected by fire be important in the recovery of the forest?

3. What kind of environmental factors might affect how a forest regrows after a fire?

4. Some plants have seeds that only germinate after a fire. Why might these types of plants increase in number after a fire?

5. What happens to the total number of plant taxa over time since a disturbance and why might this be?

6. (a) Why might the stem density of *E. regnans* decrease over time?

   (b) Would you expect this trend to continue? What factors might alter your prediction? Explain:

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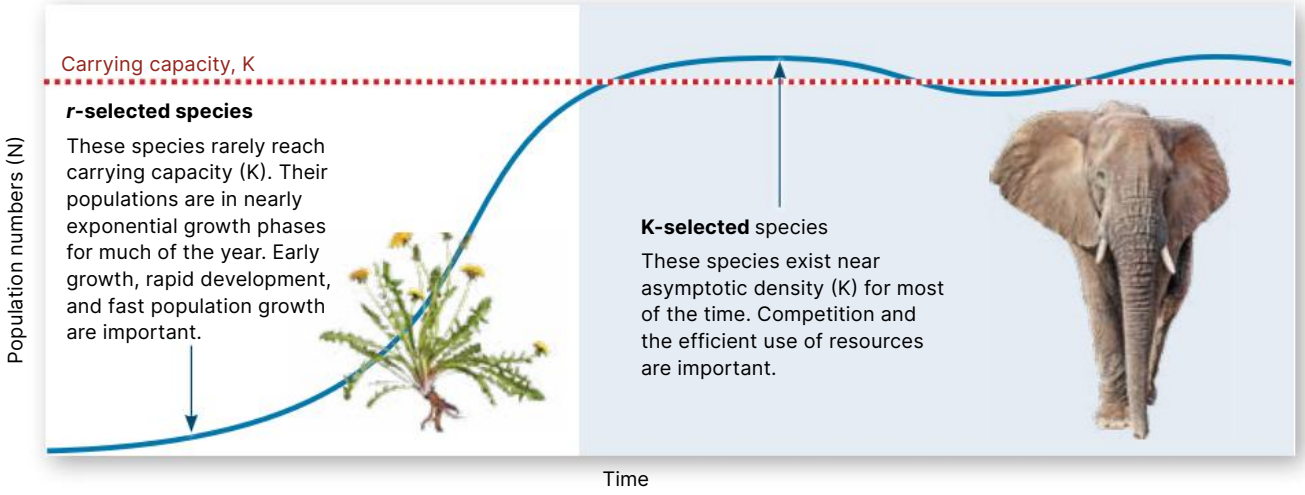
71 *r* and K Selected Species

Key Idea: *r*-selected species have high biotic potentials (*r*) and are typical early colonisers in ecological successions. K-selected species have lower biotic potentials and typically late successional species, existing near carrying capacity.

The maximum rate at which a population can grow (its intrinsic rate of increase or *r*) is called its biotic potential. It is a measure of reproductive capacity and is assigned a set value that is specific to the organism involved. Species with high biotic potentials are called **r-selected** species (*r* dominates in the life cycle). They include algae, bacteria, rodents, many insects, and most annual plants. These species grow rapidly in disturbed environments and are typically early colonisers in **ecological successions**. **K-selected** species have lower biotic potentials, typically live longer and are usually late successional or climax species, existing at or near carrying capacity (K). They include most large mammals, birds of prey, and large, long-lived plants. Whereas rapid growth, early reproduction, and productivity are important for colonising species, efficiency of resource use and competitive ability dominate in late successional communities.

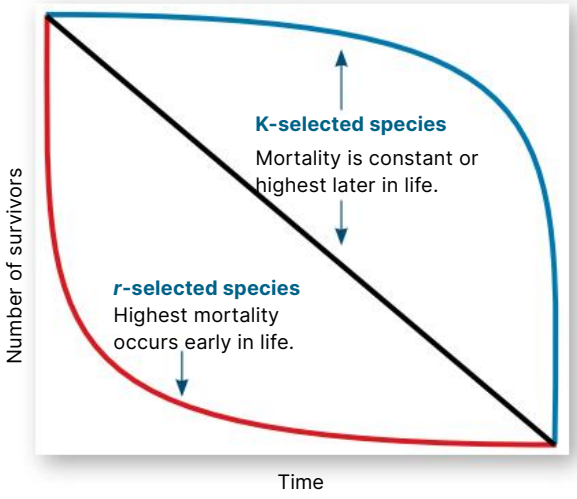


Recall the features of *r* and K selected species described earlier.

r-selected species have short lives and produce many offspring, most of which die early (right). Population size fluctuates widely.

K-selected species have long life spans and fewer offspring, many of which survive to maturity. Population size is relatively stable.

As with many things in biology, life history strategies are on a continuum, with some species falling between pure *r* or pure K strategies.



1. Explain why r-selected species tend to predominate in unstable, disturbed, or early successional communities:

2. Explain why many K-selected species tend to predominate in stable, climax communities:

3. Describe factors that might cause a change in the predominance of K-selected species in a climax community:

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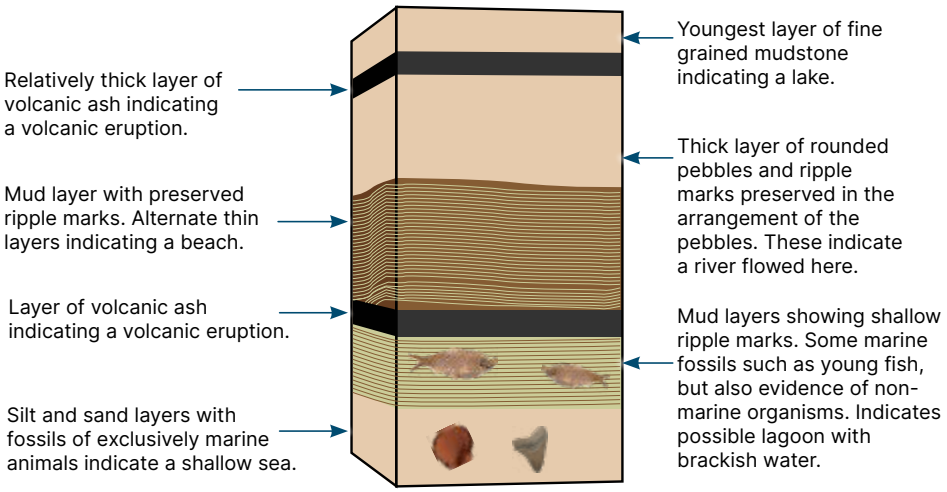
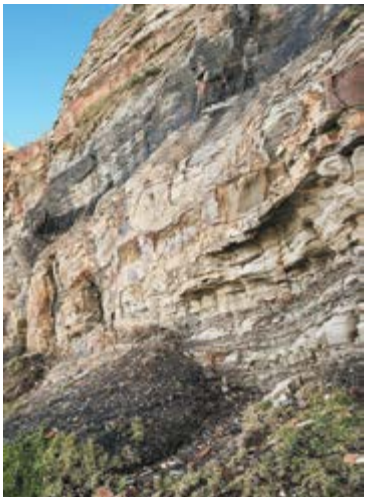
72 Interpreting Past Environments

Key Idea: Studying rocks and fossils can tell us about past environments and changes that have occurred through time. Studying rock strata can tell us about the geological history of a region. Different environments and geological events leave characteristic formations in rocks that give us clues to the past habitats, environments, and life of the area.

Interpreting rock strata

Rock strata hold clues that can be interpreted to provide information about past environments. The rock strata below illustrate how strata might change over time in a coastal area.




Sedimentary strata, New South Wales

Fossils can provide valuable information about the organisms present and their past environment. The fossils can be compared to similar organisms alive today to give us clues about the past environment. For example, stromatolites are layered rocky structures formed in shallow water by the accumulation of sediment by microbial mats (particularly cyanobacteria). Stromatolites are found today at Shark Bay in Western Australia in shallow, highly saline water. Stromatolite fossils have been found in many places around Australia indicating warm shallow seas were present over the early Australian continent.

Rygel, M.C. CC 3.0 via wikipedia

Locations of Australian stromatolite fossils

1. Write an interpretation of the history of the area around the strata shown at the top of the page. Justify your interpretation with evidence in the rocks:

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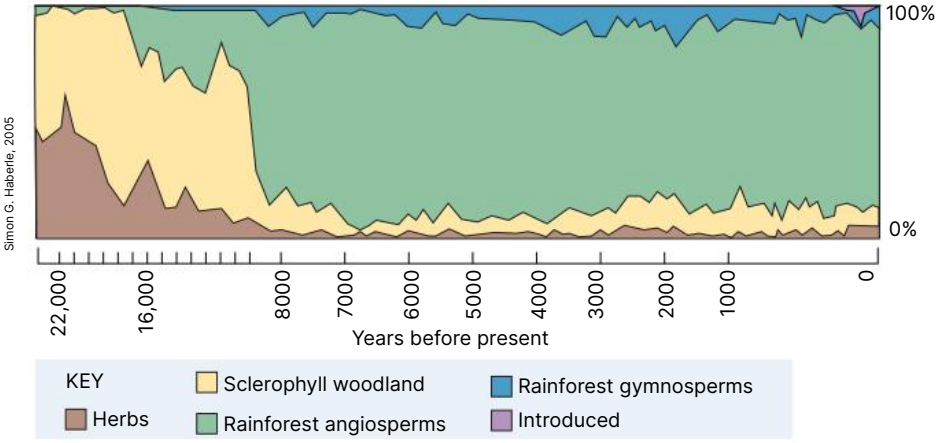
73 Analysing Ecosystem Change

Key Idea: Data from various parts of the fossil record can be used to understand ecosystem change in Australia.

Fossil records, including fossilised leaves and pollen records, can help interpret the history of **ecosystem** change in Australia. Pollens in sediments laid down on lake beds is especially useful for identifying plant types, because different plant taxa have distinctive pollen structures. Many of Australia's plant species are unique: 80% of the flowering plants occur nowhere else in the world. The eucalypts and the acacias dominate the flora over much of Australia. Many Australian flowering plants are sclerophylls, which means they are plants with hard and often small leaves. Woody, fire adapted sclerophyll species have become more common with the increase in the incidence of fire.

Pollen record from Lake Euramoo, Northern Queensland

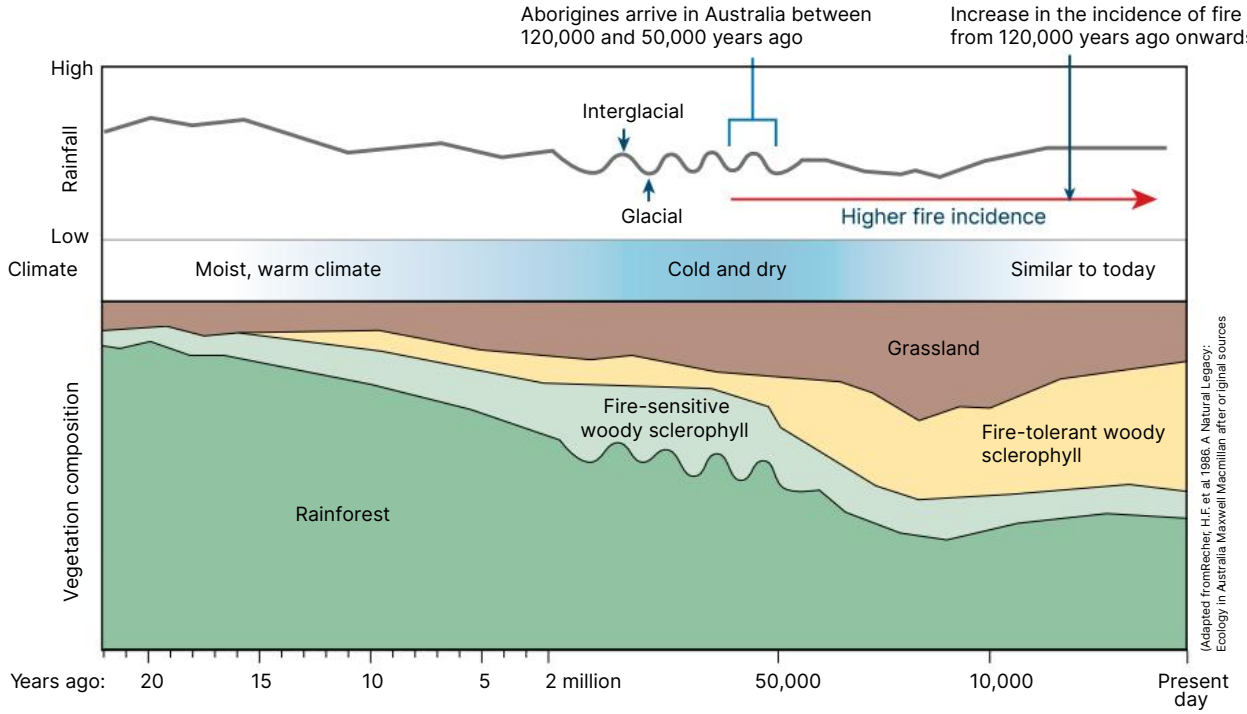


Simon G. Haberle, 2005

Glpww cc 4.0

Lake Euromoo, Tablelands, north Qld

Changes in Australian climate and vegetation



(Adapted from Recher, H.F. et al 1986. A Natural Legacy: Ecology in Australia. Maxwell Macmillan after original sources

1. (a) How has the forest around Lake Euramoo changed over the last 22,000 years?

(b) Why is taking pollen cores a good way to find out about the natural history of the forests of the region?

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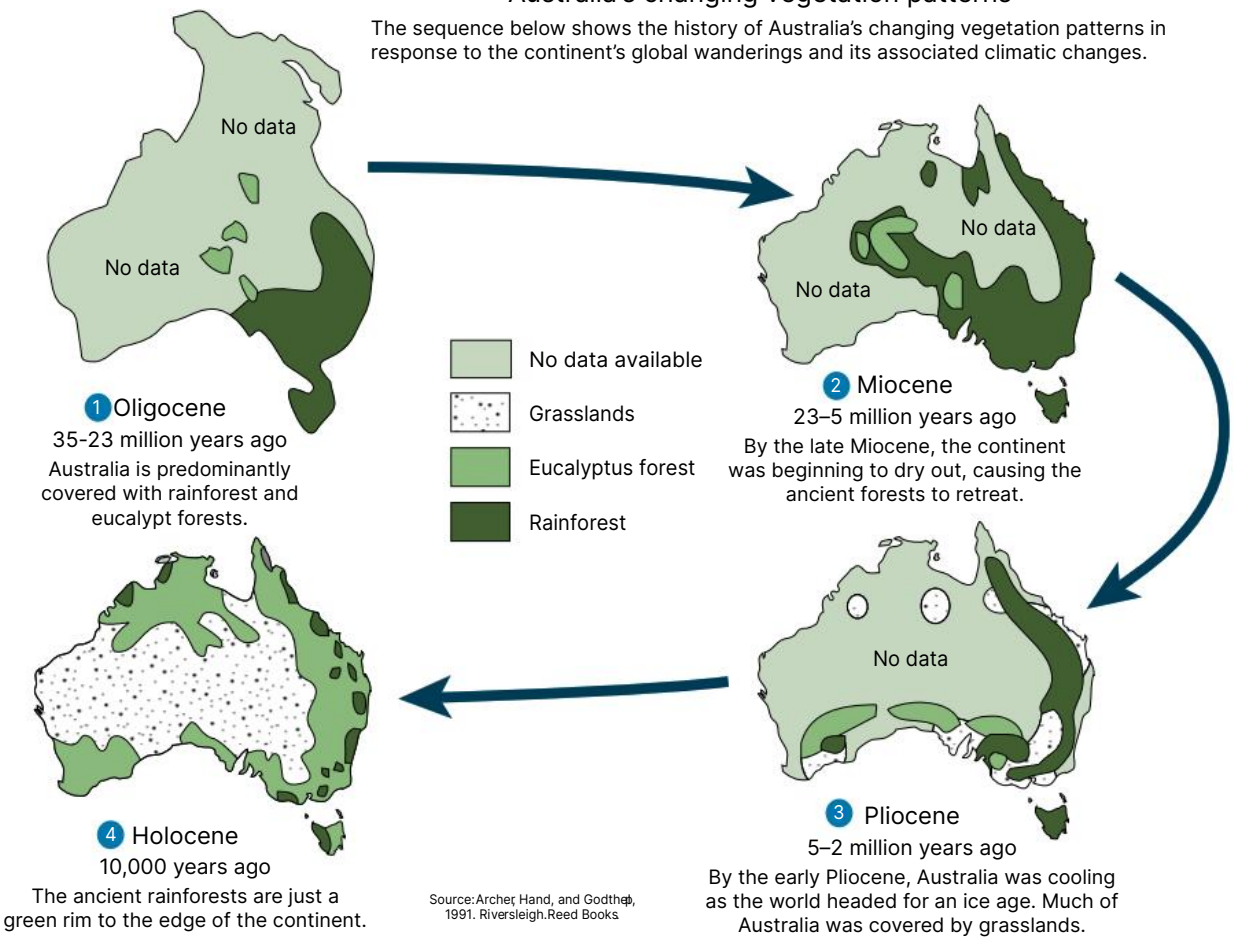
Australia's changing vegetation patterns

The sequence below shows the history of Australia's changing vegetation patterns in response to the continent's global wanderings and its associated climatic changes.



Source: Archer, Hand, and Godthelp, 1991. Riversleigh. Reed Books.

2. Describe the conditions during the glacials and interglacials, 2 million to 10,000 years ago:

   (a) Rainfall: _____

   _____

   (b) Climate: _____

3. During this time, the extent of the rainforests varies (oscillates), as well as generally declining.

   (a) What was the likely cause of the oscillations in rainforest abundance? _____

   (b) Why was there a general decline in rainforest abundance? _____

4. The grasslands have gradually expanded their range and become more abundant.

   (a) Approximately when did this expansion begin? _____

   (b) What was the likely cause? _____

   _____

5. The abundance of fire-tolerant woody sclerophyll forest increased towards the end of the glacial periods.

   (a) What physical factor was probably responsible for this increase? _____

   (b) Why are early humans also implicated? _____

6. Research the globe's climatic zones. How do these help explain Australia's current vegetation? _____

   _____

   _____

   _____

   _____

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74 Changing Environments Affect Carrying Capacity

Key Idea: Organisms may need to exploit several different habitats to get the resources they need to survive.

Some animals range over a variety of habitats, partly in order to obtain different resources from different habitats, and sometimes simply because they are forced into marginal habitats by competition. Dingoes are found throughout Australia, in **ecosystems** as diverse as the tropical rainforests of the north to the arid deserts of the central Australia. Within each of these ecosystems, they may frequent several habitats or microhabitats.

Habitats provide resources

Species may tolerate wide variations in a range of physical and biotic factors. As a result of this tolerance range, the habitat that is occupied by members of a species may be quite variable.

The important thing is that the habitat provides resources for the organisms that live there. These resources include water, food, shelter, and places to raise offspring.

Some habitats can be richer in resources than others and are usually described with reference to their main features. For example, riverine habitats (rivers and creeks containing water and thick vegetated cover) provide water, food, and cover (right).

Dingo habitats

Dingoes (right) are wild dogs found throughout Australia. The table on the far right gives information about five dingo packs at one location, including how much of their territory is made up of riverine areas. Kangaroos are the main prey for these dingoes.

Dingo pack name	Territory area (km^2)	Pack size	Dingo density	% of total territory made up of riverine areas
Pack A	113	12	10.6	10
Pack B	94	12		14
Pack C	86	3		2
Pack D	63	6		12
Pack E	45	10		14

1. Calculate the density of each of the dingo packs per 100 km^2 using the equation below, and record it in the table above. The first one has been done for you.

Density = pack size ÷ territory area x 100

2. (a) Plot a scatter graph (right) of dingo density per 100 km^2 versus how much of their territory is made up of riverine areas for each pack.

(b) Describe the relationship between dingo density and amount of riverine area:

_____

_____

_____

_____

(c) Can you explain why this relationship might occur?

_____

_____

_____

_____

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75 The Impact of Humans on Ecosystems

Key Idea: The exploitation of environmental resources by humans has had a negative impact on the environment.

Human activity can have very negative effects on surrounding **ecosystems**. Unrestricted mining, logging, or harvesting of natural populations can alter the balance of ecosystems and affect their ability to provide services such as carbon storage and water purification. There are many examples illustrating how overexploitation of resources affects the diversity, functioning, and stability of natural ecosystems, sometimes even resulting in species extinctions.

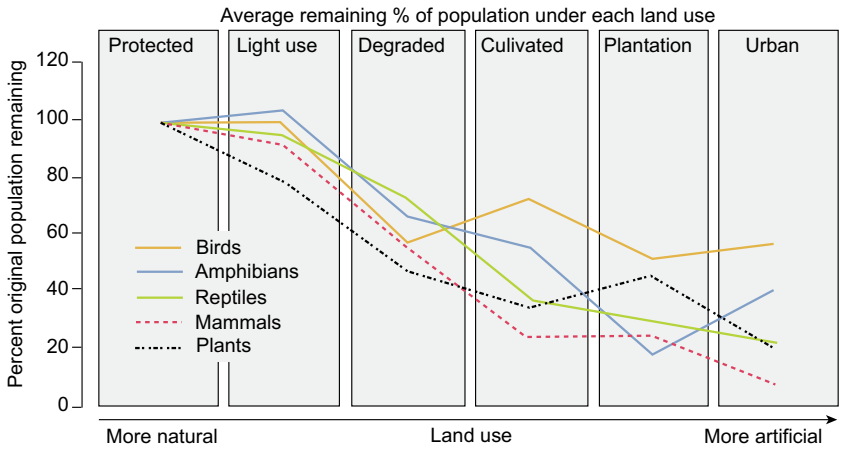
Piet Spaans cc2.5

Human exploitation of natural populations has driven some species to the brink of extinction, or significantly reduced their populations. Examples include the hunting of whales and overfishing of many fish populations such as orange roughy.

One of the most important drivers of ecosystem change is habitat destruction. Wild areas are cleared to make way for farms, mining, or housing. This dramatically reduces **biodiversity** and ecosystem services and can affect both the local and wider climate.

Demand for food increases as the population grows. Modern farming techniques favour monocultures (growing a single crop type) to maximise yield and profit. However, monocultures are low diversity systems and do not allow for many different organisms to thrive.

Many industries depend on the combustion of fossil fuels and this contributes to global warming (the continuing rise in the average temperature of the Earth's surface). Global warming and associated shifts in climate will affect species distributions, breeding cycles, and patterns of migration. Species unable to adapt are at risk of extinction.



Nearly 40% of the Earth's land surface is devoted to agricultural use. In these areas, the original biodiversity, a polyculture of plants and animals, has been severely reduced. Many of these areas are effectively monocultures, where just one type of plant is grown. The graph (above) shows that, as the land is more intensively used, the populations and variety of plants and animals fall.

1. As a group, discuss the effects of human activities on local and global ecosystems. After the discussion, make your own predictions about the effect of an expanding human population on biodiversity and the scale and rate of ecosystem change. Summarise your predictions and your reasoning below:

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Plastic pollution in the Pacific

It is estimated that around 8 million tonnes of plastic enters the oceans each year. Some of this comes from plastic waste thrown away in cities, but the vast majority comes from abandoned fishing gear. The circulation of the oceans tends to concentrate the plastic into certain areas of the ocean. In the South Pacific, plastic is concentrated by the South Pacific Gyre, a huge system of ocean currents that rotates in an anticlockwise direction. In the North Pacific, plastic is concentrated by the North Pacific Gyre, which rotates in a clockwise direction. The concentration of plastic in the North Pacific is sometimes called the Great Pacific Garbage Patch.

The effect of plastic in the marine environment can be dramatically seen on islands near the centre of these gyres. Henderson Island in the South Pacific is one.

Plastic is often mistaken by seabirds, e.g. albatross, for food and is eaten or fed to chicks on the nest. Every year, thousands of albatross young die from ingesting plastic products.

Henderson Island

Henderson Island sits in the South Pacific Ocean. It is part of the Pitcairn group and is about 5000 km from the nearest significant land mass. The island is just 37.3 km^2 and uninhabited. A study in 2017, led by Jennifer Lavers, measured the amount of plastic on the island's beaches. Her team measured the amount of plastic already on the beach, and then cleared a control area to measure the rate at which plastic accumulated. They estimated that over 13,000 items accumulated per kilometre of beach per day.

Plastic debris on beach, Henderson Island

	Mean density on beach (items per m^2)	Estimated total debris on beach (items)		Estimated island total including buried items and back beach (items)	
Site		**Number**	**Mass (kg)**	**Number**	**Mass (kg)**
North Beach	30.3	812,116	2985	7,634,052	4,744
East Beach	239.4	3,053,901	12,611	30,027, 343	12,857
Total		3,866,017	15,597	37,661,395	17,601

Jennifer L. Lavers. Exceptional and rapid accumulation of anthropogenic debris on one of the world's most remote and pristine islands, 2017

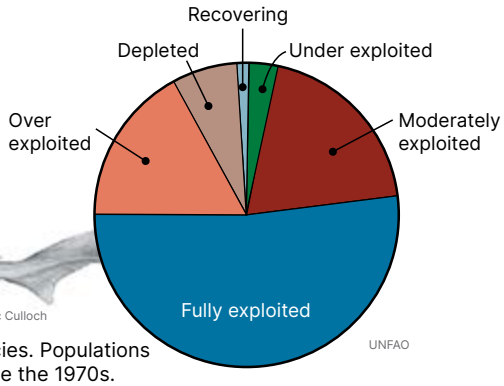
The effect of overfishing

52% of the world's fished species is already fully exploited. Any increase in catch from these species would result in over-exploitation. 7% of the fish species are already depleted and 17% are over-exploited.

In Australia, 14% of managed fish stocks are over exploited and 21% are uncertain. Overexploitation of a fish population can result in the population declining rapidly, especially if mature, breeding individuals are targeted more often than young or old individuals.

The decline of a fish population can mean that other species increase to fill the gap and this can alter the local marine ecosystem. If a predatory species is over exploited, prey species can increase, or other predatory species can increase to take their place.

Percentage exploitation of global fisheries



A. R. Mc Culloch

Gulper sharks are an overexploited species. Populations have dropped by an estimated 99% since the 1970s.

2. Explain how plastic thrown away in a city on the east coast of Australia can end up on a beach on Henderson Island:

3. How does plastic in the ocean affect seabirds on isolated Pacific islands?

4. How can overexploitation of a species of fish affect an ecosystem?

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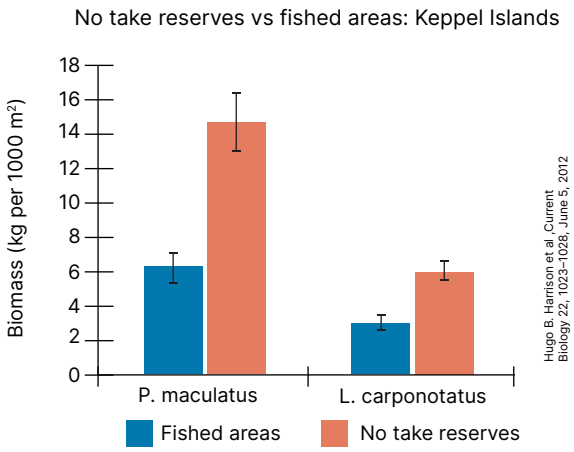
76 Marine Parks and Their Effects

Key Idea: Marine parks deliver both direct and indirect protection to marine organisms.

Marine parks in Australia are divided between marine parks managed by the Australian government and marine parks managed by state governments. For example, the Great Barrier Reef is a national marine park (The Great Barrier Reef Marine Park). However, the area of sea between the land and the reef is the Great Barrier Reef Coast Marine Park, managed by the Queensland Government. Two other state marine parks, the Moreton Bay Marine Park and the Great Sandy Marine Park, are also established in Queensland waters. Establishing marine parks allows the government to vary the level of protection for marine environments depending on various environmental and community factors.

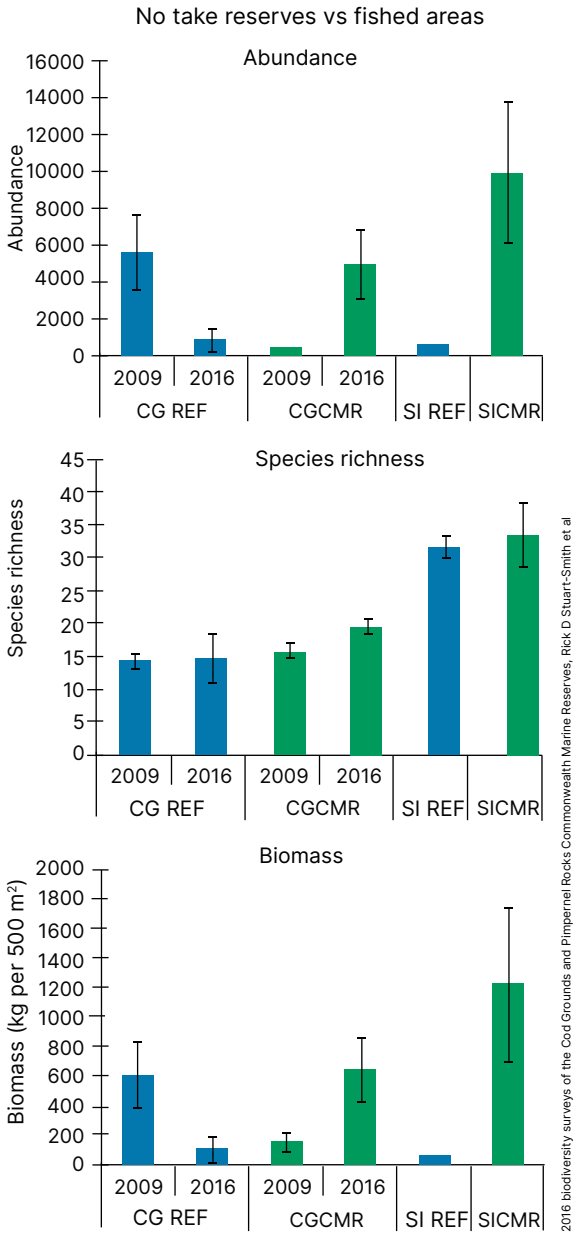
Marine parks export fish to other areas

There are different levels of protection within marine parks. National park zones (green zones) are no take areas, where fishing is completely banned. Studies have shown that not only is the density of marine life higher in these zones than elsewhere (right, top graph), but they are exporters of juvenile fish to other areas. A study in 2012 focussed on popular fisheries species: coral trout, *Plectropomus maculatus*, and stripey snapper, *Lutjanus carponotatus*, around the Keppel Island group in the Great Barrier Reef Marine Park. It found that 83% of coral trout juveniles and 55% of stripey snapper juveniles were exported to other parts of the reef. It estimated the no-take zone that covered 28% of local reef area produced at least half of the juvenile fish within 30 km of the reserve.



Marine parks provide comparisons to exploitation areas

No take marine parks provide comparisons to places where fishing is allowed. The Cod Grounds Commonwealth Marine Reserve (CGCMR) is located four nautical miles from the coast of New South Wales off Camden Head. Pimpernel Rock is located in the Solitary Islands Marine Park, about 3 nautical miles (5.5 km) from the coast of New South Wales off Brooms Head but has Commonwealth Marine Reserve (SICMR) status. Both of these sites were compared to reference sites (REF) that had similar geographic and marine characteristics but where fishing was allowed. The results of the study are shown on the right.



1. What is the purpose of marine parks and reserves?

2. Describe the evidence that no-take marine parks and reserves fare better than marine areas with no fishing protection:

3. Why is it important to protect and monitor a wide range of marine environments?

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77 The Importance of Indigenous Knowledge

Key Idea: Recognising traditional ecological knowledge can lead to more resilient socio-ecological systems.

Increasingly, the scientific community is recognising that the inclusion of indigenous perspectives and knowledge is critical to developing strategies for more resilient and equitable natural resource management. Integrating Western science with indigenous or traditional ecological knowledge (TEK) is more likely to result in sustainable solutions to resource management problems because the knowledge, skills, and perspectives of all affected parties are included.

Bush fires and indigenous knowledge

Large parts of Australia experience extremely high temperatures in the dry season. Combined with a dry and flammable landscape, this leads to often large and dangerous bush fires. For many decades, conservation of bushland based on Western ideals has focussed on preventing fires. Only recently has it been acknowledged that this practice has contributed to some of the largest wildfires in decades because it allowed the build up of dry undergrowth and debris that would ordinarily be removed by fire every few years.

In Australia, Aboriginal knowledge of fire use for bush management is beginning to be employed, including the use of back burning and controlled burns. Traditional Aboriginal knowledge of cool fires, soils, and flowering and fruiting of trees can all be used to decide when and where controlled burns can be used to manage the bush, reduce wildfires, and encourage plant growth and animal diversity.

Arsonists in the skies

Fires are known to jump across fire breaks but in some cases fires were beginning up to a kilometre from the fire break. Stories among indigenous people of North Australia held that birds were actually starting the fires. This was taken into account by Aboriginal rangers but was often met with official skepticism. In 2017, this behaviour was finally observed and documented by researchers, some 53 years after indigenous doctor Phillip W. Roberts wrote of it in his 1964 autobiography. Researchers observed at least three bird of prey species picking up smouldering twigs and flying up to a kilometre before dropping them in dry grassland. Groups of birds will then wait along the fire's edge, feeding on any prey species that flee the fire.

Fisheries management

The Torres Strait between northern Queensland and Papua New Guinea has some 580 coral reefs and some of the most extensive seagrass beds in the world. These are grazed by dugongs, a traditional source of food for the Torres Strait Islanders. The dugong is critically endangered. Using TEK, policies are being developed to help conserve the dugong and other traditional seafoods while still allowing access to this traditional food source.

Fire control, Northern Queensland

Birds of prey exploit fire front, Queensland

Dugong

Julien Willem CC 3.0

1. Why is traditional ecological knowledge important when developing forest, marine, and wildlife management policies?

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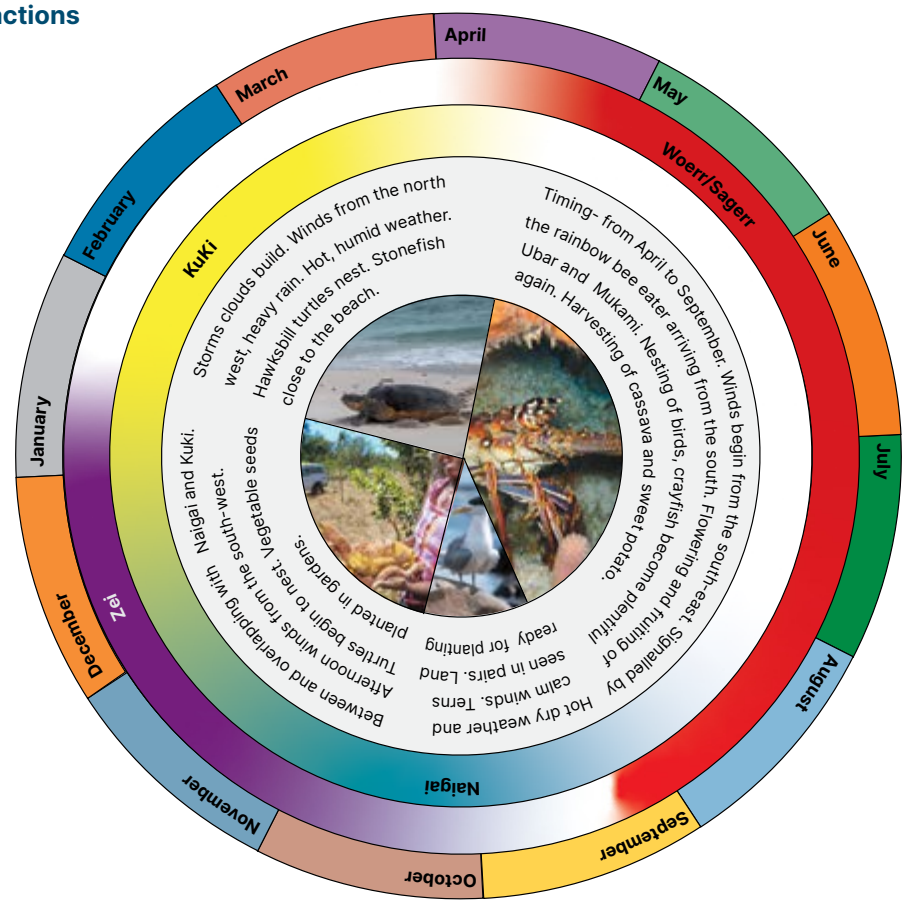
SI SHE

Calendars and ecosystems interactions

The Gregorian calendar, used by much of the world, is designed mainly around organising social events, e.g. religious holidays.

- From it, we are able to obtain exact dates as to when ecological events will (or should) occur. Seasonal dates worked into the calendar are essentially arbitrary (e.g. summer starts on December 1, not on November 30, or December 2).
- Indigenous or seasonal calendars usually operate around ecological events, such as the beginning of the wet season or flowering of certain plant species. These calendars emphasise cyclical processes, acknowledging interactions within **ecosystems**. For example, the return of the a certain bird from migration indicates certain fruits will soon be ripening.
- Seasonal calendars are linked to places, so they vary regionally. The calendar, right, is based on the area around the Masig (Yorke) Islands in the Torres Strait.



2. What is the main difference between the use of the Gregorian calendar and a seasonal calendar?

3. Describe how the seasonal calendar shows relationships within the ecosystem it is linked to:

4. Why is the indigenous seasonal calendar more useful in predicting ecosystem events than a Gregorian calendar:

5. Explain how seasonal calendars are a good way of preserving traditional knowledge:

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78 Did You Get it?

1. Test your vocabulary by matching each term to its definition, as identified by its preceding letter code.

(i) ecological succession ☐

(ii) sere ☐

(iii) K-selection ☐

(iv) primary succession ☐

(v) r-selection ☐

(vi) secondary succession ☐

A Selection that occurs in an environment at or near carrying capacity, favouring the production of a few, highly competitive offspring.

B A succession occurring on land with no plants or soil (bare rock or lava).

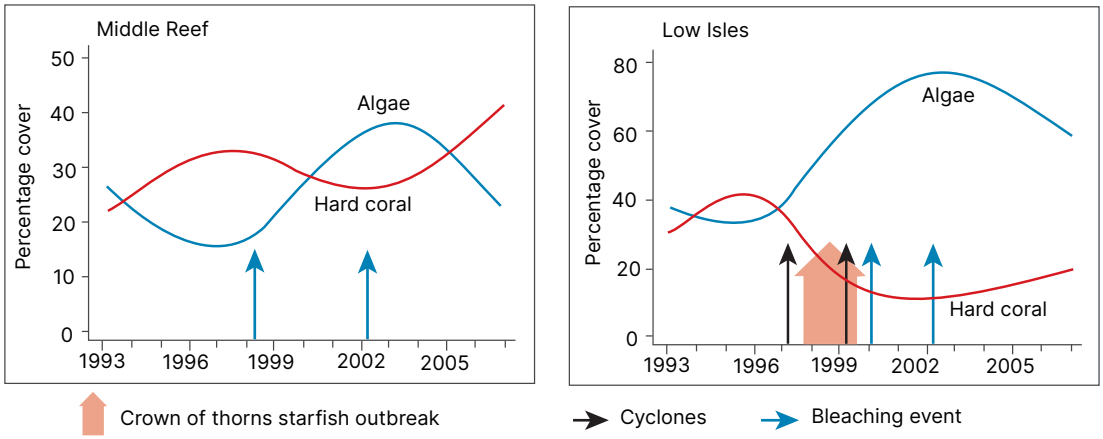
C An intermediate stage in an ecological succession.

D Selection favouring rapid rates of population increase especially prominent in species that colonise transient environments.

E A succession sequence that takes place after a land clearance event (e.g. forest fire or landslide). It does not involve the loss of seeds and root stock.

F The progression from colonisation of a newly cleared area to a climax community.

2. A study of coral and algal cover at two locations in Australia's Great Barrier Reef (below) showed how ecosystems recover after disturbance (cyclones, bleaching events, crown of thorns starfish (predator) outbreaks).



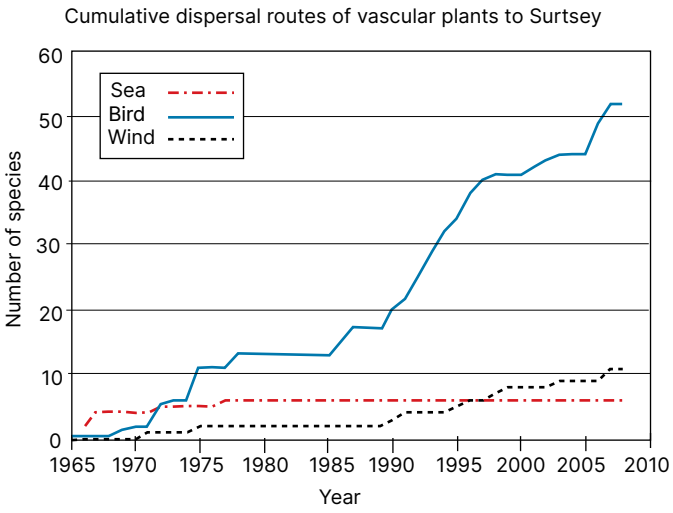
Based on the evidence, give a likely explanation for why the coral at Middle Reef remained abundant from 1993 to 2005 but the coral at Low Isles did not?

3. The graph on the right shows the dispersal routes of plants to Surtsey Island on the southern coast of Iceland.

(a) Which is the most common route by which plants reach the island?

(b) A gull colony established on the island in 1985. What was the effect of this.

(c) Suggest why the number of species arriving by sea peaked early before quickly levelling off:



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79 Synoptic Questions: Unit 3, Topic 2

1. The plot (right) shows the results of the experimental removal of the starfish *Pisaster* from a region of an ecosystem:

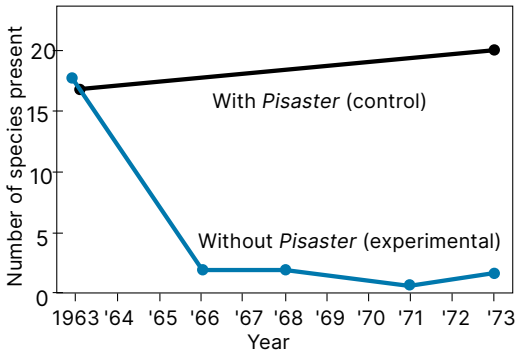
   (a) What does the graph show? _____

   _____

   (b) What do the results suggest about *Pisaster*'s role in this ecosystem?

   _____

   _____



2. (a) Use the following labels to complete the diagram of the carbon cycle shown right: a*tmosphere, geosphere, oceans, respiration (R), photosynthesis (PS)*.

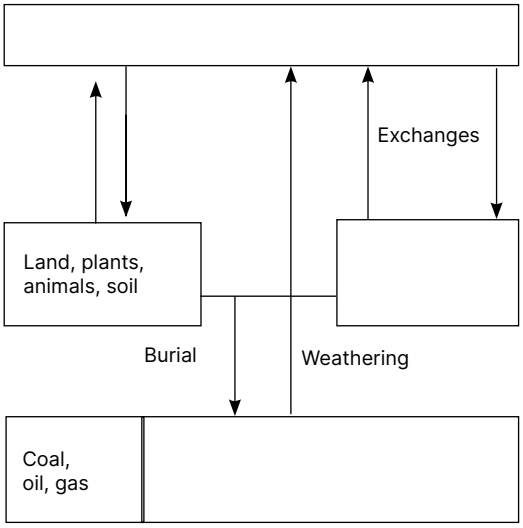
   (b) Add arrows to show deforestation (D) and combustion (C) of fossil fuels:

   (c) Combustion and deforestation result in another 9 petagrams of carbon being added to the carbon cycle. Add this value to the diagram.

   (d) About 3 petagrams is taken up by photosynthesis and 2 petagrams is taken up by the oceans. Add these values to the appropriate labels on the diagram.

   (e) How much extra carbon is actually added to the atmosphere by deforestation and combustion?

   _____



3. (a) The graph (right) shows primary production in the oceans. Explain the shape of the curves:

   _____

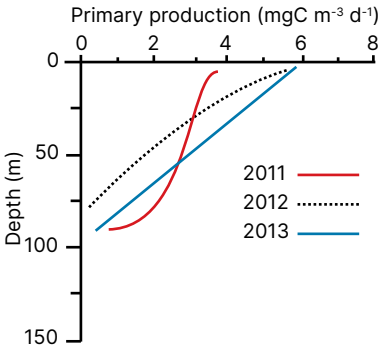
   _____

   (b) About 90% of all marine life lives in the photic zone (the depth to which light penetrates). Suggest why this is so:

   _____

   _____

   _____



4. Explain the difference between *r* and K selected species and describe the role each of these would play in the ecological succession of a disturbed environment:

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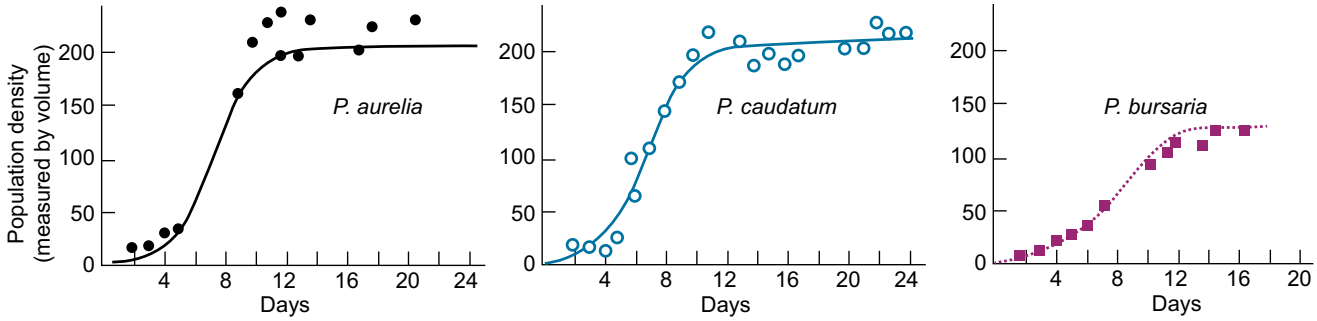
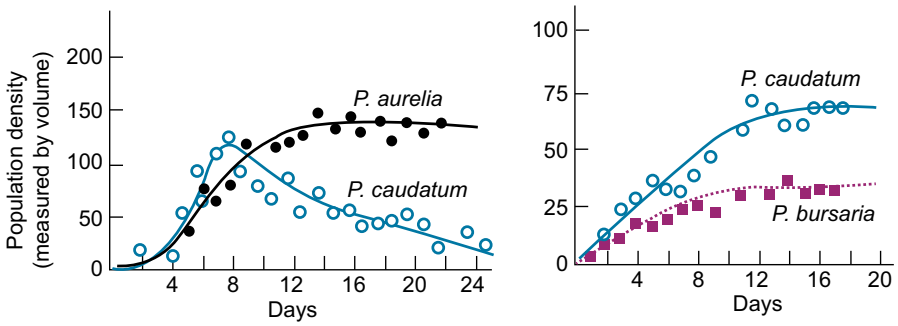
5. In 1934, Georgii Gause, a Russian biologist, carried out a series of experiments on *Paramecium*. The results led him to propose the **competitive exclusion principle**, a fundamental idea in ecology. In the first stage of the experiments, he grew three species of *Paramecium* in isolation in a nutritive medium containing their essential resource (bacterial food). Their growth curves are shown below:

Paramecium grown in isolation



In the second stage of the experiment, Gause grew *P. aurelia* and *P. caudatum* together. He found that *P. caudatum* was always out-competed and became extinct from the culture. Gause then grew *P. caudatum* with *P. bursaria*. He found they were able to exist together (but at lower numbers). Investigation found that *P. caudatum* occupied the oxygen rich top half of the culture tube, whereas *P. bursaria* retreated to the lower, poorly oxygenated region. *P. bursaria* contains symbiotic algae, which release oxygen in photosynthesis. This allows *P. bursaria* to remain in the anoxic zone.

Paramecium grown in competition



(a) What is meant by the "competitive exclusion principle"?_____

_____

_____

(b) What type of growth curve do the *Paramecium* species show when grown in isolation? _____

_____

(c) Why could *P. caudatum* and *P. aurelia* not exist together but *P. caudatum* and *P. bursaria* could? _____

_____

_____

(d) Do the experiments support Gause's competitive exclusion principle? _____

_____

_____

_____

_____

(e) Why kind(s) of competition is occurring here? Explain: _____

_____

_____

_____

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Guidance on Internal Assessments 1 and 2

Key Concepts

- Carry out an experiment by designing a method to gather and analyse data related to biodiversity or ecosystem dynamics, ensuring ethical and safety considerations are met.
- Analyse data and provide valid conclusions. Communicate conclusion and evaluations using an appropriate format or presentation.

Assessment objectives IA1		Activity Number
☐ 1	Apply your understanding of biodiversity or ecosystem dynamics to determine unknown scientific quantities or features.	80
☐ 2	Analyse evidence about biodiversity or ecosystem dynamics to identify trends, patterns, relationships, limitations or uncertainty in data.	80
☐ 3	Interpret evidence about biodiversity or ecosystem dynamics to draw conclusions based on the analysis of data.	80

Assessment objectives IA2

For this assessment task, you are required to modify (refine, extend, or redirect) an experiment in order to address your own hypothesis or question about biodiversity or ecosystem dynamics. The purpose of this chapter is to provide you with some guidelines for your experiment and its analysis and presentation.

To complete the assessment, you must:

☐ 4	Describe ideas and experimental findings related to biodiversity, ecosystem dynamics, or populations.	81
☐ 5	Apply understanding of biodiversity, ecosystem dynamics or populations to modify an experimental method and process primary data.	81
☐ 6	Analyse, interpret, investigate, and evaluate experimental evidence about biodiversity, ecosystem dynamics or populations.	81

Key considerations IA2

☐ 7	Show an understanding of the biological concepts and terms as relevant to your investigation.	81
☐ 8	Demonstrate an understanding of the characteristics of scientific research methods and techniques for collecting primary data as relevant to your investigation. Determine your aim and hypothesis, ask questions, and make predictions that can be tested.	81
☐ 9	Explain and justify your experimental design (including, in field work, why a fair test may not be possible). Show awareness of assumptions in your investigation.	81
☐ 10	Show understanding of precision, accuracy, reliability, and validity when collecting your data. Precision, accuracy, and reliability are features of the assessment or measurement tools used, whereas validity is a feature of design. Explain how you will minimise bias, ensure accuracy (e.g. through calibration of equipment), and maximise precision of measurements.	81
☐ 11	Demonstrate an ability to carry out an investigation safely and ethically.	81
☐ 12	Use appropriate means to organise, analyse, and evaluate primary data to identify patterns and relationships. Include reference to sources of error and limitations of data or methods.	81
☐ 13	Make clear, accurate scientific drawings as appropriate to your investigation.	81
☐ 14	Present and explain the key findings of your investigation as a scientific report or poster presentation to include a title, introduction, methodology, results, discussion, conclusion, and references and acknowledgements. Include appropriate biological terminology and representations, standard abbreviations, and units of measurement, and acknowledge all sources of information.	81

80 IA1: Data Test

This summative internal assessment requires you to work individually.

1. Students wanted to use Simpson's diversity index to compare the diversity of insects in a planted barley field and a natural hedgerow. They collected insects from a randomly selected point at each site. Their results are tabulated below.

Barley field		
Species	n	n(n – 1)
A	32	
B	78	
C	1	
D	0	
E	0	
F	0	
G	0	
H	0	
I	0	
J	0	
K	85	
L	0	
N(N – 1) =	196	∑n(n-1) =
D =		

Under hedgerow		
Species	n	n(n – 1)
A	0	
B	1	
C	2	
D	12	
E	8	
F	9	
G	4	
H	3	
I	2	
J	5	
K	0	
L	7	
N(N – 1) =	53	∑n(n-1) =
D =		

(a) Describe the relative species richness and species evenness at each site: _____

(b) Complete the tables by calculating the missing values for the column n(n – 1).

(c) Use $\mathbf{D} = 1 - \frac{\sum n(n-1)}{N(N-1)}$ to calculate Simpson's diversity index for each site. Enter the values below each table:

(d) Describe the relative diversity of insect species at each site: _____

(e) Give a possible explanation for the difference in the two sites: _____

(f) Identify a limitation of this data set in terms of making conclusions about the biodiversity present? _____

2. Students gathered plant species data at three other sites: a regularly grazed paddock, a forest, and the border area between the forest and paddock. The calculated diversities were: paddock: 0.60, forest edge: 0.91, inside forest: 0.83.

What do the results mean and suggest an explanation for them: _____

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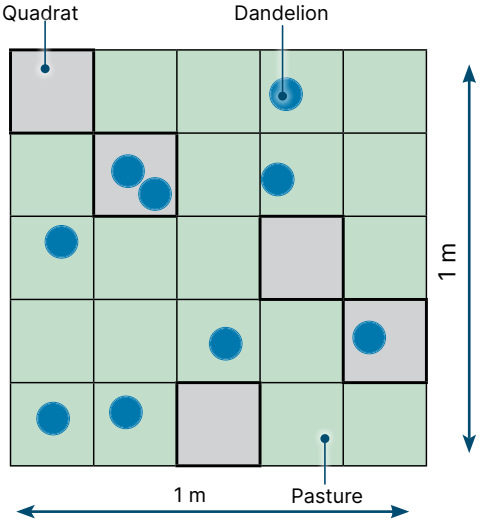
3. The diagram, right, shows an area of pasture invaded by dandelions. Quadrats (area 0.04 m^2) have been used to sample the dandelions. The grey quadrats represent the samples:



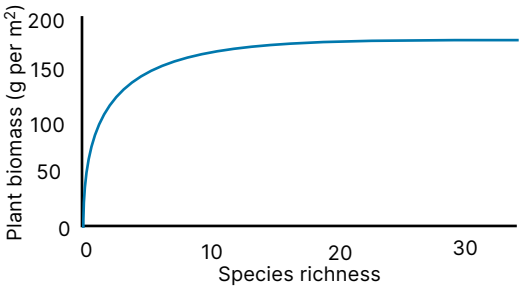
(a) From the quadrat based sample, what is the density of dandelions? Use the formula:

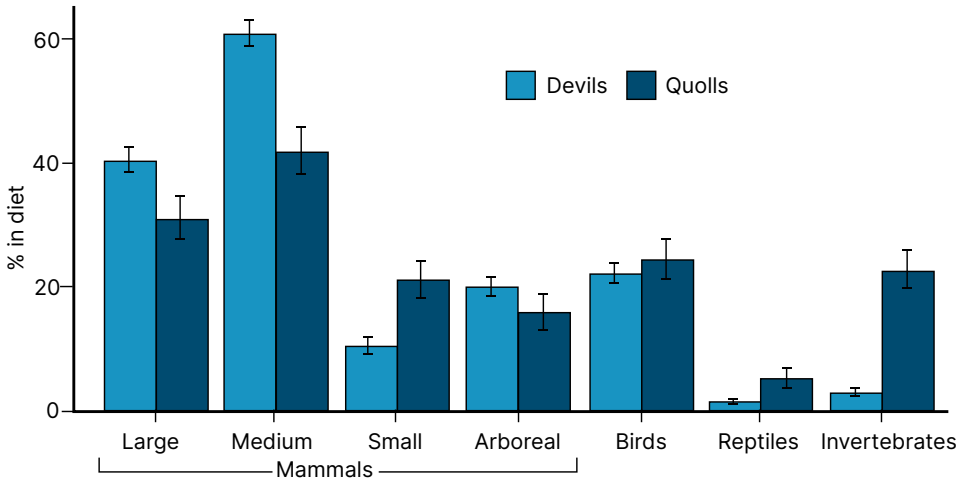
$$\text{Density} = \frac{\text{Total number in all quadrats sampled}}{\text{No. of quadrats sampled x area of quadrat}}$$

(b) From a direct count, what is the actual population density?

(c) Does this sample over- or underestimate the extent of the dandelion invasion? Can you suggest why?

4. Study the graph, right. What can be said about the relationship between species richness and plant biomass in a grassland ecosystem?





5. The graph show the diet of the carnivorous species Spotted Tailed Quolls and Tasmanian devils. The two species co-exist in Tasmania.

Use the graph to explain how these two species are able to coexist and what concept with respect to niche is demonstrated in the data.

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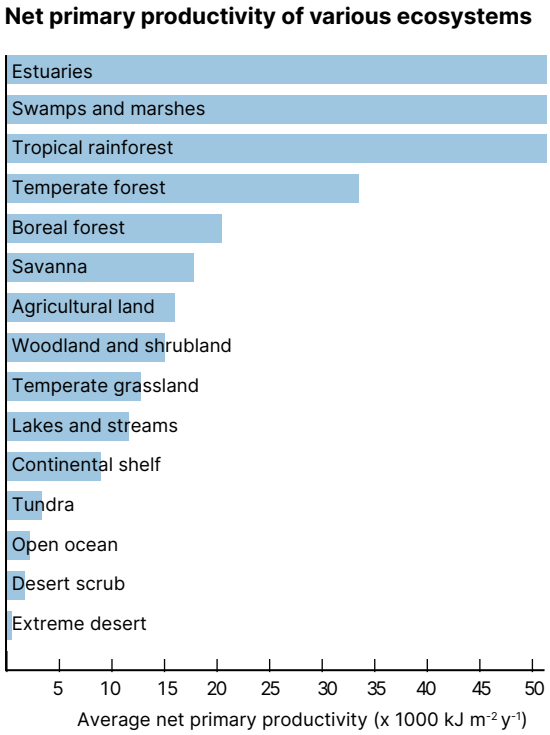
6. Study the ecosystem NPP graph on the right:



(a) Identify the three most productive ecosystems:

_____

_____

(b) What factors are likely to contribute to this high productivity?

_____

_____

_____

(c) Why do deserts have low NPP? _____

_____

_____

(d) Why is primary productivity lower in the open ocean than in estuaries?

_____

_____

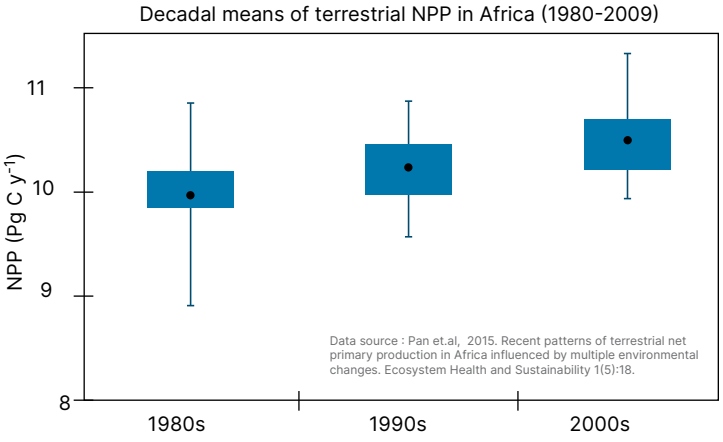
_____

7. Study the information and graph of NPP in Africa below:

The effect of climate change on NPP

Maintaining NPP above a certain level is important for food security and ecosystem sustainability. Some regions, such as the African continent, are highly vulnerable to climate variability. More than 40% of Africa's population live in arid or semiarid regions, and changes in rainfall (e.g. drought) can severely reduce productivity (reduced NPP), including that of food crops.

Africa has undergone a number of climatic changes, all of which have affected NPP. These include a 5°C increase in air temperature over the last 100 years, and an increase in CO_2 from 280 ppm (preindustry) to 380 ppm in 2005. Spatial variations in rainfall across the continent were also a contributing factor. Some areas received more rainfall, others less, and some suffered from drought. Nitrogen deposition (in the form of added fertiliser) is also a major factor in determining NPP. These changes have a strong effect on NPP in Africa (right).



The plot above shows how terrestrial NPP has changed over three decades. These changes are primarily due to variation in precipitation (rainfall) levels, elevated CO_2 levels, and nitrogen deposition. Circles = mean NPP. Boxes = the first and third quartiles (medians of the lower and upper halves of the data set respectively). Whiskers = minimum and maximum values.

(a) Describe the trend in NPP between 1980 - 2009: _____

_____

_____

(b) Identify the factors contributing to this trend: _____

_____

_____

_____

(c) Predict the effect a sustained drought would have on NPP: _____

_____

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8. The partially completed table below is from an investigation of the ecosystem around Silver Springs, Florida. It shows the energy available in each trophic level.

	Energy in organisms kJ m^{-2} yr^{-1}	Energy lost (respiration/ waste)	Energy passed to next level	% available to next level
Producers (P)	31,897	27,279	***4618***	
Herbivores (C1)	***4618***	4154		
Carnivores (C2)		444		
Top carnivores (C3)		20		

Based on data from Odum, 1957. Ecological Monographs 27(1), 55–112.

(a) Complete the table above:

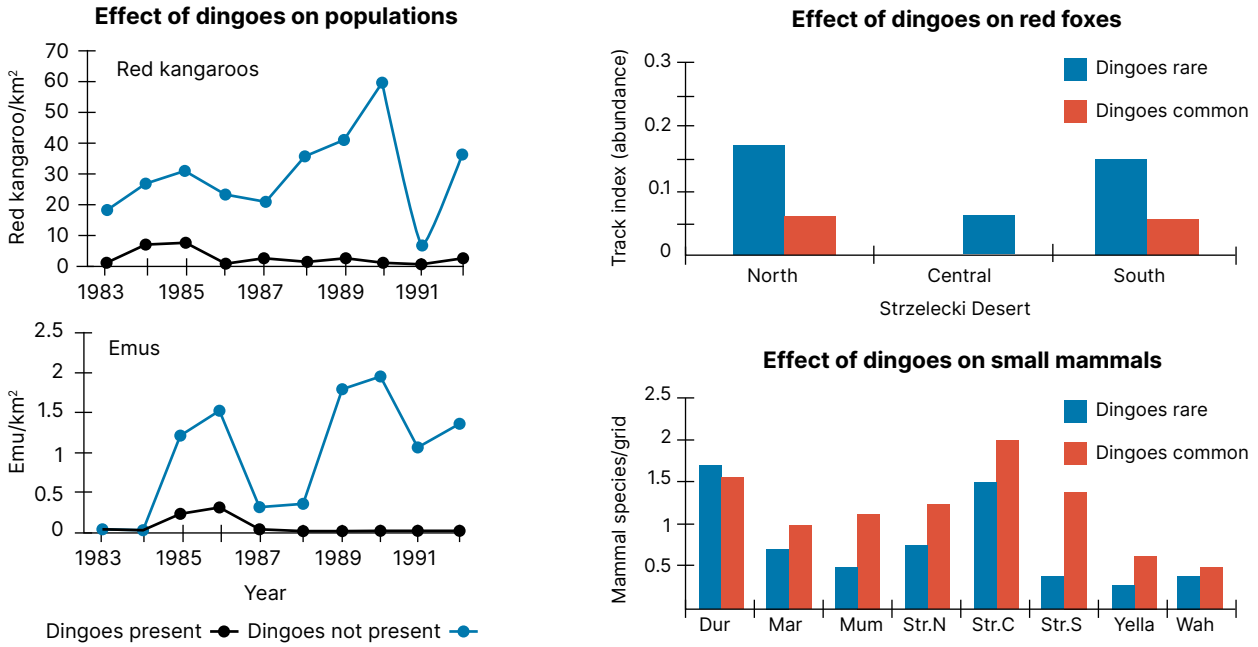
(b) Draw an energy pyramid from the Silver Springs ecosystem in the space on the right:

(c) Why can energy pyramids never be inverted? _____

_____

_____

9. The dingo is an apex predator in Australia, filling the role of large marsupial predators that disappeared about the same time as the dingo arrived. The dingo fence was established to protect pastoral areas in southern Queensland and spans 5600 km from Yalata in the south, to north of Brisbane. It has provided ecologists with the opportunity to study ecosystems in the presence and absence of a top predator. The graphs below compare the effect of the presence and absence of dingoes in various regions:



(a) Kangaroo and emu populations tend to fluctuate with environmental factors including climate and food supply. Which appears to have a greater effect, the presence of dingoes or the amount of food present? Explain your answer.

_____

_____

_____

_____

(b) What is the effect of the presence of dingoes on small mammal species? _____

_____

(c) Explain this effect: _____

_____

_____

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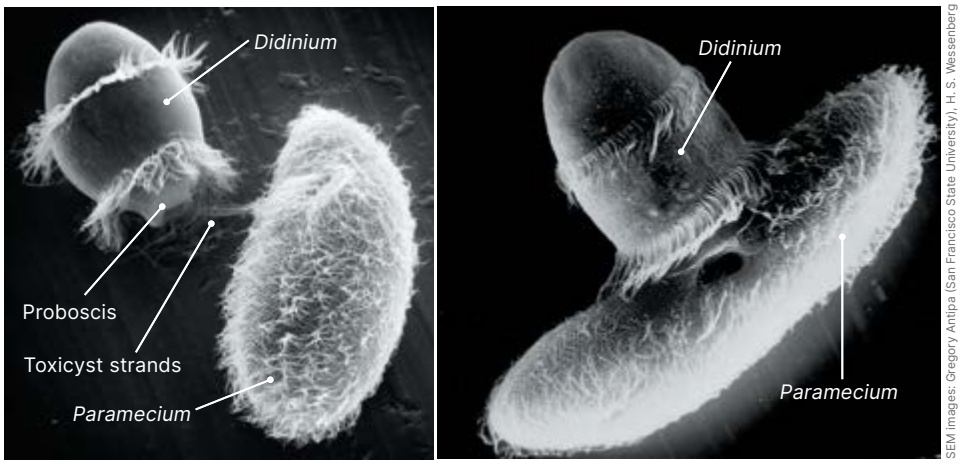
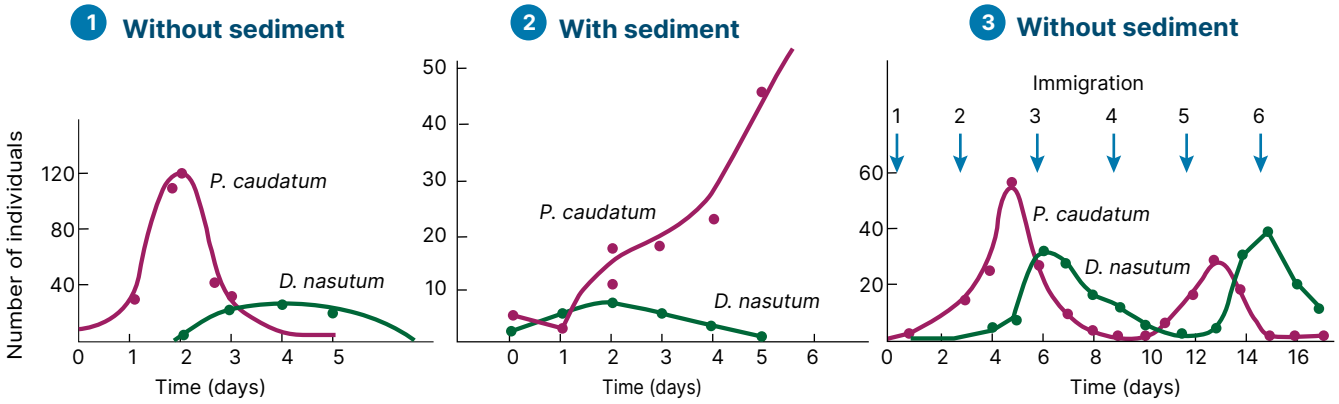
Predator-prey experiments

Gause studied predator-prey interactions in two protists, *Paramecium* and its predator *Didinium,* in simple test tube 'microcosms'. The results are shown in the graphs below. In the first and third experiments, there was no sediment in the test tube. In the second experiment, sediment was added to the test tube.



SEM images: Gregory Antipa (San Francisco State University), H. S. Wessenberg

Didinium, a unicellular ciliate, feeds almost exclusively on *Paramecium*. It captures *Paramecium* by shooting toxicysts into the *Paramecium* (left). It then reels the *Paramecium* into its proboscis.



Five *Paramecium* were added to the medium and three *Didinium* added after two days.

Same regime as experiment 1 but the medium included sediment.

One *Paramecium* and one *Didinium* were introduced into the microcosm at day 0 and then every third day (immigration).

10. Why did the *Paramecium* die out in the first experiment? _____

_____

11. Why did the *Paramecium* survive in the second experiment? _____

_____

12. Why is there a lag in the predator population compared to the prey population in the third experiment?

_____

_____

_____

13. (a) What did Gause's simple microcosm experiments tell us about the role of predation in limiting prey populations?

_____

_____

_____

(b) What did Gause's simple microcosm experiments tell us about the role of the environment in predator prey interactions?

_____

_____

_____

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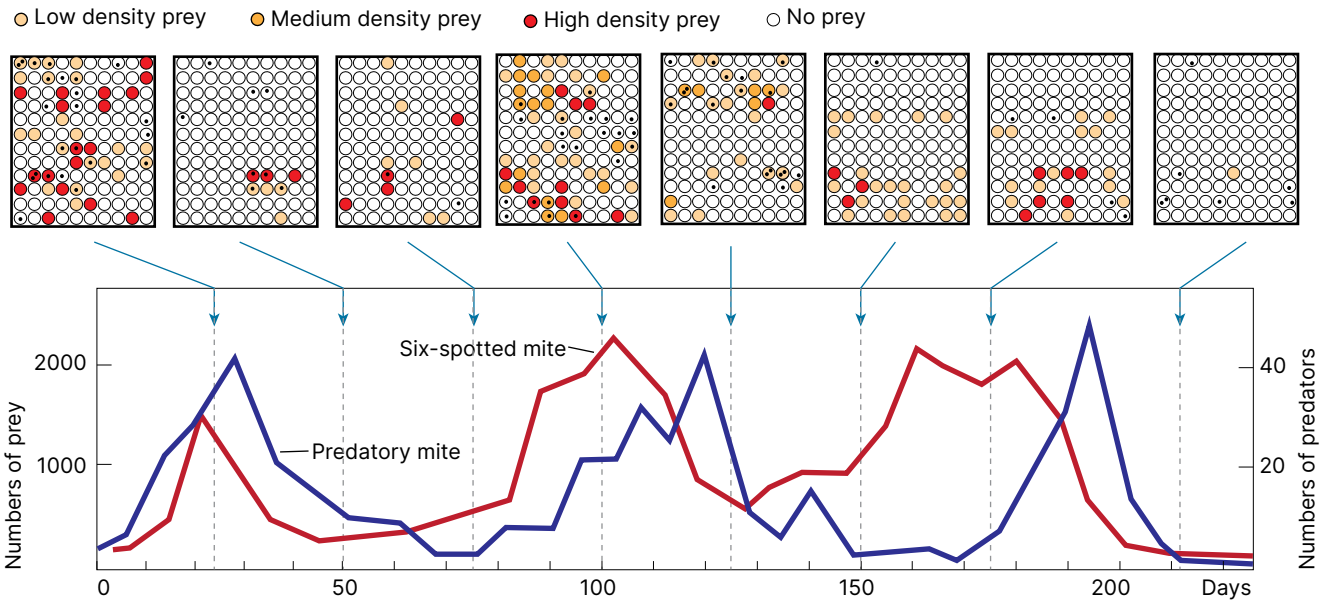
- Huffaker built on Gause's findings and attempted to design artificial systems that would better model a real world system. He worked on two mite species: the six spotted mite and its predator. Oranges provided both the habitat and the food for the prey.
- In a simple system, such as a small number of oranges grouped together, predators quickly ate all the prey and then died out.
- Huffaker then created a more complex system with arrays of 120 oranges (below). The amount of available food on each orange was controlled by sealing off parts of each orange with wax. Patchiness in the environment was created using balls (representing unsuitable habitat). Sticks aided dispersal of prey mites and petroleum jelly was used to form barriers for predatory mite dispersal. In this system, the predator and prey coexisted for three full cycles (> year). In the diagram below, the arrays depict the distribution and density of the populations at the arrowed points. The circles represent oranges or balls and the dots the predatory mites.



14. (a) Mark the three population cycles completed in Huffaker's experiment on the plot above.

    (b) In a different colour, mark the lag in the predator population response to change in prey numbers.

    (c) What does the lag represent? _____

15. How well do you think Huffaker's model system approximated a real ecosystem? Use evidence from the arrays to discuss how variation in habitat makes it possible for populations to persist despite periodic declines in their numbers.

16. In 1960, the Alaska Department of Fish and Game released two wolves onto Coronation Island (116 km^2) to control the deer population. By 1961, indications were the wolves had begun breeding and the population was increasing. By 1964, there were at least 13 wolves on the island. In 1965, wolves were seen on all the beaches but there were few signs of deer. In 1968 only one wolf was sighted on the island. In 1983, there were no wolves, but plentiful deer once more.

    (a) From the information above, which of Gause's experiments (opposite) does this data most closely follow?

    (b) Outline why the predator-prey populations behaved as they did: _____

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81 IA2: Student Experiment

Key Idea: Carrying out an investigation requires planning and research. Records of work should be kept for later review.

This activity will help you to design and undertake a practical investigation of your own related to biodiversity or ecosystem dynamics. This activity will provide background information, which, combined with your own scientific knowledge, will help you design and carry out your experiment and analyse and present the data. Remember that ethical and safety issues must be taken into consideration in your experimental design. Think carefully how you will collect and analyse your data so your results are meaningful and allow you to make valid conclusions about your findings.

Health and safety considerations

Field studies present their own set of health and safety considerations. The Australian environment can be harsh and bushland may contain wildlife, plants, and even geographic features that can be hazardous if not treated with respect. Make sure you research the hazards of the area before beginning any field studies.

Make sure you know the hazards and look out for them.

TydeNet CC 3.0

Even field studies may require some laboratory work, especially if samples found in the field need to be identified. This may require the use of chemicals or may produce hazardous biological material. Hazards in the lab fall into three general categories: chemical, biological, and physical.

- **Chemical**: Chemicals could be ingested, absorbed through the skin, or inhaled. Examples include cleaning agents, disinfectants, and reagents (powdered and liquid). Some chemicals can cause fires or explosions if not handled correctly.
- **Biological**: All biological material should be treated as potentially hazardous to avoid contamination and possible harm. Examples include microbial samples, animal tissue, fluid samples, and plant samples.
- **Physical**: There are numerous potential physical hazards ranging from the laboratory environment itself to the equipment you are using. Common hazards include injury caused by not using the equipment correctly (electrical, thermal, or sound hazards), cluttered working spaces, and tripping or slip hazards (e.g. wet floor from spills).

Reducing risks to health and safety

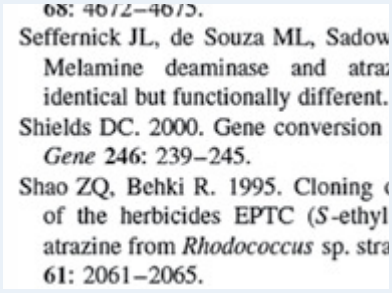
Stinging and thorned plants, like this stinging tree, can cause skin irritations.

Cgoodwin CC 3.0

- Identify potential hazards before you start and become knowledgeable about their risks.
- In the field, this includes the weather as well as your surroundings. Beware of potential hidden hazards such as wasp nests, or thorned or stinging plants.
- Know how to correctly use all equipment or machinery before you begin.
- In the lab, wear appropriate safety gear (lab coat, gloves, safety glasses, ear protection, and a mask as necessary).
- Ensure all chemicals used are clearly labelled.
- Maintain clean work spaces and floors to reduce the risk of slips and spills. Keep access ways to emergency equipment clear.

Ethical considerations

Report your true data and findings, even if they are not the results you were expecting. Changing results to fit your hypothesis is misleading and unethical.



68: 4672–4675.
Seffernick JL, de Souza ML, Sadow
Melamine deaminase and atra
identical but functionally different.
Shields DC. 2000. Gene conversion
Gene **246**: 239–245.
Shao ZQ, Behki R. 1995. Cloning
of the herbicides EPTC (*S*-ethyl
atrazine from *Rhodococcus* sp. stra
61: 2061–2065.

It is very important to acknowledge the work of others (e.g. photographs, data, reference material). Failure to do so is plagiarism.

SIR track

Have a teacher review your experimental design for ethical approval prior to beginning. Minimise the impact of your research on the environment.

With permission: Habitat News

1. Identify potential health and safety issues associated with the rocky shore study being carried out in the photo (left):

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Logbooks

A logbook provides a complete record of the ideas and work you have carried out during your investigation. Each entry must be dated and it should show in detail how you carried out your experiment or research project. The logbook provides proof that you have carried out certain activities on specific dates, and records the results of your work. Logbooks can be used to verify the authenticity and originality of your ideas.

1. Find a notebook to use that will suit your purposes (e.g. if the logbook is to be used in the field, a waterproof book is useful). A hardback A4 lined exercise book is a good choice; anything smaller will make it difficult to include photos or extra pages later on.

2. Name your logbook in a prominent location. Number the pages so you can create a good table of contents. Creating sections in your logbook with tabs helps you keep track of ideas, methods, and results easily.

3. Date and sign every entry.
Entries should be concise but contain enough information that you can understand them later on. Short notes and bullet points are often used.

4. You must be able to read your entries at a later date but don't worry too much about neatness. Logbooks are a record of your work, not the final report. It is more important to accurately record information during lab trials or field studies than to have a nice looking logbook!

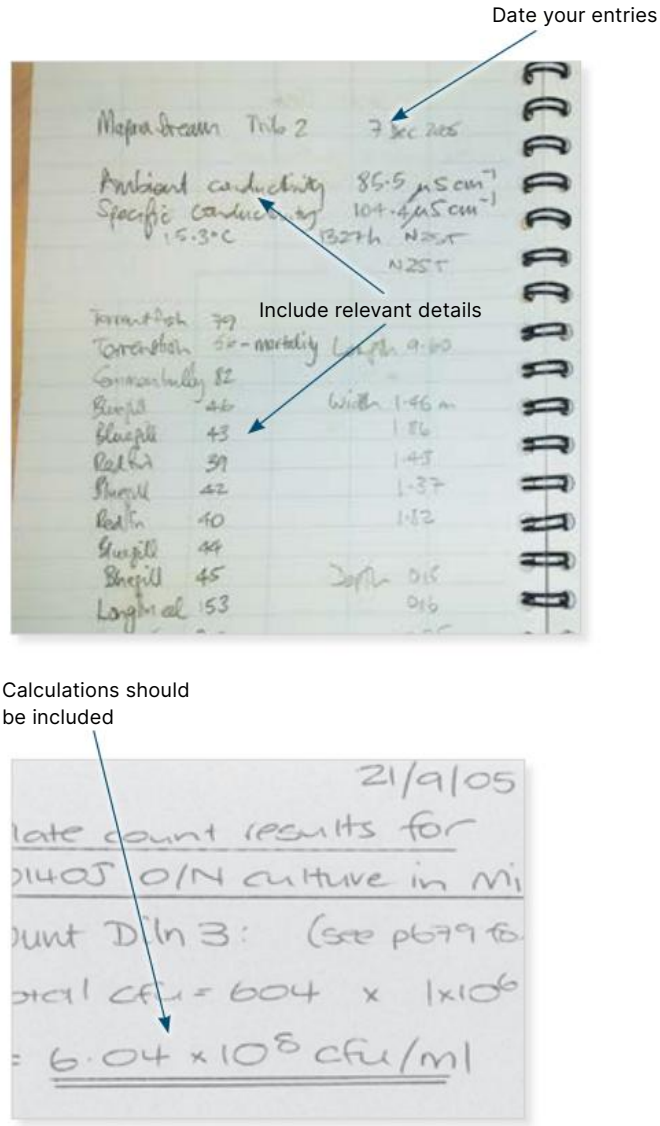
5. Your logbook should be used in all phases of your investigation, from planning to write up. Record ideas on methods or analysis, as well as results.

6. Glue, staple, or tape any loose paper or photos into your logbook. Loose papers are an annoyance, both for you to keep track of and your teacher to sort through.

7. Include any mishaps, failed experiments, or changes in methodology in your logbooks. Where possible, explain the reasons for the failure or change. Sometimes failed experiments can be just as valuable as successful experiments in understanding a result.

8. Include all observations made during your investigation and any calculations and transformations of the data.

9. Remember, systematically recording your ideas, observations, and analyses during your investigation will pay off when you have to organise the material for the final write up. It will also help to clarify any parts of your study that your teacher or marker may find confusing or incorrect, meaning you could still get credit for your work.



2. Why is it important to keep a detailed logbook during a scientific investigation? _____

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Dealing with data

Data analysis involves examining and processing the data you have collected to identify trends and patterns and establish whether or not the data support your hypothesis and help you to answer the questions you posed in your investigation. There are many ways to analyse and present data and your choice must be appropriate for the data you have collected. A statistical analysis is sometimes necessary but for simple, well designed experiments, basic descriptive statistics (e.g. means and standard deviation) may be all that is needed. Finally, you must choose how to display your results (e.g. table) so that you can present your data in an organised way.

Review your initial data

- After you have collected your first set of data (or your preliminary data) it is a good idea to spend a short period of time analysing it.
- You may discover that you need to collect your data differently to how you first planned (e.g. taking more measurements or changing the way you collect your data, such as automation for rapidly occurring changes or prolonged time series data).
- Take some time to plot the data or calculate summary statistics as these will allow you to see trends and patterns more easily than when the data is recorded in a log book. Once you are satisfied that your methods of data collection are adequate, you can continue with your investigation.

How do I analyse my data?

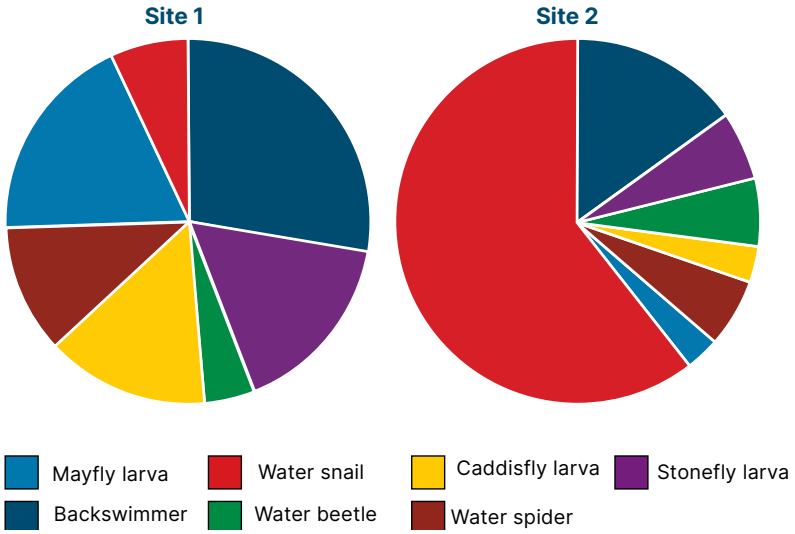
- Check your data to see that it makes sense. Do the results seem logical? Are there any outliers? If so, you must decided whether to include them in your analysis.
- Raw data may need to be transformed to see trends and patterns. Recall that these transformations are often quite simple (e.g. percentages, rates, ratios). Other transformations are used to normalise the data so that it can undergo further analysis (e.g. log transformations when working with large numbers).
- Descriptive statistics (e.g. mean and standard deviation) provide a way to summarise your data, and provide results that can easily be presented and compared across groups. Summary statistics are also useful in identifying trends and patterns in the data.
- Sometimes an appropriate statistical analysis is required to test the significance of results. However, with simple experiments, if the design is sound, the results are often clearly shown in a plot of the data.

Presenting your data

Tables and graphs provide a way to organise and visualise data in a way that helps to identify trends. Each has a different purpose. Tables provide an accurate record of numerical values and allow you to organise your data so that relationships and trends are apparent. Graphs provide a visual representation of trends in the data in a minimum of space and are an excellent choice for displaying results. Whether or not data will be presented as a chart depends on the type of data collected. Data collected by quadrats in a survey of stream invertebrates could be presented in the following way:

Species	Site 1	Site 2
Backswimmer	12	5
Stonefly larva	7	2
Water beetle	2	2
Caddisfly larva	6	1
Water spider	5	2
Mayfly larva	8	1
Water snail	3	20

The data table presents concise information on the number of individuals collected at site 1 and site 2



Presenting the data as pie charts clearly shows the differences between the communities at the two sites.

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A student carried out an investigation of the effect of manure on earthworm populations. The student threw quadrats randomly on to two regions of cultivated ground to mark out 8 sample areas in each region. One area had been regularly manured and the other had not. The results are shown below.

Plot 1 (manured)		Plot 2 (not manured)	
Quadrat	Worms per m^2	Quadrat	Worms per m^2
1	6	1	5
2	10	2	4
3	12	3	7
4	10	4	8
5	11	5	6
6	8	6	4
7	6	7	4
8	9	8	6

3. Why is it a good idea to review your preliminary data before proceeding with the investigation? _____

4. (a) Why was the student's method of randomly selecting quadrat areas not truly random? _____

   (b) How should they have located the quadrats? _____

5. (a) What would be the null hypothesis for the investigation? _____

   (b) What kind of statistical test could be carried out on this data to test the null hypothesis? _____

6. (a) Why are data often presented as tables or graphs? _____

   (b) How would you recommend the student presents their earthworm data in a scientific report? _____

   (c) Explain your choice: _____

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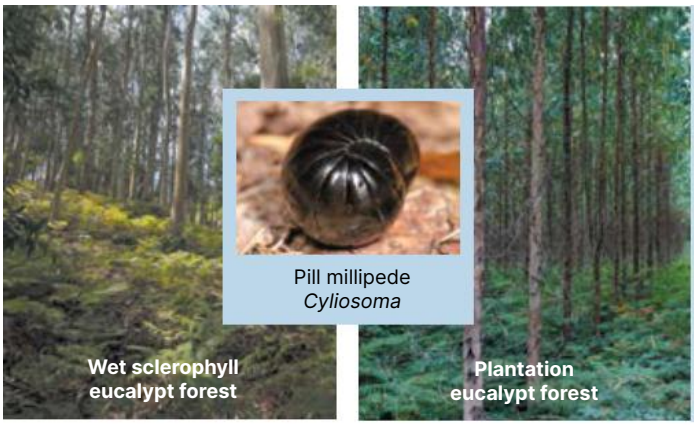
An experimental design

The figure below provides an example and some ideas for designing a field study. It provides a framework which can be modified for most simple comparative field investigations. For reasons of space, the full methodology is not included.



Pill millipede: Marshal Hedin CC 2.0

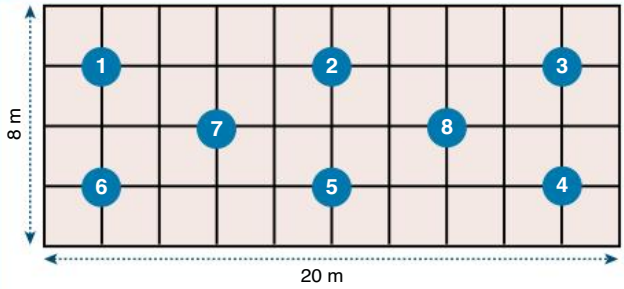
Observation

A student read that a particular species of pill millipede (left) is extremely abundant in forest leaf litter, but a search in the litter of a eucalypt plantation near his home revealed only very low numbers of this millipede species.

Hypothesis

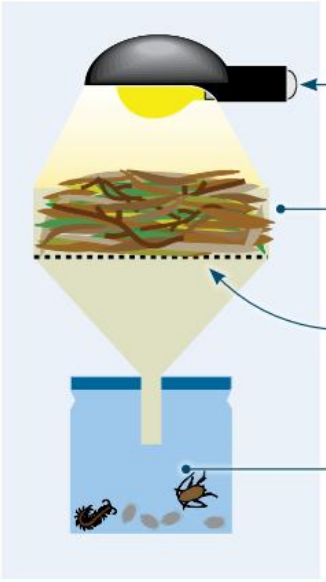
This millipede species is adapted to a niche in the leaf litter of humid forests and is abundant there. However, it is rare in the litter of drier plantation forests. The null hypothesis is that there is no difference between the abundance of this millipede species in wet sclerophyll and plantation forests.

Wet sclerophyll or plantation forest



1 Sampling sites numbered 1-8 at evenly spaced intervals on a 2 × 2 m grid within an area of 20 m x 8 m.

Sampling equipment: leaf litter light trap



Light from a battery operated lamp drives the invertebrates down through the leaf litter.

Large (diameter 300 mm) funnel containing leaf litter resting on a gauze platform.

Gauze allows invertebrates of a certain size to move down the funnel.

Collecting jar placed in the litter on the forest floor traps the invertebrates that fall through the gauze and prevents their escape.

Notes on collection and analysis

- Mean millipede abundance was calculated from the counts from the eight sites. The difference in abundance at the sites was tested using a Student's *t* test.
- After counting and analysis of the samples, all the collected invertebrates were returned to the sites.

Sampling program

A sampling program was designed to test the prediction that the millipedes would be more abundant in the leaf litter of wet sclerophyll forest than in plantation eucalypt forest.

Equipment and procedure

Sites: For each of the two forest types, an area 20 × 8 m was chosen and marked out in 2 × 2 m grids. Eight sampling sites were selected, evenly spaced along the grid as shown.

- The general area for the study chosen was selected on the basis of the large amounts of leaf litter present.
- Eight sites were chosen as the largest number feasible to collect and analyse in the time available.
- The two forests were sampled on sequential days.

Capture of millipedes: At each site, a 0.4 × 0.4 m quadrat was placed on the forest floor and the leaf litter within the quadrat was collected. Millipedes and other leaf litter invertebrates were captured using a simple gauze lined funnel containing the leaf litter from within the quadrat. A lamp was positioned over each funnel for two hours and the invertebrates in the litter moved down and were trapped in the collecting jar.

- After two hours each jar was labelled with the site number and returned to the lab for analysis.
- The litter in each funnel was bagged, labelled with the site number and returned to the lab for weighing.
- The number of millipedes at each site was recorded.
- The numbers of other invertebrates (classified into major taxa) were also noted for reference.

Assumptions

- The areas chosen in each forest were representative of the forest types in terms of millipede abundance.
- Eight sites were sufficient to adequately sample the millipede populations in each forest.
- A quadrat size of 0.4 × 0.4 m contained enough leaf litter to adequately sample the millipedes at each site.
- The millipedes were not preyed on by any of the other invertebrates captured in the collecting jar.
- All the invertebrates within the quadrat were captured.
- Millipedes moving away from the light are effectively captured by the funnel apparatus and cannot escape.
- Two hours was long enough for the millipedes to move down through the litter and fall into the trap.
- Note that these last two assumptions could be tested by examining the bagged leaf litter for millipedes after returning to the lab.

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The importance of sample size

In any field study, two of the most important considerations are the sample size (the number of samples you will take) and the size of the sampling unit (e.g. quadrat size). An appropriate choice will enable you to collect sufficient, unbiased data to confidently estimate the population parameters of interest (e.g. mean population size). The number of samples you take will be determined largely by the resources and time that you have available to collect and analyse your data (your sampling effort).

Yohan euan 04

Based on the design of this investigation, the information provided, and your own knowledge of ecological sampling, design your own investigation of the biodiversity of an area. Use the questions below to guide you.

7. Carry out background research before you begin your experimental design so you have good knowledge of the topic. In the space below note down any information sources you have used. You will need to acknowledge these in your write up.

8. State an aim and a hypothesis for your experiment: _____

9. In the space below summarise your method as step by step instructions and draw or map your experimental set up:

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10. (a) What kind of risk assessment is needed and how might you reduce risks? _____

(b) Identify any ethical issues associated with your investigation: _____

11. (a) What data will you collect? _____

(b) How will you collect it? _____

(c) In the space below, draw a template to record your data:

12. (a) Identify any sources of error and limitations in the methods and/or results: _____

(b) What changes would you make to improve the experiment? _____

13. Write your conclusions here: _____

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Presenting your findings

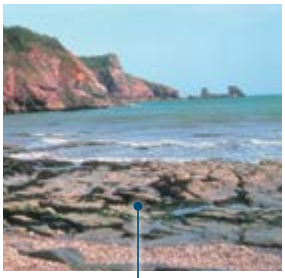
At the conclusion of your practical investigation, you may present your findings as a written report or a scientific poster.

Presenting a report

When writing your report, it is useful to write the methods or the results first, followed by the discussion and conclusion. The introduction should be one of the last sections that you write. Writing the other sections first gives you a better understanding of your investigation within the context of other work in the same area.

Methods

The methods section of a report should include enough detail to enable the study to be repeated, but should omit the details of standard procedures (e.g. how to use a balance). Details of statistical analyses can be included, as well as the rationale for these. The diagram below describes the information that should be included in the methods of a field study. It is not exhaustive, but indicates the sort of information that should be presented.



Study site & organisms

- Site location and features
- Why that site was chosen
- Species involved

Specialised equipment

- pH and oxygen meters
- Thermometers
- Nets and traps

Data collection

- Number and timing of observations/collections
- Time of day or year
- Sample sizes and size of the sampling unit
- Temperature at time of sampling
- Methods of sample preservation or staining
- Weather conditions on the day(s) of sampling
- Methods of measurement/ sampling
- Methods of recording

Results

The results section is arguably the most important part of any research report; it is the place where you can bring together and present your findings. When properly constructed, this section will present your results clearly and in a way that shows you have organised your data and carefully considered the appropriate analysis. A portion of the results section from a scientific paper on the habitat preference of New Zealand black mudfish is presented below (Hicks, B. and Barrier, R. (1996), NZJMFR. 30, 135-151). It highlights some important features of the results section and shows you how you can present information concisely, even if your results are relatively lengthy. Use it as a guide for content when you write up this section.

Keep your statement of important findings brief. Only include results, not a discussion.

Graphs (figures) illustrate trends in the data. Be sure to choose the correct type of graph and allocate enough space to it in the report.

summer wate
nificantly diffe
mudfish (t-test, p ≥ 0.016: Table 5). Mean summe
s
with mudfish, compared to 22.6 cm at sites without. Winter and maximum water depths were also less at sites with mudfish than at sites without mudfish. Mean turbidity was 11.5 nephelometric turbidity units (NTU) at sites with mudfish, but 21.3 NTU at sites without mudfish. Conductivity, total
he water surface, humic concentration, pH, an
s (t-test, P > 0.153: Table 5). Catch rates at site
er trap per night (geometric mean 0.70: Table 5).

Label figures and tables clearly and in sequence so that they can be referred to easily in the text.

Fig. 2 Catch rates in turbid water

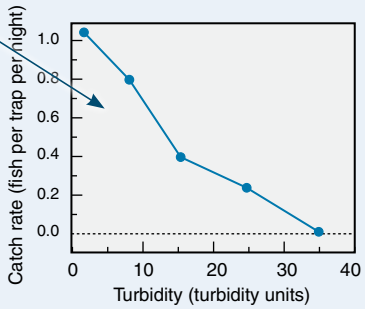


Table 5: Characteristics of sites with and without mudfish

	Sites with mudfish		Sites without mudfish		Probability
	Mean ± CI	SD	Mean ± CI	SD	
	0.70 ± 1.31	0.84	0.00		
	2.1 ± 1.9	2.2	22.6 ± 7.8	24.7	<0.001
Winter water depth /cm	28.9 ± 4.3	5.8	40.2 ± 7.7	24.4	0.012
Turbidity /NTU	11.5 ± 2.5	13.3	21.3 ± 7.1	22.6	0.012

Tables and figures are referred to in brackets.

Tables summarise raw data, any transformations, and the results of statistical tests.

The significance of statistical tests are included

14. Explain why you should make reference to tables and figures in the body of the text:

_____

_____

15. Explain why you might present the same data in a table and as a figure: _____

_____

_____

_____

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Discussion

In the discussion section of your report, you must interpret your results in the context of the specific questions you set out to answer in the investigation. You should also place your findings in the context of any broader relevant issues. If your results coincide exactly with what you expected, then your discussion will be relatively brief. However, be prepared to discuss any unexpected or conflicting results and critically evaluate any problems with your study design. The discussion section may (and should) refer to the findings in the results section, but it is not the place to introduce new results. Try to work towards a point in your discussion where the reader is lead naturally to the conclusion. The conclusion may be presented within the discussion or it may be included separately after the discussion as a separate section.

Support your statements with reference to Tables and Figures from the Results section.

The discussion describes the relevance of the results of the investigation.

Black mudfish habitat in the W escribed for predictive purposes by four variables that are easy to measure: summer wat nt of disturbance (as indicated by vegetation), and turbidity. Catch rates of black mudfish ent study, catch rates ranged from 0.2 to 8.4 mudfish per trap per night (mean 0.70) between May and October 1992, and were similar to those of Dean (1995) in September 1993 and October 1994 in the Whangamarino Wetland complex (0.0-2.0 mudfish per trap pe ch rate in our study, 8.4 mudfish per trap per night, was at Site 24 (Table 1, Figure 1). The s trap per night) was at Site 32, in a drain about 4 km east of Hamilton. Black mudfish in the monly found at sites in wetlands with absence of water in summer, moderate depth of water in winter, limited modification of the vegetation (low DSR), and low turbidity (Fig. 2). There are similarities between the habitat requirements of black mudfish and those of brown mudfish and the common river galaxias (*Galaxias vulgaris*). Brown mudfish inhabited shallow water, dies, but were usually absent from water deeper than about 30-50 cm (Eldon a preference for shallow water, occupying river margins < 20 cm deep (Jowett

State any limitations of your approach in carrying out the investigation and what further studies might be appropriate.

Sites where black mudfish were found were not just shallow or dry in summer, but also had substantial seasonal variation in water depth. A weakness of this study is the fact that sites were trapped only once; however, five traps were spread relatively widely at each site to maximise the chance of catching any fish that were there. Cover was important for black mudfish, in the form of emergent or overhanging vegetation, or tree roots. The significance of cover in determining the presence or absence of black mudfish is predictable, considering the shallow nature of their habitats. Mudfish, though nocturnally active as adults, are likely to require cover during the to protect them from avian predators, such as bitterns (*Botaurus stellaris poiciloptilus*) and kingfishers (*Halcyon sancta vagans*). Predation of black mudfish by a swamp bittern has been recorded (Ogle & Cheyne 1981). Cover is also fish (Eldon 1978). Black mudfish were found at sites with the predatory mosquitofish and juv drying of their habitats may be a key to the successful coexistence of mudfish with their pr known predators of mudfish fry (Barrier & Hicks 1994), and eels would presumably also prey on black mudfish, as they do on Canterbury mudfish (Eldon 1979b). If, however, black mudfish are relatively uncompetitive and vulnerable to predation, the question remains as to how they manage to coexist with juvenile eels and mosquitofish. The habitat variables measured in this study can be used to classify fish in future. The adaptability of bla in some altered rains. From this study, we can conc of suitable ant to black mudfish than the presence of predators and competitors. This study has also improved methods of identifying suitable mudfish habitats in the Waikato region.

Reference is made to the work of others.

Further research is suggested

A clear conclusion is made towards the end of the discussion.

References

Proper referencing of sources of information is an important aspect of report writing. It shows that you have explored the topic and recognise and respect the work of others. There are two aspects to consider: citing sources within the text (making reference to other work to support a statement or compare results) and compiling a reference list at the end of the report. A bibliography lists all sources of information, but these may not necessarily appear as citations in the report. In contrast, a reference list should contain only those texts cited in the report. Citations in the main body of the report should include only the authors' surnames, publication date, and page numbers (or internet site) and the citation should be relevant to the statement it claims to support (see above).

Example of a reference list

Lab notes can be listed according to title if the author is unknown.

Advanced biology laboratory manual (2000). Cell membranes. pp. 16-18. Sunhigh College.

References are listed alphabetically according to the author's surname.

Cooper, G.M. (1997). *The cell: A molecular approach* (2nd ed.). Washington D.C.: ASM Press

Book titles in italics — Publisher

Davis, P. (1996). Cellular factories. *New Scientist* 2057: Inside science supplement.

Journal titles in italics

Publications from a single author are listed from oldest to most recent.

Indge, B. (2001). Diarrhea, digestion and dehydration. Biological Sciences Review, 14(1), 7-9.

Article title — Volume (Issue number), Pages

Indge, B. (2002). Experiments. Biological Sciences Review, 14(3), 11-13.

Last name and initials of authors.

Kingsland, J. (2000). Border control. New Scientist 2247: Inside science supplement.

Internet sites change often so the date accessed is included. The person or organization in charge of the site is also included.

http://www.cbc.umn.edu/~mwd/cell_intro.html (Dalton, M. "Introduction to cell biology" 12.02.03)

Publication date

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A poster

A poster is a visual summary of your research. Every piece of information on the poster provides key information to your audience so that they have an overview of your findings. Getting the right balance of information is crucial. Too much information can make the poster busy and hard to read, but too little information leaves your audience with a poor understanding of the work. The example shown below shows an effective poster presentation, although deliberately on a topic you would be unlikely to choose. The message is focussed, it uses graphics with minimal text, and presents material in a clear sequence.

Leaf breakdown in streams

Adapted from a poster by Brendan J. Hicks & J. Lee Laboyrie, Dept of Biological Sciences, University of Waikato, NZ. Modified with permission.

Introduction

Fallen leaves can provide a major energy source for forest stream ecosystems, but decomposition by microbes is necessary to lower the C:N ratio and increase the food value of leaves to aquatic invertebrates.

The aims of this investigation were to:
(1) compare rates of mass loss between leaves of different tree species,
(2) determine changes in C:N ratio during the conditioning process,
(3) make preliminary estimates of invertebrate colonisation.

If leaf litter provides food and habitat for stream invertebrates, we expect they will colonise in-stream leaf bags. Breakdown rates will vary, so colonisation will be influenced by leaf type.

Methods

1. Fallen leaves were collected from the forest floor, and placed in mesh bags after drying and weighing.
2. The leaf bags were strung onto a wire and left in the Mangoatama Stream, Waikato. The mean water temperature was 14.5°C.

Leaves incubating in mesh bags

3. The leaf bags were retrieved after 28 days. The leaves were gently washed, the aquatic insects were sorted, and the leaves and insects were dried and weighed.
4. The carbon and nitrogen content of the leaves were determined before and after incubation to determine the change in food quality.

Results

1. Food quality of the leaves was increased. Mean C:N ratio fell from 45:1 to 35:1 with incubation.
2. These aquatic insects were commonly found in the leaf bags:

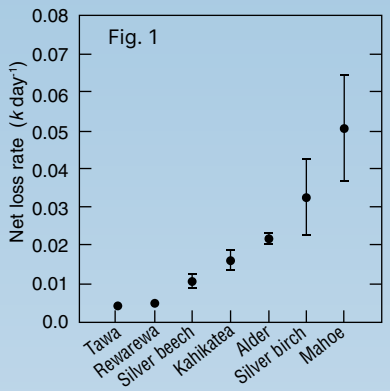
Insect photos: Stephen Moore

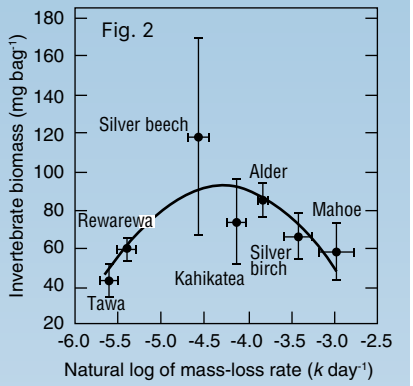
Mayfly larva, *Deleatidium* *(collector-browser)*

Beetle larva (Elmidae) *(collector-browser)*

Caddisfly larva, *Olinga* *(generalist feeder)*

3. Mahoe and silver birch leaves broke down fast compared to rewarewa and tawa (Fig. 1).
4. There were more aquatic insects on the leaves with intermediate rates of breakdown than on those with very fast or very slow rates (Fig. 2).





Conclusions

1. Leaves of different tree species showed a range of breakdown rates. Progression of leaf breakdown determined the colonisation of leaves by aquatic insects. Slower breakdown provides habitat. Faster breakdown provides energy quickly.
2. The food quality (C:N ratio) of leaves was improved by breakdown.
3. Leaves of trees planted in riparian zones should have a range of breakdown rates to give energy that is quickly available (e.g. mahoe) as well as to provide habitat structure (e.g. silver beech).

The hypothesis was supported. Further research will investigate suitable mixes of tree species to maximise invertebrate community diversity.

References

Hicks, B.J.; Laboyrie, J.L. 1999. Preliminary estimates of mass-loss rates, changes in stable isotope composition, and invertebrate colonisation of evergreen and deciduous leaves in a Waikato, New Zealand, stream. NZ Journal of Marine and Freshwater Research 33.

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- The key to an excellent poster presentation is to provide all the required information in a simple format and not to overload the poster with too much text. Bulleted or numbered text blocks present information in an easy-to-read format.
- Use graphics where possible to communicate information in a space efficient manner. Where possible, use graphs to present results as they are easier to read than large tables and provide a quick summary of your results at a glance.
- Choose a simple background that does not detract from your message. Choose text font, size, and colours that can be easily read and that do not blend into your background.
- A scientific poster has a particular structure, which leads the reader through the study and presents and explains its findings. Key section headings and a checklist are provided below to help you plan your own scientific poster.
- Story-boarding your poster (left) before you start laying it out can help to produce a good poster.

Poster format and content

Purpose and checklist

Title
A clear, brief description of the investigation. A well constructed title make a clear statement about the content of the poster.

- ☐ Clearly indicates the type and extent of the study
- ☐ Includes species scientific and common name if this is appropriate

Introduction
Includes the aim and hypothesis, and background information to the project. Not all scientific posters have an introduction, but it is an expectation for student posters at this level.

- ☐ Gives a clear statement of the aims and hypothesis
- ☐ Provides relevant background and a logical rationale for the study
- ☐ Explains specialised terminology

Methods
A description of the materials used and the experimental procedures involved. Where appropriate, photos or diagrams can be used to explain your experimental set up.

- ☐ The study design is complete and clearly outlined.
- ☐ Provides the information to enable the procedures to be repeated
- ☐ The reason for each step in the methodology is evident or explained
- ☐ Factors important in the outcome are mentioned and explained
- ☐ Includes relevant details of data collection and analysis (e.g. preparation of materials, controls, sample sizes, methods of measurement)

Results
A statement or description of the results. This section should not discuss the results, but can state trends. Raw data should not be included, but processed and presented in tables and/or graphs. Tables and graphs should be identified, e.g. Fig. 1, so that they can be clearly identified in the text.

- ☐ Provides the reader with the findings of the investigation and allows them to evaluate it themselves
- ☐ Clearly presents the findings of the study or experiment. General statements are supported with reference to the data.
- ☐ Major results are presented in tables and figures and briefly described
- ☐ Each figure or table is self-sufficient and includes title and caption
- ☐ Figures and tables are numbered sequentially

Conclusion
A clear statement describing whether or not the results of the investigation support the hypothesis.

- ☐ The conclusions are clearly stated
- ☐ You can discuss continuing research (if applicable)

Acknowledgments
A list of sources of information, including citations of written material (e.g. journals, texts), web pages, and practical and advisory help. It is important that entries are consistent within your report. Your teacher will advise you as to the format preferred.

- ☐ Acknowledges the work and expertise of others
- ☐ Allows your work to be assessed in the light of other work in the area.
- ☐ Full citations are provided for every reference cited in the report
- ☐ There are no references included that are not cited in the report.
- ☐ Each citation is correctly and consistently formatted.

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Chapter 7 Unit 4 Topic 1

DNA Structure and Replication

Resource Hub
bit.ly/3EV7Et3

Key Terms

- adenine
- anti-parallel
- base pair rule
- chromosome
- complementary base pairing
- cytosine
- deoxyribose
- DNA
- DNA helicase
- DNA polymerase
- DNA replication
- eukaryote
- guanine
- histone
- nucleotide
- nucleic acid
- nucleus
- prokaryote
- purine
- pyrimidine
- ribose
- RNA
- semi-conservative
- thymine
- uracil

Key Concepts

- DNA has a double-helix structure consisting of two anti-parallel strands held together by hydrogen bonds, storing and transmitting genetic information.
- Prokaryotic DNA is organised as a single, circular chromosome, while eukaryotic DNA is linear and packaged with histone proteins into chromosomes within the nucleus.
- DNA replication is semi-conservative and is controlled by enzymes including DNA helicase and DNA polymerase. The leading strand is copied continuously while the lagging stand is copied in short segments called Okazaki fragments.

The structure of DNA

			Activity Number
☐	1	Describe the role of DNA in living organisms and understand why it is called the 'blueprint of life'. In simple terms, describe the basic structure of a DNA molecule and how it carries genetic information.	82
☐	2	State where most of the DNA is found and describe locations where DNA may be found outside of the main chromosome or nucleus in prokaryotes and eukaryotes. Contrast the structure and organisation of the DNA in prokaryotes and eukaryotes, including plasmid DNA.	84-86
☐	3	In more detail than above, describe how the DNA in eukaryotic chromosomes is associated with histone proteins, which package and organise the DNA. State the purpose of this highly ordered organisation.	86
☐	4	Recall the structure of the nucleic acid DNA, including the composition of nucleotides, the complementary base pairing (base pairing rule) and the base-specific hydrogen bonding between anti-parallel strands. Explain how nucleotides and nucleic acids are both formed by condensation reactions.	87, 88
☐	5	Compare and contrast the structure of the nucleic acids DNA and RNA and recognise the various roles of different types of RNAs.	88
☐	6	Explore the structure of DNA further by building a physical model to illustrate the characteristics of the DNA molecule.	89
☐	7	**SHE:** Understand how the contributions of Rosalind Franklin, James Watson, and Francis Crick led to the development of the double-helix model of DNA.	90
☐	8	**SHE:** Understand the contributions of Elizabeth H Blackburn, Carol W Greider and Jack W Szostak in the discovery of chromosome structure, specifically telomeres.	86
☐	9	**SI:** Extract DNA from strawberries or kiwifruit.	83

DNA replication

☐	10	Describe the semi-conservative replication of DNA, including reference to: • the role of the enzyme DNA helicase, • the role of DNA polymerase, • the direction of synthesis and its significance. • the structure and function of Okazaki fragments	91, 92
☐	11	Explain what semi-conservative replication means and describe consequences for the newly formed DNA molecules.	91, 92

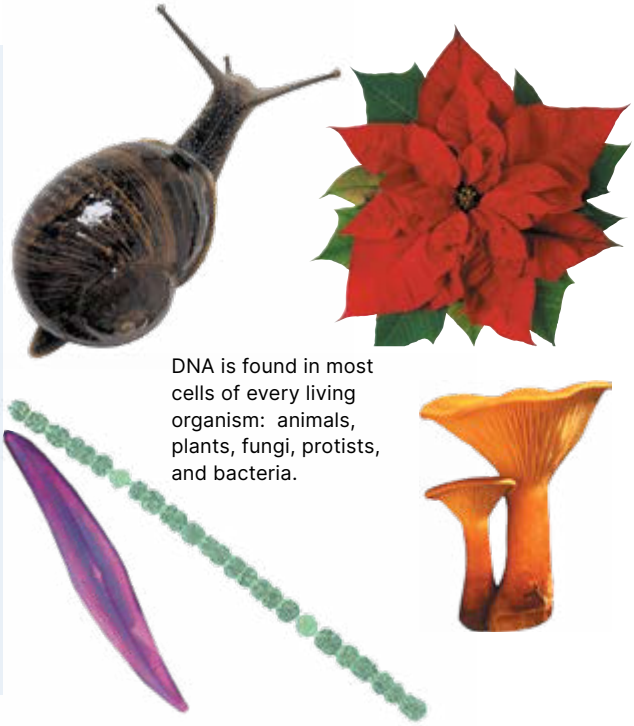
82 What is DNA?

Key Idea: DNA carries the cell's genetic information. It is organised differently in prokaryotes and eukaryotes.

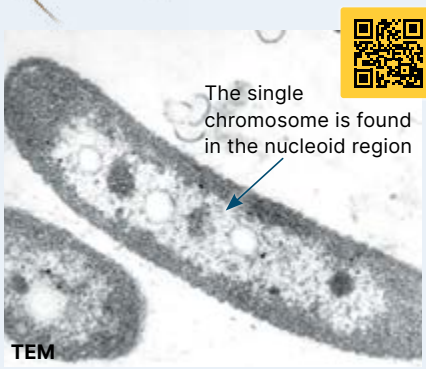
DNA is found in all living organisms. It stores information using units called bases. There are only four types of bases but the combinations of millions of bases together stores the information that controls all the functions in a cell.

About DNA

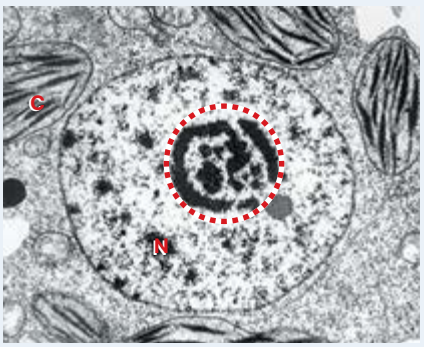
- DNA stands for **d**eoxyribo**n**ucleic **a**cid.
- DNA has a double-helix structure with two **anti-parallel** strands held together by hydrogen bonds (left). It stores and transmits genetic information.
- DNA carries all the information an organism needs to develop, function, and reproduce.
- DNA is found in most cells of all living organisms. In **eukaryotes**, most of the cell's DNA is found in the **nucleus**. In **prokaryotes**, it is free in the cytosol within a region called the nucleoid.
- If all the DNA in one human cell was unwound, it would be more than 2 m long! The linear DNA molecules are packaged with proteins into **chromosomes** so that they fit into the nucleus.
- The circular chromosome of prokaryotes is not associated with proteins (naked).



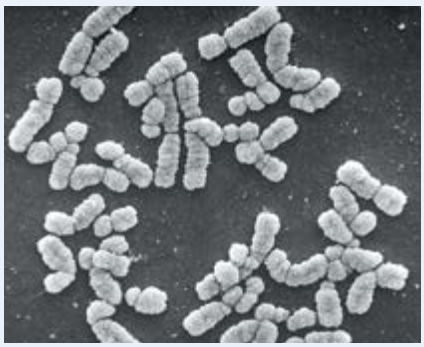
DNA is found in most cells of every living organism: animals, plants, fungi, protists, and bacteria.



The DNA of prokaryotes (bacteria) is found as a single circular molecule (called the bacterial chromosome) in direct contact with the cytoplasm. Small loops of DNA called plasmids may also be present.



In eukaryotes, most of the cell's DNA (circled above) is located in a large organelle called the nucleus (N). A very small amount is located in mitochondria, and in the chloroplasts of plants (C).



The DNA in eukaryotes is organised with proteins into chromosomes. Each chromosome contains a linear piece of DNA with two ends. The highly organised structure is necessary for packing and replication.

1. (a) What does DNA stand for? _____

   (b) What does DNA do? _____

   _____

2. Summarise the basic structure and organisation of DNA in prokaryotes and eukaryotes: _____

   _____

   _____

   _____

   _____

   _____

   _____

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SU

83 What Does DNA Look Like?

Key Idea: Strands of DNA can be extracted from any cells, but those with large amounts of DNA and large chromosomes produce the best results.

In a lab, scientists usually use extraction kits to separate **DNA** from cells. These will contain all the parts needed to accurately remove the DNA, but in general they are all based on the same technique. This includes breaking open the cells, precipitating the DNA, and removing contaminants. In a classroom, DNA is easily extracted by precipitating it out of solution using ice cold ethanol. It is good to use strawberries for this method because they are octaploid (have 8 sets of **chromosomes**) and their colour makes it easy to see the precipitating DNA. However, other fruits and vegetables such as kiwifruit, bananas, and broccoli can also be used.

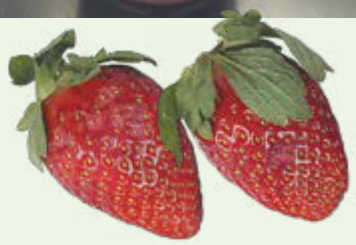
Investigation 7.1 Extracting DNA

See appendix for equipment list.

Work in pairs for this activity.

1. Take 5-6 strawberries and place them in a large zip-lock bag. Squash the strawberries into a smooth paste. This mechanically breaks up the cells, but does not release the DNA.
2. To release the DNA add 100 mL of water, 5 mL of detergent, and a pinch of salt to the paste. Reseal the bag and mix the contents by squashing and crumpling the bag. The detergent breaks down the cellular membranes and deactivates DNases, which would chop up the DNA. The salt helps to remove the proteins bound to the DNA and keeps them in solution. Positive ions in the salt also neutralise the negative charge of the DNA.
3. Place a piece of filter paper in a funnel and position the funnel so the excess fluid can drain into a beaker. Pour the contents of the bag into the filter funnel and allow it to drain. It should produce a clear reddish solution (right).
4. Gently add the ethanol on top of the strawberry solution by placing a clean glass rod into the beaker and carefully pouring the ethanol down the rod. Add ethanol until there are equal volumes of strawberry solution and ethanol.
5. Ethanol removes the water from around the DNA so it precipitates where the ethanol and the solution meet, forming whitish glue-like strands. Low temperatures speed up the precipitation and limit DNase activity.
6. The DNA strands can be centrifuged with ethanol to isolate the DNA as a pellet.

Yaminchhipa10 CC 4.0



1. In the extraction and isolation of DNA:

   (a) Why is it necessary to disrupt the cellular membranes? _____

   (b) Why does the DNA precipitate out in ethanol? _____

   (c) For a DNA extraction, why is it helpful that strawberries are octaploid? _____

   (d) Why is salt added? _____

   _____

   (e) What is the purpose of the filter funnel? _____

   _____

2. In a DNA extraction, student A obtained DNA in long threads, whereas student B obtained DNA that appeared fluffy. Account for the differences in these two results, and suggest what student B might have done incorrectly:

   _____

   _____

   _____

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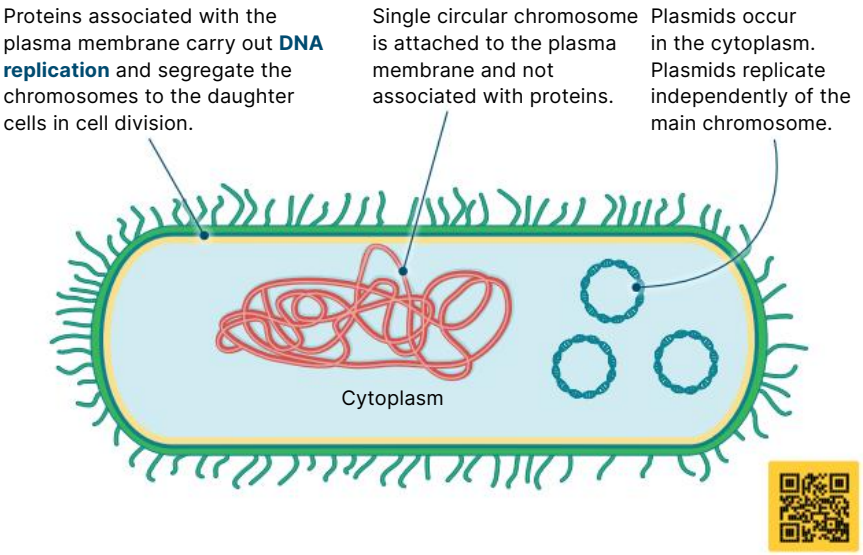
84 Prokaryotic Chromosomes

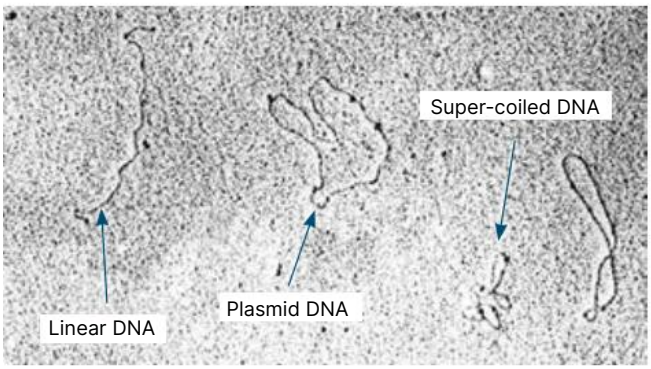
Key Idea: Prokaryotic DNA is packaged as a single circular chromosome. Smaller plasmids may be included.

DNA is packaged differently in prokaryotic and eukaryotic cells. Unlike eukaryotic **chromosomes**, the prokaryotic chromosome is not enclosed in a nuclear membrane and is not associated with protein. It is a single circular (rather than linear) molecule of double stranded DNA, attached to the plasma membrane. It is located in a nucleoid region which is in direct contact with the cytoplasm. As well as the bacterial chromosome, bacteria often contain small, circular, double-stranded DNA molecules called plasmids. Plasmids are independent of the main bacterial chromosome and usually contain 5-100 genes that are not crucial to cell survival under normal conditions.

The prokaryotic genome

- In contrast to **eukaryotes**, prokaryotic DNA consists almost entirely of protein coding genes and their regulatory sequences. It was the study of prokaryotic genomes that gave rise to the one gene-one protein hypothesis, which still holds true for bacteria.
- The chromosomal DNA is located in a nucleoid region. It is not enclosed in a membrane. The nucleoid may take up as much as 20% of the cell's volume in actively growing cells.
- Most bacteria have a single, circular chromosome. This makes them haploid for most genes, unless copies are located on plasmids (small, circular, auxiliary DNA strands). Plasmids are generally circular but can also exist as linear, or supercoiled structures.





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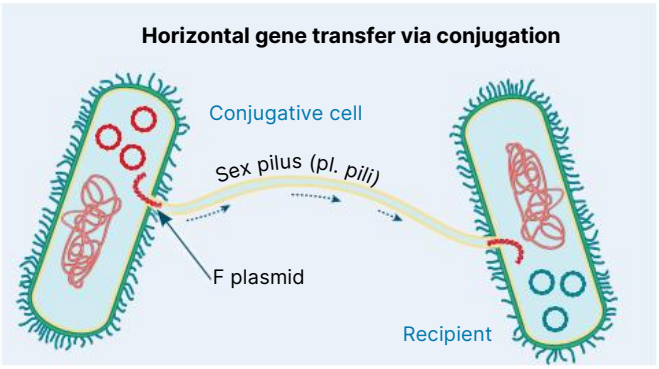

Plasmids: These vary in size from 1000 base pairs (bp) to hundreds of thousands of base pairs. In bacteria, they play an important role in providing extra genetic material, conferring extra properties such as antibiotic resistance. Plasmids can be transferred between bacterial cells in the process of plasmid transfer called conjugation (right).

Conjugation: Special conjugative (F) plasmids contain transfer genes, which enable conjugation and the transfer of genetic information between bacterial cells. Transfer occurs via a sex pilus, which briefly connects the donor and the recipient. Conjugation provides another route for acquiring genes in addition to transfer via binary fission.

1. State three important ways in which prokaryotic chromosomes differ from eukaryotic chromosomes:

   (a) _____

   (b) _____

   (c) _____

2. Explain the consequences to protein synthesis of the prokaryotic chromosome being free in the cytoplasm:

   _____

   _____

3. Most of the bacterial genome comprises protein coding genes and their regulatory sequences. What is the consequence of this to the relative sizes of bacterial and eukaryotic genomes?

   _____

   _____

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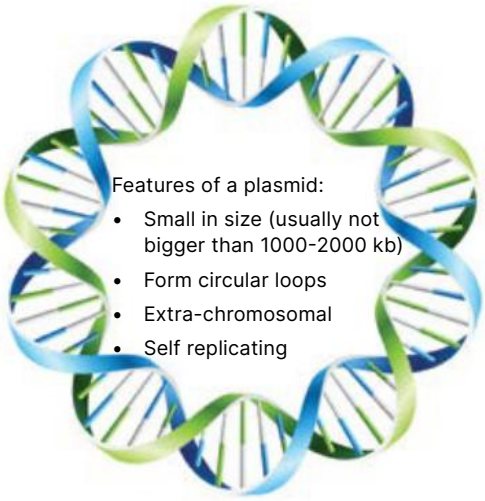
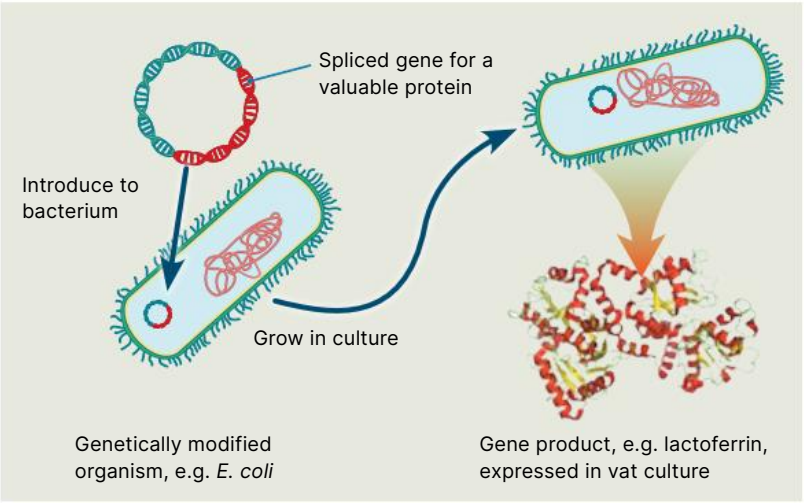
85 Plasmid DNA

Key Idea: Plasmids play a special role in storing DNA in prokaryotes. Plasmids can be exploited for gene manipulation.

Prokaryotes store most of their genetic information in one large chromosome but a small proportion can commonly be found as independently replicating, circular, extra-chromosomal pieces of **DNA** known as plasmids. Plasmids may carry important genes, such as those for the production of toxins that eliminate prokaryote competitors. Plasmids are less common in **eukaryotes** but some species, such as the yeast, *Saccharomyces,* do have them. The genetic material from viruses may form plasmid-like structures called episomes once they have infected a cell.

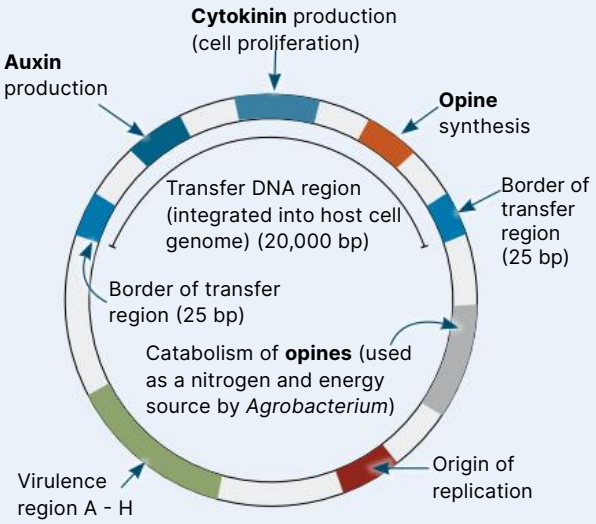


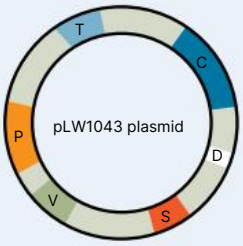


The properties of plasmids enable them to be used as tools to introduce genetic material into organisms. A gene is spliced into a plasmid and the plasmid is inserted into a recipient organism, e.g. a bacterium. The recipient will then produce the gene product as part of its normal metabolism. This technique has enabled the industrial-scale production of valuable gene products, such insulin, from bacteria.

The make-up of plasmids

The Ti plasmid





The pLW1043 plasmid

Genes for
- C Conjugative ability
- T Trimethoprim resistance
- V Vancomycin resistance
- D Disinfectant resistance
- S Streptomycin resistance
- P Penicillin resistance

Plasmids often carry genes for beneficial traits, including antibiotic resistance and the ability to use new substrates. The ability of bacteria to exchange plasmids has contributed to the spread of antibiotic resistance. The pLW1043 plasmid (above) from the superbug, Methicillin Resistant *Staphylococcus aureus* (MRSA) carries several genes for antibiotic resistance, acquired progressively over time.

The bacterium *Agrobacterium tumefaciens* often contains the Ti (tumor inducing) plasmid. This plasmid is able to transfer genes into plant cells and cause disease. Several regions on the plasmid (left) help it to infect plants. The plasmid is just over 200,000 bp (base pairs) long and contains 196 genes. The mapping of its genes has made it of great importance in creating genetically modified plants.

1. What is a plasmid? _____

2. Explain how a plasmid can convey a survival advantage to bacteria under certain conditions: _____

_____

_____

3. (a) Why are plasmids (such as the Ti plasmid) useful to genetic engineers? _____

_____

(b) Into which region of the Ti plasmid would you insert a gene in order for it to be transferred into a host plant cell?

_____

SU

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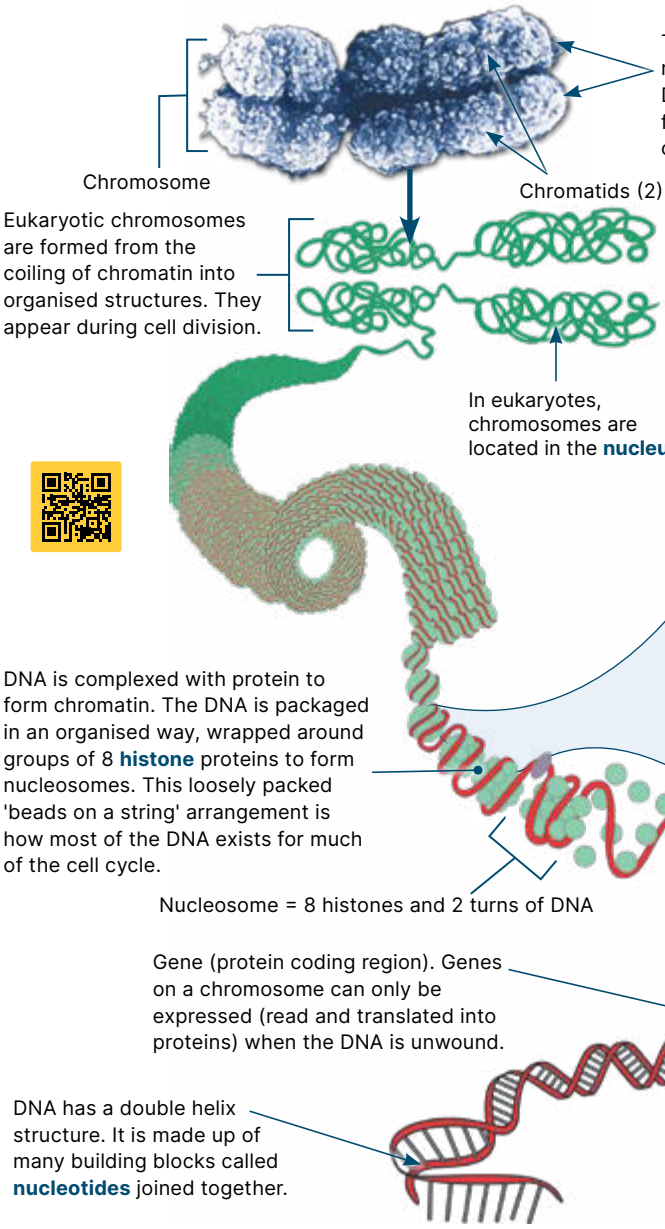
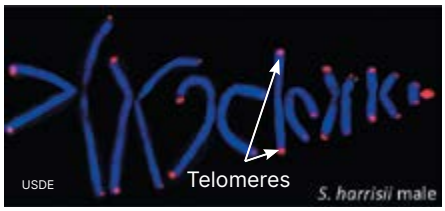
86 Eukaryotic Chromosome Structure

Key Idea: Eukaryotic DNA is located in the cell's nucleus. Linear DNA molecules are very long and must be highly organised to fit into the cell's nucleus and enable replication. Eukaryotes package their DNA as discrete linear **chromosomes**. The number of chromosomes varies from species to species. The extent of DNA packaging changes during the life cycle of the cell, but classic chromosome structures (below) appear during metaphase of mitosis.





Hannah S. Bender et al (CC 2.5)

Telomeres were first noted and named in 1938. It was not until 1977 that their structure and function was discovered, for which Elizabeth Blackburn, Carol W Greider, and Jack W Szostak were awarded Nobel prizes in physiology and medicine.

1. Explain why eukaryotic DNA needs to be packaged up to fit inside a cell nucleus? _____

2. How do histone proteins help in the coiling up of DNA? _____

3. Suggest why a cell coils up its chromosomes into tight structures when it is going to divide: _____

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Sex chromosomes and autosomes

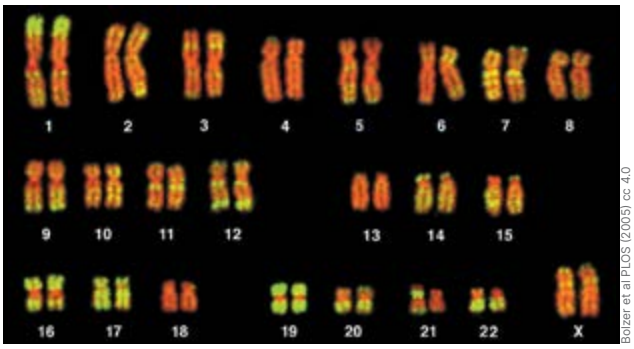
- In eukaryotes, the chromosomes are located within the cell's **nucleus**. Sexually reproducing organisms usually have two sets of chromosomes (they are diploid). One set is inherited from each parent at the time of fertilisation. The corresponding chromosomes from each parent form a homologous pair (homologous chromosomes). Chromosomes can be classified either as sex chromosomes or autosomes.

Sex chromosomes

- Sex chromosomes determine the sex of organisms and the genes they carry are called sex linked.
- Humans have two sex chromosomes (X and Y). Egg cells contain 22 autosomes and an X chromosome. Sperm cells contain 22 autosomes and either an X or Y chromosome. Humans have one pair of sex chromosomes:
  XX = females; XY = males.
- Sex chromosomes are not homologous. They differ in height, banding pattern, and centromere position. The X chromosome is much larger than the Y chromosome and contains more genes (above right). Genes on the X chromosome that are not present on the Y chromosome will always be expressed in males.

Autosomes

- Most chromosomes are autosomes (non-sex chromosomes). Their genes determine most phenotypic characteristics (but not sex).
- Human cells have 22 pairs of autosomes (1-22 below). The pairs are homologous so the chromosomes in each pair have similar heights, banding patterns, and centromere positions. They also carry the same genes, in the same location.



Bolzer et al PLOS (2005) cc 4.0

4. Summarise the differences between sex chromosomes and autosomes under the headings below:

   (a) Function:

   i) Autosome: _____

   ii) Sex chromosome: _____

   (b) Are the chromosomes homologous (Yes/No)?

   i) Autosomes: _____ ii) Sex chromosomes: _____

   (c) Number/pairs of chromosomes in humans:

   i) Autosomes: _____ ii) Sex chromosomes: _____

   (d) Are the genes sex linked (Yes/No)?

   i) Autosomes: _____ ii) Sex chromosomes: _____

5. Chromosomes are often depicted in different ways, in different sources. Search the internet for some of these depictions, print them out, and paste them into the space below. In what ways are these depictions accurate or inaccurate?

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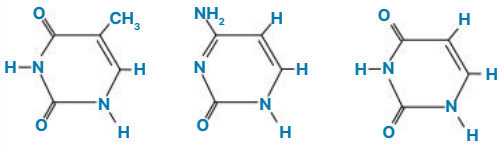
87 Nucleotides

Key Idea: Nucleotides make up nucleic acids. A nucleotide is made up of a base, a sugar, and a phosphate group.

Nucleotides are the building blocks of the **nucleic acids DNA** and **RNA**, which are involved in the transmission of inherited information. Nucleotide derivatives, such as ATP and GTP, are involved in energy transfers in cells. A nucleotide has three components: a base, a sugar, and a phosphate group. Nucleotides may contain one of five bases. The combination of bases in the nucleotides making up DNA or RNA stores the information controlling the cell's activity. The bases in DNA are the same as RNA except that **thymine** (T) in DNA is replaced with **uracil** (U) in RNA.

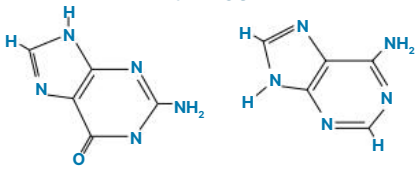
Pyrimidines



Thymine Cytosine Uracil

Pyrimidines are single ringed bases. DNA contains the pyrimidines **cytosine** (C) and thymine (T). RNA contains the pyrimidines cytosine and uracil (U).

Purines

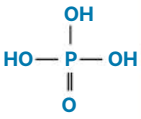


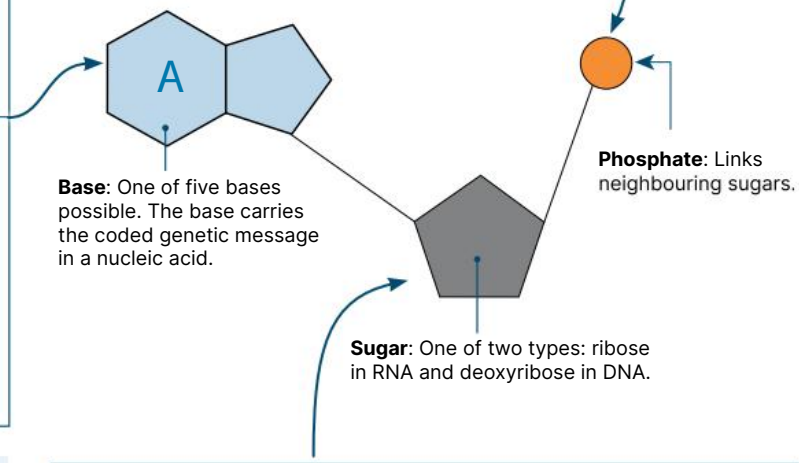
Guanine Adenine

Purines are double ringed bases. Both DNA and RNA contain the purines adenine (A) and **guanine** (G).

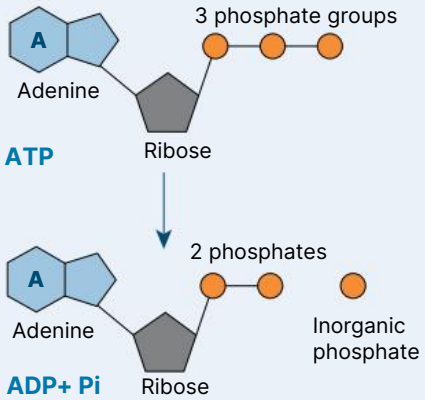
Phosphate

Phosphate groups are represented by circles. Along with the pentose sugar they form the "backbone" of the DNA or RNA molecule.





Nucleotide derivatives



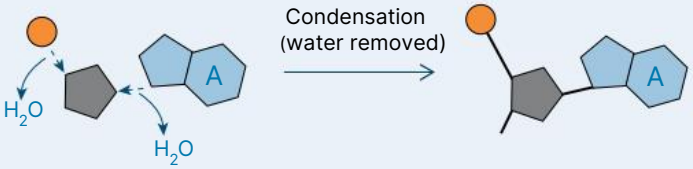
ATP is a nucleotide derivative used to provide chemical energy for metabolism. It consists of an **adenine** linked to a **ribose** sugar and 3 phosphate groups. Energy is made available when a phosphate group is transferred to a target molecule. Other nucleoside triphosphates (NTPs) have similar roles.

Sugars

Deoxyribose Ribose

Nucleotides contain one of two different sorts of sugars. **Deoxyribose** sugar is only found in DNA. Ribose sugar is found in RNA.

Nucleotide formation



In formation of a nucleotide, a phosphoric acid and a base are chemically bonded to a sugar molecule by condensation reactions in which water is given off. The reverse reaction is hydrolysis.

1. (a) List the nucleotide bases present in DNA: _____

   (b) List the nucleotide bases present in RNA: _____

2. Name the sugar present:

   (a) In DNA: _____ (b) In RNA: _____

3. How can simple nucleotide units combine to store genetic information? _____

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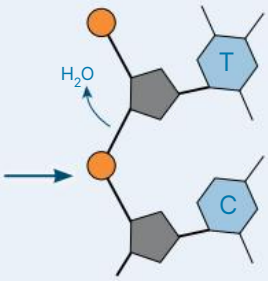
88 Nucleic Acids

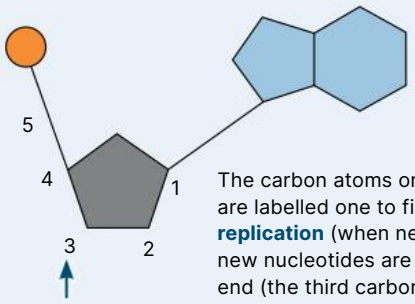
Key Idea: Nucleic acids are macromolecules made up of long chains of nucleotides, which store and transmit genetic information. DNA and RNA are nucleic acids.

DNA and **RNA** are **nucleic acids** involved in the storage and transmission of the inherited information that controls cellular activity. The central nucleic acid is called deoxyribonucleic acid (DNA). Ribonucleic acids (RNA) are involved in 'reading' and 'translating' the DNA information. All nucleic acids are made up of **nucleotides** linked together to form chains or strands. The strands vary in the sequence of the bases found on each nucleotide. It is this sequence that provides the 'genetic instructions' for the cell.

Nucleotides are joined by condensation polymerisation

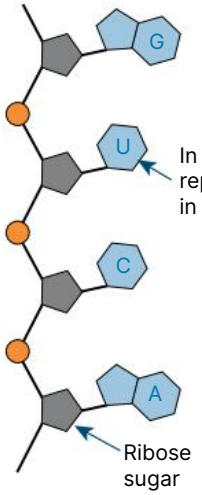
A condensation reaction joins two molecules together with the loss of a water molecule. When nucleic acids are formed, nucleotides are joined together into polymers through a condensation reaction between the phosphate of one nucleotide and the sugar of another. Water is released. Because of the way they are formed, nucleic acids are called condensation polymers.





The carbon atoms on the pentose sugar are labelled one to five. During **DNA replication** (when new DNA is made) new nucleotides are added to the 3' end (the third carbon) of the existing nucleotide chain. It is therefore said DNA replication works in the 5' to 3' direction.

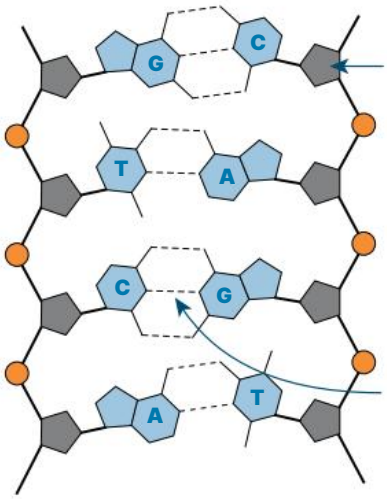
RNA molecule



In RNA, uracil replaces thymine in the code.

Ribose sugar

DNA molecule



Deoxyribose sugar

Hydrogen bonds hold the two strands together.

Only certain bases can pair.

Symbolic representation

Space filling model

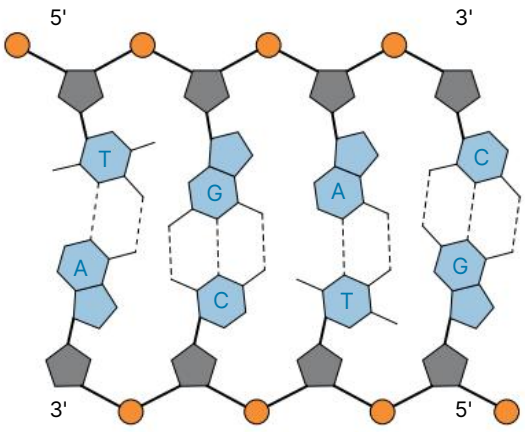
Ribonucleic acid (RNA) consists of a single strand of linked nucleotides. Although it is single stranded, it is often folded back on itself, with complementary bases joined by hydrogen bonds.

Deoxyribonucleic acid (DNA) consists of a double strand of linked nucleotides held together by hydrogen bonds. A **pyrimidine** always pairs with a **purine**. The DNA molecule is shown unwound in the symbolic representation (left). The DNA molecule takes on a double helix shape as shown in the space filling model above right.

Double-stranded DNA

The double-helix structure of DNA is like a ladder twisted into a corkscrew shape around its longitudinal axis. It is 'unwound' here to show the relationships between the bases.

- The DNA backbone is made up of alternating phosphate and sugar molecules, giving the DNA molecule an asymmetrical structure.
- The asymmetry gives a DNA strand direction. The strands run in the opposite direction to each other (**anti-parallel**).
- The ends of a DNA strand are labelled the 5' (five prime) and 3' (three prime) ends. The 5' end has a terminal phosphate group (off carbon 5), the 3' end has a terminal hydroxyl group (off carbon 3).
- DNA displays **complementary base pairing** between strands in which the base A on the one strand pairs with the base T on the other. The base C always pairs with the base G.
- The way the pairs of bases come together to form hydrogen bonds is determined by the number of bonds they can form and the configuration of the bases.



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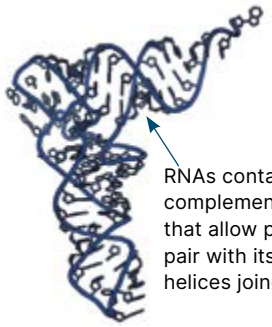
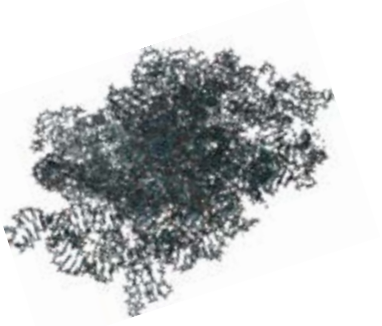
RNAs are involved in decoding the genetic information in DNA, as messenger RNA (mRNA), transfer RNA (tRNA), and ribosomal RNA (rRNA). RNA is also involved in modifying mRNA after transcription and in regulating translation.

Messenger RNA (above) is transcribed (written) from DNA. It carries a copy of the genetic instructions from the DNA to ribosomes in the cytoplasm, where it is translated into a polypeptide chain.



RNAs contain self-complementary sequences that allow parts of the RNA to pair with itself to form short helices joined by H bonds.

Transfer RNA (above) carries amino acids to the growing polypeptide chain. One end of the tRNA carries the genetic code in a three-nucleotide sequence called the anticodon. The amino acid links to the 3' end of the tRNA.



Ribosomal RNA (above) forms ribosomes from two separate ribosomal components (the large and small subunits) and assembles amino acids into a polypeptide chain.

1. Label the following parts on the diagram of the double-stranded DNA molecule at the bottom of the previous page:
   (a) Deoxyribose
   (b) Phosphate
   (c) Hydrogen bonds
   (d) Purine bases
   (e) Pyrimidine bases

2. (a) Use the diagram opposite to identify the base-pairing rule that applies in double-stranded DNA: _____

   _____

   _____

   (b) How is the base-pairing rule for RNA different? _____

   (c) What is the purpose of the hydrogen bonds in double-stranded DNA? _____

   _____

3. Briefly describe the roles of RNA: _____

   _____

4. (a) If you wanted to use a radioactive or fluorescent tag to label only the RNA in a cell and not the DNA, what molecule(s) would you label?

   _____

   (b) If you wanted to use a radioactive or fluorescent tag to label only the DNA in a cell and not the RNA, what molecule(s) would you label?

   _____

5. (a) Why do the DNA strands have an asymmetrical structure? _____

   _____

   (b) What are the differences between the 5' and 3' ends of a DNA strand? _____

   _____

6. Complete the following table summarising the differences between DNA and RNA molecules:

	DNA	RNA
Sugar present		
Bases present		
Number of strands		
Relative length		

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89 Creating a DNA Model

Key Idea: Nucleotides pair according to the base pairing rule. There are ten base pairs per turn of the DNA double helix.

DNA is made up of structures called **nucleotides**. Two primary factors control the way in which these nucleotide building blocks are linked together: 1) the available space within the DNA double helix and 2) the hydrogen-bonding capability of the bases. These factors cause the nucleotides to join together in a predictable way, referred to as the **base pairing rule**. The strands of the DNA are **anti-parallel** (they run in opposite directions) and there are 10 base pairs per 360° turn of the helix. The activity below will guide you through constructing a three dimensional model of DNA.

Chargaff's rules

Before Watson and Crick described the structure of DNA, an Austrian chemist called Chargaff analysed the base composition of DNA from a number of organisms. He found that the base composition varies between species but that within a species the percentage of A and T bases are equal and the percentage of G and C bases are equal. Validation of Chargaff's rules was the basis of Watson and Crick's base pairs in the DNA double helix model.

DNA base pairing rule

Adenine	always pairs with	**Thymine**	A ⟷ T
Thymine	always pairs with	**Adenine**	T ⟷ A
Cytosine	always pairs with	**Guanine**	C ⟷ G
Guanine	always pairs with	**Cytosine**	G ⟷ C

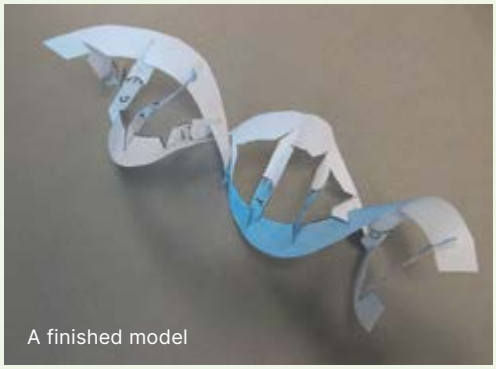
Investigation 7.2 Creating a model of a DNA molecule

See appendix for equipment list.

Work in pairs for this activity.

1. Cut out the opposite page. Cut out the template strand. Dark black lines should be cut. Make a slight fold on the red dashed lines so that the grey surfaces are facing (a valley fold). Do not cut around the grey representations of hydrogen bonds on each base. These are to show you where you will join your bases.
2. Cut out the complementary strand. The first base (G) is in position as a guide. Fold on the red dashed line so that the blue surfaces are facing each other.
3. Fill in the table (right) to help you place the remaining bases in the correct order (a)-(i) on the complementary strand:
4. Cut out the bases and slot them into the slots on the complementary strand using the order in the table above. Use short lengths of tape to fix them in position. Make sure the blue surfaces are facing and the base is in the same orientation as the guide (G).
5. Line up the first base pairs (C and G) and stick them together with tape. The tape takes the place of the hydrogen bonds holding the strands together. Note that the bases are facing in opposite directions.
6. Continue sticking base pairs together, working your way around the helix, to complete the DNA molecule.
7. Together, or in groups, search online for at least three different representations of a DNA molecule. Evaluate your model against these representations. How are they similar? How are they different? If you wish, attach pictures of the DNA representations you selected to this page.

Template strand	Complementary strand
Cytosine (C)	Guanine (G)
Guanine (G)	(a)
Thymine (T)	(b)
Adenine (A)	(c)
Thymine (T)	(d)
Adenine (A)	(e)
Thymine (T)	(f)
Thymine (T)	(g)
Cytosine (C)	(h)
Guanine (G)	(i)



A finished model

1. Describe your model in terms of the other representations you looked at. What are its strengths and deficiencies?

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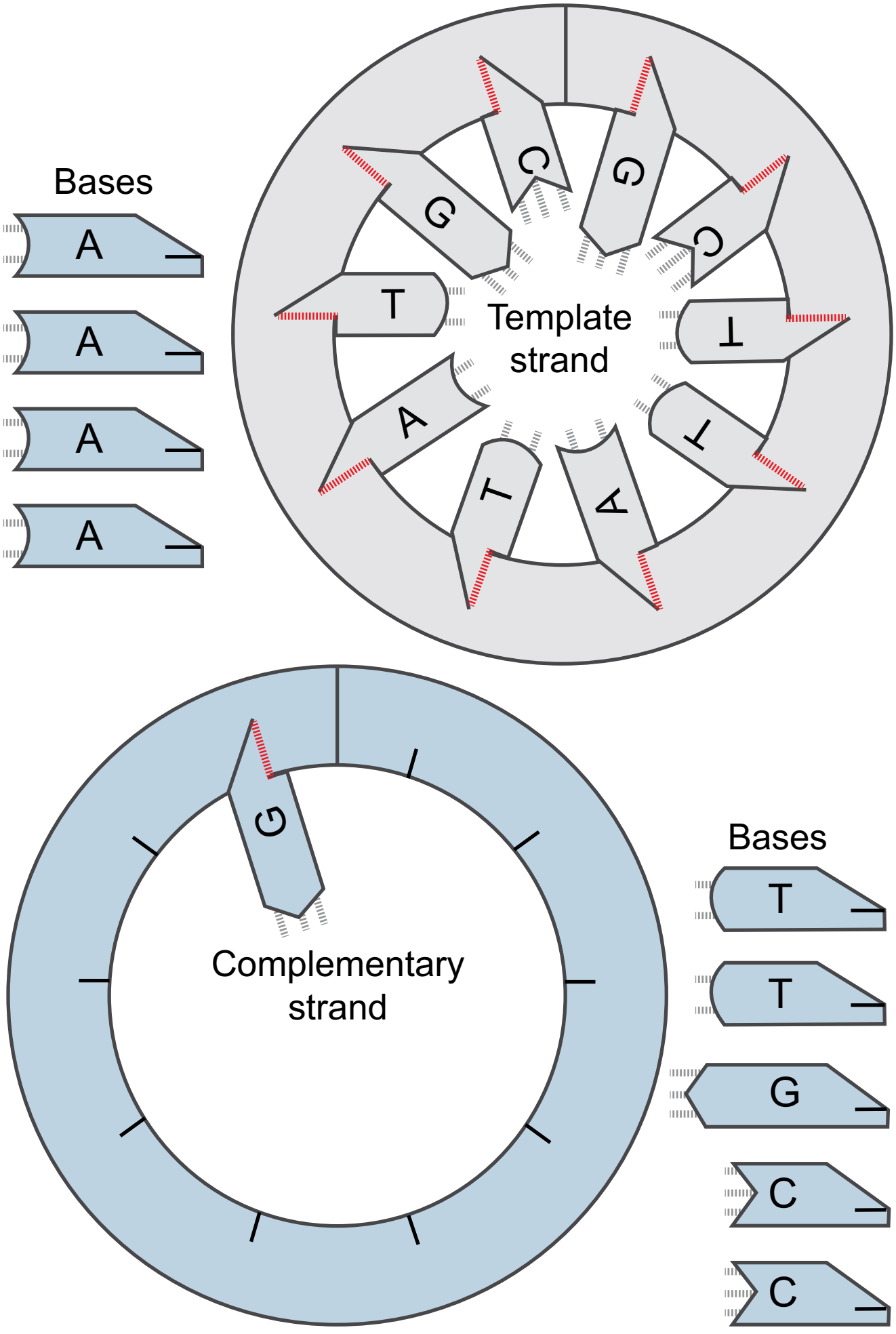

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90 Finding the Structure of DNA

Key Idea: Many scientists contributed to the discovery of DNA's structure. Once the structure of DNA was known, it immediately suggested a mechanism for its replication.

DNA is easily extracted and isolated from cells. This was first done in 1869, but it took the work of many scientists working in different areas many years to determine DNA's structure. In particular, four scientists, Watson, Crick, Franklin, and Wilkins are recognised as having made significant contributions in determining the structure of DNA. Once the structure of DNA was known scientists could determine how it was replicated.

Discovering the structure of DNA: a story of collaboration and friction

Although Watson and Crick are often credited with discovering DNA's structure, the contributions of many scientists were important. This includes not only the contributions from scientists at the time, but also from earlier researchers whose findings contributed to the body of existing knowledge.

Personal conflicts and internal politics probably prevented DNA's structure being determined earlier. Professional friction between Rosalind Franklin and Maurice Wilkins meant that they worked independently of each other. Watson and Crick analysed some of Rosalind Franklin's results, notably 'photo 51', without her knowledge or consent and Watson himself recalls that he tended to dismiss her. Photo 51 was crucial to Watson and Crick's model because it showed that DNA was a double helix. Only later did he acknowledge her considerable contribution.

Franklin was conservative by nature and opposed to prematurely building theoretical models until there was enough data to guide the model building. However, when she saw Watson and Crick's model, she readily accepted it. Despite her contribution, Franklin did not receive the Nobel prize, which cannot be awarded posthumously.

IMAGE: A. Barrington-Brown, © Gonville and Caius College, Cambridge / Coloured by Science Photo Library

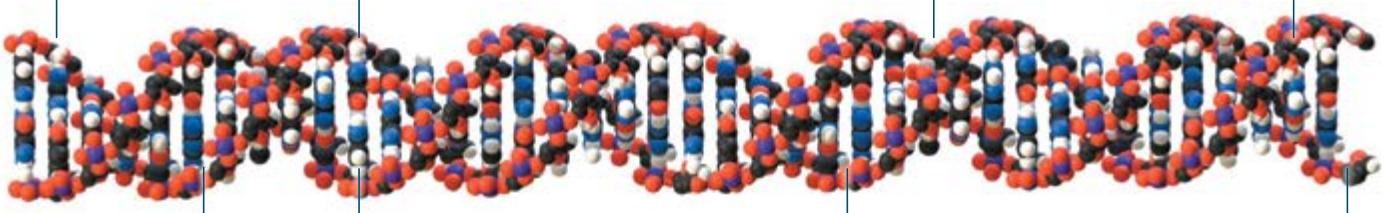
James Watson (left) and Francis Crick (right) in 1953 with their DNA model.

Late 1940s
Linus Pauling determined by x-ray crystallography that proteins have a helical structure.

1951
Rosalind Franklin studied the structure of DNA using x-ray crystallography at King's College. Maurice Wilkins, also at King's College, was also using x-ray crystallography to study DNA. Wilkins and Franklin did not get on well.

30 January 1953
Wilkins shows Watson and Crick the "photo 51" without Franklin's approval or knowledge. It provided the structural information they needed to finalise their model, completed on 7 March 1953.

16 April 1958
Franklin dies at age 37 of ovarian cancer. She was never nominated for a Nobel Prize.



1949
Chargaff's rules are announced: DNA contains equal proportions of bases A and T and G and C.

1951
James Watson and Francis Crick build their first DNA model - a three stranded helix, with bases to the outside and phosphate groups to the inside. Franklin points out that their model is incorrect and is not consistent with the data.

May 1952
Franklin produces "photo 51", showing DNA is a helix. She was working on a less hydrated form of DNA and did not return to the photo again until 1953.

1962
Watson, Crick, and Wilkins win the Nobel Prize in Physiology or Medicine. Franklin was not acknowledged.

1. As a class, work together to produce a timeline of the events leading to the discovery of DNA's structure. In small groups, choose one event or researcher and explain its/their significance. Use the information presented in this activity, as well as any information provided on **BIOZONE Resource Hub**. Take a photograph of your completed timeline and attach it to this page. How much was the discovery of DNA's structure a collaboration between scientists working in related fields? Were Watson and Crick wrong to use information they did not have permission to use? How much did their less cautious approach accelerate the determination of DNA's structure? Attach any extra notes or comments to this page.

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91 How Does DNA Replicate?

Key Idea: Semi-conservative DNA replication produces two identical copies of DNA, each containing half original material and half new material.

Before a cell can divide, it must double its **DNA**. It does this by a process called **DNA replication**. This process ensures that each resulting cell receives a complete set of genetic instructions from the parent cell. After the DNA has replicated, each **chromosome** is made up of two chromatids, joined at the centromere. The two chromatids will become separated during cell division to form separate chromosomes. During DNA replication, **nucleotides** are added at the replication fork. Enzymes are responsible for all of the key events.

Step 1
Unwinding the DNA molecule

A normal chromosome consists of an unreplicated DNA molecule. Before cell division, this long molecule of double stranded DNA must be replicated.

For this to happen, it is first untwisted and separated (unzipped) at high speed at its replication fork by an enzyme called **DNA helicase**. Another enzyme relieves the strain that this generates by cutting, winding and rejoining the DNA strands.

Step 2
Making new DNA strands

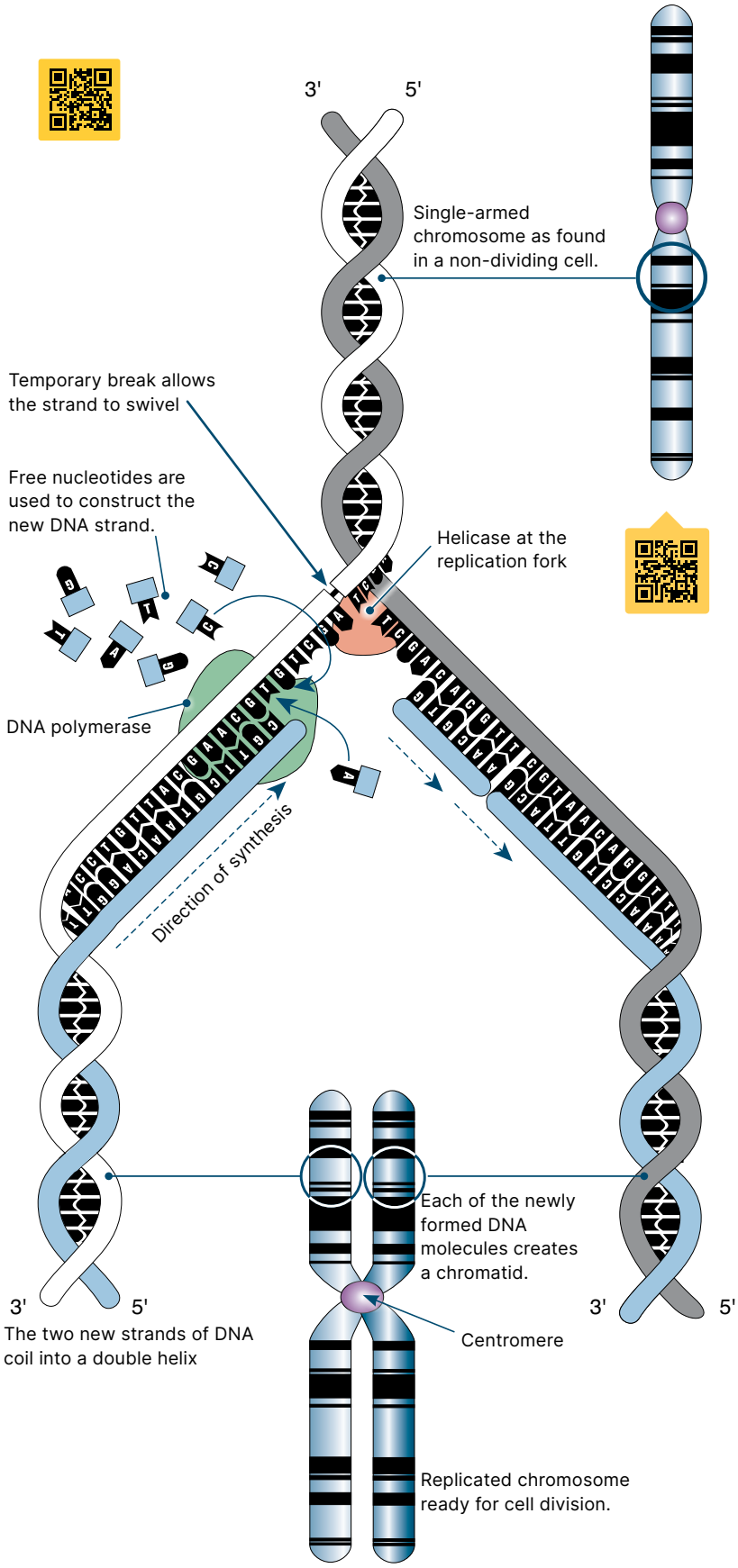
The formation of new DNA is carried out mostly by an enzyme complex called **DNA polymerase**.

DNA polymerase catalyses the condensation reaction that joins adjacent nucleotides. The strand is synthesised in a 5' to 3' direction, with the polymerase moving 3' to 5' along the strand it is reading. Thus the nucleotides are assembled in a continuous fashion on one strand but in short fragments on the other strand. These fragments are later joined by an enzyme to form one continuous length.

Step 3
Rewinding the DNA molecule

Each of the two new double-helix DNA molecules has one strand of the original DNA (dark grey and white) and one strand that is newly synthesised (blue). The two DNA molecules rewind into their double-helix shape again.

DNA replication is **semi-conservative**, with each new double helix containing one old (parent) strand and one newly synthesised (daughter) strand. The new chromosome has twice as much DNA as a non-replicated chromosome. The two chromatids will become separated in the cell division process to form two separate chromosomes.



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1. What is the purpose of DNA replication? _____

2. Summarise the three main steps involved in DNA replication:

   (a) _____

   (b) _____

   (c) _____

3. For a cell with 22 chromosomes, state how many chromatids would exist following DNA replication: _____
4. What percentage of DNA in each daughter cell is new and what percentage is original? _____
5. What does it mean when we say DNA replication is semi-conservative? _____

6. How are the new strands of DNA lengthened during replication: _____

7. What rule ensures that the two new DNA strands are identical to the original strand? _____

8. Why does one strand of DNA need to be copied in short fragments? _____

9. Match the statements in the table below to form complete sentences, then put the sentences in order to make a coherent paragraph about DNA replication and its role:

The enzymes also proofread the DNA during replication...	...is required before mitosis or meiosis can occur.
DNA replication is the process by which the DNA molecule...	...by enzymes.
Replication is tightly controlled...	...to correct any mistakes.
After replication, the chromosome...	...and half new DNA.
DNA replication...	...during mitosis.
The chromatids separate...	...is copied to produce two identical DNA strands.
A chromatid contains half original ...	...is made up of two chromatids.

Write the complete paragraph here:

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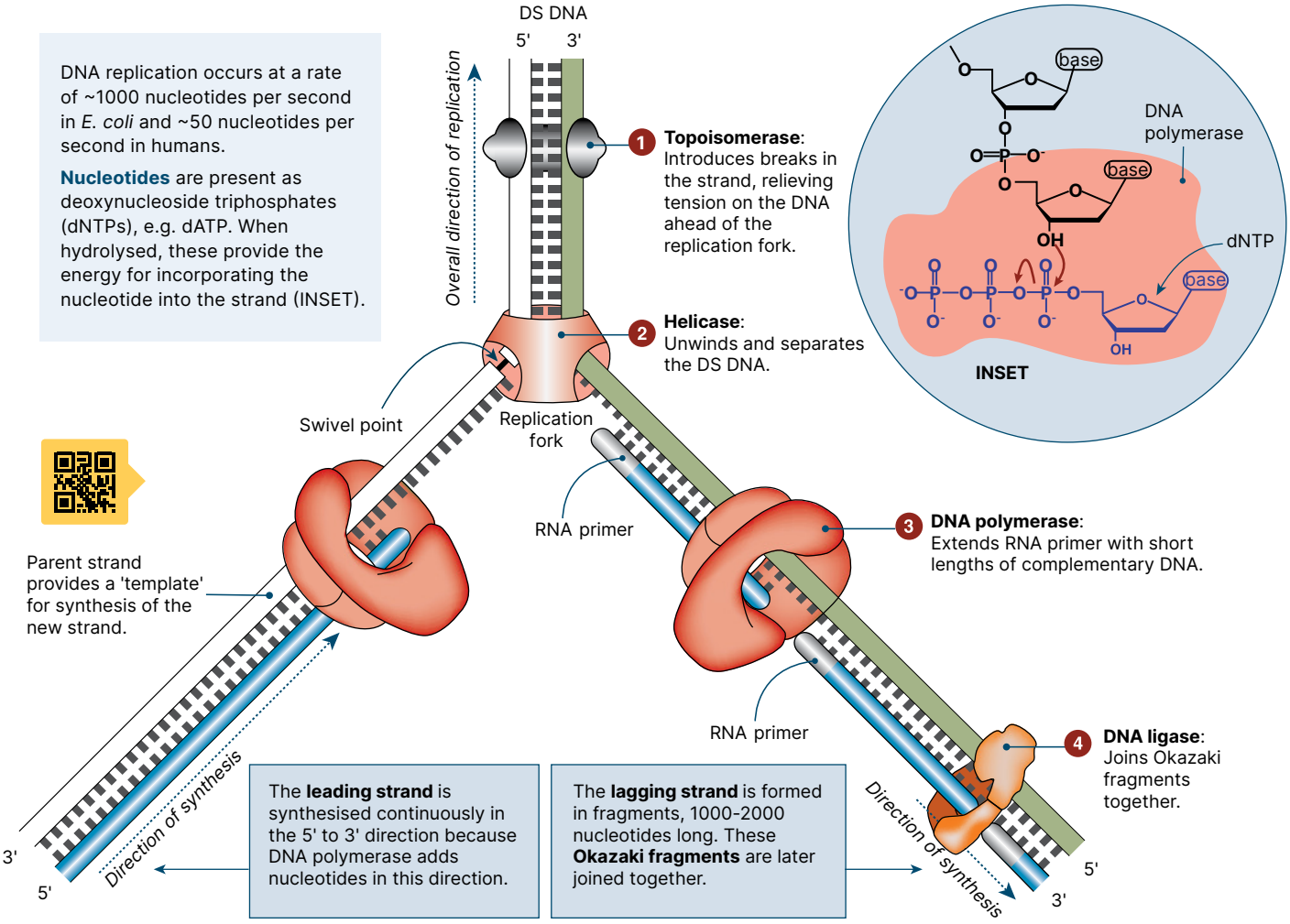
92 Enzyme Control of DNA Replication

Key Idea: The process of DNA replication is controlled by many different enzymes.

DNA replication involves many enzyme-controlled steps. They are shown below as separate, but many of the enzymes are clustered together as enzyme complexes. As the **DNA** is replicated, enzymes 'proof-read' it and correct mistakes. The polymerase enzyme can only work in one direction, so that one new strand is constructed as a continuous length (the leading strand) while the other new strand (the lagging strand) is made in short segments to be later joined together.

DNA replication occurs at a rate of ~1000 nucleotides per second in *E. coli* and ~50 nucleotides per second in humans.

Nucleotides are present as deoxynucleoside triphosphates (dNTPs), e.g. dATP. When hydrolysed, these provide the energy for incorporating the nucleotide into the strand (INSET).



1. Explain the general role of enzymes in DNA replication: _____

_____

_____

_____

2. Explain the specific role of each of the following enzymes in DNA replication:

   (a) Helicase: _____

   (b) Topoisomerase: _____

   (c) DNA polymerase: _____

   (d) Ligase: _____

3. *E. coli* has 4.6 ×10^6 base pairs in a single circular chromosome and all of it is replicated in two directions from a single point of origin. Determine how long it would take to replicate its DNA:

_____

4. Explain how the energy for DNA replication is supplied: _____

_____

SU

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93 Did You Get It?

1. List the differences between RNA and DNA: _____

2. What does antiparallel mean? Use DNA as an example or antiparallel: _____

3. Explain the importance of Okazaki fragments: _____

4. In the boxes below draw and label a series of diagrams to illustrate how a strand of DNA replicates:

DNA unzips	Nucleotides are added to the parent strands	The parent and daughter strands rewind to form two new DNA strands

5. (a) Which base does the base thymine (T) pair with in DNA? _____

   (b) Which base does the base cytosine (C) pair with in DNA? _____

6. What is the difference between a chromosome, a chromatid, and chromatin? _____

7. Under the headings Unwind, Replicate, Rewind, describe the stages of DNA replication: _____

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Chapter 8 Unit 4 Topic 1

Cell Replication and Variation

Resource Hub
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Key Terms

- anaphase I
- anaphase II
- chromosome
- crossing over
- diploid
- fertilisation
- gamete
- haploid
- homologous pair
- independent assortment
- interphase
- meiosis
- metaphase I
- metaphase II
- mitosis
- oogenesis
- prophase I
- prophase II
- recombination
- sexual reproduction
- spermatogenesis
- telophase I
- telophase II

Key Concepts

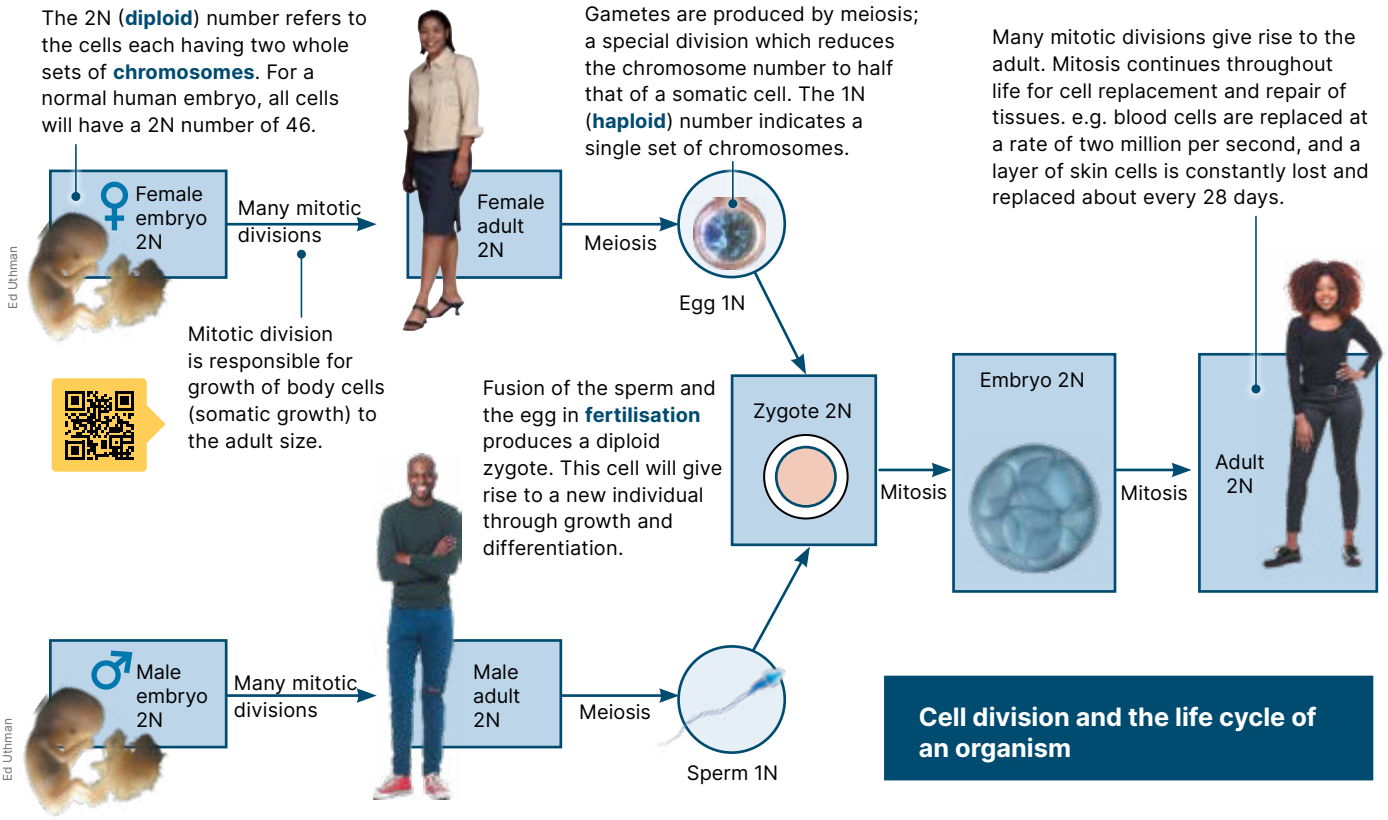
- Cells divide by either mitosis or meiosis. Mitosis is for growth and repair. Meiosis is for the production of gametes for reproduction. Meiosis produces haploid cells.
- Meiosis is a continuous process but can be divided into stages based on the structures present in the dividing cells. Meiosis produces variation in offspring by independent assortment and crossing over.

Meiosis and Cell Division		Activity Number
☐ 1	State that cells replicate by cell division which is preceded by duplication of the genetic material by DNA replication. Distinguish between mitotic and meiotic division in terms of their genetic outcome and biological role.	94
☐ 2	Describe the key events in the two divisions of meiosis including the behaviour and role of homologous chromosomes: • Meiosis I: prophase I, metaphase I, anaphase I, and telophase I • Meiosis II: prophase II, metaphase II, anaphase II, and telophase II	95
☐ 3	Describe the processes of crossing over and recombination between non-sister chromatids of homologous chromosomes.	95
☐ 4	Explain the significance of the following events in meiosis: • Crossing over between homologous chromosomes in prophase I of meiosis • Recombination of alleles as a result of crossing over • Independent assortment of homologous pairs in metaphase I • The non-dividing centromere in metaphase I	95
☐ 5	Explain that gametes produced by meiosis are brought together in fertilisation to restore the diploid number of the organism.	94, 95, 97
☐ 6	Using a model, demonstrate how crossing over and recombination and the independent assortment of homologous chromosomes contribute to genetic variation in the gametes. Use the model to also show how random fertilisation of genetically variable gametes contributes to genotypic variation in the offspring.	96
☐ 7	Compare and contrast the processes of spermatogenesis and oogenesis with reference to haploid and diploid cells.	97

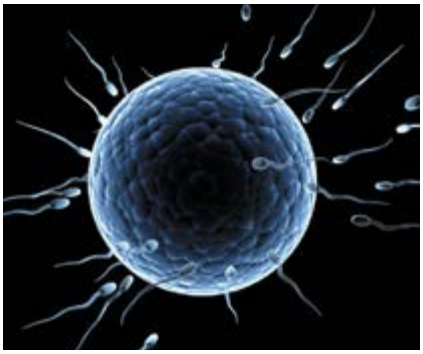
94 Cell Division

Key Idea: There are two types of cell division in eukaryotes, mitosis and meiosis, but only meiosis produces cells that are genetically different to the parent cell.

New cells are formed when existing cells divide. There are two forms of cell division in eukaryotes, **mitosis** and **meiosis**. Mitosis produces two identical daughter cells from a parent cell. Meiosis is a special type of cell division, it produces sex cells (**gametes** or spores) for **sexual reproduction**. In sexual reproduction, sex cells from two parents combine to form a new individual that is genetically different to its parents.

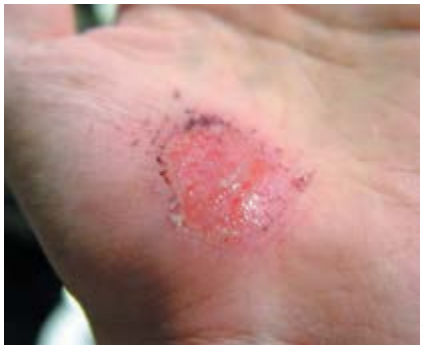


Cell division and the life cycle of an organism



The sex cells in humans, called eggs and sperm, are produced by meiosis. Events occurring during meiosis creates gametes with unique combinations of gene variants and so creates genetic variability.

Sexual reproduction rearranges and reshuffles the genetic material into new combinations. This is why family members may look similar, but they'll never be identical (except for identical twins).



Jpbarrass

Mitosis produces genetically identical cells. This characteristic allows the body to produce cells to heal itself when it is damaged, and is also responsible for the production of the cells required for growth.

1. (a) Where does mitosis take place in animals? _____

   (b) Describe the roles of mitosis in the human body: _____

   _____

   (c) In mitosis, the daughter cells are genetically different to the parent cell. True or False? _____

2. (a) Where does meiosis take place in animals? _____

   (b) What is the purpose of meiosis? _____

   _____

   (c) In meiosis, the sex cells are genetically different to the parent cell. True or False? _____

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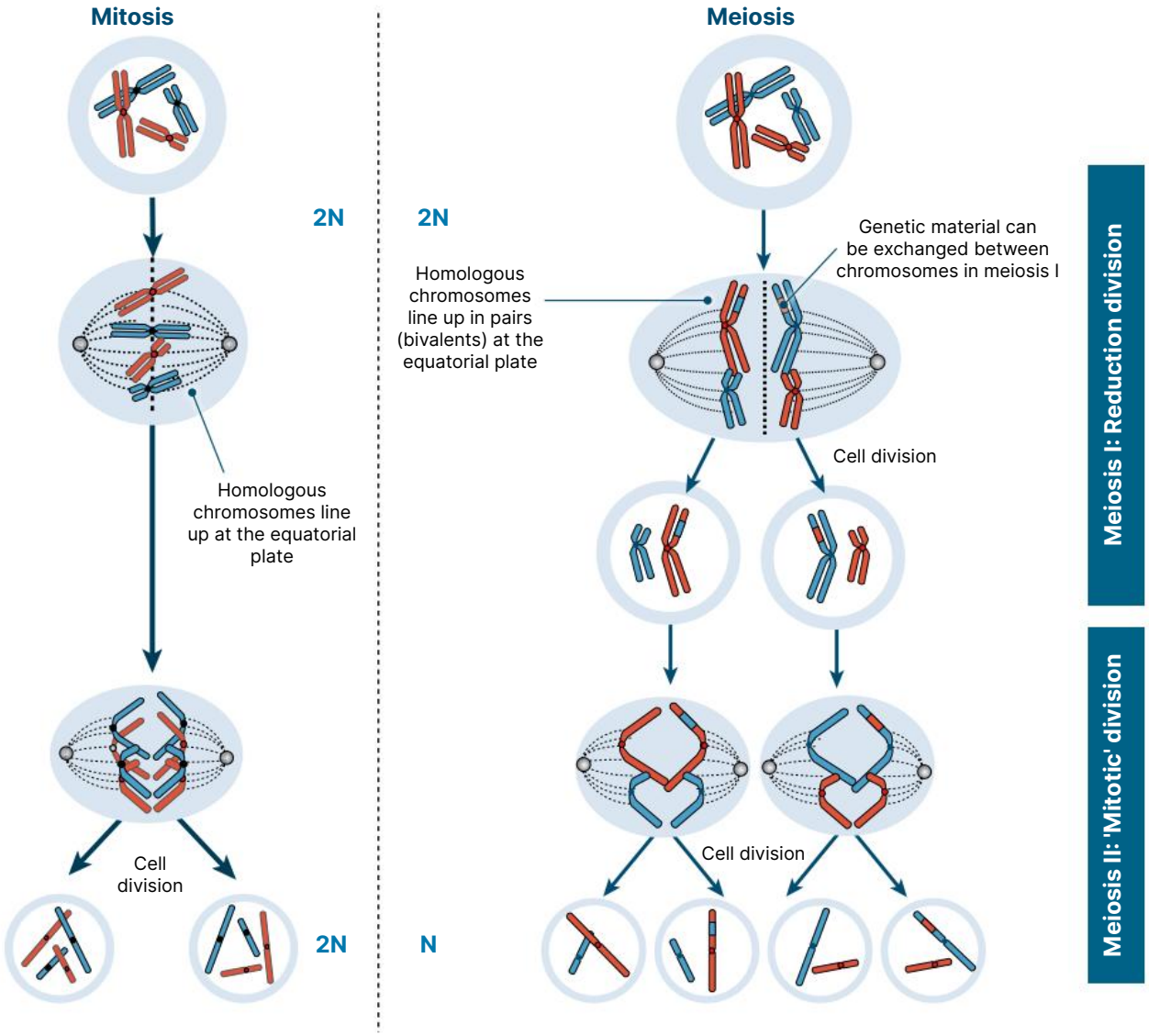
- Mitosis and meiosis have quite different purposes and genetic outcomes.
- Mitosis is the simpler process and produces two identical daughter cells from each parent cell. It is responsible for growth and repair in multicellular organisms and reproduction in single-celled and asexual eukaryotes.
- Meiosis involves a reduction division in which haploid gametes are produced for the purposes of sexual reproduction.



3. Explain how mitosis conserves chromosome number while meiosis reduces the number from diploid to haploid:

4. Describe a fundamental difference between the first and second divisions of meiosis:

5. How does meiosis introduce genetic variability into gametes and offspring (following gamete fusion in fertilisation)?

6. If the DNA in a chromatid was affected by a mutation in a cell about to undergo meiosis, what is the probability of a daughter cell being affected by the mutation?

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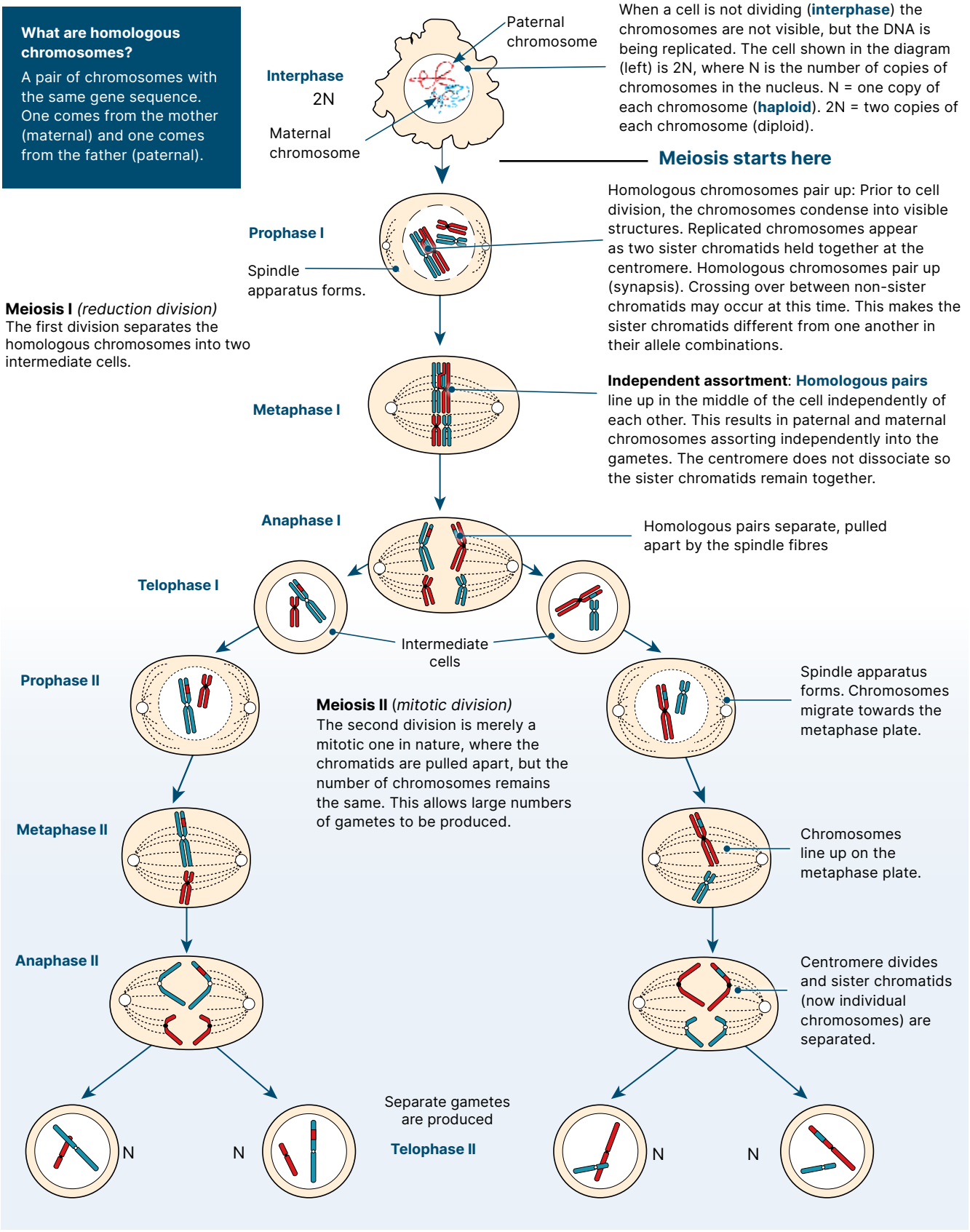
95 Meiosis

Key Idea: Meiosis is a special type of cell division. It produces sex cells (gametes) for the purpose of sexual reproduction.

Meiosis involves a single chromosomal duplication followed by two successive nuclear divisions, and results in a halving of the **diploid chromosome** number. Meiosis occurs in the sex organs of animals and the sporangia of plants. If genetic mistakes (gene and chromosome mutations) occur here, they will be passed on to the offspring (they will be inherited). Meiosis creates genetic variation in the sex cells through **crossing over** and **independent assortment**. Crossing over refers to the mutual exchange of pieces of chromosome (and their genes) between homologous chromosomes. In independent assortment, homologous chromosomes are randomly distributed to the **gametes**.

What are homologous chromosomes?

A pair of chromosomes with the same gene sequence. One comes from the mother (maternal) and one comes from the father (paternal).



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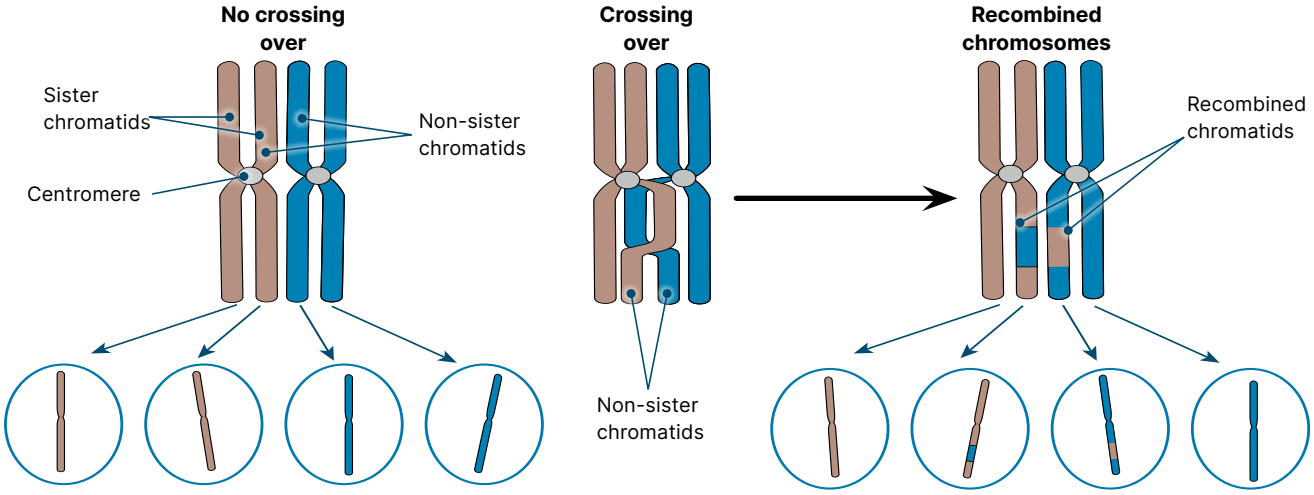
Crossing over and recombination

- Chromosomes replicate during interphase, before meiosis, to produce replicated chromosomes with sister chromatids held together at the centromere (see below). When the replicated chromosomes are paired during the first stage of meiosis, non-sister chromatids may become entangled and segments may be exchanged in a process called crossing over. Crossing over results in the **recombination** of alleles (variations of the same gene) producing greater variation in the offspring than would otherwise occur.

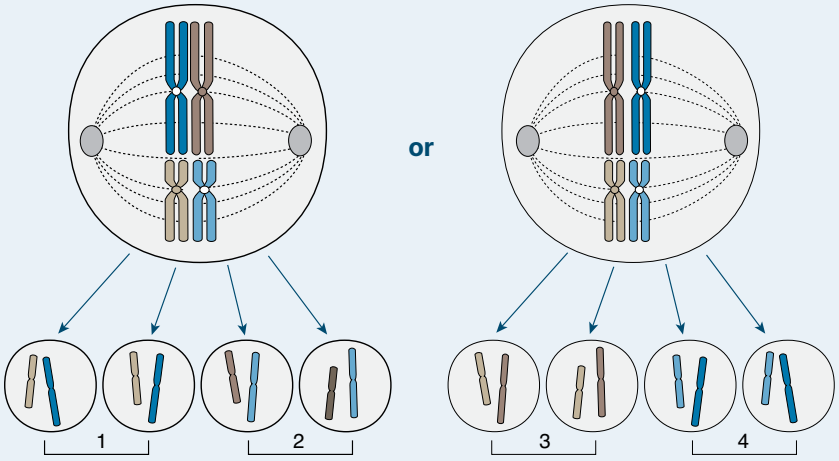


Possible gametes with no crossing over

Possible gametes with crossing over

Independent assortment

Independent assortment is the random alignment and distribution of chromosomes during meiosis. Independent assortment is an important mechanism for producing variation in gametes. During the first stage of meiosis, replicated homologous chromosomes pair up along the middle of the cell. The way the chromosomes pair up is random. For the homologous chromosomes right, there are two possible ways in which they can line up resulting in four different combinations in the gametes. The intermediate steps of meiosis have been left out for simplicity.



1. Describe the behaviour of the chromosomes in the first and then the second division in meiosis: _____

2. How does independent assortment increase the variation in gametes? _____

3. (a) What is crossing over? _____

   (b) How does crossing over increase the variation in the gametes (and hence the offspring)? _____

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96 Modelling Meiosis

Key Idea: We can simulate crossing over, gamete production, and the inheritance of alleles during meiosis using ice-block sticks to represent chromosomes.

This practical activity simulates the production of **gametes** (sperm and eggs) by **meiosis** and shows you how **crossing over** increases genetic variability. This is demonstrated by studying how two of your own alleles are inherited by the 'child' produced at the completion of the activity. Completing this activity will help you to visualise and understand some of the important aspects of events in meiosis.

Investigation 8.1 Modelling meiosis using ice-block sticks

See appendix for equipment list.

To study the effect of crossing over on genetic variation, you will work in pairs to simulate the inheritance of two of your own traits: ability to tongue roll and handedness. This activity will take 25-45 minutes.

1. Record your phenotype and genotype for each trait in the table (right). If you have a dominant trait, you will not know if you are heterozygous or homozygous for that trait, so you can choose either genotype.

2. Before you start the simulation, partner up with a classmate. Your gametes will combine with theirs (fertilisation) at the end of the activity to produce a 'child'. Decide who will be female, and who will be male. You will need to work with this person again at step 7.

3. Collect four ice-block sticks. These represent four chromosomes. Colour two sticks blue or mark them with a P. These are the paternal chromosomes. The plain sticks are the maternal chromosomes. Write your initials on each of the four sticks. Label each chromosome with its number. Label four sticky dots with the alleles to describe your phenotype and stick each onto the appropriate chromosome. In the example shown, the person is heterozygous for tongue rolling so sticky dots with alleles T and t are placed on chromosome 10. The person is also left handed, so alleles r and r are placed on chromosome 2 (right).

4. Randomly drop the chromosomes onto a table. This represents a cell in either the testes or ovaries.

   Duplicate your chromosomes by adding four more identical ice-block sticks to the table (right).
   What are you simulating with this action?

   _____

5. Simulate the first stage of meiosis by lining the duplicated chromosome pair with their homologous pair (below). For each chromosome number, you will have four sticks touching side-by-side (A, below).

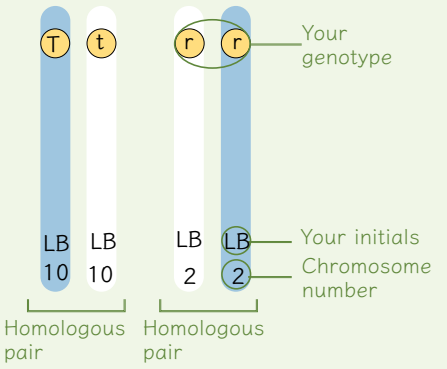
   At this stage crossing over occurs. Simulate this by swapping sticky dots from adjoining homologues (B, below).

Chromosome number	Phenotype	Genotype
10	Tongue roller	TT, Tt
10	Non-tongue roller	tt
2	Right handed	RR, Rr
2	Left handed	rr

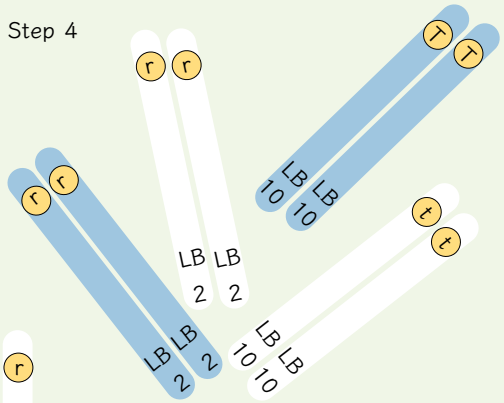
Step 1

Trait	Phenotype	Genotype
Handedness		
Tongue rolling		

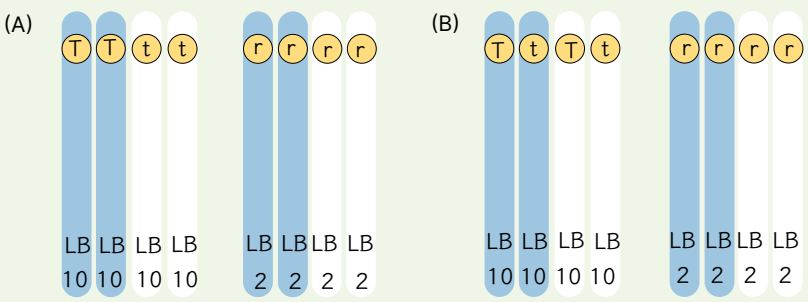
Step 3



Step 4



Step 5



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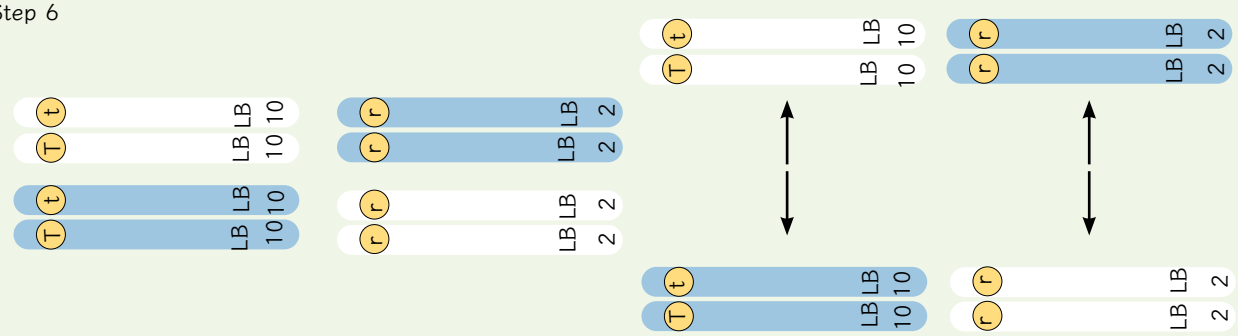
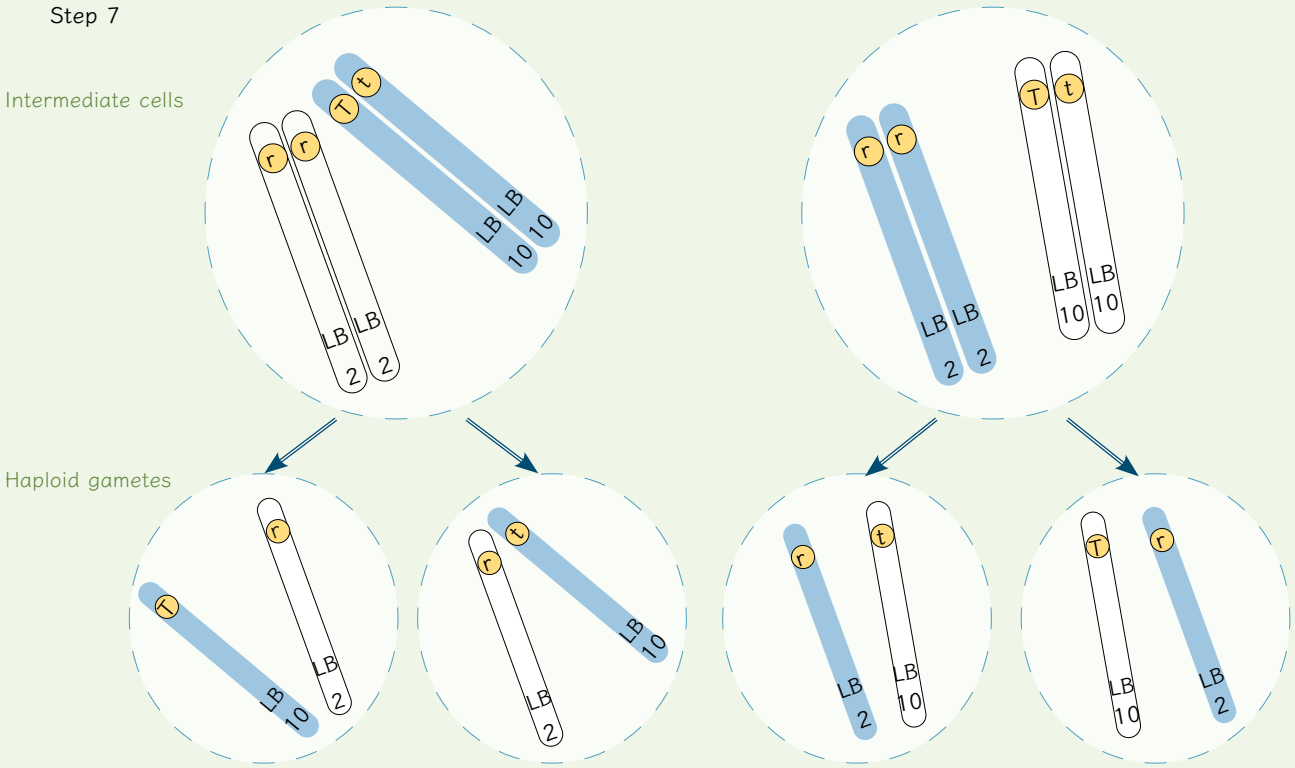
6. Randomly align the homologous chromosome pairs to simulate alignment across the cell's centre (equator) (as occurs in the next phase of meiosis). Simulate the separation of the chromosome pairs.
For each group of four sticks, two are pulled to each pole (end) of the cell.

Step 6



7. Two intermediate cells are formed. If you have completed step 5 correctly, each intermediate cell will be haploid (half the diploid chromosome number shown in step 3) with a mixture of maternal and paternal chromosomes. This is the end of the first division of meiosis. Your cells now need to divide for a second time. Repeat steps 4 and 5 but this time there is no crossing over and you are now separating replicated chromosomes, not homologues. At the end of this process each intermediate cell will have produced two haploid gametes. Each will have a maternal chromosome (white) and a paternal chromosome (blue) (below).

Step 7



8. Pair up with the partner you chose at the beginning of the exercise to carry out fertilisation. Randomly select one sperm and one egg cell. The unsuccessful gametes can be removed from the table. Combine the chromosomes of the successful gametes. You have created a child! Fill in the following chart to describe your child's genotype and phenotype for tongue rolling and handedness.

Trait	Phenotype	Genotype
Handedness		
Tongue rolling		

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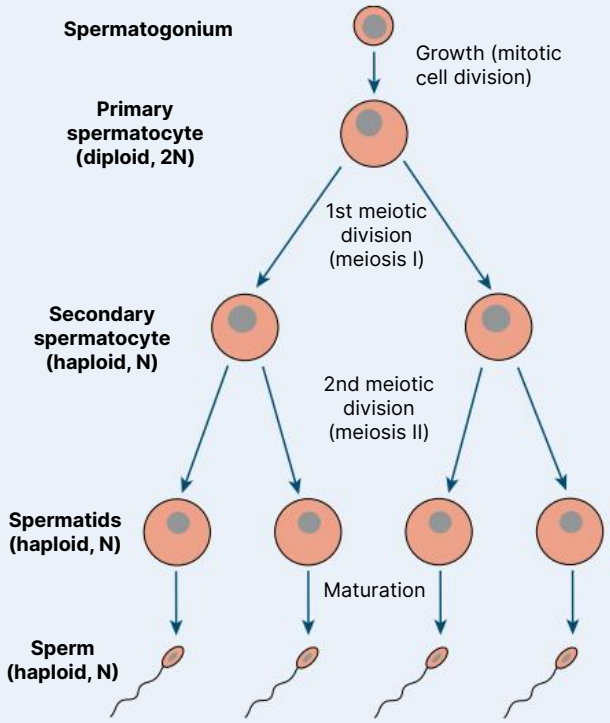
97 Producing Sex Cells

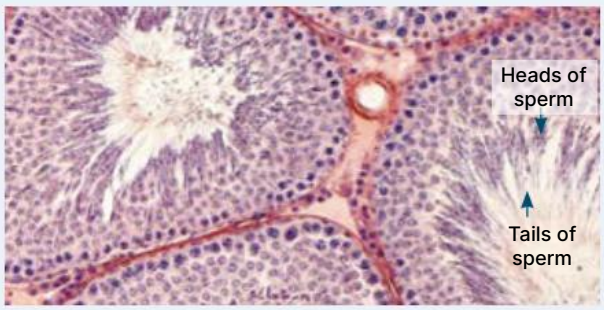
Key Idea: Sperm are the male gametes. They are produced in the testes by spermatogenesis. Eggs are the female gametes. They are produced by oogenesis in the ovaries.

Male **gametes,** or sperm, are produced by a process called **spermatogenesis** in the testes. Mammalian sperm are highly motile. In human males, sperm are produced in large numbers throughout adult life. Thousands are produced every second, and take approximately two months to fully mature. The production of egg cells (ova) in females occurs by **oogenesis**. Unlike spermatogenesis, no new eggs are produced after birth. Instead, a human female is born with her entire complement of immature eggs.

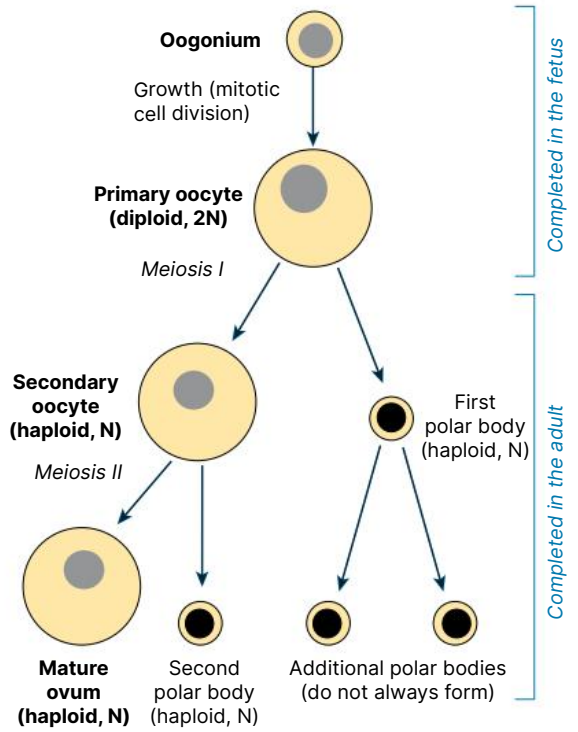
Spermatogenesis



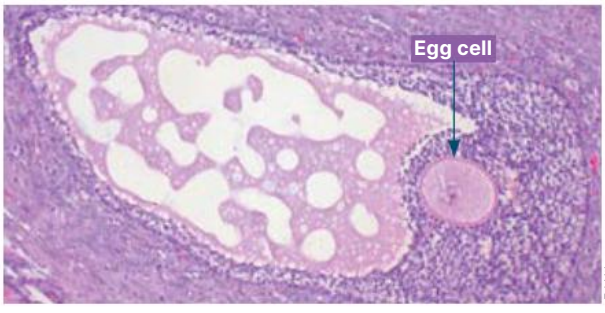
Spermatogenesis is the process by which mature sperm are produced in the testes. In humans, they are produced at the rate of about 120 million per day. Spermatogonia, in the outer layer of the seminiferous tubules, multiply throughout reproductive life. Some of them divide by meiosis into spermatocytes, which produce spermatids. These are transformed into mature sperm by the process of spermiogenesis in the seminiferous tubules of the testis (below). The sperm complete maturation in the epididymis.



Oogenesis



During growth of the female fetus, future egg cells start **meiosis** in the ovaries. The cells remain arrested in **prophase** of meiosis I throughout childhood. After puberty, most commonly a single egg cell is released from the ovaries at regular monthly intervals as part of the menstrual cycle. These egg cells are arrested in **metaphase** of meiosis II. This second meiotic division is only completed upon **fertilisation**. The release of egg cells ceases at menopause, when menstruation stops and the woman is no longer fertile.



1. How are diploid (2N) cells maintained during sexual reproduction: _____

2. What are the main differences between spermatogenesis and oogenesis? _____

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98 Did You Get It?

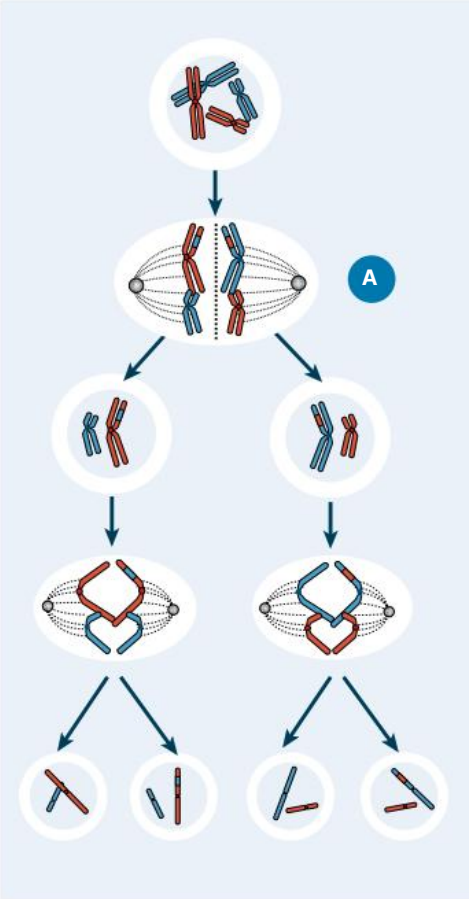
1. Identify the process shown on the right: _____

2. What is the purpose of this process? _____

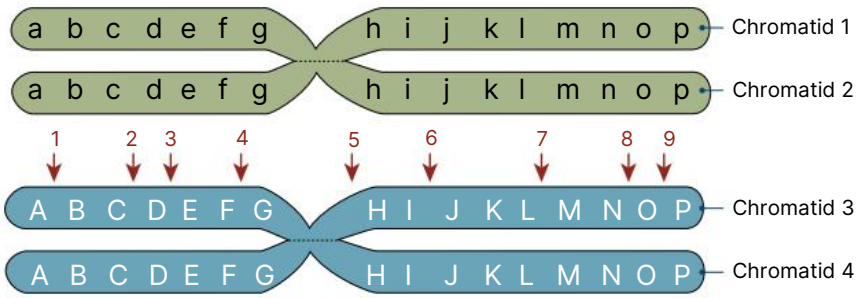
3. (a) Describe the two events that have occurred at point A on the diagram:

(b) How do these events increase genetic variation in the offspring? ____

(c) What other event contributes to variation in the offspring:



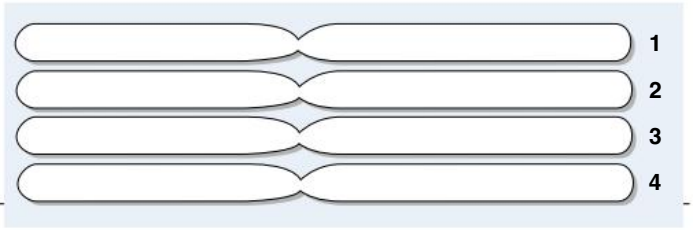
4. The possible crossing over points between the chromosomes below are indicated with red arrows.



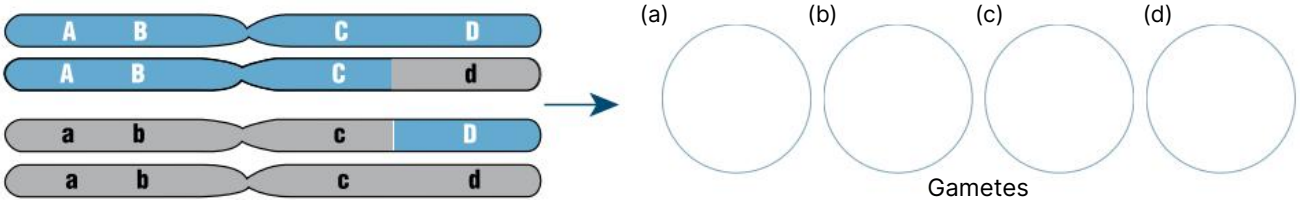
(a) Draw the gene sequences for the four chromatids (above), after crossing over has occurred at crossover point 2:

(b) Which genes have been exchanged between the homologous chromosomes?

_____



5. Complete the diagram below (a) - (d) by drawing the gametes formed:



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Chapter 9 Unit 4 Topic 1

Gene Expression

Resource Hub
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Key Terms

- amino acid
- anticodon
- coding strand
- codon
- degeneracy
- epigenetics
- exon
- gene
- gene expression
- genetic code
- genome
- intron
- polypeptide
- protein
- regulatory gene
- ribosome
- RNA (mRNA, rRNA, tRNA)
- redundancy
- structural gene
- template strand
- transcription
- transcription factor
- translation

Key Concepts

- Gene expression involves transcription in the nucleus, editing of the primary mRNA transcript, and translation in the cytoplasm to produce proteins.
- Regulatory genes encode transcription factors that control gene expression, while structural genes code for proteins that maintain cell structure and function.
- Gene expression and cellular differentiation is influenced by the environment. Environmental cues can cause the attachment of chemical tags to DNA that affect chromatin structure.

Eukaryotic gene structure and protein synthesis

		Activity Number
☐ 1	Define the terms genome and gene and recognise structural and regulatory genes. Distinguish between exons and introns and identify the roles of intronic DNA, including as centromeres and telomeres, and in regulating gene expression.	99
☐ 2	Summarise the steps in gene expression in eukaryotes to include transcription of genes, the editing of a primary mRNA transcript, and the translation of the mRNA into proteins. Identify where in the cell each of these steps occurs.	100
☐ 3	Describe the features of the genetic code, including: • The 4-letter alphabet and the 3-letter triplet code (codon) of base sequences • The non-overlapping, linear nature of the code, which is read from start to finish in one direction. The specific punctuation codons and their significance • The universal nature and degeneracy of the code	101
☐ 4	Describe transcription in eukaryotes, including reference to the start and end points, the direction of transcription, and the role of RNA polymerase.	102, 104
☐ 5	Describe translation of mRNA into an amino acid sequence (polypeptide) at the ribosome, including reference to the role of transfer RNA, codons, and anticodons.	103, 104
☐ 6	**SHE:** Understand our knowledge of genetics and heredity is a result of the collaboration and combined effort of many different scientists and scientific disciplines.	99, 102, 109

Regulating gene expression

☐ 7	Explain how gene expression is regulated including: • Regulatory genes encode transcription factors which control transcription • Post transcriptional modification of the mRNA and post translational modification of the gene product • Environment, including the epigenetic environment	105- 109
☐ 8	Explain how transcription in eukaryotes involves the interaction of transcription factors with specific DNA sequences so that RNA polymerase can transcribe the protein-coding gene into a primary RNA transcript. Describe how this affects cellular differentiation.	105
☐ 9	Describe how the environment can alter gene expression so that phenotype is modified. Explain how the environment can be internal (e.g. growth factors during development) or external (e.g. environmental temperature). Understand that the environment's effect on gene expression is often moderated by epigenetic factors.	107
☐ 10	Explain how epigenetic factors can influence the level of gene expression. Describe some of the evidence for epigenetic regulation, including from twin studies.	108
☐ 11	Describe an example of a regulatory (transcription factor) gene that regulates morphology (e.g. HOX gene family).	109

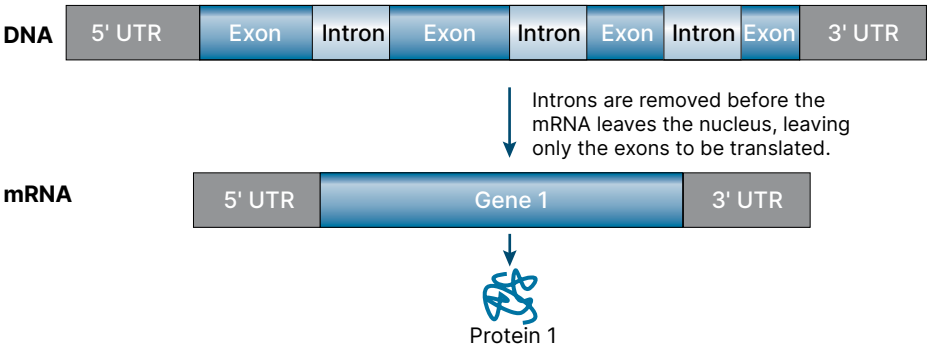
99 Eukaryotic Gene Structure

Key Idea: Structural genes code for all proteins except for regulatory proteins. Regulatory genes code for the molecules involved in controlling the expression of structural genes.

Genes are sections of **DNA** that code for **mRNA** products (e.g. **proteins**). **Structural genes** code for any protein product other than a regulatory protein. The proteins encoded by structural genes are diverse and have roles in maintaining the structure or function of a cell. **Regulatory genes** (or sequences) code for proteins and other small molecules, such as microRNAs, that control the expression of structural genes. Regulatory genes may be some distance from the structural genes they control. Within a section of DNA, expressed structural genes are enclosed on either side by untranslated regions (UTRs). UTRs contain regulatory sequences that directly control protein synthesis. The very simplified structure of a eukaryotic gene is pictured below.

Eukaryotic gene structure

- Structural genes are under the control of regulatory sequences. Each structural gene is enclosed by untranslated regions (UTRs).
- It is important to remember that before the primary **RNA** transcript is translated in eukaryotes, the non-protein coding **introns** are removed (only the protein-coding **exons** form the mature mRNA for **translation**).



The fact that eukaryote genes are not contiguous strings of DNA but contain introns, non coding sections, that are removed from the mature mRNA was discovered by Phillip Sharp and Richard Roberts. They received the Nobel prize in 1993 for their work.

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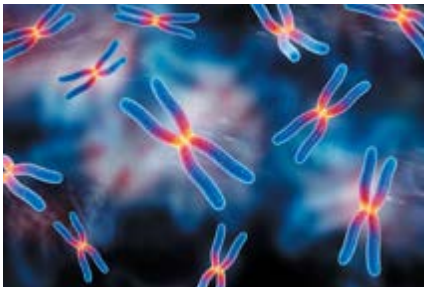
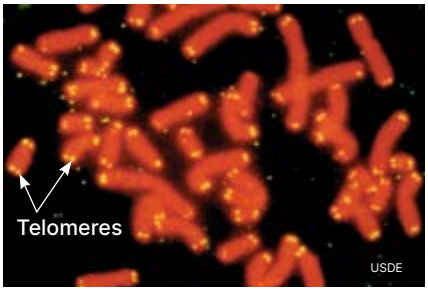
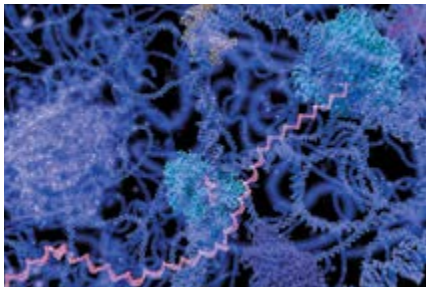
Structures outside the gene



Centromeres are non-coding DNA sequences that hold sister chromatids together after replication. During mitosis, spindle fibres attach to the centromere to pull the chromatids apart.



Telomeres are repeating non-coding DNA sequences that are not part of a gene. They are found at the end of chromosomes and protect the chromosomes from degradation during replication.



Regulatory genes (elements/sequences) are sequences of the DNA that regulate non-regulatory protein-coding genes. They include promoters and enhancers that facilitate **transcription** of genes.

1. What is the difference between a regulatory gene and a structural gene? _____

2. How is a mature mRNA different from the DNA it was coded from? _____

3. Describe two functions of non-protein coding DNA: _____

SU SHE

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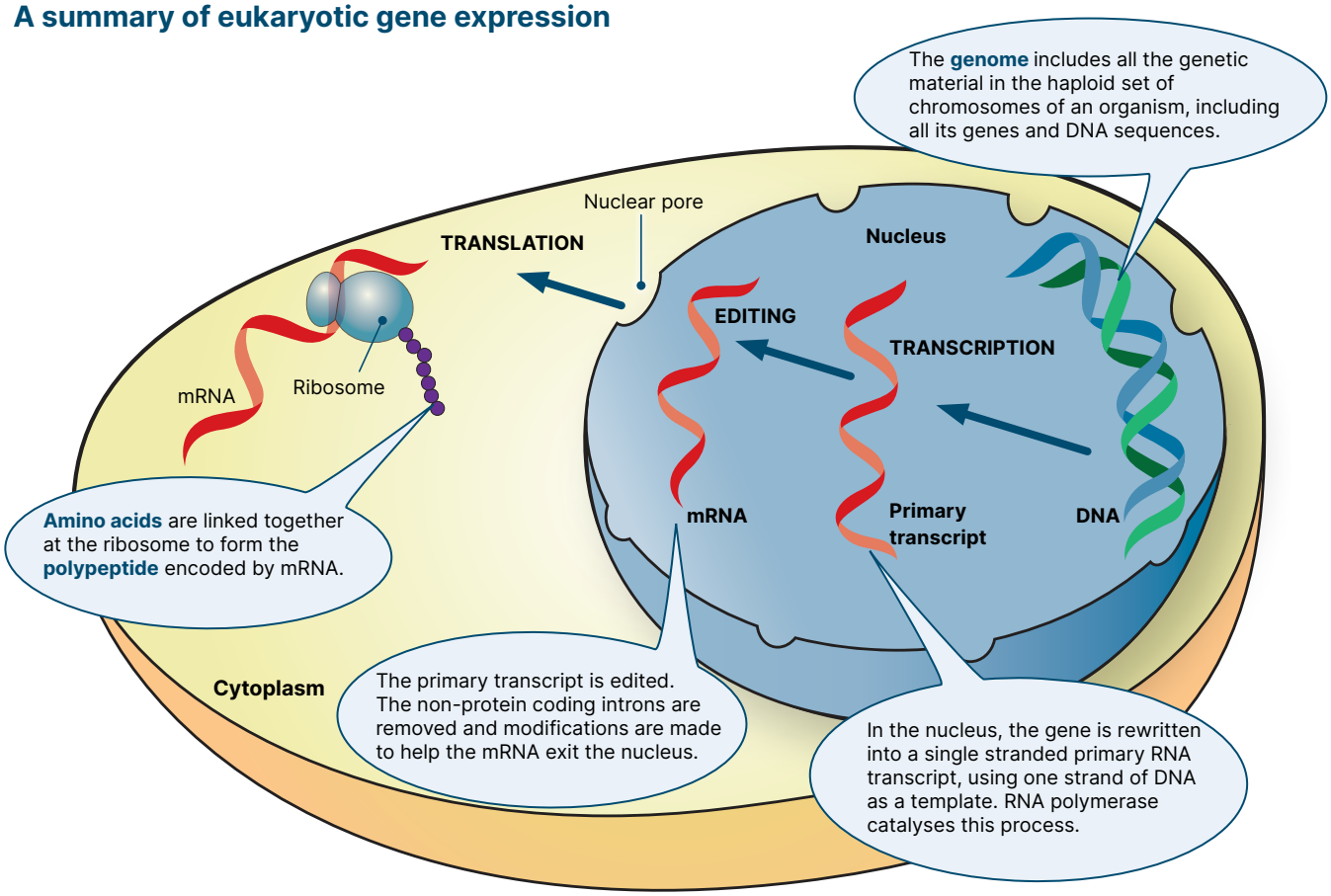
100 What is Gene Expression?

Key Idea: Genes are sections of DNA that code for proteins. Genes are expressed when they are transcribed into messenger RNA (mRNA) and then translated into a protein.

Gene expression is the process by which the information in a **gene** is used to synthesise a **protein**. It involves **transcription** of the **DNA** into **mRNA** and **translation** of the mRNA into protein. Eukaryotic genes include non-protein coding regions called **introns**. These regions of intronic DNA must be edited out before the mRNA is translated by the **ribosomes**. Transcription of the genes and editing that primary transcript to form the mature mRNA occurs in the nucleus. Translation of the protein by the ribosomes occurs in the cytoplasm.

A summary of eukaryotic gene expression



1. What is a gene? _____

_____

2. (a) What does gene expression mean? _____

_____

(b) What are the three stages in gene expression in eukaryotes and what happens in each stage?

(i) _____

(ii) _____

(iii) _____

3. The photograph right shows an SEM of a giant polytene chromosome. These chromosomes are common in the larval stages of flies, which must grow rapidly before changing to the adult form. They form as a result of repeated cycles of DNA replication without cell division. This creates many copies of genes. Within these chromosomes, visible 'puffs' indicate regions where there is active transcription of the genes.

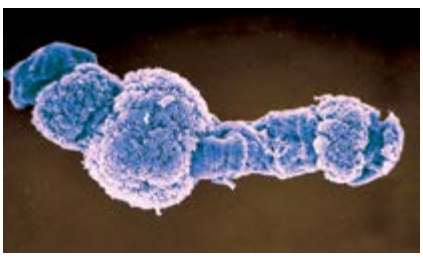
(a) What is the consequence of active transcription in a polytene chromosome?

_____

(b) Why might this be useful in a larval insect? _____

_____

_____



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101 The Genetic Code

Key Idea: The genetic code is the set of rules by which the genetic information in DNA or mRNA is translated into proteins.

The genetic information for the assembly of **amino acids** is stored as a three-base sequence. These three letter codes on **mRNA** are called **codons**. Each codon represents one of 20 amino acids used to make **proteins**. The code is effectively universal, being the same in all living things (with a few minor exceptions). The **genetic code** is summarised in a mRNA-amino acid table, which identifies the amino acid encoded by each mRNA codon. The code is degenerate, meaning there may be more than one codon for each amino acid. Most of this **degeneracy** is in the third nucleotide of a codon.

The mRNA - amino acid table

The table on the right is used to 'decode' the genetic code. It shows which amino acid each mRNA codon codes for. There are 64 different codons possible, 61 code for amino acids, and three are stop codons.

Amino acid names are written as three letter abbreviations (e.g. Ser = serine). To work out which amino acid a codon codes for, carry out the following steps:

i Find the first letter of the codon in the row on the left hand side of the table. AUG is the start codon.

ii Find the column that intersects that row from the top, second letter, row.

iii Locate the third base in the codon by looking along the row on the right hand side that matches your codon.

e.g. **GAU** codes for Asp (aspartic acid)

Read second letter here

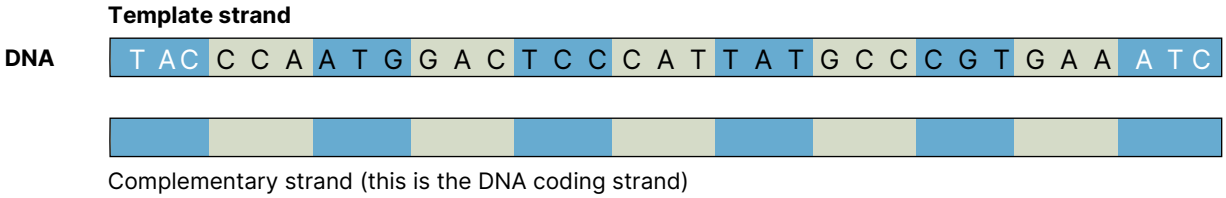
First letter	Second letter: U	Second letter: C	Second letter: A	Second letter: G	Third letter
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
	UUA Leu	UCA Ser	UAA STOP	UGA STOP	A
	UUG Leu	UCG Ser	UAG STOP	UGG Trp	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC Leu	CCC Pro	CAC His	CGC Arg	C
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
	AUC Ile	ACC Thr	AAC Asn	AGC Ser	C
	AUA Ile	ACA Thr	AAA Lys	AGA Arg	A
	AUG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC Val	GCC Ala	GAC Asp	GGC Gly	C
	GUA Val	GCA Ala	GAA Glu	GGA Gly	A
	GUG Val	GCG Ala	GAG Glu	GGG Gly	G

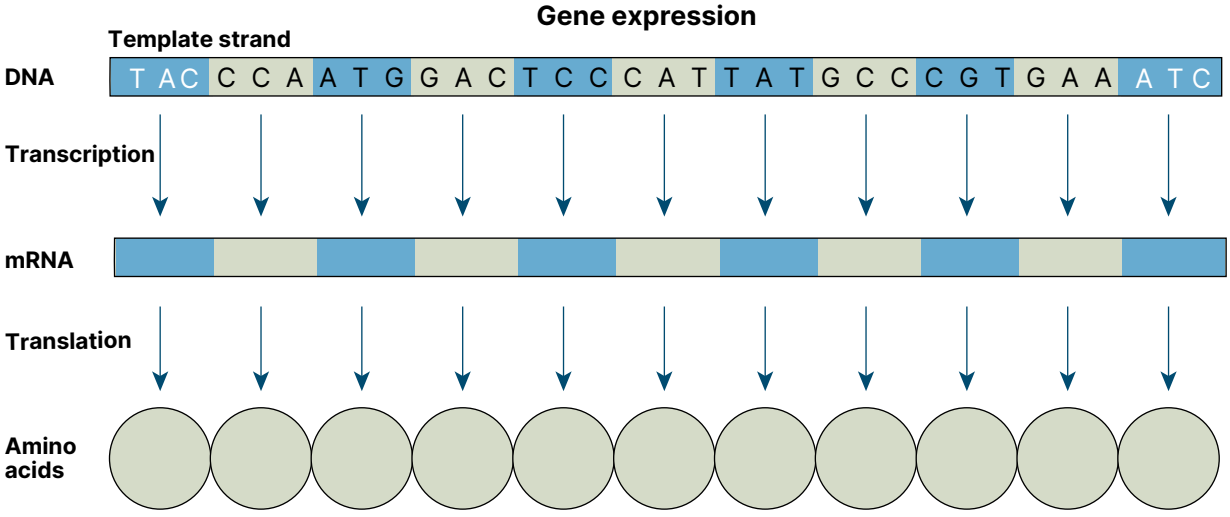
Read first letter here

Read third letter here

1. (a) Use the base-pairing rule to create the complementary strand for the DNA template strand shown below.

   (b) For the same DNA template strand, determine the mRNA sequence and use the mRNA - amino acid table above to determine the amino acid sequence. Note that in mRNA, uracil (U) replaces thymine (T) and pairs with adenine.





2. What do you notice about the sequence on the DNA coding strand and the mRNA strand? _____

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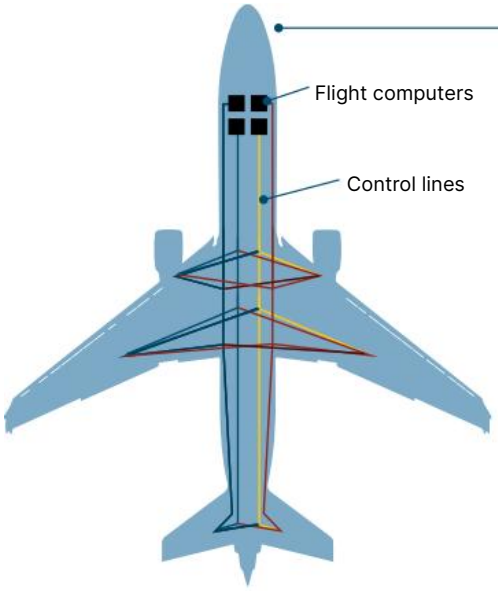
Redundancy and degeneracy

Redundancy and degeneracy are important concepts in understanding the genetic code.

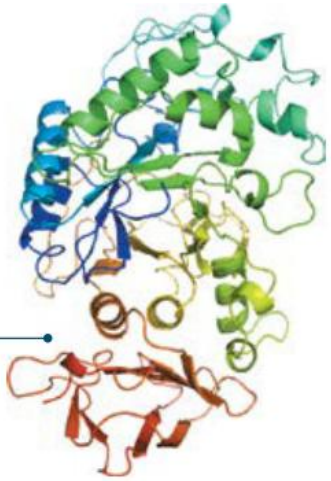
- **Redundancy** is when several situations code for or control the actions of one specific thing.
- **Degeneracy** is when a particular output can be produced by several different pathways.

Examples of redundancy and degeneracy are illustrated below. In modern aircraft redundant features add safety by making sure if one system fails others will ensure a smooth, safe flight. Degeneracy can be seen in proteins when different proteins have the same function.



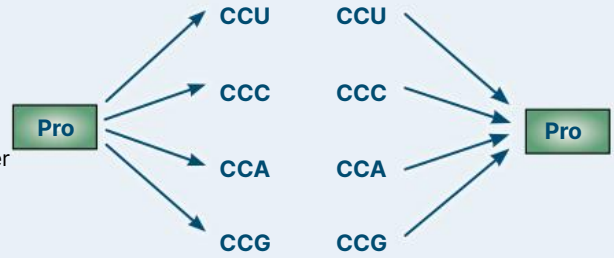
Modern aircraft (left) have multiple redundant features for safety. Often there are three or four flight computers linked independently to the flight surfaces and other input/output devices. If one computer or control line fails the others can continue to fly the plane normally.

Degeneracy is seen in the production of the enzymes salivary and pancreatic amylase. Salivary amylase breaks down carbohydrates in the mouth, whereas pancreatic amylase does so in the small intestine. The enzymes are encoded by different genes (AMY1A and AMY2A) but have the same functional role (right).



Salivary amylase (above) is structurally different to pancreatic amylase, but has the same function.

The genetic code shows degeneracy. This means that a number of 3 base combinations specify one amino acid. The codons for the same amino acid often differ by only a single letter (often the second or third). For example, proline is encoded by four different codons.



The degeneracy of the genetic code creates redundancy, so that several codons code for the same amino acid (e.g. CCU, CCC, CCA, and CCG code for proline). Note that although there is redundancy, there is no ambiguity - none of the codons encodes any other amino acid.

3. Explain how degeneracy adds "safety" to the coding of protein chains: _____

4. The genetic code shows redundancy but no ambiguity. What does this mean and why is it important?

5. Identify the following:

   (a) The codons that encode valine (Val): _____

   (b) The codons that encode aspartic acid (Asp): _____

6. (a) Arginine (Arg) is encoded in how many ways? _____

   (b) Glycine (Gly) is encoded in how many ways? _____

   (c) Which amino acid(s) are encoded in only one way? _____

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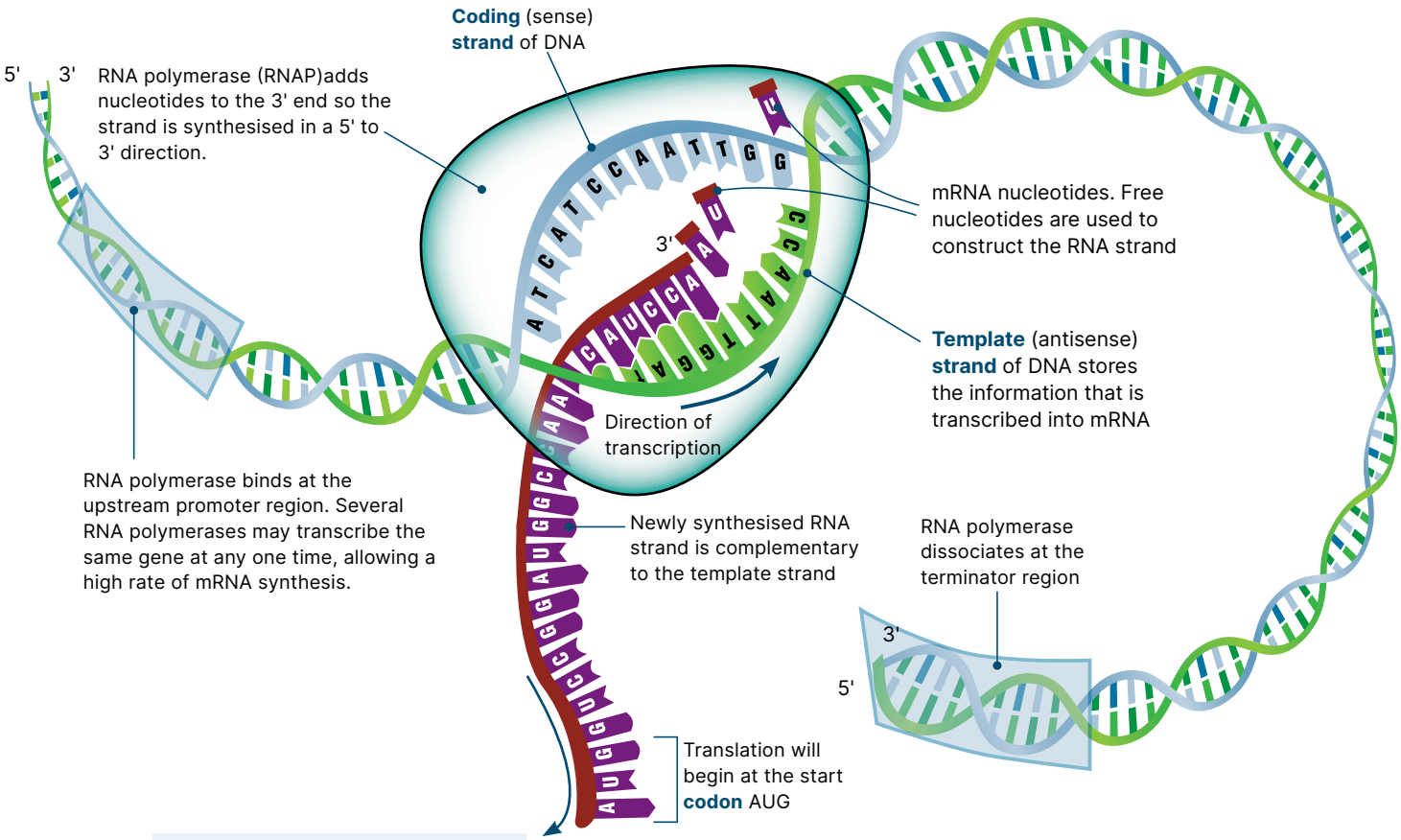
102 Transcription in Eukaryotes

Key Idea: Transcription is the first step of gene expression. It involves the enzyme RNA polymerase rewriting the information into a primary RNA transcript. In eukaryotes, transcription takes place in the nucleus.

Transcription is the first stage of **gene expression**. It takes place in the nucleus and is carried out by the enzyme RNA polymerase, which rewrites the **DNA** into a primary **RNA** transcript using a single **template strand** of DNA. The protein-coding portion of a **gene** is bounded by an upstream start (promoter) region and a downstream terminator region. These regions control transcription by telling RNA polymerase where to start and stop transcription. In eukaryotes, non protein-coding sections called **introns** must first be removed and the remaining **exons** spliced together to form the mature **mRNA** before the gene can be translated into a **protein**. This editing process also occurs in the nucleus.

Transcription is carried out by RNA polymerase (RNAP)



This primary RNA transcript is edited to form the mature mRNA, which then passes to the cytoplasm where the nucleotide sequence is translated into a **polypeptide**.

Many scientists have contributed to our understanding of how the information in DNA is read. Nobel prize winner Roger D. Kornberg has possibly contributed more than most, discovering and characterising numerous processes and dozens of proteins involved in transcription.

1. (a) Name the enzyme responsible for transcribing the DNA: _____

   (b) What strand of DNA does this enzyme use? _____

   (c) The code on this strand is the [same as / complementary to] the RNA being formed (circle correct answer).

   (d) Which nucleotide base replaces thymine in mRNA? _____

   (e) On the diagram, use a coloured pen to mark the beginning and end of the protein-coding region being transcribed.

2. (a) In which direction is the RNA strand synthesised? _____

   (b) Explain why this is the case: _____

   _____

   _____

3. (a) Why is AUG called the start codon? _____

   (b) What would the three letter code be on the DNA coding strand? _____

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103 Translation

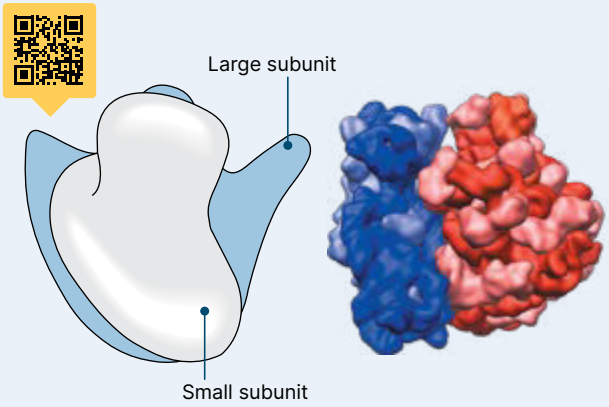
Key Idea: Translation is the final stage of gene expression in which ribosomes read the mRNA and decode (translate) it to synthesise a protein. This occurs in the cytoplasm.

In eukaryotes, **translation** occurs in the cytoplasm either at free **ribosomes** or ribosomes on the rough endoplasmic reticulum. Ribosomes translate the code carried in the **mRNA** molecules, providing the catalytic environment for the linkage of **amino acids** delivered by transfer **RNA** (**tRNA**) molecules. **Protein** synthesis begins at the start **codon** and, as the ribosome wobbles along the mRNA strand, the **polypeptide** chain elongates. On reaching a stop **codon**, the ribosome subunits dissociate from the mRNA, releasing the protein.

Ribosome structure

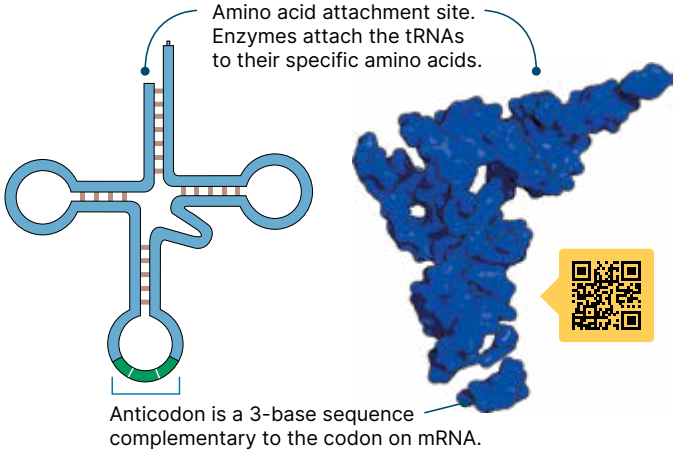
Ribosomes are made up of a complex of ribosomal RNA (**rRNA**) and ribosomal proteins. These small cellular structures direct the catalytic steps required for protein synthesis and have specific regions that accommodate transfer RNA (tRNA) molecules loaded with amino acids.

Ribosomes exist as two separate sub-units (below) until they are attracted to a binding site on the mRNA molecule, when they come together around the mRNA strand.



tRNA structure

tRNA molecules are RNA molecules, about 80 nucleotides long, which transfer amino acids to the ribosome as directed by the codons in the mRNA. Each tRNA has a 3-base **anticodon**, which is complementary to a mRNA codon. There is a different tRNA molecule for each possible codon and, because of the **degeneracy** of the **genetic code**, there may be up to six different tRNAs carrying the same amino acid.



1. Describe the structure of a ribosome: _____

_____

2. What is the role of each of the following components in translation?

   (a) Ribosome: _____

   (b) tRNA: _____

   (c) Amino acids: _____

   (d) Start codon: _____

   (e) Stop codon: _____

3. There are many different types of tRNA molecules, each with a different anticodon (HINT: see the mRNA table).

   (a) How many different tRNA types are there, each with a unique anticodon? _____

   (b) Explain your answer: _____

   _____

   _____

   _____

   (c) Determine the mRNA codons and the amino acid sequence for the following tRNA anticodons:

   tRNA anticodons: U A C U A G C C G C G A U U U

   Codons on the mRNA: _____

   Amino acids encoded: _____

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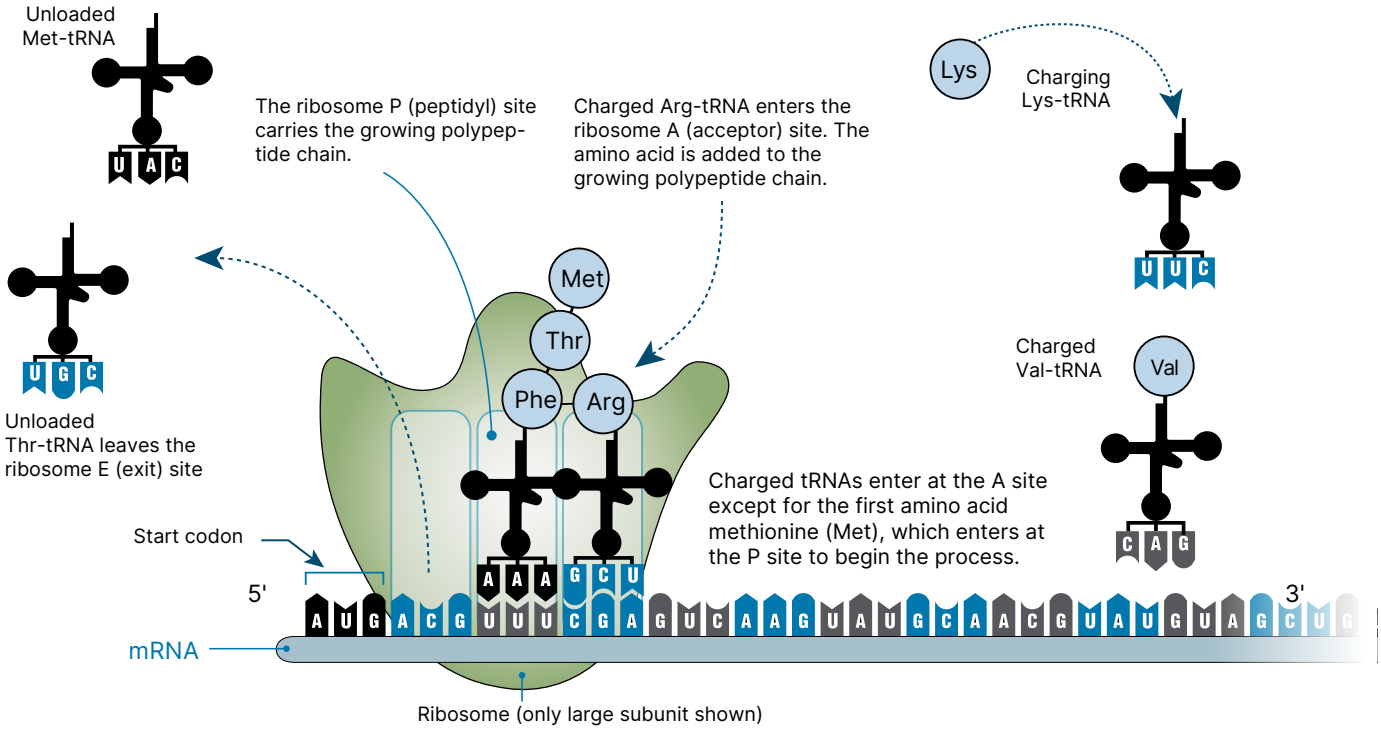
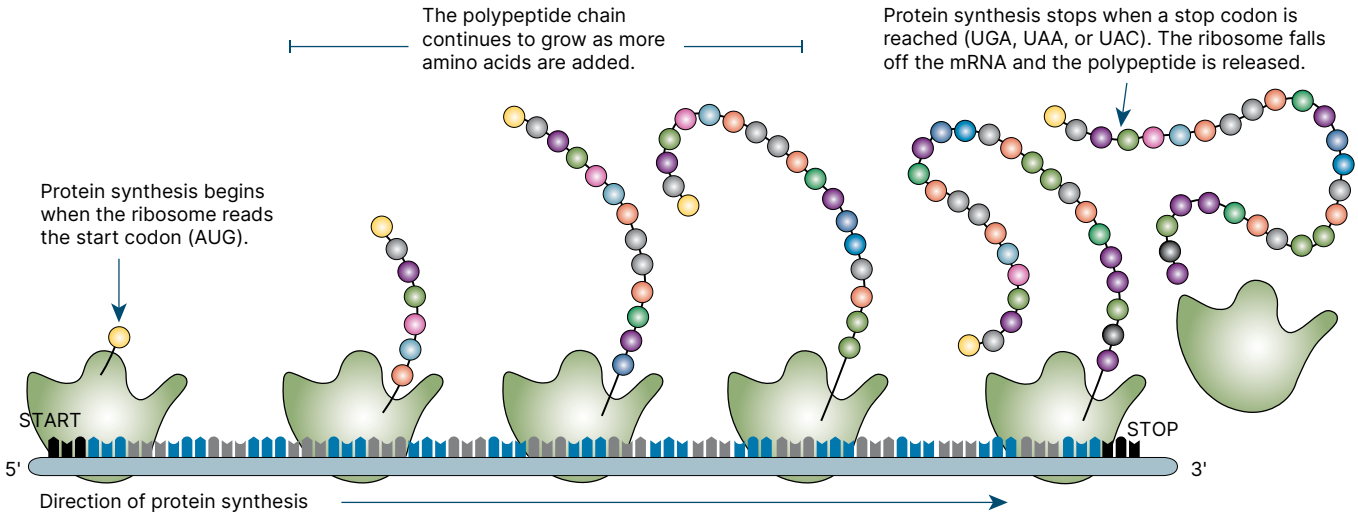
tRNA molecules deliver amino acids to ribosomes

tRNA molecules match amino acids with the appropriate codon on mRNA. As defined by the genetic code, the anticodon specifies which amino acid the tRNA carries. The tRNA delivers its amino acid to the ribosome, where enzymes join the amino acids to form a polypeptide chain. During translation, the ribosome "wobbles" along the mRNA molecule joining amino acids together. Enzymes and energy are involved in charging the tRNA molecules (attaching them to their amino acid) and elongating the peptide chain.



The polypeptide chain grows as more amino acids are added



4. Describe the events occurring during translation: _____

_____

_____

_____

5. Many ribosomes can work on one strand of mRNA at a time (a polyribosome system). What would this achieve?

_____

_____

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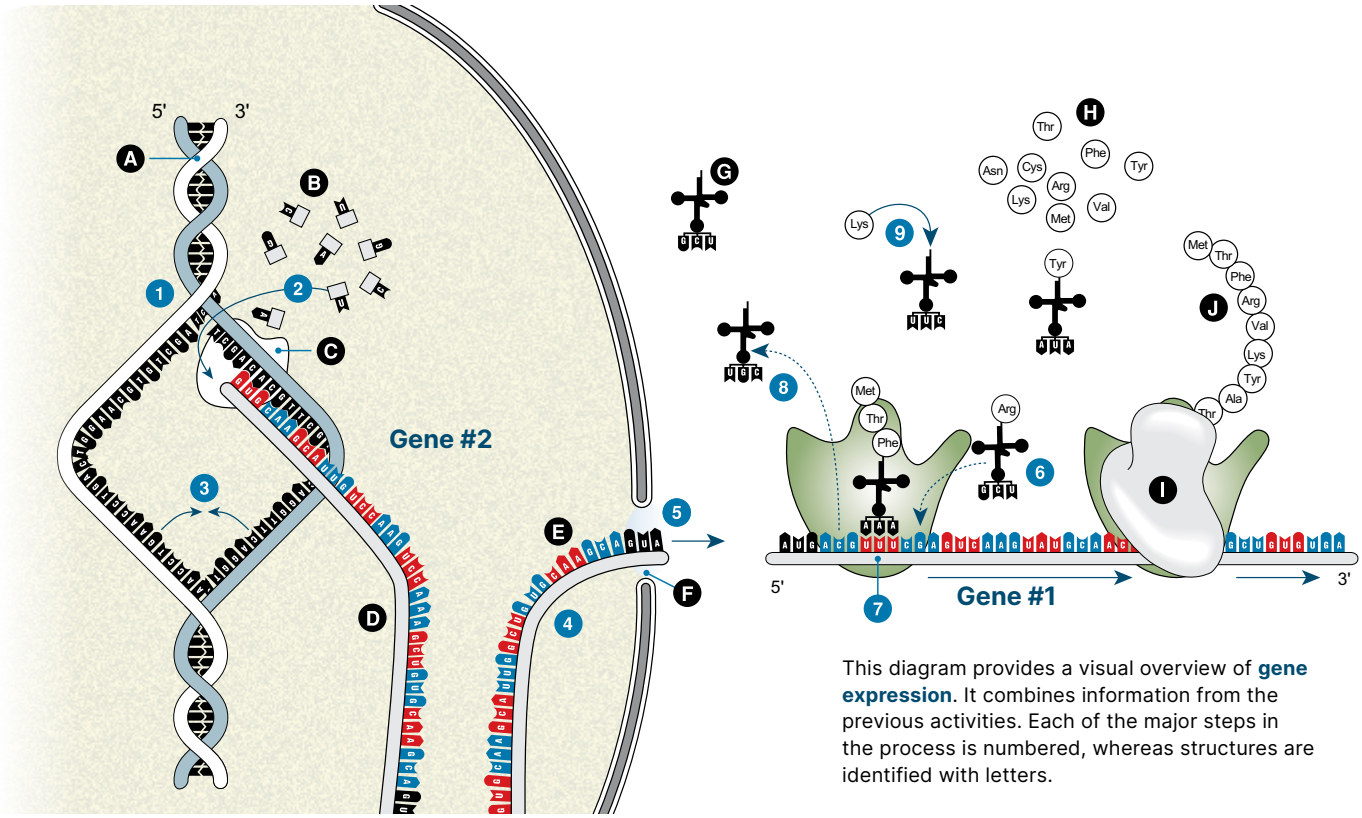
104 Gene Expression Summary



This diagram provides a visual overview of **gene expression**. It combines information from the previous activities. Each of the major steps in the process is numbered, whereas structures are identified with letters.

1. Briefly describe each of the numbered processes in the diagram above:

   (a) Process 1: _____

   (b) Process 2: _____

   (c) Process 3: _____

   (d) Process 4: _____

   (e) Process 5: _____

   (f) Process 6: _____

   (g) Process 7: _____

   (h) Process 8: _____

   (i) Process 9: _____

2. Identify each of the structures marked with a letter and write their names below in the spaces provided:

   (a) Structure A: _____ (f) Structure F: _____

   (b) Structure B: _____ (g) Structure G: _____

   (c) Structure C: _____ (h) Structure H: _____

   (d) Structure D: _____ (i) Structure I: _____

   (e) Structure E: _____ (j) Structure J: _____

3. Describe two factors that would determine whether or not a particular protein is produced in the cell:

   (a) _____

   _____

   (b) _____

   _____

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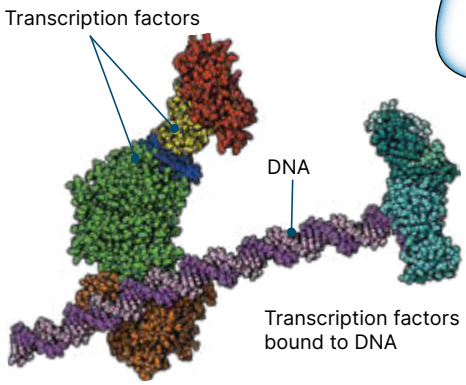
105 Transcriptional Control of Gene Expression

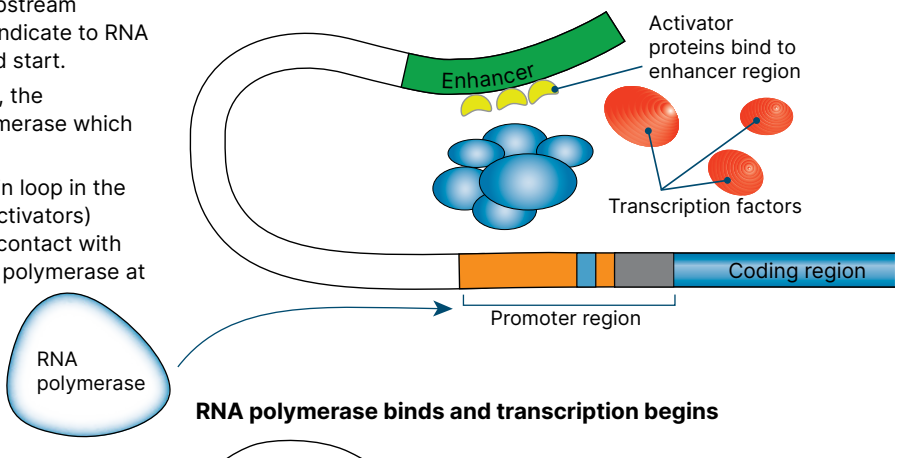
Key Idea: In eukaryotes, transcription is initiated by proteins called transcription factors.

Transcription factors are encoded by **regulatory genes** and have a role in creating an initiation complex for **transcription** (below). The transcription factors bind to specific regions of the **DNA** and help position the RNA polymerase on the DNA where transcription will begin. Some of the specific regions of DNA are far away from the protein-coding gene itself. Transcription factors attached to these regions come together when the DNA forms a 'hair-pin loop'. Transcription factors are an important part of regulating cellular differentiation. Different transcription factors active at different times determine the fate of cells by regulating their developmental pathway.

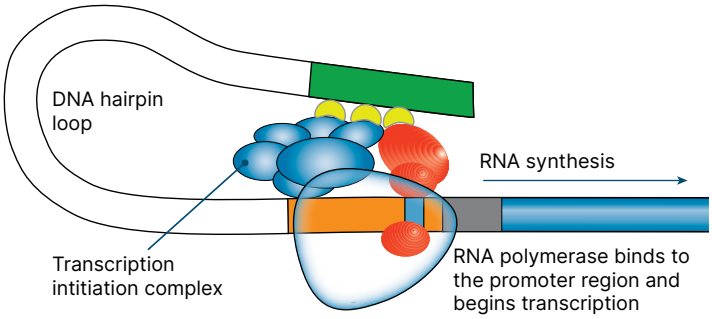
- Transcription factors bind to distinct regions of the DNA, including the promoter and upstream enhancers. They will act as a guide to indicate to RNA polymerase where **transcription** should start.
- Once bound to the promoter sequence, the transcription factors capture RNA polymerase which can then begin transcription.
- Transcription is activated when a hairpin loop in the DNA brings the transcription factors (activators) attached to the enhancer sequence in contact with the transcription factors bound to RNA polymerase at the promoter (bottom).



Assembly of the transcription initiation complex

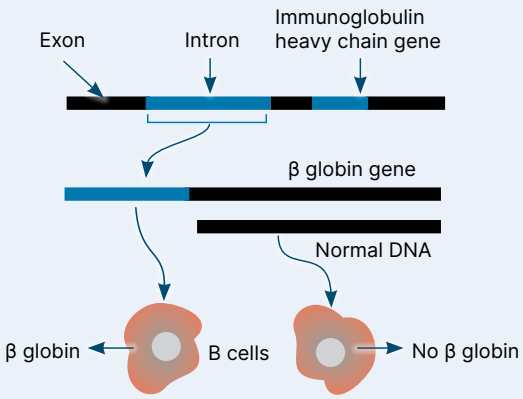


RNA polymerase binds and transcription begins



Parts of the DNA act as enhancers

- In the early 1980s, Julian Banerji and colleagues carried out several experiments identifying that parts of the DNA enhanced transcription and that some of those parts are specific to certain cells.
- In one experiment, they removed the large **intron** from the **gene** coding for the immunoglobulin heavy chain and attached it to the gene coding for β globin. The immunoglobulin heavy chain is only expressed in B cells of the immune system. However, β globin is not.
- The recombined DNA containing the intron and the β globin gene was inserted into B cells. An unaltered gene was also inserted in separate B cells to act as a control. When the cells were tested for the presence of β globin, only the cell with the recombined DNA produced the chain.



1. (a) What is a transcription factor? _____

_____

(b) What sort of genes encode transcription factors? _____

(c) How are transcription factors involved in regulating gene expression? _____

_____

_____

_____

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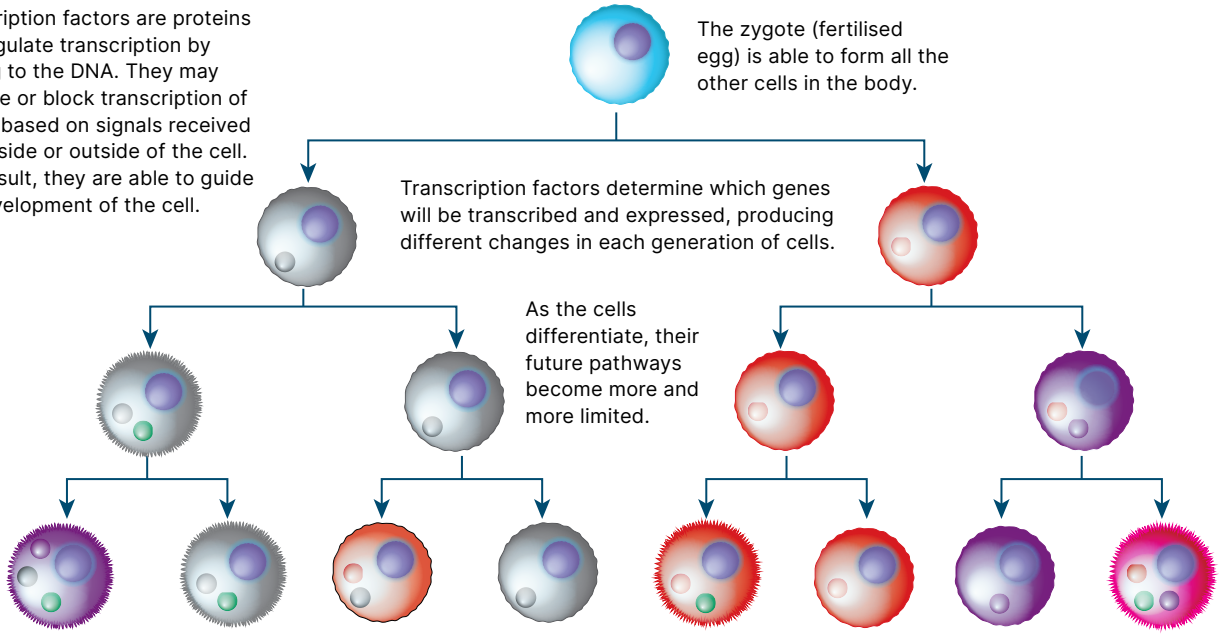
Transcription factors and cellular differentiation

Transcription factors are proteins that regulate transcription by binding to the DNA. They may promote or block transcription of genes based on signals received from inside or outside of the cell. As a result, they are able to guide the development of the cell.

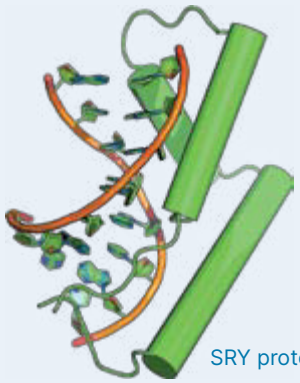


By using different transcription factors at different times, a large variety of different cells is produced.

Sex determination and the SRY gene

The *SRY* (sex determining region) gene is found on the Y chromosome and produces a DNA binding protein, the SRY protein. The SRY protein acts as a transcription factor that causes the up regulation (greater production) of other transcription factors.

When gestation begins, the primordial gonad cells may develop into ovaries (female) or testes (male). SRY initiates differentiation of the primordial gonad cells into cells of the testis.



SRY protein bound to DNA

XY female and XX male?

During the meiotic divisions that produce sperm cells, genetic material can be swapped between homologous chromosomes by crossing over. Very rarely, the region on the Y chromosome containing the SRY gene can cross over with the X chromosome producing a Y chromosome with no SRY gene and an X chromosome with an SRY gene. In these cases an XX karyotype develops into a male and an XY karyotype develops into a female. In both cases, the person would be infertile.

2. What evidence is there that introns can be involved in regulating gene expression?_____

3. Multicellular organisms consist of many different cell types. Use the diagram above to explain how it is possible for these all to arise from a single fertilized egg (zygote):

4. Why would a XY person without an SRY gene on the Y chromosome appear female? _____

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106 Changes after Transcription and Translation

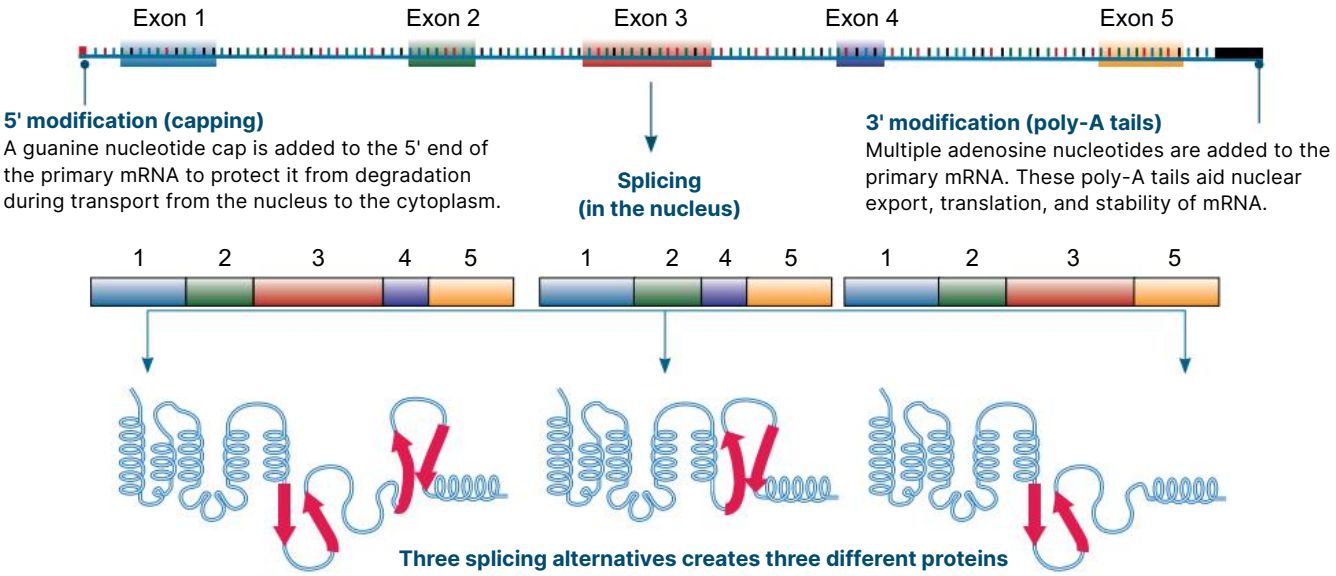
Key Idea: Modifications of the primary mRNA after transcription are needed before mRNA can exit the nucleus. Post-transcriptional and post-translational modifications also account for how cells are able to produce a wide variety of proteins from a smaller number of genes.

Once a **gene** is transcribed, the primary transcript is modified to produce the **mRNA** strand that will be translated in the cytoplasm. Caps and tails assist transport of the mRNA from the nucleus and increase its stability in the cytoplasm. **Exon** splicing produces exon combinations that result in different **protein** products. Modification of proteins after **translation** further increases the variety of proteins produced.

Post transcriptional modification

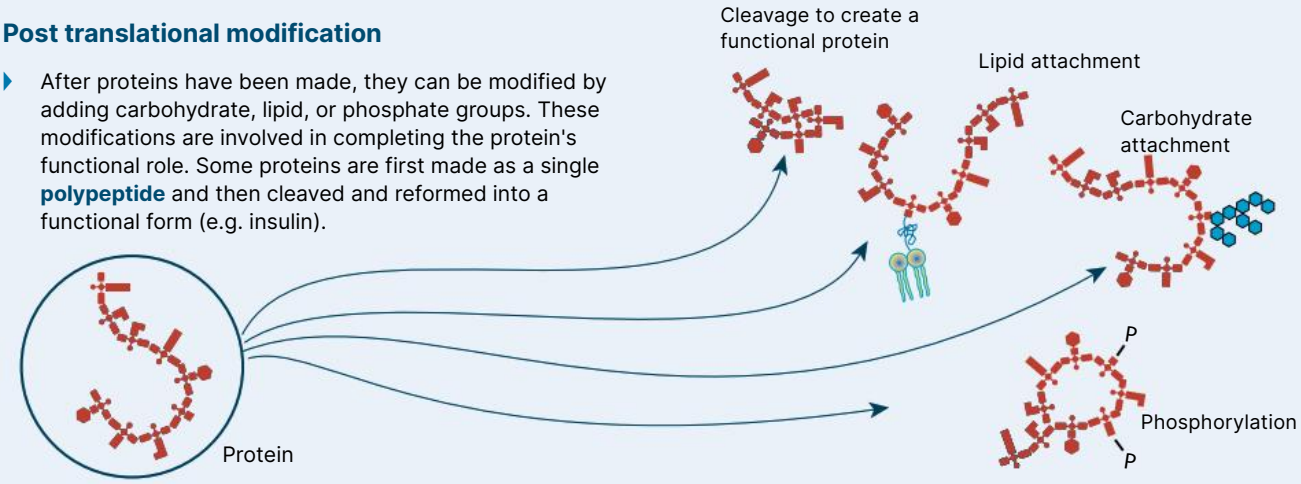
- As seen earlier, **introns** are removed from the primary **mRNA** transcript and the exons are spliced together. However, exons can be spliced together in different ways to create variations in the translated proteins. In mammals, the most common method of alternative splicing involves exon skipping, in which not all exons are spliced into the final mRNA (below).

Human DNA contains 25,000 genes, but produces up to 1 million different proteins. Modifications after transcription and translation allow several proteins to be produced from just one gene.



Post translational modification

- After proteins have been made, they can be modified by adding carbohydrate, lipid, or phosphate groups. These modifications are involved in completing the protein's functional role. Some proteins are first made as a single **polypeptide** and then cleaved and reformed into a functional form (e.g. insulin).



1. How can so many proteins be produced from so few genes? _____

_____

_____

2. What is the advantage of being able to modify the mRNA to produce different proteins? _____

_____

3. If a human produces 1 million proteins, but human DNA only codes for 25,000 genes, on average how many proteins are produced per gene?

_____

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107 Gene Expression and the Environment

Key Idea: The environment can affect phenotype, often by influencing how genes are expressed and even inherited.

As we have seen, **gene expression** is influenced by the **genes** themselves, e.g. some genes are expressed in response to or along with other genes. However, gene expression is also influenced by the internal or external environment. Some genes are expressed in response to an internal or external chemical (including hormones and growth factors) or a critical temperature. These environmental factors (and others) can turn genes on (genes are expressed) or off. If and when genes are expressed (and for how long) can have a considerable influence on an organism's eventual phenotype.

The effect of temperature

The sex of some animals is determined by incubation temperature during embryonic development. Examples include turtles, crocodiles, and the American alligator. In some species, high incubation temperatures produce males and low temperatures produce females. In other species, the opposite is true. Temperature regulated sex determination may be advantageous because it helps to prevent inbreeding (since all siblings will tend to be of the same sex).

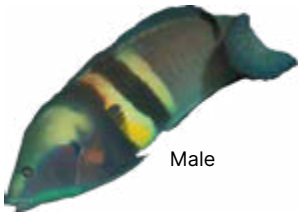
Colour-pointing in breeds of cats and rabbits (e.g. Siamese, Himalayan) is a result of a temperature sensitive mutation in one of the enzymes in the metabolic pathway from tyrosine to melanin. The dark pigment is only produced in the cooler areas of the body (face, ears, feet, and tail), while the rest of the body is a paler version of the same colour, or white.

The effect of other organisms

For some animals, the presence of other individuals of the same species may control sex determination.

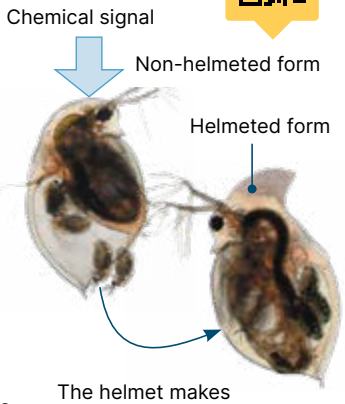
Female

Some fish species, including some in the wrasse family (e.g. *Coris sandageri*, right), show this phenomenon. The fish live in groups consisting of a single male with attendant females and juveniles. In the presence of a male, all juveniles become females. When the male dies, the dominant female will undergo changes in physiology and appearance to become a male.



Male

Some organisms respond to the presence of harmful organisms by changing their morphology or body shape. When the water flea *Daphnia* is exposed to predatory phantom midge larvae it develops a helmet and/or tail spine and also produces young with the same defensive structures. These responses are mediated through chemicals produced by the predator.



The helmet makes *Daphnia* more difficult to attack and handle by the predatory midge.

1. Give an example where the environment affects an organism's phenotype (other than those shown above):

_____

2. (a) How is helmet and spine development in *Daphnia* a response to environment? _____

_____

_____

(b) How does the phenotypic response help the animal survive? _____

_____

_____

3. Why are the darker patches of fur in colour-pointed cats and rabbits found only on the face, paws and tail:

_____

_____

_____

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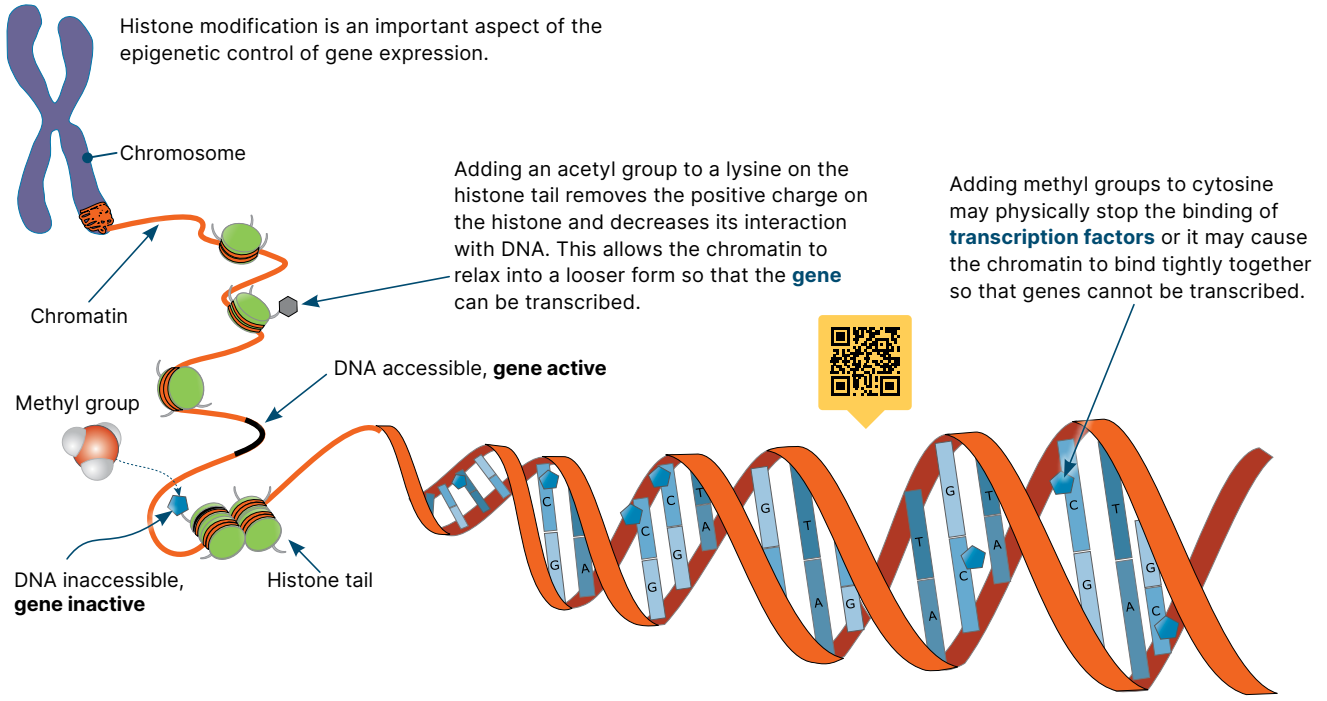
108 Epigenetic Regulation of Gene Expression

Key Idea: The mechanisms by which the environment modifies the expression of genes are often epigenetic.

As you saw earlier, **gene expression** can be influenced in part by the environment. But how is the influence of environment moderated? Sometimes (as with colour pointing) the environment directly influences a **protein**'s function. Most often though, the regulation is **epigenetic**. Epi- means 'on top of' or 'extra to'. Thus epigenetic factors are those external to the gene itself (e.g. chemical tags) that influence how that gene is expressed. Epigenetic regulation is achieved by modifying the way the **DNA** is packaged and its availability to be transcribed. The DNA sequence is unchanged.

The regulation of gene expression in eukaryotes is a complex process beginning before the DNA is even transcribed. The packaging of DNA regulates gene expression either by making the nucleosomes in the chromatin pack together tightly (heterochromatin) or more loosely (euchromatin). This affects whether or not RNA polymerase can attach to the DNA and transcribe the DNA.



1. What is epigenetics? _____

_____

_____

2. (a) Describe the effect of histone modification and adding methyl groups on DNA packaging: _____

_____

_____

(b) How do these processes affect transcription of the DNA? _____

_____

_____

3. The graphs right show the relative amount of genomic methylation and the effect of this on the frequency of gene expression. Describe the relationship between methylation and gene expression:

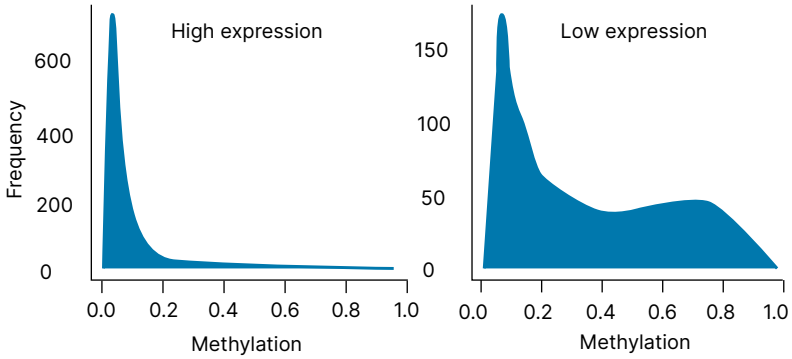
_____

_____

_____

_____

_____



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Epigenetics and gene expression

Epigenetics affects development

- One of the biggest debates in the study of development is the idea of nature versus nurture. To what extent do genes or the environment affect development and phenotype?
- A 2004 study of the grooming of rat pups by their mothers helps provide some insight. In this study, the quality of care by a pup's mother affected how the pup behaved when it reached adulthood.
- Rat pups that were groomed more often by their mother were better at coping with stress than pups that received less grooming. What's more, it was shown that the effect was caused by changes in the expression of the glucocorticoid receptor, which plays a role in the response to stress.
- DNA analysis found differences in the way the DNA was chemically tagged. Rats that received a lot of grooming had DNA that allowed for greater transcription and so had higher expression of the glucocorticoid receptor. The opposite was true for rats who received little grooming.

Twins in space

NASA

- Twin studies can provide a lot of information about how the environment affects gene expression. The studies are often done when identical twins have been separated at birth (usually because one or both of them are adopted out). Their similarities and differences can then be studied to assess how much the environment influenced their development.
- In 2015, NASA astronaut Scott Kelly blasted into space for a year long stay on the International Space Station. His identical twin brother Mark remained on Earth. This gave NASA a chance to study the real effects of space travel on the human body. Importantly, the gene expression of the men could be measured before and after Scott went to space.
- It was found that six months after Scott's return, 7% of his genes had not returned to their normal level of gene expression. Also, although there was no decrease in Scott's cognitive abilities, there was a decrease in his speed and accuracy until his readjustment to Earth gravity. The space environment had altered Scott Kelly's gene expression compared to his identical twin Mark Kelly.

4. (a) Describe how grooming by mother rats on their pups affected the pups in the long term: _____

   _____

   (b) How could this have been achieved by epigenetics? _____

   _____

   _____

5. How might twin studies help the study of gene-environment responses? _____

   _____

   _____

   _____

6. What evidence is there that epigenetics can have long term to permanent effects on gene expression?

   _____

   _____

   _____

   _____

7. When a zygote forms at fertilisation most of the epigenetic tags are erased so that cells return to a genetic 'blank slate' ready for development to begin. However some epigenetic tags are retained and inherited. Why do you think it might be advantageous to inherit some epigenetic tags from a parent?

   _____

   _____

   _____

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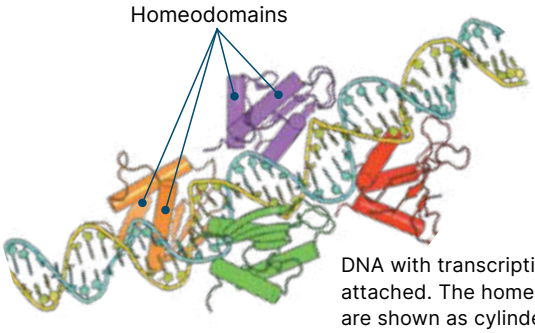
109 Regulating Morphology

Key Idea: Transcription factors regulate gene expression, and so also cellular differentiation and morphology.

Recall that **genes** can structural or regulatory. **Regulatory genes** produce **proteins** that regulate how other genes are expressed. Examples of these regulatory genes include the *Hox* genes. *Hox* genes play a major part in determining morphology because they regulate genes that then regulate networks of other genes.

Homeobox genes

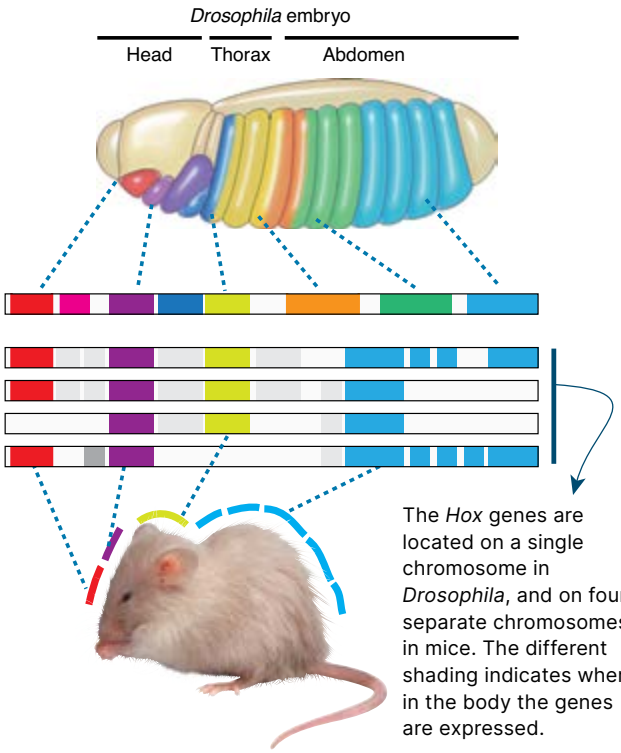
- Homeobox genes are genes containing a highly conserved (unchanging) sequence called the homeobox. The homeobox is about 180 base pairs long and encodes a string of about 60 **amino acids** called a homeodomain, which can bind to DNA.
- Proteins containing the homeodomain act as **transcription factors** and so regulate **transcription** of other genes.
- A homeobox gene is not one gene. It is a large, ancient group of genes that all contain the homeobox sequence. In humans, there are about 235 homeobox genes, but homeobox genes are found in all eukaryotes, including plants, animals, and fungi. The genes themselves may be different, but the homeobox sequence itself hasn't changed much at all throughout evolution.



DNA with transcription factors attached. The homeodomains are shown as cylinders.

The role of *Hox* genes

Hox genes are a special group of homeobox genes found only in animals. *Hox* genes control the development of the back and front parts of the animal body. The same genes (or homologous ones) are present in essentially all animals, including humans.



The *Hox* genes are located on a single chromosome in *Drosophila*, and on four separate chromosomes in mice. The different shading indicates where in the body the genes are expressed.

Studying *Drosophila*

The 1995 Nobel Prize for Medicine and Physiology was award to Edward B Lewis, Christiane Nüsslein-Volhard and Eric F Wieschaus for their work on how *HOX* genes control embryonic development using *Drosophila* as their model. *Drosophila* is used because its genetic make up is relatively simple, many of its genes are similar to human genes, and it reproduces quickly and produces many offspring, allowing genetic studies over many generations to proceed quickly.

Edward B Lewis was a founder in the field of evolutionary developmental biology (Evo-Devo), discovering the bithorax complex (BX-C) of *HOX* genes in *Drosophila*, which controls the development of the posterior two-thirds of embryo development. Christiane Nüsslein-Volhard and Eric F Wieschaus identified the 15 genes responsible for the segmented pattern in the Drosophila embryo and directing the fertilised egg cell to form a new fly.

These findings have helped generate new understanding on how new structures evolve and on genetic disorders.

Expression of the *HOX* gene *Antp* in the wrong region of the body can result in legs growing where antenna should be (right).

Toony cc3.0

1. What are *Hox* genes and how do they function? _____

2. Hox genes contain highly conserved sequences of DNA. What does this mean and how can it help identifying evolutionary relationships?

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110 Did You Get It?

1. For the following DNA sequence on the template strand, give the mRNA sequence and then identify the amino acids that are encoded. You may consult the mRNA-amino acid table earlier in the chapter.

   DNA (template strand): G A A A C C C T T A C A T A T C G T G C T

   mRNA: _____

   Amino acids: _____

2. Complete the following paragraph by deleting one of the words in the bracketed () pairs below:

   In eukaryotes, gene expression begins with (transcription/translation) which occurs in the (cytoplasm/nucleus). (Transcription/Translation) is the copying of the DNA code into (mRNA/tRNA). The (mRNA/tRNA) is then transported to the (cytoplasm/nucleus) where (transcription/translation) occurs. Ribosomes attach to the (mRNA/tRNA) and help match the codons on (mRNA/tRNA) with the anticodons on (mRNA/tRNA). The (mRNA/tRNA) transports the animo acids to the ribosome where they are added to the growing (polypeptide/carbohydrate) chain.

3. All worker bees and the queen bee (circled) in a hive have the same genome, yet the queen looks and behaves very differently from the workers. Only bee larvae fed a substance called royal jelly will develop into queens.

   Research shows that royal jelly contains factors that silence the activation of a gene called Dnmt3, which itself silences many other genes. Studies on bee development have focussed on the Dnmt3 gene. One study switched off the Dnmt3 gene in 100 bee larvae. All the larvae developed into queens. Leaving the gene switched on in larvae causes them to develop into workers. Compare these results to feeding larvae royal jelly. Which results mimic feeding larvae royal jelly? Explain:

   _____

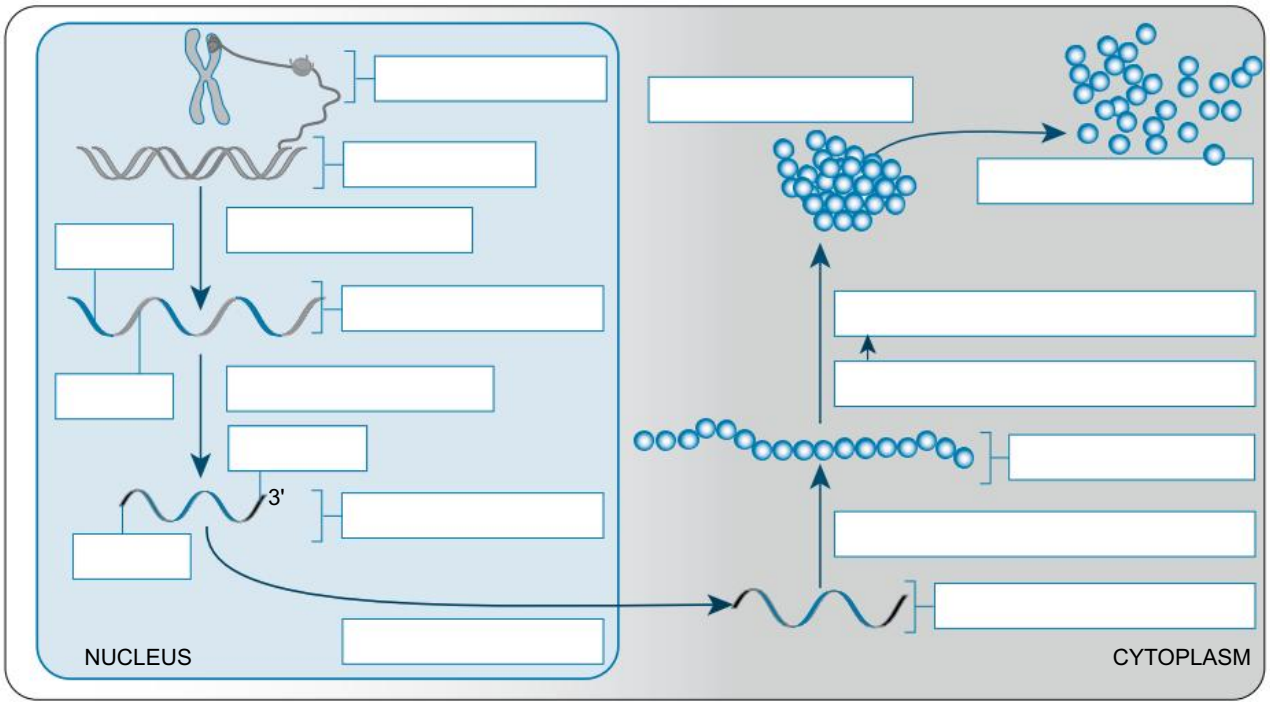
   _____

   _____

   _____

4. The schematic below shows the levels of control in gene expression. Fill in the boxes indicating the structures and processes, choosing from the following word list. Use a highlighter or different coloured pens to distinguish processes (in red or black) and structures (in blue).

   Word list: *5' cap, mRNA in the nucleus, polypeptide, mRNA in the cytoplasm, DNA packing, exon, intron, functional protein, folding and assembly, poly A tail, gene, cleavage or chemical modification, primary mRNA, protein degradation, translation, transcription, exon splicing, nuclear export.*



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Chapter 10 Unit 4 Topic 1

Mutations

Resource Hub
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Key Terms

- allele
- aneuploidy
- carcinogenic
- chromosome mutations
- frameshift
- gene
- gene mutation
- karyogram
- karyotyping
- mutagen
- mutagenic
- mutation
- non-disjunction
- point mutation

Key Concepts

- Mutations are permanent changes in DNA that can be caused by errors in replication, non-disjunction, or exposure to mutagens, and they are the source of new alleles.
- Gene mutations can involve point mutations (substitution, insertion, deletion) or frameshifts, with frameshifts being more disruptive to protein function.
- Karyotyping is used to identify chromosomal abnormalities, such as aneuploidy, by analyzing the size, shape, and banding patterns of chromosomes.

Causes of mutations

			Activity Number
☐	1	Explain how mutations can occur in DNA as a result of: • errors in DNA replication prior to cell division (point and frameshift mutations) • non-disjunction during cell division • Chromosome mutations • damage to DNA by mutagens.	111 - 116
☐	2	Explain what is meant by a gene mutation. Describe the consequences of different types of point mutations and explain why a frameshift has a more detrimental effect than a base substitution. Identify some examples of point mutations.	112, 113
☐	3	Identify examples of mutagens and explain how they cause mutations. Understand that many chemical mutagens are also carcinogens, interacting directly with DNA and interrupting the normal controls over cell division.	114
☐	4	Explain what is meant by a chromosome mutation. Describe the consequences of different types of chromosome mutations including insertions, deletions, inversions, and translocations.	116

Karyotypes and chromosome abnormalities

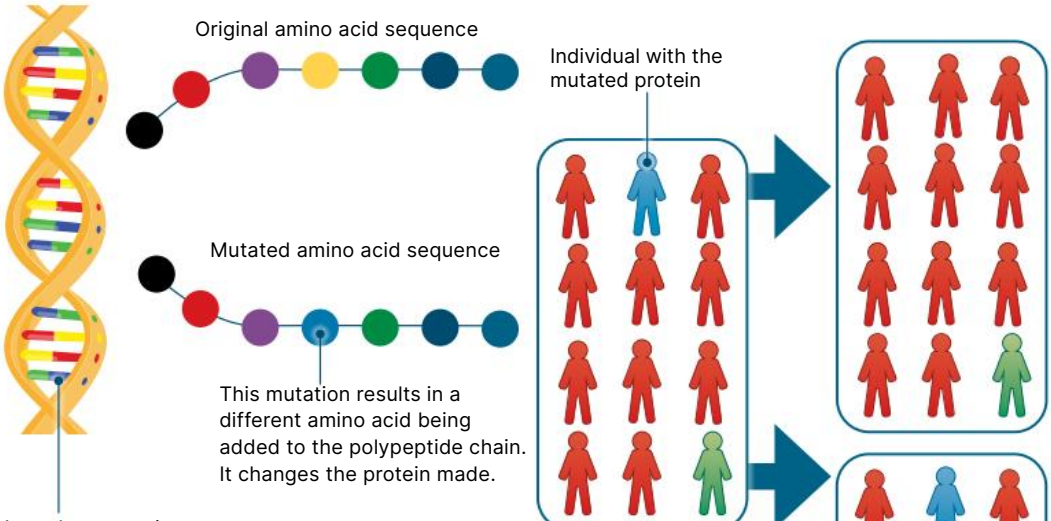
☐	5	Explain what is meant by non-disjunction. Describe how non-disjunction occurs and how it leads to aneuploidy. Identify and describe examples of changes in ploidy in humans and/or plants.	115
☐	6	Explain what is meant by a karyogram. Describe the use of karyotyping in the identification of chromosomal abnormalities such as aneuploidy.	117
☐	7	Use a human karyotype to identify ploidy changes and predict a genetic disorder from given data.	118
☐	8	Recognise mutations as the source of all new alleles. Using examples, describe how new alleles created by mutations can be inherited to create new phenotypic variants in the offspring. Examples include non-syndromic recessive deafness (NSRD), sickle cell disease, and human blood groups.	113

111 Mutations

Key Idea: Mutations are random events that occur in both somatic and germ cells, where the rate of mutation can increase in frequency with exposure to mutagens.

A **mutation** is a permanent change to the **DNA** sequence of an organism. Mutations are the ultimate source of new **alleles**. Most mutations are harmful because they disrupt some important cellular process, often by causing a protein to fold incorrectly. Occasionally they may cause some beneficial change, such as making an enzyme more efficient. This phenomenon is the basis of natural selection. Although the DNA replication process is very accurate, it is estimated that, in humans, a mutation occurs once every 30 million base pairs copied during DNA replication prior to **meiosis**. This means that every person has about 200-300 new mutations that their parents did not have. Mutations occurring in germ cells can be passed down to offspring.

Some mutations are retained, others are eliminated



A silent mutation is a DNA sequence change that has no phenotypic effect. This may be because the change occurs outside a protein-coding region (in **introns**), because there is no change in the amino acid (due to code degeneracy), or because an amino acid has been replaced by one with the same properties. Heritable silent mutations may be carried without effect and may only be subject to selection pressure when environmental conditions change.

1. What is a mutation? _____

2. Why are some mutations retained within a population and others eliminated? _____

3. (a) What is a silent mutation? _____

   (b) Explain the potential advantage of a silent mutation being retained within a population: _____

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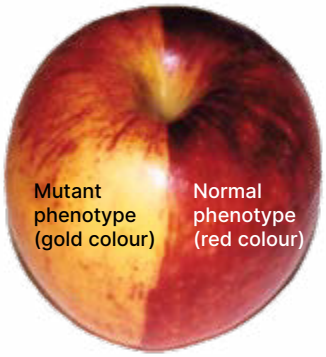
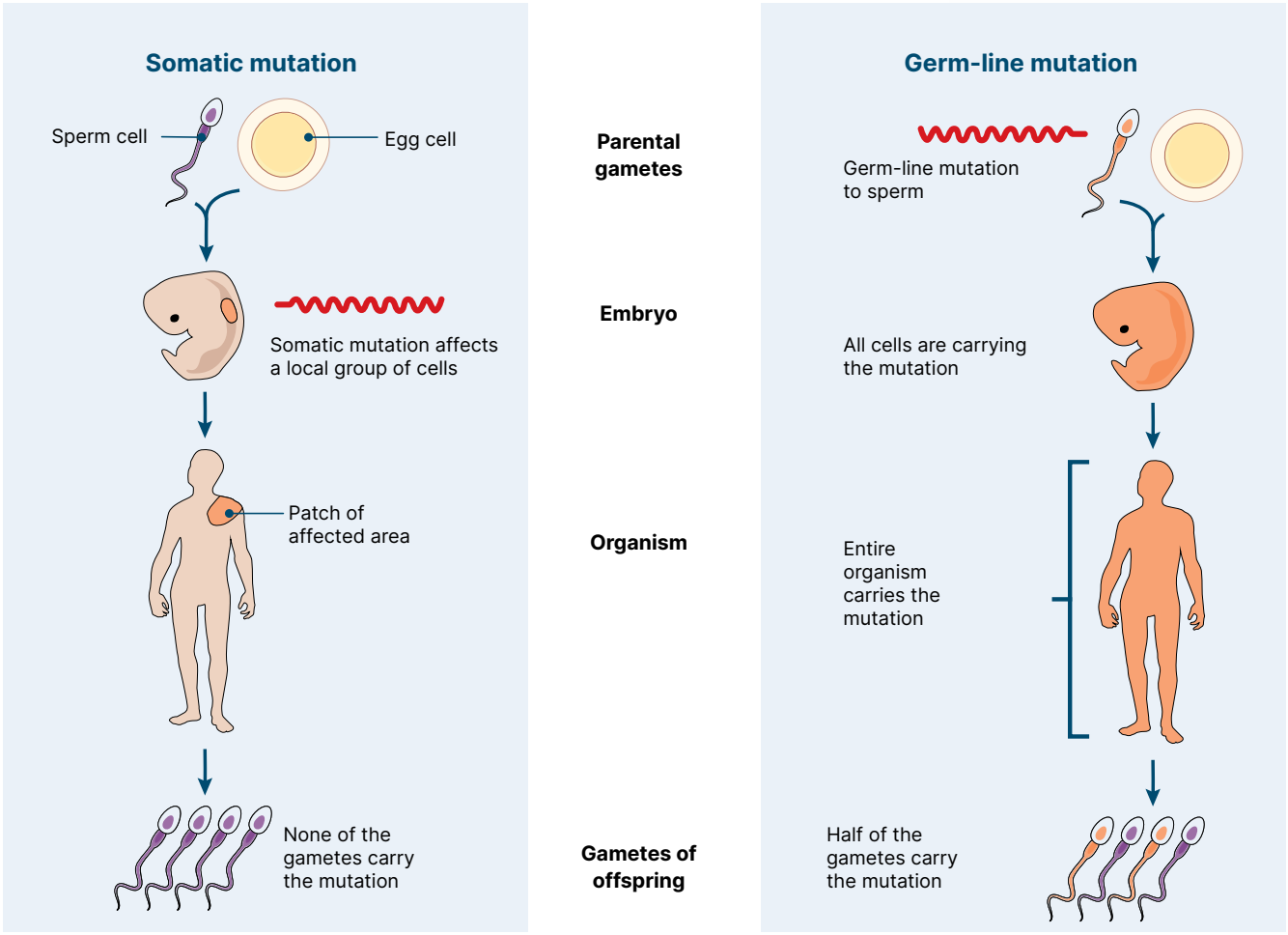
Somatic vs germ cell mutations

- Gametic cells are the reproductive (sex) cells of an organism (the egg and sperm). Mutations occurring in these cells are called germ-line mutations, or gametic mutations.
- Somatic cells (body cells) are all the remaining cells. Mutations to these cells are called somatic mutations.
- Only germ-line mutations will be inherited. Somatic mutations are not inherited but may affect an organism in its lifetime, e.g. a cancer.
- The red delicious apple (right) is a natural chimera (an organism with a mixture of two or more different genotypes). In the apple, a mutation occurred in the part of the flower that developed into the fleshy part of the apple. The seeds are unaffected by the mutation, so it is not inherited.





4. Distinguish between somatic and germ-line mutations: _____

5. Explain the consequences of these different mutation locations: _____

6. Chimeras can be produced artificially in both plants and animals. Suggest what kind of information these organisms could provide in studies of gene expression and gene regulation:

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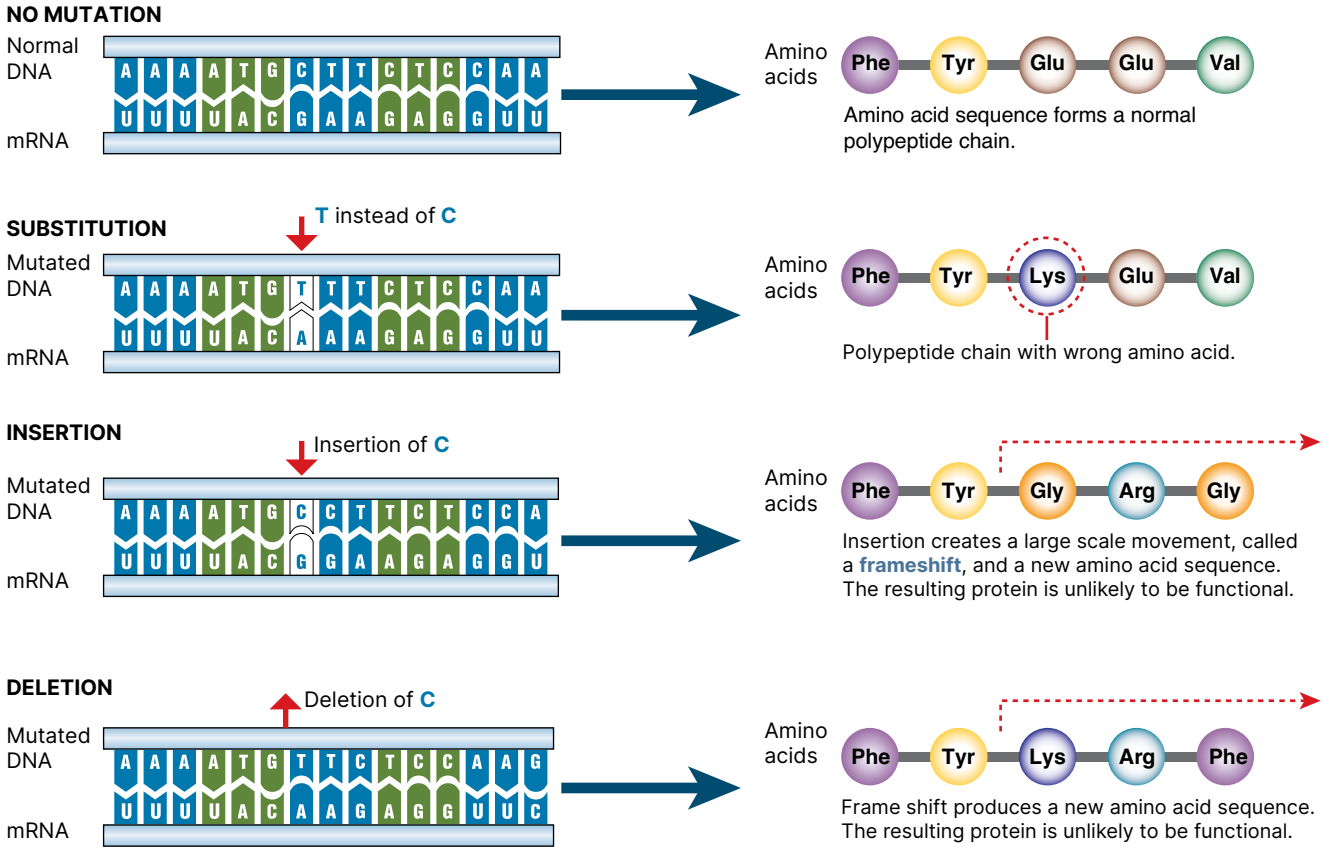
112 Gene Mutations

Key Idea: Gene mutations are localised changes to the DNA base sequence. The effects can be minimal or large.

Gene mutations are small, localised changes in the base sequence of a **DNA** strand caused by a **mutagen** or an error during DNA replication. The changes may involve a single nucleotide (a **point mutation**) or a change to a triplet. Point mutations can occur by substitution, insertion, or deletion of bases. These changes alter the **mRNA** transcribed from the mutated DNA. A point mutation may not alter the **amino acid** sequence because more than one codon can code for the same amino acid. Mutations that result in a change in the amino acid sequence will usually be harmful.



1. Some gene mutations are more disruptive to an organism than others.

   (a) Which type of gene mutations are generally the most damaging to an organism? _____

   _____

   (b) Explain why they are the most disruptive: _____

   _____

   (c) Describe what type of gene mutation is least likely to cause a change in protein structure and explain your answer:

   _____

   _____

2. In the following DNA sequence, replace the **G** of the second codon with **A** to create a mutated DNA strand. Determine the new mRNA sequence and the amino acid sequence. Use the mRNA-amino acid table to identify the amino acids:

   (a) Original DNA: AAA ATG TTT CTC CAA GAT

   Mutated DNA: _____

   mRNA: _____

   Amino acids: _____

   (b) Identify the amino acid coded by codon 2 (ATG) in the original DNA: _____

   (c) Explain the effect of the mutation: _____

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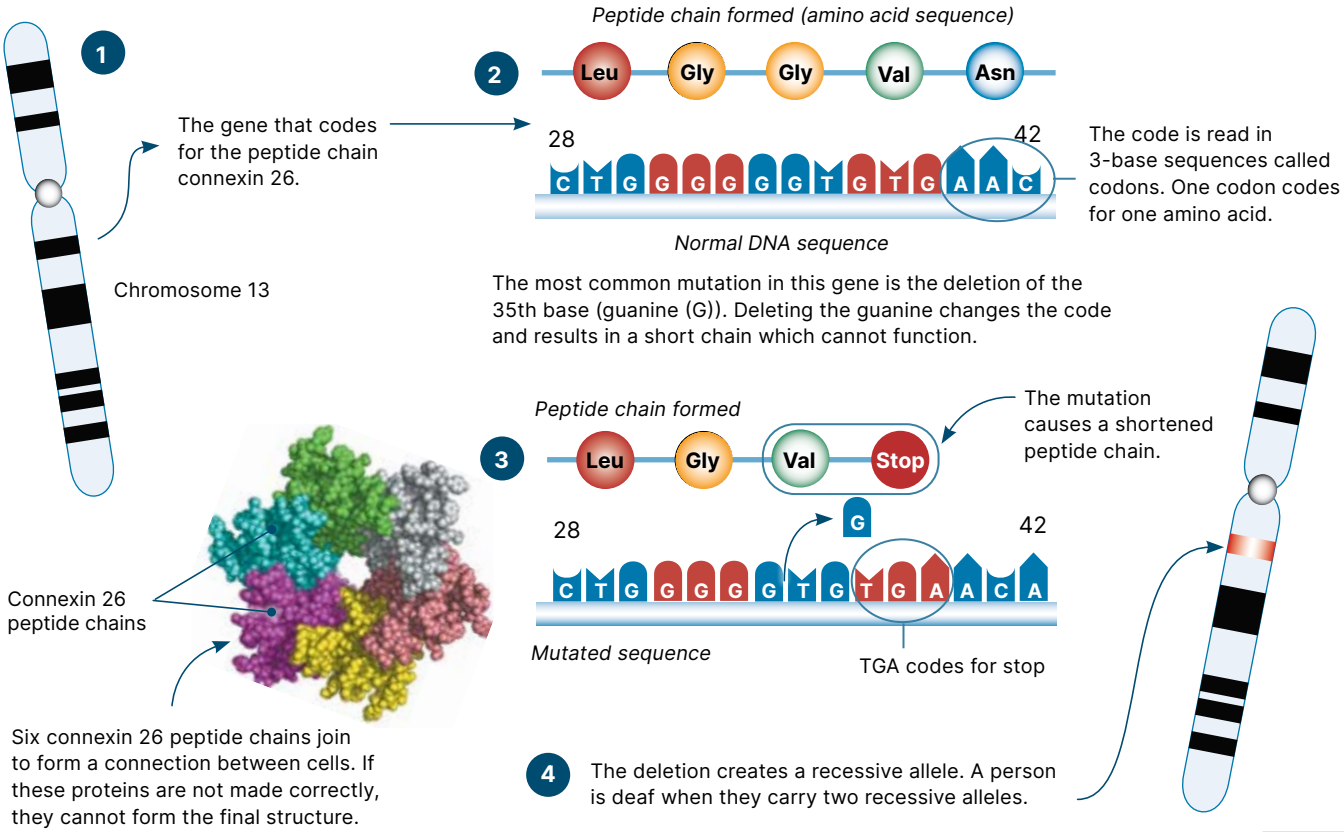
113 Mutations Can Alter Phenotype

Key Idea: Mutations are the ultimate source of new genetic information, i.e. new alleles.

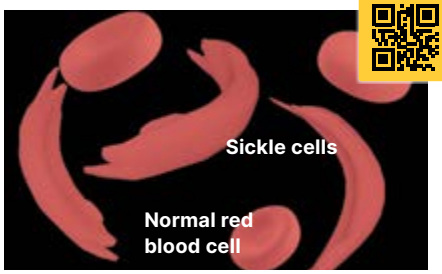
Recall that mutations are changes to the **DNA** sequence. They may involve small changes to the DNA (e.g. a base substitution) or movements of large parts of chromosomes. **Mutation** is the only way to create new **alleles** (an allele is a **gene** variant). Mutations are usually harmful, but occasionally they can be beneficial and sometimes they are silent (result in no change in the phenotype (appearance) of the individual). The example below describes a mutation that produces a new allele for the gene coding for the protein connexin 26. This mutation causes a form of inherited deafness (NSRD).

Mutation for non-syndromic recessive deafness (NSRD)



In mammals, production of the enzyme lactase, which digests the sugar lactose in milk, stops after childhood. In humans of European, East African, or Indian descent, a mutation about 10,000 years ago produced a dominant allele for the lactase gene. This kept the lactase gene active, allowing adults to continue to digest dairy products.

In humans, there are three major blood groups, A, B, and O, controlled by the alleles A, B, and O. The alleles produce enzymes that modify carbohydrates (sugars) on the surface of blood cells. Different blood groups have different carbohydrates on the cell surface. It is believed that the A allele group evolved first, followed by O, and then B.



Red blood cells are packed with the oxygen-carrying protein haemoglobin, encoded by the HBB gene. A substitution mutation to the HBB gene produces an allele that causes the haemoglobin to distort the red blood cells into a sickle shape. The homozygous condition is lethal but the mutation persists because heterozygotes are more resistant to malaria.

1. What is a mutation? _____

2. The NSRD mutation is a harmful mutation. Why might someone with this mutation not actually be affected?

_____

3. Why would the appearance of the persistent lactase allele be an advantage? _____

_____

_____

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114 Mutagens

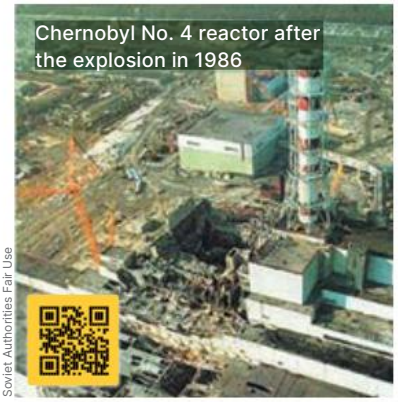
Key Idea: Mutagens are chemical or physical agents that cause a change in the DNA sequence.

Mutations occur spontaneously in all organisms. The natural rate at which a **gene** will undergo change is normally very low, but this rate can be increased by environmental factors such as ionising radiation and **mutagenic** chemicals. Only **mutations** in cells producing sex cells (gametic mutations) will be inherited. If they occur in a body cell after the organism has begun to develop, they are called somatic mutations. In some cases, somatic mutations may disrupt the normal controls over gene regulation and expression and trigger the onset of cancer (abnormal cell growth).

Mutagen and effect

Ionising radiation

High energy radiation in the form of ultraviolet radiation, x-rays, gamma rays and particle emission from radioactive isotopes can penetrate tissue and cause DNA damage. Rates of thyroid cancer increased in areas near Chernobyl after the explosion of the No. 4 reactor there. Skin cancer (from high exposure to ultraviolet) is increasingly common with fair skinned people at low latitudes at greatest risk. Safer equipment has reduced the risks to those working with ionising radiation (e.g. radiographers).



Chernobyl No. 4 reactor after the explosion in 1986

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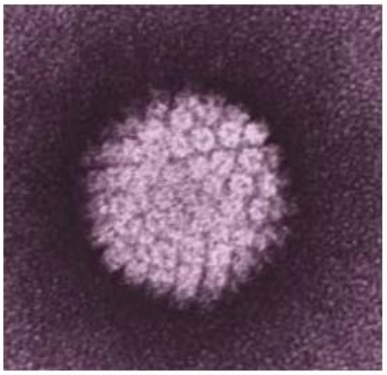
Viruses and microorganisms

Some viruses integrate into the human chromosome, upsetting genes and triggering cancers. Examples include hepatitis B virus (liver cancer), HIV (Kaposi's sarcoma), Epstein-Barr virus (Burkitt's lymphoma, Hodgkin's disease), and HPV (right) which is implicated in cervical cancer. Aflatoxins produced by the fungus *Aspergillus flavus* are potent inducers of liver cancer.

Those at higher risk of viral infections include intravenous drug users and those with unsafe sex practices



NIH

Poisons and irritants

Many chemicals interact directly with DNA to trigger cancer (they are **carcinogenic**). Synthetic and natural examples include organic solvents (e.g. benzene), tobacco tar, formaldehyde, vinyl chlorides, coal tars, some dyes, and nitrites. Those most at risk include workers in the chemicals industries, including the glue, paint, rubber, resin, and leather industries, and those in the coal and other mining industries.

Right: Firefighters and those involved in environmental clean-up of toxic spills are at high risk of exposure to **mutagens**.

Diet, alcohol and tobacco smoke

Diets high in fat, especially those containing burned or fatty, highly preserved meat, slow the passage of food through the gut giving time for mutagenic irritants to form in the lower bowel.

High alcohol intake increases the risk of some cancers and increases susceptibility to tobacco-smoking related cancers.

Tobacco tar is one of the most damaging constituents of tobacco smoke. Tobacco tars contain at least 17 known carcinogens (cancer inducing mutagens) that cause chronic irritation of the gas exchange system and cause cancer in smokers.

1. Describe examples of environmental factors that induce mutations under the following headings:

(a) Ionising radiation: _____

(b) Chemical agents: _____

2. Explain how mutagens cause mutations:

3. Distinguish between gametic and somatic mutations and comment on the significance of the difference:

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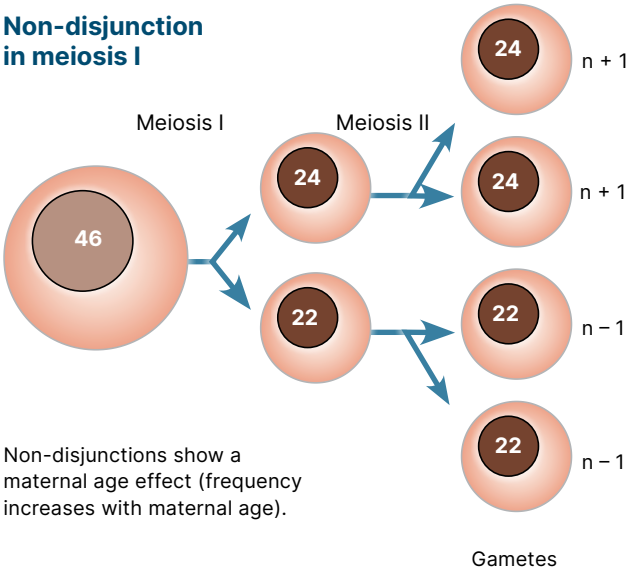
115 Non-Disjunction Can Produce Aneuploidies

Key Idea: Non-disjunction during meiosis results in incorrect apportioning of chromosomes to the gametes.

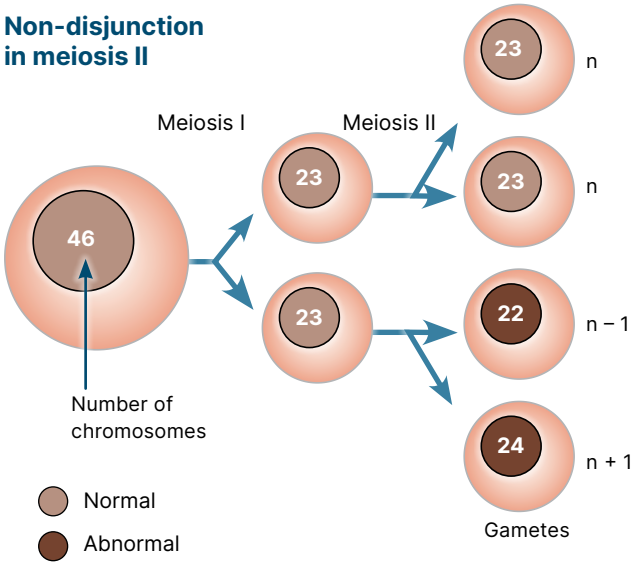
In **meiosis**, **chromosomes** are usually distributed to daughter cells without error. Occasionally, homologous chromosomes fail to separate properly in meiosis I, or sister chromatids fail to separate in meiosis II. In these cases, one **gamete** receives two of the same type of chromosome and the other gamete receives no copy. This error is known as **non-disjunction** and it results in abnormal numbers of chromosomes in the gametes. The union of an aberrant and a normal gamete at fertilisation produces offspring with an abnormal chromosome number. This condition is known as **aneuploidy**.

Non-disjunction in meiosis I



Non-disjunctions show a maternal age effect (frequency increases with maternal age).

Non-disjunction in meiosis II



Down syndrome (trisomy 21)

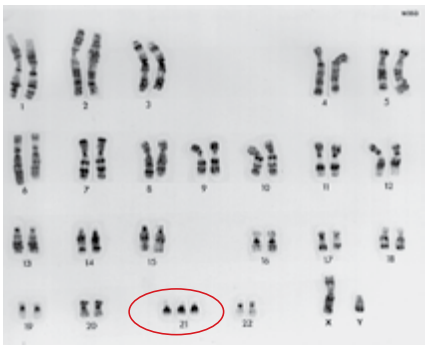


Photo: Waikato Hospital

Down syndrome is the most common of the human aneuploidies. The incidence rate in humans is about 1 in 800 births for women aged 30 to 31 years, with a maternal age effect (the rate increases rapidly with maternal age). Nearly all cases (approximately 95%) result from non-disjunction of chromosome 21 during meiosis. When this happens, a gamete (most commonly the oocyte) ends up with 24 rather than 23 chromosomes, and fertilisation produces a trisomic offspring. *Above: A karyogram for an individual with trisomy 21. The affected chromosomes are circled.*

Datura stramonium

Agnieszka Kwiecie, license: CC-BY 3.0

The plant *Datura stramonium* has 12 sets of chromosomes. There are 12 known aneuploids, each trisomic for a different chromosome. Interestingly each aneuploid has its own variety of seed pod shape, ranging from buckling (trisomy 3) to cocklebur (trisomy 6) and spinach (trisomy 10). All the aneuploids survive to be viable adult plants indicating plants are better able to accommodate genetic shuffling than animals.

1. Describe the consequences of non-disjunction during meiosis: _____

2. Explain why non-disjunction in meiosis I results in a higher proportion of faulty gametes than non-disjunction in meiosis II:

3. How does non-disjunction lead to aneuploidy? _____

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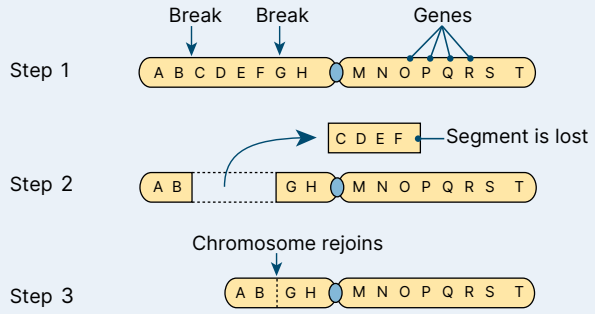
116 Chromosome Mutations

Key Idea: Large scale mutations occurring during meiosis can fundamentally change chromosome structure.

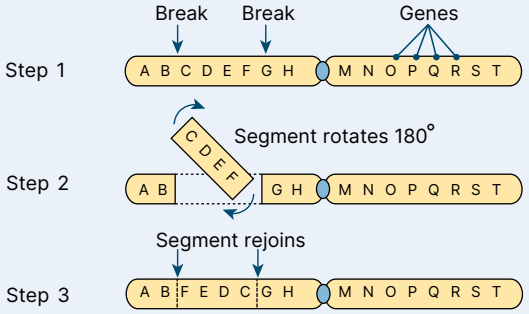
Chromosome mutations, also called block mutations, involve the rearrangement of whole blocks of **genes** involving many bases, rather than individual bases within a gene. They commonly occur during meiosis and they alter the number or sequence of whole sets of genes on the chromosome (represented by letters below). Translocations may sometimes involve the fusion of whole chromosomes, thereby reducing the chromosome number of an organism. This is thought to be an important evolutionary mechanism by which instant speciation can occur.

Deletion



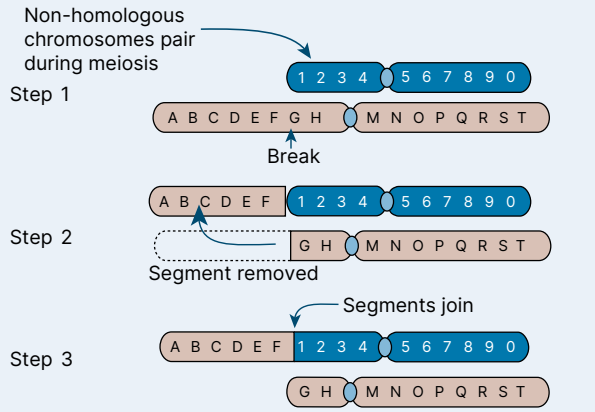
A break may occur at two points on the chromosome and the middle piece of the chromosome falls out. The two ends then rejoin to form a chromosome deficient in some genes. Alternatively, the end of a chromosome may break off and is lost.

Inversion



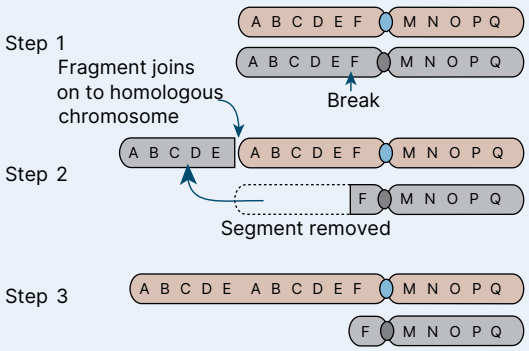
The middle piece of the chromosome falls out and rotates through 180° and then rejoins. There is no loss of genetic material. The genes will be in a reverse order for this segment of the chromosome.

Translocation



In translocation mutations, a group of genes moves between different chromosomes. The large chromosome (brown) and the small chromosome (blue) are not homologous. A piece of one chromosome breaks off and joins to the other. When the chromosomes are passed to gametes, some gametes will receive extra genes, while some will be deficient.

Duplication



A segment is lost from one chromosome and added to its homologue. In the diagram, the darker chromosome on the bottom is the 'donor' of the duplicated piece of chromosome. The chromosome with the segment removed is deficient in genes. Some gametes will receive double the genes while others will have no genes for the affected segment.

1. Which of the chromosome mutations above results in a loss of genetic information? _____

2. For each of the chromosome (block) mutations below, write the new gene sequence after the mutation has occurred:

	Original sequence	Mutated sequence
(a) Inversion:	ABCDEFGHMNOPQRST	_____
(b) Translocation:	1 2 3 4 5 6 7 8 9 0	_____

3. Which type of block mutation is likely to be the least damaging to the organism? Explain your answer:

_____

_____

4. Why do translocations sometimes reduce the total number of chromosomes? _____

_____

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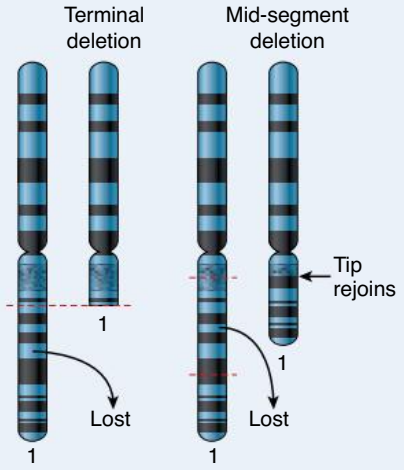
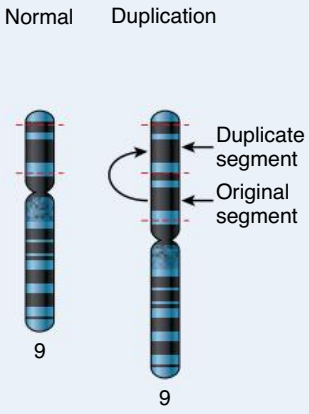
Examples of chromosome mutations in humans



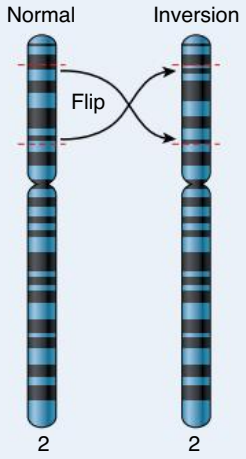
Deletion

Two types of deletion are known to occur on chromosome 1: a '*terminal deletion*' on the left removes a portion at the end, while a '*mid-segment deletion*' on the right removes a central block of a chromosome.



Duplication

In this chromosome **9** duplication mutation, the extra chromosomal segment could arise via an unequal exchange of chromatids during crossing over with its homologue.



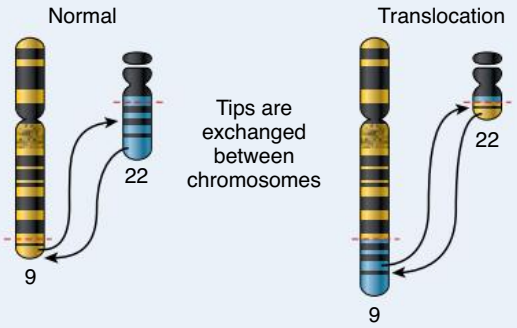
Inversion

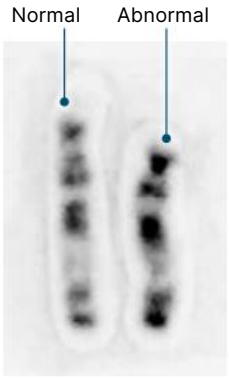
This diagram shows a chromosome **2** inversion. There has been no change in the genetic content; it has only been rearranged. However, this has important consequences during crossing over.

Translocation

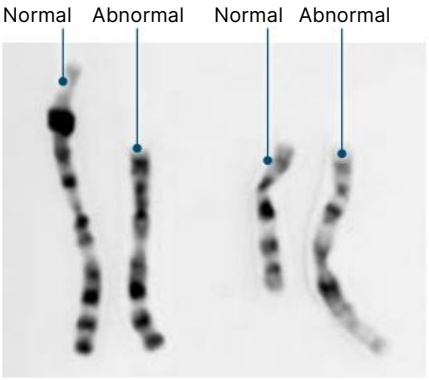
The chromosome on the right shows a two-way translocation where the tips of chromosomes **9** and **22** are exchanged. This specific translocation is associated with chronic myeloid leukaemia.

This translocation is a vivid demonstration that if the stability of the chromosome structure is upset too greatly, the resulting phenotype may have impaired fitness (reduced ability to survive and reproduce). This example did not even involve the loss of genetic material, just a movement of genes from one chromosome to another. It may be that an effect on a specific gene at the point of the break caused the illness.

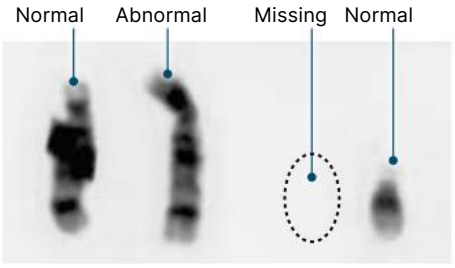




Chromosome 15



Chromosome 1 **Chromosome 10**



Chromosome 14 **Chromosome 21**

Offspring inheriting two normal chromosome 21s as well as the abnormal chromosome 14 have a rare type of Down syndrome (they have three copies of the genes on chromosome 21).

The examples above illustrate block mutations in human chromosomes. Individuals with these karyotypes could produce faulty gametes, leading to recognisable genetic disorders in the offspring. Individuals with translocated chromosomes could produce normal gametes but also gametes either missing or with extra genetic material. *Photos and information: Cytogenetics Department, Waikato Hospital, Hamilton, NZ.*

5. The photographs above were taken by the cytogenetics department at a hospital. Using the diagram explanations on this page as a guide, draw arrows to show the movement of chromosome segments on the photographs.

6. Identify the type of chromosome rearrangement shown in each photo involving:

   (a) Chromosome 15: _____

   (b) Chromosome 1 and 10: _____

   (c) Chromosome 14 and 21: _____

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117 Karyotyping

Key Idea: The karyotype is the number and appearance of chromosomes in the nucleus of a eukaryotic cell. The karyotype can be pictured in a standard format, called a karyogram, in which the chromosomes are ordered by size.

Karyotyping begins with 'freezing' the nuclei of cultured white blood cells in metaphase of mitosis. A photograph of the chromosomes is then cut up and the chromosomes are organised on a grid, with homologous pairs together, to produce a **karyogram**. In humans, the male karyotype has 44 autosomes (non-sex chromosomes), and an X and a Y chromosome (44 + XY). The female karyotype has two X chromosomes (44 + XX).

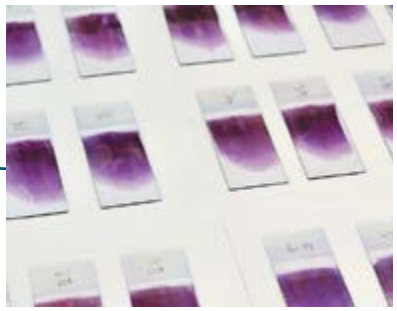
Preparing a karyotype

1 A sample of cells is taken from the person of interest. This may be from the amniotic fluid surrounding a fetus or from a blood sample from an adult or child.

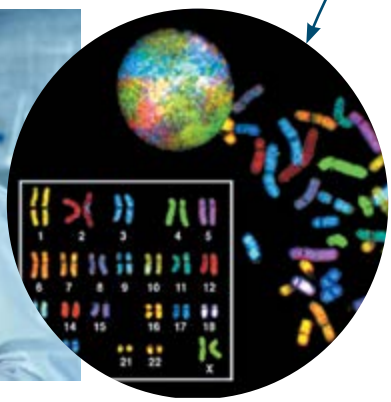
2 The sample is centrifuged and the lymphocytes (a type of white blood cell) are removed and induced to divide (mitosis).

They are grown for several days in culture and then treated to halt the cycle at the metaphase stage.

3 A drop of the cell suspension in preservative is spread on a microscope slide, dried and stained with a dye that causes a banding pattern to appear on each chromosome.



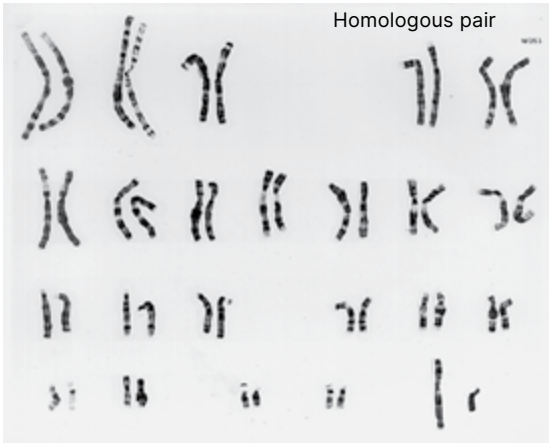
Microscope slides with stained smears



4 The stained white blood cells are viewed under a microscope and a clearly arranged spread of chromosomes is photographed.

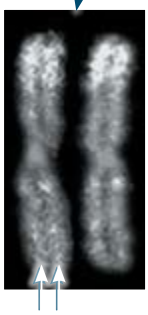
Newer techniques use fluorescent probes to colour-code chromosomes and provide a spectral karyogram (left).

5 The photograph is cut up (manually or electronically with the use of a computer) so that each chromosome is separate from the others. The chromosomes are then arranged into homologous pairs according to size, shape, and banding pattern (or colour).



Karyotypes: Cytogenetics Dept, Waikato Hospital

Conventional karyogram (male): 44 + XY



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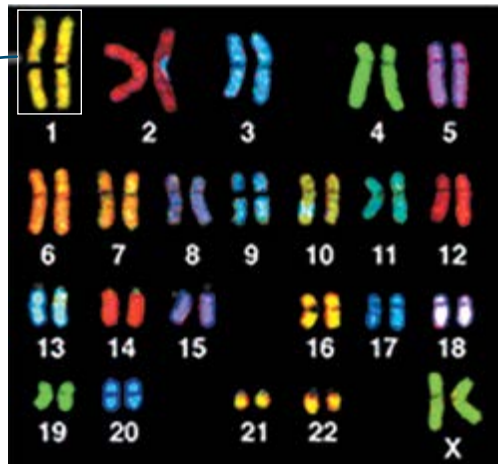
Close up reveals two chromatids



Spectral karyogram (female): 44 + XX

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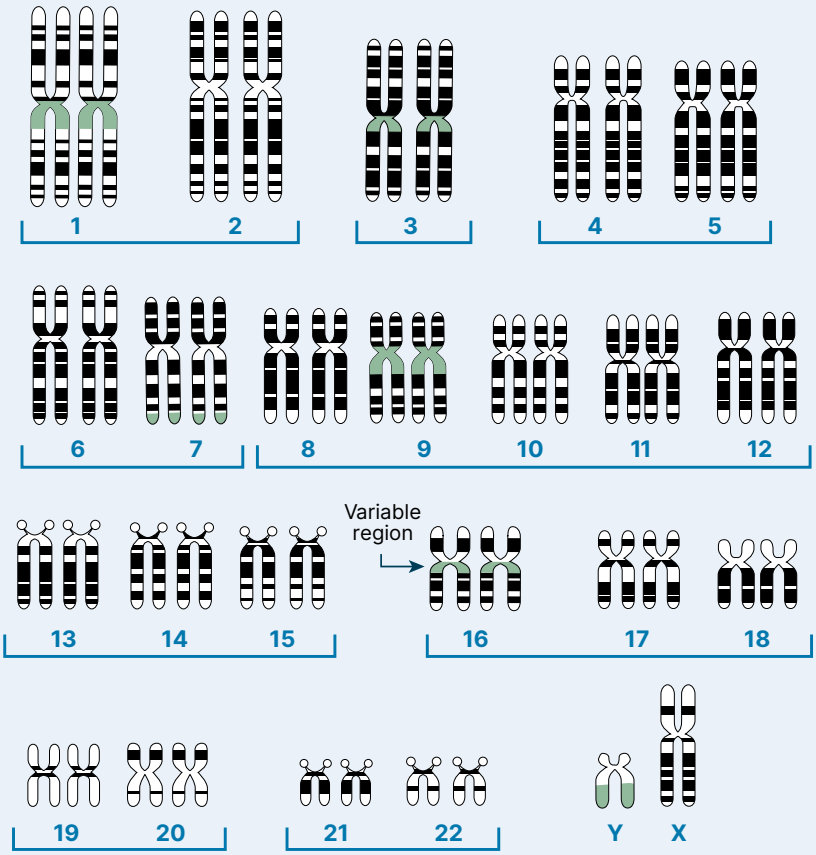
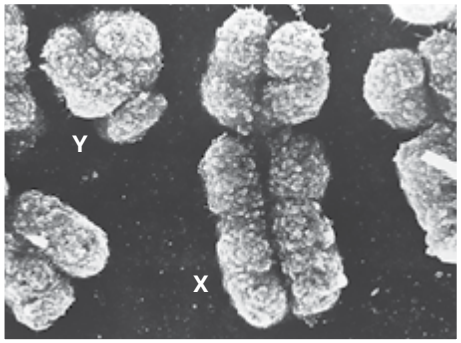
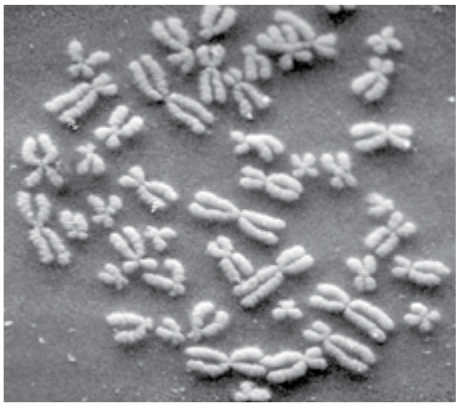
Typical layout of a human karyogram





SEM showing human X and Y chromosomes. Although these two are the sex chromosomes, they are not homologous.



A scanning electron micrograph (SEM) of human chromosomes clearly showing their double chromatids.

1. (a) What is a karyogram? _____

   _____

   (b) What information can it provide? _____

   _____

2. On the male karyogram on the previous page, number each homologous pair of chromosomes using the diagram above as a guide.
3. Circle the sex chromosomes (**X** and **Y**) in the karyogram of the female and the male.
4. Write down the number of autosomes and the arrangement of sex chromosomes for each sex:

   (a) Female: No. of autosomes: _____ Sex chromosomes: _____

   (b) Male: No. of autosomes: _____ Sex chromosomes: _____
5. State how many chromosomes are found in a:

   (a) Normal human (somatic) body cell: _____ (b) Normal human sperm or egg cell: _____
6. Distinguish between autosomes and sex chromosomes: _____

   _____

   _____
7. What features of the chromosomes allow them to be paired up for a karyogram? _____

   _____

   _____
8. Why are the X and Y chromosomes not homologous? _____

   _____

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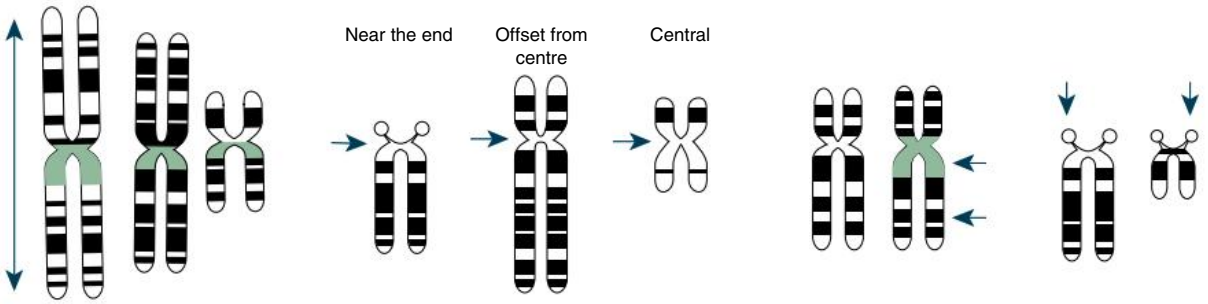
118 Making a Karyogram

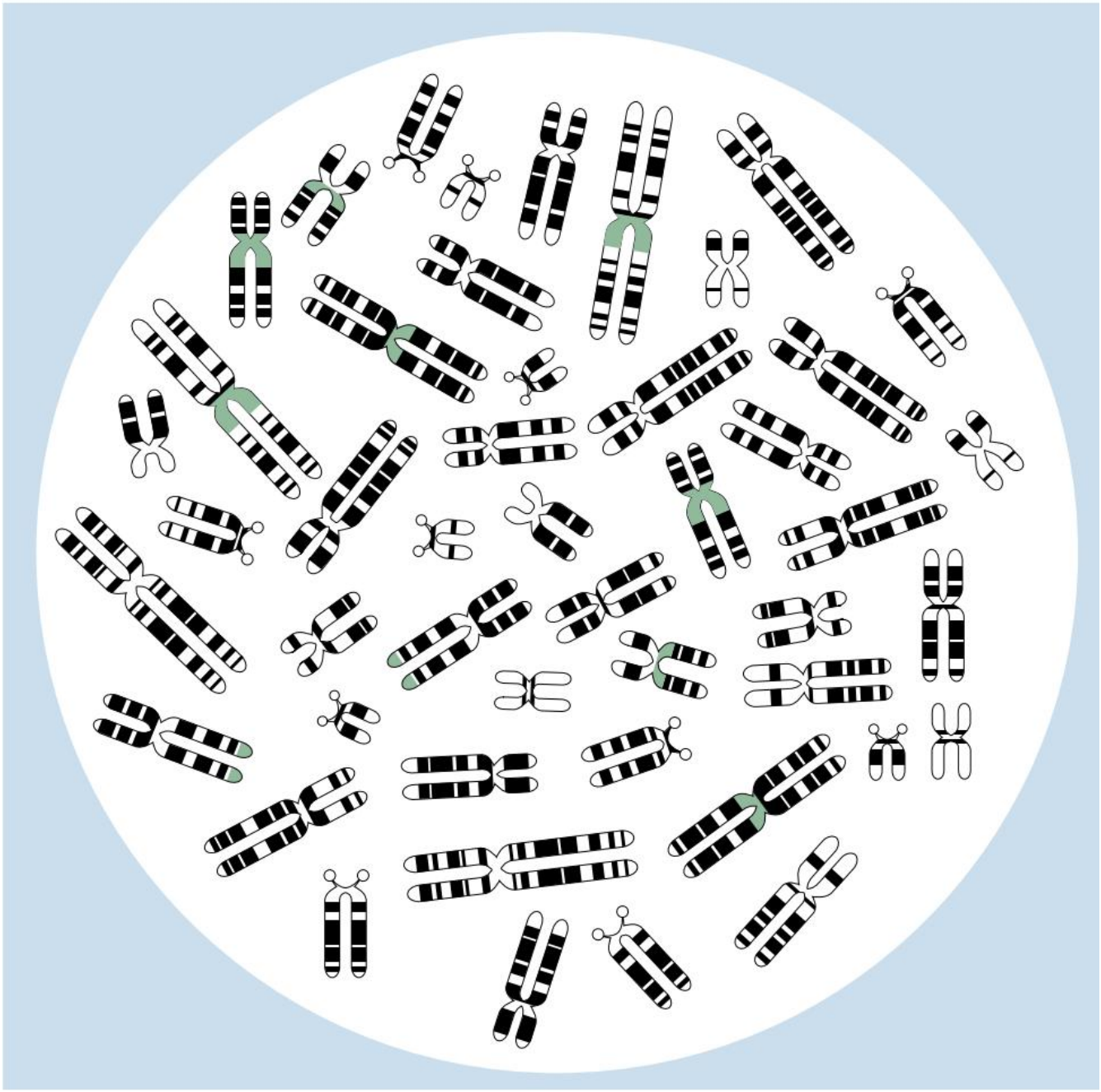
Key Idea: A karyogram can be created by matching the size and banding pattern of individual chromosomes.

Each chromosome has specific distinguishing features. Chromosomes are stained in a special technique that gives them a banded appearance in which the banding pattern represents regions containing up to many hundreds of genes. Cut out the chromosomes below and arrange them on the record sheet on p215 in order to determine the sex and chromosome condition of the individual whose karyotype is shown. The **karyograms** presented on the previous pages and the hints on how to recognise chromosome pairs can be used to help you complete this activity.

Distinguishing characteristics of chromosomes



Chromosome length | **Centromere position** | **Banding pattern** | **Satellite endings**



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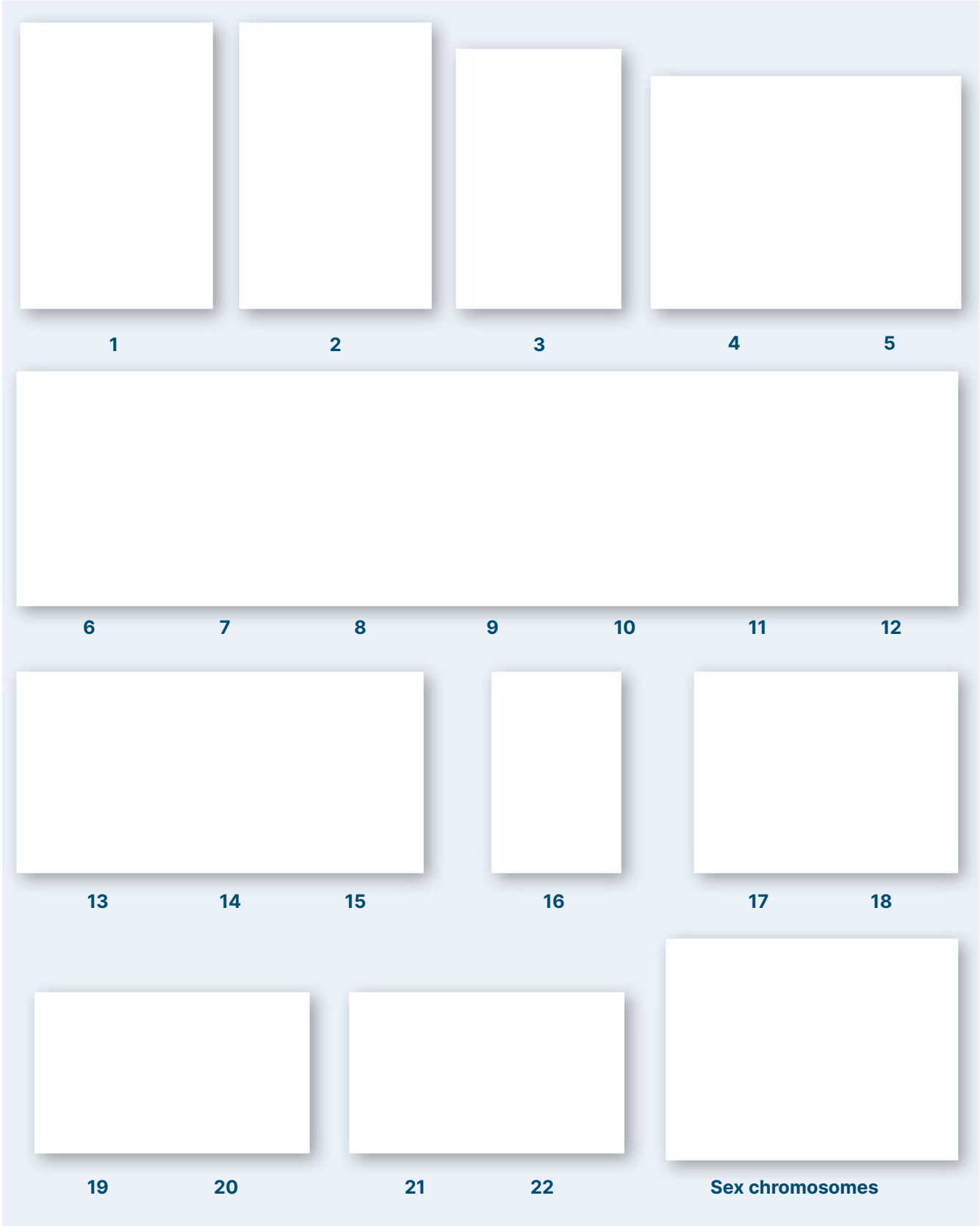
1. Cut out the chromosomes on page 213 and arrange them on the record sheet below in their homologous pairs.
2. (a) Determine the sex of this individual: **male** or **female** (circle one)

   (b) State whether the individual's chromosome arrangement is: **normal** or **abnormal** (circle one)

   (c) If the arrangement is abnormal, state in what way and name the syndrome displayed: _____

   _____



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119 Did You Get It?

1. Test your vocabulary by matching each term to its definition, as identified by its preceding letter code.

(i) aneuploidy ☐

(ii) karyogram ☐

(iii) karyotype ☐

(iv) non-disjunction ☐

(v) trisomy ☐

A The number and appearance of chromosomes in the nucleus of a eukaryotic cell.

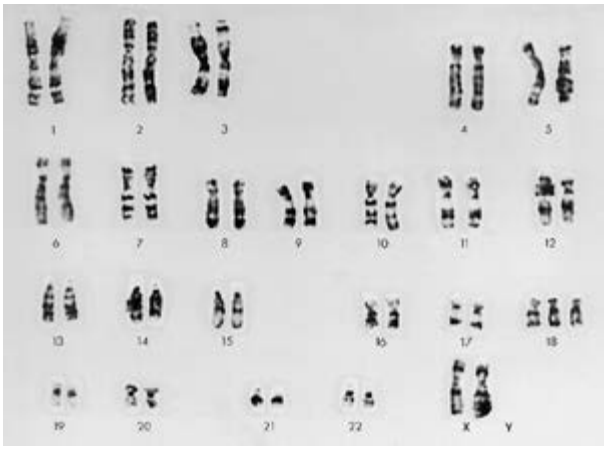
B Condition in which there is one extra chromosome in the body's cells.

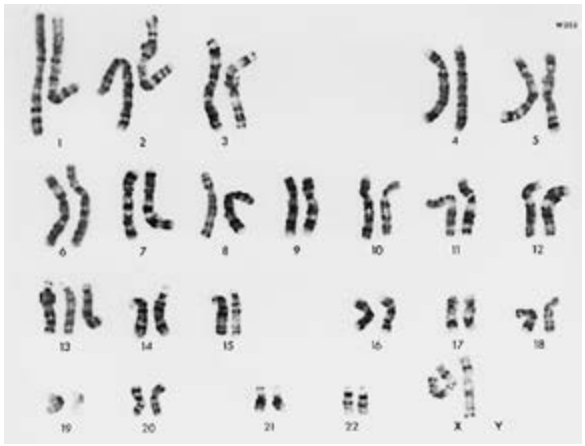
C The rearrangement of a micrograph of chromosomes into a standard image and format.

D The condition of having a chromosome number that is not an exact multiple of the normal diploid (2N) condition.

E An error during meiosis in which homologous chromosomes or sister chromatids do not separate correctly.

2. For each of the karyograms shown below, determine the sex of the individual, state whether the karyotype is normal/abnormal (circle any abnormality), and describe the abnormality if there is one.





i) Sex: _____ Normal / Abnormal

Abnormality: _____

ii) Sex: _____ Normal / Abnormal

Abnormality: _____

3. An original DNA sequence is shown right: **GCG TGA TTT GTA GGC GCT CTG**

For each of the following DNA mutations, state the type of mutation that has occurred:

(a) **GCG TGT TTG TAG GCG CTC TG** _____

(b) **GCG TGA TTT GTA AGG CGC TCT G** _____

(c) **GCG TGA TTT GGA GGC GCT CTG** _____

(d) **GCG TGA GTA GGC GCT CTG** _____

4. For the DNA sequence **G** G T C T C C G T A A T A T T show the effect of the following by writing the new DNA sequence (note: position one in the sequence starts with the bold **G** on the left hand side):

(a) A deletion of the T at position 5: _____

(b) A substitution of C at position 7 with A: _____

(c) A deletion of the bases from positions 10 - 12: _____

5. How do mutagens cause mutations? _____

_____

6. Explain how a mutation might cause a new phenotype: _____

_____

_____

_____

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Chapter 11 Unit 4 Topic 1

Inheritance

Resource Hub
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Key Terms

- allele
- codominance
- cross (genetic cross)
- dominant
- genotype
- heterozygous
- homozygous
- incomplete dominance
- locus
- multiple alleles
- multiple genes (=polygenes)
- pedigree chart
- phenotype
- probability
- Punnett square
- recessive
- sex linked gene
- trait
- X-linkage

Key Concepts

- Understand the principles of inheritance, including key terms: alleles, genotype, phenotype, and Punnett squares.
- Describe different inheritance patterns including autosomal dominance, incomplete dominance, codominance, and sex-linked traits.
- Use histograms to show continuous variation in polygenic phenotypes.
- Analyse pedigree charts to trace inheritance patterns and identify carriers or affected individuals.

Alleles and inheritance		Activity Number
☐ 1	Recall the difference between genes and alleles. Demonstrate understanding of the terms used in studying inheritance: allele, locus, trait, heterozygous, homozygous, genotype, phenotype, cross. Use symbols to represent genotypes and distinguish between alleles in genetic crosses.	120-122
☐ 2	Giving examples, distinguish between recessive and dominant traits for autosomal genes.	123
☐ 3	Understand the rules for calculating probability and apply them to predictions of the genotype and phenotype ratios of genetic crosses.	121
☐ 4	Describe non-Mendelian inheritance patterns, including incomplete dominance and co-dominance.	124, 125
☐ 5	Using an example, explain what is meant by a sex-linked gene. Describe the characteristics of X-linked inheritance of dominant traits and recessive traits. Explain how to distinguish X-linked from Y-linked inheritance.	126

Predicting inheritance		
☐ 6	Use Punnett squares to predict the frequencies of genotypes and phenotypes in crosses involving autosomal dominance. Give examples of human disorders that follow an autosomal dominant pattern of inheritance.	123, 127
☐ 7	Use Punnett squares to predict the frequencies of genotypes and phenotypes in crosses involving incomplete dominance. Describe the characteristics of this type of inheritance.	124
☐ 8	Use Punnett squares to predict the frequencies of genotypes and phenotypes in crosses involving codominance. Describe the characteristics of this type of inheritance.	125
☐ 9	Using an example, explain how multiple allele systems allow for many possible dominance relationships. Use Punnett squares to predict the frequencies of genotypes and phenotypes in crosses involving codominance of multiple alleles.	125
☐ 10	Use Punnett squares to predict the outcome of crosses involving sex-linked genes.	126
☐ 11	Predict the frequencies of genotypes and phenotypes for polygenic inheritance involving three genes. State how many phenotypes are expected in an F1 cross involving a three-gene polygenic system.	128
☐ 12	Investigate a polygenic phenotype (e.g height), using a histogram to display the frequency of traits.	128
☐ 13	Study and produce pedigree charts showing the inheritance of traits over generations.	129

120 Alleles

Key Idea: Eukaryotes generally have paired chromosomes. Each chromosome contains many genes and each gene may have a number of versions called alleles.

Sexually reproducing organisms usually have paired sets of **chromosomes**, one set from each parent. The equivalent chromosomes that form a pair are termed homologues. They carry equivalent sets of **genes**, but there is the potential for different versions of a gene (**alleles**) to exist in a population.

Homologous chromosomes

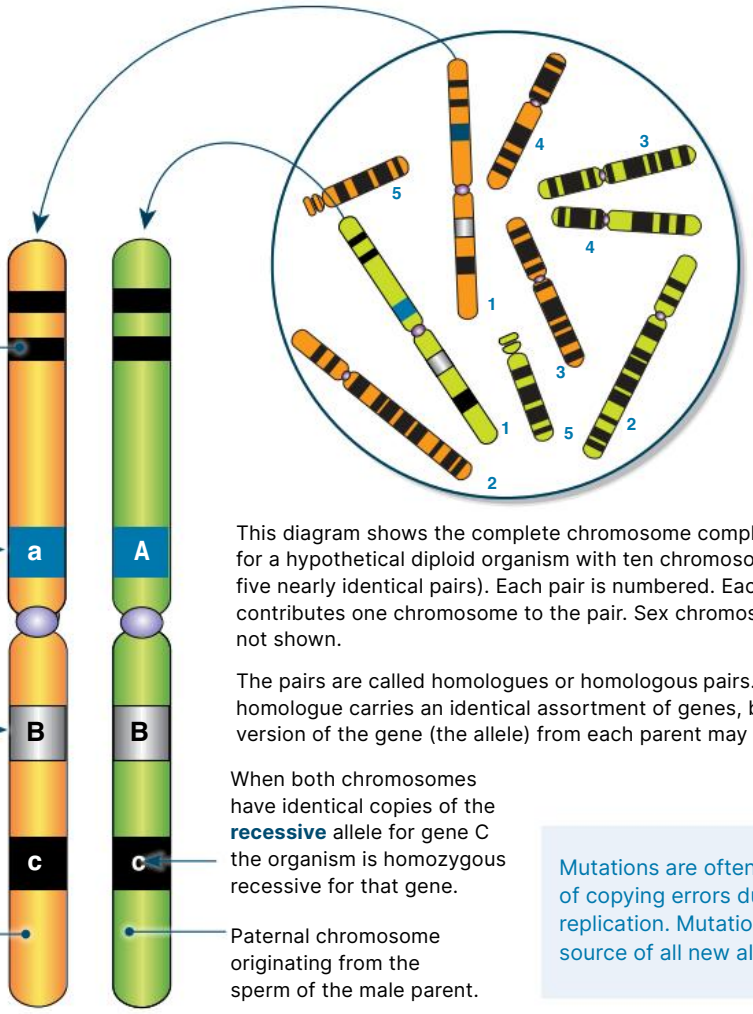
Most cells in sexually reproducing organisms have a homologous pair of **chromosomes** (one from each parent). Chromosomes are formed from **DNA** tightly wound around special proteins. This diagram shows the position of three different genes on the same chromosome that control three different **traits** (A, B and C).

A gene is the unit of heredity. Genes occupying the same **locus** or position on a chromosome code for the same phenotypic character (e.g. eye colour).

Having two different versions (alleles) of gene A is called the **heterozygous** condition. Only the **dominant** allele (A) will be expressed. Alleles differ by only a few bases.

When both chromosomes have identical copies of an allele, they are termed **homozygous**. If both alleles are the dominant allele for gene B the organism is homozygous dominant for that gene.

Maternal chromosome originating from the egg of the female parent.



This diagram shows the complete chromosome complement for a hypothetical diploid organism with ten chromosomes (as five nearly identical pairs). Each pair is numbered. Each parent contributes one chromosome to the pair. Sex chromosomes are not shown.

The pairs are called homologues or homologous pairs. Each homologue carries an identical assortment of genes, but the version of the gene (the allele) from each parent may differ.

When both chromosomes have identical copies of the **recessive** allele for gene C the organism is homozygous recessive for that gene.

Paternal chromosome originating from the sperm of the male parent.

Mutations are often the result of copying errors during DNA replication. Mutations are the source of all new alleles.

1. Define the following terms used to describe the allele combinations in the genotype for a given gene:

   (a) Heterozygous: _____

   (b) Homozygous dominant: _____

   (c) Homozygous recessive: _____

2. For a gene given the symbol 'A', name the alleles present in an organism that is identified as:

   (a) Heterozygous: _____ (b) Homozygous dominant: _____ (c) Homozygous recessive: _____

3. What is a homologous pair of chromosomes? _____

4. Discuss the significance of genes existing as alleles: _____

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121 Dominant and Recessive Traits

Key Idea: A phenotype refers to the observable characteristics of an organism. A variant of a phenotypic characteristic is a trait. Traits may result from dominant or recessive alleles.

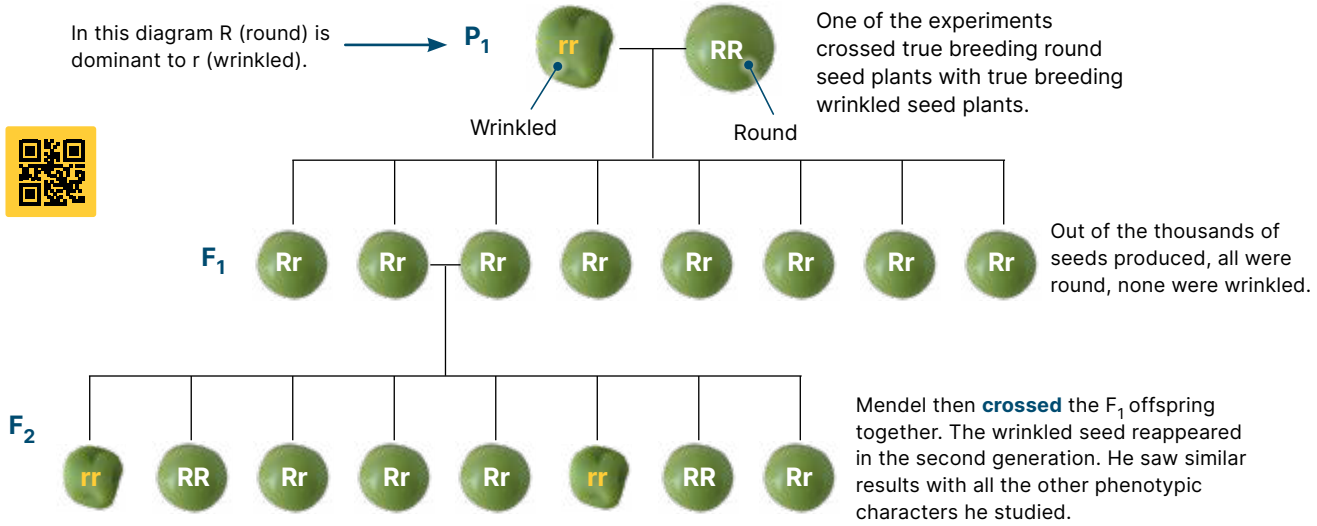
Traits are particular variants of phenotypic (observed physical) characters. For example, a phenotypic character is eye colour, a trait is blue eye colour. Traits may be controlled by one gene or many genes and can show continuous variation, e.g. height in humans, or discontinuous variation, e.g. flower colour in pea plants. What trait appears depends on the **alleles** present. **Dominant** alleles will produce a dominant trait. **Recessive** alleles will only produce a recessive trait if both alleles present are recessive.

Some of the best known experiments in **phenotypes** (appearance) are the experiments carried out by Gregor Mendel (right) on pea plants. During one of the experiments (shown below) he noticed how traits expressed in one generation disappeared in the second generation, but reappeared in the third generation. In his experiments, Mendel used true breeding plants. When self-crossed, true breeding organisms produce offspring with the same phenotypes as the parents.

Mendel's experiments

Mendel studied seven phenotypic characters of the pea plant:

- Flower colour (violet or white)
- Pod colour (green or yellow)
- Height (tall or short)
- Position of the flowers on the stem (axial or terminal)
- Pod shape (inflated or constricted)
- Seed shape (round of wrinkled)
- Seed colour (yellow or green)



How can this be explained?

Mendel was able to explain his observations in the following way:

- Traits are determined by a unit, which passes unchanged from parent to offspring (we now know these units are genes).
- Each individual inherits one unit (gene) for each trait from each parent (each individual has two units).
- Traits may not physically appear in an individual, but the units (genes) for them can still be passed to its offspring.

1. (a) Define a trait: _____

_____

_____

(b) Define true breeding: _____

_____

_____

2. (a) What was the ratio of smooth seeds to wrinkled seeds in the F_2 generation? _____

_____

(b) Why did the wrinkled seed trait not appear in the F_1 generation? _____

_____

_____

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Probability in genetics

Many events cannot be predicted with absolute certainty, however we can determine how likely it is that an event will happen. This calculated likelihood of an event occurring is called **probability**. The probability of an event ranges from 0 to 1. The sum of all probabilities equals 1.

In biology, probability is used to calculate the statistical significance of a difference between means or the probability of an event occurring, e.g. getting an offspring with a certain genotype and phenotype in a **genetic cross**s.

$$\text{Probability of an event happening} = \frac{\text{Number of ways it can happen}}{\text{Total number of outcomes}}$$

- Tossing a coin and predicting whether it will land heads (H) up or tails (T) up is a good example to illustrate probability.
- There are two possible outcomes; the coin will either land heads up or tails up, and only one outcome can occur at a time. Therefore the probability of a coin landing heads up is 1/2. The likelihood of a coin landing tails up is also 1/2.
- Remember probability is just an indication of how likely something will happen. Even though we predict that heads and tails will come up 50 times each if we toss a coin 100 times, it might not be exactly that.

3. Calculate the probability that a 6 will occur when you roll a single dice (die):

Diacritica cc 3.0

The rules for calculating probability

- Probability rules are used when we want to predict the likelihood of two events occurring together or when we want to determine the chances of one outcome over another.
- The rules are useful when we want to determine the probably of certain outcomes in genetic crosses, especially when large numbers of alleles are involved.
- The probability rule used depends on the situation.

PRODUCT RULE for independent events

For independent events, A & B, the probability (P) of them both occurring (A&B) = P(A) X P(B)

Example: If you roll two dice at the same time, what is the probability of rolling two sixes?

Solution: The probability of getting six on two dice at once is 1/6 × 1/6 = 1/36.

SUM RULE for mutually exclusive events

For mutually exclusive events, A & B, the probability (P) that one will occur (A or B) = P(A) + P(B)

Example: A single die is rolled. What are the chances of rolling a 2 **or** a 6?

Solution: P(A or B) = P(A) + P(B). 1/6 + 1/6 = 2/6 (1/3). There is a 1/3 chance that a 2 or 6 will be rolled.

4. In a cross Aa x Aa, use the sum rule to determine the probability of the offspring having a dominant phenotype:

5. Use the product rule to determine the probability of a first and second child born to the same parents both being boys?

6. In a cross of rabbits both heterozygous for genes for coat colour and length (BbLl x BbLl), determine the probability of the offspring being BbLl.
HINT: Calculate probabilities for Bb and Ll separately and then use the product rule. Test your calculation using the Punnett square (right).

7. In a cross of two individuals with various alleles of four unlinked genes: AaBbCCdd x AabbCcDd, explain how you would calculate the probability of getting offspring with the dominant phenotype for all four traits?

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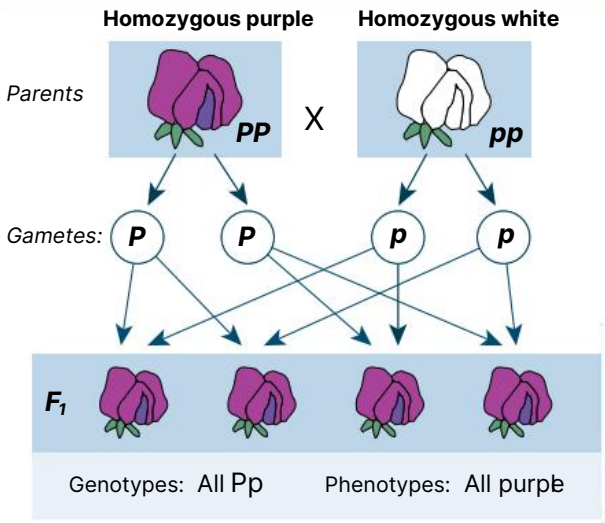
122 Basic Genetic Crosses

Key Idea: The outcome of a cross depends on the parental genotypes and can be predicted using Punnett squares.

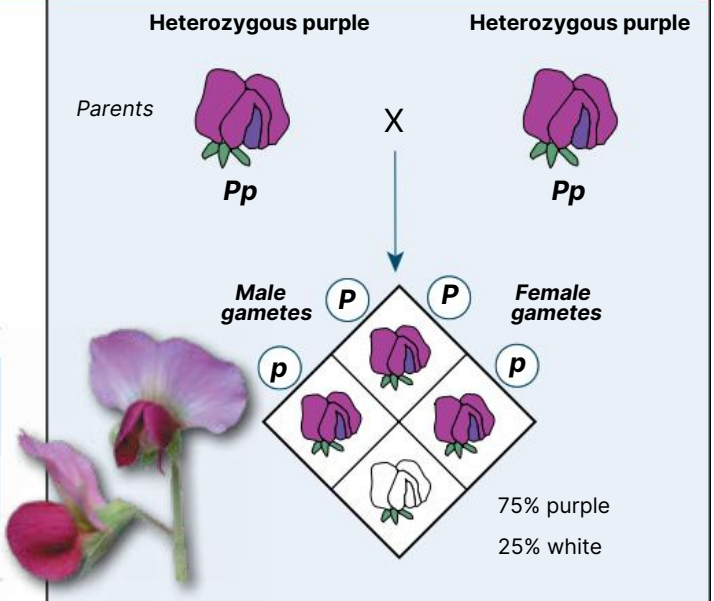
Examine the diagrams below on monohybrid (one gene) and dihybrid (two gene) inheritance. The F1 generation describes the offspring of a **cross** between true-breeding (**homozygous**) parents. A back cross is a cross between an offspring and one of its parents. If the back cross is to a homozygous **recessive**, it can be used as a test cross.

Monohybrid cross F_1



A true-breeding organism is homozygous for the gene involved. The F_1 offspring of a cross between two true breeding parent plants are all purple (Pp).

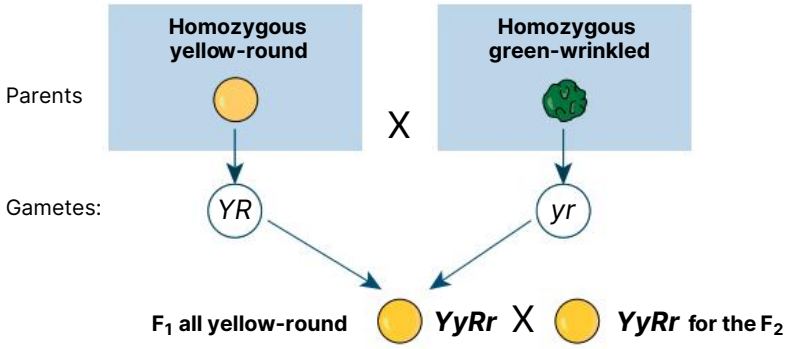
Monohybrid cross F_2



A cross between the F_1 offspring (Pp x Pp) would yield a 3:1 ratio in the F_2 of purple (PP, Pp, Pp) to white (pp).

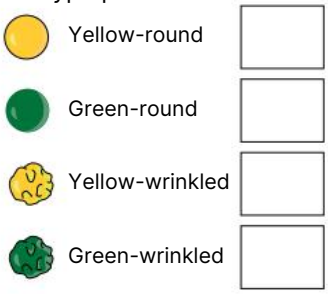
Dihybrid cross

A dihybrid cross studies the inheritance patterns of two genes. In pea seeds, yellow colour (Y) is dominant to green (y) and round shape (R) is dominant to wrinkled (r). Each true breeding parental plant has matching alleles for each of these characters (YYRR or yyrr). F_1 offspring will all have the same genotype and phenotype (yellow-round: YyRr).



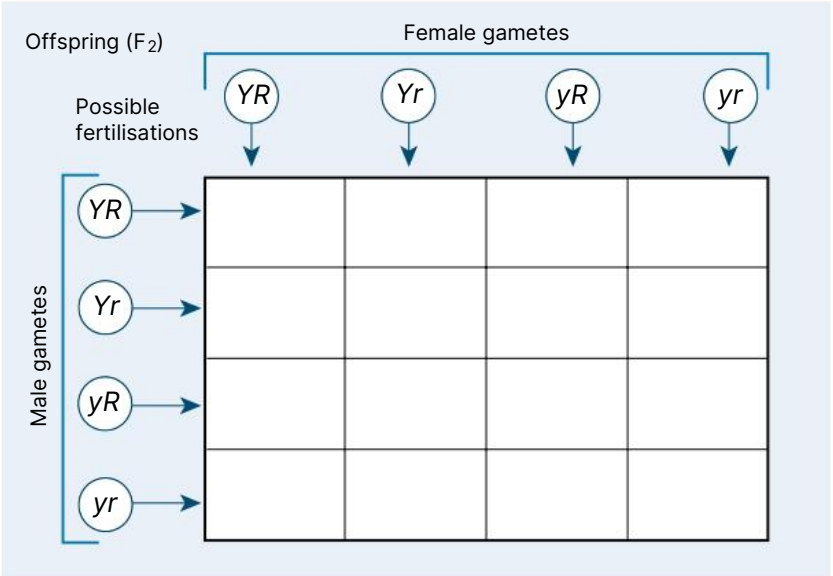
1. Fill in the Punnett square (below right) to show the genotypes of the F_2 generation.

2. In the boxes below, use fractions to indicate the numbers of each phenotype produced from this cross.



3. Express these numbers as a ratio:

_____



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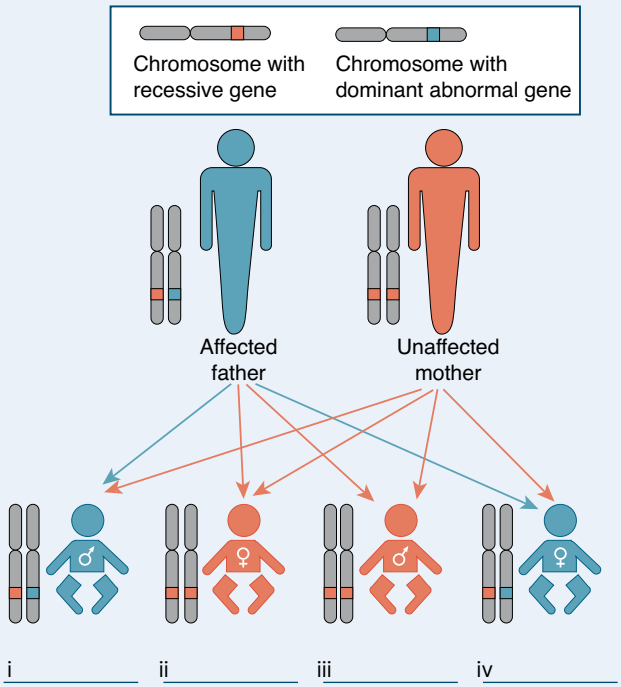
123 Autosomal Inheritance

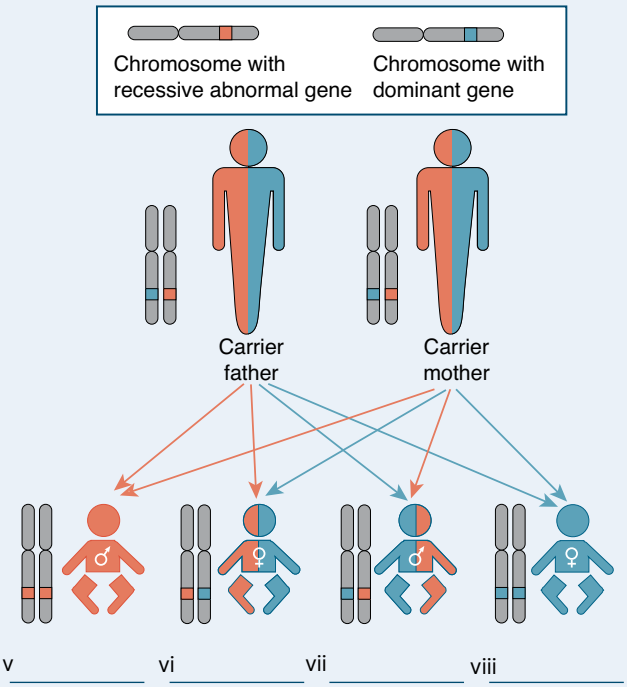
Key Idea: Autosomal dominant traits are always expressed regardless of whether there is one or two copies of the allele. An autosomal gene refers to a gene that is carried on an autosome (not a sex chromosome). A **dominant allele** will always be expressed in the **phenotype** regardless of whether it exists in the **homozygous** (two copies) or the **heterozygous** (one copy) condition. For alleles that cause a recognisable disease, an autosomal dominant condition is easily recognised because people with only one copy of the allele will be affected. This is the case with the most common form of polycystic kidney disease (ADPKD) condition. Its inheritance pattern is shown below left. A less common form of the disease is inherited only when a person carries two copies of a mutation to a related gene (below right).

Autosomal dominant inheritance



Example: Autosomal Dominant PKD (ADPKD)
Mutation to PKD1 or PKD2 genes.

Autosomal recessive inheritance



Example: Autosomal Recessive PKD (ARPKD)
Mutation to PKDH1 gene.

1. Explain the inheritance pattern of an autosomal dominant allele: _____

2. Fill in the spaces (i-viii) in the diagram above to identify the children as **affected**, **carrier**, or **unaffected**. A carrier carries the mutated allele but does not show any symptoms of the disease.

3. The diagram above left shows inheritance when the father is heterozygous for the affected allele. Describe what the phenotype of the offspring would be if the father had been homozygous for the affected allele:

4. Contrast the pattern of inheritance for an autosomal dominant and an autosomal recessive condition:

5. Some diseases caused autosomal dominant alleles, such as Huntington's disease, do not become apparent until well into adulthood. Suggest how this might explain why such diseases persist in the population:

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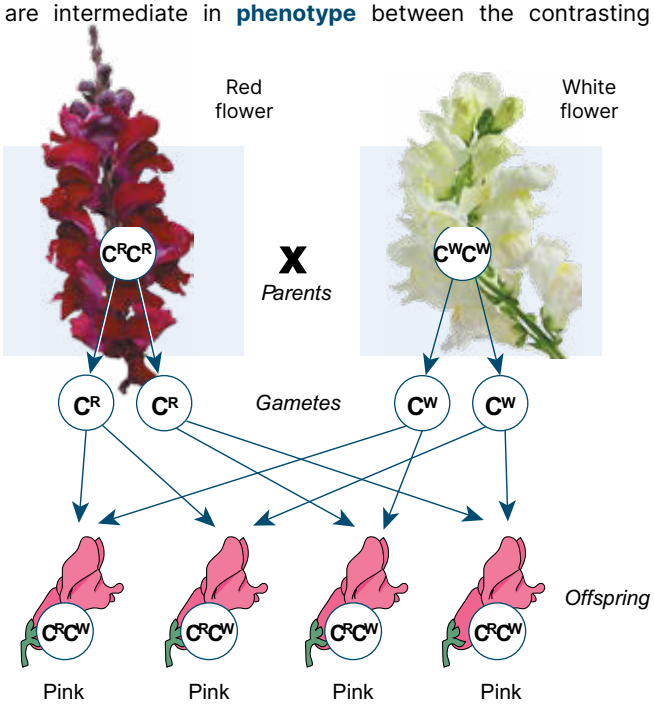
124 Incomplete Dominance

Key Idea: Incomplete dominance describes the situation where the action of one allele does not completely mask the action of the other and neither allele shows dominance in determining the trait.

In **incomplete dominance** the **heterozygous** offspring are intermediate in **phenotype** between the contrasting **homozygous** parental phenotypes. In **crosses** involving incomplete dominance, the phenotype and **genotype** ratios are identical. The phenotype of heterozygous offspring results from the partial influence of both **alleles**. Examples of incomplete dominance includes flower colour in snapdragons (*Antirrhinum*) and four o'clocks (*Mirabilis*) (below).



Pure breeding snapdragons produce red or white flowers (left). When red and white-flowered parent plants are crossed, a pink-flowered offspring is produced. If the offspring (F_1 generation) are then crossed together, all three phenotypes (red, pink, and white) are produced in the F_2 generation.

Four o'clocks (above) are also known to have flower colours controlled by alleles that show incomplete dominance. Pure breeding four o'clocks produce crimson, yellow or white flowers. Crimson flowers (above) crossed with yellow flowers produced reddish-orange flowers, while crimson flowers crossed with white flowers produce magenta (reddish-pink) flowers.

1. Explain how incomplete dominance of alleles differs from complete dominance: _____

_____

_____

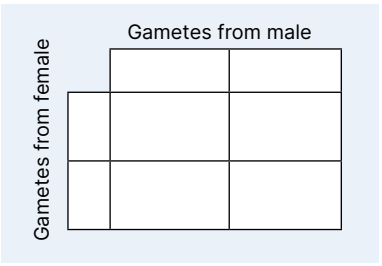
_____

2. A plant breeder wanted to produce snapdragons for sale that were only pink or white (i.e. no red). Determine the phenotypes of the two parents necessary to produce these desired offspring. Use the Punnett square (right) to help you:

_____

_____

_____



3. Another plant breeder crossed two four o'clocks, known to have its flower colour controlled by alleles that show incomplete dominance. Pollen from a magenta flowered plant was placed on the stigma of a crimson flowered plant.

   (a) Fill in the spaces on the diagram on the right to show the genotype and phenotype for parents and offspring.

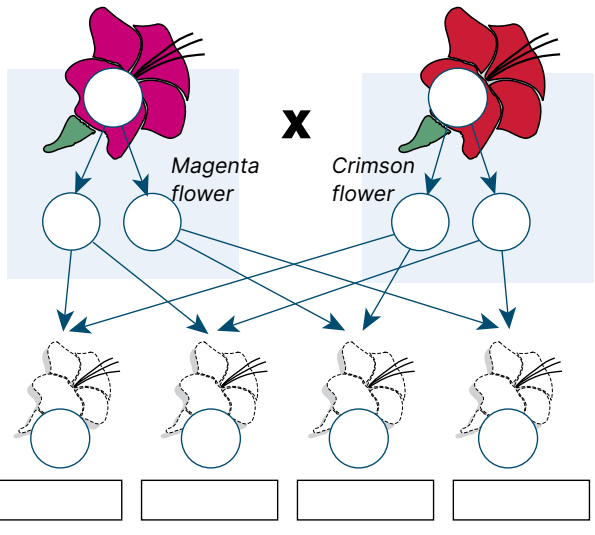
   (b) State the phenotype ratio:

_____

_____

_____

_____



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- In its normal form, the MSTN **gene** produces an enzyme that inhibits muscle growth. The mutated form does not operate correctly and mammals with this mutation exhibit enhanced muscle development (called double muscling).
- This **trait** has been used to breed Belgian blue cattle (right) for beef production.
- The MSTN gene displays incomplete dominance. Heterozygous cattle also have enhanced muscle development, while cattle homozygous for the mutant gene show even greater muscle development, to the extent that giving birth is difficult for female cattle.
- Because of this, many breeders opt for cross breeding full Belgian blues with other cattle breeds to produce a manageable increase in muscle growth.

4. (a) A cattle breeder crosses a bull homozygous for double muscling ($M^D M^D$) with a heterozygous cow ($M^D M$). What is the probability that the calf will be heterozygous?

(b) What should the breeder do if a 100% chance of producing heterozygous calves is required?

- A dog's coat colour is governed by at least eight genes and coat texture by at least four genes, most of which have **multiple alleles**. These genes produce all the coat types and colours seen in dogs.
- The gene producing the merle (M) pattern shows incomplete dominance and is associated with a mottled coat pattern. The **genotype** MM gives a very light, almost white merle pattern but can produce serious health defects including problems with sight and hearing. The homozygous genotype mm produces a normal (not merle) coat pattern. Mm produces the merle pattern, but no serious health effects.

mm **Mm** **MM**

5. A breeder wants to produce dogs with merle coats but wants to avoid both using dogs and producing puppies that are homozygous for the merle gene (MM). Explain how the breeder can do this in one cross, and provide the genotype/phenotype probabilities of the puppies:

6. A puppy is born with a merle coat (genotype Mm). What is the probability that only one of the parents had the Mm genotype as well? Use the space below for working:

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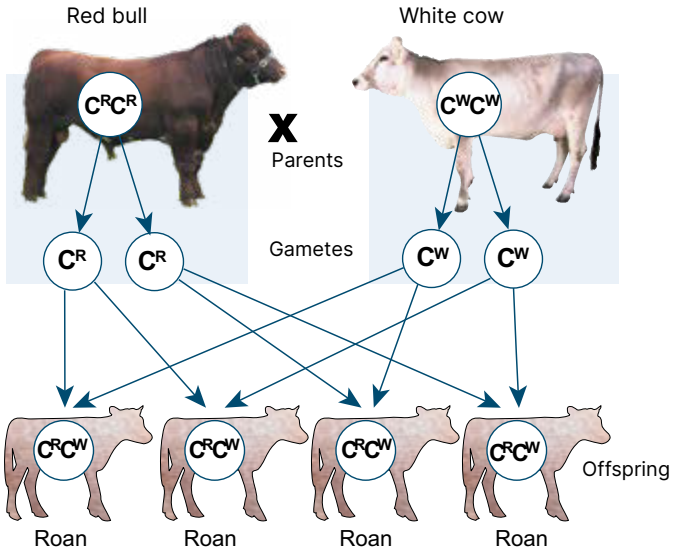
125 Codominance

Key Idea: In the inheritance of codominant alleles, neither allele is recessive. Both alleles are equally and independently expressed in the heterozygote.

Codominance is an inheritance pattern in which both **alleles** in a heterozygote contribute to the **phenotype** and both alleles are independently and equally expressed. Examples include the human blood group AB and certain coat colours in horses and cattle. Reddish coat colour is equally **dominant** with white. Animals that have both alleles have coats that are roan (both red and white hairs are present).



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In the shorthorn cattle breed, coat colour is inherited. White shorthorn parents always produce calves with white coats. Red parents always produce red calves. However, when a red parent mates with a white one, the calves have a coat colour that is different from either parent: a mixture of red and white hairs, called roan. Use the example (left) to help you to solve the problems below.

1. Explain how codominance of alleles can result in offspring with a phenotype that is different from either parent:

_____

2. A white bull is mated with a roan cow (right):

   (a) Fill in the spaces to show the genotypes and phenotypes for parents and calves:

   (b) What is the phenotype ratio for this cross?

   _____

   (c) How could a cattle farmer control the breeding so that the herd ultimately consisted of only red cattle:

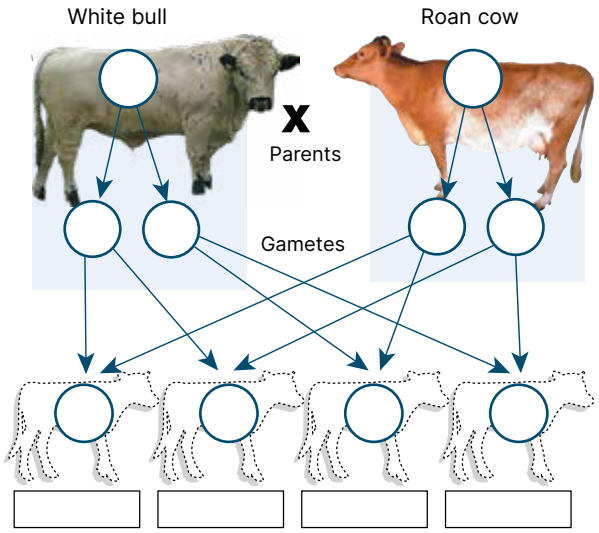
   _____

   _____

   _____

   _____

   _____



3. A farmer has only roan cattle on his farm. He suspects that one of the neighbours' bulls may have jumped the fence to mate with his cows earlier in the year because half the calves born were red and half were roan. One neighbour has a red bull, the other has a roan.

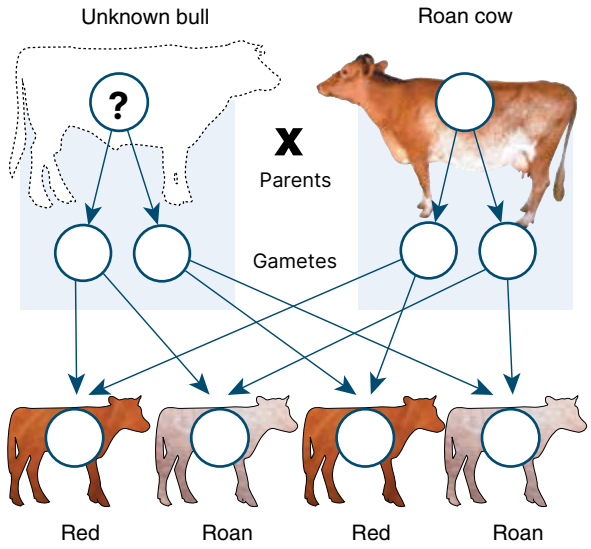
   (a) Fill in the spaces (right) to show the genotype and phenotype for parents and calves.

   (b) Which bull serviced the cows, red or roan? _____

4. Describe the classical phenotypic ratio for a codominant gene resulting from the cross of two heterozygous parents (e.g. a cross between two roan cattle):

   _____

   _____



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- The human ABO blood group system also shows codominance. The four common blood groups of the human 'ABO blood group system' are determined by three alleles: A, B, and O. The ABO antigens consist of sugars attached to the surface of red blood cells. The alleles code for enzymes (proteins) that join these sugars together.
- The allele O is **recessive**. It produces a non-functioning enzyme that cannot make any changes to the basic sugar molecule.
- The other two alleles (A, B) are codominant and are expressed equally. They each produce a different functional enzyme that adds a different, specific sugar to the basic sugar molecule.
- The blood group A and B antigens are able to react with antibodies present in the blood of other people so blood must always be matched for transfusion.

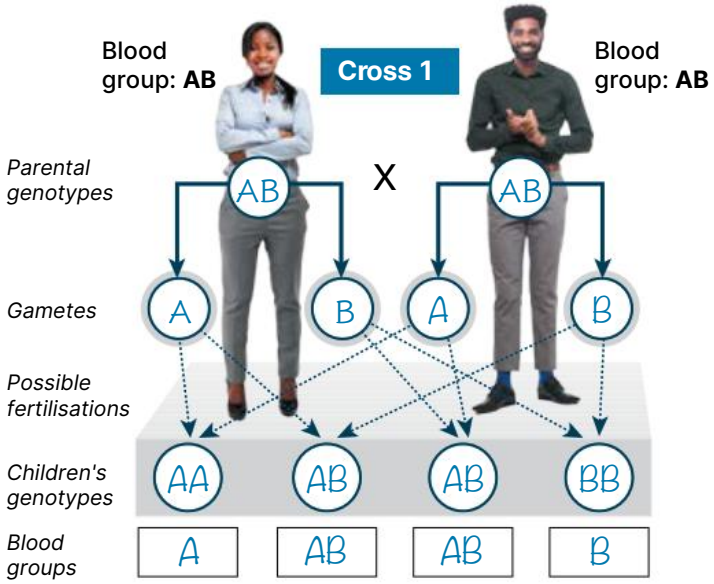
Recessive allele: ***O*** produces a non-functioning protein
Dominant allele: ***A*** produces an enzyme which forms **A antigen**
Dominant allele: ***B*** produces an enzyme which forms **B antigen**

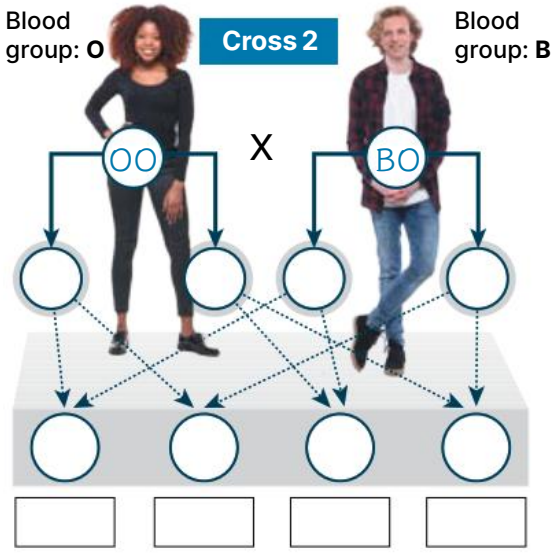
If a person has the AO allele combination then their blood group will be group A. The presence of the recessive allele has no effect on the blood group in the presence of a dominant allele. Another possible allele combination that can create the same blood group is AA.

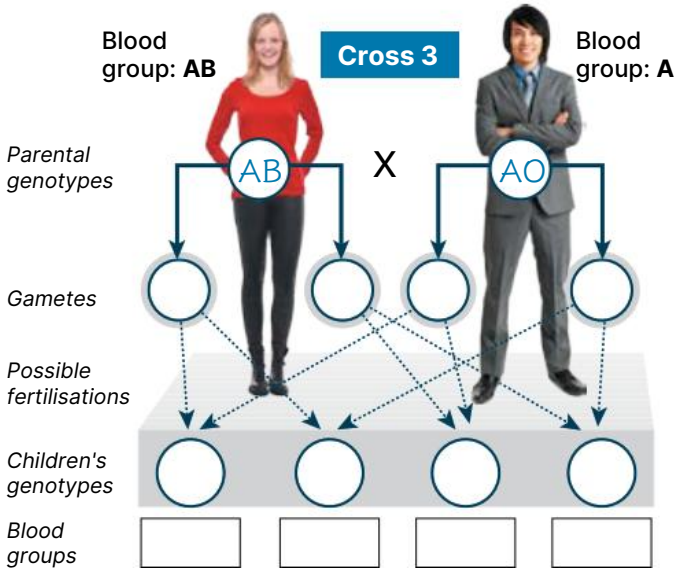
Blood group (phenotype)	Possible genotypes	Frequency in Australia
O	OO	49%
A	AA AO	38%
B		10%
AB		3%

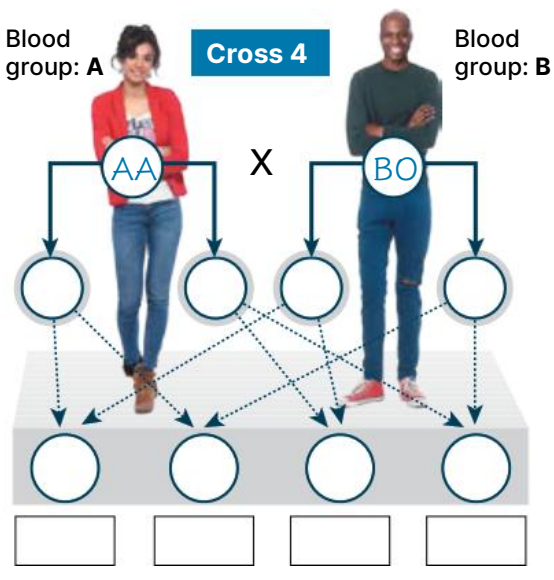
5. Use the information above to complete the table for the possible genotypes for blood group B and group AB.

6. Below are four crosses possible between couples of various blood group types. The first example has been completed for you. Complete the genotype and phenotype for the other three crosses below:









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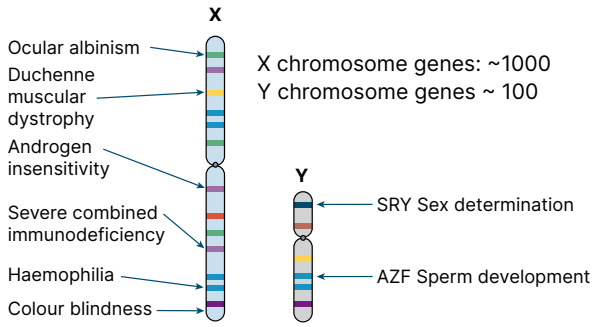
126 Sex Linkage

Key Idea: Many genes on the X chromosome do not have a match on the Y chromosome. In males, which are XY, a recessive allele on the X chromosome will be expressed.

Sex linkage refers to the way genes on the sex **chromosomes** are inherited and expressed. In humans, the sex chromosomes are X and Y, but sex linkage usually involves genes on the X chromosome, which has many more **genes** than the Y chromosome. **X-linked** recessive **traits** are usually seen only in males (XY) and occur rarely in the females (XX) because females may be **heterozygous** (carriers). X-linked dominant traits do not necessarily affect males more than females. In humans, recessive **sex linked genes** are responsible for a number of heritable disorders in males. Y-linked disorders are rare and usually associated with infertility.

Sex linkage

- Sex linkage refers to the way genes on the sex chromosomes are inherited and expressed. In humans, the sex chromosomes are X and Y, but sex linkage usually involves genes on the X chromosome, which has many more genes than the Y chromosome.
- X-linked **recessive traits** are usually seen only in males (XY) and occur rarely in the females (XX) because females may be heterozygous (carriers). X-linked **dominant** traits do not necessarily affect males more than females. In humans, recessive sex linked genes are responsible for a number of heritable disorders in males. Y-linked disorders are rare and usually associated with infertility.



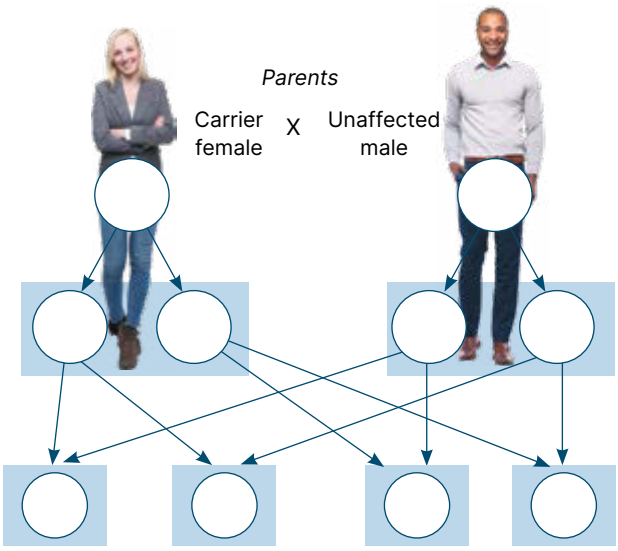
Genetic comparison of X and Y chromosomes

1. Explain why sex linked conditions are more likely linked to alleles on the X chromosome than on the Y chromosome:

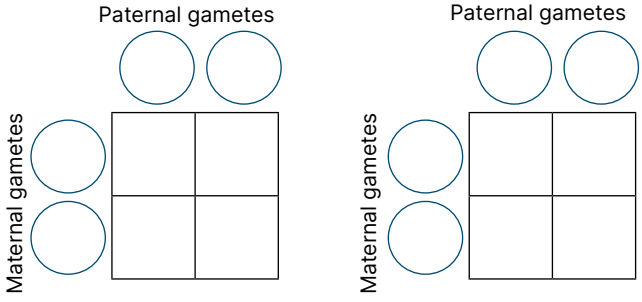
- Haemophilia is a recessive disorder linked to the X-chromosome that results in ineffective blood clotting when a blood vessel is damaged. The most common type, haemophilia A, occurs in 1 in 5000 male births. Any male who carries the gene will express the **phenotype**. Haemophilia is extremely rare in women.

2. A couple wishes to have children. The woman knows she is a carrier for haemophilia. The man is not a haemophiliac. Use the notation X^h for haemophilia and X^H for the dominant allele to complete the diagram on the right including the parent genotypes, gametes and possible fertilisations. Write the genotypes and phenotypes in the table below.

	Genotypes	Phenotypes
Male children		
Female children		



3. A second couple also wishes to have children. The woman knows her maternal grandfather was a haemophiliac, but neither her mother or father were. Determine the probability she is a carrier (X^HX^h) Use the Punnett squares, right, to help you:



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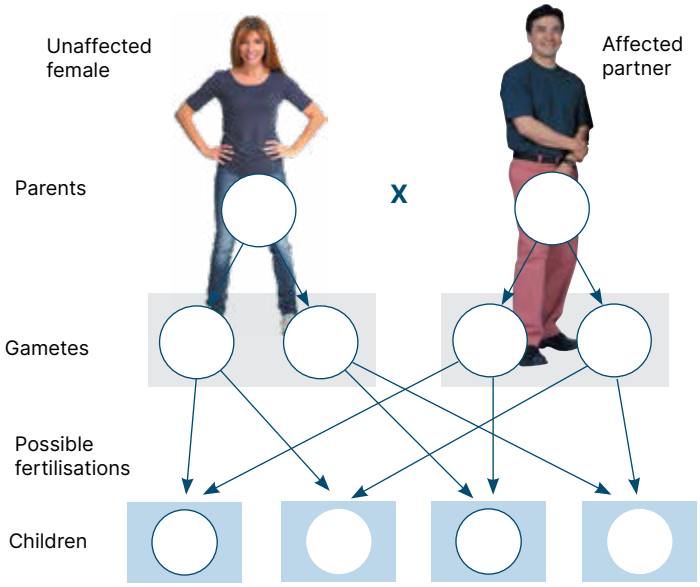
Dominant allele in humans

A rare form of rickets in humans is determined by a dominant allele of a gene on the X chromosome (it is not found on the Y chromosome). This condition is not successfully treated with vitamin D therapy. The allele types, **genotypes**, and **phenotypes** are as follows:

Allele types		Genotypes		Phenotypes
X^R	= affected by rickets	X^RX^R, X^RX	=	Affected female
X	= normal	X^RY	=	Affected male
		XX, XY	=	Unaffected female, male

As a genetic counsellor you are presented with a married couple where one of them has a family history of this disease. The husband is affected by this disease and the wife is not. The couple, who are thinking of starting a family, would like to know what their chances are of having a child born with this condition. They would also like to know what the probabilities are of having an affected boy or affected girl. Use the symbols above to complete the diagram right and determine the probabilities stated below (expressed as a proportion or percentage).



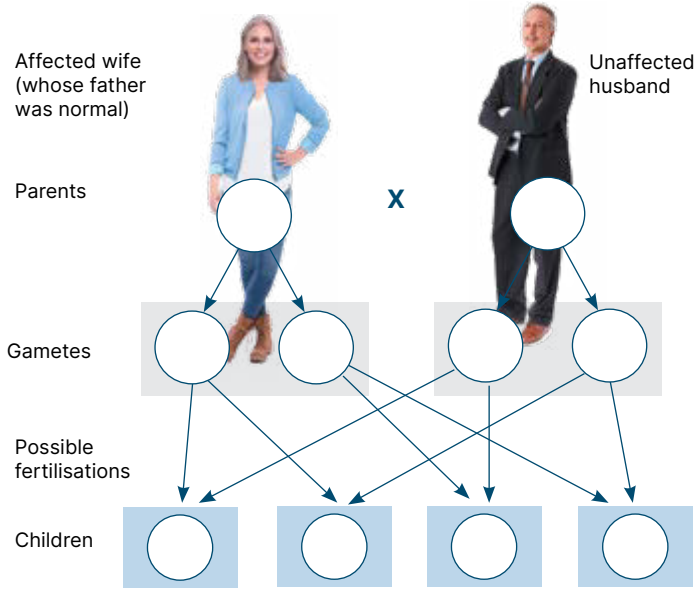
4. Determine the probability of having:

   (a) Affected children: _____

   (b) An affected girl: _____

   (c) An affected boy: _____

Another couple with a family history of the same disease also come in to see you to obtain genetic counselling. In this case, the husband is unaffected and the wife is affected. The wife's father was not affected by this disease. Determine what their chances are of having a child born with this condition. They would also like to know what the probabilities are of having an affected boy or affected girl. Use the symbols above to complete the diagram right and determine the probabilities stated below (expressed as a proportion or percentage).



5. Determine the probability of having:

   (a) Affected children: _____

   (b) An affected girl: _____

   (c) An affected boy: _____

6. Why are males much more likely to inherit X-linked recessive disorders than females? _____

_____

_____

_____

7. From what you know about sex linkage, what two features could you use to detect a Y-linked disorder in a pedigree?

   (a) _____

   (b) _____

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127 Inheritance Patterns

Key Idea: Sex-linked traits and autosomal traits have different inheritance patterns.

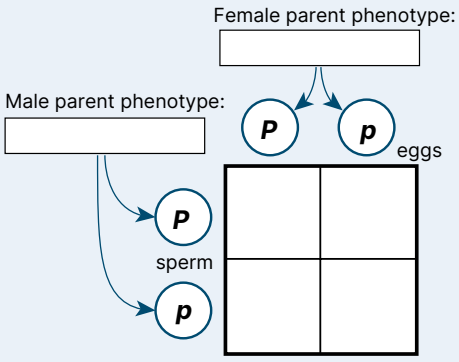
Complete the following monohybrid **crosses** for different types of inheritance patterns in humans: autosomal **recessive**, autosomal **dominant**, **sex linked** recessive, and sex-linked dominant inheritance.

1. **Inheritance of autosomal recessive traits**
   Example: Albinism
   Albinism (lack of pigment in hair, eyes and skin) is inherited as an autosomal recessive allele (not sex-linked).
   Using the codes: PP (normal) Pp (carrier)
   pp (albino)
   (a) Enter the parent phenotypes and complete the Punnett square for a cross between two carrier genotypes.

   (b) Give the ratios for the phenotypes from this cross.

   Phenotype ratios: _____

   _____

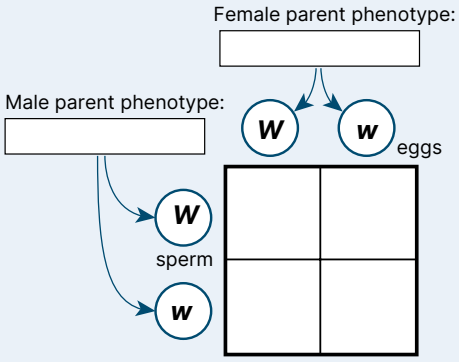


2. **Inheritance of autosomal dominant traits**
   Example: Woolly hair
   Woolly hair is inherited as an autosomal dominant allele. Each affected individual will have at least one affected parent.
   Using the codes: WW (woolly hair)
   Ww (woolly hair, heterozygous)
   ww (normal hair)
   (a) Enter the parent phenotypes and complete the Punnett square for a cross between two heterozygous individuals.

   (b) Give the ratios for the phenotypes from this cross.

   Phenotype ratios: _____

   _____

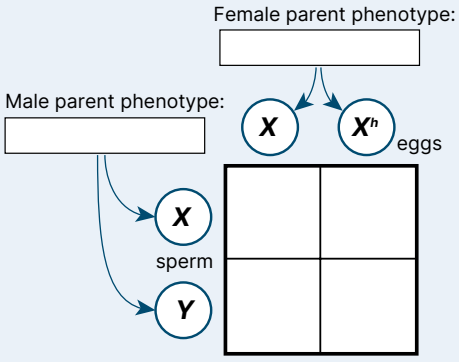


3. **Inheritance of sex linked recessive traits**
   Example: Haemophilia
   Inheritance of haemophilia is sex linked. Males with the recessive (haemophilia) allele, are affected. Females can be carriers.
   Using the codes: XX (unaffected/normal female)
   X^hX (carrier female)
   X^hX^h (haemophiliac female)
   XY (unaffected/normal male)
   X^hY (haemophiliac male)
   (a) Enter the parent phenotypes and complete the Punnett square for a cross between an unaffected male and a carrier female.

   (b) Give the ratios for the phenotypes from this cross.

   Phenotype ratios: _____

   _____

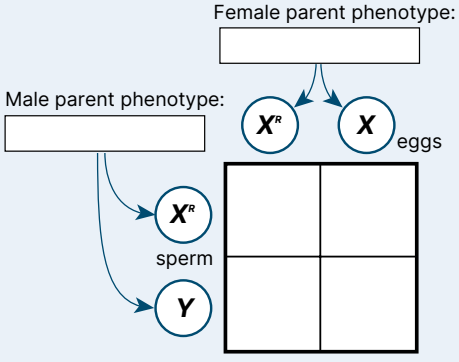


4. **Inheritance of sex linked dominant traits**
   Example: Sex linked form of rickets
   A rare form of rickets is inherited on the X chromosome.
   Using the codes: XX (unaffected female); XY (unaffected male)
   X^RX (affected heterozygote female)
   X^RX^R (affected female)
   X^RY (affected male)
   (a) Enter the parent phenotypes and complete the Punnett square for a cross between an affected male and heterozygous female.

   (b) Give the ratios for the phenotypes from this cross.

   Phenotype ratios: _____

   _____



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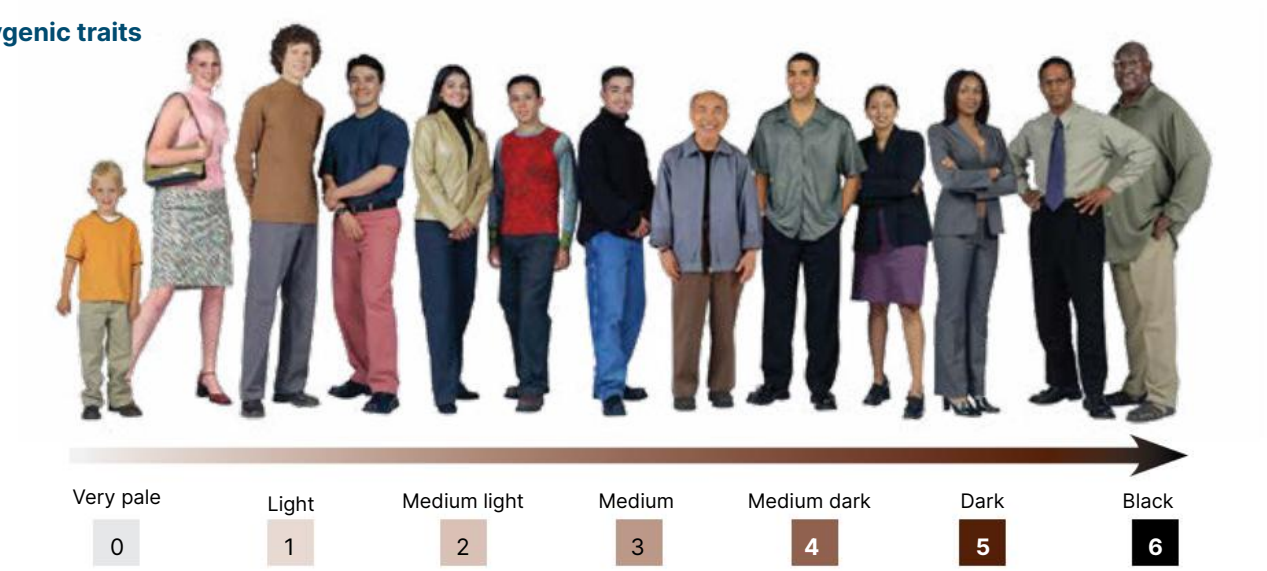
128 Polygenes

Key Idea: Many phenotypes are affected by multiple genes.

Many **phenotypes** are controlled by more than one **gene**. This is called polygeny or polygenic inheritance. As phenotype is controlled by many genes and alleles, a large range is possible. Combined with environmental effects, this produces continuous variation within the population. Two examples in humans are skin colour and height.

Polygenic traits



Polygenic **traits** are usually identified by:

- Traits are usually quantified by measuring rather than counting.
- Two or more genes contribute to the phenotype.
- Phenotypic expression is over a wide range (often in a bell shaped curve).
- Polygenic phenotypes include skin colour, height, eye colour, and weight.

Multiple genes *(many genes contributing to a phenotype) are quite different to* **multiple alleles** *(many alleles present in the population for one phenotypic characteristic).*

It is estimated that skin colour is controlled by at least eight genes (probably more). There are various ways to compare skin colour. One is shown above, in which there are seven shades ranging from very pale to very dark. Most individuals are somewhat intermediate in skin colour.

The table (right) shows a cross between three genes involved in skin colour, A, B, and C, each with two alleles (AaBbCc x AaBbCc). This is sufficient to give the seven shades of skin colour shown above. The shaded boxes indicate their effect on skin colour when combined. No dominant allele results in a lack of dark pigment (aabbcc). Full pigmentation (black) requires six dominant alleles (AABBCC). Note that for three genes with two alleles each there are $2^3 \times 2^3 = 8 \times 8 = 64$ possible **genotypes**.

Gametes	ABC	ABc	AbC	Abc	aBC	aBc	abC	abc
ABC	AABB CC	AABB Cc	AABb CC	AABb Cc	AaBB CC	AaBB Cc	AaBb CC	AaBb Cc
ABc	AABB Cc	AABB cc	AABb Cc	AABb cc	AaBB Cc	AaBB cc	AaBb Cc	AaBb cc
AbC	AABb CC	AABb Cc	AAbb CC	AAbb Cc	AaBb CC	AaBb Cc	Aabb Cc	Aabb Cc
Abc	AABb Cc	AABb cc	AAbb Cc	AAbb cc	AaBb Cc	AaBb cc	Aabb Cc	Aabb cc
aBC	AaBB CC	AaBB Cc	AaBb CC	AaBb Cc	aaBB CC	aaBB Cc	aaBb CC	aaBb Cc
aBc	AaBB Cc	AaBB cc	AaBb Cc	AaBb cc	aaBB Cc	aaBB cc	aaBb Cc	aaBb cc
abC	AaBb CC	AaBb Cc	Aabb CC	Aabb Cc	aaBb CC	aaBb Cc	aabb CC	aabb Cc
abc	AaBb Cc	AaBb cc	Aabb Cc	Aabb cc	aaBb Cc	aaBb cc	aabb Cc	aabb cc

1. (a) What is polygeny? _____

_____

(b) How does polygeny contribute to continuous variation? _____

_____

_____

2. Study the cross between the A, B, and C genes above. Write down the frequencies of the seven phenotypes (0-6):

_____

_____

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Investigation 11.1 Measuring continuous variation

See appendix for equipment list.

1. Choose one variable which occurs as a result of continuous variation (e.g. height, weight, hand span, or foot length) and write the variable you will be investigating here:
2. Select 30-50 classmates to be your sample. Measure the variable of interest (to one decimal place) and record the results in the space for raw data below.
3. Decide on appropriate frequency for the data, then record it as a tally chart in the space below.

Raw data

Tally chart

4. Summarise the features of your data in the table (right). You can enter your data on a spreadsheet to make it easier to calculate if you want.
5. Plot the tally chart data as a histogram on the grid (next page).

Number of entries
Sum
Mean
Standard deviation

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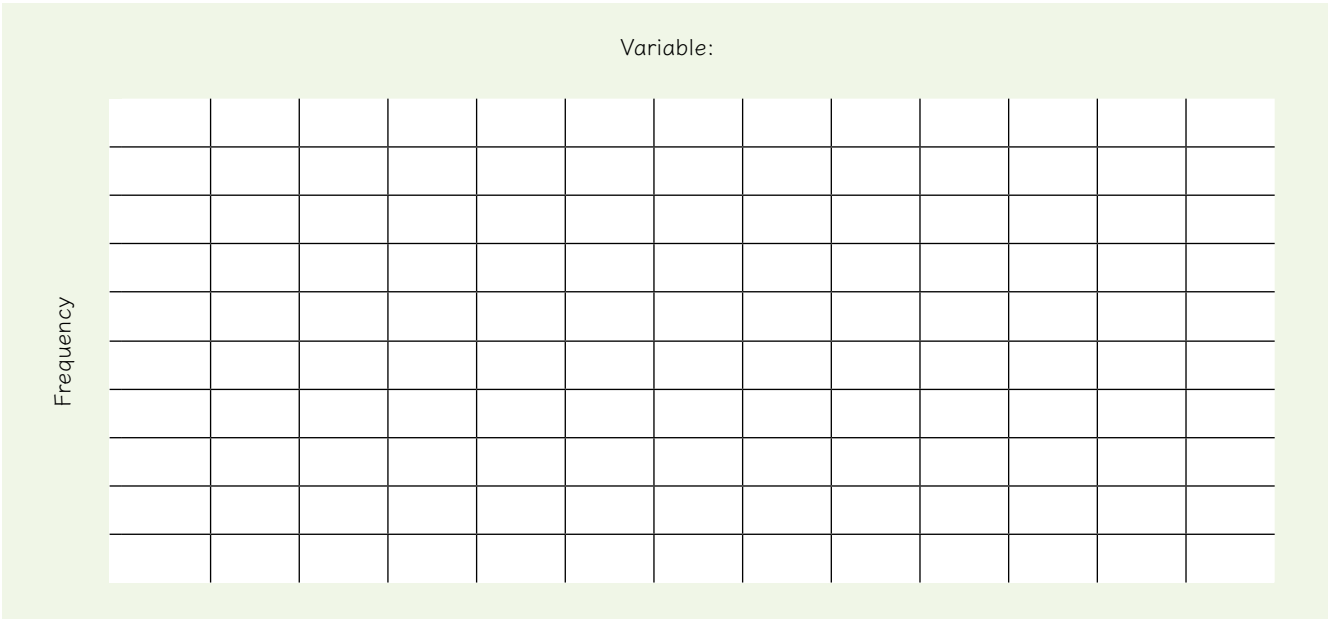

3. (a) Describe the pattern of the distribution shown in your graph: _____

(b) What is the genetic basis of this distribution? Give a brief explanation of what this means:

(c) What is the importance of a large sample size when gathering data relating to a continuous variable?

4. Explain the differences between continuous and discontinuous variation, giving examples to illustrate your answer:

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129 Pedigree Analysis

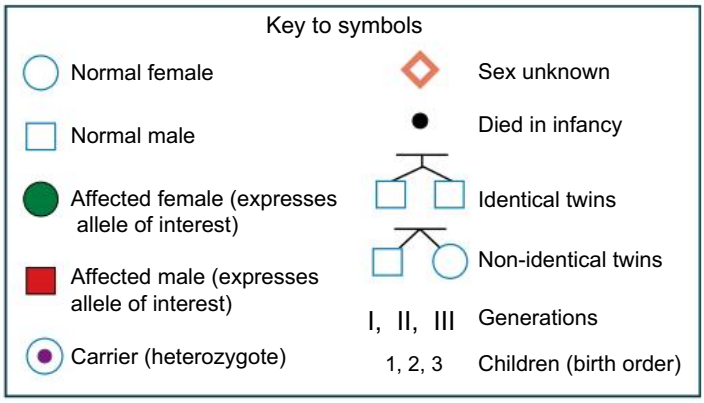
Key Idea: Pedigree charts are a way to graphically illustrate inheritance patterns over a number of generations.

One way in which to analyse the family history of an observable **trait** is to use a **pedigree chart**, which follows certain rules and uses particular symbols to indicate the sex and **genotype** of individuals across generations.

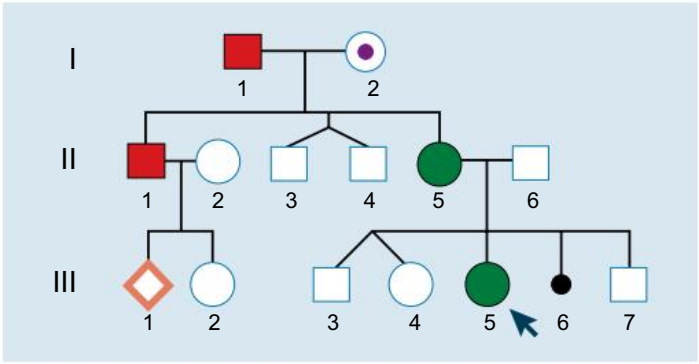
Pedigree charts

A pedigree chart is a diagram that shows the occurrence of a particular **gene** or trait from one generation to the next. In humans, pedigree charts are often used to analyse the inheritance of heritable conditions. In domestic animals, pedigree charts are often used to trace the inheritance of traits in selective breeding programs.

Pedigree charts use symbols to indicate an individual's particular traits. The key (right) explains the meaning of the symbols. Particular individuals are identified by their generation number and their order in that generational row. For example, **II-6** is the sixth person in the second generation. The arrow indicates the person through whom the pedigree was discovered (i.e. reported the condition).



The chart on the right represents three generations: grandparents (I-1 and I-2) with three sons and one daughter. Two of the sons (II-3 and II-4) are identical twins, but did not have any children. The other son (II-1) had a daughter and another child (sex unknown). The daughter (II-5) had two sons and two daughters, plus a child that died in infancy. Pedigrees can also indicate if a trait shows autosomal or **sex linked** inheritance. In autosomal patterns, both males and females are generally equally affected (more or less).



For the particular trait being studied, the grandfather was expressing the **phenotype** (showing the trait) and the grandmother was a carrier. One of their sons and one of their daughters also show the trait, together with one of their granddaughters (arrow).

1. (a) Very few traits are truly monogenic (controlled by a single gene). Most traits that behave in a monogenic way are in fact the outcome of multiple linked-genes inherited as one unit, effectively acting as a single gene. The ability to taste phenylthiocarbamide or PTC is one such trait. PTC is an organic molecule that for some people tastes very bitter, and for others is tasteless. The ability to taste PTC follows a very strong dominant/recessive inheritance pattern. The ability to taste PTC (T) is dominant to not tasting (t).

   A PTC tasting man (A), whose mother is a nontaster and whose father is a taster, marries a nontasting woman (B) whose parents both PTC tasters. They have a daughter who is a nontaster. Draw a pedigree showing all four grandparents, the two parents, and the daughter. Indicate each individual's possible genotype. Use filled shapes to indicate the recessive trait.

(b) Identify the individuals that are definitely heterozygous (carriers): _____

(c) Identify the individual that could be heterozygous (a carrier): _____

(d) What is the probability of couple A and B having a nontaster boy as their next child? _____

(e) Explain your reasoning: _____

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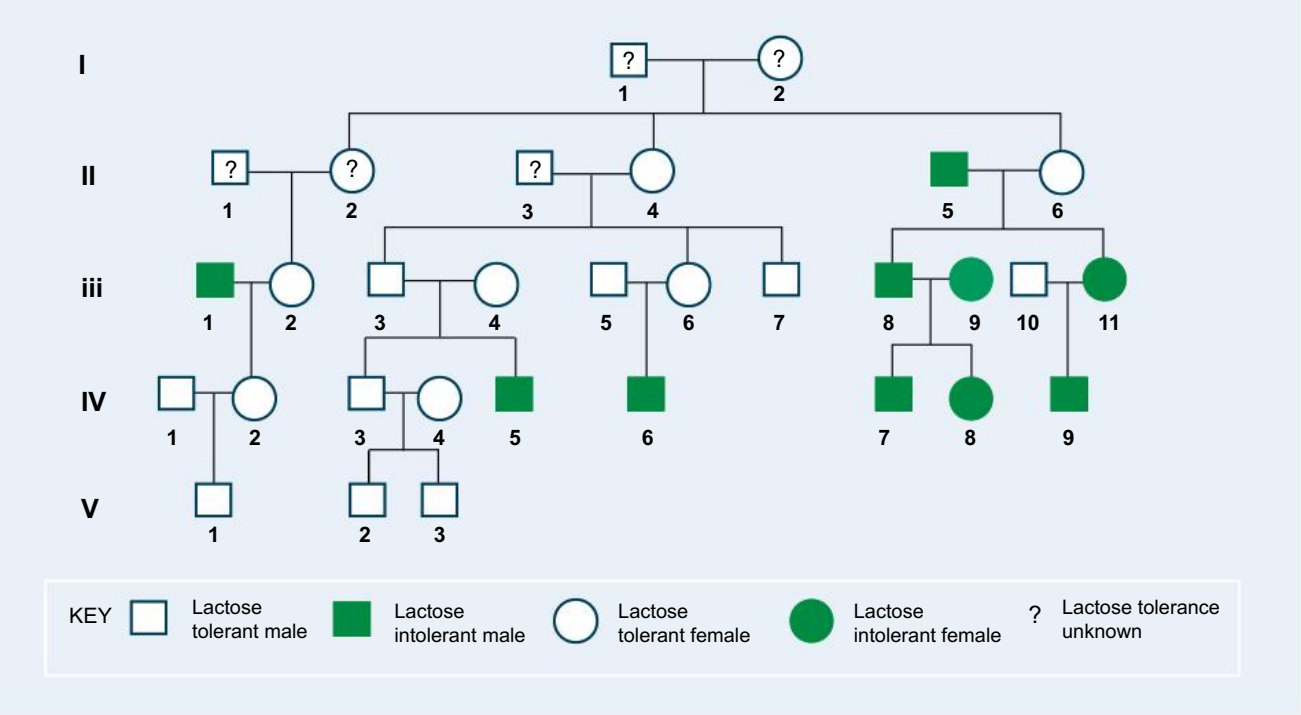
The pedigree of lactose intolerance

Lactose intolerance is the inability to digest the milk sugar lactose. It occurs because some people do not produce lactase, the enzyme needed to break down lactose. The pedigree chart below was one of the original studies to determine the inheritance pattern of lactose intolerance.



2. Use an analysis of the pedigree above to make a claim about the inheritance pattern of lactose intolerance. Support your claim with at least two pieces of evidence:

3. (a) Use the Punnett square below to show the cross between III-10 and III-11 in the pedigree chart above. Use the capital letter L for the dominant allele and the letter l for the recessive allele.

   (b) Explain how you can be certain about III-10's genotype:

	Male alleles	
Female alleles		

4. What is the probability that V-1 is heterozygous for lactose intolerance (Ll)? Show your working or justification:

5. How do we know that the original parents (row I) could not both have been homozygous dominant? Explain:

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6. **Autosomal recessive traits**
Albinos lack pigment in the hair, skin and eyes. This is an autosomal recessive trait.

(a) Write the genotype for each of the individuals on the chart using the following letter codes: **PP** normal skin colour; **P-** normal, but unknown if homozygous; **Pp** carrier; **pp** albino.

(b) Why must the parents (II-3) and (II-4) be carriers of a recessive allele?

_____

_____

7. **Sex linked recessive traits**
Haemophilia is a disease where blood clotting is affected. A person can die from a simple bruise (which is internal bleeding). The clotting factor gene is carried on the X chromosome.

(a) Write the genotype for each of the individuals on the chart using the codes: **XY** normal male; **X_hY** affected male; **XX** normal female; **X_hX** female carrier; **X_hX_h** affected female:

(b) Why can males never be carriers? _____

_____

_____

_____

_____

8. **Autosomal dominant traits**
An unusual trait found in some humans is woolly hair (not to be confused with curly hair). Each affected individual will have at least one affected parent.

(a) Write the genotype for each of the individuals on the chart using the following letter codes:
WW woolly hair; **Ww** woolly hair (heterozygous); **W-** woolly hair, but unknown if homozygous; **ww** normal hair

(b) Describe a feature of this inheritance pattern that suggests the trait is the result of a dominant allele:

_____

_____

9. **Sex linked dominant traits**
A rare form of rickets is inherited on the X chromosome. All daughters of affected males will be affected. More females than males will show the trait.

(a) Write the genotype for each of the individuals on the chart using the following letter codes:
XY normal male; **X_RY** affected male; **XX** normal female; **X_{R-}** female (unknown if homozygous); **X_RX_R** affected female.

(b) What is the probability a male offspring will be affected if either of the parents (one or the other) are affected?

_____

(c) What is the probability a female offspring will be affected if either of the parents (one of the other) are affected?

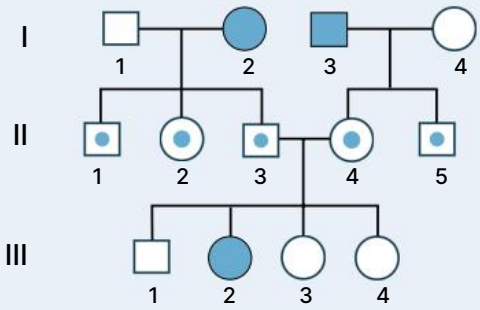
_____

(d) Why will more females than males be affected?

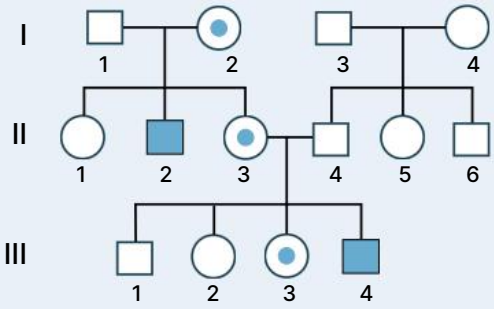
_____

_____

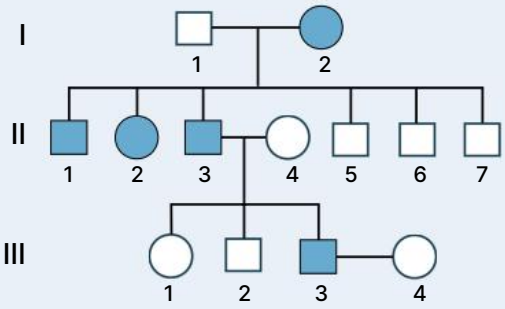
Albinism in humans



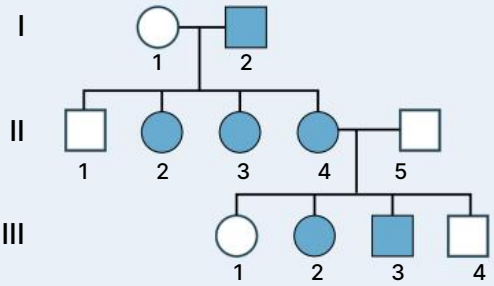
Haemophilia in humans



Woolly hair in humans



A rare form of rickets in humans



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130 Did You Get It?

1. Test your vocabulary by matching each term to its correct definition, as identified by its preceding letter code.

(i) allele	
(ii) dominant	
(iii) heterozygous	
(iv) homozygous	
(v) phenotype	
(iv) recessive	

A Observable characteristics in an organism.

B Possessing two different alleles for a gene, one inherited from each parent.

C One of a number of alternative versions of a gene

D Possessing two identical alleles of a gene, one inherited from each parent.

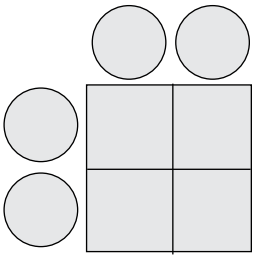
E Allele that expresses its trait irrespective of the other allele.

F An allele that will only express its trait in the absence of the dominant allele.

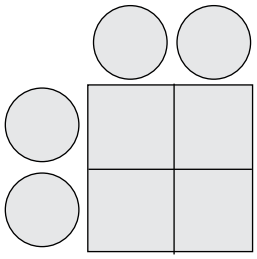
2. A plant breeder crossed a group of true breeding red flowers with a group of true breeding purple flowers and collected the seeds. When they were grown it was found that all the plants had flowers that were wine coloured. When these plants were crossed and the seeds collected and grown it was found that of 124 plants, 30 had red flowers, 33 had purple flowers, and 61 had wine coloured flowers.

   (a) Complete the Punnett squares below. Use the alleles F^R and F^P for the alleles for the red and purple flowers:

Parental cross



F_1 cross



   (b) What kind of inheritance pattern is shown here? _____

3. A breeder has two guinea pigs, one with black hair and the other with white. The two are bred together and all the offspring are black. Two of the offspring are then crossed. Four offspring are born, one is white the rest are black.

   (a) What phenotypic character is being investigated here? _____

   (b) Which phenotypic trait is dominant? _____

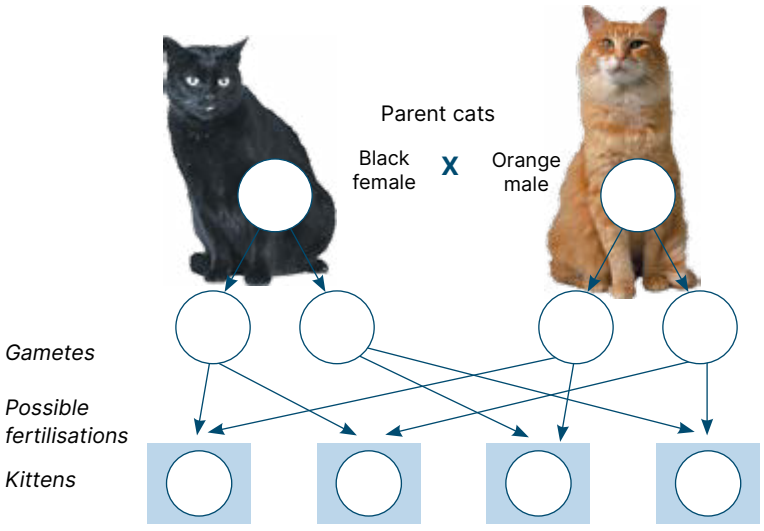
4. One of the gene loci controlling coat colour in cats is sex-linked. The two alleles, red and non-red (or black), are found only on the X-chromosome. Use the alleles listed to answer the following questions:

Allele types		Genotypes		Phenotypes
X_O =	Non-red (=black)	X_OX_O, X_OY	=	Black coated female, male
X_O =	Red	X_OX_O, X_OY	=	Orange coated female, male
		X_OX_o	=	Tortoiseshell, i.e. mix of black and orange in fur (female cats only)

An owner of a cat is thinking of mating her black female cat with an orange male cat. Before she does this, she would like to know what possible coat colours could result from such a cross. Use the symbols above to fill in the diagram on the right. Summarise the possible genotypes and phenotypes of the kittens in the tables below.

	Genotypes	Phenotypes
Male kittens		

Female kittens		



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Chapter 12 Unit 4 Topic 1

Biotechnology

Resource Hub
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Key Terms

- annealing
- bioinformatics
- CRISPR-Cas9
- DNA
- DNA amplification
- DNA ligase
- DNA polymerase
- DNA profiling
- DNA sequencing
- forensics
- gel electrophoresis
- genetic modification
- GMO
- marker gene
- plasmid
- polymerase chain reaction (PCR)
- primer
- recognition site
- recombinant DNA
- recombinant plasmid
- restriction enzyme
- transgenic organism

Key Concepts

- Understand the process of genetic modification, including adding, altering, or deleting genes to produce recombinant DNA and create genetically modified organisms (GMOs) or transgenic organisms.
- Explore the use of DNA technologies such as PCR and gel electrophoresis, and their application in DNA profiling, paternity testing, genetic disease analysis, and vaccine development.
- Study the benefits and risks of GMOs in agriculture, genetic screening, pharmaceuticals, and environmental applications.

Recombinant DNA		Activity Number
☐ 1	Explain what is meant by genetic modification and briefly describe the ways in which organisms can be genetically modified. State that genetic modification may involve adding novel genes to an organism to create a transgenic organism.	131
☐ 2	Describe the process of making recombinant DNA Including: • isolation of the DNA • cutting the DNA using restriction enzymes (including CRISPR-Cas9) • joining (annealing) the DNA using DNA ligase • amplification of the recombinant DNA by bacterial transformation (gene cloning)	132
☐ 3	Explain how transformed bacteria are identified and isolated. Understand that these transformed bacteria are transgenic organisms. Study an example of bacterial transformation in the lab.	133, 134
☐ 4	**SHE:** Describe gene editing using CRISPR. Understand that the development of this technology was the combined result of the research of many different scientists.	135
☐ 5	**SHE:** Discuss the potential advantages and consequences of GMOs (including transgenic organisms) of using agriculture and pharmaceutical development.	136, 137

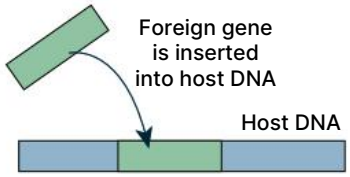
DNA technologies and applications		
☐ 6	Describe DNA amplification using the polymerase chain reaction (PCR). Explain the role of PCR in DNA analyses such as sequencing and profiling.	138
☐ 7	Explain the basis for separation of DNA fragments using gel electrophoresis.	139
☐ 8	Distinguish between DNA sequencing and DNA profiling. Recognise the applications of DNA sequencing in genome mapping and DNA profiling to identify unique genetic information.	140, 141
☐ 9	**SI:** Interpret DNA profiles from gel electrophoresis. Explore the use of DNA profiles in forensics and paternity testing.	140, 141
☐ 10	**SI/SHE:** Explain how genome sequencing projects (e.g. the Human Genome Project or HGP) can advance our understanding of genes and gene function and are major drivers in the development of modern technology and knowledge, even outside of the field of genetics.	142
☐ 11	**SI:** Explain the use of bioinformatics in analysing biological data, such as DNA sequences (e.g. the HGP). Describe some applications of this information.	143
☐ 12	**SI:** Investigate how advances in genetics have helped change the way disease can be diagnosed and treated. Understand the implications of easily available genetic tests.	144, 145
☐ 13	**SI/ SHE:** Explore the contributions of the many scientists who and scientific disciplines that have added to our understanding of gene technology.	135, 147
☐ 14	**SHE:** Appreciate the wide variety of genetically modified organisms that are grown today and their importance to human food and medical supplies. Understand that there are still concerns over the possible unchecked spread of these organisms.	136, 137

131 What is DNA Manipulation?

Key Idea: DNA manipulation alters an organism's DNA either by adding new DNA or editing the existing DNA.

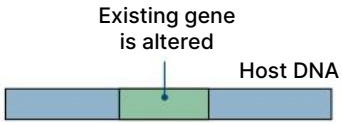
DNA manipulation (also called genetic engineering) involves the direct manipulation of an organism's genome using biotechnology. This can be achieved by introducing new **DNA** into an organism or by editing its existing DNA. DNA manipulation aims to repair damage or to produce improved or novel organisms with specific traits. Genetic engineering has wide applications in food technology, industry, agriculture, environmental clean up, pharmaceutical production, and vaccine development. Organisms that have had their DNA altered are called genetically modified organisms (**GMO**s).

How are genetically modified organisms produced?



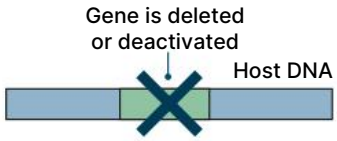
Add a foreign gene

A novel gene (foreign to the recipient) is inserted from another species. This will enable the GMO to express the trait encoded by the new gene. Organisms genetically altered in this way are referred to as **transgenic**.



Alter an existing gene

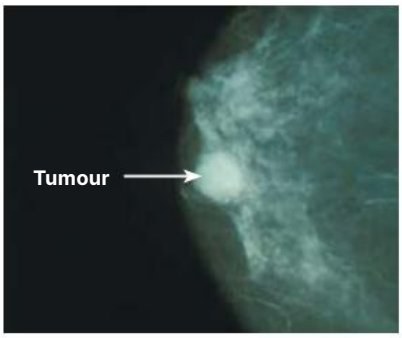
An existing gene may be altered to make it express at a higher level (e.g. growth hormone) or in a different way (in tissue that would not normally express it). The technique may provide a way to fix a malfunctioning gene.



Delete or 'turn off' a gene

An existing gene may be deleted or deactivated (switched off) to prevent the expression of a trait (e.g. the deactivation of the ripening gene in tomatoes produced the Flavr-Savr tomato).

Human insulin, used to treat diabetic patients, is produced by inserting the insulin gene into bacteria and yeast.



Gene editing technologies, such as **CRISPR**, are being explored to treat breast cancer (above) and sickle cell disease.

Manipulating gene action is one way in which to control processes such as ripening in fruit so it stays fresher longer.

1. (a) What is DNA manipulation? _____

(b) Using examples, discuss the ways in which an organism may be genetically modified: _____

2. Describe some of the applications of DNA manipulation: _____

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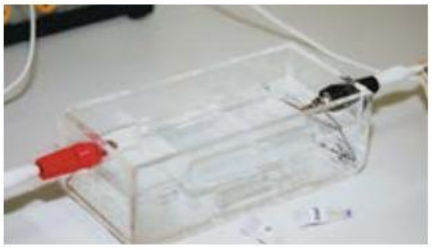
132 Making Recombinant DNA

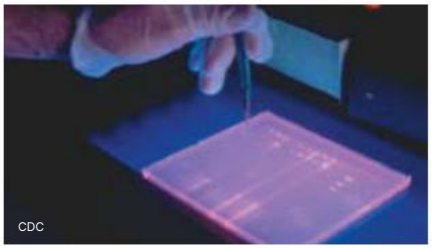
Key Idea: Recombinant DNA (rDNA) is produced by first isolating (or synthesising) a DNA sequence, then inserting it into the genome of a different organism, e.g. a bacterium.

Recombinant DNA (rDNA) is produced by combining genetic material from two or more different sources. The production of rDNA is possible because the **DNA** of every organism is made of the same building blocks (nucleotides). rDNA allows a gene from one organism to be moved into, and expressed in, a different organism. Two important tools are used to create rDNA. Endonucleases (such as **restriction enzymes** or the **CRISPR-Cas9** system) cut the DNA and the enzyme **DNA ligase** is used to join the sections of DNA together.

Overview: How is recombinant DNA made?



Fragments of **DNA** produced by restriction enzymes (below) are mixed with ethidium bromide, a molecule that fluoresces under UV light. The DNA fragments are then placed on an electrophoresis gel to separate the different lengths of DNA.

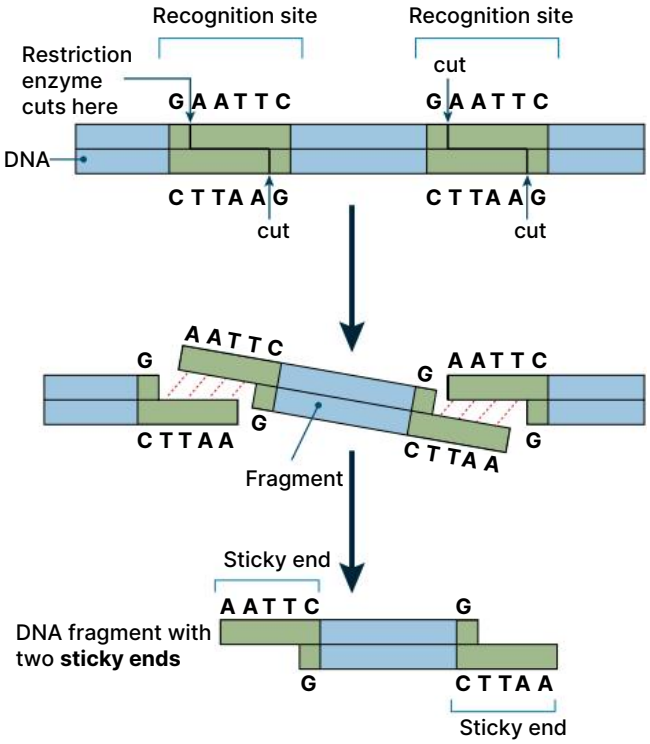


Once the DNA fragments are separated, the gel is placed on a UV viewing platform. The area of the gel containing the DNA fragments of the correct length is cut out and placed in a solution that dissolves the gel. This releases the DNA into the solution.

The solution containing the DNA is centrifuged at high speed to separate out the DNA. Centrifugation works by separating molecules of different densities. Once isolated, the DNA can be spliced into another DNA molecule.

What are restriction enzymes?

- A restriction enzyme is an enzyme that cuts a double-stranded DNA molecule at a specific **recognition site** (a specific DNA sequence). There are many different types of restriction enzymes and each has a unique recognition site.
- Some restriction enzymes produce DNA fragments with two sticky ends (right). A sticky end has exposed nucleotide bases at each end. DNA cut in such a way is able to be joined to other piece of DNA with matching sticky ends. Such joins are specific to their recognition sites.
- Some restriction enzymes produce a DNA fragment with two blunt ends (ends with no exposed nucleotide bases). The piece it is removed from is also left with blunt ends. DNA cut in such a way can be joined to any other blunt end fragment. Unlike sticky ends, blunt end joins are non-specific because there are no sticky ends to act as specific recognition sites.



1. What is the purpose of restriction enzymes in making recombinant DNA? _____

_____

_____

2. What is the difference between sticky end and blunt end fragments? _____

_____

_____

3. Why is it useful to have many different kinds of restriction enzymes? _____

_____

_____

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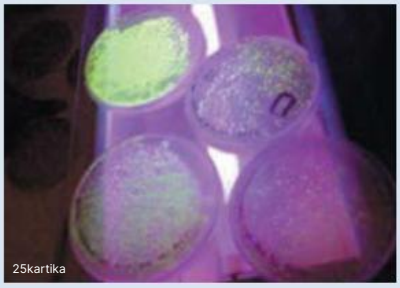
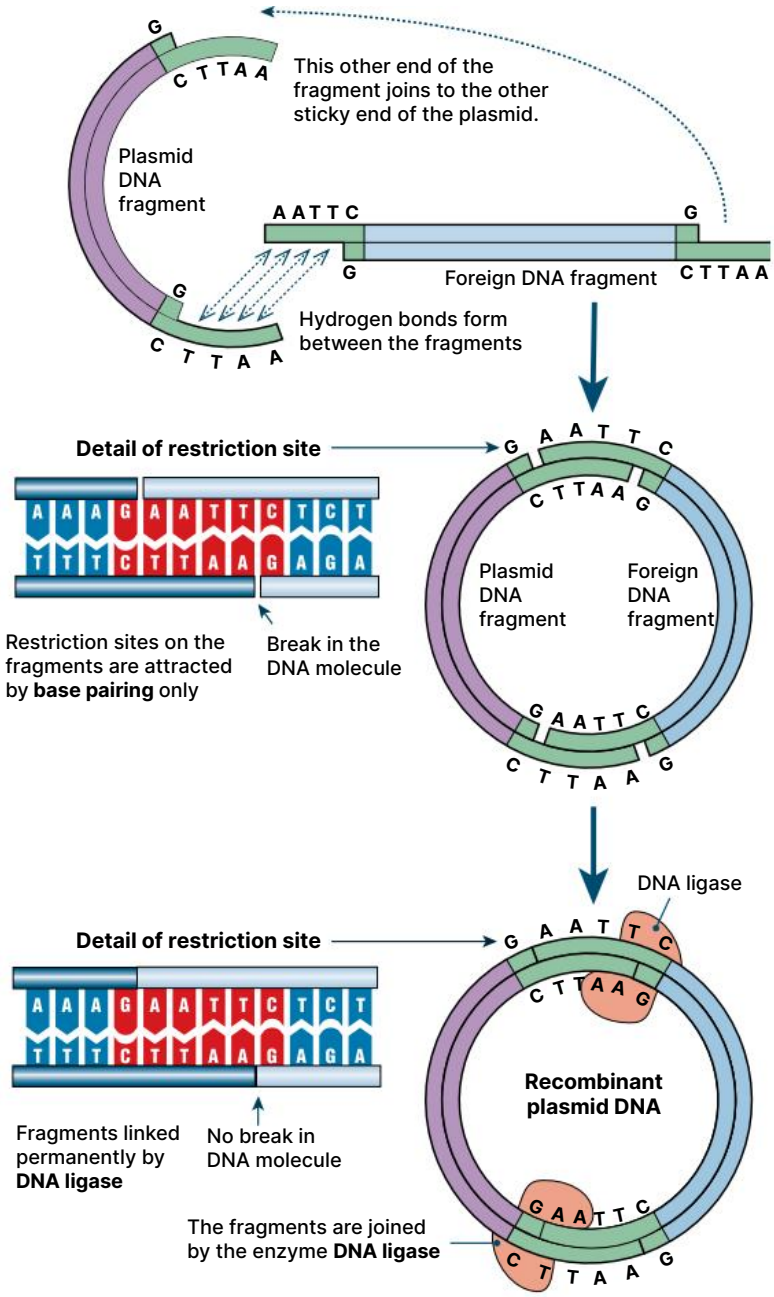
Creating a recombinant DNA plasmid

1. Two pieces of DNA are cut by the same restriction enzyme (they will produce fragments with matching sticky ends).
2. Fragments with matching sticky ends can be joined by base-pairing. This process is called **annealing**. This allows DNA fragments from different sources to be joined. The DNA fragments are joined by the enzyme DNA ligase, which catalyses the formation of a phosphodiester bond. This produces a molecule of **recombinant DNA**.
3. The joined fragments will usually form either a linear or a circular molecule, as shown here (right) as **recombinant plasmid** DNA.



pGLO is a **plasmid** engineered to contain Green Fluorescent Protein (*gfp*). pGLO has been used to create fluorescent organisms, including the bacteria above (bright patches on agar plates).



4. Explain in your own words the two main steps in the process of joining two DNA fragments together:

   (a) Annealing: _____

   _____

   (b) DNA ligase: _____

   _____

5. Explain why ligation can be considered the reverse of the restriction digestion process: _____

   _____

6. Why can recombinant DNA be expressed in any kind of organism, even if it contains DNA from another species?

   _____

   _____

   _____

   _____

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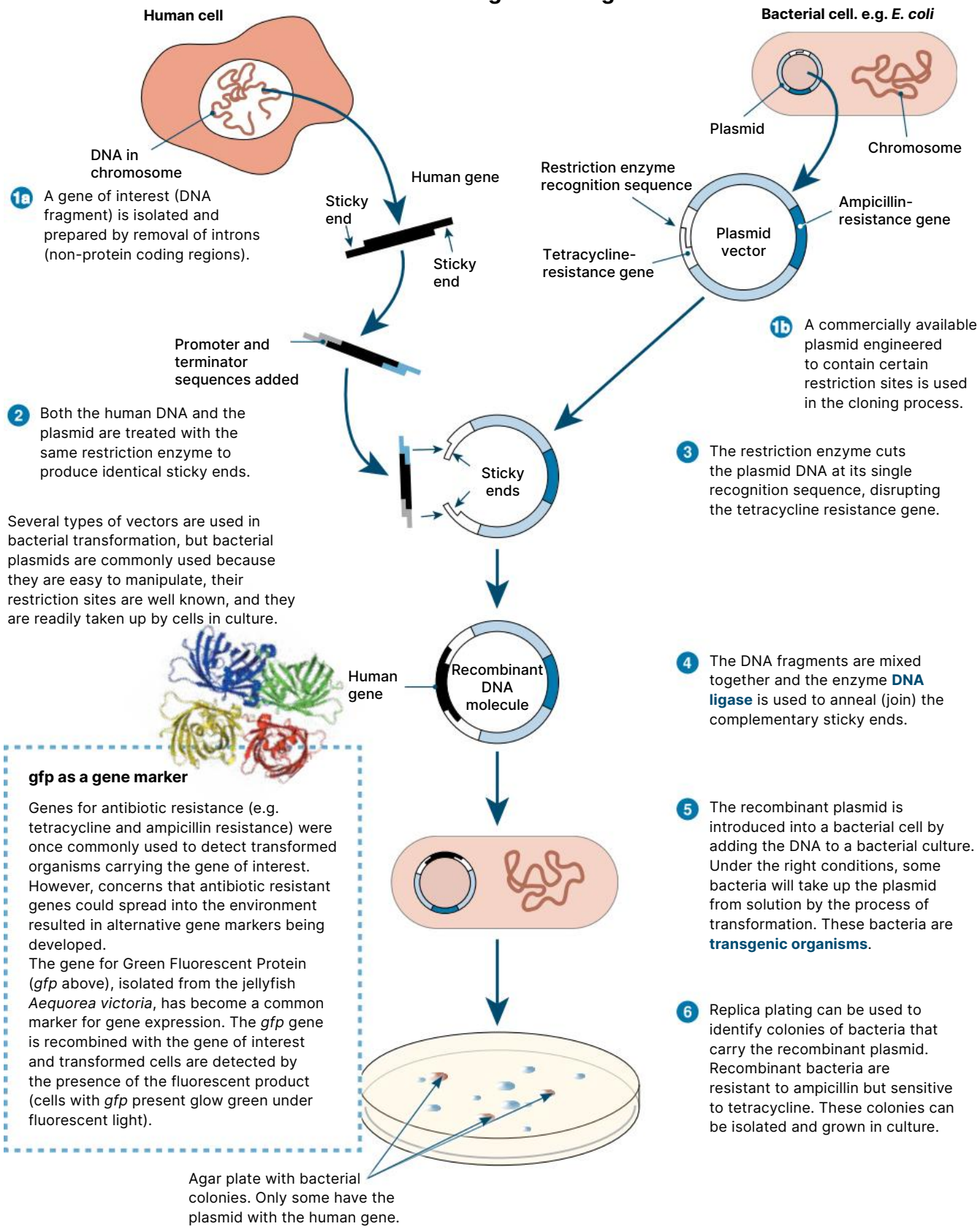
133 DNA Amplification Using Bacterial Transformation

Key Idea: Recombinant plasmids taken up into a host organism are replicated when the host's DNA is replicated. This produces large quantities of the recombinant DNA.

We have already seen that **recombinant DNA** techniques can be used to insert a **gene** into a **plasmid**. The plasmid can then be used to transmit the gene to another organism (e.g. *E. coli* bacteria). Once inside *E. coli*, the gene is replicated along with the host **DNA**. This technique is called gene cloning and produces multiple copies of the gene. The **recombinant plasmid** must be able to replicate inside its host, it must have one or more sites at which a **restriction enzyme** can cut, and it must have some kind of genetic marker that allows them to be identified. Replica plating is often used to identify organisms that have produced the gene of interest.

Cloning a human gene



gfp as a gene marker

Genes for antibiotic resistance (e.g. tetracycline and ampicillin resistance) were once commonly used to detect transformed organisms carrying the gene of interest. However, concerns that antibiotic resistant genes could spread into the environment resulted in alternative gene markers being developed.

The gene for Green Fluorescent Protein (*gfp* above), isolated from the jellyfish *Aequorea victoria*, has become a common marker for gene expression. The *gfp* gene is recombined with the gene of interest and transformed cells are detected by the presence of the fluorescent product (cells with *gfp* present glow green under fluorescent light).

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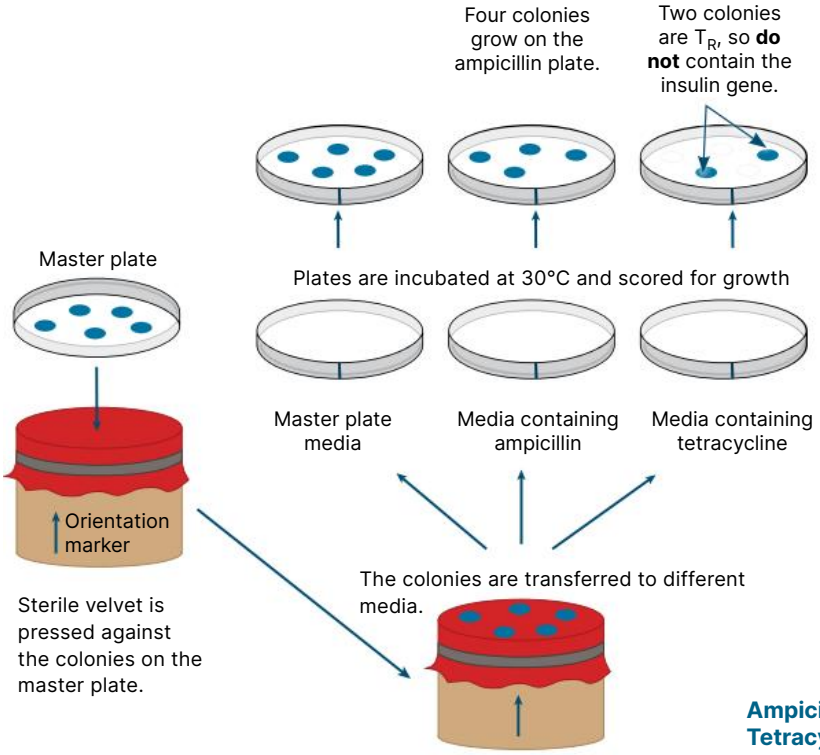
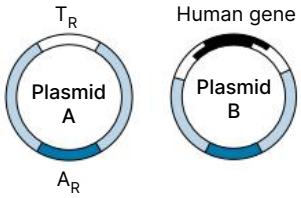
Replica plating identifies colonies with desirable qualities



After gene cloning, it is important to be able to identify the colonies in which transformation has occurred. This is achieved by replica plating.

Replica plating transfers colonies from a master plate to test plates enriched with specific nutrients or antibiotics. The original pattern of colonies is maintained during the transfer. Growth (or lack of) on the test plates can be used to identify colonies of interest (e.g. colonies containing the insulin gene).

In the example on the left, colonies are tested for their susceptibility to the antibiotic tetracycline. Those with ampicillin resistance but no tetracycline resistance contain the insulin gene (plasmid B). The insertion of the insulin gene has interrupted the tetracycline gene, so they are sensitive to tetracycline.



Ampicillin resistance (A_R):	**YES**	**YES**
Tetracycline resistance (T_R):	**YES**	**NO**

1. What is the purpose of gene cloning? _____

2. Explain how a human gene is removed from a chromosome and placed into a plasmid: _____

3. (a) What is the purpose of replica plating? _____

   (b) In the replica plating example above, explain how the colonies with the recombinant plasmids are identified:

   (c) What can you say about the colony that did not grow on the ampicillin plate? _____

4. Why is the *gfp* marker a more desirable gene marker than genes for antibiotic resistance? _____

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134 Testing for Transformation

Key Idea: Bacteria are able to obtain new genetic information by taking up genetic material from the environment. This process is called transformation.

Bacteria are able to take up extracellular naked **DNA** from their environment. This is called transformation. In biotechnology, scientists often use **recombinant plasmids** as the naked DNA source to insert a novel gene into bacteria. This allows them to produce gene products (e.g. insulin) on an industrial scale. The efficiency of the uptake is measured by calculating transformation efficiency.

Aim

To investigate the efficiency of transformation in *E. coli* bacteria when mixed with a plasmid containing a variant of GFP (green fluorescent protein) gene and the ampicillin resistance gene.

Background

GFP is a **marker gene** that is used to identify bacterial colonies that have acquired a target **plasmid** (+plasmid). GFP glows under fluorescent light. The variant of this gene also causes the bacterial colonies to turn yellow-green in ordinary white light (*E. coli* colonies normally have a whitish appearance).

In this example, both ampicillin resistance and GFP genes are being used because only transformed bacterial colonies are being counted. The ampicillin resistance makes this simpler because untransformed colonies can be eliminated by using ampicillin-containing agar plates.

Colonies can be assumed to be derived from individual bacterial cells, so the number of colonies relates directly to the number of cells originally on the agar plate.

Method for transforming *E. coli*

250 µL of ice cold $CaCl_2$ was transferred to two microcentrifuge tubes using a sterile transfer pipette. One tube was labelled +plasmid, the other was labelled -plasmid (the control, no plasmid added)). Both tubes were placed on ice. A starter colony of *E. coli* was transferred to each tube using a sterile inoculation loop. The tubes were inverted to mix, then returned to the ice.

10 µL of 0.005 µg μL^{-1} solution of plasmid was transferred by sterile pipette to the tube labelled +plasmid only. The +plasmid and -plasmid tubes were the incubated on ice for 10 minutes. The tubes were then placed in a water bath at 42°C for 50 seconds to heat shock the bacteria (this helps plasmid uptake), then the tubes were returned to ice for two minutes. Each tube then had 250 µL of nutrient broth added and were incubated at room temperature for 10 minutes.

Two plates containing nutrient agar only and two plates containing nutrient agar and ampicillin were prepared. 100 µL of -plasmid was transferred to one of each type of plate and streaked using a sterile inoculating loop. The same was done with the +plasmid.

The plates were covered and placed in an incubator at 37°C for 24 hours. The number of colonies on the plate containing the +plasmid and ampicillin agar were counted and recorded.

Results

The four agar plates are shown below:

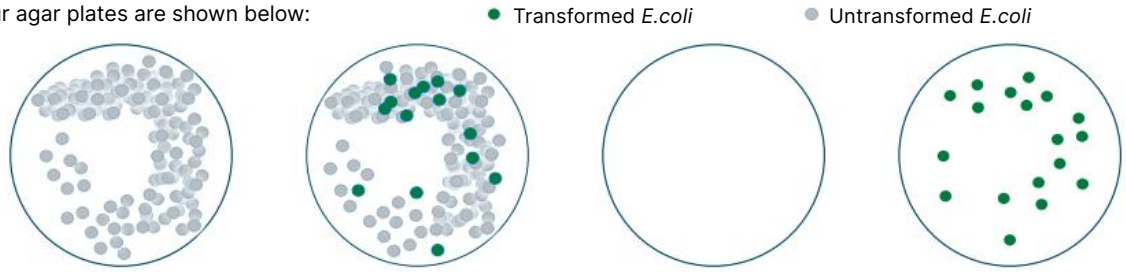

Plate 1: Nutrient agar only (no ampicillin) -plasmid

Plate 2: Nutrient agar only (no ampicillin) +plasmid

Plate 3: Nutrient agar + ampicillin -plasmid

Plate 4: Nutrient agar + ampicillin +plasmid

1. (a) Determine the mass of plasmid pipetted into the microcentrifuge tubes.
Use the formula mass (µg) (of plasmid) = concentration (µg μL^{-1}) x volume (µL):

_____

(b) Determine the fraction of this amount spread on the plate (volume spread on plate ÷ total volume in tube):

_____

(c) Determine the mass of plasmid spread on the plate (answer 1(a) x answer 1(b)): _____

(d) Calculate the transformation efficiency (transformants per µg) using the number of colonies ÷ mass of DNA spread:

_____

2. How has plate 4 made counting the transformed colonies easier compared to plate 2? _____

_____

3. What would growth on plate 3 tell you? _____

_____

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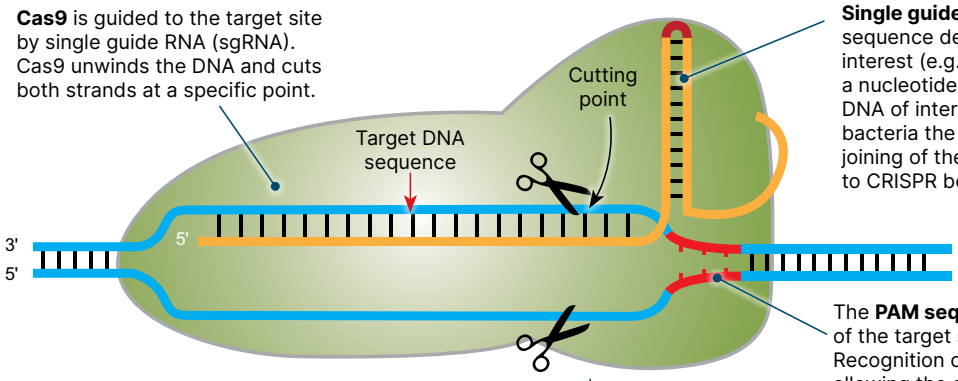
135 CRISPR

Key Idea: CRISPR is a complex made up of a Cas9 endonuclease and sgRNA. The CRISPR complex cuts DNA at very specific sequences and can be used to edit genes.

CRISPR-Cas9 (shortened to CRISPR and pronounced crisper) occurs naturally in bacteria, which use it to edit the DNA of invading viruses. It is an endonuclease complex, i.e. it cleaves the phosphodiester bond in DNA. CRISPR is able to target specific stretches of DNA and edit it at very precise locations. Two key components are required for CRISPR to work: an RNA guide that locates and binds to the target piece of DNA and the Cas9 endonuclease that unwinds and cuts the DNA. The technology has potential applications in correcting mutations responsible for disease, switching faulty genes off, adding new genes to an organism, or studying the effect of specific genes. It represents a major advance because it allows precise and efficient gene editing.

Cas9 is guided to the target site by single guide RNA (sgRNA). Cas9 unwinds the DNA and cuts both strands at a specific point.



Single guide RNA (sgRNA) is a short synthetic RNA sequence designed to guide Cas9 to the site of interest (e.g. a faulty gene sequence). It contains a nucleotide section that is complementary to the DNA of interest. It is called a single guide because in bacteria the RNA is two separate pieces. It was the joining of these two pieces in the lab that led directly to CRISPR being a usable editing tool.

The **PAM sequence** (NGG)* lies directly downstream of the target sequence on the non-target DNA strand. Recognition of PAM by Cas9 destabilises the DNA allowing the sgRNA to be inserted. Cas9 will not function if PAM is absent. *N can be any nucleotide. CRISPR can be made to recognise different versions of the PAM sequence.

CRISPR stands for Clustered Regularly Interspaced Short Palindromic Repeats (a palindrome is a sequence that reads the same forwards and backwards).

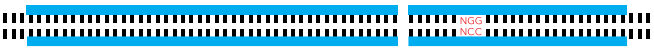
The cut DNA can be repaired using one of the following methods:

Gene knock in 'gene editing'

A new DNA sequence is inserted into the DNA break. For example allows a faulty gene sequence can be replaced with the correct sequence to restore normal gene function.

Gene knock out "gene silencing"

Errors occur as the cell's normal repair mechanisms mend the broken DNA, causing the insertion or deletion of bases. The resulting frame-shift mutation changes the way the nucleotide sequence is read, either disabling gene function or producing a STOP signal. This technique can be used to silence a faulty gene.



Like many scientific discoveries, the discovery and development of CRISPR editing involved many years and many different scientists in many different countries working on projects as diverse as gene cloning to yoghurt production.

However, is was the work of Emmanuelle Charpentier and Jennifer A Doudna that led to the CRISPR complex used today. They realised that two short sections of RNA used in the bacterial CRISPR complex could be joined into one piece and that, if that piece was synthetically and specifically made, the CRISPR complex could be used to target any section of DNA for editing. This work won them the Nobel prize in Chemistry in 2020.


Jennifer A Doudna

Cmichel67 CC4.0

1. What are the roles of the following in CRISPR gene editing:

   (a) Cas9? _____

   (b) sgRNA? _____

2. Outline two ways that CRISPR can be used to edit genes: _____

   _____

   _____

   _____

3. What benefits are offered by CRISPR technology? _____

   _____

   _____

   _____

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136 Applications of Genetically Modified Organisms

Key Idea: GMOs are widely used to increase yields or quality in agriculture, or to produce pharmaceutical products.

Recall that organisms that have had their DNA altered are called genetically modified organisms (**GMO**s). Incorporation of a new gene into a species can optimism their performance (e.g. growth) or stimulate production of a desirable product (e.g. higher vitamin levels). Current applications are highly varied and include food and enzyme technology, industry and medicine, environmental clean up, and agriculture. Some medical and agricultural applications are given below.

GMOs and agriculture

In Australia, the use of genetically modified crops is tightly regulated and approval is needed before they can be grown. Strict regulation is in place because transgenes (literally 'transferred genes') are easily spread between plant species and could result in plants accidently acquiring foreign genes.

What GM crops are grown in Australia?

Five GM crops are currently authorised to be grown in Australia, canola (right), cotton, safflower, Indian mustard, and banana. There are a number of experimental field trials also in progress. These include, barley, ryegrass, sugarcane, and wheat.

Why GM crops?

There are many different reasons to genetically modify crops. Common uses are to increase crop yield, decrease the cost of production, improve crop genetics, or to enhance nutritional qualities.

IRRI CC2.0

Scott Bauer, USDA ARS

Crop improvement: The nutrient content of crops can be enhanced to have higher protein or vitamin levels (e.g. golden rice has higher levels of β-carotene, which is needed to make vitamin A). Plants can also be engineered to use less water or to grow in conditions they could not normally tolerate (e.g. saline soils).

Pest or herbicide resistance: Large amounts of money are spent on spraying chemicals to control plant pests. Plants can be engineered to express genes for insect toxins or herbicide resistance. Pest resistant crops do not require spraying and herbicide resistance allows the grower to control weeds without damaging the crops.

Extending shelf life: Food that spoils before it can be sold reduces profit. Shelf life in fresh produce (e.g. tomatoes) can be extended by switching off the genes for specific enzymes involved in the fruit ripening process (e.g. the enzymes involved in softening of the fruit wall or controlling the production of ethylene).

GMOs and pharmaceuticals

Production of bioactive proteins: Transgenic bacteria are widely used to produce desirable commodities, such as hormones. Large quantities of a product can be produced commercially in large bioreactors. One example is injectable human insulin (above) produced in recombinant bacteria or yeast. Transgenic sheep carrying the human gene for a protein called α-1-antitrypsin, produce the protein in their milk. The antitrypsin is extracted from the sheep's milk and can be used to treat hereditary forms of the breathing disorder emphysema.

Vaccine development: Genes encoding antigenic components (e.g. viral proteins) are inserted into a bacterial cell, which then expresses the genes. The gene product is purified to make a vaccine and generates an immune response without the risk of ever causing the disease.

1. Suggest one economic advantage of extending shelf life in fresh produce: _____

_____

_____

2. Explain the benefit of using GE bacteria to produce a human hormone such as insulin?_____

_____

_____

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Engineering herbicide resistance

Bt toxin

Bacillus thuringiensis is a soil living bacterium. It also occurs naturally in the gut of caterpillars and on leaf surfaces. The bacteria form spores that are associated with crystalline proteins called δ-endotoxins. These are lethal to lepidopteran (butterfly and moth) larvae but do not affect other insects such as beetles or bees (or any other animal). For this reason the Bt toxin has been used as a targeted insecticide since the 1960s.

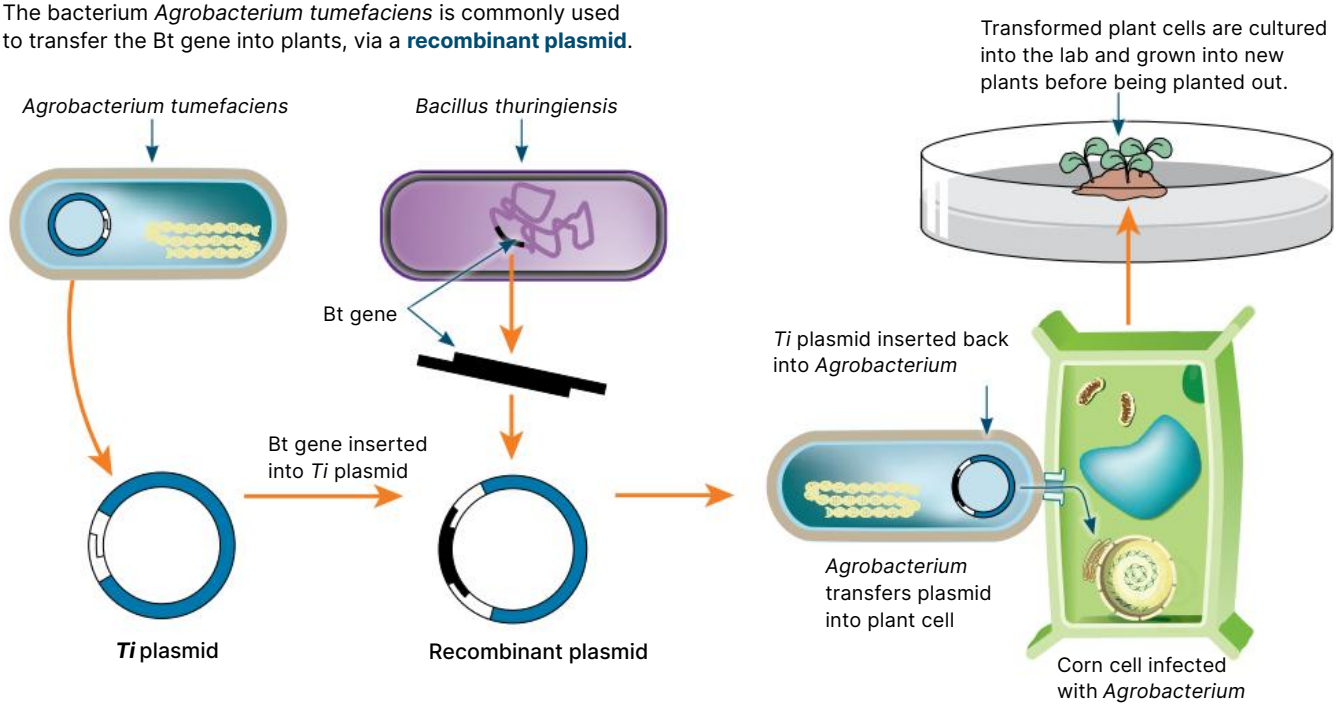
In 1996 the seed company Monsanto released its first versions of Bt corn. This corn had been genetically modified to contain the gene that produces the Bt protein. The target insect pest for Bt corn is the larval stage of the European corn borer, which causes hundreds of millions of dollars worth of damage to crops annually.

Both photos USDA

The effects of the Bt toxin on insect deterrence. The plant on the right has been treated with Bt toxin before being exposed to caterpillars. The plant on the left had not been treated with Bt toxin.

Producing a Bt plant

Genetic engineering has been used to produce transgenic cotton, corn, and potato varieties that produce the Bt toxin. The bacterium *Agrobacterium tumefaciens* is commonly used to transfer the Bt gene into plants, via a **recombinant plasmid**.



3. Explain why it is safer to produce a vaccine using gene technology, rather than the pathogen itself?

_____

4. What is meant by a transgenic organism? _____

_____

5. Name the bacteria that produces Bt toxin: _____

6. Why is Bt toxin a useful insecticide? _____

_____

7. What is the primary target of the Bt toxin in Bt corn? _____

8. Explain how transgenic Bt corn is produced using *Agrobacterium tumefaciens*: _____

_____

_____

_____

_____

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137 GMOs and the Environment

Key Idea: There are many potential benefits, risks, and ethical questions in using genetically modified organisms.

Genetically modified organisms (**GMO**s) or **transgenic organisms** have many potential benefits, but their use raises a number of biological and ethical concerns. Some of these include risk to human health, animal welfare issues, and environmental safety. A constant matter of concern to people is the adequacy of government regulations controlling the use of GMOs and GMO products. Some of this concern comes from the potential consequences of DNA crossing species boundaries and producing "superweeds" or pesticide resistant insect pests. Other concerns include labelling of GMO products in food or the effect of GMOs on non target organisms (e.g. pesticide producing plants).

Potential benefits of GMOs

1. Increase in crop yields, including crops with more nutritional value and that can be stored for longer.
2. Decrease in use of pesticides, herbicides, and animal remedies.
3. Production of crops that are drought tolerant or salt tolerant.
4. Improvement in the health of the human population and the medicines used to achieve it.
5. Development of animal factories for the production of proteins used in manufacturing, the food industry, and health.

Potential risks of GMOs

1. Possible (uncontrollable) spread of transgenes into other species of plants, or animals.
2. Concerns that the release of GMOs into the environment may be irreversible.
3. Animal welfare and ethical issues: GM animals may suffer poor health and reduced life span.
4. GMOs may cause the emergence of pest, insect, or microbial resistance to traditional control methods.
5. May create a monopoly and dependence of developing countries on companies who are seeking to control the world's commercial seed supply.

Issues and solutions

Issue: The accidental release of GMOs into the environment.

Problem: **Recombinant DNA** may be taken up by non-target organisms. These have the potential to become pests or cause disease.

Solution: Rigorous controls on the production and release of GMOs. GMOs could have specific genes deleted so that their growth requirements are met only in controlled environments.

Issue: Adding genes to organisms to produce pharmaceuticals for human use or study.

Problem: There are concerns with animal health. Many genetically modified mammals have congenital defects and reproductive difficulties (low conception to term rates).

Solution: Testing and monitoring animal health is important. Continued development of non-animal based methods for developing proteins.

Issue: Targeted use of transgenic organisms in the environment.

Problem: Once their desired function, e.g. environmental clean-up, is completed, they may be undesirable invaders in the ecosystem.

Solution: GMOs can be engineered to contain "suicide genes" or metabolic deficiencies so that they do not survive for long in the new environment after completion of their task.

1. Choose one of the following topics to research:

   (a) Choose one genetically modified crop grown in Australia (e.g. canola, cotton, or safflower) and research the advantages and disadvantages of its use compared to a non-GMO crop. Summarise your ideas on a shared document for the class to comment on.

   (b) Edible plants can be engineered to carry antigenic proteins. If you could save lives by producing an edible vaccine in a GM crop would you do it? Research this topic and write a discussion on the potential of edible vaccines to deliver vaccines safely and at low cost. Post your ideas in a shared document for your classmates to see and discuss.

   (c) There will always be pros and cons of any new technology. GMOs and transgenic organisms tend to evoke polar opinions in people. Carry out a survey of people in and out of your class and summarise their opinions on the use of GMOs outside of the lab. Write an evaluation of these opinions including their validity (for or against).

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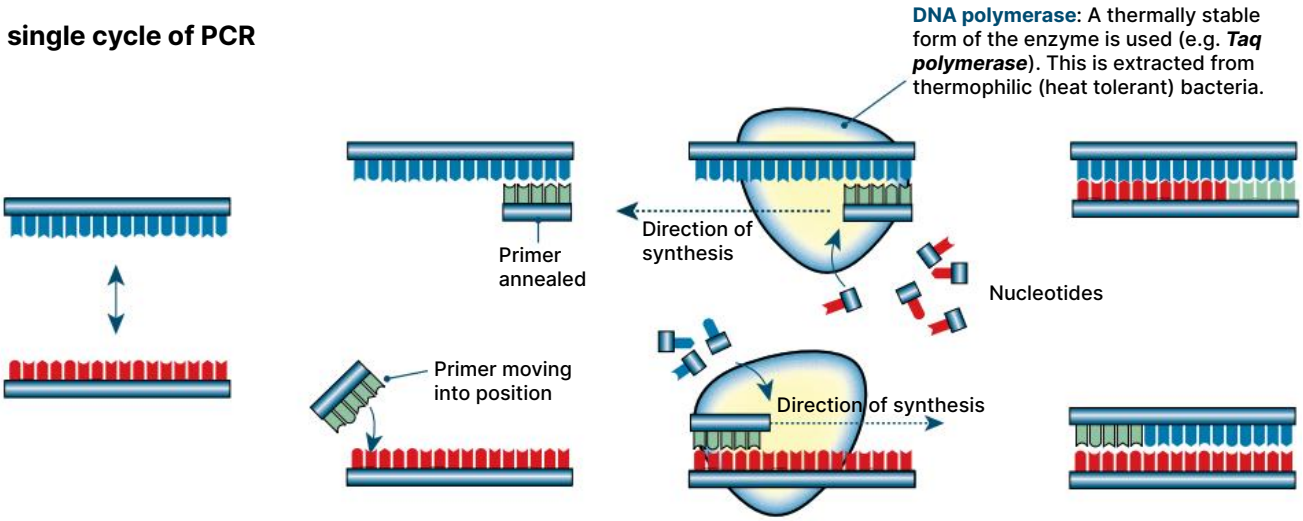
138 DNA Amplification Using PCR

Key Idea: PCR uses a polymerase enzyme to copy a DNA sample, producing billions of copies in a few hours.

Often it is very hard to get enough **DNA** to analyse (e.g. DNA from a crime scene or from an extinct organism). Researchers need to increase the amount of DNA they have to work with (**DNA amplification**), this is done using **polymerase chain reaction** (PCR). PCR can make billions of copies of a target DNA sequence of interest so that it can be analysed. The technique is carried out *in vitro* (e.g. in tubes) rather than in a living organism. An overview of PCR is given below.

A single cycle of PCR



1. Denaturing
A DNA sample (called target DNA) is obtained. It is denatured (DNA strands are separated) by heating at 98°C for 5 minutes.

2. Annealing
The sample is cooled to 60°C. **Primers** are annealed (bonded) to each DNA strand. In PCR, the primers are short strands of DNA; they provide the starting sequence for DNA extension.

3. Extension/elongation
Free nucleotides and DNA polymerase are added. DNA polymerase binds to the primers and synthesises complementary strands of DNA, using the free nucleotides.

4. Completed strands
After one cycle, there are now two copies of the original DNA.

Repeat cycle of heating and cooling until enough copies of the target DNA have been produced

1. Outline the process of PCR: _____

2. (a) Explain the purpose of PCR: _____

   (b) Give two examples where PCR is needed to amplify DNA: _____

3. After only two cycles of replication, four copies of the double-stranded DNA exist. Calculate how much a DNA sample will have increased after:

   (a) 10 cycles: _____ (b) 25 cycles: _____

4. Researchers take great care to avoid DNA contamination during PCR preparation. Explain why: _____

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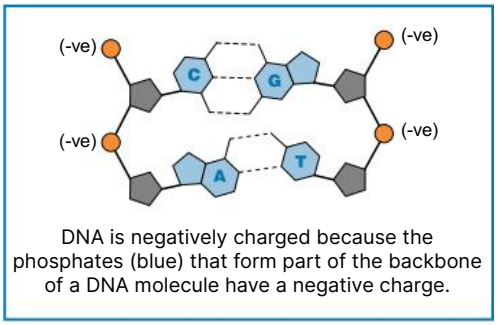
139 Gel Electrophoresis

Key Idea: Gel electrophoresis is used to separate DNA fragments on the basis of size.

Gel electrophoresis is a tool used to isolate DNA of interest for further study. It is also used for **DNA profiling** (comparing individuals based on their unique **DNA** banding profiles). DNA has an overall negative charge, so when an electrical current is run through a gel, the DNA moves towards the positive electrode. The rate at which the DNA molecules move through the gel depends primarily on their size and the strength of the electric field. The gel they move through is full of pores (holes). Smaller DNA molecules move through the pores more quickly than larger ones. At the end of the process, the DNA molecules can be stained and visualised as a series of bands. Each band contains DNA molecules of a particular size. The bands furthest from the start of the gel contain the smallest DNA fragments.



DNA is negatively charged because the phosphates (blue) that form part of the backbone of a DNA molecule have a negative charge.

DNA solutions: Mixtures of different sizes of DNA fragments are loaded in each well in the gel.

DNA markers, a mixture of DNA molecules with known molecular weights (size) are often run in one lane. They are used to estimate the sizes of the DNA fragments in the sample lanes. The figures below are hypothetical markers (bp = base pairs).

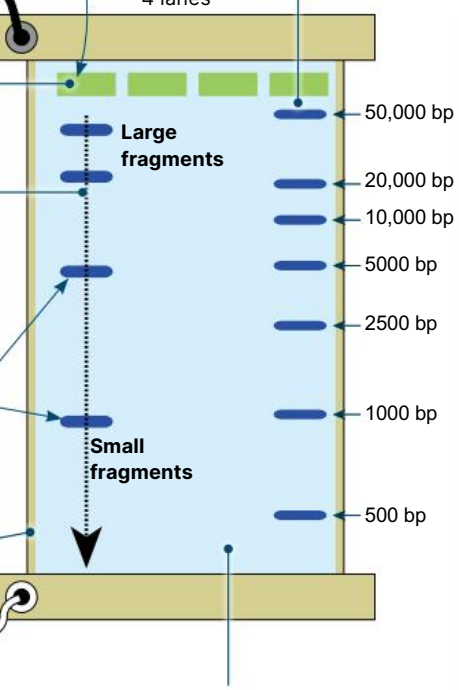
Negative electrode (–)

4 lanes

Wells: Holes are made in the gel with a comb, acting as a reservoir for the DNA solution.

DNA fragments move: The gel matrix acts as a sieve for the negatively charged DNA molecules as they move towards the positive terminal. Small fragments move easily through the matrix, whereas large fragments don't.

As DNA molecules migrate through the gel, large fragments lag behind small fragments. As the process continues, the separation between larger and smaller fragments increases.



Tray: The gel is poured into this tray and allowed to set.

Positive electrode **(+)**

Gel: A gel is prepared, which will act as a support for separation of the fragments of DNA. The gel is a jelly-like material, called agarose.

Steps in the process of gel electrophoresis of DNA

1. The gel is placed in an electrophoresis chamber and the chamber is filled with buffer, covering the gel. This allows electric current from electrodes at either end of the gel to flow through it.
2. DNA samples are mixed with a "loading dye" to make the DNA sample visible. The dye also contains glycerol or sucrose to make the DNA sample heavy so that it will sink to the bottom of the well.
3. The gel is covered, electrodes are attached to a power supply and turned on.
4. When the dye marker has moved through the gel, the current is turned off and the gel is removed from the tray.
5. DNA molecules are made visible by staining the gel with methylene blue or ethidium bromide which binds to DNA and will fluoresce in UV light.
6. The band or bands of interest are cut from the gel and dissolved in chemicals to release the DNA. This DNA can then be studied in more detail (e.g. its nucleotide sequence can be determined).

1. What is the purpose of gel electrophoresis? _____

_____

_____

2. Describe the two forces that control the speed at which fragments pass through the gel:

   (a) _____

   (b) _____

3. Why do the smallest fragments travel through the gel the fastest? _____

_____

_____

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Recognition sites for selected restriction enzymes

Enzyme	Source	Recognition sites
***Eco*RI**	*Escherichia coli* RY13	G A A T T C
HaeIII	*Haemophilus aegyptius*	G G C C
***Hind*III**	*Haemophilus influenzae* Rd	A A G C T T
***Hpa*I**	*Haemophilus parainfluenzae*	G T T A A C
***Hpa*II**	*Haemophilus parainfluenzae*	C C G G
***Rsa*I**	*Rhodopseudomonas sphaeroides*	G T A C
***Taq*I**	*Thermus aquaticus*	T C G A

- DNA fragments for gel electrophoresis are produced by restriction digestion of DNA using **restriction enzymes**. Restriction enzymes are produced by bacteria as a method of eliminating foreign DNA. About 3000 different restriction enzymes have been isolated. Around 600 are commonly used in laboratories.
- Restriction enzymes are named according to the species they were first isolated from, followed by a number to distinguish different enzymes isolated from the same organism.

4. (a) A scientist uses *Hpa*II to cut a length of DNA. State the recognition site for *Hpa*II: _____

   (b) Circle where on the DNA sequence below *Hpa*II would cut the following DNA sequence:

   GTTAGGCCCGGCTAGCTTGACCAGTCCCGGGTCACAGTCTCTGACCCGGCTTTAGACACACTCCGGTTACTACCG

5. In 1988, the disease BLAD (Bovine Leukocyte Adhesion Deficiency) specific to Holstein cattle was affecting the US dairy industry. The disease is recessive and two alleles are needed for its expression. The disease is caused by two mutations of the CD18 gene. One of the affected regions is shown below. The DNA of three individuals is shown: an unaffected animal, a carrier, and an affected animal. Only a single strand of DNA from each chromosome is shown to save space.

Unaffected	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGGCCTGTACTACCTGATGGACCTCT	Allele 1
	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGGCCTGTACTACCTGATGGACCTCT	Allele 2
Carrier	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGACCTGTACTACCTGATGGACCTCT	Allele 1
	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGGCCTGTACTACCTGATGGACCTCT	Allele 2
Affected	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGACCTGTACTACCTGATGGACCTCT	Allele 1
	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGACCTGTACTACCTGATGGACCTC	Allele 2

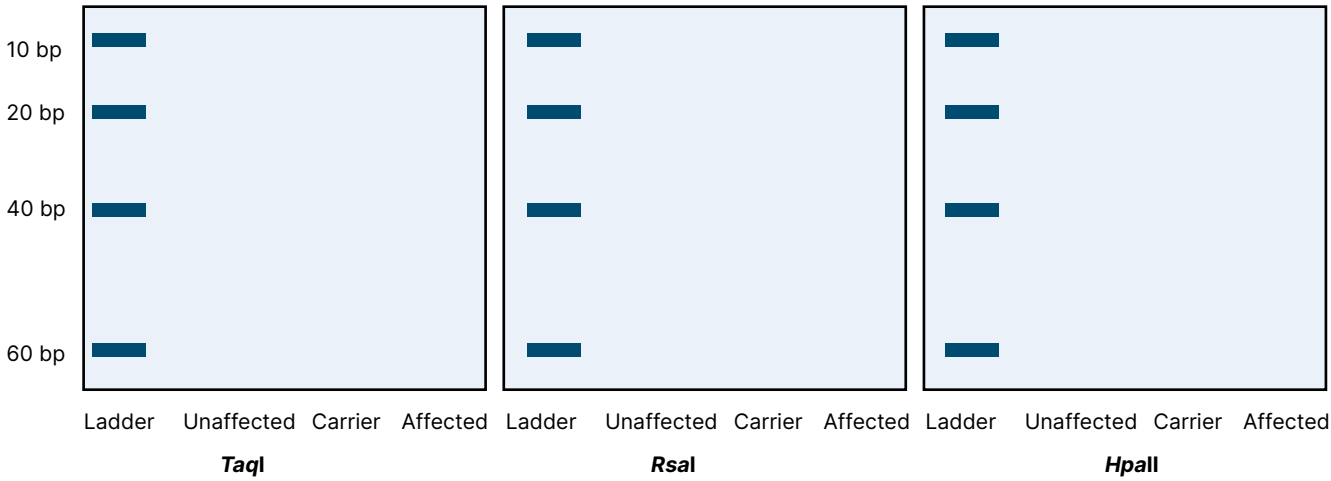
   (a) Use the restriction enzymes *Taq*I, *Hae*III, and *Hpa*II to "cut" the sequences. Write the length of the segments (in bases) produced in the spaces below. **U** = unaffected; **C** = carrier; **A** = affected.
   NOTE: *Taq*I cuts between T and C. *Rsa*I cuts between T and A. *Hpa*II cuts between C and C:

   *Taq*I: **U**: _____ **C**: _____ **A**: _____

   *Rsa*I: **U**: _____ **C**: _____ **A**: _____

   *Hpa*II: **U**: _____ **C** _____ **A**: _____

   (b) On the gels below draw in the bands that would be seen for each individual for each restriction enzyme:



   (c) Decide which restriction enzyme(s) would be useful for identifying carriers of BLAD: _____

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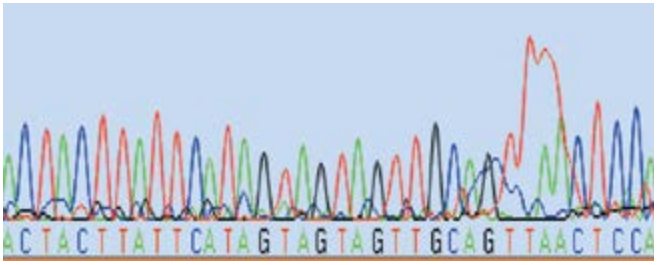
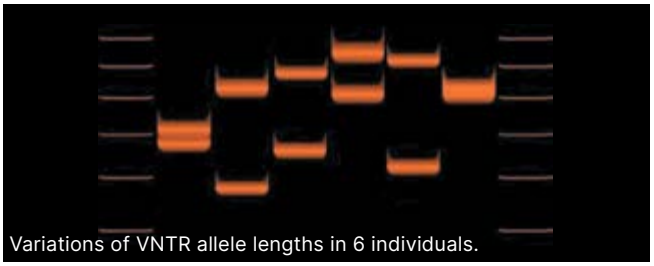
140 Applications of DNA Analysis

Key Idea: DNA profiling involves the comparison of DNA samples. DNA sequencing is the process of determining the order of nucleotides in DNA.

DNA can be analysed in different ways depending on what information a researcher is seeking. **DNA sequencing** determines the sequence of nucleotides (As, Ts, Cs, and Gs) in a gene or section of DNA. Sequencing has many applications including in molecular biology, evolutionary biology, and medicine. **DNA profiling** looks at a specific DNA pattern (profile) and compares it to another. Like DNA sequencing, DNA profiling has applications in many areas of science, but is most notable in **forensics**. DNA profiling is used in criminal cases, for paternity testing, and even in identifying animal products illegally made from endangered species.





Variations of VNTR allele lengths in 6 individuals.

Palewhalegail CC 3.0

DNA sequencing

DNA sequencing can be used to sequence all of an organism's genetic material (its genome). It was once an expensive, time consuming, and laborious process, with large genomes needing to be broken down into small pieces and amplified using **polymerase chain reaction** first, then visualised using **gel electrophoresis**. Supercomputers were needed to analyse long overlapping DNA sequences. Current high throughput sequencing technologies have automated DNA sequencing and there are a number of different ways the sequencing is carried out. The sequencing of a cell's DNA can now be done in hours, rather than months.

Once the sequence is obtained, the information can be used to:

- Locate specific genes (e.g. associated with a disease) and target genes in gene therapy (correcting a defective gene).
- Determine the function of a gene.
- Provide information on the evolutionary history and/or relatedness between species.
- To improve **genetic modification** techniques.

DNA profiling

DNA profiling is also called DNA fingerprinting. Unlike sequencing, profiling does not attempt to determine DNA sequence. Instead the DNA profiles of individuals are compared to determine if a sample of DNA has come from a particular individual or not.

Within DNA there are regions containing short repeating DNA sequences. The sequences, called short tandem repeats (STRs), are only 2-6 base pairs long. STRs can repeat up to 100 times so there is STR variation between individuals. This variation can be used to identify a person's unique STR profile. Longer sequences of tandem repeats, called variable number tandem repeats (VNTRs), are also used in profiling (above).

Two common applications of DNA profiling are:

- Paternity testing (determining who the father of a child is).
- Forensic investigations. The DNA profile of a suspect is compared to DNA evidence collected at a crime scene to see if they were involved in the crime.

1. Explain the difference between DNA sequencing and DNA profiling: _____

2. There are about 3.2 billion base pairs in the human genome. 99.9% of the genome is identical between humans. Calculate the number of base pairs that are variable in humans:

3. (a) What are short tandem repeats? _____

   (b) Explain how STRs cause variation between individuals: _____

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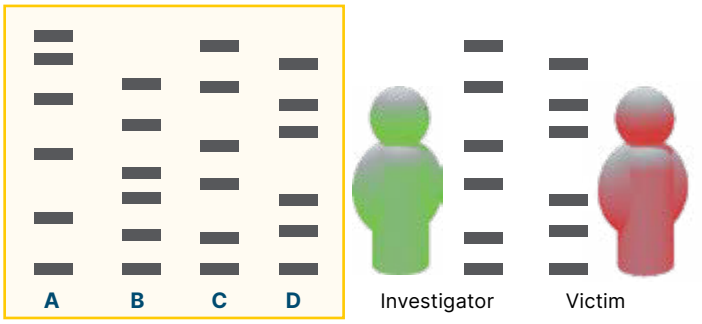
Using DNA to solve crimes

Although it does not make a complete case on it own, DNA profiling (in conjunction with other evidence) is one of the most powerful tools in identifying offenders or unknown tissues.

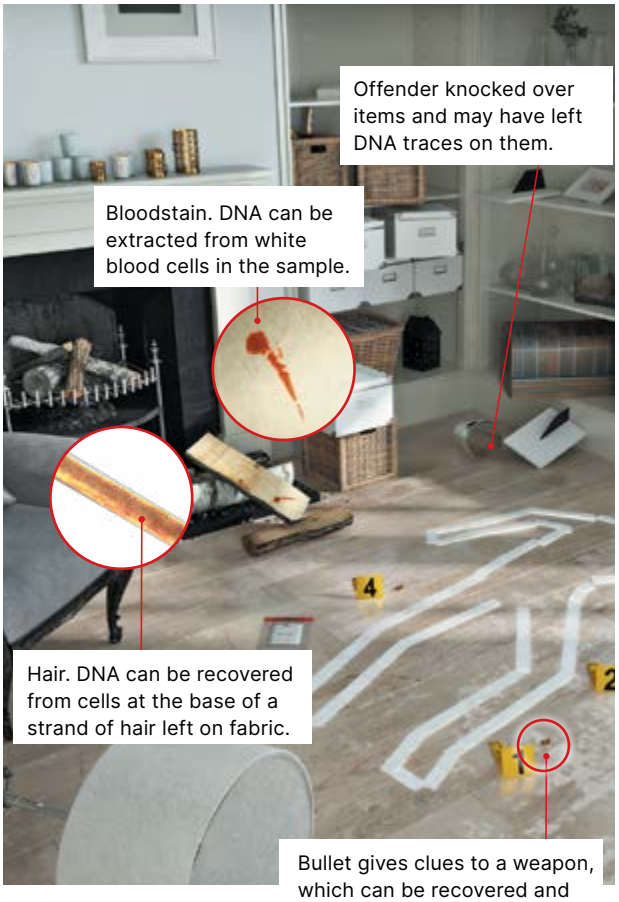
A lot of DNA is found at crime scenes and the information collected can be used to help identify the criminal. However, not all of the DNA collected will be from the criminal. Other DNA could belong to the victim, people who came to their aid (e.g. paramedics) or the police investigators (if they have not taken correct precautions).

In the example (right) the criminal who broke into this home has left behind several samples of their DNA. Samples of material that may contain DNA are taken for analysis. At a crime scene, this may include blood and body fluids as well as samples of clothing or objects that the offender might have touched. Samples from the victim and the investigator are also taken to eliminate them as a possible source of contamination (below). In this example, the DNA of the people who live in the house will also be collected so that their profiles can be eliminated. A calibration or standard is run so that the technician knows the profile has run correctly.



Calibration

Profiles of DNA at the crime scene



There are two different ways an offender can be identified through DNA profiling. If a person is suspected of a crime, a sample of their DNA can be taken (e.g. blood sample) and compared to DNA evidence collected at the crime scene. A match indicates they are the offender. If there is no match, the person can be cleared as a suspect. In cases where the suspect is unknown, biological evidence from the crime scene is analysed and the profile is compared to known offender profiles in DNA databases. The profile may match that of a known offender.

4. Below are the DNA sequences for four different species:

   Cow DNA sequence: **TGA TTG TAA GCT TTC AGG GTG GGT GAT TA**

   Sheep DNA sequence: **TAG TTG TAG GCT TTT TGG GTG GGT GAT TA**

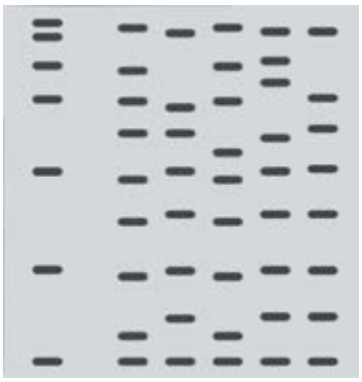
   Goat DNA sequence: **TGG TTG TAG GCT TTC TGG GTG GGT AAT TA**

   Horse DNA sequence: **TGT TTG TAG GCC TTT AGA GTG GGT GAT TA**

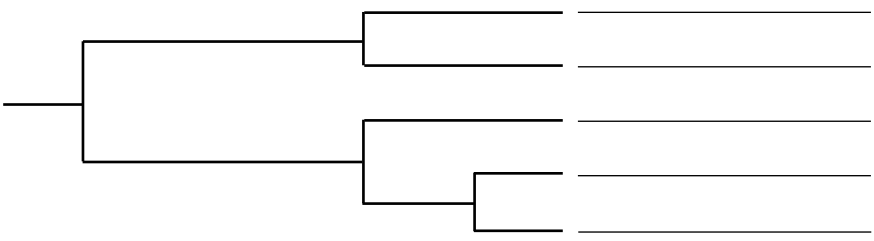
   Based on the number of differences in the DNA sequences:

   (a) Identify the two species that are most closely related: _____

   (b) Identify the two species that are the least closely related: _____



5. Determine the relatedness of each individual (A-E) using each banding pattern on the set of DNA profiles (left). When you have done this, complete the phylogenetic tree by adding the letter of each individual.



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Paternity testing

DNA profiling can be used to determine paternity (and maternity) by looking for matches in alleles between parents and children. It is used in cases such as child support or inheritance. DNA profiling can establish the certainty of paternity (and maternity) to a 99.99% probability of parentage.

Every STR allele is given the number of its repeats as its name, e.g. 8 or 9. In a paternity case, the mother may be 11, 12 and the father may be 8, 13 for a particular STR. The child will have a combination of these. The table below illustrates this:

DNA marker	Mother's alleles	Child's alleles	Father's alleles
CSF1PO	7, 8	8, 9	9, 12
D10S1248	14, 15	11, 14	10, 11
D12S391	16, 17	17, 17	17, 18
D13S317	10, 11	9, 10	8, 9

The frequency of the each allele occurring in the population is important when determining paternity (or maternity). For example, DNA marker CSF1PO allele 9 has a frequency of 0.0294 making the match between father and child very significant (whereas allele 12 has a frequency of 0.3446, making a match less significant). For each allele, a paternity index (PI) is calculated. These indicate the significance of the match. The PIs are combined to produce a probability of parentage. 10-13 different STRs are used to identify paternity. Mismatches of two STRs between the male and child is enough to exclude the male as the biological father.

Whale DNA: tracking illegal slaughter

Under International Whaling Commission regulations, some species of whales can be captured for scientific research and their meat can be sold legally. Most whales, including humpback and blue whales, are fully protected and to capture or kill them is illegal.

Between 1999 and 2003, researchers used DNA profiling to investigate whale meat sold in markets in Japan and South Korea. They found 10% of the samples tested were from fully protected whales including western grey whales and humpbacks. They also found that many more whales were being killed than were being officially reported.

6. Which of the profiles A-D at the top of the previous page belong to:

   (a) The victim: _____ (b) The investigator: _____ (c) Unknown suspect: _____

7. Study the profile on the right.

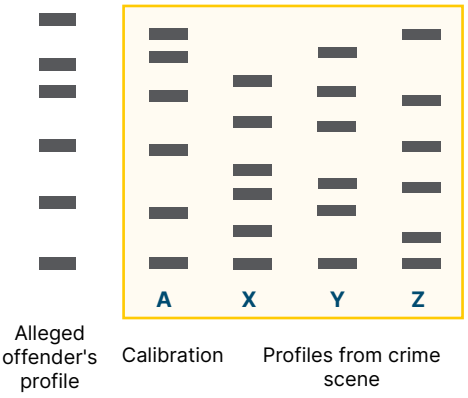
   (a) Is the alleged offender innocent or guilty?_____

   (b) Explain your decision: _____

   _____

   _____

   _____



8. For the STR D10S1248 in the example below right, what possible allele combinations could the child have?

   _____

9 A paternity test was carried out and the abbreviated results are shown right:

   (a) Could the man be the biological father? _____

   (b) Explain your answer: _____

   _____

   _____

   _____

DNA marker	Mother's alleles	Child's alleles	Man's alleles
CSF1PO	7, 8	8, 9	9, 12
D10S1248	14, 15	11, 14	10, 11
D19S433	9, 10	10,15	14, 16
D13S317	10, 11	9, 10	8, 9
D2S441	7, 15	7, 9	14, 17

10. How could DNA profiling be used to refute official claims of the type of whales captured and sold in fish markets?

    _____

    _____

    _____

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141 How Well Does DNA Profiling Work?

Key Idea: The type of DNA sample influences the success of DNA profiling in forensic cases.

DNA profiling to identify an offender at a crime scene is an important aspect of **forensic** investigations. To cope with the large number of samples analysed in Australia, investigators are continually improving their processes to increase throughput but still maintain the accuracy and reliability of the data produced.

Efficiencies cannot be increased at the expense of reliability. Identifying the wrong person could mean they are convicted for a crime they didn't commit, while the person who committed the crime goes unpunished (and may offend again). Several factors increase the chances of obtaining a successful profile. One factor is the type of sample used to obtain the DNA (below).

How does sample type affect profiling success?

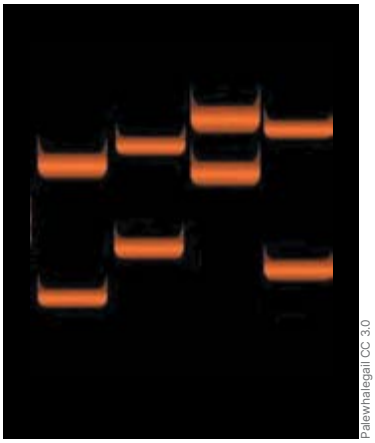
Between 2012 and 2013, new **DNA** analysis kits were introduced into forensic laboratories in Australia. The new kits analysed more DNA markers than the old kits. A project was carried out to compare the results from the old kits with those from the new kits.

One of the study areas examined how sample type affected the success rate. These results are shown in Table 1. The criterion for a successful match was matching more than 6 alleles. When fewer than 6 alleles matches were obtained, the match was recorded as unsuccessful. DNA analysis was carried out using blood, saliva, and trace DNA samples. Trace DNA is any sample that falls below the recommended thresholds for the analysis, and cannot be defined by a precise picogram amount.

Table 1. DNA profile success rates from different samples using two different types of DNA analysis kits, the older Profiler Plus and newer Powerplex 21.

	Sample type	Profiler plus kit		Powerplex 21 kit	
		Number of items	Successful profiles (%)	Number of items	Successful profiles (%)
Swab	Blood	43	92.6	20	90.4
Clothing	Blood	3	100.0	6	100.0
Cigarette butt	Saliva	53	71.1	9	66.6
Mouth/rim bottle	Saliva	54	68.5	1	100.0
Clothing	Trace	50	70.0	57	50.8
Items: Probable friction	Trace	16	37.5	41	48.7
Items: No probable friction	Trace	27	55.5	133	46.6

Data: DNA Profiling success rates on volume crime cases to determine the optimal number and type of samples that should be analysed per case. Linzi Wilson-Wilde, Mojca Kegolvic, and Simon Walsh. Presented to the 25th Congress of the International Society for Forensic Genetics, 2 – 7 September 2013.



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1. Explain why it is important that a fast analysis time is balanced with high accuracy rate: _____

_____

_____

_____

2. Table 1 shows the successful rates of DNA profiles obtained from a number of different sample types.

   (a) Identify the sample type with the highest successful profiles: _____

   (b) Identify which sample type is the least likely to produce a successful profile: _____

   (c) Explain why the sample you named in (b) is the less likely to produce a successful profile: _____

_____

_____

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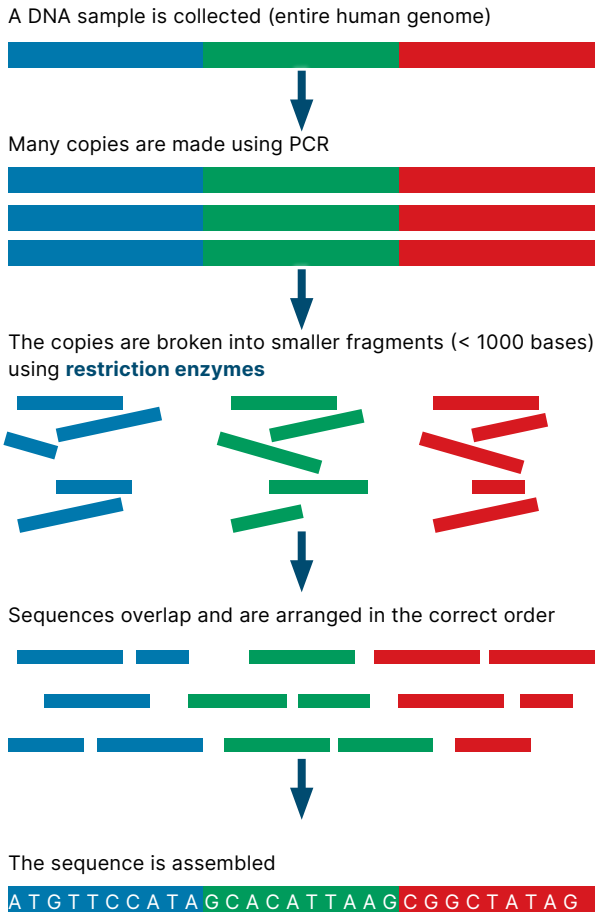
142 The Human Genome Project

Key Idea: The Human Genome Project (HGP) sequenced the entire human genome. The information is used in many fields of science and medicine.

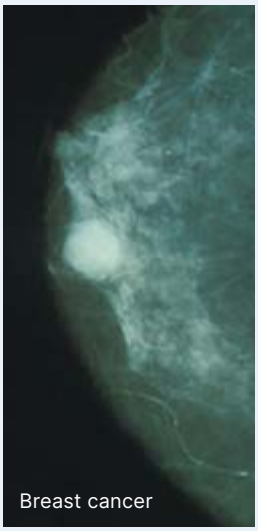
The Human Genome Project (HGP) was an international collaboration to sequence the entire human genome (about 3.2 billion base pairs from a small number of individuals). It took 13 years to complete and cost US$1 billion dollars. The sequence information was made freely available so that it could be used for various purposes in a variety of scientific fields (below). Since the HGP, sequencing technology has advanced at an extraordinary rate. An individual genome can now be sequenced in 2 days at a cost of less than US$5000.

A hierarchical shotgun method was used to sequence the human genome

The HGP began when sequencing technology was relatively primitive compared to today. Sequencing methods could only sequence DNA molecules that were around 1000 basepairs long. This meant that the human genome had to be broken up into millions of short sections that needed to be sequenced (being scattered like gun shot). Those short sequences then need to be arranged back into the correct order. To do this, newer, more powerful computers were needed. In many ways, the HGP helped boost not only gene sequencing technology but also the capabilities of computers.

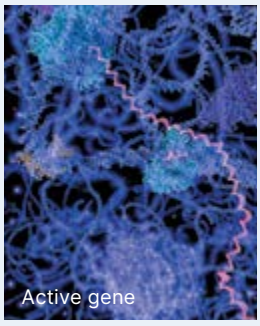


How is the information from the HGP used?

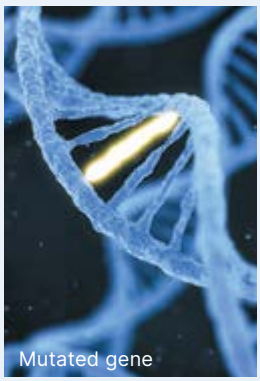


Identifying and treating disease: By comparing the genomes of healthy individuals to those with a particular disease, it is possible to see if a particular variation is associated with the disease. The information can be used to predict disease risk and to take measures to reduce risk where possible.

Researchers have developed tests to look for specific diseases and design new medicines to treat disease. For example, 20% of breast cancers are caused by the HER-2 mutation. Herceptin was developed to specifically treat women with the HER-2 mutation and increase patient survival.



Identifying genes and functionality: Before the HGP the genome was thought to encode ~100,000 genes. We now know that number is much smaller (~20,000). Projects such as ENCODE identify functional elements of the DNA sequence, helping us to understand how genes (and metabolic processes) are regulated. The knowledge could be used to switch off undesirable genes.



Evolution and species comparisons: The DNA sequences for particular genes between species can be compared to learn about their evolutionary history. Species with fewer differences are more closely related than species with more differences. Researchers can determine the effects of human genes by studying the same gene in other species. For example, studying the genes for DNA repair in rodents has provided information about cancer development in humans.

1. (a) What was the purpose of the Human Genome Project? _____

   _____

   (b) Identify uses of this information: _____

   _____

2. Why do you think it was important that the information was made freely available to scientists and researchers?

   _____

   _____

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143 Bioinformatics

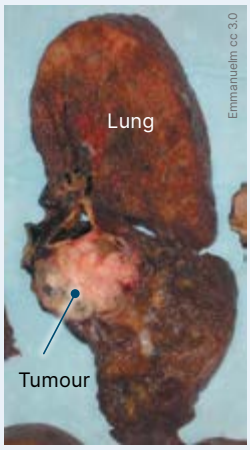
Key Idea: Bioinformatics uses powerful computing and mathematical tools to collect, store, and analyse large amounts of biological information, such as HGP data.

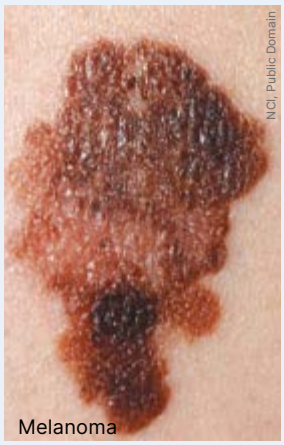
Bioinformatics is the collection, storage, and mathematical analysis of biological information using computers. It is often used in the fields of molecular phylogenetics and genome studies. The information is stored in databases where it can easily be retrieved, analysed, and compared. Improved technology (e.g. faster computing power) allows large amounts of data to be analysed very quickly. Bioinformatics has been important in the rapid analysis of the data from the HGP. Some bioinformatics applications are described below.

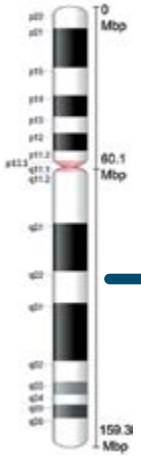
Using bioinformatics and genome analysis to tackle cancer

The Cancer Genome Atlas (**TCGA**) was a project with the aim of improving the diagnosis, treatment, and prevention of cancer and is an excellent example of the use of bioinformatics. It ran for 12 years and closed in 2018. The data is now available on line at the TCGA website. During the time it ran the TCGA:

- Collected data from 11,000 patients.
- Produced over 2.5 petabytes of data (that is equivalent to 212,000 DVDs of data).
- Characterised 33 different types of cancers.
- Used the data to detect cancerous mutations, identify cancer markers, and understand the molecular and functional basis of tumour behaviour.
- Provided information for the development and delivery of highly specific cancer drugs (see below).

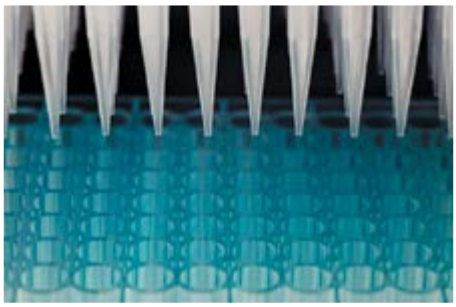






The EGFR gene is located between 55 and 55.2 Mbp on the p arm of chromosome 7.

Sequencing and gene mapping (knowing a gene's location) allows researchers to identify mutations that can cause cells to become cancerous. For example, mutations causing over-expression of the EGFR gene causes many cancers.



Understanding the role of specific genes in cancer helps researchers develop therapeutic drugs. The use of bioinformatics and high throughput screening of potential new drugs means many drugs can be developed and tested for effectiveness in a short space of time. Researchers use the information from the HGP to develop drugs to target specific types of cancer. This is called targeted drug therapy.

An ideal targeted drug therapy acts on a specific type of abnormal cell while leaving normal cells unaffected. Often, these drugs have fewer side effects as a result. Iressa (above) is an example of targeted drug therapy. Iressa is designed to treat cancerous cells in the lung with a mutation to the EGFR gene. Iressa blocks signals to the cancer cell telling it to grow and divide. It will not work on tumours without the EGFR mutation.

1. What is bioinformatics? _____

2. How has bioinformatics made projects like The Cancer Genome Atlas possible? _____

3. Using an example, explain how detailed genomic information can be used for targeted therapy: _____

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144 Genome Sequencing For All!

Key Idea: Many companies offer cheap genetic testing directly to the public. However, the testing procedure and interpretation are not always accurate.

Several companies sell cheap DNA test kits directly to the public, often for less than $300. It is now possible to test the **DNA** of pets, mostly dogs, to identity or confirm breeding ancestry. All the consumer has to do is provide a saliva sample and send it off for analysis. The most common tests purchased provide information about ancestry, but some also test for genetic health risks. The tests are very popular, and consumers often see them as harmless fun. But there are some serious consequences people often don't think about. How reliable are the results and what happens to your information once it is collected?

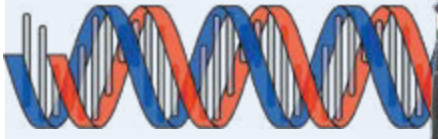
What does my DNA tell me?

People use DNA testing to find out all sorts of information about themselves. This includes:

- Where did my ancestors come from?
- What diseases could I develop in the future?
- Could I pass on an inherited disease to my future children?
- Who is my father?

Hundreds of companies (including Australian ones) offer to provide answers to these questions. The tests are incredibly popular, millions of people have taken DNA tests, including at least 20,000 Australians.

At the moment most kits look for specific genes, but whole genome sequencing for less than $1000 may be available soon.



Can I trust the results?

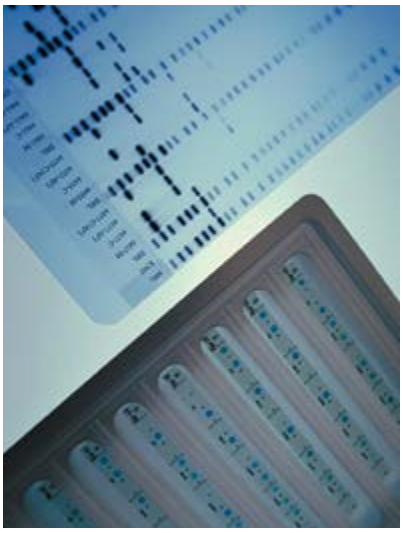
No, not always. Some companies have very rigourous testing procedures while others do not. There have been multiple reports of people sending dog DNA to human ancestry testing companies or sending human DNA to dog ancestry testing companies only for the company to not notice and insist the (obviously incorrect) results are correct. There are also many examples when people have had their ancestry analysed using different companies and come up with very different results. Often the difference is because of differences in their reference databases. Different results are returned based on the size and population sample your DNA is compared to, and as these data sets change over time, so to will the results.

What if testing shows you have a gene linked to a certain disease? Having a particular gene means there is a risk you could develop the disease, but it does not mean you definitely will. Other factors, such as lifestyle and environment also contribute. A positive outcome of the discovery is that you could make lifestyle changes and have regular checks to reduce your disease risk and improve your chances of detecting disease. However, a person could spend their lifetime worrying unnecessarily about a disease that may not develop.

What happens to your information once it is collected?

Most people assume their genetic information is not able to be accessed again or is destroyed, but this is not always the case. Many companies may store the information, and most will have to make it available to authorities in cases of criminal investigations. Company terms and conditions are also subject to change which may put your genetic data at risk. For example in 2018 the company 23andMe made a very low key announcement that they were selling customers' DNA data to GlaxoSmithKline, a large pharmaceutical company. Consumers had to scroll through pages of terms and conditions to find this information in the small print. 23andMe stated the data was being on-sold to the pharmaceutical company so that new drugs could be developed. Additionally there is the risk of data breaches by internet hackers who can then use that data for criminal activities. Other things to considered include:

- A testing company selling customer data is making money, but the customer gets no money.
- Your personal information is being shared with (or stolen by) other parties. Your unique genetic data could be shared and used anywhere without your consent.
- Several studies have shown it is actually possible to track an individual person within a large database based on their genetic information. This information could be misused. For example a political candidate may be disadvantaged because they have a risk of developing Alzheimer's.



1. Work in pairs to discuss the pros and cons of cheap genetic testing, then join with another pair to hear their discussion points. At the end of your discussion decide whether you think DNA testing kits are a good or bad idea.

   Summarise you ideas and staple them to this page.

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145 Genetic Technology and Disease Treatment

Key Idea: The genome can be scanned to identify possible disease risk and identify a treatment.

The genetic screening of gametes, embryos, children, and adults for some diseases is now possible. Genetic screening has many applications including in the detection and treatment of diseases. Genetic screening has many positive applications, but it raises a number of ethical issues. This is particularly the case for the screening of embryos and fetuses because it may result in their destruction if they have genetic defects, or even an undesirable genotype (e.g. the wrong sex). Screening allows doctors to tailor a course of medicine to more efficiently treat a patient.

Why carry out genetic screening?

Carrier testing: A person with a family history for a disease may want to be tested to see if they carry the gene for that disease. The result may influence whether or not they choose to have children.

Pharmacogenetics: Genetic screening can be used to help decide what type, or dose, of medicine will be best for an individual. Targeted treatment can increase the chances of the medicine working.

USAF

Newborn screening: Newborns are screened for a range of metabolic disorders (e.g. phenylketonuria). If a disease is detected, treatment can begin immediately and the child's prognosis is improved.

Arguments for genetic screening

- Testing allows potential carriers to be screened for a disease so they can decide whether they have children or not. This is important for diseases that do not show any symptoms until later in life (e.g. Huntington's disease).
- Researchers can study individuals with the gene(s) associated with a disease and this may help them to develop a treatment or cure for that disease.
- Knowing a person's genetic make-up can be used to optimise drug therapies and improve treatment outcomes.
- Knowing the risk of developing a disease allows informed decisions to be made about medical options. For example, breast cancer can be treated, so an individual may decide to increase screening to increase the chance of early detection. They may choose to reduce risk factors (e.g. breast removal if they are at high risk of breast cancer).
- The discovery of a genetic defect in an unborn child provides an opportunity to come to terms with the situation and prepare for the delivery and ongoing care of a special needs child.

Arguments against genetic screening

- Genetic tests can only tell you if you carry a gene for an associated disorder. They cannot yet predict when and if you will develop the disease, or to what extent. Testing therefore carries the risk of causing unnecessary anxiety.
- An individual's privacy may be compromised by testing. The knowledge that you may develop a genetic disorder in the future could be used against you (e.g. medical insurance could be declined or an employer may no longer want to employ you).
- Designer babies could be produced where parents pick certain characteristics they want their child to have. This is already seen in countries where more value is placed on the birth of a boy child than a girl, and unwanted female fetuses are terminated.
- The discovery of a genetic defect in an unborn child may lead to the decision to terminate the pregnancy, an action some people believe is morally wrong because they feel it devalues human life.

1. How can genetic screening influence societal perspectives on ethical issues, such as the value of human life and privacy concerns?

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Using genetic studies to identify disease risk and treatment

- Recall that the human genome is 99.9% the same between any two people. Much of the 0.1% difference comes in the form of single nucleotide polymorphisms or SNPs, which are single base-pair differences in a DNA sequence or gene.
- Groups of single nucleotide polymorphisms (SNPs) found close together are called haplotypes. Population wide studies of haplotypes allow scientists to associate different haplotypes, or groups of haplotypes, with diseases.

Identifying a relationship

- To study the genetic component of a disease, researchers require two main study groups: people with the disease and people without the disease (known as phenotype first).
- A genome wide association study (GWAS) is carried out on each individual in each group. The study looks for SNPs (changes to single base pairs) to see if there are differences between the control group and the afflicted group. There are over 100 million SNPs spread throughout the human genome and there are numerous ways to identify them, including **DNA sequencing** and using **restriction enzymes**.
- Once the SNPs are identified, their frequencies are analysed to see if any are significantly different between the groups. SNPs found to be associated with a disease do not always just appear in people with the disease. Often, they can be found in people without the disease. This lack of a definitive link makes linking a disease to a specific DNA profile a matter of probability and risks.

Using profiling to analyse disease risk

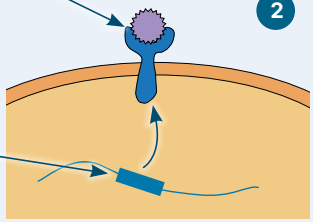
Using **DNA profiling** as a tool to analyse disease risk is a relatively new field. Although it promises a new way of diagnosing disease, to date it has produced inconsistent results because of the complexity of diseases involving large numbers of genes. One promising use of DNA profiling in disease analysis is the ability to determine response to albuterol in the treatment of asthma.

Albuterol is used to relieve the symptoms of asthma. It works well on some people but not on others.

1

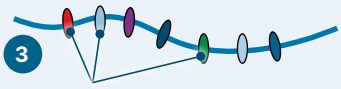
Albuterol binds to the beta2 adrenergic receptor in a cell's plasma membrane and causes the relaxation of smooth muscle in the airways.

2



The beta2 AR protein is encoded by the ADRB2 gene. Scientists wondered if genetic differences in or near this gene affected how well albuterol worked.

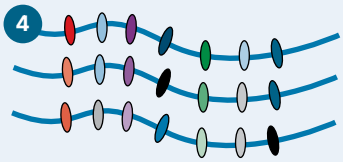
3



SNP

Scientists analysed a 3000 base pair piece of DNA near the ADRB2 gene and identified 13 SNPs.

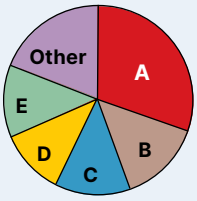
4



The SNPs are found arranged in combinations called haplotypes. 12 different haplotypes have been identified.

% haplotypes in population

5



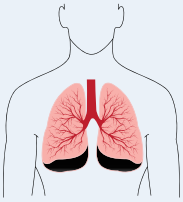
Every person has a haplotype profile relating to the ADRB2 gene. Five of the haplotypes are relatively common.

6

A	Poor
B	Good
C	Fair
D	None
E	Very good

Some of the haplotypes seem to be related to the effect of albuterol on people. Some haplotypes are found mainly in people who have a poor response to albuterol (D), while others are found in people who respond well to the drug (B, E).

7



Patient responsive to albuterol.

This data could possibly be used by doctors when prescribing albuterol. In the future, other profiles could be used to determine the effect of other drugs on people.

2. Explain the use of population wide studies of haplotypes: _____

_____

_____

_____

3. (a) Why is a set of SNPs (a haplotype) used when identifying a genetic disease, rather than just a single SNP?

_____

_____

(b) Why is the use of SNPs not a definitive way to assess the risk of a genetic disease? _____

_____

_____

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146 Did You Get It?

1. The electrophoresis gel (below, right) shows four profiles containing five STR sites: the mother (A) her daughter (B) and two possible fathers (C and D). Which of the possible fathers is the biological father?

   (a) The biological father is: _____

   (b) Why do profiles B and D only have 9 bands?

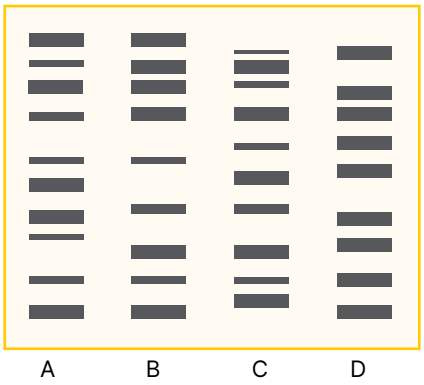
   _____

   _____

   _____

   _____

   _____



2. Distinguish between VNTRs and STRs and outline their uses in modern genetics: _____

   _____

   _____

   _____

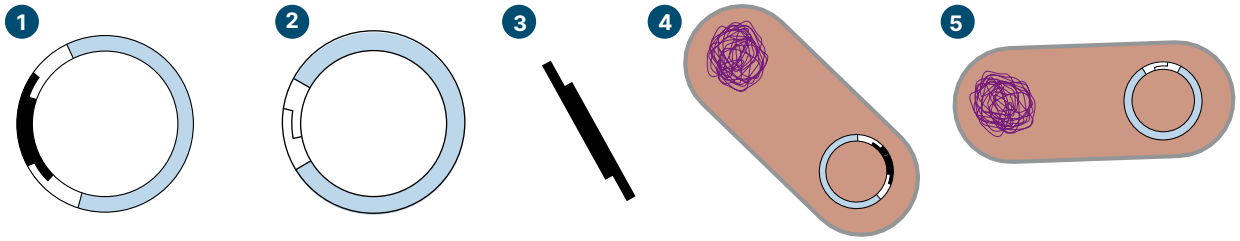
   _____

3. Below is a DNA sequence of sections A, B, C, D, E, F and G and A', B', C', D', E', F' and G'. You want to isolate the sections B, C, D and E as a continuous group by PCR (and B', C', D', E'). Primers are E' and B. How many PCR cycles are needed to fully isolate the sequence B, C, D, and E, and B', C', D', and E'?

A	B	C	D	E	F	G
A'	B'	C'	D'	E'	F'	G'

   _____

4. Put the numbered items in the correct order for producing a transformed bacterial cell and provide a description of each step in the process:



   _____

   _____

   _____

   _____

   _____

   _____

   _____

5. Define the following terms:

   (a) Recombinant DNA: _____

   (b) transgenic organism: _____

   _____

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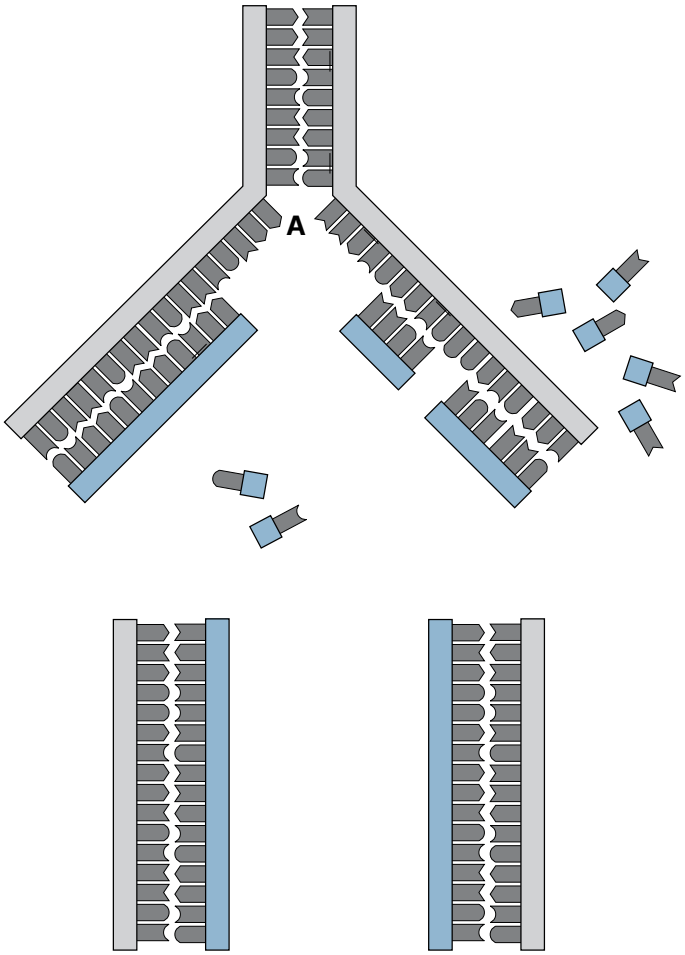
147 Synoptic Questions: Unit 4, Topic 1

1. The diagram below shows a simplified overview of DNA replication. Summarise the process by labelling the diagram according to the questions below:



(a) Label the 5' and 3' ends of all strands on the DNA being replicated.

(b) Label:
- (i) A parent strand
- (ii) A daughter strand
- (iii) Free nucleotides
- (iv) The new chromatids
- (v) The leading strand
- (vi) The lagging strand

(c) Draw in the likely positions of:

- (i) DNA polymerase
- (ii) Helicase

(d) What is happening at position A?

_____

_____

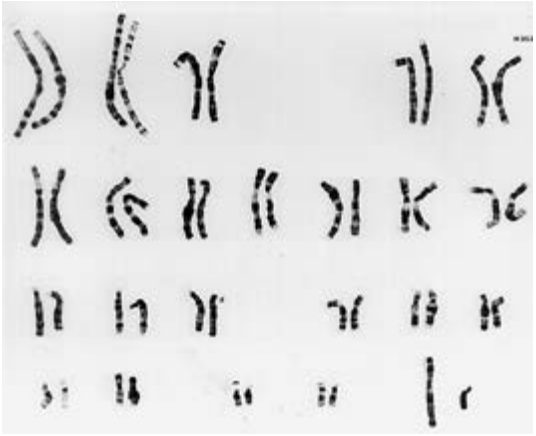
_____

_____

(e) Circle the nucleotide to be added next to the leading strand and use an arrow to show where it will go.

(f) Circle the nucleotide to be added next to the lagging strand and use an arrow to show where it will go.

2. The preparation of a karyogram involves arranging the chromosomes of an individual into homologous pairs in order.



Cytogenetics Dept, Waikato Hospital

(a) Study the karyogram on the right. Circle the sex chromosomes:

(b) State the sex of this individual: _____

(c) Determine if the karyotype shown is normal/abnormal:

(d) Explain the reason for the answer you have given in (c):

_____

_____

_____

_____

3. (a) What would you expect to see in the karyogram of an individual with Down syndrome?

_____

(b) What type of disorder is Down syndrome? _____

(c) Explain the cause of Down syndrome: _____

_____

_____

_____

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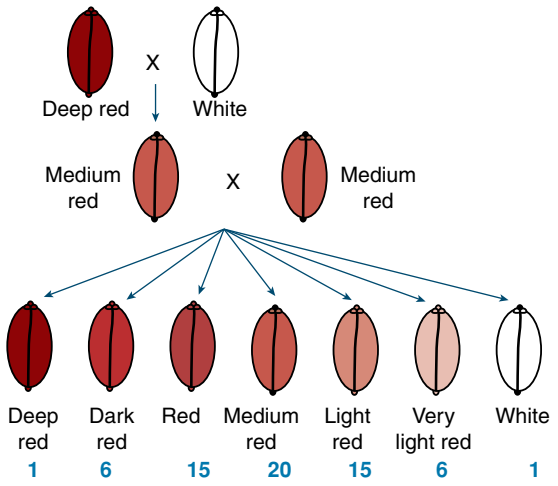
SI SHE

4. The Swedish geneticist Nilsson-Ehle studied the inheritance of wheat kernel colour. Using Mendelian methods, he crossed pure-breeding red-kernel strains with pure-breeding white-kernel strains. The F_1 plants produced seeds intermediate in colour between the two parents. When he then crossed these F_1 plants, the F_2 generation segregated as shown in the diagram right.



(a) What type of inheritance is involved in this example?

_____

(b) How many genes are involved: _____

(c) What other factor could be influencing the outcome of the cross and how could you test for its influence?

_____

_____

_____

(d) Identify another phenotypic character with this type of inheritance pattern: _____

5. The diagram below shows a simplified eukaryotic gene.

(a) What are the grey coloured regions and what is their general role? _____

_____

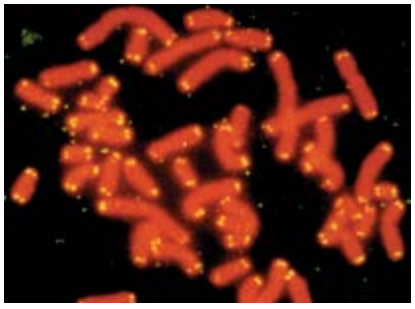
(b) What is the fate of the exon regions of the gene?_____

_____

(c) What is the fate of the intron regions of the gene? _____

_____

6. (a) Identify the white regions on the human chromosomes pictured right:



_____

(b) What are they made up of? _____

_____

(c) What is their role? _____

_____

7. Explain the role of each of the following tools in the processes identified:

(a) PCR in genome mapping:_____

_____

_____

(b) Gel electrophoresis in DNA profiling:_____

_____

_____

(c) Restriction enzymes in making a transgenic organism: _____

_____

_____

8. Our understanding of genetics and heredity has resulted from collaboration of many different scientists and scientific disciplines, many of which have been mentioned in chapters of this topic (chapters 8-13). Pick one of the scientists mentioned and, on a separate piece of paper, write a short description (max 100 words) of their contributions to science. Attach your answer to this page.

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Chapter 13 Unit 4 Topic 2

Evolution

Resource Hub
bit.ly/3GLZDaI

Key Terms

- cladogram
- comparative genomics
- evolution
- evolutionary radiation
- extinction
- homology
- macroevolution
- mass extinction
- microevolution
- phylogenetics
- phylogeny
- phylogram

Key Concepts

- Evolution involves heritable genetic changes in populations over time, occurring at two scales: microevolution (changes within species) and macroevolution (formation of new species or genera).
- Comparative genomics, protein homology, and DNA sequencing provide robust evidence for evolutionary relationships, enabling the construction of phylogenetic trees and understanding species divergence.
- Extinction events, such as the Permian and Cretaceous extinctions, create opportunities for evolutionary radiations, resulting in diversity and the emergence of new species.

What is evolution?		Activity Number
☐ 1	What do you understand by the term evolution. Distinguish between microevolution and macroevolution and give examples of each.	148
☐ 2	Determine episodes of evolutionary radiation and mass extinctions from an evolutionary timescale of life on Earth. What were the different causes of evolutionary radiations (increases in taxonomic diversity) and how did they operate? Evolutionary radiations are often associated with and increase in morphological differences between taxa. Can you give an example? Recognise adaptive radiation as a rapid evolutionary radiation within a lineage involving adaptation to different niches	150, 162
☐ 3	**SHE:** Many scientists have contributed to the modern theory of natural selection. Their ideas have been tested and corroborated in accordance with the scientific method. Evolutionary models and theories have been contested and refined or replaced as new evidence has been found, or when a new model or theory has had a greater explanatory power.	149

Comparative genomics and phylogeny		
☐ 4	Understand that the evidence for evolution comes from many disciplines, including morphological comparisons, but increasingly from comparative genomics.	151-153
☐ 5	Comparative genomics compares the genomic information of different organisms in order to determine similarities and differences as well as evolutionary history. Genomic information can include DNA sequences and genes but also proteins, RNA, and regulatory regions. Outline the different ways to obtain genomic information, including (but not restricted to): • Protein homology (e.g. haemoglobin, immunological proteins) • Highly conserved proteins such as cytochrome c • Sequence comparisons by DNA hydridisation • Sequence comparisons by DNA sequencing • Bioinformatics and large scale DNA and protein databases	151-154
☐ 6	Understand the basis of DNA barcoding and molecular phylogenetics. Analyse data from molecular sequences to infer species evolutionary relatedness. Describe the applications of this molecular information.	155
☐ 7	Explain what is meant by a phylogenetic tree. Distinguish between monophyletic, polyphyletic, and paraphyletic taxa in phylogenetic trees.	156
☐ 8	Explain what is meant by a clade and describe the basis of classifying organisms using cladistics. Identify the assumptions of cladistics including shared common ancestry, bifurcation (branching), and parsimony. Interpret cladograms to infer the evolutionary relatedness between groups of organisms.	157
☐ 9	**SHE:** Explain how developments in comparative genomics and bioinformatics, including genome databases and BLAST, provide evidence of evolutionary relationships among organisms.	151-155, 159
☐ 10	**SI:** Explain how phylogenetic data can be used to trace viral evolution and to trace human migration over thousands of years.	160-161
☐ 11	**SI:** Explore the many different areas of science that produce evidence for evolution including morphology, genetics, biogeography, and palaeontology.	151-154

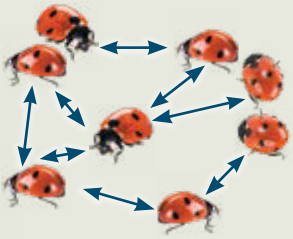
148 What is Evolution?

Key Idea: Evolution of taxonomic groups (macroevolution) results from evolution within species (microevolution).

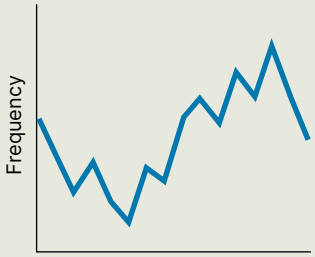
Evolution refers to the heritable genetic changes occurring in a population over time. Importantly, evolution refers to populations, not to individuals and the changes must be passed on to the next generation. Evolutionary processes can be considered at two scales. **Microevolution** refers to changes in the gene or allele frequencies within a species. Microevolution is responsible for changes in a species' genetic make-up in response to environmental changes (e.g. spread of antibiotic resistance). **Macroevolution** refers to evolution above the species level, e.g. the formation of new species or genera. It encompasses increases in taxonomic diversity or morphological differences (**evolutionary radiations**).

Mutation
Mutations produce new alleles (gene variants) and DNA sequences. Many small mutations can result in large changes over many generations.

Natural selection
Individuals with beneficial variations will have an advantage. They will leave more offspring, increasing the frequency of that variation in later generations.



Gene flow
Genetic information flowing into or out of the population affects the population over time. As populations diverge, gene flow is reduced.



Genetic drift
Random changes in gene frequencies between generations affect the genes available for recombining in later generations.

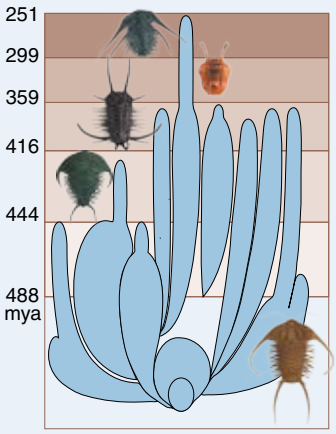
MICROEVOLUTION

MACROEVOLUTION

Zebra karyogram

Horse karyogram

Lions and leopards are more closely related than either are to tigers.



Genomic divergence
Large scale patterns in the number of chromosomes, genes, and genomic organisation reflect evolutionary relationships.

Morphological divergence
Evolutionary radiations are often accompanied by differences in the morphology of taxa. The amount of difference indicates the relatedness of organisms.

Taxonomic diversity
Taxonomy is the science of classifying the diversity that has resulted from macroevolution. Organisms form taxa based on shared characteristics.

Trends and patterns
Macroevolution encompasses trends or patterns in evolution above the species level, such as evolutionary radiation (above) and convergence.

1. Define evolution: _____

_____

_____

2. Using examples, distinguish between macroevolution and microevolution: _____

_____

_____

_____

_____

_____

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149 A Pictorial History of Evolutionary Thought

Key Idea: The modern theory of evolution is the result of many different scientists refining theories based on new evidence.

Although Charles Darwin is largely credited with the development of the theory of **evolution** by natural selection, his ideas did not develop in isolation but within the context of the work of others before him. The modern synthesis of evolution (below) has a long history with contributors from all fields of science. The diagram below summarises just some of the important players in the story of evolutionary biology. This is not to say they were collaborators or always agreed. However, the work of many has contributed to a deeper understanding of evolutionary processes. This understanding continues to develop with the use of molecular techniques and work between scientists across many disciplines.

1900 to present day

1800s

Pre 1800

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GEOLOGY - EARTH'S HISTORY -	PALEONTOLOGY - LIFE'S HISTORY -	THE MECHANISMS OF EVOLUTION	DEVELOPMENT AND GENETICS
			Modern evo-devo *Stephen Jay Gould*
			Genetic similarities *Wilson, Sarich, Sibley, & Ahlquist*
Radiometric dating *Clair Patterson*	Endosymbiosis *Lynn Margulis*	Speciation *Ernst Mayr*	DNA *James Watson & Francis Crick*
THE MODERN SYNTHESIS OF EVOLUTION Brought together many disciplines and showed how mutation and natural selection could produce large-scale evolutionary change. *Theodosius Dobzhansky*			
1900	Human evolution *Huxley & Dubois*		The founding of population genetics *Fisher, Haldane, & Sewall Wright*
			Chromosomes and mutation *Thomas Hunt Morgan*
Biogeography *Wallace & Wegener*			
			Early evo-devo *Ernst Haeckel*
	Evolution by natural selection *Charles Darwin and Alfred Russel Wallace*		
			Genes are discrete *Gregor Mendel*
Uniformitarianism *Charles Lyell*			
			Chromosomal basis of heredity *August Weismann*
Biostratigraphy *William Smith*			
		Evolution *Lamarck*	Developmental studies *Karl Von Baer*
1800	Extinctions *Georges Cuvier*		
Old Earth and ancient life *Comte de Buffon*		The ecology of human populations *Thomas Malthus*	
	The order of nature *Carl Linnaeus*		
1700			
	Fossils and the birth of paleontology		
Observation and natural theology *Important because it addressed the question of how life works*			
	Comparative anatomy *Andreas Vesalius*		

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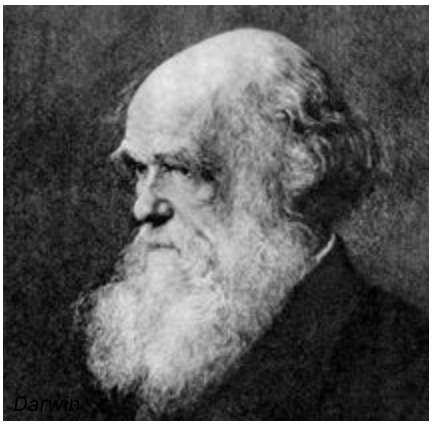
The development of the modern synthesis


Darwin


Wallace

Charles Darwin (1809-1882) and **Alfred Russel Wallace** (1823-1913) jointly and independently proposed the theory of evolution by natural selection. Both amassed large amounts of supporting evidence: Darwin from his voyages aboard the Beagle and in the Galápagos Islands and Wallace from his studies in the Amazon and the Malay archipelago. Wallace wrote to Darwin of his ideas, spurring Darwin to publish *The Origin of Species*.

Gregor Mendel (1822-1884) developed ideas of the genetic basis of inheritance. Mendel's *particulate model of inheritance* was recognized decades later as providing the means by which natural selection could occur.


From the Theodosius Dobzhansky Papers held by the APS. Used under Fair Use licence.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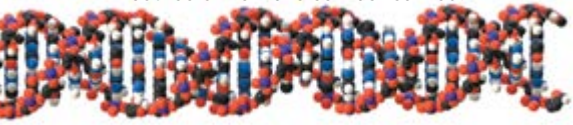
Theodosius Dobzhansky (1900-1975) was a Ukrainian who synthesized the ideas of genetics and evolutionary biology and defined evolution as "a change in the frequency of an allele within a gene pool". Dobzhansky worked on the genetics of wild *Drosophila* species and was famously quoted as saying "Nothing in biology makes sense except in the light of evolution".

Ernst Mayr (1904-2005) was a German evolutionary biologist who collaborated with Dobzhansky to formulate the modern evolutionary synthesis. He worked on and defined various mechanisms of speciation and proposed the existence of rapid speciation events, which became important for later ideas about punctuated equilibrium.

Ronald Fisher, **JBS Haldane**, and **Sewall Wright** founded population genetics, building sophisticated mathematical models of genetic change in populations. Their models, together with the work of others like Mayr and Dobzhansky contributed to the development of the modern synthesis**.** Haldane was quoted as saying the Creator must have "an inordinate fondness for beetles".

The modern synthesis today

James Watson and **Francis Crick**'s discovery of DNA's structure in 1953 revolutionized evolutionary biology. The genetic code could be understood and deciphered, and the role of mutation as the source of new alleles was realized.



After Haeckel's flawed work on embryology, the evolutionary study of embryos was largely abandoned for decades. However, in the 1970s, **Stephen Jay Gould**'s work on the genetic triggers for developmental change brought studies of embryological development back into the forefront. Today, evo-devo (evolutionary developmental biology) provides strong evidence for how novel forms can rapidly arise.


Stephen Jay Gould (1941-2002)
Kathy Chapman online cc 3.0

In recent decades, DNA and protein analyses have revolutionized our understanding of **phylogeny**. **Allan Wilson** was one of a small group of pioneers in this field, using molecular approaches to understand evolutionary change and reconstruct phylogenies, including those of human ancestors.

1. Using a separate sheet, research and then write a 150 word account of the development of evolutionary thought and the importance of contributors from many scientific disciplines in shaping what became the modern synthesis. You should choose specific examples to illustrate your points of discussion.

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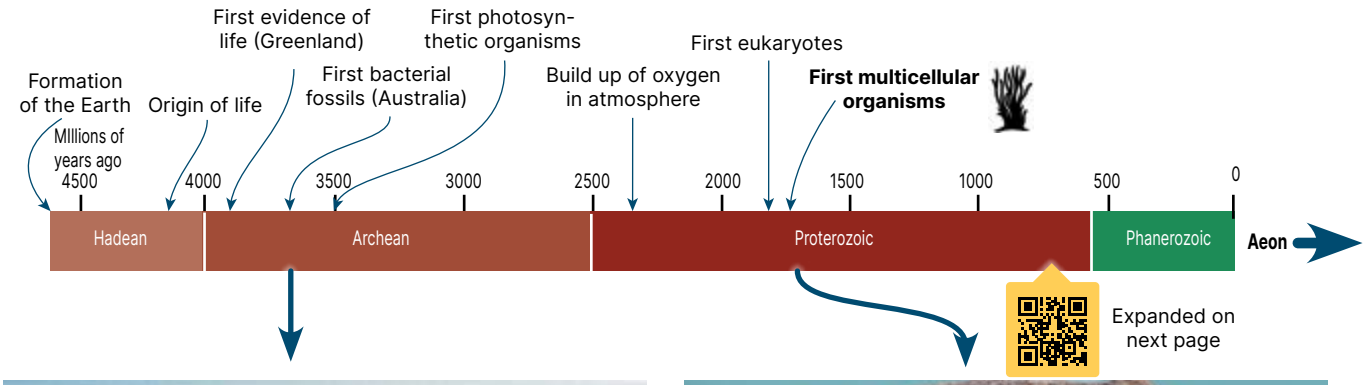
150 Earth's Evolutionary History

Key Idea: Life on Earth originated about 4100 million years ago, but complex life evolved much more recently than this.

Life forms on Earth originally arose from primitive cells living some 4100 million years ago in conditions quite different to those on Earth today. The earliest fossil records of living things show only simple cell types. It is thought that the first cells arose as a result of **evolution** at the chemical level in a 'primordial soup' (a rich broth of chemicals in a warm pool of water, perhaps near a volcanic vent). Life appears very early in Earth's history, but did not evolve beyond the single cell stage until much later (about 600 mya). This would suggest that the evolution of complex life forms required greater hurdles to be overcome. The build up of free atmospheric oxygen, released as a by-product of oxygenic photosynthesis, was important for the evolution of eukaryotes and paved the way for the evolution of multicellular life.

Timeline of Earth's biodiversity



Fossil jellyfish

RA

Stromatolites (such as the ones shown above from Shark Bay, Western Australia), represent some of the most ancient living things on Earth. Few examples exist today, but fossil remains can be dated back to 3.7 billion years ago. Stromatolites are rock-like structures formed from the accretion of sediment by microorganisms, especially cyanobacteria (blue-green photosynthetic bacteria). Ancient representatives of cyanobacteria are thought to have been responsible for the production of oxygen in the atmosphere after they evolved oxygenic photosynthesis (light capture and carbon fixation resulting in oxygen production). It resulted in what is called the Great Oxygenation Event (a rise in atmospheric oxygen), which caused the **extinction** of many anaerobic bacteria but eventually led to the rise of multicellular life forms.

Multicellular organisms arose soon after the evolution of eukaryotes. Multicellularity was a major evolutionary event as it allowed organisms to diversify the tissues and cells of their bodies to perform specialised tasks. The origin of multicellularity is much debated but one hypothesis is that unicellular organisms began to associate together (e.g. cyanobacteria stick together after binary fission and form long chains called filaments). Different cells in the group produced molecules useful to others and so the group benefited by staying together. As the different cell lines became more dependent on others for certain molecules, a greater need to remain together also developed (in low nitrogen conditions, some of the cells in filamentous cyanobacteria transform into nitrogen-fixing cells, and this benefits the other cells in the filament).

1. (a) What was the significance of the buildup of free oxygen in the atmosphere for the evolution of life?

_____

_____

(b) How long did it take for free oxygen to build up in the atmosphere? _____

2. Explain how multicellular life evolved: _____

_____

_____

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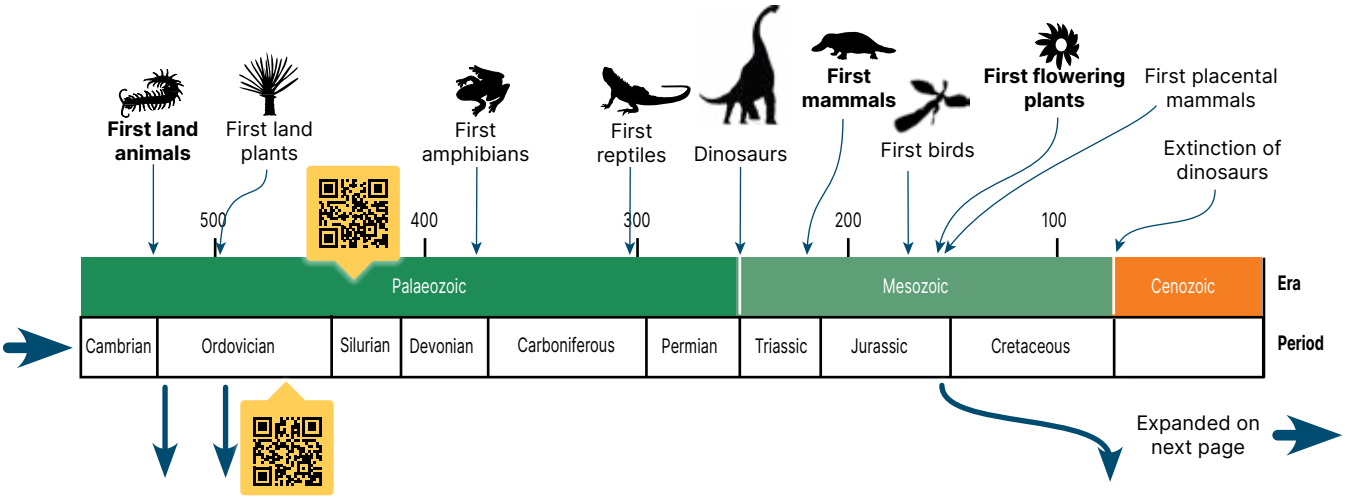
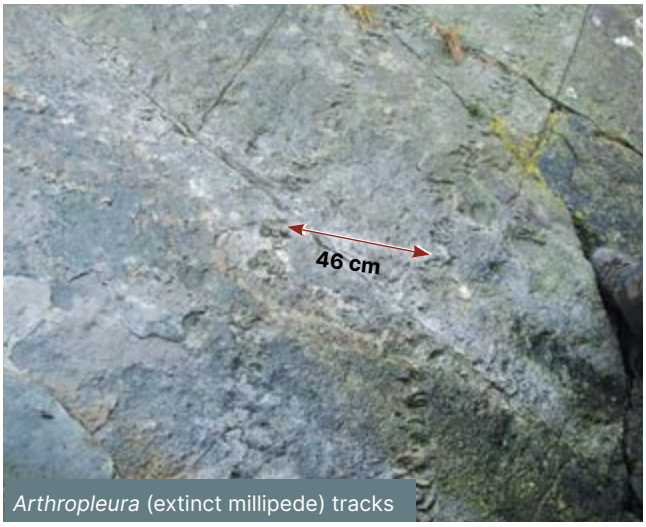
Phanerozoic





Arthropleura (extinct millipede) tracks

Ashley Dace

Animals may have ventured onto land before plants, with evidence suggesting they did so about 530 million years ago. The earliest land animals were invertebrates, perhaps similar to horseshoe crabs, which come ashore to lay eggs on the sand. Strategies like this would have been an advantage at a time when there were no land animals to eat the eggs. Similarly, some of the first excursions onto land may have been to take refuge from aquatic predators. **Plants** may have arrived soon after animals, possibly as early as 500 million years ago. The earliest terrestrial plants had no vascular tissue, like mosses and liverworts today. Vascular plants (e.g. ferns) did not appear until about 425 million years ago but (like many animal taxa) underwent a number of **evolutionary radiations** (increases in taxonomic diversity) once they colonised land.

Flowering plants (angiosperms) are the most successful terrestrial plants. With at least 350,000 species, they make up 90% of all living plant species. Flowering plants first appeared about 160 million years ago. They began to diversify rapidly about 120 million years ago. The evolution of flowers helped to make sexual reproduction more efficient. Flowers attracted insects (and later birds) with the use of colours and rewards (such as nectar). The insects and birds then spread pollen from flower to flower. This system has become so successful that many insects and birds now rely on flowers for food and plants rely on their pollinators for reproduction. Genetic evidence suggests the evolution of flowers was linked to at least two rounds of whole genome duplication, which might explain why angiosperms appeared suddenly in the fossil record.

3. What were the earliest land animals and what circumstances may have caused them to come on to the land?

4. Explain why the evolution of flowers was an advantage to plants. What was the result?

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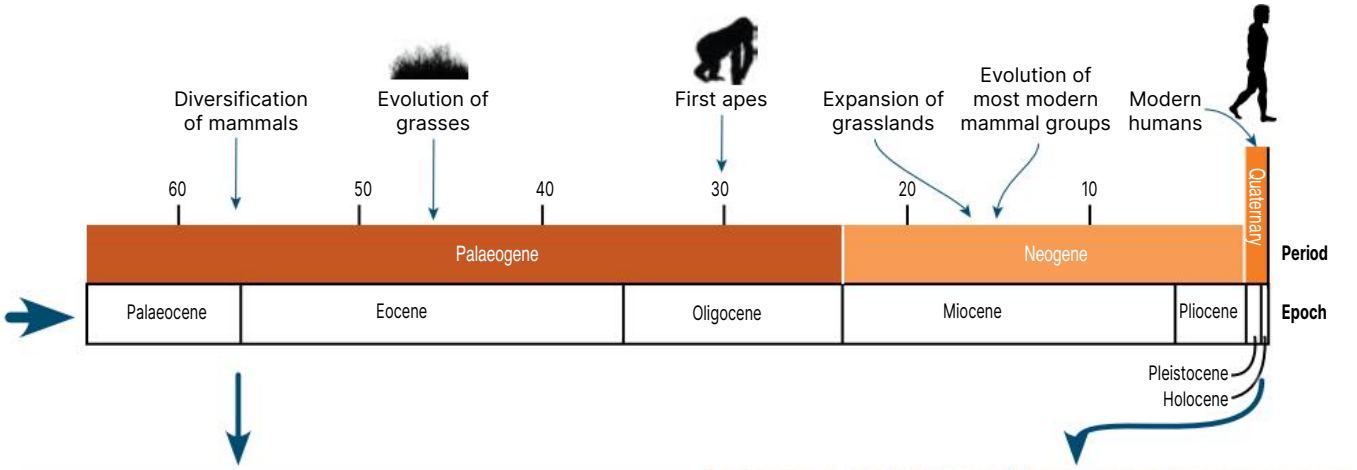
Cenozoic



Both photos NASA

Mammalian evolution can be traced back to the Carboniferous period with the appearance of the synapsids (e.g. *Dimetrodon*), one of the two major clades of tetrapod vertebrates (the other clade gave rise to the reptiles and birds). However, it was not until the Triassic period that the first true mammals appeared. The monotremes (egg laying mammals) appeared about 210 million years ago. Marsupials and placentals probably split about 160 million years ago. Today, marsupials are found almost exclusively in Central and South America and Australia (the North American opossum being the exception). While there are 334 species of marsupials, there are nearly 4000 species of placental mammal. The **evolutionary radiation** of the mammal lineage happened after the **extinction** of the dinosaurs at the end of the Cretaceous. Mammals diversified rapidly to occupy the vacant niches and give rise to the many taxa we see today.

Human ancestors first appeared about 4 million years ago, with the genus *Homo* appearing about 2 million years ago. Modern humans evolved in Africa about 200,000 years ago. In the short time since then, humans have spread across the globe and now influence every single part of the planet in a way no other living thing ever has since photosynthetic organisms changed the nature of the atmosphere 3 billion years ago. Humans, however, have changed the planet in a much shorter time scale, so much so that it has been suggested that the epoch of recent human existence should be called the Anthropocene. This would have begun the same time that humans began to change the Earth on a large scale, perhaps 12,000 years ago, although some proposals would define it as beginning with the Trinity nuclear test in 1945. In many cases, evidence of human activity can be seen in changes in sediments, especially in lake beds (above).

5. Explain why mammals did not diversify until the Palaeocene epoch, even though they first appeared in the Triassic period.

6. The evolution of life on Earth is a history of some lineages diversifying over time and some lineages dying out. Use some examples to explain why diversification takes place:

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151 Protein Homology and Phylogeny

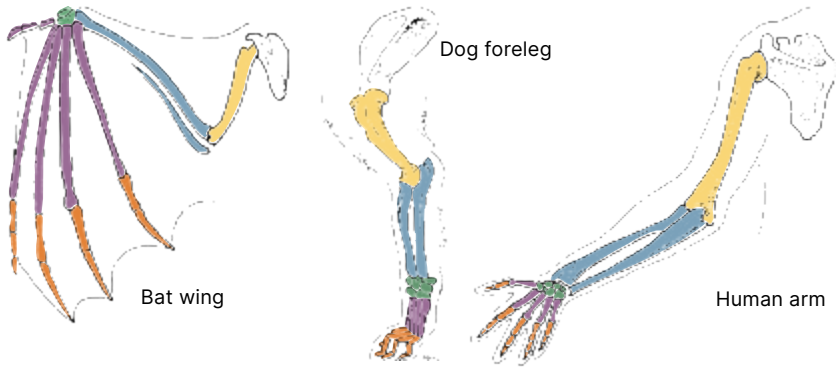
Key Idea: Proteins are the product of gene expression, so an analysis of the differences between the same protein in different taxa gives an indication of species relatedness.

Traditionally, phylogenies were based largely on anatomical traits, and biologists attempted to determine the relationships between taxa based on similarity or by tracing the appearance of key characteristics. With the advent of new molecular techniques, homologies (similarities arising from shared ancestry) could be studied at the molecular level as well and the results compared to phylogenies established using other methods. Protein sequencing provides an excellent tool for establishing homologies. A protein has a specific number of amino acids arranged in a specific order. Any differences in the sequence reflect changes in the DNA sequence. Commonly studied proteins include blood proteins, such as haemoglobin.

What is homology?

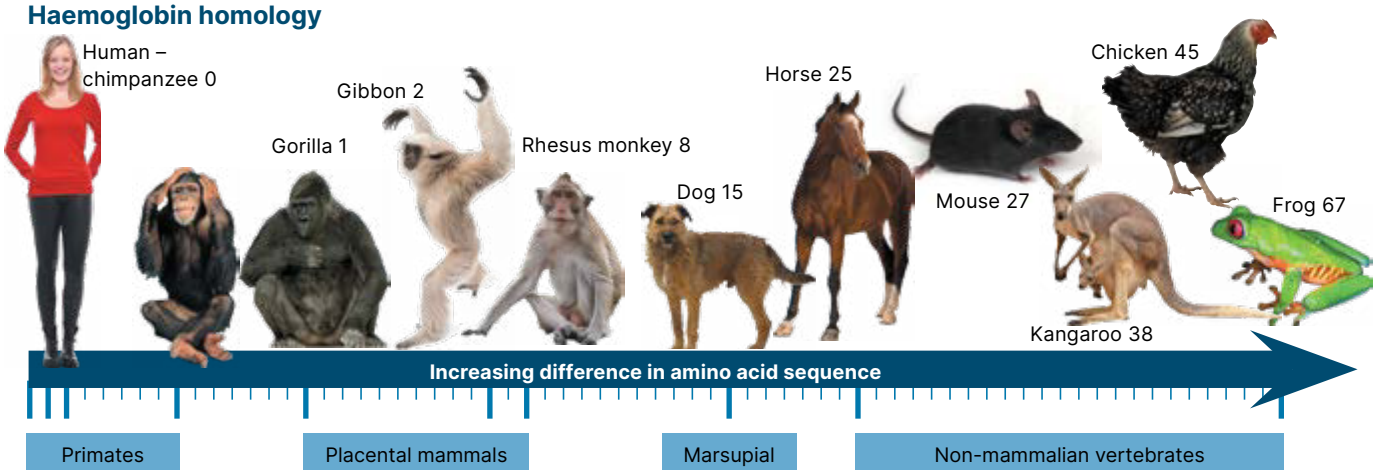
Homology is the similarity between structures, genes, or proteins arising as a result of shared ancestry. In vertebrates, homology can be seen in the bones of the forelimbs (right). It can also be seen in the wings of different insects.

All living things are related through DNA, and DNA includes genes, and genes code for proteins. It follows that, if organisms are related, then that relatedness should be evident in their DNA and proteins. The closer the relatedness, the more homologies we should see.



A bat's wing, a dog's foreleg, and a human arm are all homologous structures.

Haemoglobin homology



Haemoglobin is the oxygen-transporting blood protein found in most vertebrates. The beta chain haemoglobin sequences from different organisms can be compared to determine evolutionary relationships.

As genetic relatedness decreases, the number of amino acid differences between the haemoglobin beta chains of different vertebrates increases (above). For example, there are no amino acid differences between humans and chimpanzees, indicating they recently shared a common ancestor. Humans and frogs have 67 amino acid differences, indicating they had a common ancestor a very long time ago.

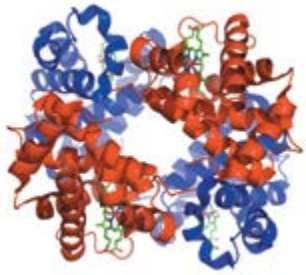


Image: Zephyris CC 3.0

Haemoglobin protein

1. What is homology and how can it be used as evidence for evolutionary processes? _____

2. Compare the differences in the haemoglobin sequence of humans, rhesus monkeys, and horses. What do these tell you about the relative relatedness of these organisms?

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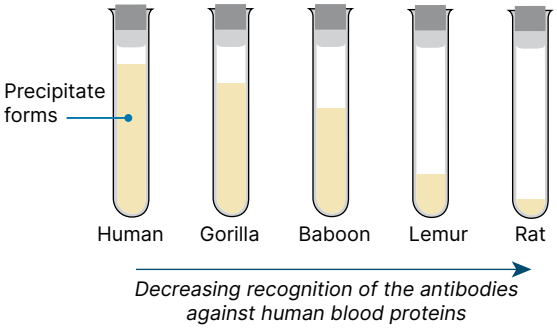
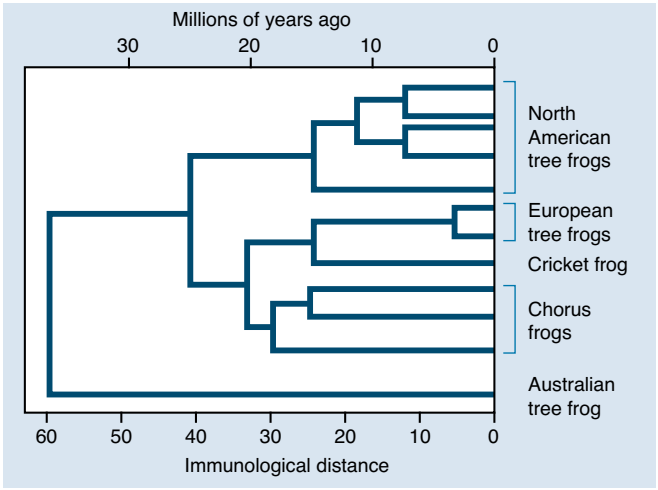
Using immunology to determine phylogeny

The immune system of one species will recognise the blood proteins of another species as foreign and form antibodies against them. This property can be used to determine the extent of relatedness between species. Blood proteins, such as albumins, are used to prepare antiserum in rabbits, a distantly related species. The antiserum contains antibodies against the test blood proteins (e.g. human) and will react to those proteins in any blood sample they are mixed with. The extent of the reaction indicates how similar the proteins are: the greater the reaction, the more similar the proteins. This principle is illustrated (right) for antiserum produced to human blood and its reaction with the blood of other primates and a rat.





The relationships among tree frogs have been established by immunological studies based on blood proteins such as immunoglobulins and albumins. The immunological distance is a measure of the number of amino acid substitutions between two groups. This, in turn, has been calibrated to provide a time scale showing when the various related groups diverged.

3. In humans, the amino acid chain for the protein insulin has 110 amino acids (before post-translational cleaving). The sequences below show the amino acid sequence for amino acids (aa) 1 to 60 of the insulin protein in humans compared to other vertebrates. Each letter stands for a different amino acid:

	1	**60**
Human aa sequence:	FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG	
Chimpanzee aa sequence:	FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG	
Grey wolf aa sequence:	FVNQHLCGSHLVEALYLVCGERGFFYTPKARREVEDLQVRDVELA GAPGEGGLQPLALEG	
Mouse aa sequence:	FVKQHLCGSHLVEALYLVCGERGFFYTPMSRREVEDPQVAQLELGGGPGAGDLQTLALEV	
Jungle fowl aa sequence:	ANQHLCGSHLVEALYLVCGERGFFYSPKARRD VEQPLVSS- PLRGEAGVLPFQQEEYEK	

(a) How many differences are there between a human and chimpanzee insulin? _____

(b) Convert this a percentage similarity: _____

(c) How many differences are there between a human and grey wolf insulin? _____

(d) Convert this a percentage similarity: _____

(e) Do the differences in the insulin protein shown above agree with the differences between human haemoglobin and other vertebrates shown earlier?

_____

4. (a) Explain how a phylogeny (evolutionary history) can be produced from comparing the reaction of blood to antibodies:

_____

_____

_____

(b) Does the amino acid data in Question 3 agree with the haemoglobin information on the previous page? _____

(c) How does this affect our conclusion about the relatedness of organisms? _____

_____

_____

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152 Gene Duplication and Evolution

Key Idea: Genomic comparisons reveal that diversification among arthropod taxa is linked to the duplication and modification of genes and their expression.

Evolutionary developmental biology (evo-devo) is an area of evolutionary biology that examines how changes to developmental processes can result in the novel features we see appearing in **evolutionary radiations**. Genomic comparisons among taxa have been important in revealing how duplication and mutation of the genes regulating development have been important in the **evolution** of novel structures and body plans. In particular, it explains how new characteristics can appear with apparent suddenness.

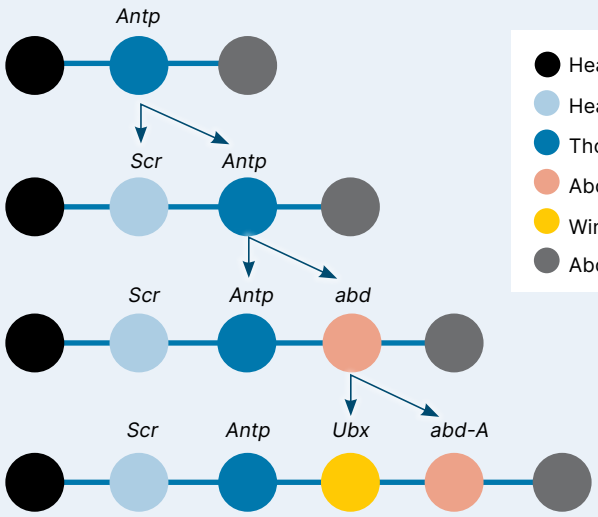
Evolution: you work with what you've got!

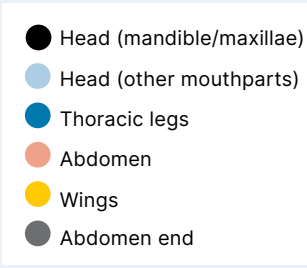
- Genomic studies have revealed the role of developmental genes in the evolution of novel forms and structures, and given valuable insight into the genetic mechanisms underlying evolutionary radiations.
- Arthropods, annelids, and vertebrates, all have highly modular bodies, i.e. the body is made up of repeating units. In arthropods, changes to individual segments through duplication and modification of genes has seen the evolution of a diverse range of body forms.
- For example, a gene involved in the development of appendages in arthropods can be duplicated and the duplicate gene modified. This produces modifications to some appendages, enabling a new set of functions without having to modify all other the appendages.

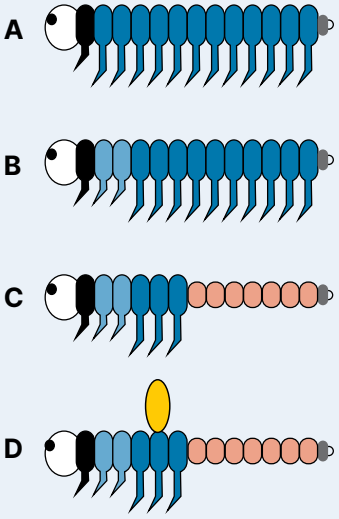
Myriopods | Insects | Arachnids | Crustaceans

Evolution works with what is already present, and 'new' structures are just modifications of pre-existing structures. Segmental modifications produce a large amount of morphological variation in arthropods.

Developmental genes and arthropods







By looking at the DNA sequences in a series of genes we can piece together the order in which genes were duplicated and modified. The sequence above shows the order in which genes that are expressed in various parts of an arthropod appeared, starting with the original antennapedia (Antp) gene, which controls the development of appendages near the head.

We can identify which body segments the genes are expressed in and so work out the order in which body segments were modified. Above we start with a primitive arthropod (**A**). Three genes control development of the head, the middle segments, and the tail. Subsequent duplication and modification of genes produces an arthropod resembling a centipede (**B**), then a primitive wingless insect (**C**), and finally a modern winged insect (**D**).

1. Explain how comparisons of developmental genes among different taxa can provide evidence for how different organisms are related and their evolutionary history:

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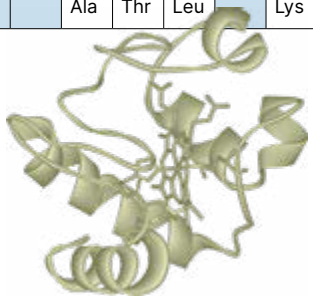
153 What Can Highly Conserved Proteins Tell Us?

Key Idea: Some proteins change very little between even unrelated species. These proteins are called highly conserved.

Some proteins are common in many different species. These proteins are called highly conserved proteins, meaning they change (mutate) very little over time. This is because they have critical roles in the organism (e.g. in cellular respiration) and mutations are likely to be lethal. Evidence indicates that highly conserved proteins are homologous and have been derived from a common ancestor. Because they are highly conserved, changes in the amino acid sequence are likely to represent major divergences between groups during the course of **evolution**. Examples of highly conserved proteins are cytochrome c, a respiratory protein (below) and the Pax-6 protein (bottom).

Cytochrome c compared between species

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
Human	Gly	Asp	Val	Glu	Lys	Gly	Lys	Lys	Ile	Phe	Ile	Met	Lys	Cys	Ser	Gln	Cys	His	Thr	Val	Glu	Lys
Pig											Val	Gln			Ala							
Chicken			Ile						Val		Val	Gln			Ala							
Dogfish									Val		Val	Gln			Ala							Asn
Drosophila <<									Leu		Val	Gln	Arg		Ala							Ala
Wheat <<		Asn	Pro	Asp	Ala		Ala				Lys	Thr	Arg		Ala						Asp	Ala
Yeast <<		Ser	Ala	Lys			Ala	Thr	Leu		Lys	Thr	Arg		Glu	Leu						

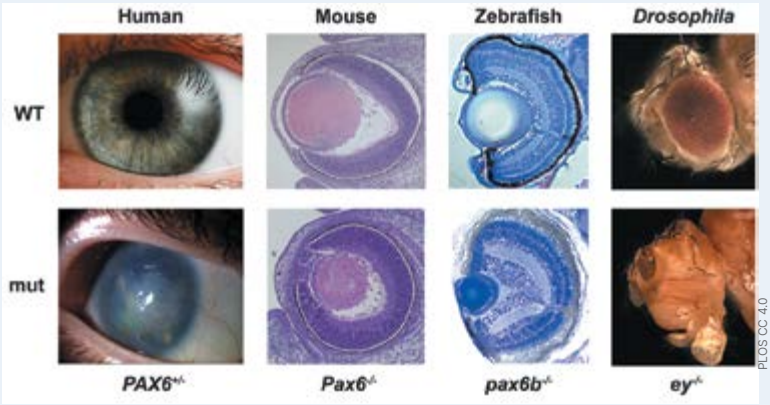


Cytochrome C (right) is a respiratory protein located in the electron transport chain in mitochondria. Highly conserved proteins, such as cytochrome c, change very little over time and between species because they carry out important roles and if they changed too much they may no longer function properly.

The table above shows the N-terminal 22 amino acid residues of human cytochrome c, with corresponding sequences from other organisms aligned beneath. Sequences are aligned to give the most position matches. A shaded square indicates no change. In every case, the cytochrome's heme group is attached to the Cys-14 and Cys-17. In *Drosophila*, wheat, and yeast, arrows indicate that several amino acids precede the sequence shown.

The Pax-6 protein provides evidence for evolution

- The Pax-6 gene belongs to a family of master genes that regulate the formation of a number of organs, including the eye, during embryonic development.
- The Pax-6 gene produces the Pax-6 protein, which acts as a transcription factor to control the expression of other genes.
- Scientists know the role of Pax-6 in eye development because they created a knockout model in mice where the Pax-6 gene is not expressed. The knockout model is eyeless or has very underdeveloped eyes.
- The Pax-6 gene is so highly conserved that the gene from one species can be inserted into another species, and still produce a normal eye.
- This suggests the Pax-6 proteins are homologous, and the gene has been inherited from a common ancestor.



The images above show the effect of a non-functional Pax-6 gene. In all cases, a non-functional gene leads to non-functional eyes. In the case of the *Drosophila*, the eye is missing. Experiments have shown that Pax-6 genes work across species. When a mouse Pax-6 gene was inserted into fly DNA and turned on in the fly's legs, the fly developed morphologically normal eyes on its legs!

1. (a) What is a highly conserved protein? _____

_____

(b) What type of proteins tend to be highly conserved? _____

_____

(c) Why are the proteins named in (b) highly conserved? _____

_____

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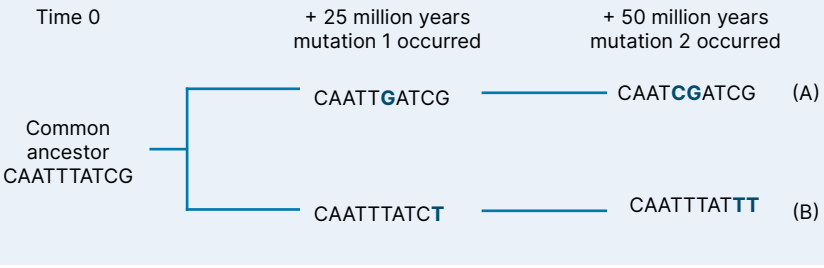
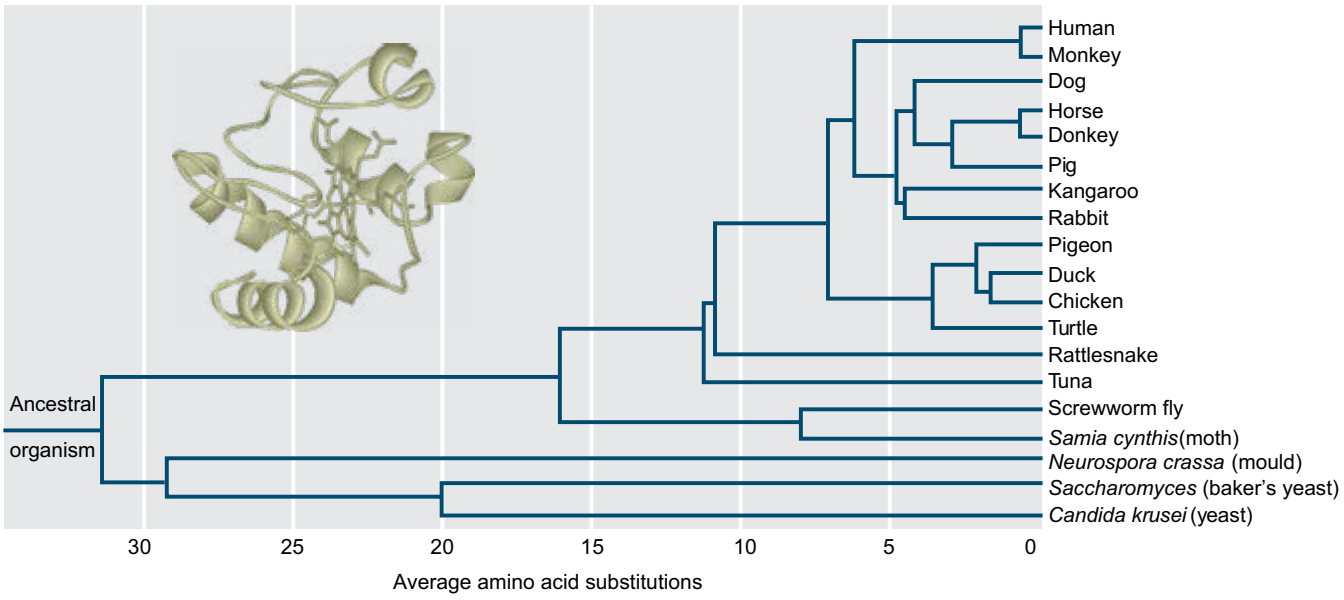
Cytochrome c and phylogeny

Because conserved proteins are found across many species, they can be used to create a **phylogeny** showing species relationships based on their mutations. The molecular clock hypothesis states that mutations occur at a relatively constant rate for any given gene. The genetic difference between any two species can indicate when two species last shared a common ancestor and can be used to construct a phylogenetic tree. The molecular clock for each species, and each protein, may run at different rates, so molecular clock data is calibrated with other evidence (e.g. morphological) to confirm phylogeny. Molecular clock calculations are carried out on DNA or amino acid sequences.

In this hypothetical example, the DNA sequence for a gene in two species (A and B) alive today differs by four bases. The mutation rate for the gene is approximately one base per 25 million years. Based on this rate, it can be determined that the common ancestor for these two species lived 50 million years ago.





2. For cytochrome *c*, suggest why amino acids 14 and 17 are unchanged in all the organisms shown in the table:

_____

3. (a) Describe the role of the Pax-6 gene: _____

_____

_____

(b) What evidence is there that the Pax-6 protein is highly conserved? _____

_____

_____

4. (a) Describe a limitation of using molecular clocks to establish phylogeny: _____

_____

_____

(b) Why are highly conserved proteins good for constructing phylogenies? _____

_____

_____

_____

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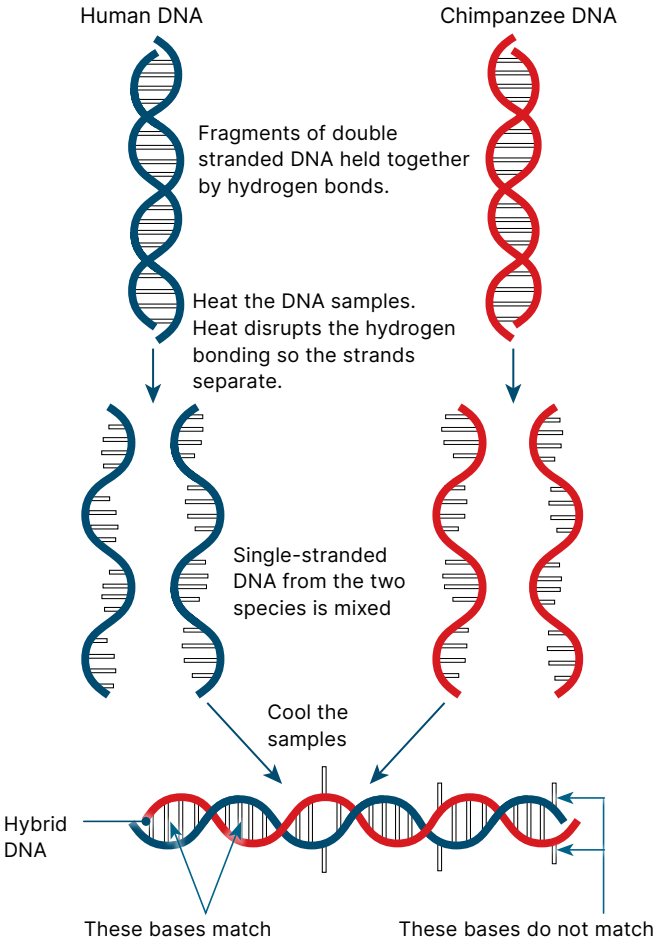
154 Genomic Comparisons and Relatedness

Key Idea: Relationships between species can be assessed by comparing the DNA directly.

Protein studies can show relatedness between species, but since those proteins are based on the DNA sequence, it makes sense to study the DNA directly. There are two main methods of doing this. An older technique is called DNA hybridisation (below). The method provides information only about how much of the DNA is the same but cannot provide specific information about what the similarities or differences are. It has largely been superseded by direct DNA sequencing (opposite), which provides more accurate information about where the differences in the DNA occur.

DNA hybridisation technique

1. DNA from the two species to be compared is extracted, purified and cut into short fragments.
2. The mixture is heated so the DNA separates. The DNA from the two species is mixed together.
3. As it cools, bonds form between compatible nucleotides. Hybrid, double-stranded DNA forms.
4. If species share low similarity, the hybrid DNA will have few bonds (and the strands will be weakly held together). The number of bonds (and therefore the strength of the hybrid DNA) increases with increasing similarity.
5. The similarity is measured by heating the hybrid DNA to force it to form single strands. The greater the similarity, the more heat is required to break the hybrid DNA apart.

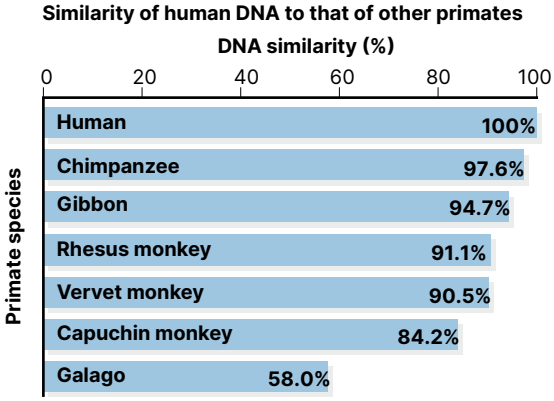


1. How can DNA hybridisation give a measure of genetic relatedness between species?

2. Why do the double strands of DNA break when they are heated?

3. What is responsible for the hybridisation between the DNA strands?

4. The graph below shows the results of a DNA hybridisation between humans and other primates.



(a) Which primate is most closely related to humans?

(b) Which primate is most distantly related to humans?

5. Hybrid DNA from species A and B comes apart at a lower temperature that of species A and C. Which species is A most closely related to?

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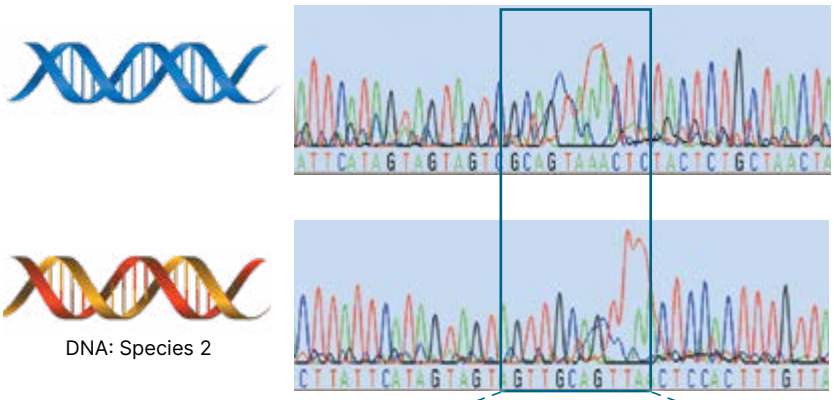
DNA sequencing

DNA sequencing provides the precise order of nucleotides in a DNA molecule. This information, which can now be analysed using sophisticated computing, allows researchers to compare sequences between species in much more detail than is possible with DNA hybridisation. Not only can areas of difference be identified, but the variation between the nucleotides at a certain position can be determined. This information allows researchers to more accurately determine the relatedness between species, even between those with very minor differences.

Comparing DNA sequences

Improved DNA sequencing techniques and powerful computing software have allowed researchers to accurately and quickly sequence and compare entire genomes (all an organism's genetic material) within and between species.

Once DNA sequences have been determined, they are aligned and compared to see where the differences occur (right). DNA sequencing generates large volumes of data and the rise in computing power has been central to modern sequence analyses. The technological advances have been behind the new field of bioinformatics, which uses computer science, statistics, mathematics, and engineering to analyse and interpret biological data.



What type of sequences are compared?

Highly conserved sequences are often used for comparative genomic analysis because they are found in many organisms. The changes (mutations) of the sequences over time can be used to determine evolutionary relationships. As with other forms of molecular analysis, species with fewer nucleotide differences are more closely related than those with many.

Whole genome analysis has been important in classifying the primates. Historical views attributed special status to humans which often confused primate classification schemes. DNA evidence provides impartial quantitative evidence and modern classification schemes have been based on this data.

Based on DNA evidence, chimpanzees are more closely related to humans than they are to gorillas and there is no taxon called "great apes".

6. (a) What advantages does DNA sequence comparison have over DNA hybridisation? _____

_____

_____

_____

(b) How is this an advantage in determining evolutionary relationships? _____

_____

_____

7. Three partial DNA sequences for three different species are presented below.

Species 1 A T G G C C C C C A A C A T T C G A A A A T C G C A C C C C C T G C T C A A A A T T A T C A A C

Species 2 A T G G C A C C T A A C A T C C C C A A C T C C C A C C G T G T A C T C A A A A T C A T C A A G

Species 3 A T G G C A C C C A A T A T C C G C A A A T C A C A C C C C C T G T T A A A A A C A A T C A A C

Based on the number of differences in the DNA sequences:

(a) Identify the two species that are most closely related: _____

(b) Identify the two species that are the least closely related: _____

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155 How Technology Helps Us Understand Evolution

Key Idea: DNA sequencing is many times faster than even a decade ago. This allows DNA sequences to be easily compared between species.

The advancement of DNA sequencing has produced enormous amounts of sequencing information. The collection, storage, and analysis of this information using computers is called bioinformatics. Bioinformatics allows DNA sequence comparisons between species, a field called **comparative genomics**. Comparative genomics has provided the information to support (or overturn) established phylogenies.

DNA sequencing continually advances

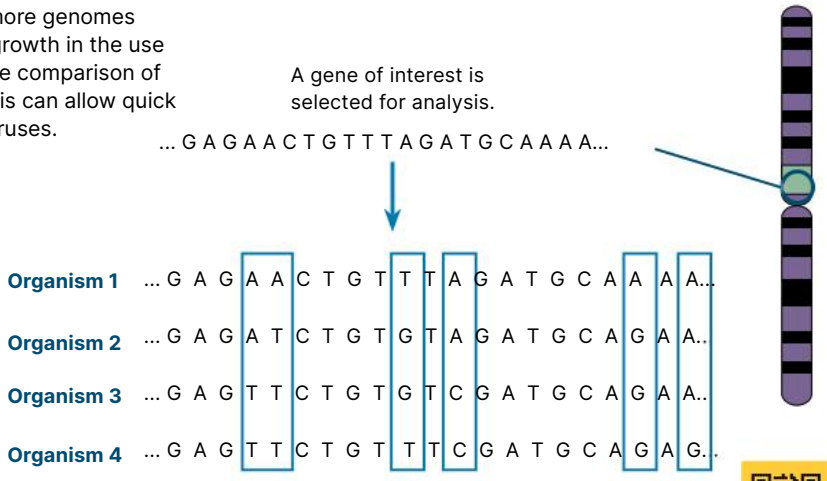
- Early DNA sequencing technologies, such as the Sanger method, required that the sample sequence was copied using modified DNA, producing various lengths of DNA. These then had to be separated on a gel and read on a UV bed or as they passed by a laser.
- High throughput sequencers read the DNA as it is being copied, a technique called sequencing by synthesis. Thousands to millions of sequences can be read at once, allowing million to billions of DNA fragments to be sequenced at the same time. The resulting sequences are compared by computer and aligned based on overlapping sequences.
- Next generation sequencers have dramatically improved the feasibility and reduced the costs of whole-genome sequencing. The very latest sequencers simply run the sample DNA through a nanopore in a membrane and analyse the electric signal produced by each DNA nucleotide as it passes through.

The MinION, developed by Oxford Nanopore Technologies.

The latest sequencing technology is now small enough to fit on a chip/reader that is little bigger than a USB memory stick and can read about 150 million base pairs per run.

Using the sequence data

As genome sequencing has become faster and more genomes are sequenced there has been a corresponding growth in the use of bioinformatics. Online DNA databases allow the comparison of DNA being studied to known DNA sequences. This can allow quick identification of species, especially bacteria or viruses.

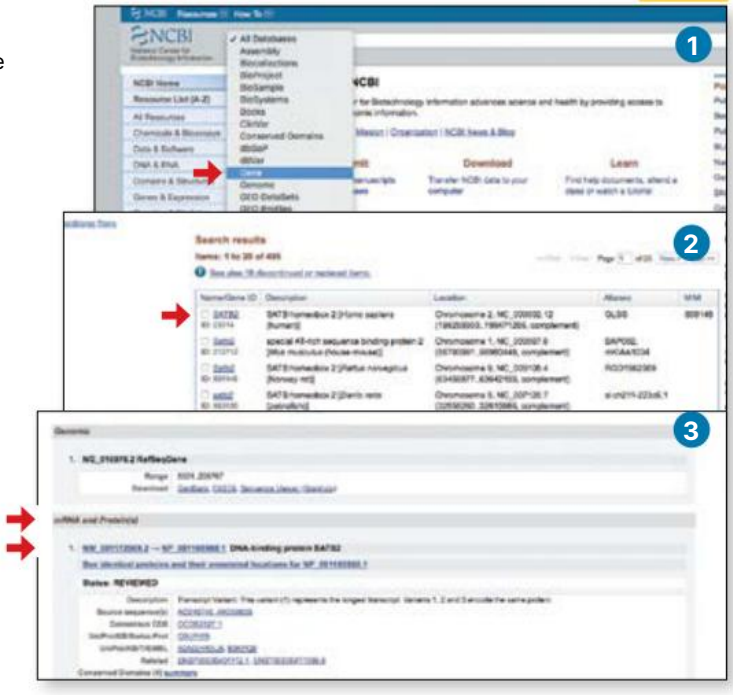


Powerful computer software can quickly compare the DNA sequences of many organisms. Commonalities and differences in the DNA sequence can help to determine the organism and its evolutionary relationship to other organisms. The blue boxes indicate differences in the DNA sequences.

Online databases

There are many easily accessible online databases where DNA sequences can be studied. The example below uses NCBI data base at **www.ncbi.nlm.nih.gov** (use the QR code n the right).

1. There is a search box at the top of the page with a drop down menu. Use the menu: find and click **Gene** (image 1).
2. In the search box, type SATB2. This is a homeobox gene on the 2nd human chromosome. Homeobox genes control the formation of many body structures during early development.
3. Click **search** and a new window appears showing the results.
4. Find the SATB2 on the list with the ID 23314 (image 2). A new window appears showing known information on the SATB2 gene. Scrolling down the screen provides a huge amount of information about this gene.
5. Scroll down to the heading **NCBI Reference Sequences**. Under this is the smaller heading **mRNA and proteins** (image 3) listing all the mRNA transcripts of this gene.
6. Click the first on the list **(NM_001172509.2**).
7. This brings up information on the transcript. Scroll to the bottom and the DNA sequence for the mRNA is shown.
8. Highlight and copy this sequence.



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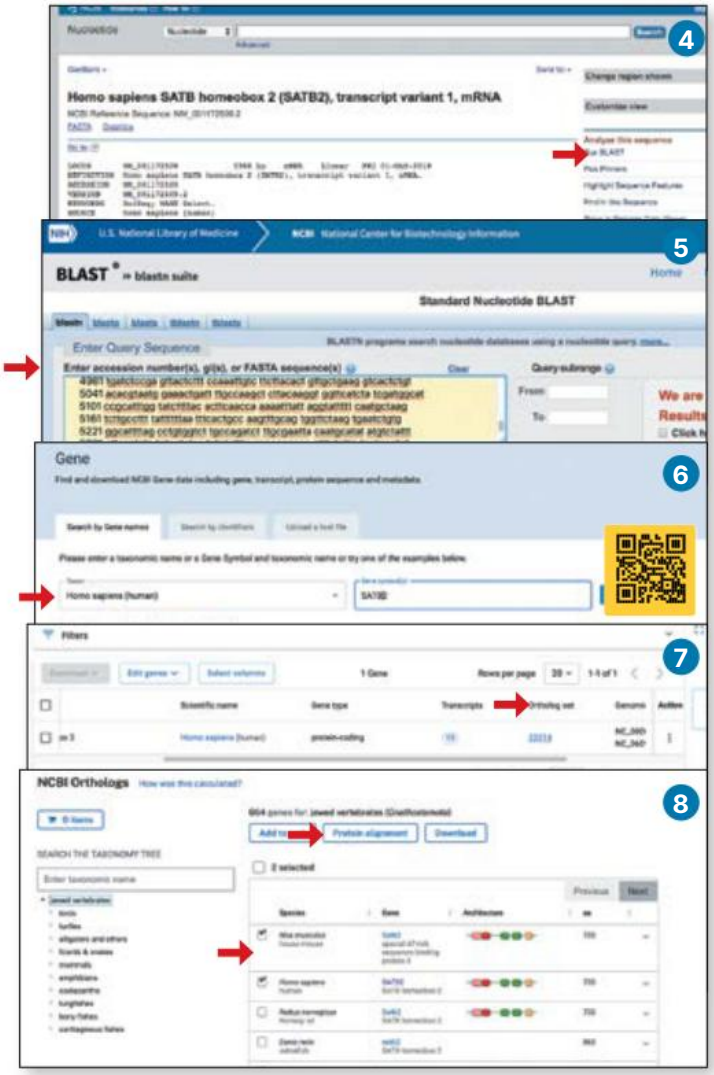
11. Scroll back to the top of the page. On the right is the heading **Analyze this sequence** (image 4). Under this, click the heading **Run BLAST**. This opens a search box where you can compare the SATB2 sequence from the previous website to other sequences.
12. Paste the SATB2 DNA sequence in your paste buffer into the box headed "**Enter accession number(s), gi(s), or FASTA sequence(s)**" or use the reference number shown in the box (image 5). Click on **BLAST** at the bottom of the page. The search may take a minute or so.
13. A new screen appears showing the BLAST results. Scroll down to see a list of all the species that have similar SATB2 sequences. Clicking on a species shows a match up of all the DNA in the sequences.
14. Once you are familiar with this process go to **www.ncbi.nlm.nih.gov/datasets/** (use the QR code right). Click on the **Gene** tab. A new window appears with a Taxon drop down menu and a field to enter a gene. Make sure the Taxon menu reads “Homo sapiens (human)”. In the gene symbol field type **SATB2** and click **search** (image 6).
15. Use the side scroll bar at the bottom of the result page to scroll until you see the heading **Ortholog set**. Click the link (image 7).
16. Another window appears comparing the human SATB2 gene with SATB2 genes from other animals. You can see how similar parts of the gene are arranged in other animals.
17. By clicking on the check boxes you can compare the gene from different animals. Check the first two, *Mus musculus* (mouse) and *Homo sapiens* (humans). Click the button **Protein alignment** at the top (image 8). Leave the check box “one sequence per gene” checked and click **Align**.
18. Another window appears. Click **Align** again. After a short time the results appear. Scroll down to see how the amino acids in the SATB2 protein align between the two species.
19. Go back to ortholog page (image 7). This time select human and zebrafish (*Danio rerio*) to do a protein alignment following the previous steps.



The steps above are a highly simplified step-through of the databases. These databases are capable of many different searches and investigations and stores millions of DNA and gene sequences. Even this simple process shows the power of technology in the investigation of species relationships.

1. Using the SATB2 gene and the NCBI gene data base answer the following:

   (a) What is the % similarity of the DNA between a human and a chimpanzee for the SATB2 gene? _____

   (b) What is the % similarity of the DNA between a human and a domestic dog for the SATB2 gene (variant X1)?

   _____

2. Computers scan the DNA sequences to find where the sequences most closely align. At what number DNA base pairs do the domestic dog (*Canus lupus familiaris*) and human DNA begin to align?

   _____

3. Using the Gene data set (from step 15 above) answer the following:

   (a) What is the % similarity between the human and dog SATB2 amino acid sequence? _____

   (b) At what number amino acids do the differences occur? _____

4. Go to the NCBI web page shown in image 5 above. The search box is useful in that the DNA sequence can be typed directly into the search box. How might this be useful in identifying the origin of a DNA sequence?

   _____

   _____

   _____

5. Type a short DNA sequence of your choosing in the search box (about 20 to 30 letters). Click Blast and see if there are any matches. The search may take some time. Have you "found" a unique DNA sequence or is it from a known species?

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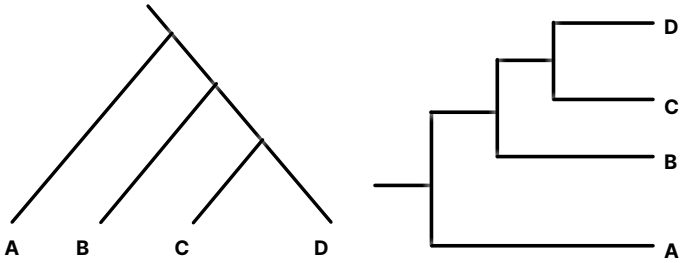
156 What is a Phylogenetic Tree?

Key Idea: Phylogenetic trees represent possible evolutionary relationships among organisms. They can be constructed based on appearance or molecular data.

Phylogenetics is the study of the evolutionary history of organisms or groups of organisms. These relationships are often shown as a diagram called a phylogenetic tree. A phylogenetic tree represents a likely hypothesis of the evolutionary relationships among biological taxa (*sing*. taxon). A taxon may consist of an individual species or it may be a larger group (e.g. an order). Traditionally, phylogenetic trees have been constructed based on similarities in appearance (morphology) but increasingly, molecular comparisons are used, especially to distinguish closely related taxa. Molecular phylogenetics can reveal differences not seen in morphological comparisons, and have resulted in the revision of some morphological phylogenies where organisms could not be separated on appearance. Phylogenetic trees are often constructed based on cladistic criteria (below).

What do phylogenetic trees look like?

Phylogenetic trees represent possible evolutionary histories, and there are many different ways they can be drawn (right). Depending on how the tree is constructed, some represent evolutionary time or the amount of character change through the length of the branches (lines) (called **phylograms**). Phylogenetic trees based on cladistics (**cladograms**) do not represent evolutionary time.

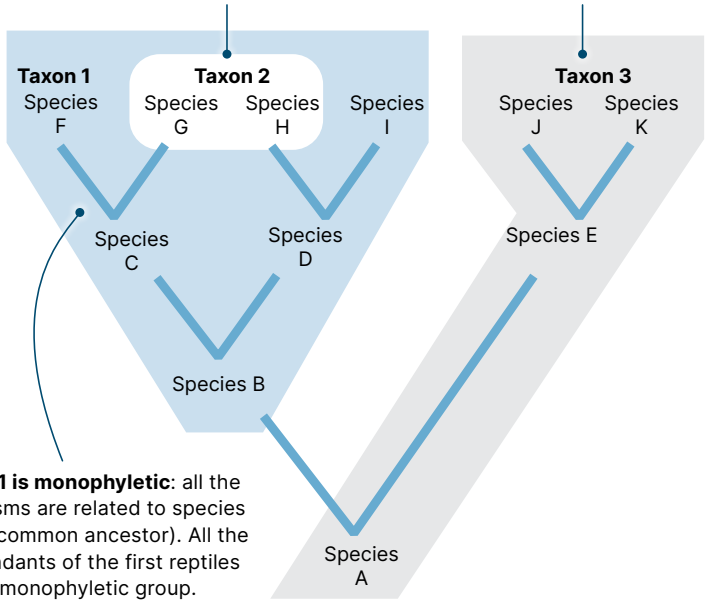


Determining phylogenetic relationships

- Increasingly, analyses to determine evolutionary relationships rely on cladistic analyses of character states. Cladistic analysis groups species according to their most recent common ancestor on the basis of shared derived characteristics. All other characteristics are ignored.
- A **phylogeny** constructed using cladistics thus includes only monophyletic groups, i.e. the common ancestor and all of its descendants. It excludes both paraphyletic and polyphyletic groups (right). It is important to understand these terms when constructing **cladograms** and to also understand that the terms are relative to wherever you start in the phylogenetic tree (i.e. where the common ancestor is).
- The cladistic approach creates an unambiguous branching tree. One problem with this approach is that a strictly cladistic classification could theoretically have an impractically large number of taxonomic levels and may be incompatible with a Linnaean system.

Taxon 2 is polyphyletic: it includes organisms with different ancestors. The group "warm-blooded (endothermic) animals" is polyphyletic as it includes birds and mammals.

Taxon 3 is paraphyletic: it includes species A without including all of A's descendants. The traditional grouping of reptiles is paraphyletic because it does not include birds.



Taxon 1 is monophyletic: all the organisms are related to species B (the common ancestor). All the descendants of the first reptiles form a monophyletic group.

1. What does a phylogenetic tree show? _____

_____

_____

2. Why might phylogenetic trees based on molecular differences be preferred over phylogenies based on appearance?

_____

_____

3. Define the following:

(a) Monophyletic: _____

(b) Polyphyletic: _____

(c) Paraphyletic: _____

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157 Constructing Phylogenies Using Cladistics

Key Idea: Cladograms are phylogenetic trees constructed on the basis of shared derived characteristics.

A **cladogram** is a phylogenetic tree constructed using a taxonomic tool called cladistics. Cladistics groups organisms on the basis of their shared derived characters (features arising in an ancestor and shared by all its descendants) and ignores features that are not the result of shared ancestry. A clade, or branch on the tree, includes a common ancestor and all its descendants (i.e. it is monophyletic). Increasingly, cladistic methods rely on molecular data (e.g. DNA sequences) to determine phylogenies. Highly conserved DNA sequences are used because changes are likely to signal a significant evolutionary divergence. Cladograms may not always agree completely with phylogenies constructed using traditional methods but similarities in the trees indicate that the proposed relationships are likely to be correct.

Derived vs ancestral characters

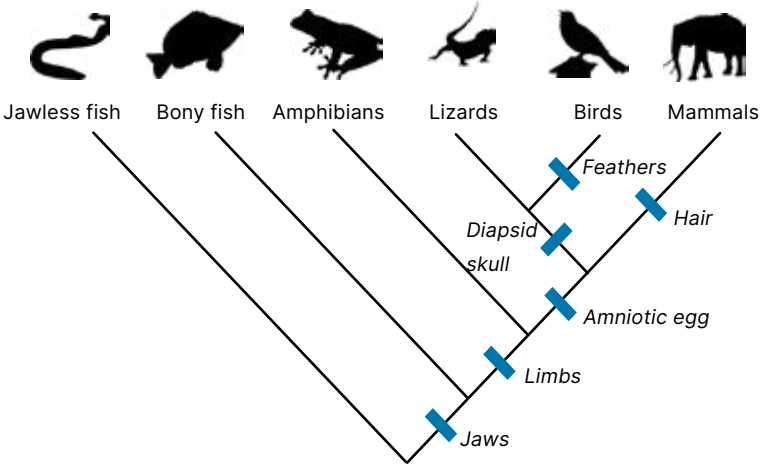
When constructing cladograms, shared derived characters are used to separate the clades (branches on the tree). Using ancestral characters (those that arise in a species that is ancestral to more than one group) would result in distantly related organisms being grouped together and would not help to determine the evolutionary relationships within a clade. Whether or not a character is derived depends on the taxonomic level being considered. For example, a backbone is an ancestral character for mammals, but a derived character for vertebrates. Production of milk is a derived character shared by all mammals but no other taxa.

The backbone in a mammal, e.g. rat, is an ancestral character common to all vertebrate taxa. However, the production of milk from mammary glands is a derived character, shared by all mammals but no other taxa.

Constructing a simple cladogram

- A table listing the features for comparison allows us to identify where we should make branches in the cladogram. An outgroup (one which is known to have no or little relationship to the other organisms) is used as a basis for comparison.
- The table (right) lists features shared by selected taxa. The outgroup (jawless fish) shares just one feature (vertebral column), so it gives a reference for comparison and the first branch of the cladogram. As the number of taxa in the table increases, the number of possible trees that could be drawn increases exponentially.
- Several different cladograms can be constructed from the same data. To determine the most likely relationships, the rule of parsimony is used. Parsimony assumes that the tree with the simplest explanation (the least number of evolutionary events) is most likely to show the correct evolutionary relationship.
- A possible cladogram for the data in the table is shown on the right. Its construction assumed that six evolutionary events took place (labelled as blue bars on the cladogram). If other cladograms were constructed, but involved more evolutionary events, the one shown would be assumed to be correct because it is the most parsimonious.
- Parsimony can lead to some confusion. Some evolutionary events have occurred multiple times. An example is the **evolution** of the four chambered heart, which occurred separately in both birds and mammals. The use of fossil evidence and DNA analysis can help to solve problems like this.

Comparative features	Jawless fish (outgroup)	Bony fish	Amphibians	Lizards	Birds	Mammals
Vertebral column	✓	✓	✓	✓	✓	✓
Jaws	x	✓	✓	✓	✓	✓
Four supporting limbs	x	x	✓	✓	✓	✓
Amniotic egg	x	x	x	✓	✓	✓
Diapsid skull	x	x	x	✓	✓	x
Feathers	x	x	x	x	✓	x
Hair	x	x	x	x	x	✓



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1. (a) Distinguish between a shared derived characteristic and a shared ancestral characteristic: _____

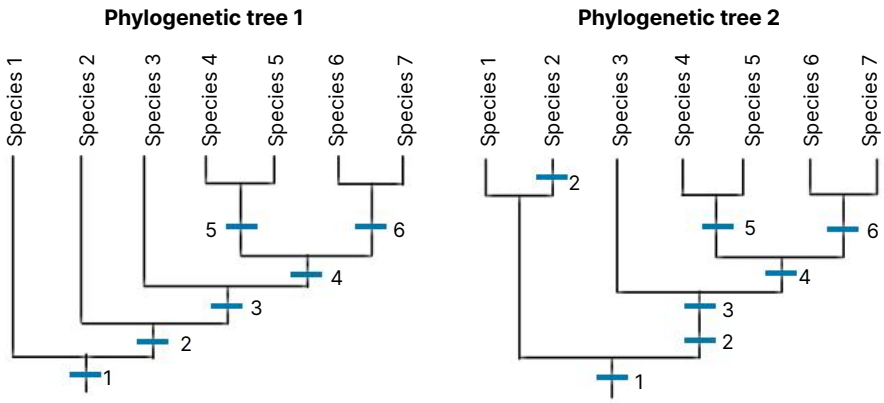
(b) Why are ancestral characteristics not useful in constructing evolutionary histories? _____

2. What assumption is made when applying the rule of parsimony in constructing a cladogram? _____

3. Two possible phylogenetic trees constructed from the same character table are shown below. The numbers next to a blue bar represent an evolutionary event.

(a) Which tree is more likely to be correct?

(b) State your reason:

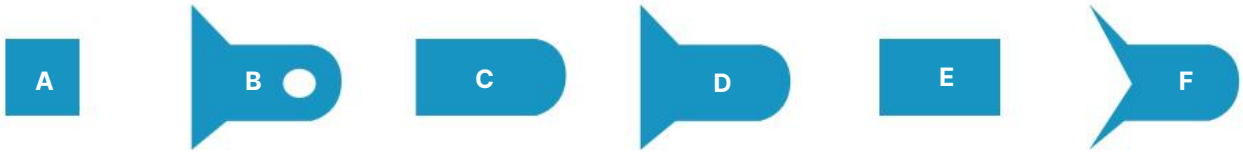


(c) Identify the event which has occurred twice in phylogenetic tree 2:

_____

4. A phylogenetic tree is a hypothesis for an evolutionary history. How could you test it? _____

5. Use the shapes below to construct a cladogram that shows their phylogenetic relationships (hint: A is the outgroup).



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158 Constructing a Cladogram

Key Idea: A table of selected characteristics can be organised systematically as a matrix and used to construct a **cladogram**.

Taxon	Character												
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
Zebra-perch sea chub	0	0	0	0	0	0	0	0	0	0	0	0	0
Barred surfperch	1	0	0	0	0	0	0	0	0	1	1	0	0
Walleye surfperch	1	0	0	0	0	1	0	1	0	1	1	0	0
Black perch	1	1	1	0	0	0	0	0	0	0	0	1	0
Rainbow seaperch	1	1	1	0	0	0	0	0	0	0	0	1	0
Rubberlip surfperch	1	1	1	1	1	0	0	0	0	0	0	0	1
Pile surfperch	1	1	1	1	1	0	0	0	0	0	0	0	1
White seaperch	1	1	1	1	1	0	0	0	0	0	0	0	0
Shiner perch	1	1	1	1	1	1	0	0	0	0	0	0	0
Pink seaperch	1	1	1	1	1	1	1	1	0	0	0	0	0
Kelp perch	1	1	1	1	1	1	1	1	1	0	0	0	0
Reef perch	1	1	1	1	1	1	1	1	1	0	0	0	0

Steve Lonhart (SIMoN / MBNMS) PD NOAA

Surfperches are viviparous (live bearing) and the females give birth to relatively well developed young. Some of the characteristics (below, left) relate to adaptations of the male for internal fertilisation. Others relate to deterring or detecting predators. In the matrix, characteristics are assigned a 0 or 1 depending on whether they represent the ancestral (0) or derived (1) state. This coding is common in cladistics because it allows the data to be analysed by computer.

Selected characters for cladogram assembly

1.	Viviparity (live bearing)	0 No	1 Yes
2.	Males with flask organ	0 No	1 Yes
3.	Orbit without bony front wall	0 Yes	1 No
4.	Tail length	0 Short	1 Long
5.	Body depth	0 Deep	1 Narrow
6.	Body size	0 Large	1 Small
7.	Length of dorsal fin base	0 Long	1 Short
8.	Eye diameter	0 Moderate	1 Large
9	Males with anal crescent	0 No	1 Yes
10	Pectoral bone with process	0 No	1 Yes
11.	Length of dorsal sheath	0 Long	1 Short
12.	Body mostly darkish	0 No	1 Yes
13.	Flanks with large black bars	0 No	1 Yes

Notes and working space

1. This activity provides the taxa and character matrix for 11 genera of marine fishes in the family of surfperches. The outgroup given is a representative of a sister family of rudderfishes (zebra-perch sea chub), which are not live-bearing. Your task is to create the most parsimonious cladogram from the matrix of character states provided. To help you, we have organised the matrix with genera having the smallest blocks of derived character states (1) at the top following the outgroup representative. Use a separate sheet of graph paper, working from left to right to assemble your cladogram.

   Identify the origin of derived character states with horizontal bars, as shown in the previous activity. CLUE: You should end up with 15 steps. Two derived character states arise twice independently. Staple your cladogram to this page.

2. (a) Why are the character states organised in a matrix? _____

   _____

   (b) Why is it useful to designate the characters states as 0 (ancestral) or derived (1)? _____

   _____

3. In the cladogram you have constructed for the surfperches, two characters have evolved twice independently:

   (a) Identify these two characters: _____

   (b) What selection pressures do you think might have been important in the evolution of these two derived states?

   _____

   _____

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159 Molecular Phylogenetics

Key Idea: Molecular phylogenetics analyses heritable molecular differences to find out about an organism's evolutionary relationships. It has many applications including in cladistics and in DNA barcoding.

The advent of rapid throughput DNA sequencing and the analysis of biological data using computers (bioinformatics) has given rise to a new field of science called molecular **phylogenetics**. Molecular phylogenetics uses computers to compare and align different DNA sequences to produce the maximum number of matches. The number of matches and unique DNA bases can be used to produce phylogenetic trees. New standards such as DNA barcoding that use particular sequences of DNA have produced a vast amount of data that can be used in molecular phylogenetics.

The DNA barcode

DNA barcoding uses short highly conserved sequences of DNA to produce species-specific information. The sequence of DNA that is chosen for analysis depends on the type of organism (e.g. plant, animal, fungus, bacterium).

Plant barcoding uses up to three genes in the chloroplasts and one in the nuclear DNA.

The barcode from animals is taken from the cytochrome c oxidase 1 gene (CO1 gene).

Fungal barcoding uses the nuclear ribosomal internal transcribed spacer (ITS).

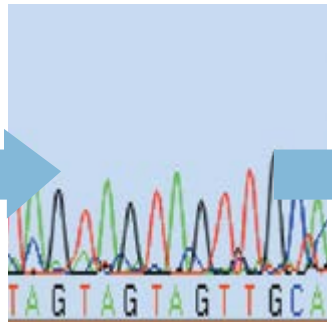
The goal of DNA barcoding to be able to identify individual species from short sequences of DNA. This information can then be applied wherever species-specific knowledge is important. Applications include evolutionary biology, conservation, detection of invasive species, dietary analysis (to help describe food webs), and food safety.

Barcoding and molecular phylogenetics

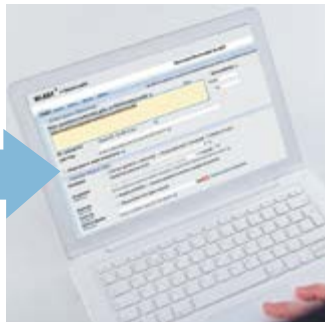
DNA barcoding and molecular phylogenetics work on the assumption each species' DNA is different but that the more closely related species are, the more similar their DNA will be. Conserved genes found throughout the range of organisms being studied are assumed to evolve (gain mutations) at a constant rate, thus differences between the genes reflect differences between species.

Isolate DNA from sample.

Identify and isolate target DNA.



Sequence the target DNA.



Compare sequence with database to identify species.

A brief recap on definitions

The language of classification and evolutionary relationships can be confusing and many terms are used somewhat interchangeably. To help you, refer to the definitions below:

- **Phylogenetic tree**: A diagram representing a possible evolutionary history of an organism. Many different trees may be proposed for any one taxon.
- **Cladogram**: A phylogenetic tree constructed using a cladistic approach.
- **Phylogram**: A phylogenetic tree in which the branch lengths represent length of time or amount of character change.
- **Monophyletic**: Consisting of an ancestor and all its descendants.
- **Molecular phylogenetics**: A branch of science that analyses heritable molecular differences to find out about an organism's evolutionary relationships.
- **Cladistics**: An approach to biological classification in which organisms are organised in groups, called clades, based on the most recent common ancestor. Taxa must be monophyletic. Phylogenetic classifications are essentially cladistic whereas traditional classifications may not be.

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Using molecular phylogenetics

Differences in DNA can be used to build phylogenetic trees. Once the DNA from several species is sequenced, the DNA can be compared. Consider the following DNA sequences:

>1 AGATGATCTCGCTGATAGCTCGATGATCGTCGATAGAGACAGATACAGTCG

>2 AAATGATCTCGCTGATAGCTCGATGATCGTCGATAGAGACAGATACAGTCG

>3 AAATGATCTCGTTGATAGCTCGATGATCGTCGATAGAGACAGATACAGTCG

>4 AAATGATCTCGTTGATAGCTCGATGATCGTCGATACAGTCAGATACAGTCG

>5 AGATGATCTCGCTGATAGCTCGATGATCGTCGATAGAGACTTATACAGTCG

>6 AGATGATCTCGCTGATAGCTCGATGATCGTCGATAGAGACTTATACACTCG

>7 AGATGACTCGCTGATAGCTCGATGATCGTCAGATAGACTTATACACTCGGC

The sequences are similar but have some differences. Additionally, the sequences need to be correctly aligned before they can be useful. If you study 6 and 7 carefully, you will see the sequences are very similar but fail to align perfectly.

1. Do a rough analysis of the sequences above. Can you identify two groups that the sequences fall into?

A computer program can to be used to align and then analyse the phylogeny of the DNA quickly. There are many online programs to do this. One of the simplest to use is https://www.phylogeny.fr/index.cgi
Use the QR code, right, to access the website.

2. (a) Using a computer go to the Phylogeny.fr home page.
   (b) Once you are there, click on Phylogeny Analysis in the menu bar and select "**One Click**"
   (c) You may name your anaylsis. In the large box, you need to copy in the DNA sequences above as per the screen shot (right). You can find these sequences as a PDF in the **BIOZONE Resource Hub** or type them in manually. Make sure the formatting is correct as in the screen shot.
   (d) Now click **Submit** below the box (don't worry about email address).
   (e) The program will align and analyse the sequences then draw a phylogenetic tree. This may take a minute or so.*
   (f) At the bottom of the page you can change the type of tree produced. You can save the diagram as a PNG or PDF file.

3. Draw the phylogenetic tree produced by Phylogeny.fr in the box below:

*If the phylogenetic tree is not displayed, you may need to click the "data and settings" tab again, then click the "tree rendering" tab.

4. What is the purpose of molecular phylogenetics: _____

5. Why is using a conserved gene such as cytochrome oxidase useful when producing DNA barcodes for species?

6. How does DNA barcoding help molecular phylogenetics? _____

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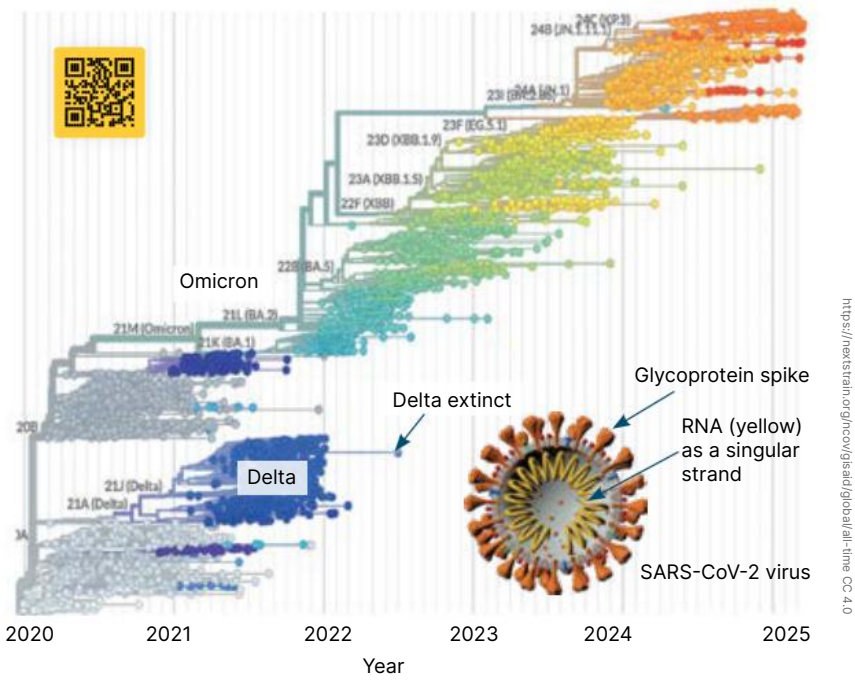
160 Using Phylogenetics

Key Idea: Phylogenetics can be used to trace the lineage of disease, helping to make predictions of future outbreaks.

Many pathogens, especially those producing relatively short lived, easily spread infections, evolve relatively quickly. This is because they must overcome a host population's collective immune system. As the population becomes immune to a pathogen, either by the death of individuals whose immune system could not deal with the pathogen, leaving only naturally immune individuals in the population, or by the population becoming immune by each individual developing immunity during an infection, the pathogen must evolve to evade this new immunity. Two contemporary examples of this are the influenza virus which causes the flu, and the SARS-CoV-2 virus which causes Covid-19. The SARS-CoV-2 virus is a particularly good example as its global presence went from no cases to tens of millions in a few years, and it has been extensively studied during that time.

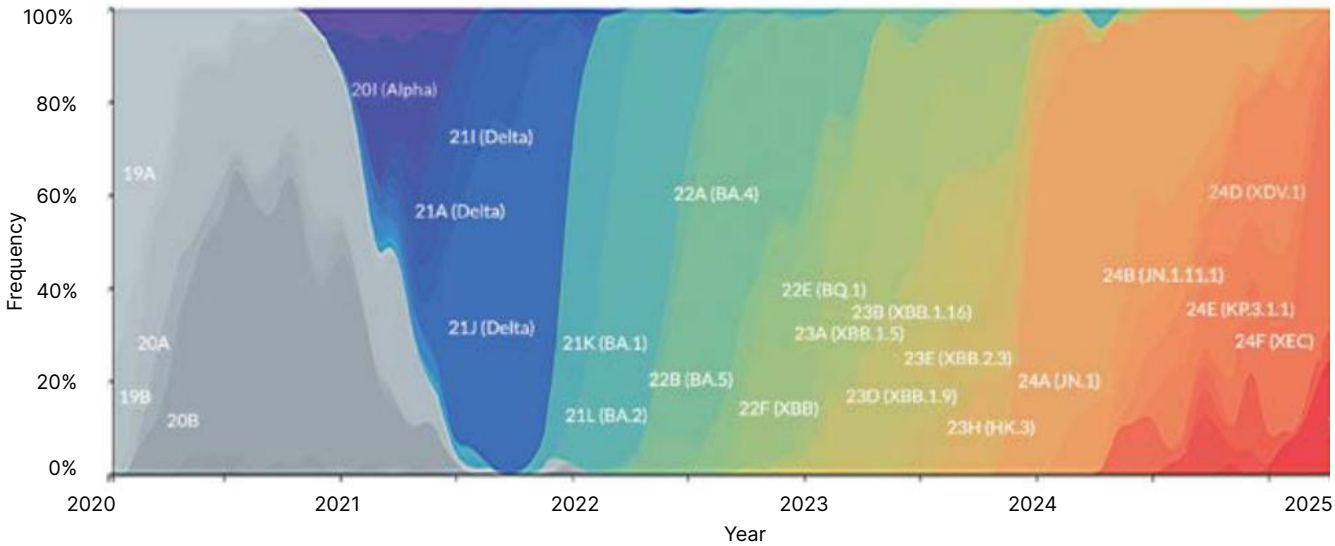
- Covid-19 is the disease caused by infection with the SARS-CoV-2 virus (right). The virus affects the respiratory system.
- The SARS-CoV-2 virus has a genome of around 30,000 bases, making sequencing the entire genome relatively simple. More than 16 million SARS-CoV-2 sequences had been added to public databases by 2023.
- This amount of data means the **phylogeny** of SARS-CoV-2 can be determined.
- Based on the virus's phylogeny, predictions can be made on which strains may cause future outbreaks.
- The immune system remembers characteristics of pathogens and will react to other pathogens with similar characteristics, called cross reactivity. Using **phylogenetics**, researchers can see the most common strains of pathogens and how they relate to each other. They can then develop vaccines that cross react to protect against these strains, increasing the vaccine's efficiency.

SARS-CoV-2 phylogeny



https://nextstrain.org/ncov/gisaid/global/all-time CC 4.0

SARS-CoV-2 frequency of strains over time



https://nextstrain.org/ncov/gisaid/global/all-time CC 4.0

- The graph above shows the **evolution** of the strains of the SARS-CoV-2 virus over time. Over time, the symptoms of the virus and its transmissibility have changed. As the population has developed immunity, after infection or vaccination, strains of the virus that are better adapted to evading the population's current immune response have developed.
- Some of these characteristics include the ability to invade different cell types (one of the reasons newer strains no longer affect taste or smell as much), or becoming more transmissible but less severe. Any of these changes may give the virus an increased fitness compared to other strains, which allows it to spread faster and out-compete those strains.
- The SARS-CoV-2 virus shows in real-time the evolution/**extinction** cycles of much larger species. Before 2021, alpha, beta, and gamma were the dominant strains but in 2022 these were declared extinct. Soon after, the delta stain was also declared extinct, while the omicron strain became the dominant one.

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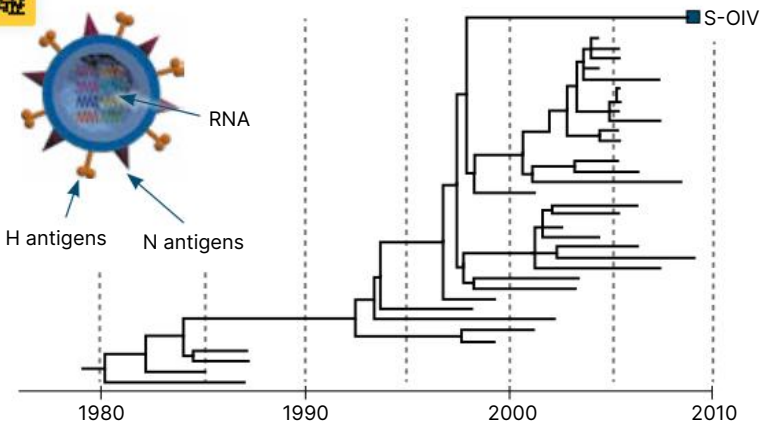
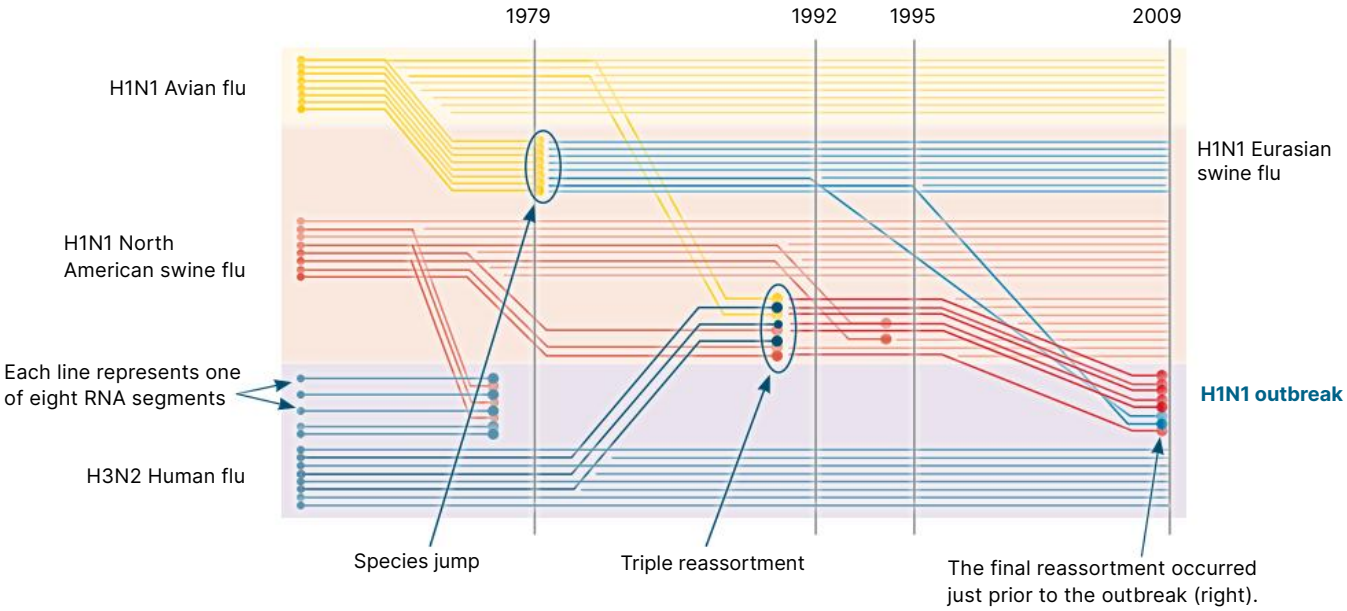
Influenzavirus

- Influenza (flu) is a disease of the upper respiratory tract caused by the viral genus *Influenzavirus*.
- *Influenzavirus* subtypes are classified by the N and H antigens (e.g. H1N1) which cover their surface. The genetic material in *Influenzavirus* is stored as eight RNA sequences. All eight RNA segments can be reassorted. Two of the RNA segments code for the H and N antigens.
- In 2009, a reassortment of the eight RNA sequences produced an influenza strain (called S-OIV) that resulted in the swine flu pandemic. By examining the phylogeny (right) of each RNA sequence, it was possible to determine the sequence of events that produced the S-OIV strain (below).





1. How does mapping the phylogeny of SARS-CoV-2 help predict future outbreaks?

2. How can phylogenetics improve vaccine development for SARS-CoV-2?

3. What can be said about the relationship of the delta and omicron strains of SARS-CoV-2?

4. What can be said about the relationship of the PB2 RNA sequence from the S-OIV influenzavirus with PB2 RNA sequences from other strains of influenza virus?

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161 Using Genome Data to Trace Human Migration

Key Idea: Large scale genetic studies have helped answer questions about how humans evolved and migrated across the globe.

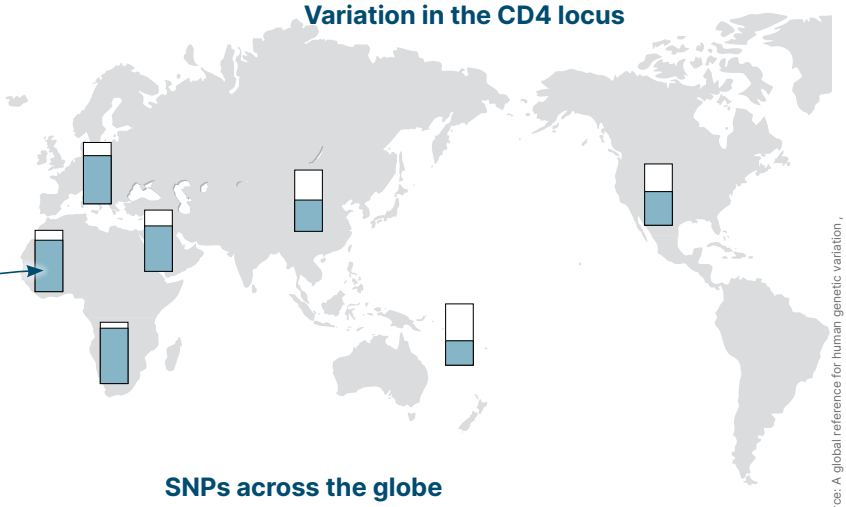
Fossil and genetic evidence shows modern humans evolved around 200,000 years ago in East Africa and then spread across the globe in a series of migrations. Genetic information has shown that modern African populations tend to have the greatest diversity in their genes. Genetic diversity tends to decrease the further from Africa a population is. As humans migrated out of Africa they encountered and interbred with small populations of Neanderthals and Denisovans. Interbreeding with these groups has left traceable amounts of DNA in the genome. The amount varies from region to region across the globe.

Out of Africa

- One of the great debates over human **evolution** is: did modern humans evolve in Africa and then migrate across the globe (the Out-of-Africa hypothesis), or did they evolve from an earlier migration of *Homo erectus* which produced populations throughout the Old World that evolved together as they interbred (the multiregional hypothesis)?
- Genetic evidence from studies involving groups across the globe shows that genetic diversity is greatest in Africa and becomes less so outside Africa. This is consistent with a subset of humans migrating out of Africa and populating the globe (right).
- Humans, in general, have very little genetic diversity. An average person's DNA varies about 0.6% from the 2015 reference genome.

	Diversity (0 = low)		
Locus (measurement)	Africa	Europe	Asia
30 microsatellites	0.807	0.730	0.685
Xq 13.3 (short arm X chromosome)	0.035	0.034	0.025
50 autosomal sequences	0.115	0.064	0.061
mt DNA control region	2.08	1.08	1.75

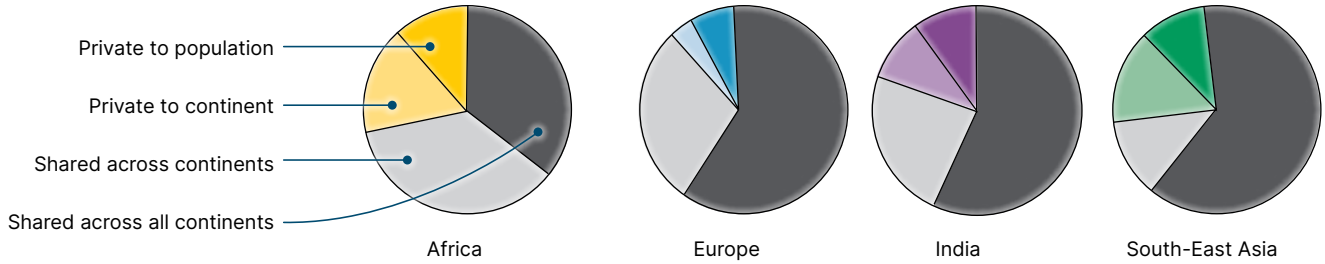
Variation in the CD4 locus



Diversity in the CD4 locus on chromosome 12. (Blue shading represents the amount of diversity).

Source: A global reference for human genetic variation, 1000 Genome Project, 2015. See credits for full reference.

SNPs across the globe



- Recall that SNPs are single nucleotide polymorphisms. The pie graphs above show the percentage of SNPs in humans in different parts of the globe which are shared and which are found only in specific continents or populations.

1. Describe the Out of Africa and multiregional hypotheses: _____

2. Which hypothesis does the genetic evidence support and why? _____

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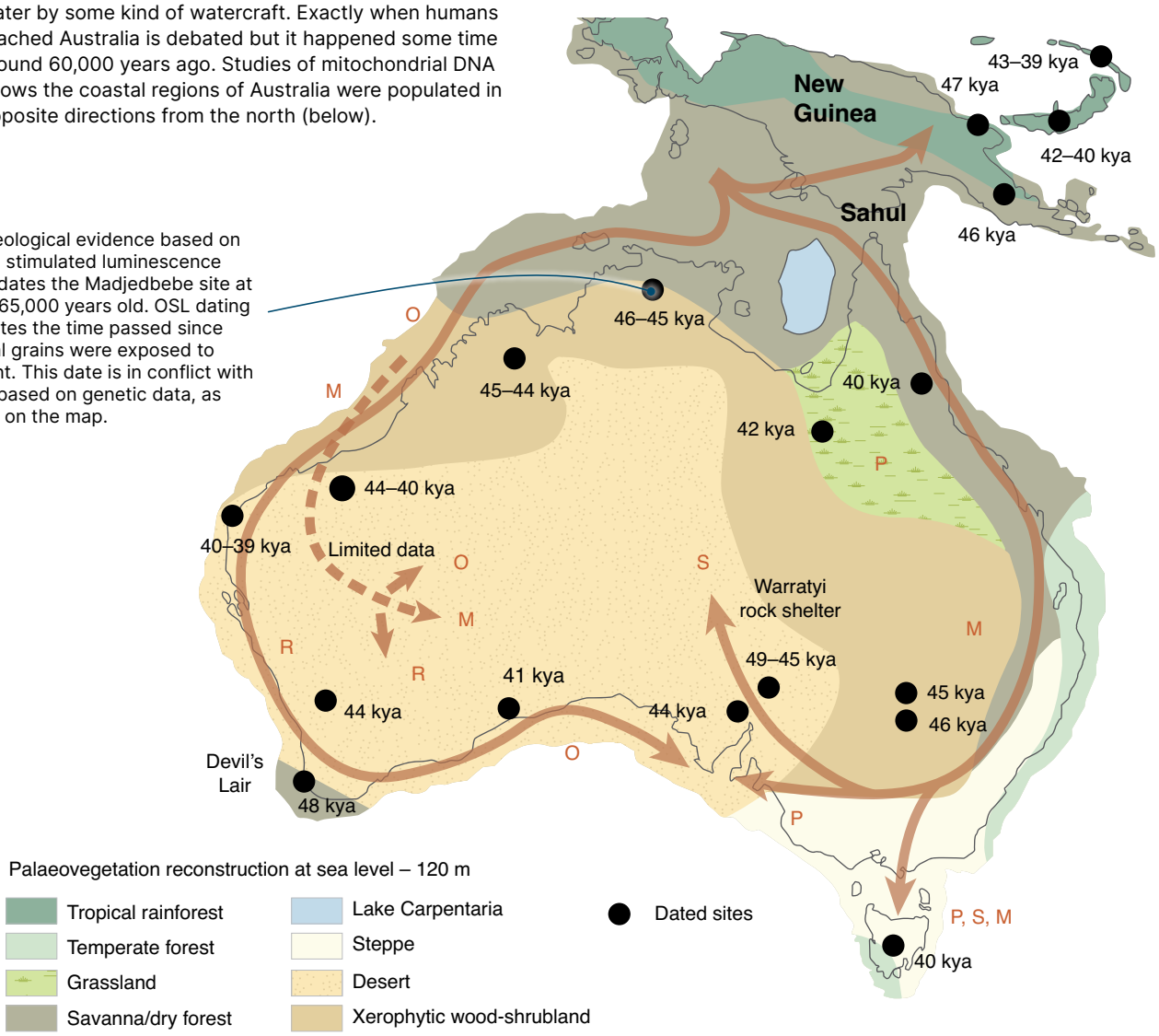
Using haplotypes to track the populating of Australia

- After it split from Gondwana, the Australian continent (technically known as Sahul) has remained disconnected from the rest of the world. Low sea levels 70–60,000 years ago saw a land bridge form between mainland Australia and the island of New Guinea to the north, but there has been no connection of Sahul to the other continents.
- To reach Sahul, humans must have travelled across open water by some kind of watercraft. Exactly when humans reached Australia is debated but it happened some time around 60,000 years ago. Studies of mitochondrial DNA shows the coastal regions of Australia were populated in opposite directions from the north (below).

Archaeological evidence based on optical stimulated luminescence (OSL) dates the Madjedbebe site at about 65,000 years old. OSL dating estimates the time passed since mineral grains were exposed to sunlight. This date is in conflict with dates based on genetic data, as shown on the map.



Adapted from Tobler *et al* Nature, 2017. See credits for full reference.

- The latest and most comprehensive mitochondrial DNA analysis has shown the modern Aboriginal Australians are directly related to the first humans to populate Australia. Analysis of Aboriginal mitochondrial haplotypes show they fall into five major groups labelled S, O, M, P and R. The movement of these groups is shown on the map above.
- Results are consistent with the hypothesis that a wave of modern humans migrated out of Africa 80–70,000 years ago. Some of those humans arrived in Australia around 60,000 years ago. Interestingly, Aboriginal Australians diverged from Papuans about 40,000 years ago, long before the physical separation of the two countries 10,000 years ago.
- The diagram above shows the estimated routes taken during the populating of Sahul based on the five mitochondrial haplotypes.

3. Describe the route taken in the populating of Australia: _____

_____

4. Looking at the dates on the map, what can be said about the rate at which Australia was populated?

_____

5. Looking at the locations where the major haplotypes are found, what can be said about migration within Australia after the initial population event?

_____

_____

_____

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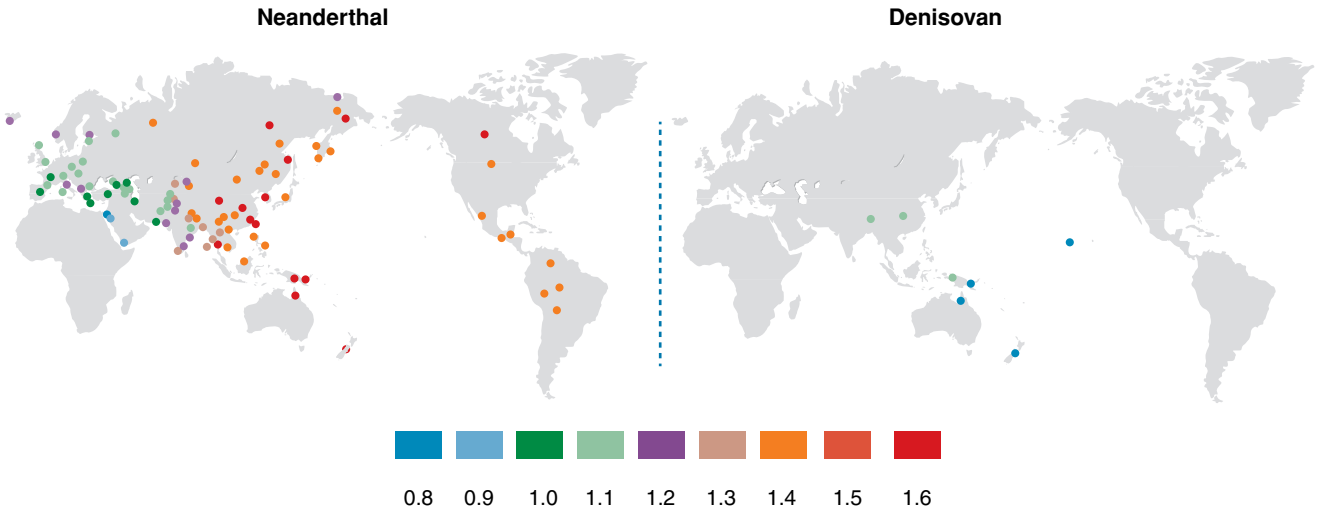
Large scale DNA analysis of human groups shows interbreeding with Neanderthals and Denisovans

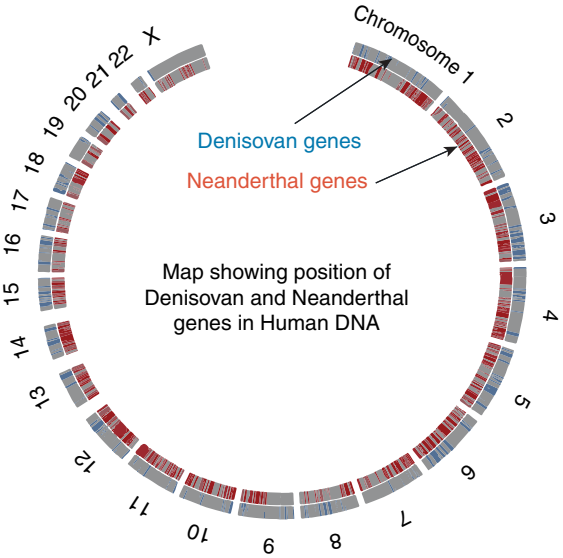
- As modern humans migrated out of Africa they encountered populations of other *Homo* species that had evolved from earlier migrations of *Homo heidelbergensis* out of Africa about 650,000 years ago. These populations were the Neanderthals in Europe and the Denisovans in Asia.
- Until around the late 2000s, it was generally assumed that modern humans simply out-competed the Neanderthals, if they met at all. However, when the first Neanderthal DNA was sequenced in 2010, it hinted at a more complex relationship. In 2016, analysis of Neanderthal and human DNA showed that about 2% of the human genome was made up of Neanderthal genes. Further analysis has shown that interbreeding occurred a number of times.
- In 2010, analysis of mtDNA from a tooth found in the Denisova cave in Siberia showed the tooth was from a previously unknown *Homo* species, neither human nor Neanderthal. Comparison of Denisovan and human DNA shows that Denisovan DNA appears in the DNA of peoples of Oceania and Malaysia. Denisovan DNA does not appear in peoples of Europe and Africa.

Percentage Neanderthals or Denisovan DNA in modern human groups



Percentage Neanderthal or Denisovan DNA in modern human groups

Based on data from The landscape of Neandertal ancestry in present-day humans, Sriram Sankararaman et al, 2014



- Denisovan and Neanderthal DNA is spread throughout the human genome. Denisovan DNA appears in larger chunks than Neanderthal DNA, indicating a more recent interbreeding event.
- A recent study on a 45,000 year old human leg bone found in Siberia showed it had 2.1% Neanderthal DNA, the same as a human today. However, the DNA was in large chunks rather than dispersed as it is in our modern genome.
- This indicates the interbreeding event with Neanderthals had recently occurred. Using this as a marker, scientists were able to date the migration out of Africa by modern humans at around 55,000 years ago.

Neanderthal skull

Image: Bone clones

6. Explain how the presence of Neanderthal and Denisovan DNA in modern humans agrees with the theory of a migration out of Africa by modern humans, around 70,000 years ago.

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162 Extinction

Key Idea: Extinction is a natural process. Most species that have ever lived are now extinct. There have been five major mass extinctions in the history of life on Earth.

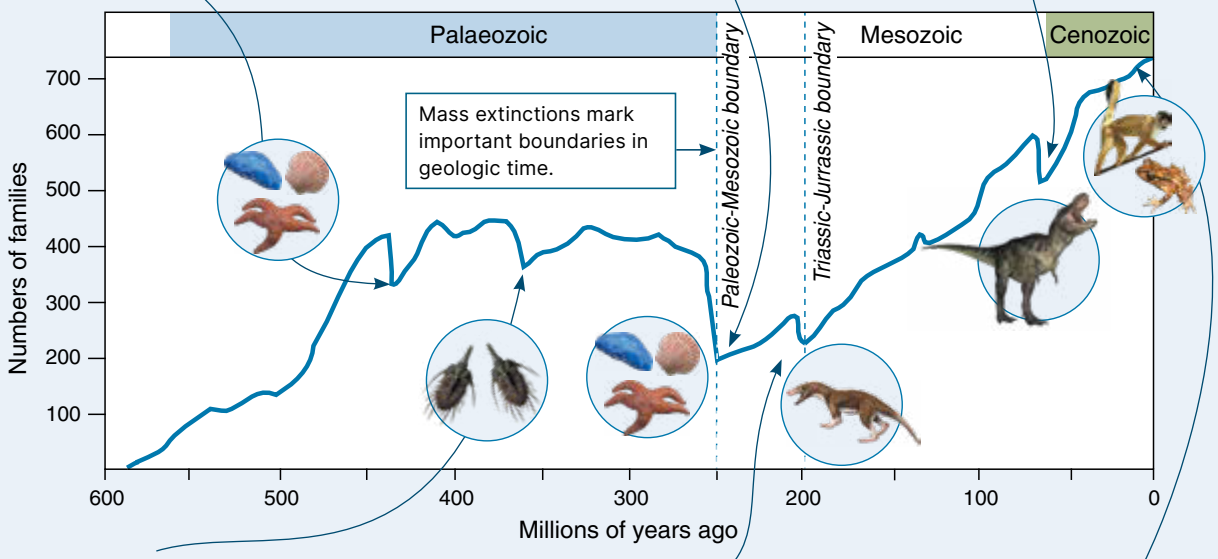
Extinction is important in **evolution** because it provides opportunities, in the form of vacant niches, for the evolution of new species. The species alive today make up only a fraction of the total list of species that have lived on Earth throughout its history. The duration of a species is thought to range from as little as 1 million years for complex larger organisms to as long as 10-20 million years for simpler organisms. This constant extinction of species is called the background extinction rate. Superimposed on this rate are catastrophic events or **mass extinctions** that wipe out vast numbers of species in relatively brief periods of time in geologic terms. The diagram below shows how the number of species has varied over the history of life on Earth. The number of species is indicated on the graph by families: a taxonomic group consisting of many genera and species. There have been five major extinction events and a sixth likely event, which began in the Late Pleistocene and continues today.

Major mass extinctions

Ordovician extinction (450 mya)
Second largest extinction of marine life: >60% of marine invertebrates died. One of the coldest periods in Earth's history.

Permian extinction (250 mya)
Nearly all life on Earth perished. More than 90% of marine species and many terrestrial species die out. Many families and genera lost.

Cretaceous extinction (65 mya)
Marked by the extinction of nearly all dinosaur species (their descendants the birds survive). Generally accepted as being caused by a massive asteroid that collided with Earth.



Devonian (374 mya)
Marine life affected, especially brachiopods, trilobites, and reef building organisms.

Triassic extinction (201.3 mya)
At least half of the species present became extinct, vacating niches and ushering in the age of the dinosaurs.

Sixth extinction (Holocene)
The large numbers of extinctions across many families is attributed to human activity.

1. Why would counting the number of families that became extinct in a mass extinction provide more useful data than counting the number of species that became extinct?

2. (a) What has happened to the diversity of life soon after each mass extinction? _____

(b) Why would this occur? _____

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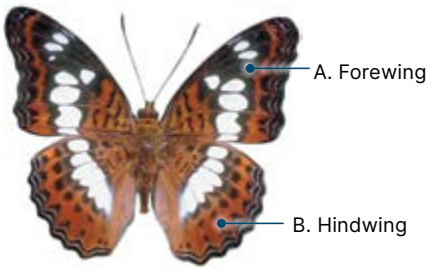
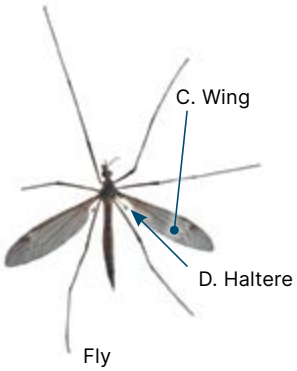
163 Did You Get It?

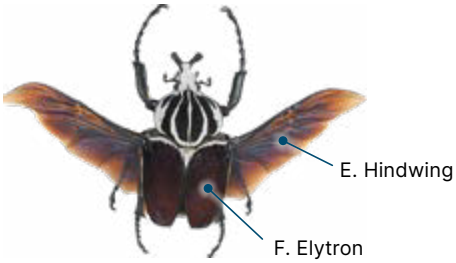
1. Insects are extremely adaptable and have a wide range of body forms. Consider the wing structure of the insects below:



Butterfly



Fly



Beetle

(a) Use the letters to identify the wing structures that are homologous on the images above: _____

(b) What does the homology of these structures indicate? _____

_____

_____

2. Compare and contrast DNA hybridisation and DNA sequence comparison as methods for generating phylogenies:

_____

_____

_____

_____

_____

3. Explain how determining variation in some genes in different populations helps explain human migration patterns:

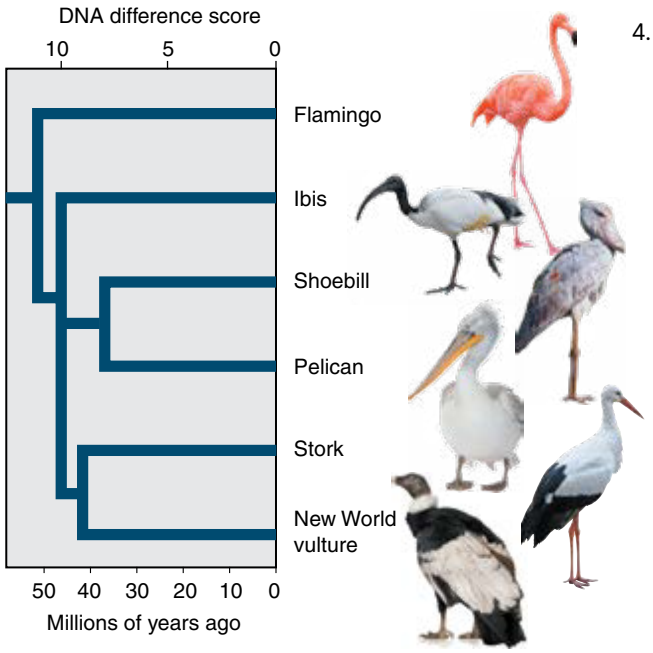
_____

_____

_____

_____

_____



4. The diagram left shows the evolutionary relationship of a group of birds based on DNA similarities:

(a) Place an X on the last common ancestor of all the birds:

(b) How many years ago did storks diverge from vultures?

_____

(c) What are the most closely related birds? _____

_____

(d) What is the difference in DNA (score) between:

i: Storks and vultures: _____

ii: Ibises and shoebills: _____

(e) Which of the birds is the least related to vultures?

_____

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Chapter 14 Unit 4 Topic 2

Natural Selection and Microevolution

Resource Hub
bit.ly/434H7kT

Key Terms

- adaptation
- allele frequency
- directional selection
- disruptive selection
- founder effect
- gene flow
- gene pool
- genetic drift
- genotypic change
- microevolutionary process
- mutation
- natural selection
- phenotypic variation
- stabilising selection

Key Concepts

- Natural selection, mutation, gene flow, and genetic drift all contribute to changes in allele frequencies within populations, driving evolution.
- Natural selection includes stabilising, directional, and disruptive selection. Natural selection drives evolution by favouring adaptive phenotypes that enhance survival and reproduction in specific environments.
- Random allele frequency changes (genetic drift) and isolated founder populations (founder effect) can affect genetic diversity. This is noticeable in smaller populations.

Natural selection and changes in gene pools		Activity Number
☐ 1	Recall what is meant by microevolution. Recognise natural selection as one of the four important microevolutionary processes in gene pools. Explain how natural selection sorts natural variation and establishes adaptive phenotypes. Remember that natural selection is simply the differential survival and reproduction of individuals due to differences in phenotype. It selects for adaptive phenotypes and against phenotypes that are less well suited to the environment at the time.	164, 165
☐ 2	Explain what is mean by a gene pool and by allele frequency. Understand the concept of genetic equilibrium and explain why populations evolve because the conditions for genetic equilibrium are seldom met. Use simple models to show how natural selection can alter the allele frequencies in a population over time.	166, 167
☐ 3	Describe what is meant by an adaptation and the connection between adaptation and fitness. Describe some adaptations in Australian organisms and explain how they enable the organism to exploit its niche (functional role in the ecosystem).	168
☐ 4	Interpret data and describe the three main type of natural selection: stabilising selection, directional selection, and disruptive selection. Using examples, explain how each type affects the phenotypic mean and the environmental conditions under which each type is likely to operate.	169-173
☐ 5	Interpret data to describe and explain the evolution of chemical resistance in modern populations. Identify the selective pressure involved in each case. Recognise that the evolution of chemical resistance occurs by natural selection. • Antibiotic resistance in bacteria (including horizontal gene transmission) • Pesticide resistance in insects	174
☐ 6	SI: Use a computer simulation to analyse genotypic changes for a selective pressure in a gene pool.	167, 176

Other processes in microevolution		
☐ 7	Recall that natural selection is just one process in microevolution, the others being mutation, gene flow, and genetic drift. Summarise the effect of each of these on the allele frequencies of a population remembering that mutation is the source of all new genetic variation.	165
☐ 8	Explain how emigration of a small number of founders to a new environment can result in a new population with an allele frequency that differs from the original parent population. Analyse data to explain the role of this 'founder effect' in the rapid evolution of isolated populations, especially when they are small. Include reference to the role of genetic drift.	175
☐ 9	Analyse data, including from a computer simulation, to explain the effect of population size on genetic drift. Using an Australian example, explain how genetic drift affects the allelic diversity of small founder populations. Explain why genetic drift is regarded as an important agent of evolution, especially in small populations.	176

164 Variation and Natural Selection

Key Idea: Natural selection is the evolutionary mechanism by which organisms that are better adapted to their environment survive to produce a greater number of offspring.

Evolution is simply the change in inherited characteristics in a population over generations. Darwin recognised this as the consequence of four interacting factors: (1) the capacity of populations to increase in numbers, (2) the **phenotypic variation** of individuals, (3) that there is competition for resources, and (4) proliferation of individuals with better survival and reproduction.

Natural selection is the varying survival and reproduction of individuals due to differences in phenotype. Organisms with more favourable phenotypes will survive in greater numbers to produce a greater number of viable offspring. The proportion of their alleles in subsequent generations will therefore increase. This is the basis of Darwin's theory of evolution by natural selection. Natural selection is one of the most important **microevolutionary processes**.

We can demonstrate the basic principles of evolution using the analogy of a 'population' of M&M's candy.

In a bag of M&M's, there are many colours, which represents the variation in a population. As you and a friend eat through the bag of candy, you both leave the blue ones, which you both dislike, and return them to bag.

The blue candy becomes more common...

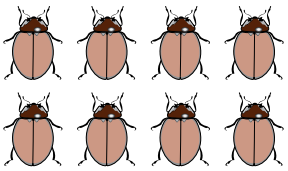
Eventually, you are left with a bag of blue M&M's. Your selective preference for the other colours changed the make-up of the M&M's population. This is the basic principle of selection that drives evolution in natural populations.

Darwin's theory of evolution by natural selection

Darwin's theory of evolution by natural selection is outlined below. It is widely accepted by the scientific community today and is one of the founding principles of modern science.

Overproduction

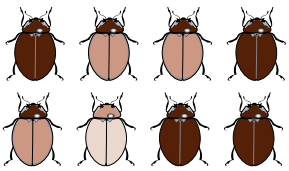
Populations produce too many young; many must die.



Populations generally produce more offspring than are needed to replace the parents. Natural populations normally maintain constant numbers. A certain number will die without reproducing.

Variation

Individuals show variation; some variations are more favourable than others.



Individuals in a population have different phenotypes and therefore, genotypes. Some traits are better suited to the environment, and individuals with these have better survival and reproductive success.

Natural selection

Natural selection favours the individuals best suited to the environment at the time.

Individuals in the population compete for limited resources. Those with favourable variations will be more likely to survive. Relatively more of those without favourable variations will die.

Inherited

Variations are inherited: the best suited variants leave more offspring

The variations (both favourable and unfavourable) are passed on to offspring. Each generation will contain proportionally more descendants of individuals with favourable characters.

1. Identify the four factors that interact to bring about evolution in populations: _____

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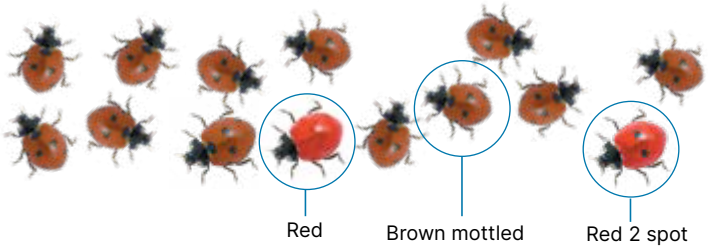
Variation, selection, and population change

Natural populations, like the ladybird population above, show genotypic (and therefore phenotypic) variation. This is a result of **mutation** (which creates new alleles) and sexual reproduction (which produces new combinations of alleles). Some phenotypic variants are more suited to the environment of the time than others. These variants will leave more offspring, as described for the hypothetical population (right).

1. Variation through mutation and sexual reproduction:
In a population of brown beetles, mutations independently produce red colouration and 2 spot marking on the wings. The individuals in the population compete for limited resources.



2. Selective predation:
Brown mottled beetles are eaten by birds but red ones are avoided.

3. Change in the genetics of the population:
Red beetles have better survival and fitness and become more numerous with each generation. Brown beetles have poor fitness and become rare.

2. What produces the genetic variation in populations? _____

3. Define evolution: _____

_____

4. Explain how the genetic make-up of a population can change over time: _____

_____

_____

_____

_____

_____

_____

5. Complete the table below by calculating the percentage of beetles in the example above right.

Beetle population	% Brown beetles	% Red beetles	% Red beetles with spots
1			
2			
3			

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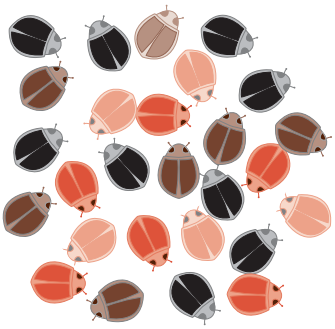
165 Microevolutionary Processes in Gene Pools

Key Idea: Mutations, gene flow, genetic drift, and natural selection all contribute to changes in the genetic makeup (frequency of different alleles) of a population.

A population can be regarded as a collection of all its alleles (the **gene pool**). Changes in the frequency of these alleles in the population over time is what we call evolution. As we have seen, **mutation** and sexual reproduction create genotypic (and therefore phenotypic) variation and **phenotypic variation** is the raw material for **natural selection**. Four **microevolutionary processes** can contribute to genetic change in populations. Mutation creates new alleles. Migration creates **gene flow** as alleles enter or leave a population. Natural selection sorts variation and establishes adaptive phenotypes and is a major agent of evolution. **Genetic drift** alters alleles frequencies randomly and its effects are due to chance events. Increasingly, genetic drift is being recognised as an important agent of change, especially in small, isolated populations (e.g. island colonisers).

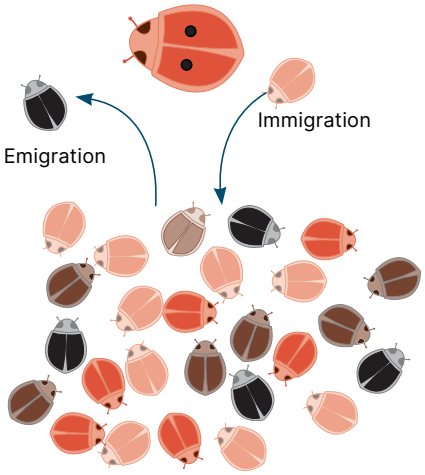
Genetic variation

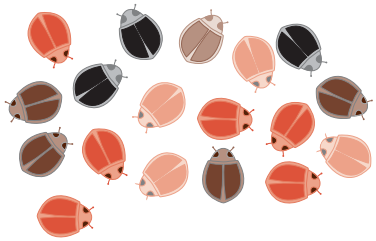
Genetic variation refers to the number of different types of alleles in a population. Genetic variation produces phenotypic variation (e.g. colour of ladybirds). It is this phenotypic variation that is the raw material for natural selection. This ladybird population has five different phenotypes (black, dark brown, tan, brick red, and pale).

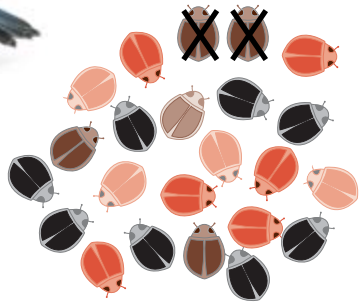


As we have seen in earlier activities, genetic variation arises through mutations and the recombination of alleles through sexual reproduction.

For example, a mutation produces a ladybird with a new spotted phenotype (below).







Natural selection

Natural selection acts on populations to maintain favourable phenotypes and eliminate unfavourable phenotypes. Over time, favourable phenotypes become more common in the population because those individuals reproduce more.

For example, black ladybirds are more easily seen by birds and are eaten more often than the other phenotypes. The lighter phenotypes become more common in the next generation.

Genetic drift

Genetic drift is the change in a population's allele frequency due to random events. Genetic drift has a more pronounced effect in small populations.

For example, falling rocks kill a number of ladybirds, but more of the dark brown ladybirds are crushed than any other phenotype. The proportion of dark brown ladybirds remaining in the population is drastically reduced, and their representation in the next generation is also reduced.

Migration (gene flow)

Migration is the movement of individuals into and out of a population. Through immigration or emigration, alleles can enter or leave the population. Gene flow tends to decrease the genetic differences between populations because alleles are being exchanged.

In the example above, several black ladybirds have left and some very pale ladybirds have arrived changing the proportion of remaining phenotypes in the population.

1. Define the following terms:

(a) Gene flow: _____

_____

_____

(b) Genetic drift: _____

_____

_____

(c) Natural selection: _____

_____

_____

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2. One of the important theoretical concepts in population genetics is that of genetic equilibrium, which states that "***for a large, randomly mating population, allele frequencies do not change from generation to generation***". If allele frequencies in a population are to remain unchanged, all of the following criteria must be met: the population must be large, there must be no mutation or gene flow, mating must be random, and there must be no natural selection. Evolution is a consequence of few if any of these conditions ever being met in natural populations. For each of the five factors (a-e) below, describe how and why each would affect the allele frequency in a gene pool. Use the diagrams to help you.

(a) Population size: _____

(b) Mate selection: _____

(c) Gene flow: _____

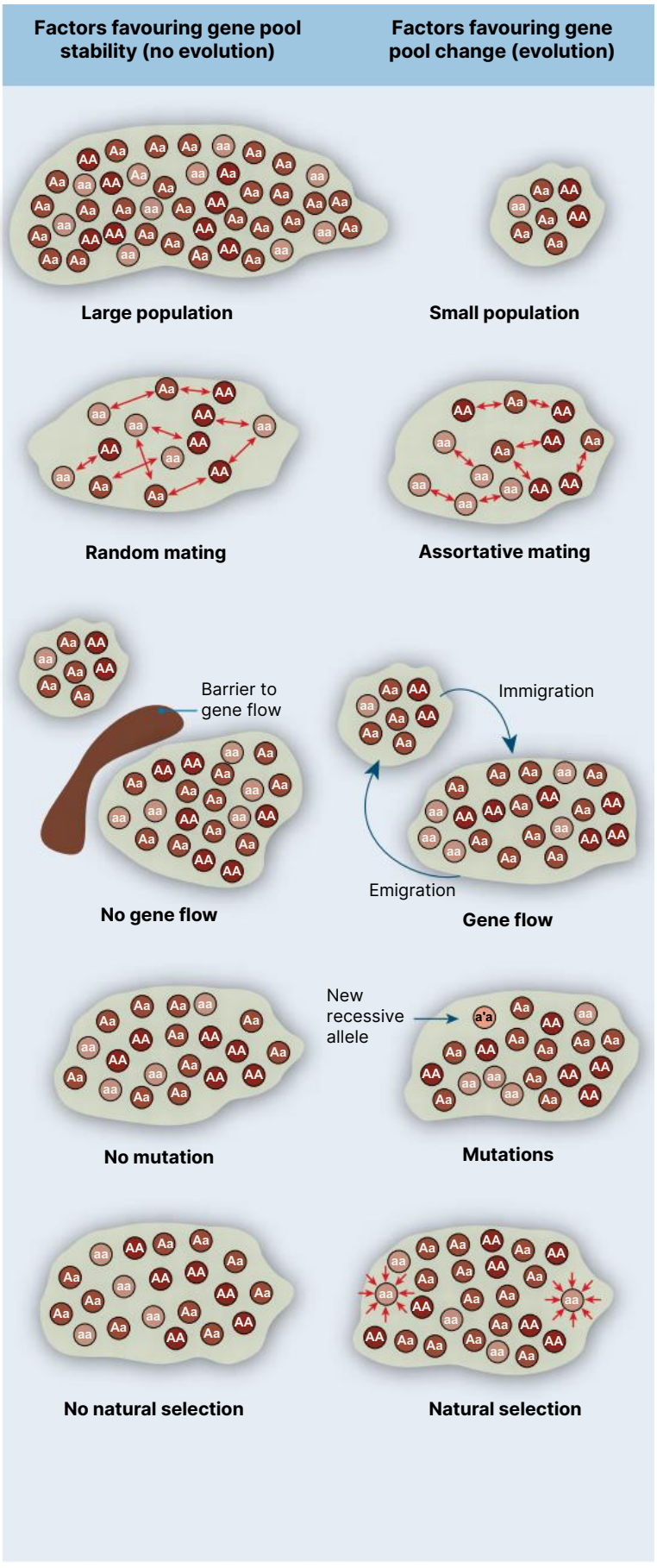
(d) Mutation: _____

(e) Natural selection: _____

3. Identify a factor that tends to:

(a) Increase genetic variation in populations:

(b) Decrease genetic variation in populations:



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166 Analysing Allele Frequencies

Key Idea: The frequency in which alleles appear in different populations varies. Allele frequencies can be used in many genetic studies and forensic tests.

Recall that an allele is a version of a gene. Analysing how often an allele occurs relative to the total number of alleles (the **allele frequency**) can be useful in population studies. Recording how allele frequencies change over time can give insight in the evolution of a population. Comparing allele frequencies between populations can show important differences between populations.

Calculating allele frequency

- The frequency of an allele represents how often an allele appears in a **gene pool** or population. The frequency is calculated by dividing the number of times the allele is observed by the total number of alleles for that gene or genetic locus.

$$\text{Allele frequency} = \frac{\text{Number of copies of a specific allele}}{\text{Total number of alleles in population}}$$

- For example, in Awassi sheep (right), a **mutation** in the gene CNGA3 produces an allele that, in homozygous recessive animals, causes day blindness. In a population of 423 sheep 74 were found to be carriers (heterozygous for the mutation). Therefore the frequency of the mutant allele is 74 ÷ (423 × 2) = 0.087.

Allele frequencies and gene pools

- Recording changes in gene pools can give insight into the evolution of a population. In Olney, Illinois, there is a unique population of albino (white) and grey squirrels. Between 1977 and 1990, students at Olney Central College carried out a study of this population. They recorded the frequency of grey and albino squirrels. The albinos displayed a mutant allele expressed as an albino phenotype only in the homozygous recessive condition. The recorded results are shown below:

Population of grey and white squirrels in Olney, Illinois (1977-1990)

Year	Grey (GG)	Grey (Gg)	White (gg)	Total	Freq. of G	Freq. of g
1977	211	391	182	784	0.52	0.48
1978	170	342	172	683		
1979	175	307	134	616		
1980	180	309	133	622		
1981	187	349	163	699		
1982	238	380	151	769		
1983	139	280	141	560		
1984	137	241	106	484		
1985	163	285	125	573		
1986	191	345	155	691		
1987	*No data collected this year*					
1988	281	371	122	774		
1989	206	346	146	698		
1990	262	341	111	714		

1. Explain the equation for calculating the frequency of the mutant allele in Awassi sheep: _____

2. Complete the table above by calculating the frequency of the G and g alleles in the squirrel population:

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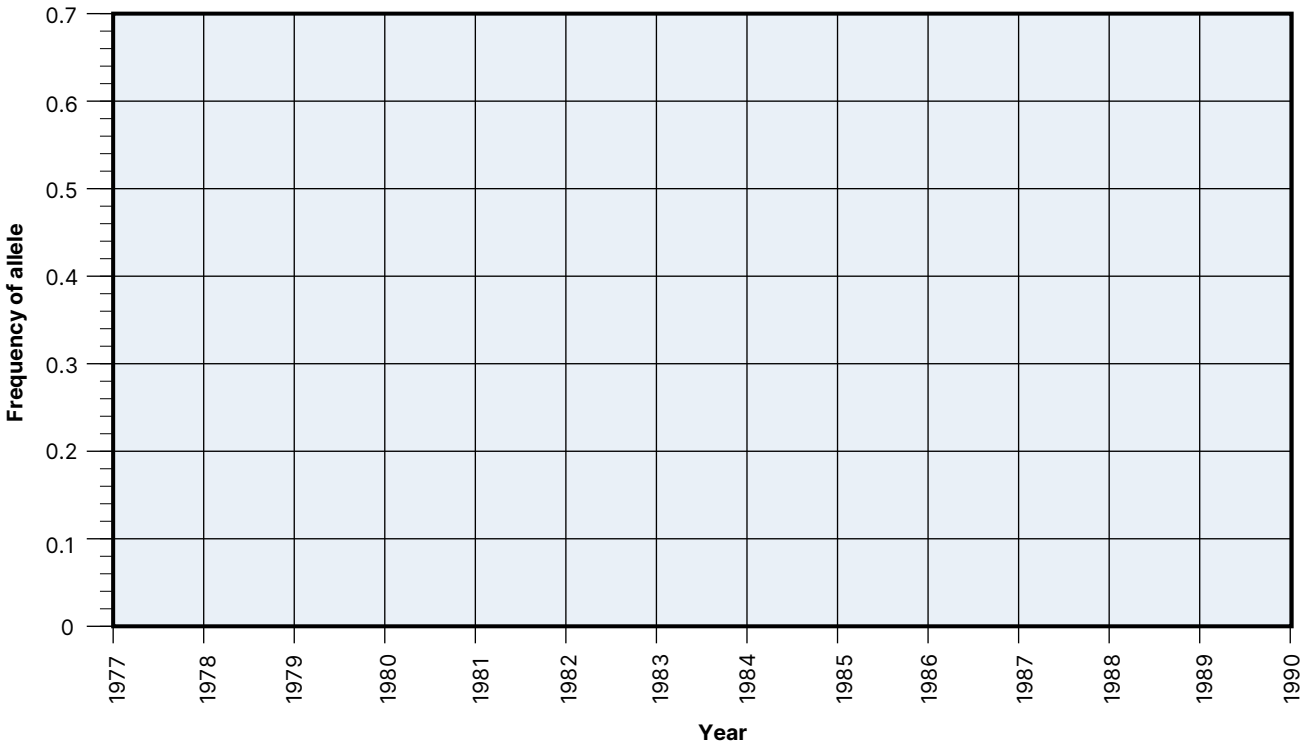
3. Plot a graph of the frequency of the G and g alleles over time:



4. Describe the shape of the graph and what this means for the evolution of the squirrel's gene pool:

Allele frequencies and SNPs

- Recall that Single nucleotide polymorphisms (SNPs, pronounced 'snips') are the most common genetic variation among people. A SNP is a single nucleotide change at a specific DNA locus, normally found in at least 1% of the population. For example a sequence of DNA may have two polymorphisms: AAC**G**TGT or AAC**T**TGT.
- SNPs are mostly found in between genes and therefore have little effect on gene function. However, a particular SNP or set of SNPs may be associated with a gene or, more specifically, with an allele of a gene. This means they are close enough to the gene that they are inherited with it. As a result, a SNP can be used as a gene marker, i.e. a specific SNP identifies a specific allele.
- Large numbers of SNPs have been identified in humans. Specific groups of SNPs are called haplotypes and specific haplotypes may be associated with specific diseases, or how people react to certain medication.
- Identifying haplotypes gives scientists a way of identifying the genetic cause of disease or to devise better treatments for a person's illness.

5. What is a SNP?

6. Explain why SNP markers need to be close to their respective gene:

7. Why would identifying haplotypes associated with how a person reacts to treatment help scientists devise better treatments?

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167 Changes in a Gene Pool

Key Idea: Natural selection and migration can alter the allele frequencies in gene pools.

The diagram below shows a hypothetical population of beetles undergoing changes as it is subjected to two 'events'. The three phases represent a progression in time, i.e. the same **gene pool**, undergoing change. The beetles have two phenotypes, dark and pale, determined by the amount of pigment deposited in the cuticle. The gene controlling this character is represented by two alleles A and a. Your task is to analyse the gene pool as it undergoes changes.

1. For each phase in the gene pool below fill in the following tables. The first has been done for you:

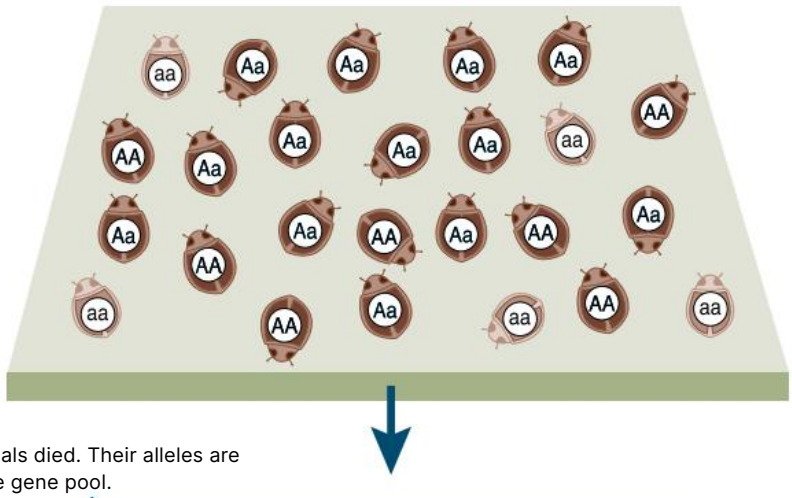
   (a) Count the number of 'A' and 'a' alleles separately. Enter the count into the top row of the table (left hand columns).
   (b) Count the number of each type of allele combination (AA, Aa and aa) in the gene pool. Enter the count into the top row of the table (right hand columns).
   (c) For each of the above, work out the frequencies as percentages (bottom row of table):

Allele frequency (%) = No. counted alleles ÷ Total no. of alleles x 100

Phase 1: Initial gene pool

	A	a	AA	Aa	aa
No.	27		7		
%	54		28		

Allele types *Allele combinations*



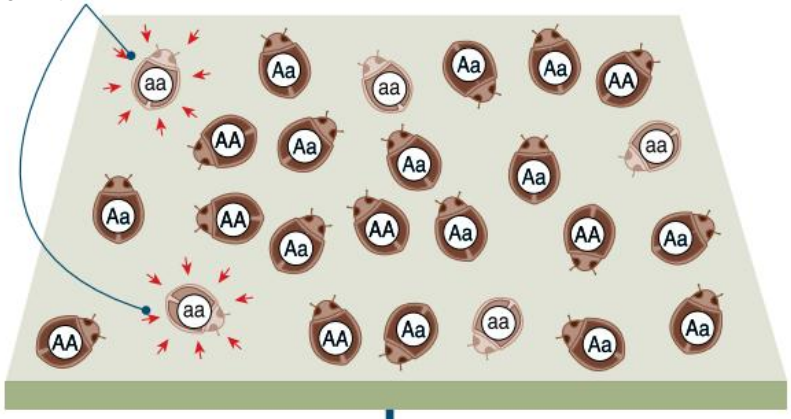
Two pale individuals died. Their alleles are removed from the gene pool.

Phase 2: Natural selection

In the same gene pool at a later time there was a change in the allele frequencies. This was due to the loss of certain allele combinations due to natural selection. Some of those with a genotype of aa were eliminated (poor fitness).

These individuals (surrounded by small red arrows) are not counted for allele frequencies; they are dead!

	A	a	AA	Aa	aa
No.					
%					



This individual is entering the population and will add its alleles to the gene pool.

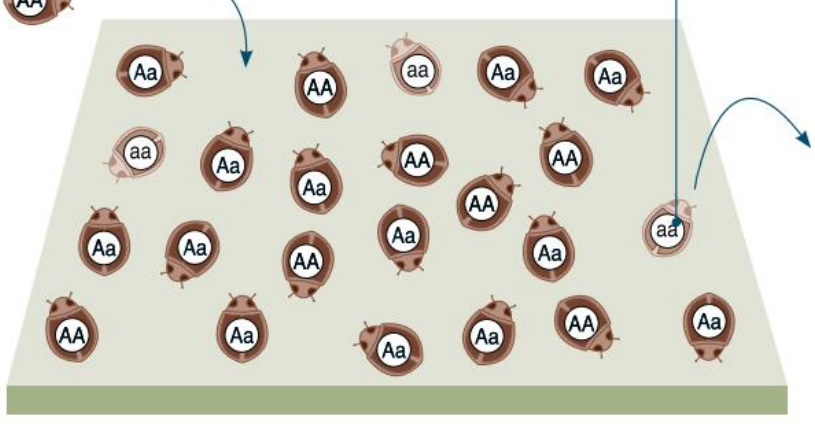
This individual is leaving the population, removing its alleles from the gene pool.

Phase 3: Immigration and emigration

This particular kind of beetle exhibits wandering behaviour. The allele frequencies change again due to the introduction and departure of individual beetles, each carrying certain allele combinations.

Individuals coming into the gene pool (AA) are counted for allele frequencies, but those leaving (aa) are not.

	A	a	AA	Aa	aa
No.					
%					



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Modelling natural selection

Changes in gene pools are often modelled using physical representations of the genotypes in a population. This type of modelling is tedious and subject to human error. Modelling **genotypic changes** using a spreadsheet is quicker and allows the model to be changed to simulate different scenarios occurring in the gene pool.

Investigation 14.1 Investigating natural selection

Some natural selection labs work by manually placing tokens representing alleles into a bag and withdrawing them randomly to make genotypes. A certain genotype is then selected against by not returning it to the bag and the next generation is drawn from the remaining alleles. This exercise is long and difficult to manipulate, and it reduces the population numbers over time so that an accurate simulation is not entirely possible.

These problems can be solved by using a spreadsheet to compute allele changes over time. Once the formulae are in place, the spreadsheet can be manipulated in different ways to produce a more accurate, yet still simple, simulation. This spreadsheet can also be used to simulate genetic drift in Activity 176.

Download the spreadsheet from the **BIOZONE Resource Hub** or use the notes and screenshots below to recreate the spreadsheet yourself.

PART 1: Setting Up the spreadsheet

1. Open a new spreadsheet. The first thing to do is to switch off automatic calculation. This makes calculation of future allele frequencies simpler and under manual control, so that you can calculate them when you're ready. Each spreadsheet program will have slightly different ways of doing this. For Microsoft Excel click on the **Formulas** tab then on the **Calculation Options** menu and click **Manual**. Calculations can then be made using the **Calculate Now** button beside the Calculation Options menu or using the **F9** button.

2. The headings A and B represent the alleles A and a. This is necessary because the COUNTIF formula used later in the spreadsheet is not case sensitive (it does not recognise the difference between A and a).

3. 0.5 is the frequency of the A allele in the initial population (generation 0). The frequency of the B allele in the population is equal to 1-A. In our initial population, 50% of the alleles will be A and 50% will be B (A and a in the population).

	A	B	C	D
1	Allele frequency			
2	A	B		
3	0.5	=1-A3		
4				
5				
6	Gamete 1	Gamete 2		Zygote
7	=IF(RAND()<=$A$3,"A","B")	=IF(RAND()<=$A$3,"A","B")		=CONCATENATE(A7,B7)
8	=IF(RAND()<=$A$3,"A","B")	=IF(RAND()<=$A$3,"A","B")		=CONCATENATE(A8,B8)
9	=IF(RAND()<=$A$3,"A","B")	=IF(RAND()<=$A$3,"A","B")		=CONCATENATE(A9,B9)
10	=IF(RAND()<=$A$3,"A","B")	=IF(RAND()<=$A$3,"A","B")		=CONCATENATE(A10,B10)
11	=IF(RAND()<=$A$3,"A","B")	=IF(RAND()<=$A$3,"A","B")		=CONCATENATE(A11,B11)

4. The RAND formula produces a random number between 0 and 1 and compares it to the number in cell A3. If the random number is less than or equal to the number in cell A3 then an A is displayed in the cell. If the random number is greater, a B is displayed. The $ symbol tells the spreadsheet that cell A3 is a reference cell and must not change.

5. The CONCATENATE formula takes gametes A and B and puts them together to make the zygote.

6. Highlight cells and copy down all formulas to row 56 to produce 100 random gametes containing alleles A or B and 100 zygotes.

7. You now need to count up the number of AA, AB, and BB genotypes

	F	G	H	I	J
1	AA	AB	BB		Total Genotypes
2	=COUNTIF($D$7:$D$56,"AA")	=COUNTIF($D$7:$D$56,"AB")+COUNTIF($D$7:$D$56,"BA")	=COUNTIF($D$7:$D$56,"BB")		=SUM(F2:H2)
3					
4					

8. The COUNTIF formula counts up the number of AA, AB, and BB genotypes.

9. The SUM formula adds up the number of genotypes. It should add up to 50.

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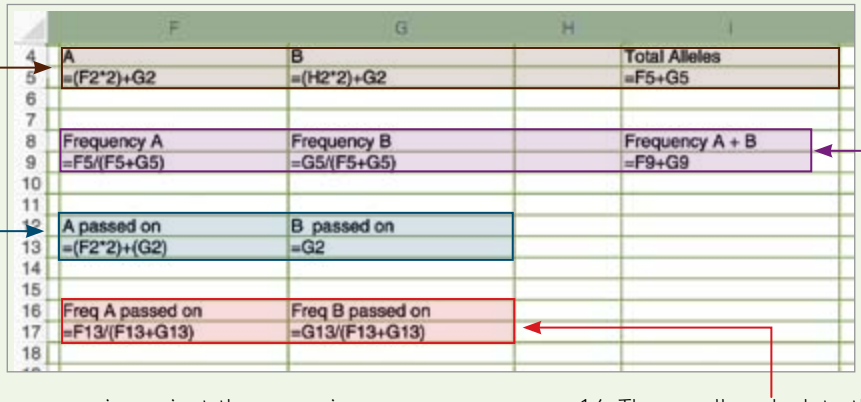
10. Now you must calculate the number of A and B alleles present in this generation (Generation 1).In cell **F4** type the heading **A** and in cell **G4** type the heading **B**. In cell **I4**, type the heading **Total Alleles**.

11. Cell F5 adds up all the alleles from the AA genotype and the A alleles from the AB genotype. Cell **G5** adds up all the B alleles. Cell I5 adds up all the alleles. Click **Calculate Now** and you should see the number 100 appear.

12. Cells F9 and G9 calculate the frequency of As and Bs in Generation 1. Cell I9 adds up cell F9 and G9. This should add to 1.

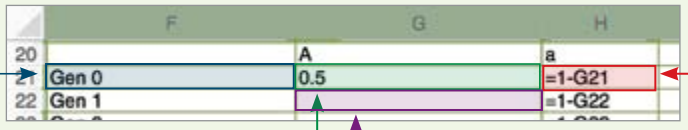


13. The **selection pressure** is against the recessive phenotype. The alleles in the recessive genotype (BB) will not be passed on, so the frequency of alleles in the population is different to the frequency of alleles that will be passed on. These cells calculate the **number** of alleles that will be passed on (excluding those in genotype BB).

14. These cells calculate the frequency of alleles that will be available to the next generation.

15. Finally, you must keep a record of each generation's allele frequencies before mating (i.e. before BB is excluded).

16. Gen 0 was your starting population. Copy down to cell **F31** to get ten generations.



17. The frequency of A in Gen 0 was 0.5

18. The frequency of *a* is simply 1-A. Copy down to **H31.**

19. Click **Calculate Now**. Note the numbers that appear in cells **F9** and **G9**. Type the number in **F9** into **G22**. This is the frequency of the A allele in the first generation.

20. Now type the number in cell **F17** into cell **A3** and click **Calculate Now** to produce the second generation of alleles in cells F9 and G9. Again, enter the number in **F9** into **G23** and the number in **F17** into **A3** before clicking **Calculate Now**.

21. Each time you do this, the spreadsheet calculates a new generation of genotypes and their alleles based in the number you enter into A3.

22. Save your spreadsheet.

PART 2: Natural Selection lab

Now that you have built the spreadsheet and are familiar with it, you can begin the natural selection lab.

1. To do this you will select against the recessive phenotype (and hence the *aa* genotype, represented as BB in the spreadsheet). In this scenario any BB individuals never get to breed (it is irrelevant what the phenotype is, what is important is that no BB individuals will enter their alleles into the next generation).

2. To start the lab, make sure **0.5** is entered into cell **A3**. Enter **0.5** into cell **G21** and make sure the cells below them are clear. Highlight cells **F17** and **G17** and under the **Format** menu click **Cells**, then click the **Number** category and set it to **2** decimal places. Click **OK.**

3. It is also worth tracking the numbers of AA, Aa and aa individuals before breeding. You can do this by simply recording the numbers on a new part of the spreadsheet, the same way as recording the A and a allele frequencies. Theoretically, Generation 0 will start as 12.5 AA, 25 Aa, and 12.5 aa, but because only whole numbers of individuals are allowed these will need to be rounded to the nearest whole number that still

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produces a total of 50 (12, 26, 12). In cell **F35**, type the heading **Gen0**. **Highlight** the cell and copy it down to cell **F45**. In cell **G34**, type the heading **AA**, Cell **H34** type Aa and in **I34** type ***aa***. Into cell **G35** type **12**, in **H35** type **26**, and in **I35** type **12**.

	F	G	H	I
35	Gen 0	12	26	12
36	Gen 1			
37	Gen 2			

4. Click **Calculate Now**.
5. Enter the results in cell **F9** into Generation 1 A (cell **G22**). Enter the numbers in **F2**, **G3**, and **H2** into **G36**, **H36**, and **I36**. Enter the number from **F17** into **A3** and click **Calculate Now** again.
6. Repeat this until you have ten generations of alleles.

PART 3: Graphing the data

1. You can now produce a graph of the results. Highlight the cells **F20** to **H31** and click **Insert** then click on a **line graph** with markers.
2. The graph should automatically produce two lines for A and a. Give the graph appropriate titles and axes labels by clicking **Add Chart Element** (depending on your spreadsheet programme) and selecting **title** and **axes** labels.
3. Repeat this for the AA, Aa, and aa individuals.
4. Print the graphs and staple them to this page.

1. (a) What happens to the frequency of the a alleles over ten generations when the aa genotype is totally excluded from passing its alleles to the next generation?

_____

_____

_____

(b) What happens to the frequency of the A alleles over ten generations when the aa genotype is totally excluded from passing its alleles to the next generation?

_____

_____

_____

(c) Why do your observations from (a) and (b) happen? _____

_____

_____

(d) What is the effect on the phenotypes over time? (Assume AA and Aa produce the same dominant phenotype and aa is the recessive phenotype).

_____

_____

_____

(e) Predict what might happen if some of the aa genotype were able to breed: _____

_____

_____

_____

_____

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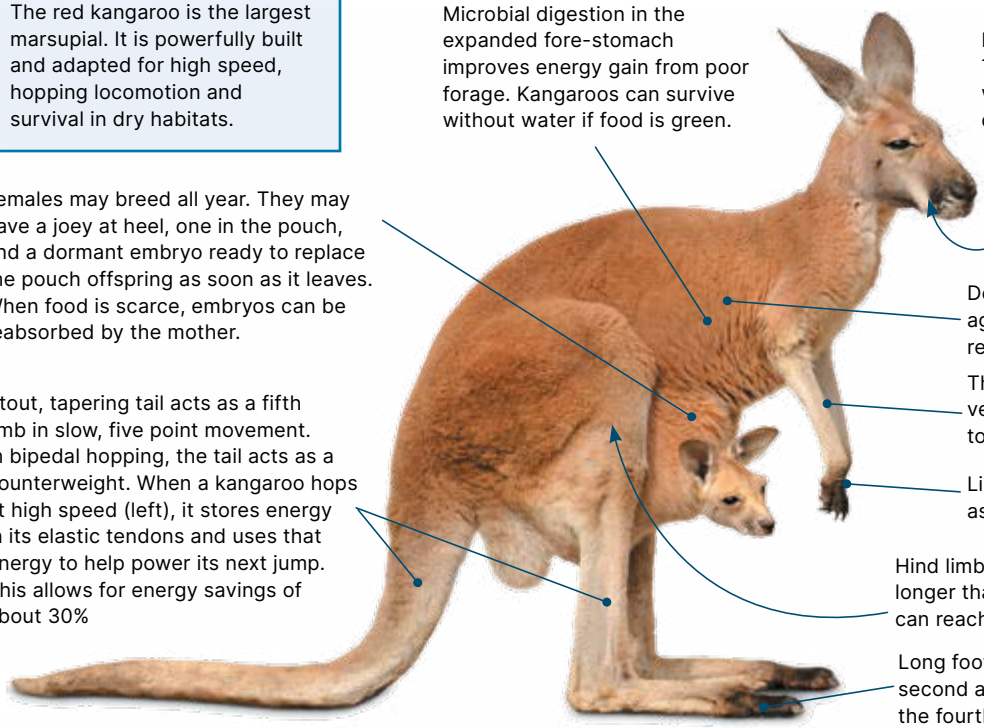
168 Adaptation and Fitness

Key Idea: Adaptive features enhance an individual's fitness.

An **adaptation** (adaptive feature) is a heritable trait that suits an organism to its functional role in the environment (its niche). These traits may be structural, physiological, or behavioural. Adaptations promote fitness, which is a mathematical measure of the contribution an organism makes to the next generation. The adaptations of species are a result of evolution in particular environments. Traits that do not contribute to an increase in fitness will not be favoured and will be lost. Over generations, small incremental changes to genes fine-tune an organism's adaptations, leading to the specialisations we see in organisms all around us.

The red kangaroo is the largest marsupial. It is powerfully built and adapted for high speed, hopping locomotion and survival in dry habitats.



Microbial digestion in the expanded fore-stomach improves energy gain from poor forage. Kangaroos can survive without water if food is green.

Robust, high crowned molar teeth. The molars are replaced as they wear down as an adaptation to a diet of abrasive grasses.

Females may breed all year. They may have a joey at heel, one in the pouch, and a dormant embryo ready to replace the pouch offspring as soon as it leaves. When food is scarce, embryos can be reabsorbed by the mother.

Dense, fine fur provides insulation against heat loss or gain. Fur is reflective, especially on the flanks.

Thin skin well supplied with blood vessels, especially on the forelimbs, to assist heat loss by evaporation.

Stout, tapering tail acts as a fifth limb in slow, five point movement. In bipedal hopping, the tail acts as a counterweight. When a kangaroo hops at high speed (left), it stores energy in its elastic tendons and uses that energy to help power its next jump. This allows for energy savings of about 30%

Licking the pads of the front paws assists in cooling by evaporation.

Hind limbs are more heavily muscled and longer than the forelimbs. Hopping speeds can reach 50 km per hour.

Long foot bones help balance. The second and third digits are fused and the fourth digit is much larger and longer than the others. The heel is elongated for load bearing.

1. Explain the evolutionary significance of adaptations. You can use the red kangaroo example to illustrate your points:

2. The photograph (right) shows the heritage-listed curtain fig tree in the Tablelands Region, Queensland. It belongs to the strangler fig species *Ficus virens*. These trees eventually smother and kill the host tree but are not parasitic. Use the photograph and do some research of your own to find out about *Ficus virens*. Describe its adaptations below, including how they increase fitness in the fig's rainforest environment:

Paste cc 3.0

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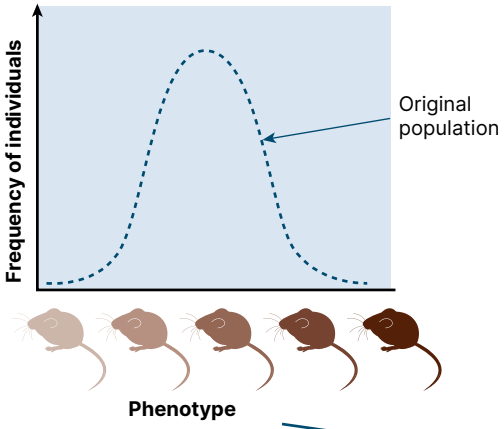
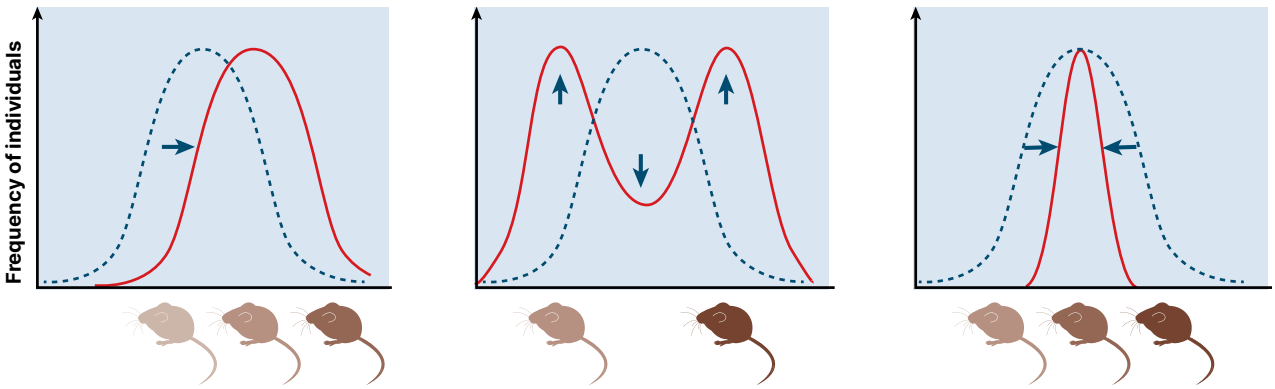
169 Types of Natural Selection

Key Idea: Natural selection is responsible for the differential survival of some phenotypes (and the associated DNA) over others. It is an important cause of genetic change in populations.

Natural selection operates on the phenotypes of individuals, produced by their particular genetic make up in the particular environment. It results in the differential survival of some phenotypes over others. Individuals with phenotypes better suited to the environment at the time will become relatively more numerous in the population. Over time, natural selection may lead to a permanent change in the genetic makeup of a population. Natural selection is always linked to the suitability of the phenotype to the current environment so it is a dynamic process. It may favour existing phenotypes or shift the phenotypic median, as is shown below.



Natural selection acts on **phenotypic variation**. Even slight variations may be enough for selection to occur. The white streak on the mouse on the right may make it stand out to predators. The darker mouse may be able to more easily hide in the shadows.



Directional selection

In **directional selection** an environmental pressure, e.g. predation, or higher temperatures, selects against one of the phenotypic extremes. The adaptive phenotype is shifted in one direction and one phenotype is favoured over others.

Disruptive selection

Disruptive selection favours two phenotypic extremes at the expense of intermediate forms. Disruptive selection may occur when environments or resources are fluctuating or distinctly divergent.

Stabilising selection

Extreme variations are selected against and the middle range (most common) phenotypes are retained in greater numbers. **Stabilising selection** decreases variation for the phenotypic character involved.

1. Explain why fluctuating (as opposed to stable) environments favour disruptive (diversifying) selection:

2. What would be the likely effect of rapid environmental change on a population with very low phenotypic variation?

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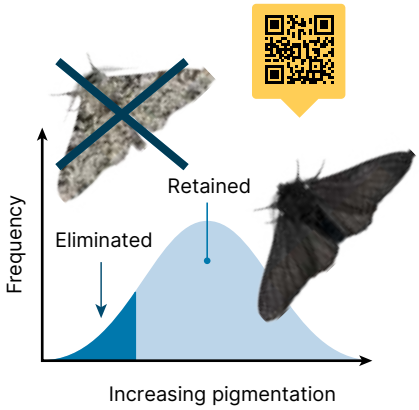
Examples of selection

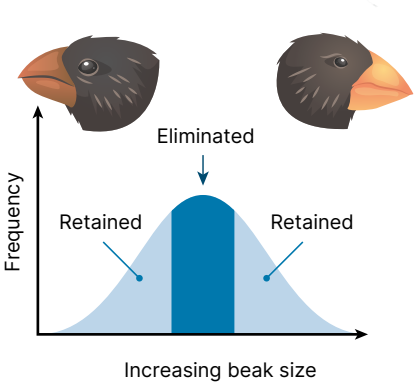
Directional selection



Moths Olaf Leillinger

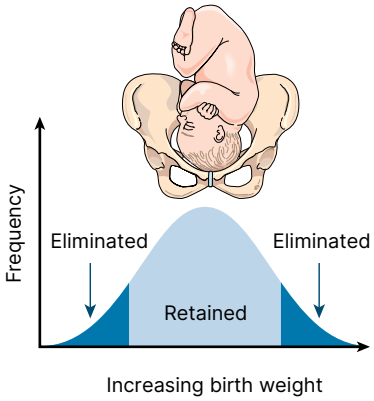
Directional selection was observed in peppered moths in England during the Industrial Revolution when soot-covered trees were common. In England's current environment, the selection pressures on the moths are more balanced, although lighter morphs predominate.

Disruptive selection



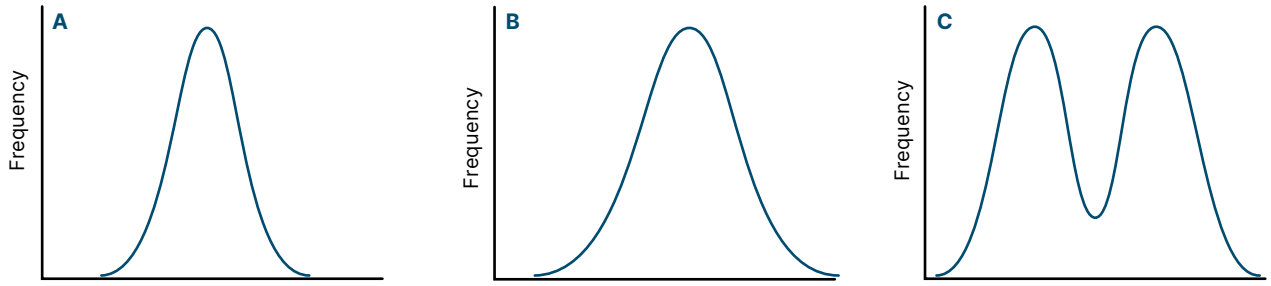
A prolonged drought on Santa Cruz Island in the Galápagos, resulted in a population of ground finches that was bimodal for beak size. Competition for the usual medium-sized seed sources was so intense that selection favoured birds able to exploit either small or large seeds.

Stabilising selection



Stabilising selection operates most of the time in most populations and acts to prevent divergence from the adaptive phenotype, e.g. birth weight of human infants or number of eggs laid in a nest.

3. Which of the graphs below relate to the examples above:



A: _____

B: _____

C: _____

4. Disruptive selection can be important in the formation of new species:

   (a) Describe the evidence from the ground finches on Santa Cruz Island that provides support for this statement:

   _____

   _____

   (b) The ground finches on Santa Cruz Island are one interbreeding population with a strongly bimodal distribution for the phenotypic character beak size. Suggest what conditions could lead to the two phenotypic extremes diverging further:

   _____

   (c) Predict the consequences of the end of the drought and an increased abundance of medium sized seeds as food:

   _____

5. Explain why the number of eggs in a bird's nest is most likely governed by stabilising selection:

   _____

   _____

   _____

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170 Directional Selection in Moths

Key Idea: Selection pressures on the peppered moth during the Industrial Revolution shifted the common phenotype from the grey form to the melanic (dark) form.

Genetically determined melanism is a common polymorphism in animals (meaning different forms exist in the population). In the peppered moth (*Biston betularia*), during the Industrial Revolution, selection favoured the proliferation of dark (melanic) forms over the pale (non-melanic) forms. Intensive coal burning during this time caused trees to become dark with soot, offering melanic forms greater camouflage against predatory birds. The shift in phenotype at this time is an example of **directional selection**.

The gene controlling colour in the peppered moth is located on a single locus. The allele for the melanic (dark) form (**M**) is dominant over the allele for the grey (light) form (**m**).

Melanic form
Genotype: MM or Mm

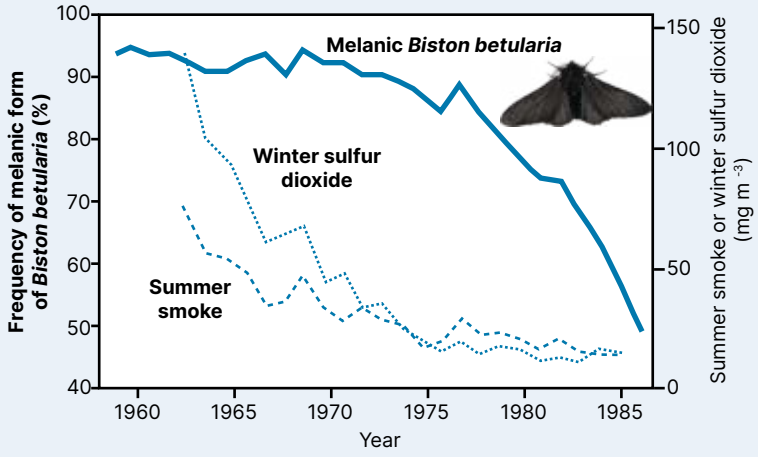
Grey form
Genotype: mm

The peppered moth, *Biston betularia*, has two forms: a grey mottled form, and a dark melanic form. During the Industrial Revolution, the relative abundance of the two forms changed to favour the dark form. The change was thought to be the result of selective predation by birds. It was proposed that the grey form was more visible to birds in industrial areas where the trees were dark. As a result, birds preyed upon them more often, resulting in higher numbers of the dark form surviving.

Museum collections of the peppered moth over the last 150 years show a marked change in the frequency of the melanic form (above right). Moths collected in 1850, prior to the major onset of the Industrial Revolution in England, were mostly the grey form (above left). Fifty years later the frequency of the darker melanic forms had increased.

In the 1940s and 1950s, coal burning was still at intense levels around the industrial centres of Manchester and Liverpool in the UK. During this time, the melanic form of the moth was still very dominant. In the rural areas further south and west of these industrial centres, the occurrence of the grey form increased dramatically. With the decline of coal burning factories and the introduction of the Clean Air Act in cities, air quality improved between 1960 and 1980. Sulfur dioxide and smoke levels dropped to a fraction of their previous levels. This coincided with a sharp fall in the relative numbers of melanic moths (right).

Frequency of melanic peppered moth related to reduced air pollution



1. The populations of peppered moth in England have undergone changes in the frequency of an obvious phenotypic character over the last 150 years. What is the phenotypic character?

2. Describe how the selection pressure on the grey form has changed with change in environment over the last 150 years:

3. Describe the relationship between allele frequency and phenotype frequency:

4. The level of pollution dropped around Manchester and Liverpool between 1960 and 1985. How did the frequency of the darker melanic form change during this period?

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171 Directional Selection in Darwin's Finches

Key Idea: The effect of directional selection on a population can be verified by making measurements of phenotypic traits.

Natural selection acts on the phenotypes of a population. Individuals with phenotypes that produce more offspring have higher fitness, increasing the proportion of the genes corresponding to that phenotype in the next generation. Many population studies have shown natural selection can cause phenotypic changes in a population relatively quickly.

The finches on the Galápagos Islands (Darwin's finches) are famous in that they are commonly used as examples of how evolution produces new species. In this activity you will analyse data from the measurement of beak depths of the medium ground finch (below) on the island of Daphne Major near the centre of the Galápagos Islands. The measurements were taken in 1976 before a major drought hit the island and in 1978 after the drought (survivors and survivors' offspring).

Beak depth (mm)	No. 1976 birds	No. 1978 survivors
7.30-7.79	1	0
7.80-8.29	12	1
8.30-8.79	30	3
8.80-9.29	47	3
9.30-9.79	45	6
9.80-10.29	40	9
10.30-10.79	25	10
10.80-11.29	3	1
11.30+	0	0

Beak depth of offspring (mm)	Number of birds
7.30-7.79	2
7.80-8.29	2
8.30-8.79	5
8.80-9.29	21
9.30-9.79	34
9.80-10.29	37
10.30-10.79	19
10.80-11.29	15
11.30+	2

1. Use the data above to draw two separate sets of histograms:

   (a) On the left hand grid draw side-by-side histograms for the number of 1976 birds per beak depth and the number of 1978 survivors per beak depth.

   (b) On the right hand grid draw a histogram of the beak depths of the offspring of the 1978 survivors.

2. (a) Mark the approximate mean beak depth on the graphs of the 1976 beak depths and the 1978 offspring.

   (b) How much has the average moved from 1976 to 1978? _____

   (c) Is beak depth heritable? What does this mean for the process of natural selection in the finches?

   _____

   _____

3. The 1976 drought resulted in plants dying back and not producing seed. Based on the graphs, what can you say about competition between the birds for the remaining seeds, i.e. in what order were the seeds probably used up?

   _____

   _____

   _____

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172 Disruptive Selection in Darwin's Finches

Key Idea: Disruptive selection in the finch *Geospiza fortis* produces a bimodal distribution for beak size.

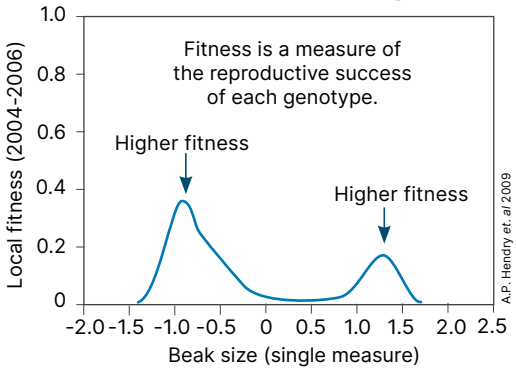
The Galápagos Islands, 970 km west of Ecuador, are home to the finch species *Geospiza fortis*. A study during a prolonged drought on Santa Cruz Island showed how **disruptive selection** can change the distribution of genotypes in a population. During the drought, large and small seeds were more abundant than the preferred intermediate seed size.

Beak sizes of *G. fortis* were measured over a three year period (2004-2006), at the start and end of each year. At the start of the year, individuals were captured, banded, and their beaks were measured.

The presence or absence of banded individuals was recorded at the end of the year when the birds were recaptured. Recaptured individuals had their beaks measured. The proportion of banded birds in the population at the end of the year gave a measure of fitness. Absent individuals were presumed dead (fitness = 0).

Fitness related to beak size showed a bimodal distribution (left) typical of disruptive selection.

Beak size vs fitness in *Geospiza fortis*

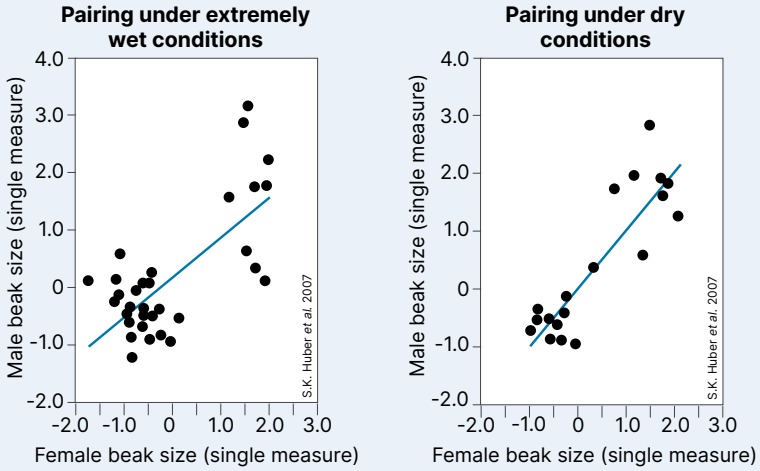


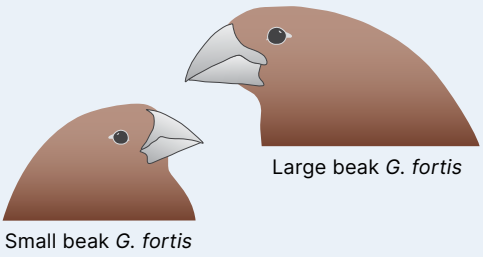
Fitness showed a bimodal distribution (arrowed) being highest for smaller and larger beak sizes.

Measurements of the beak length, width, and depth were combined into one single measure.

Jeff Podos

Beak size pairing in *Geospiza fortis*





A 2007 study found that breeding pairs of birds had similar beak sizes. Male and females with small beaks tended to breed together, and males and females with large beaks tended to breed together. Mate selection maintained the bimodal distribution in the population during extremely wet conditions. If beak size wasn't a factor in mate selection, the beak size would even out.

1. (a) How did the drought affect seed size on Santa Cruz Island? _____

_____

(b) How did the change in seed size during the drought create a selection pressure for changes in beak size?

_____

_____

_____

_____

2. How does beak size relate to fitness (differential reproductive success) in G. fortis? _____

_____

_____

_____

3. (a) Is mate selection in G. fortis random / non-random? _____

(b) Give reasons for your answer: _____

_____

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173 Selection for Human Birth Weight

Key Idea: Stabilising selection operates to keep human birth weight within relatively narrow constraints.

Selection pressures operate on populations in such a way as to reduce mortality. For humans, selection pressures act to constrain birth weight to within narrow limits. This is a good example of **stabilising selection**. It is possible to document this effect by plotting birth weights for a large sample of the population. Carry out the steps below.

Step 1: For this activity, you will need a sample of 100 birth weights. You can search birth records online or use the data provided in the appendix at the back of this book.

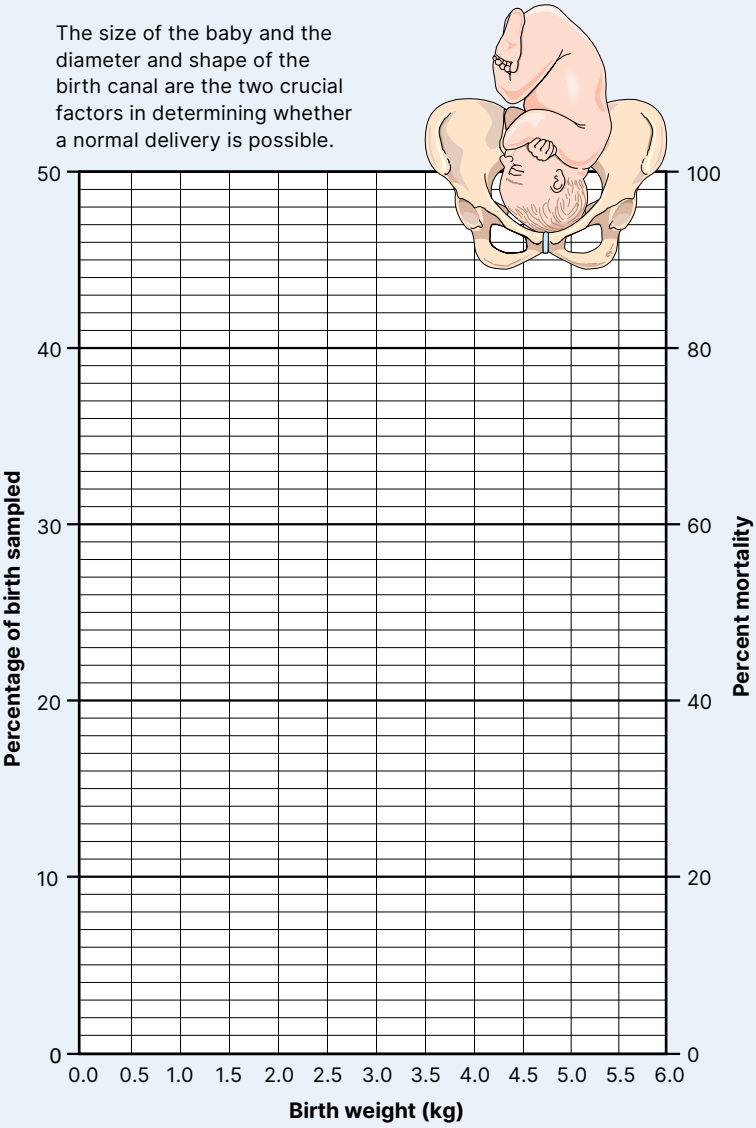
Step 2: Group the weights into each of the 12 weight classes indicated on the graph template provided. Calculate the percentage in each weight class.

Step 3: Graph these in the form of a histogram for the 12 weight classes (use the graphing grid provided right). Be sure to use the scale provided on the left vertical (y) axis.

Step 4: Create a plot of percentage mortality of newborns in relation to their birth weight. Use the scale on the right y axis and data provided (below). Draw a line of best fit through the points.

Weight (kg)	Mortality (%)
1.0	80
1.5	30
2.0	12
2.5	4
3.0	3
3.5	2
4.0	3
4.5	7
5.0	15

Evidence indicates that the phenotypic norm is shifting. Researchers estimate that cases where the baby cannot fit down the birth canal have increased from 30/1000 in the 1960s to 36/1000 births today, indicating that there is less selection against women with a narrow pelvis and babies with larger heads.



1. Describe the shape of the histogram for birth weights: _____
2. What is the optimum birth weight in terms of the lowest newborn mortality? _____
3. Describe the relationship between newborn mortality and birth weight: _____
4. Describe the selection pressures that are operating to control the range of birth weight: _____
5. How might modern medical intervention during pregnancy and childbirth have altered these selection pressures?

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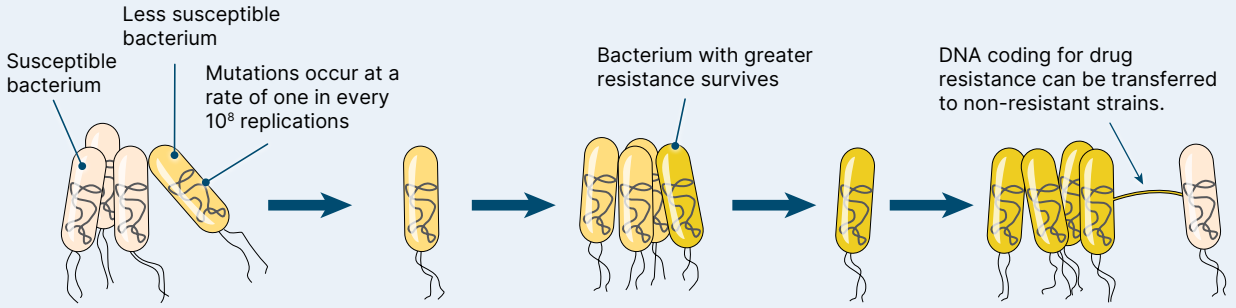
174 Modern Drivers in Evolution

Key Idea: Widespread use of antibiotics and pesticides has created a selective environment for the proliferation of chemical resistance in populations of bacteria and insects.

Resistance to antibiotics and pesticides is becoming a more common occurrence in the modern world. It can occur when chemical control agents do not remove all the targeted organisms. Those that survive due to their suite of specific inherited characteristics are able to pass on these genes and so resistance becomes more common in subsequent generations (i.e. **natural selection**). Resistance to antibiotics in bacteria and to pesticides in insects poses serious threats to human health and food supplies.

The evolution of antibiotic resistance in bacteria

Antibiotic resistance arises when genetic changes allow bacteria to tolerate levels of antibiotic that would normally inhibit growth. Resistance may arise spontaneously through **mutation** or by transfer of DNA between microbes (horizontal gene transfer). Genomic analyses from 30,000 year old permafrost sediments show that the genes for antibiotic resistance predate modern antibiotic use. In the current selective environment of widespread antibiotic use, these genes have proliferated and antibiotic resistance has spread. For example, methicillin resistant strains of *Staphylococcus aureus* (MRSA) have acquired genes for resistance to all penicillins. Such strains are called superbugs.

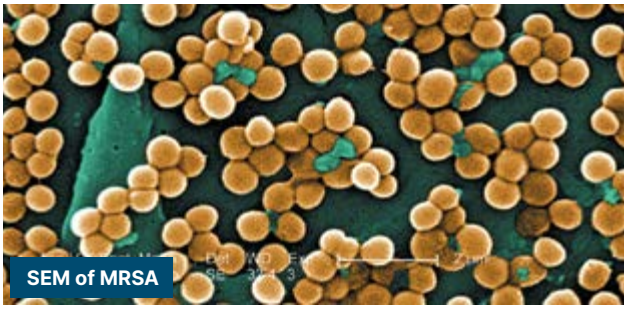


Any population, including bacterial populations, includes variants with unusual traits, in this case reduced sensitivity to an antibiotic. These variants arise as a result of mutations in the bacterial chromosome.

When a person takes an antibiotic, only the most susceptible bacteria will die. The more resistant cells remain alive and continue dividing. Note that the antibiotic does not create the resistance; it provides the environment in which selection for resistance can take place.

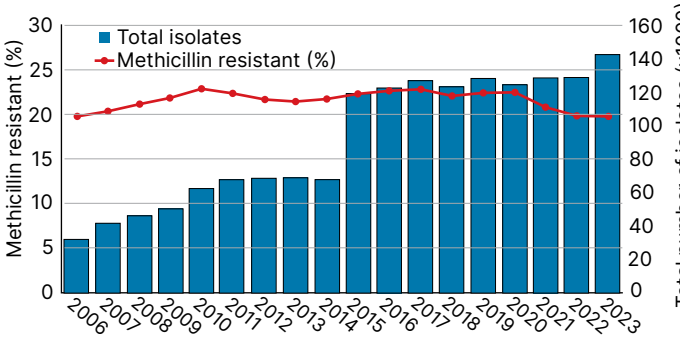
If the amount of antibiotic delivered is too low, or the course of antibiotics is not completed, a population of resistant bacteria develops. Within this population too, there will be variation in susceptibility. Some will survive higher antibiotic levels than others.

A highly resistant population has evolved. The resistant cells can exchange genetic material with other bacteria (via horizontal gene transmission), passing on the genes for resistance. The antibiotic initially used against this bacterial strain will now be ineffective.



Staphylococcus aureus is a common bacterium responsible for several minor skin infections in humans. MRSA is a strain that has evolved resistance to penicillin and related antibiotics. MRSA is troublesome in hospital-associated infections because patients with open wounds, invasive devices (e.g. catheters), or poor immunity are at greater risk for infection than the general public.

Percentage of *Staphylococcus aureus* methicillin resistance



In Australia, MRSA has remained steady at around 20% of all isolates due to greater reporting measures and cleaning standards since the early 2000s.

Australian Passive AMR Surveillance An update of resistance trends in multidrug-resistant organisms – 2006 to 2023

1. Describe how resistance develops in a population: _____

2. How can antibiotic resistance be transferred between strains of bacteria? _____

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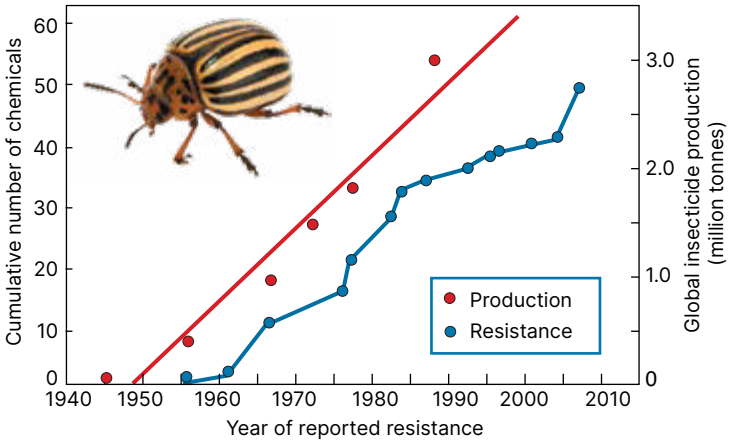
Insecticide resistance

- Insecticides are pesticides used to control pest insects. They have been used for hundreds of years but their use has increased since synthetic insecticides were first developed in the 1940s.
- Insecticide resistance can arise through behavioural, anatomical, biochemical, and physiological mechanisms but, like antibiotic resistance, the underlying process is a form of natural selection in which the most resistant organisms survive to pass on their genes to their offspring.
- To combat increasing resistance, higher doses of more potent pesticides are sometimes used. This drives the selection process so that increasingly higher dose rates are required to combat rising resistance. This phenomenon is made worse by the development of multiple resistance in some pest species.
- Insecticides are widely used so the development of resistance has serious environmental and economic consequences.

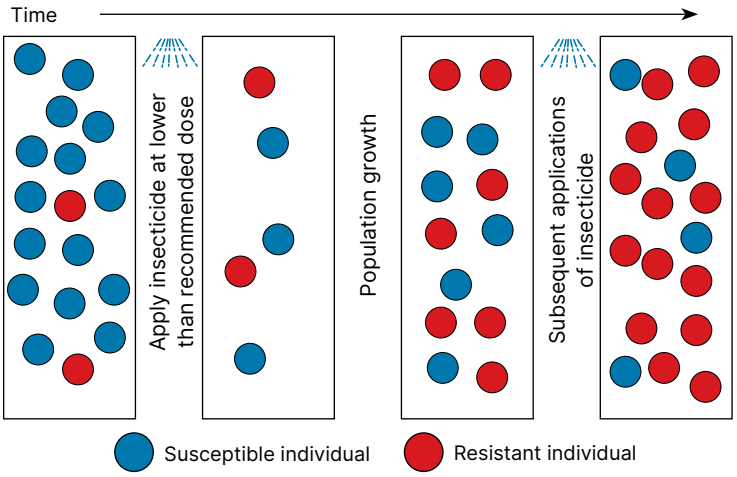


The Colorado potato beetle is a major potato pest that was originally found living on buffalo-bur (*Solanum rostratum*) in the Rocky mountains. Since synthetic insecticides began to be produced, it has become resistant to more than 50 different types.

How does resistance spread?

The application of an insecticide can act as a selective agent for chemical resistance in pest insects. Insects with a low natural resistance die from an insecticide application, but a few (those with a naturally higher resistance) will survive, particularly if the insecticide is not applied properly. These individuals will reproduce, giving rise to a new generation which will, on average, have a higher resistance to the insecticide.

As the diagram, right, demonstrates, a small proportion of the population will have the genetic makeup to survive the first application of a pesticide. The genes for pesticide resistance are passed to the next generation. The proportion of resistant individuals increases following subsequent applications of insecticide. Eventually, almost all of the population is resistant.



3. With reference to MRSA, describe the implications to humans of widespread antibiotic resistance:

4. Explain how repeated insecticide applications act as a selective agent for evolutionary change in insect populations:

5. With reference to synthetic insecticides, discuss the implications of insecticide resistance to human populations:

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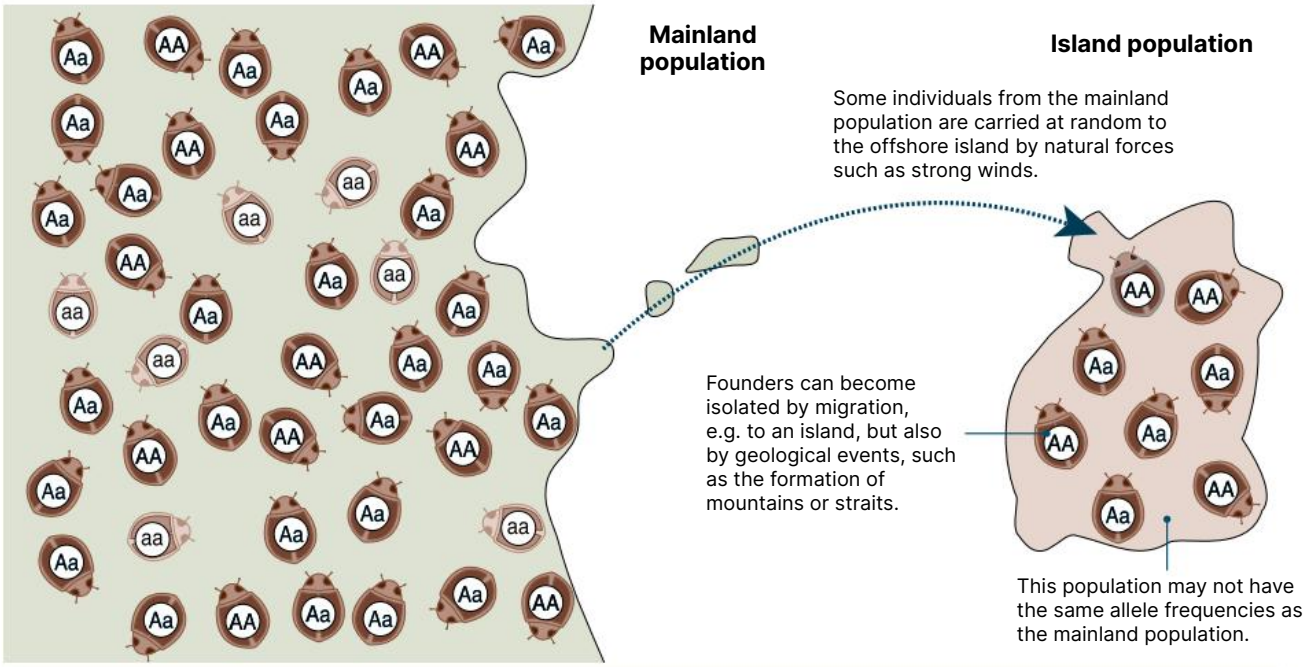
175 The Founder Effect

Key Idea: The founder effect can result in differences in allele frequencies between a parent and founder populations.

If a small number of individuals from a large population becomes isolated from their original parent population, their sample of alleles is unlikely to represent the allele proportions of the parent population. This phenomenon is called the **founder effect** and it can result in the colonising (founder) population evolving in a different direction to the parent population. This is particularly the case if the founder population is subjected to different selection pressures in a new environment and if the population is missing alleles that are present in the parent population.



Mainland population

	Allele frequencies		Phenotype frequencies	
	Actual numbers	Calculate %	Dark	Pale
Allele A				
Allele a				
Total				

Colonising island population

	Allele frequencies		Phenotype frequencies	
	Actual numbers	Calculate %	Dark	Pale
Allele A				
Allele a				
Total				

1. Compare the mainland population to the population which ended up on the island (use the spaces in the tables above):
   (a) Count the phenotype numbers for the two populations (i.e. the number of black and pale beetles).

   (b) Count the allele numbers for the two populations: the number of dominant alleles (A) and recessive alleles (a). Calculate these as a percentage of the total number of alleles for each population.

2. How are the allele frequencies of the two populations different? _____

   _____

3. (a) What changes are likely when a founder population is isolated in a new environment? _____

   _____

   _____

   (b) What factors might influence the end result or the speed of the changes? _____

   _____

   _____

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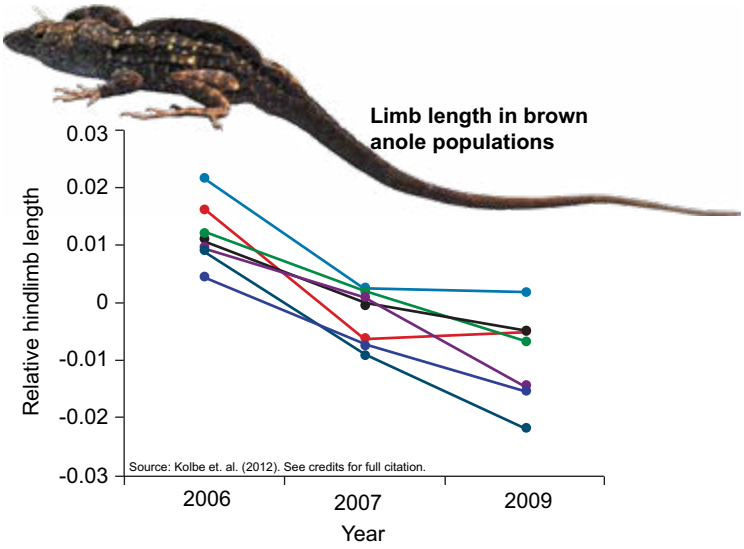
Founder effect in brown anole lizards

- In 2004 Hurricane Francis wiped out the brown anole lizard (*Anolis sagrei*) populations on several cays (small sandy islands) around the Bahamas. Scientists used this as a chance to study the founder effect. They took pairs of lizards from the mainland and placed them on different cays.
- The vegetation on the cays is much smaller and scrub-like with thin branches or twigs compared to the much larger trees of the mainland. On the mainland, scientists noted that the lizards use their long limbs to climb around the trees. They hypothesised that the populations isolated on the cays would eventually evolve shorter limbs to adapt to the scrub-like, less supportive vegetation. They measured the limb length over several years.
- It was found that limb length indeed became shorter over successive generations in all the populations. Importantly, populations founded by lizards with the longest legs still had the longest legs and populations founded by lizards with the shortest legs still had the shortest legs. The characteristics of the founder populations influenced the descendant populations.



Founder effect in human populations

thinboyfatter CC 2.0

Due to the many episodes of human migration around the world there are many instances of the founder effect in human populations. In 1790, nine mutineers from the ship HMS Bounty along with six Tahitian men, eleven Tahitian women, and a baby girl settled on Pitcairn island. The population eventually grew to 193 by 1856.

In 1856 the entire population of Pitcairn Island resettled on Norfolk Island after it was decided Pitcairn was over populated. The effect of this can still be seen in genetic studies of the Norfolk Island population. In 1859, 16 people returned to Pitcairn Island and founded a new population, that eventually reached 250 people by 1936. The population is now around 56.

Brian Gratwicke CC 2.0

Tristan da Cunha sits 2,400 km from Africa and more than 3,500 km from South America. The current settlement of Tristan da Cunha was founded by the English in 1817. In 1961, a genetic study traced 14% of all genes in the population of 300 to one founding couple. Around 47% of the population are affected by asthma. Of the 15 original settlers, at least three had asthma.

4. (a) Why were conditions good for setting up an experiment on the founder effect on the cays around the Bahamas?

(b) Describe how the founder effect was demonstrated in the brown anole lizards:

5. (a) The rate of asthma in the UK is about 8%. Calculate the rate of asthma in the original Tristan da Cunha settlers:

(b) How has this affected the current population of Tristan da Cuhna?

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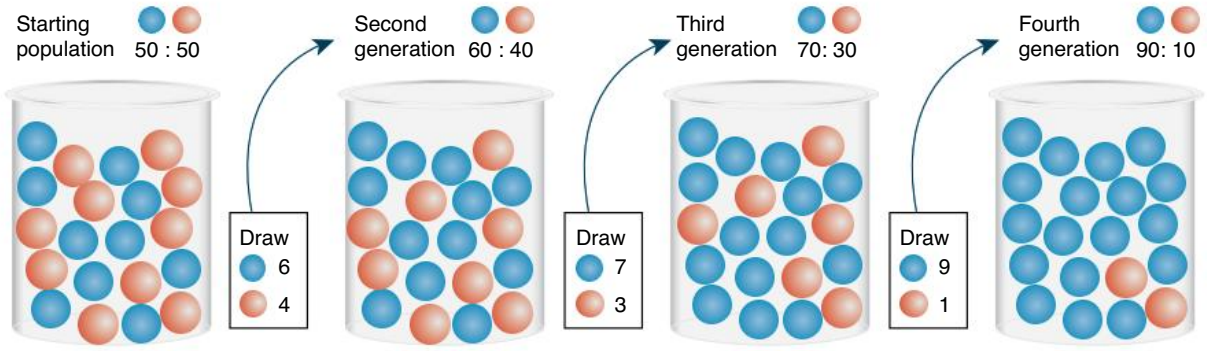
176 Genetic Drift

Key Idea: Genetic drift describes the random changes in allele frequency that occur in all populations. It has a more pronounced effect in small populations.

Not all individuals, for various reasons, will be able to contribute their genes to the next generation. This random change in allele frequencies is called **genetic drift**. It is the result of 'sampling error' in the selection of alleles from the current **gene pool** for the next generation (not an error of how we might observe or record breeding events). The effect of genetic drift on a gene pool is more pronounced in small populations. Alleles may become lost from the gene pool (frequency = 0%) or fixed as the only allele present for the gene (frequency = 100%). Recall that in your **natural selection** spreadsheet, even starting with 0.5 *A* and 0.5 *a* the next generation of alleles were not 0.5 *A* and 0.5 *a* (even before selection had occurred). Due to the random mating set in the simulation, sometimes more or less than 0.5 *A* alleles were passed on. This directly affects the frequencies in the next generations's gene pool. Even without any selection, random changes in the gene pool can have important effects.

How does genetic drift reduce variation in populations?

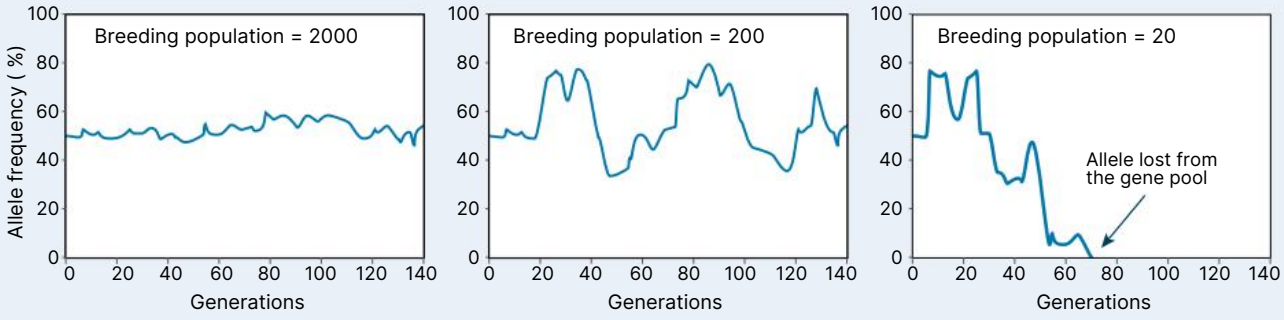
The change in allele frequencies within a population through genetic drift can be illustrated using the random sampling of marbles from a jar. The diagram below represents a population of 20 individuals. The different alleles are represented by blue and orange marbles. The starting population contains an equal number of blue and orange marbles. Random mating is represented by selecting 10 marbles at random. Twenty marbles representing the new allele proportions are placed into a new jar to represent the second generation, and the process is repeated for subsequent generations.



Computer simulations of genetic drift

- Computer simulations are used to carry out population experiments which are impractical to fully observe in wild populations. For example, the generation times may be too long or obtaining genetic samples impossible, or the population size can be changed, to observe the effect.
- In the example above, the orange marbles are becoming less frequent within the population and the amount of genetic variation within the population is reducing. Unless the proportion of orange marbles increases, it will eventually be lost from the population altogether and the allele for the blue marble becomes fixed (the only variant). How might the effect of genetic drift change larger populations of marble?

Below are displayed the change in allele frequencies in a computer simulation showing random genetic drift. The breeding population progressively gets smaller from left to right. Each simulation was run for 140 generations.



Large breeding population
Fluctuations are minimal because large numbers buffer the population against random loss of alleles. On average, losses for each allele type will be similar in frequency and little change occurs.

Small breeding population
Fluctuations are more severe in smaller breeding populations because random changes in a few alleles cause a greater percentage change in allele frequencies.

Very small breeding population
Fluctuations in very small breeding populations are so extreme that the allele can become fixed (frequency of 100%) or lost from the gene pool altogether (frequency of 0%).

- You can use the spreadsheet you made in Activity 167 to investigate the effect of population size on **allele frequency** changes due to genetic drift (see next page). You will need to modify the spreadsheet to make random changes to the frequency with which alleles are passed on to the next generation. This simulates random events, removing alleles from the gene pool (as above).

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Investigation 14.2 Modelling genetic drift

Part 1

1. Modify the spreadsheet you made for Activity 167 to complete this simulation. Save the spreadsheet under a new name.
2. Open the spreadsheet. In cell **F13** (under the heading A passed on) change the formula to **=(F2*2*RAND())+(G2*RAND())**. This randomly selects a number of A alleles from the total available to pass to the next generation.
3. In cell **G13**, change the formula to **=(H2*2*RAND())+(G2*RAND()).** This randomly selects B alleles.

F	G
AA	AB
=COUNTIF($D$7:$D$56,"AA")	=COUNTIF($D$7:$D$56,"AB")+COUNTIF($D$7:$D$56,"BA")
A	B
=(F2*2)+G2	=(H2*2)+G2
Frequency A	Frequency B
=F5/(F5+G5)	=G5/(F5+G5)
A passed on	B passed on
=(F2*2*RAND())+(G2*RAND())	=(H2*2*RAND())+(G2*RAND())
Freq A passed on	Freq A passed on
=F13/(F13+G13)	=G13/(F13+G13)

4. Set cell **A3** to **0.5** and click **Calculate Now**. Record the A and a frequency for each generation, the numbers of AA, Aa, and aa individuals and produce graphs for twenty generations (stop if an allele becomes fixed) as in part 2 of Activity 102. Note Gen 0 AA = 13, Aa = 26 and aa = 13.

Part 2

1. You can now change the population number and see how genetic drift affects allele frequencies. In cell **F2**, change the COUNTIF formula to **=COUNTIF($D$7:$D$26,"AA")** to count only the first 20 individuals.
2. In cell **G2**, change the formula to **=COUNTIF($D$7:$D$26,"AB")+COUNTIF($D$7:$D$26,"BA")** and in cell **H2** change the formula to **=COUNTIF($D$7:$D$26,"BB")**. Click **Calculate Now** and cell **J2** should show **20**.
3. Set cell **A3** to **0.5** and click **Calculate Now**. Record the 'A' and 'a' frequency for each generation, the numbers of AA, Aa, and aa individuals and produce graphs for twenty generations (stop if an allele becomes fixed). Note Gen 0 AA = 5, Aa = 10 and aa = 5.
4. Now repeat the above but set the COUNTIF formulae to count to row **106**. Highlight cells **A56** to **D56** and copy them down to row **106**. Click **Calculate Now** and cell J2 should show 100.
5. Set cell **A3** to **0.5** and click **Calculate Now**. Record the A and a frequency for each generation, the numbers of AA, Aa, and aa individuals and produce graphs for twenty generations (stop if an allele becomes fixed) Note Gen 0 AA = 25, Aa = 50 and aa = 25.

1. What is genetic drift, and why are its effects more pronounced in smaller populations?_____

2. Which of the simulations you did above appears to have the most fluctuations in the A and a alleles? Explain why:

3. Suggest why genetic drift is regarded as an important process in the evolution of small populations. You can use your simulation as evidence if you wish:

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Island platypus and the perils of genetic drift

- A 2012 study of genetic diversity in platypus populations on mainland Australia, Tasmania, King Island, and Kangaroo Island has revealed very low immunological diversity in the island populations. The study (Lillie *et al.*) looked at the diversity of the MHC DZB gene and three MHC associated markers, all of which are involved in immune function. High allelic diversity in immune genes is important because it provides the variation necessary to resist different kinds of diseases. Without genetic variation, the population is likely to have low resistance to new diseases and environmental change.
- The study found that populations on the Australian mainland and in Tasmania have high levels of genetic diversity within their populations, with 57 DZB alleles identified in 70 individuals. However platypuses on King Island and Kangaroo Island (see maps), had very low levels of genetic diversity. For the King Island populations, there was no variation at all (only one allele at the DZB locus).
- Why is the genetic diversity of these island populations so low compared to the mainland populations? The Kangaroo Island population was founded from an introduction of around 20 animals in the 1930s and 1940s (founder population). The population on King Island is endemic, separated for some 14,000 years since the last ice age.
- Inbreeding in a small population and genetic drift have resulted in the loss of alleles and a dangerously low diversity in immune genes. These island populations will now need careful management to protect them from disease risk.

Klaus cc 2.0

Tentotwo cc 3.0 Nzeemin cc 3.0

Source: Diversity at the Major Histocompatibility Complex Class II in the Platypus, *Ornithorhynchus anatinus* Mette Lillie *et. al.* Journal of Heredity 2012:103(4):467–478

4. What factors have contributed to the low genetic diversity of the platypus populations on King Island and Kangaroo Island? Explain their effect(s):

5. Why would genetic drift have more impact on the genetic diversity of these populations than those on the mainland?

6. (a) Describe why a population with low MHC diversity is more likely to be affected by a new disease than a population with high MHC diversity:

   (b) Why is it important to try to keep small, isolated populations free of new diseases? _____

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177 Did You Get it?

1. Test your vocabulary by matching each term to its definition, as identified by its preceding letter code.

(i) founder effect ☐

(ii) gene pool ☐

(iii) genetic drift ☐

(iv) natural selection ☐

A The process by which heritable traits become more or less common in a population through differential survival and reproduction.

B The sum total of all alleles of all breeding individuals in a population at any one time.

C The loss of genetic variation when a new colony is formed by a very small number of individuals from a larger population.

D The change in allele frequency in a population as a result of chance events. The effect is proportionally larger in small populations.

2. Outline the effect of each of the following microevolutionary processes on the gene pool of a population:

(a) Mutation: _____

_____

(b) Gene flow: _____

_____

(c) Natural selection: _____

_____

(d) Genetic drift: _____

_____

3. Study the graphs below right.

(a) What kind of selection is occurring? _____

(b) Describe an example of this type of selection:

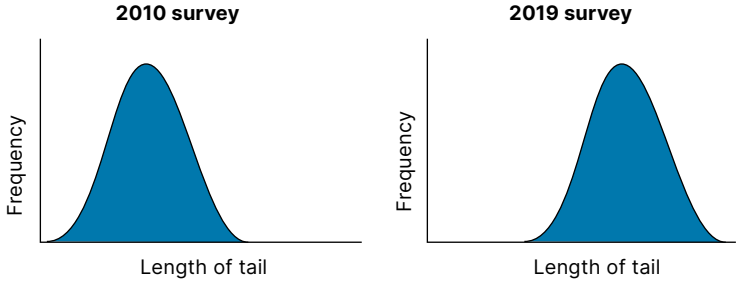
_____

_____

_____

_____

_____



4. The graph on the right shows the effect of genetic drift on the frequency of an allele (A) in populations of three different sizes.

(a) Describe how the impact of genetic drift varies depending on population size:

_____

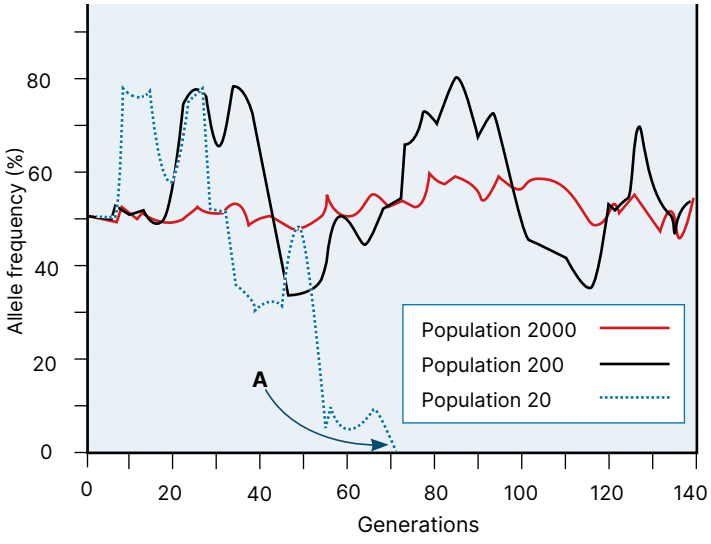
_____

_____

_____

_____

_____



(b) What has happened at point A on the diagram?

_____

_____

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Chapter 15 Unit 4 Topic 2

Speciation and Macroevolution

Resource Hub
bit.ly/4jKPQA3

Key Terms

- adaptive radiation
- allopatric speciation
- analogous structure
- coevolution
- convergent evolution
- divergent evolution
- macroevolution
- parallel evolution
- parapatric speciation
- phyletic gradualism
- population (=genetic) bottleneck
- punctuated equilibrium
- reproductive isolation
- speciation
- sympatric speciation

Key Concepts

- The mechanisms and models of evolution include divergent, convergent, parallel, and coevolution.
- Processes of speciation include allopatric, sympatric, and parapatric speciation.
- Factors including habitat fragmentation, population bottlenecks, and climate change drive genetic diversity, adaptation, and speciation, while also posing risks of extinction.

Macroevolutionary patterns		Activity Number
☐ 1	Recall that speciation and macroevolution result from the accumulation of microevolutionary changes over time. Distinguish between the four main patterns of evolution and describe the features of each: • divergent evolution (including radiations) • convergent evolution (including analogous structures) • parallel evolution (including the significance of degree of relatedness) • coevolution	178, 179, 182-184
☐ 2	Explain how the pace of macroevolutionary change can vary, as described by the punctuated equilibrium and the phyletic gradualism models.	178, 187
☐ 3	Recognise and describe examples of divergent evolution, including evolutionary radiations such as the adaptive radiation of the mammals. Explain what distinguishes adaptive radiation from other types of evolutionary divergence.	178-181
☐ 4	Recognise and describe examples of convergent evolution. Explain how analogous structures arise as a result of similar selection pressures in similar environments (similar evolutionary solutions to similar environmental challenges).	182
☐ 5	Recognise and describe examples of parallel evolution. Explain why parallelism and convergence can be difficult to distinguish and understand that the labels are somewhat arbitrary.	183
☐ 6	Recognise and describe examples of coevolution, including between competitors, plants and their pollinators, predators and prey, and hosts and parasites.	184

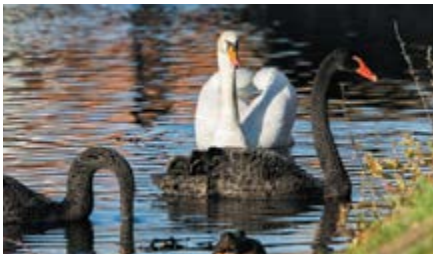
Patterns of speciation		
☐ 7	Identify the different mechanisms of isolation that operate to restrict or stop gene flow between populations prior to and after speciation events, including geographic isolation (including habitat fragmentation) and reproductive isolation.	185-188
☐ 8	Describe pre-zygotic isolating mechanisms, recognising the different levels at which they might operate during divergence of a species. Recognise geographic isolation as an important mechanism prior to reproductive isolation (which is part of the species biology).	185, 188
☐ 9	Identify and describe post-zygotic isolating mechanisms, explaining how they reinforce pre-zygotic isolation and preserve the integrity of the gene pools of closely related species.	186
☐ 10	Identify and describe different modes of speciation: allopatric, sympatric, and parapatric. Interpret data from different populations as evidence for speciation.	187, 189-191
☐ 11	Explain what is meant by a population bottleneck and explain its role in the allelic diversity and evolution of affected populations. Explain why populations with reduced genetic diversity (e.g. after a bottleneck event) are at greater risk of extinction and give some examples.	192
☐ 12	SI: Explain the importance of green corridors in connecting fragmented habitats and maintaining gene flow between populations.	193-194

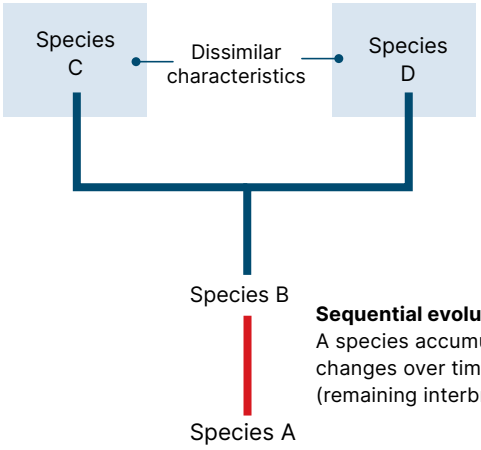
178 Patterns of Evolution

Key Idea: Populations moving into a new environment may follow particular patterns of evolution.

The diversification of one species into one or more separate species can follow one of four main patterns. **Divergent evolution** occurs when two species diverge from a common ancestor. Divergence is common in evolution and responsible for evolutionary radiations. When unrelated species evolve similar forms as a result of similar selection pressures, it is called **convergent evolution** (convergence). A similar phenomenon in related lineages is called **parallel evolution** (parallelism). The fourth pattern, **coevolution**, involves reciprocal evolution in unrelated lineages.

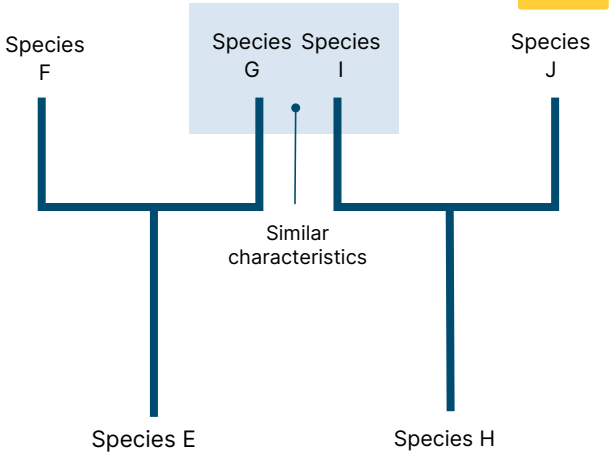
Divergent evolution (cladogenesis). A lineage splits and evolves independently due to different selection pressures in different environments. Species may later occupy the same environment, e.g. black swan (*Cygnus atratus*) and mute swan (*Cygnus olor*).



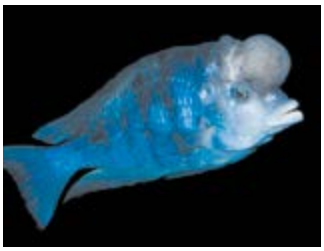


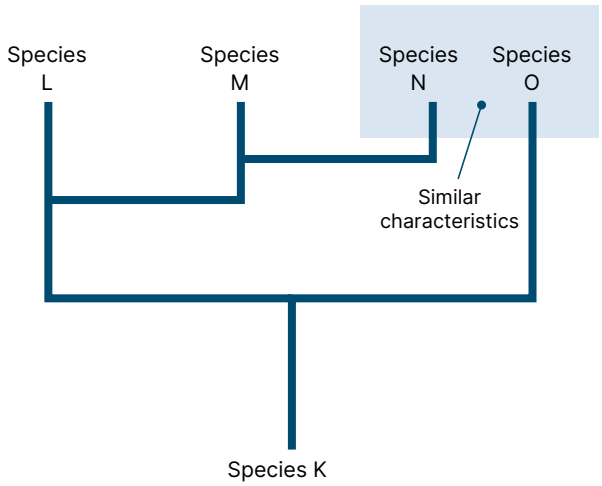
Sequential evolution (anagenesis)
A species accumulates enough genetic changes over time to form new species (remaining interbreeding).

Convergent evolution. Unrelated or distantly related species in similar environments and under similar selection pressures evolve similar features, e.g. streamlined swimming form in aquatic birds and mammals.

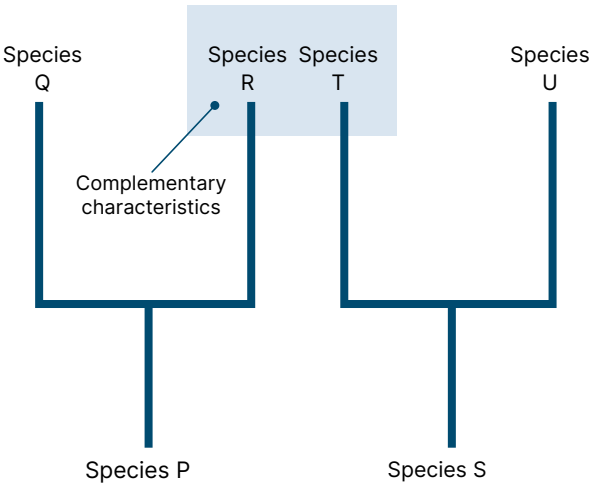


Parallel evolution. Closely related species living in separate but similar environments independently evolve similar features, e.g. the cichlid fishes of the East African Rift Valley lakes. Left: the frontosa (L. Tanganyika). Right: the Malawi blue dolphin (L. Malawi).





Coevolution. Reciprocal evolution in unrelated species as a result of selection pressures each imposes on the other. It results in complementary characteristics, e.g. flowering plants and their bird and insect pollinators.



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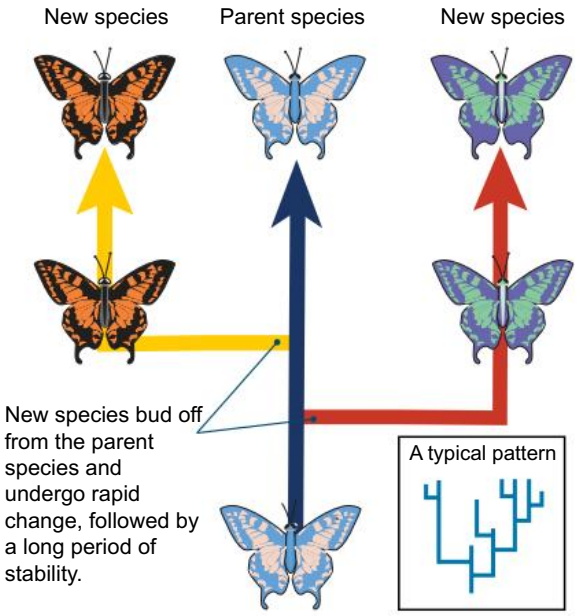
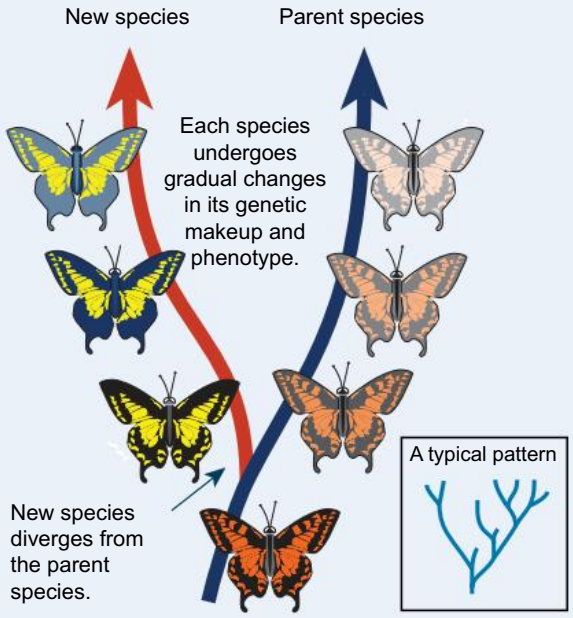
There are two basic models for the pace of evolutionary change: **phyletic gradualism** and **punctuated equilibrium**. It is likely that both mechanisms operate at different times and in different situations. Interpretations of the fossil record vary depending on the time scales involved. During its formative millennia, a species may have accumulated changes gradually (e.g. over 50,000 years). If that species survives for 5 million years, the evolution of its characteristics would have been compressed into just 1% of its evolutionary history. In the fossil record, the species would appear quite suddenly.



Punctuated equilibrium

According to the punctuated equilibrium theory, there is very little change for most of a species' existence and little time is spent in active evolutionary change. The stimulus for evolution occurs when some crucial aspect of the environment changes.



Phyletic gradualism

In a phyletic gradualism model, **speciation** is a uniform process and species diverge by slowly accumulating adaptations in response to new selection pressures. There is no clear line between an ancestral species and its descendant species.

1. What might cause divergent evolution in a species? _____

2. What is the difference between divergence and sequential evolution? _____

3. Penguins and dolphins have converged on a streamlined body form for moving through the water. What other groups of animals have also converged on this body shape?

4. How might co-evolution occur? _____

5. What rate of environmental change would support the following paces of evolution?

   (a) Punctuated equilibrium: _____

   (b) Phyletic gradualism: _____

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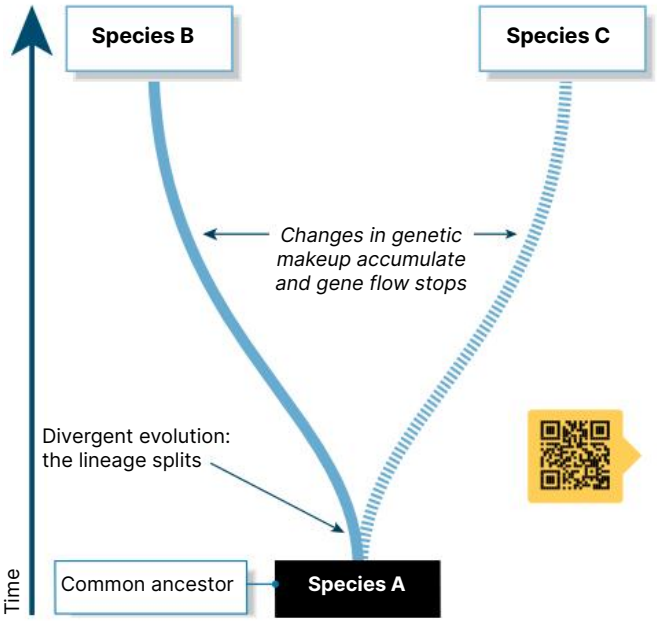
179 Divergence is an Evolutionary Pattern

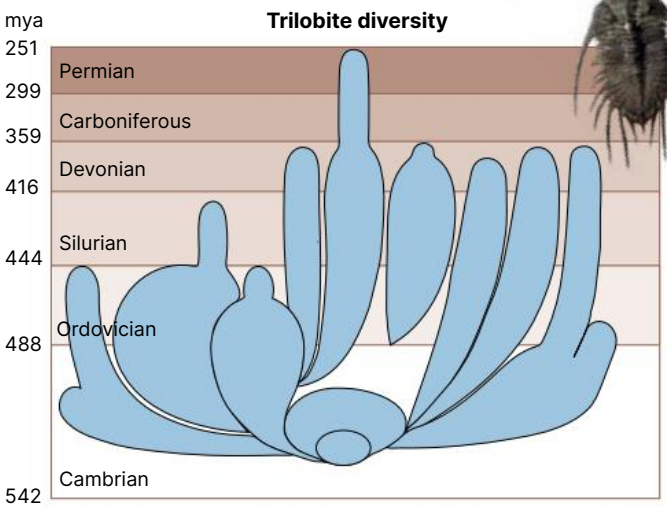
Key Idea: Divergent evolution describes the accumulation of differences between initially more similar lineages so that new species arise from a common ancestor.

Divergent evolution describes the divergence of two or more species from a common ancestor. It arises through the accumulation of genetic differences in diverging lines, usually following isolation, so that gene flow between them stops and new species arise. Divergence is a common evolutionary pattern. When it involves the diversification of a lineage into many different niches, it is called **adaptive radiation**.

An overview of divergent evolution



Divergent evolution of trilobite orders



Trilobites are extinct marine arthropods. They were one of the earliest arthropod groups and were highly successful, diverging many times during their history to exploit a wide range of niches. They appeared in the fossil record near the beginning of the Cambrian and disappeared in the Permian mass extinction. Each blue shape represents an order. Its width indicates its diversity.


Dwergenpaartje CC 3.0

Paradoxides, late Cambrian


DanielCD CC 3.0

Dalmanites, Silurian


Ghedoghedo CC 3.0

Cheirurus, Ordivician


Daderot

Walliserops, middle Devonian

Because trilobites had a hard exoskeleton, they fossilised well and have left an extensive fossil record. These fossils show that trilobites rapidly diversified early in their evolution. As many as 50,000 species of trilobite may have existed.

1. (a) Define divergent evolution: _____

_____

_____

(b) Explain the distinction between divergence and adaptive radiation: _____

_____

_____

2. (a) How would you describe the evolution of the trilobites? _____

_____

_____

(b) When was the trilobite group most diverse? _____

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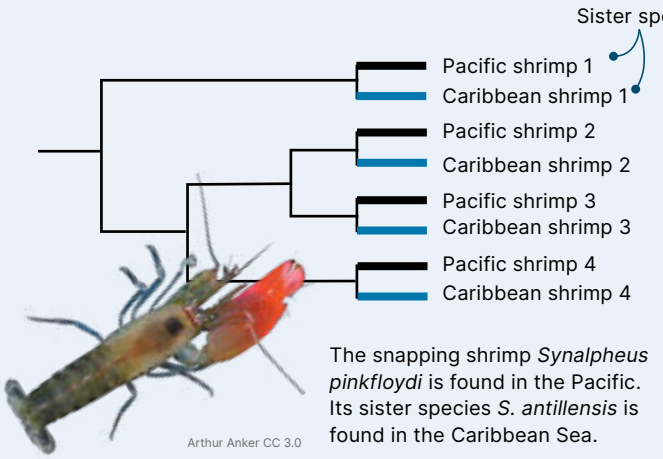
Divergent evolution: snapping shrimp

- The Isthmus of Panama separates the Pacific Ocean and Caribbean Sea in the region of Central America. The isthmus closed about 3 million years ago.
- On either side of the isthmus are numerous species of snapping shrimp. Every species on the Pacific side has a sister species on the Caribbean side.
- Genetic studies suggest that before the appearance of the isthmus there were already numerous species of snapping shrimps. After the isthmus formed, each species diverged, creating two new species, one on either side of the isthmus.



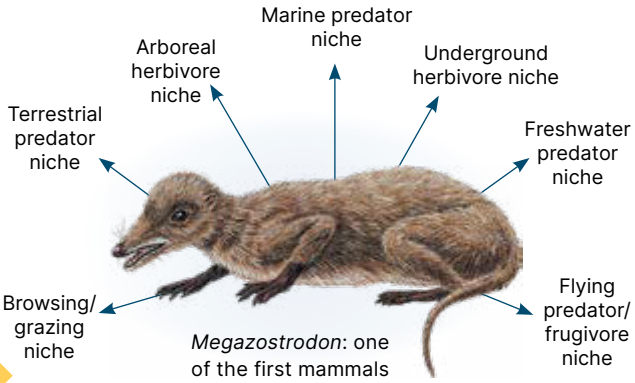
The snapping shrimp *Synalpheus pinkfloydi* is found in the Pacific. Its sister species *S. antillensis* is found in the Caribbean Sea.

Adaptive radiation

Adaptive radiation is a type of divergent evolution in which a single lineage diversifies rapidly to produce a large number of species occupying different niches. The example below right describes the radiation of the mammals, which took place after the extinction of the dinosaurs made new niches available. Note that the evolution of species may not necessarily involve branching.

The earliest true mammals evolved about 195 million years ago, long before they underwent their major adaptive radiation some 65-50 million years ago. These ancestors to the modern forms were very small (12 cm) and typically shrew-like. Many were nocturnal and fed on insects and other invertebrates. Megazostrodon is a typical example. This animal is known from fossil remains in South Africa and first appeared in the Early Jurassic period (about 195 million years ago).

It was climatic change as well as the extinction of the dinosaurs (and their related forms) that suddenly left many niches vacant for exploitation by such adaptable 'generalists'. All modern mammal orders developed very quickly and early.



3. (a) Suggest why the trilobites diversified so quickly:

(b) Considering the trilobites existed from 521 million years ago to 252 million years ago, approximately what percentage of their time in existence was spent in the evolution of new trilobite orders:

4. What evidence is there that the closing of the Isthmus of Panama was a factor in the divergence of snapping shrimps?

5. What factors were important in the adaptive radiation of the early mammals?

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180 Divergent Evolution in Ratites

Key Idea: The ratites are a group of birds descended from a single common ancestor. They lost the power of flight very early on in their evolution.

Ratites are flightless birds that possess two features that distinguish them from other birds: a flat breastbone (instead of the more usual keeled shape) and a primitive palate (roof to the mouth). Fossil evidence indicates that the ancestors of ratites were flying birds living about 80 million years ago. These ancestors also had a primitive palate but they possessed a keeled breastbone. Flightlessness in itself is not unique to ratites; there are other birds that have lost the power of flight, particularly on remote, predator-free islands. All ratites have powerful legs and many, such as the emu, can run very quickly.

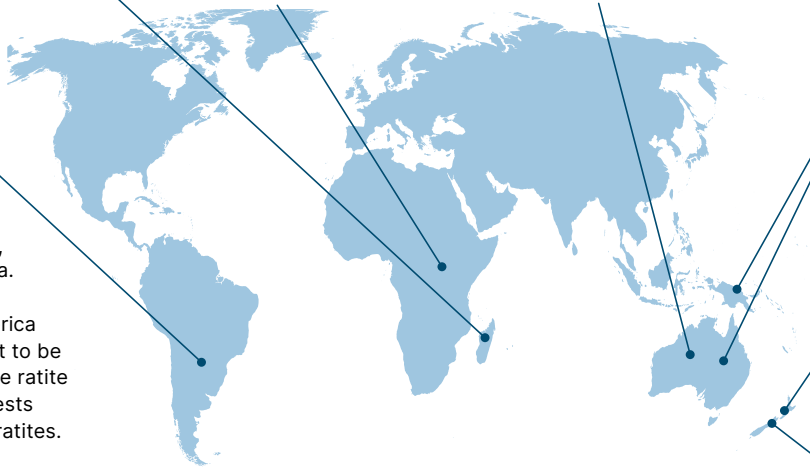
Elephant bird
Two species, extinct, Madagascar

Ostrich
Struthio camelus, Africa

Emu
Dromaius novaehollandiae, Australia.

Cassowary
Three species, Australia & New Guinea.

Rhea
Two species, South America.



Kiwi
Five species, New Zealand.

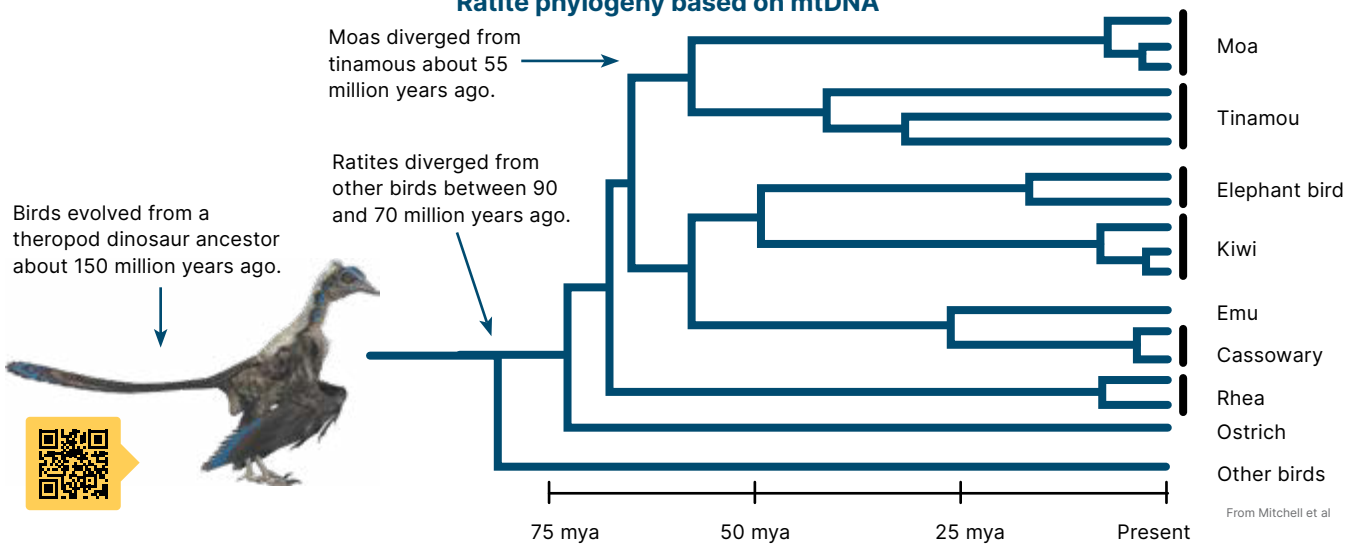
Moa
Eleven species (Lambert *et al*. 2004*), all extinct, New Zealand.

*Tinamous from South America were, until recently, thought to be related to but not part of the ratite group. New evidence suggests they should be included in ratites.

It had long been thought that the geographical distribution of modern day and extinct ratite species could be explained by continental drift. The "rafting hypothesis" suggests that the ancestral ratite population existed when the southern continents of South America, Africa, and Australia (and their major offshore islands) were joined as a single land mass called Gondwana. As the continents moved apart as a result of plate tectonics, the early ratite populations were carried with them.

Mitochondrial DNA (mtDNA) evidence now suggests kiwis are most related to the extinct elephant bird from Madagascar and slightly less closely related to emus in Australia. However, the ancestor to the kiwi arrived in New Zealand long after New Zealand separated from the rest of Gondwana. Ancestral kiwi must therefore have flown there. Moas are now thought to be closely related to tinamous (South America), which can fly. Ostriches were thought to be closely related to elephant birds but mtDNA now suggests they diverged from the other ratites early. The conclusions from these new findings suggest that the ratites evolved from flighted birds that flew between continents and independently evolved flightlessness at least six times.

Ratite phylogeny based on mtDNA



From Mitchell et al

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1. (a) Describe three physical features distinguishing all ratites (excluding tinamous) from most other birds:

   (b) Why should tinamous be included in ratites?

2. Describe two anatomical changes, common to all ratites (excluding tinamous), which have evolved as a result of flightlessness. For each, describe the selection pressures for the anatomical change:

   (a) Anatomical change:

   Selection pressure:

   (b) Anatomical change:

   Selection pressure:

3. (a) Name two other flightless birds that are not ratites:

   (b) Why are these other flightless species not considered part of the ratite group?

4. Kiwis are ratites that have remained small. They arrived in New Zealand long after the moa. What part might this late arrival have played in kiwi species remaining small?

5. (a) On the phylogenetic tree (previous page), circle the branching marking the common ancestor of moa and kiwi.

   (b) On the phylogenetic tree (previous page), circle the branching marking the common ancestor of emus and kiwi.

6. (a) Based on the rafting hypothesis which ratite would you expect to be most closely related to ostriches?

   (b) Which ratite group is actually the closest related to the ostrich?

7. The diversification of ratites from a Gondwanan ancestor may still be explained in part by continental drift. Use the data on the previous page to suggest a possible sequence of events for the distribution of ratites, assuming the phylogeny is accurate:

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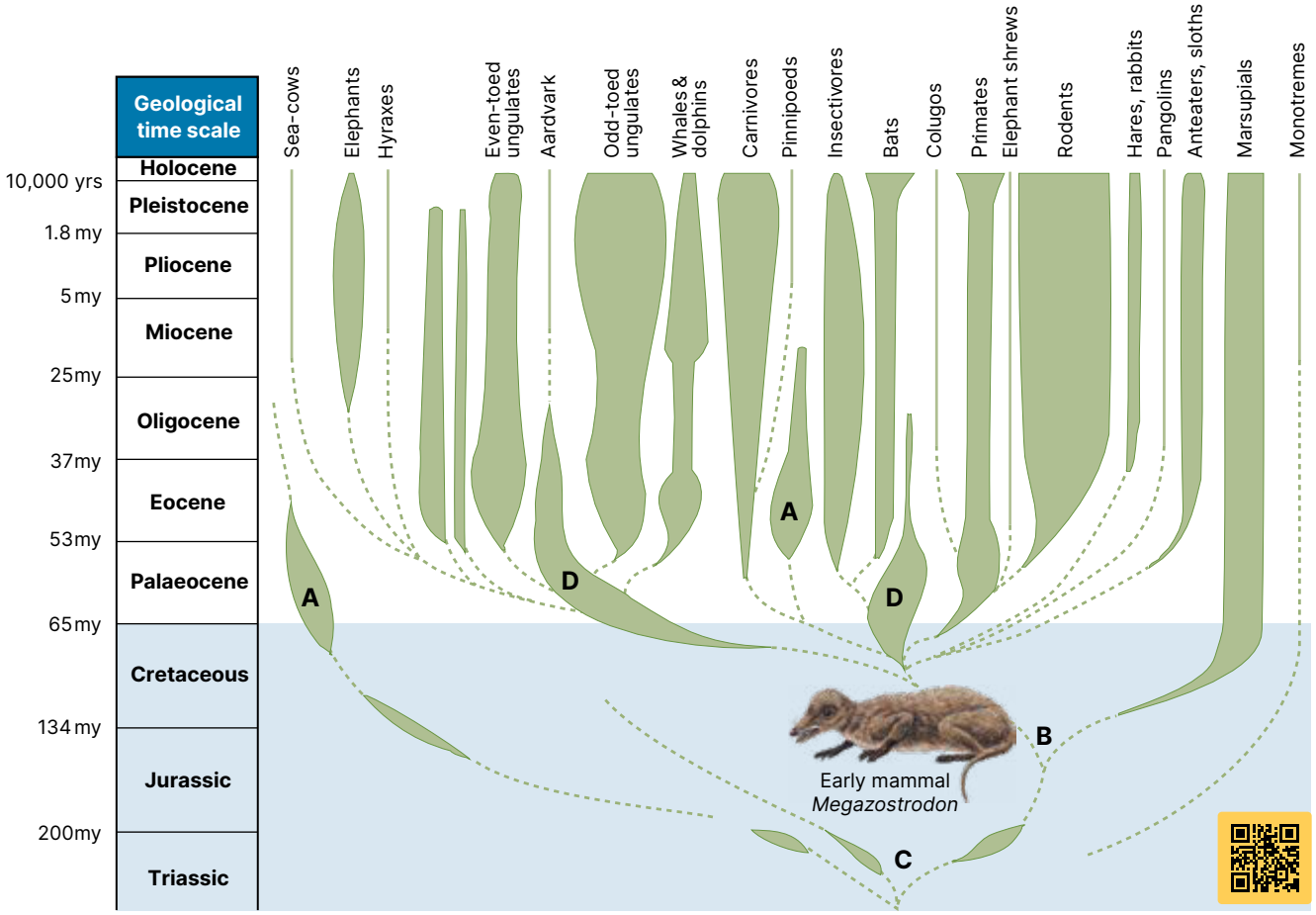
181 Adaptive Radiation in Mammals

Key Idea: Adaptive radiation of an ancestral mammal lineage about 80 million years ago resulted in the great diversity of mammal taxa we see today.

Adaptive radiation is diversification among the descendants of a single ancestral group (one lineage) to occupy different niches. Mammals underwent an extensive adaptive radiation following the extinction of the dinosaurs. Most of the modern mammalian groups became established very early on. The diagram below shows the divergence of the mammals into major orders, many occupying niches left vacant by the dinosaurs. The vertical extent of each green shape shows the time span for which a particular order has existed. Those that reach the top of the chart have survived to the present day. The width of a green shape shows how many species existed at any given time. The dotted lines indicate possible links between the orders for which there is no direct fossil evidence.



1. In general terms, describe the adaptive radiation that occurred in mammals: _____

2. Name the term that you would use to describe the animal groups at point **C** (above): _____

3. Explain what occurred at point **B** (above): _____

4. Describe one thing that the animal orders labelled **D** (above) have in common: _____

5. Identify the two orders that appear to have been most successful in terms of the number of species produced:

6. Explain what has happened to the mammal orders labelled **A** in the diagram above: _____

7. Name the geological time period during which there was the most adaptive radiation: _____

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Rodent diversity

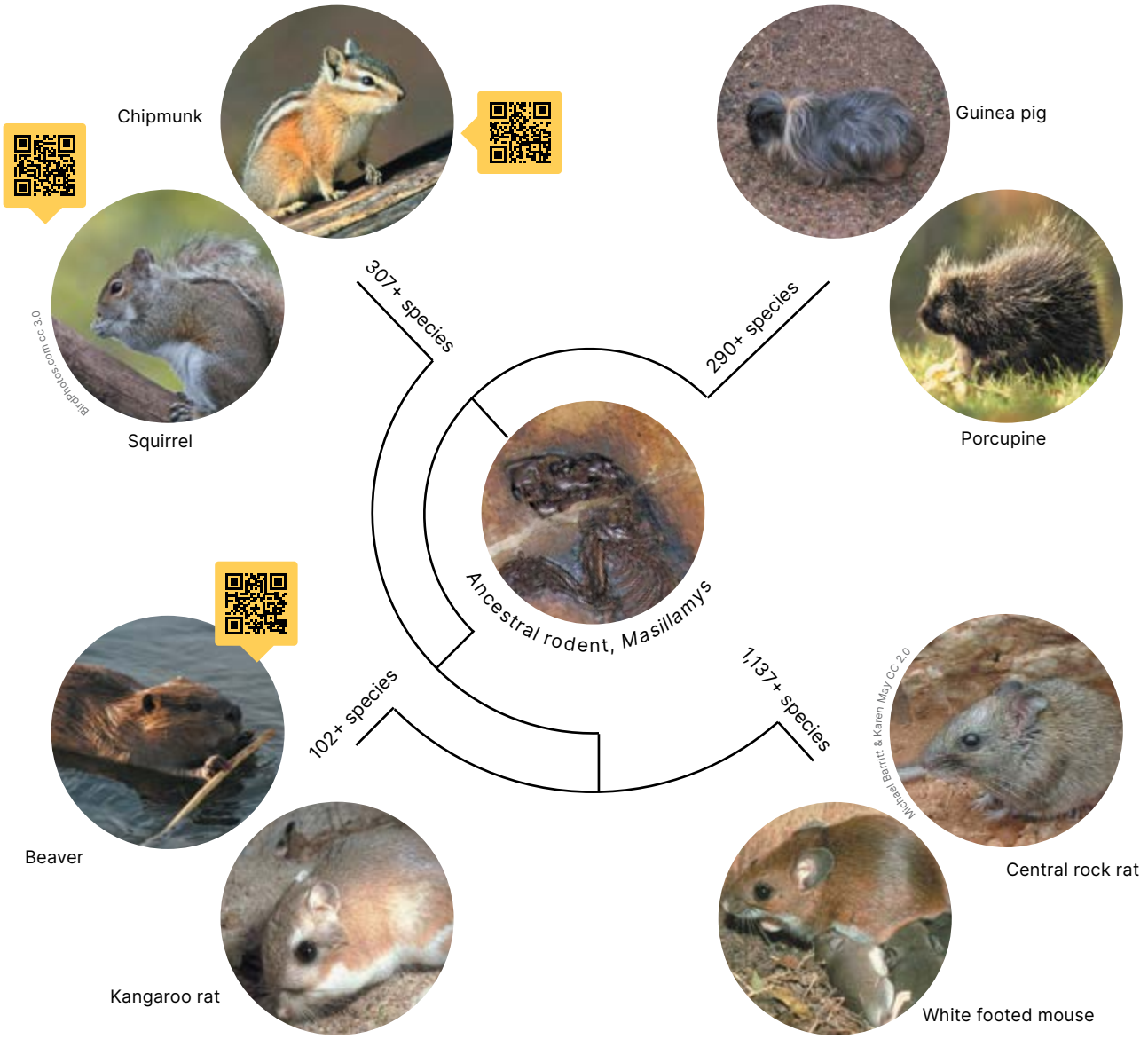
Rodents make up 40% of mammalian species, making them easily the most successful of the mammalian groups. Fossils with distinctive rodent features first appeared about 66 million years ago. All rodents have upper and lower incisor teeth that grow continuously. They are morphologically quite generalised and highly adaptable, occupying a wide number of habitats from deserts to forest. In some cases, distantly related species have occupied the same type of habitat and niche in widely separated regions, e.g. the kangaroo rat in western North America deserts (beaver-like rodents) and the jerboa in African deserts (mouse-like rodents).

Squirrel-like rodents

Squirrels are found on many continents. Their lifestyles include tree dwelling, ground dwelling, and gliding forms. Like most rodents, they are social, with prairie dogs forming large communities called towns.

Porcupine-like rodents

Capybaras are South American rodents and the largest of all rodents, occupying a range of habitats from forests to savannahs. Porcupines are found throughout the Old and New Worlds. Their spines make an almost impenetrable defence against predators. The group also includes guinea pigs, which are popular as pets.



Beaver-like rodents

Beavers are one of the larger rodents. They live near rivers, streams and lakes, chewing through small trees to build dams and lodges to live in. Gophers live in burrows, while kangaroo rats are so well adapted to the desert they rarely need to drink.

Mouse-like rodents

Rats and mice are found in virtually every part of the world thanks to their generalist adaptations and human assisted travel. There are at least 100 species of rats and mice alone. The group also includes voles, lemmings, jerboas and dormice.

8. What anatomical feature do all rodents have? _____

_____

9. Describe some of the habitats rodents have occupied: _____

_____

_____

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182 Convergent Evolution

Key Idea: Evolution in response to similar selection pressures can result in unrelated species appearing very similar.

Convergent evolution (convergence) describes the process by which species from different evolutionary lineages come to resemble each other because they have similar ecological roles, and natural selection has shaped similar adaptations.

It can be difficult to distinguish convergent and **parallel evolution**, as both produce similarity of form. Generally, similarity arising in closely related lineages (e.g. within marsupial mice) is regarded as parallelism, whereas similarity arising in more distantly related taxa is convergence (e.g. similarities between marsupial and placental mice).

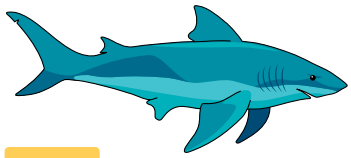
Convergence: same look, different origins

Not all similarities between species are the result of common ancestry. Selection pressures to solve similar problems in particular environments may result in similarity of form and function in unrelated (or distantly related) species. The evolution of succulence in unrelated plant groups (*Euphorbia* and the cactus family) is an example of convergence in plants. In the example (right), the selection pressures of the aquatic environment have produced a similar streamlined body shape in unrelated vertebrates. Ichthyosaurs, penguins, and dolphins each evolved from terrestrial species that took up an aquatic lifestyle. Their general body form has evolved to become similar to that of the shark, which has always been aquatic. Note that flipper shape in mammals, birds, and reptiles is a result of convergence, but its origin from the pentadactyl limb is an example of homology (common ancestry).

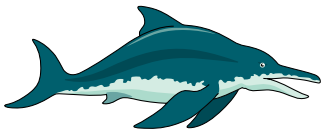
Analogous structures arise through convergent evolution

Analogous structures have the same function and often the same appearance, but different origins. The example (right) shows the structure of the **eye** in two unrelated taxa (mammals and cephalopod molluscs). The eye appears similar, but has evolved independently.

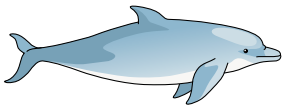
The **wings** of birds and insects are also analogous. The wings have the same function, but the two taxa do not share a common ancestor. *Longisquama*, a lizard-like creature that lived about 220 mya, also had 'wings' that probably allowed gliding between trees. These 'wings' were highly modified long scales or feathers extending from its back and not a modification of the forearm (as in birds).



Fish: Shark



Reptile: Ichthyosaur (extinct)

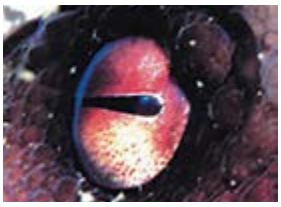


Mammal: Dolphin

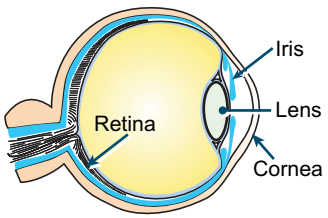
Bird: Penguin

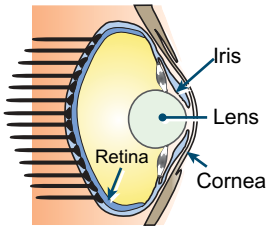
Jo Naylor cc2.0

Mammalian eye



Octopus eye





1. In the example above illustrating convergence in swimming form, describe two ways in which the body form has evolved in response to the particular selection pressures of the aquatic environment:

   (a) _____

   _____

   (b) _____

   _____

2. Describe two of the selection pressures that have influenced the body form of the swimming animals above:

   (a) _____

   (b) _____

3. When early taxonomists encountered new species in the Pacific region and the Americas, they were keen to assign them to existing taxonomic families based on their apparent similarity to European species. In recent times, many of the new species have been found to be quite unrelated to the European families they were assigned to. Explain why the traditional approach did not reveal the true evolutionary relationships of the new species:

   _____

   _____

   _____

   _____

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4. For each of the paired examples, briefly describe the adaptations of body shape, diet and locomotion that appear to be similar in both forms, and the likely selection pressures that are acting on these mammals to produce similar body forms:

Convergence between marsupials and placentals

Marsupial and placental mammals diverged very early in mammalian evolution (about 120 mya), probably in what is now the Americas. Marsupials were widespread throughout the ancient supercontinent of Gondwana as it began to break up through the Cretaceous, but then became isolated on the southern continents, while the placentals diversified in the Americas and elsewhere, displacing the marsupials in most habitats around the world. Australia's isolation from other landmasses in the Eocene meant that the Australian marsupials escaped competition with the placentals and diversified into a wide variety of forms, ecologically equivalent to the North American placental species.

Marsupial mammals

Wombat

(a) Adaptations: _____

_____

_____

_____

Selection pressures: _____

_____

_____

_____

Placental mammals

Woodchuck (groundhog or marmot)

Sugar glider (flying phalanger)

(b) Adaptations: _____

_____

_____

_____

Selection pressures: _____

_____

_____

_____

Flying squirrel

Marsupial mouse (antechinus)

(c) Adaptations: _____

_____

_____

_____

Selection pressures: _____

_____

_____

_____

Deer mouse

Long eared bandicoot (bilby)

(d) Adaptations: _____

_____

_____

_____

Selection pressures: _____

_____

_____

Jack rabbit

Patrick K59 cc 2.0

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183 Parallel Evolution

Key Idea: Parallel evolution occurs when a similar phenotype evolves independently in closely related species.

Parallel evolution is a term used to describe the evolution of similar morphology in related organisms that live in similar but separate environments. It is the result of similar selection pressures acting on the organisms. The use of the term parallel evolution is less commonly used in evolution because of its inconsistent use and definition. It is often confused with **convergent evolution** and the definitions of each often sound very similar. One of the more common distinctions used is: "If two similar traits have a similar ancestral phenotype, it is considered parallel evolution. Conversely, if two similar traits evolve from different ancestral phenotypes, it is considered convergent evolution". For example, if two related but environmentally separated species of fish converged on a similar pattern of stripes, with those stripes derived from the same origin (e.g. scale pigment), that is parallel evolution. If two unrelated fish converged on a similar pattern of stripes, but those stripes were derived from different origins (e.g. scale pigment in one but skin pigment in the other), that is convergent evolution. The problem arises when defining what is related and unrelated, and what phenotypes and characteristics are being looked at, e.g. is placental and marsupial convergence in fact parallelism because both groups are mammals? What about flight in vertebrates? Or flight in vertebrates and invertebrates?

Parallel evolution in domestic rice

- Annual rice is an important crop plant for humans. In Asia, the rice species used is *Oryza sativa*, whereas in Africa it is *Oryza glaberrima*.
- *Oryza sativa* evolved from *O. rufipogon* which has annual and perennial variants. *Oryza glaberrima* was domesticated from *O. longistaminata*, a perennial rice. *Oryza sativa* may have been domesticated 10,000 years ago in China whereas *Oryza glaberrima* may have been domesticated just 2000-3000 years ago.
- Thus annual phenotypes of the related species were produced in different environments under the same evolutionary pressures (human selection for annual growth).

African rice

Asian rice

Parallel evolution in oldfield mouse

- *Peromyscus polionotus* (the oldfield mouse) found in Florida, USA, has two major fur colorations, dark or light. Inland, most mice have dark fur and it is known as the mainland mouse. Along the beaches, lightly coloured fur is more common and it is called the beach mouse. The light fur presumably helps the mice on the beach to blend in with the light coloured sand and avoid predation.
- Genetic studies have shown that the mice populations along the Gulf coast are genetically distinct from populations on the Atlantic coast, but both are related to and form paraphyletic groups with their adjacent mainland populations.
- In 2022 genetic analysis showed that light fur in both Gulf and Atlantic coast populations was associated with a small region of the *Agouti signalling protein*. It is now believed that this new allele arose in the mainland population and spread to and was independently selected for in the coast populations, thus being an example of parallel evolution.

Alabama beach mouse

US Fish and Wildlife Service

1. What is parallel evolution? _____

2. Why could the domestication of rice be considered parallel evolution? _____

3. What are some potential problems defining parallelism and convergence in evolution?

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184 Coevolution

Key Idea: Coevolution involves the reciprocal evolution of species that have close ecological relationships, such as those involving mutualism, competition, or exploitation.

Coevolution involves the mutual (reciprocal) evolution of two or more species with an ecological relationship. Each party in the coevolution exerts selective pressures on the other and, over time, the species develop a relationship that may involve mutual dependency. Coevolution is likely to happen when different species have close ecological interactions with one another. These ecological relationships include predator-prey and parasite-host relationships, and mutualistic relationships such as those between plants and their pollinators. Competition can also drive coevolution because competitors will evolve adaptations, including those involving symbioses, that lead to niche specialisation and more efficient partitioning of available resources.

Pollinator/plant relationships

Bees are excellent pollinators. They are strong enough to enter intricate flowers and have medium length tongues which can collect nectar from many flower types. They have good colour vision, which extends into the UV, but they are red-blind, so bee pollinated flowers are typically blue, purplish, or white and they may have nectar guides that are visible as spots.

NZ's short tailed bat pollinates wood rose flowers on the forest floor

Bats are nocturnal and colour-blind but have an excellent sense of smell and are capable of long flights. Flowers that have coevolved with bat pollinators are open at night and have light or drab colours that do not attract other pollinators. Bat pollinated flowers also produce strong fragrances that mimic the smell of bats and have a wide bell shape for easy access.

Hummingbirds are important pollinators in the tropics. Their needle-like bills and long tongues can take nectar from flowers with deep tubes. Their ability to hover enables them to feed quickly from dangling flowers. As they feed, their heads are dusted with pollen, which is efficiently transferred between flowers.

Predator/prey relationships

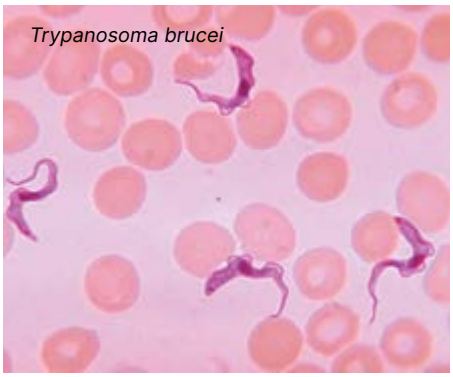
Predators have evolved strategies to successfully exploit their prey. Effective offensive weapons (e.g. claws and teeth) and hunting ability (including cooperative hunting tactics) are important. In turn, prey have evolved numerous strategies to protect themselves from predators, including large size and strength, rapid escape tactics, protective coverings, defensive weapons, and toxicity.
Lions have evolved the ability to hunt cooperatively to increase their chance of securing a kill from swift herd species such as zebra and antelope.

Competitive relationships

Crossbill

In most areas of the Rocky Mountains (USA) squirrels are the main predators of lodgepole pine seeds. In areas where there are no squirrels, crossbill birds are the main predator. Lodgepoles have evolved different pinecones depending on which is the main predator. Where squirrels dominate, the pinecones are heavy (harder to carry), have few seeds, and thin scales. Where crossbills dominate the cones are lighter with more seeds and thicker scales (harder to open). Crossbill bill shape varies depending on the region and cone type so that they can extract the seeds.

Parasite/host relationships



Trypanosoma brucei

CDC

Trypanosomes are protozoan parasites and are a good example of host-parasite coevolution. Trypanosomes have two hosts, humans and the tsetse fly. The fly vector spreads the parasite between human hosts. Trypanosomes have evolved strategies to evade their host's defences, but their virulence is constrained by needing to keep their host alive so that they can complete their life cycle. Molecular studies show that *Trypanosoma brucei* coevolved in Africa with the first hominins around 5 mya, but *T. cruzi* contact with human hosts occurred in South America only after settlements were made by nomadic cultures.

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1. (a) What is meant by coevolution? _____

(b) Why does coevolution occur? _____

2. Describe some of the strategies that have evolved in plants to attract pollinators: _____

3. Describe the limits on the parasite in the coevolution of a host-parasite relationship: _____

4. Around the Mediterranean, the mirror bee orchid (*Ophrys speculum*) has a exploitative relationship with the wasp *Dasyscolia ciliata*. The orchid's flower resembles a female wasp and produces a scent similar to the pheromones produced by the female wasp. The male wasp is therefore tricked into trying to mate with the orchid flower. The wasp becomes covered in pollen, which it will transfer to the next orchid. *D.ciliata* is the only pollinator of this orchid. Australian orchids (*Chiloglottis*) are also pollinated by this sexual deceit. In their case, the deceipt involves males of specific species of thynnine wasps.


D.ciliata pollinating orchid

Pietro Nioiu CC 3.0

(a) Why is the relationship between the mirror bee orchid and *Dasyscolia ciliata* exploitative?

(b) Discuss an evolutionary outcome if *Dasyscolia ciliata* numbers become significantly reduced over time:

5. The monarch butterfly caterpillar feeds on plants in the milkweed family. The caterpillar has adaptations to survive the toxicity of milkweed, which poisons most other animal species. The milkweed's adaptations to surviving the browse damage caused by the monarch caterpillar include a rapid regrowth response when leaf tissue is damaged.

(a) What type of **ecological** relationship is represented here? _____

(b) Describe the selection pressures on the monarch butterfly and the milkweed plant in this relationship and explain why it is an example of coevolution:

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185 Prezygotic Isolating Mechanisms

Key Idea: Reproductive isolating mechanisms prevent interbreeding between different species. Prezygotic isolating mechanisms occur before fertilisation can take place.

Reproductive isolation prevents successful interbreeding between species and is crucial to maintaining species' integrity. Prezygotic isolating mechanisms operate before fertilisation can occur and prevent "gamete wastage". They are the most common type of isolating mechanism and may be associated with behaviour, morphology, or reproductive timing. Single barriers to gene flow (such as geographical barriers) are usually insufficient to isolate a gene pool, so most species commonly have more than one type of barrier. Geographical barriers are not strictly a reproductive isolating mechanism, because they are not part of the species' biology, although they are usually a necessary precursor to reproductive isolation in sexually reproducing populations.

Geographical isolation

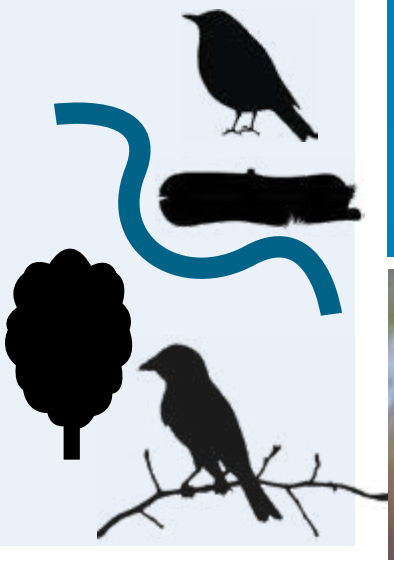
Geographical isolation describes the isolation of a species population (gene pool) by some kind of physical barrier, for example, mountain range, water body, isthmus, desert, or ice sheet. Geographical isolation is a frequent first step in the subsequent reproductive isolation of a species.

Example: Geological changes to the lake basins has been instrumental in the proliferation of cichlid fish species in the rift lakes of East Africa (far right). Similarly, many Galápagos Island species (e.g. iguanas, finches) are now quite distinct from the Central and South American mainland species from which they separated.

Ecological (habitat) isolation

Ecological isolation describes the existence of a prezygotic reproductive barrier between two species (or sub-species) as a result of them occupying or breeding in different habitats within the same general geographical area. Ecological isolation includes small scale differences (e.g. ground or tree dwelling) and broad differences (e.g. desert vs grasslands). Ecological isolation often follows geographical isolation, but in many cases the geographical barriers may remain in part.

Example: The red-browed and brown treecreepers (*Climacteris* spp.) are sympatric in south-eastern Australia and both species feed largely on ants. However the brown spends most of its time foraging on the ground or on fallen logs while the red-browed forages almost entirely in the trees.



Temporal isolation

Temporal isolation means isolated in time, and it prevents species interbreeding because they mate or they are active at different times. For example, individuals from different species do not mate because they are active during different times of the day (e.g. one species is active during the day and the other at night) or in different seasons.

Example: Closely related animal species may have different breeding seasons or periods of emergence to prevent interbreeding. The periodical cicadas (*Magicicada* genus) are an excellent example of this. Periodical cicadas are found in North America. There are several species and some have an overlapping distribution. Most of their life is spent underground as juveniles, emerging to complete their development and to mate. To prevent interbreeding, the various species spend either 13 or 17 years underground developing. Emergence of a single species is synchronised so the entire population emerges at the same time to breed.

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Gamete Isolation

The gametes (eggs and sperm) from different species are often incompatible, so even if the gametes meet, fertilization is unsuccessful. Gamete isolation is very important in aquatic environments where the gametes are released into the water and fertilisation occurs externally (e.g. reproduction in frogs, fish, and corals). Where fertilisation is internal, the sperm may not survive in the reproductive tract of another species. If the sperm does survive and reach the egg, chemical differences in the gametes prevent fertilisation. Chemical recognition is also used by flowering plants to recognise pollen from the same species. Pollen from a different species is recognised as foreign and it does not germinate.

Example: Two species of sea urchin, the red sea urchin (*Strongylocentrotus franciscanus*) and the purple sea urchin (*Strongylocentrotus purpuratus*), share the same geographic range. Sea urchins release their gametes into the sea water, but the two species do not interbreed because their gametes are not compatible.

Kirt L. Onthank cc3.0

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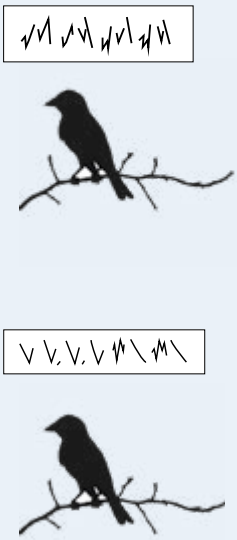
Behavioural Isolation

In many species, courtship behaviours are a necessary prelude to successful mating. These behaviours may include dances, calls, displays, or the presentation of gifts. The displays are very specific and are unique to each species. This means that mates of the same species recognise and are attracted to the individual performing the behaviour, but members of other species do not recognise or pay attention to the behaviours.

Birds exhibit a wide range of courtship displays. The use of song is widespread but ritualised movements, including nest building, are also common.

Examples: Galápagos frigatebirds have an elaborate display in which they inflate a bright red throat pouch to attract a mate. Frogs have species-specific calls.

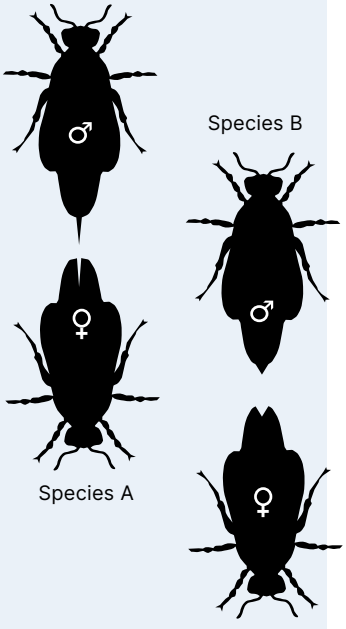


Mechanical (morphological) isolation

Structural differences (incompatibility) in the anatomy of reproductive organs prevents sperm transfer between individuals of different species. This is an important isolating mechanism preventing breeding between closely related species of arthropods.

Example: The sexual organs of empid flies have a lock-and-key mechanism. Without the right shaped genitalia, individuals cannot mate.

Many flowering plants have coevolved with their animal pollinators and have flower structures to allow only that insect access. Structural differences in the flowers and pollen of different plant species prevents cross breeding because pollen transfer is restricted to specific pollinators and the pollen itself must be species compatible.



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1. (a) What is a reproductive isolating mechanism? _____

_____

(b) What role do isolating mechanisms have in maintaining the integrity of a species? _____

_____

_____

2. What is a prezygotic isolating mechanism? _____

_____

_____

3. (a) Why is geographical isolation not regarded as a reproductive isolating mechanism? _____

_____

_____

(b) Explain why, despite this, it often precedes, and is associated with, reproductive isolation:

_____

_____

_____

_____

4. Distinguish between geographical and ecological isolation: _____

_____

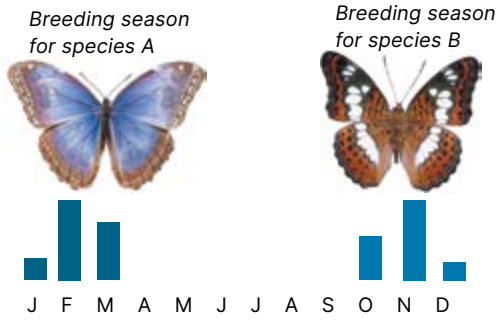
_____

_____

5. Identify the type(s) of reproductive isolation described in the following examples:

(a) Two species of butterfly (right) coexist in the same habitat but have different breeding seasons:

_____



(b) Male bowerbirds construct elaborate bowers (shelters) to attract a mate. One species, the MacGregor's bowerbird builds a tall structure and decorates it with charcoal. A second species, the satin bowerbird, decorates its bower with bright blue objects:

_____

(c) Two species of New Zealand skinks, *Oligosoma smithi* and *O. suteri* are sympatric (same area) in north-eastern New Zealand. *O. smithi* is diurnal and gives birth to live young. *O. suteri* is nocturnal and lays eggs.

_____

(d) The blackbird (*Turdus merula*) and the ring ouzel (*Turdus torquatus*) are two closely related species found in Europe. The blackbird is a woodland species and the ring ouzel tends to inhabit highlands:

_____

(e) Two species of sage plants coexist in a region of Southern California. Black sage (*Salvia mellifera*) has small flowers and is pollinated by small bees while white sage (*S. apiana*) has larger flowers providing a larger landing platform for its larger pollinator, carpenter bees. The two species of sage remain reproductively isolated.

_____

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186 Postzygotic Isolating Mechanisms

Key Idea: Postzygotic isolating mechanisms operate after fertilisation has occurred.

Postzyotic reproductive isolating mechanisms occur after fertilisation (formation of the zygote) has occurred. Postzygotic isolating mechanisms are less common than prezygotic mechanisms, but are important in maintaining the integrity of closely related species. There are several different postzygotic mechanisms operating at different stages. The first prevents development of the zygote. Even if the zygote develops into a viable offspring there are further mechanisms to prevent long term viability. These include premature death or (more commonly) infertility.

Hybrid inviability

Mating between individuals of two species may produce a zygote (fertilised egg), but genetic incompatibility may stop development of the zygote. Fertilised eggs often fail to divide because of mis-matched chromosome numbers from each gamete. Very occasionally, the hybrid zygote will complete embryonic development but will not survive for long.

For example, although sheep and goats seem similar (right) and can be mated together, they belong to different genera. Any offspring of a sheep-goat pairing is generally stillborn.


Sheep (*Ovis*) 54 chromosomes


Goat (*Capra*) 60 chromosomes

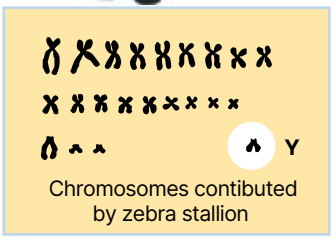
Hybrid sterility

Even if two species mate and produce hybrid offspring that are vigorous, the species are still reproductively isolated if the hybrids are sterile (genes cannot flow from one species' gene pool to the other). Such cases are common among the horse family (such as the zebra and donkey shown on the right). One cause of this sterility is the failure of meiosis to produce normal gametes in the hybrid. This can occur if the chromosomes of the two parents are different in number or structure (see the "**zebronkey**" karyotype on the right).

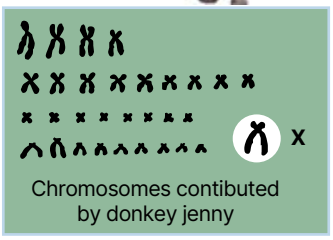
The **mule**, a cross between a donkey stallion and a horse mare, is also an example of **hybrid vigor** (they are robust) as well as **hybrid sterility**. Female mules sometimes produce viable eggs but males are infertile.

Zebra stallion (2N = 44) **X** **Donkey jenny** (2N = 62)

Karyotype of '**Zedronkey**' offspring (2N = 53)



Chromosomes contibuted by zebra stallion



Chromosomes contibuted by donkey jenny

Hybrid breakdown

Hybrid breakdown is common feature of some plant hybrids. The first generation (F_1) may be fertile, but the second generation (F_2) are infertile or inviable. Examples include hybrids between species of cotton (near right), species within the genus *Populus*, and strains of the cultivated rice *Oryza* (far right).

1. Postzygotic isolating mechanisms are said to reinforce prezygotic ones. Explain why this is the case:

2. Briefly describe how each of the postzygotic isolating mechanisms below maintains reproductive isolation:

   (a) Hybrid inviability:

   (b) Hybrid sterility:

   (c) Hybrid breakdown:

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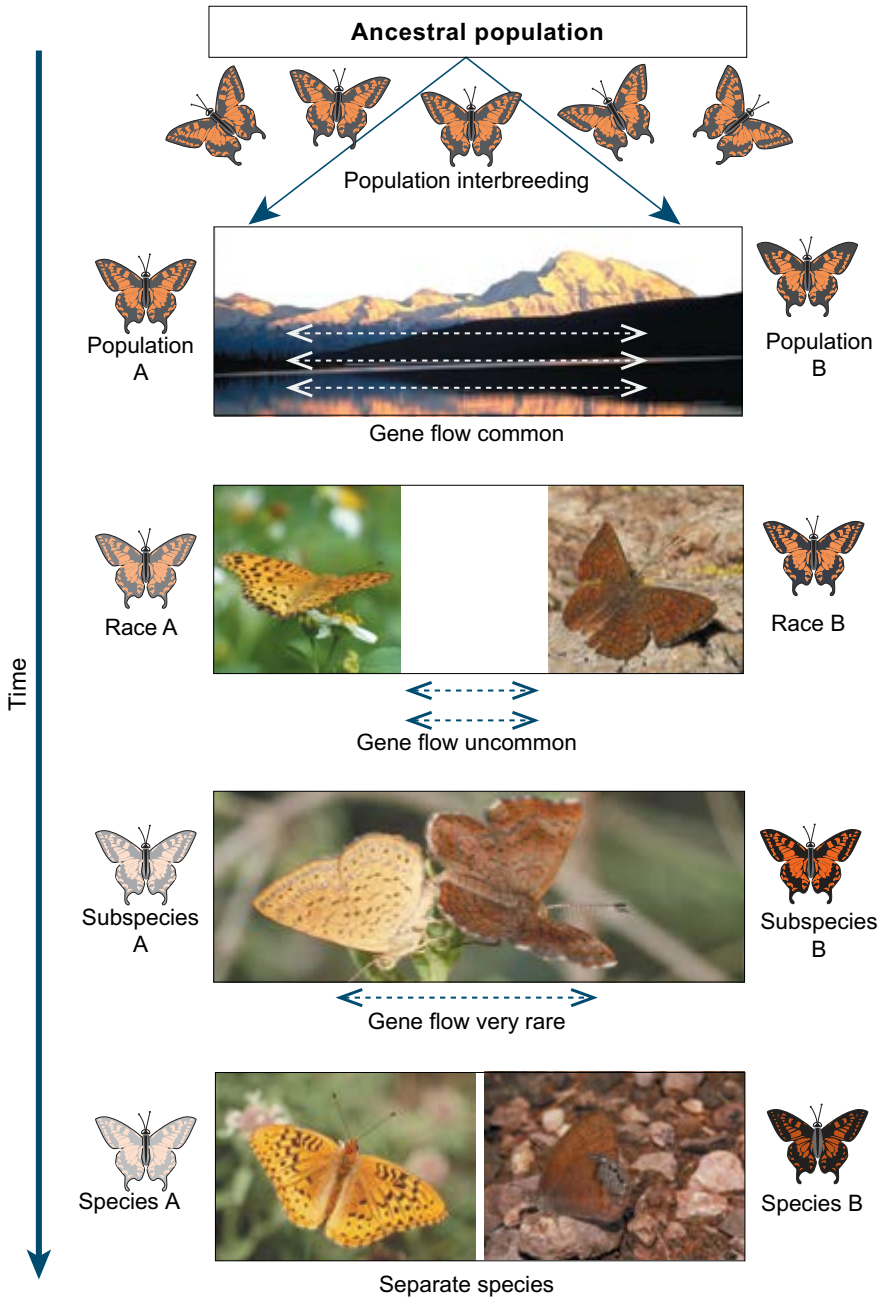
187 Stages in Species Formation

Key Idea: Speciation may occur in stages marked by increasing isolation of diverging gene pools. Physical separation is followed by increasing reproductive isolation.

The diagram below shows a possible sequence of events in evolutionary divergence by **phyletic gradualism**. Over time, the genetic differences between two populations of a parent species increase and the populations become increasingly isolated from each other. The isolation of the two gene pools may begin with a geographical barrier. This may be followed by progressively greater reduction in gene flow between the populations until the two gene pools are isolated and they each attain species status.



A species of butterfly lives on a plateau. The plateau is covered with grassland strewn with boulders. During colder weather, some butterflies sit on the sun-heated boulders to absorb the heat, while others retreat to the lower altitude grassland to avoid the cold.

Continued mountain building raises the altitude of the plateau, separating two populations of butterflies, one in the highlands the other in the lowlands.

In the highlands, boulder-sitting butterflies (BSBs) do better than grass-sitting butterflies (GSBs). In the lowlands, the opposite is true. BSBs only mate on boulders with other BSBs. Darker BSBs have greater fitness than light BSBs. (they can absorb more heat from the boulders). In the lowlands, light GSBs blend in with the grass and avoid predators better than darker butterflies.

Over time, only boulder-sitting butterflies are found in the highlands and grass-sitting butterflies in the lowlands. Occasionally, wind brings members of the two groups together but if they mate, the offspring are usually not viable or have a much lowered fitness.

Eventually, gene flow between separated populations ceases as variation between the populations increases. They fail to recognise each other as members of the same species.

1. Identify the variation in behaviour in the original butterfly population: _____

2. What were the selection pressures acting on boulder sitting butterflies in the highlands and grass sitting butterflies in the lowlands respectively?

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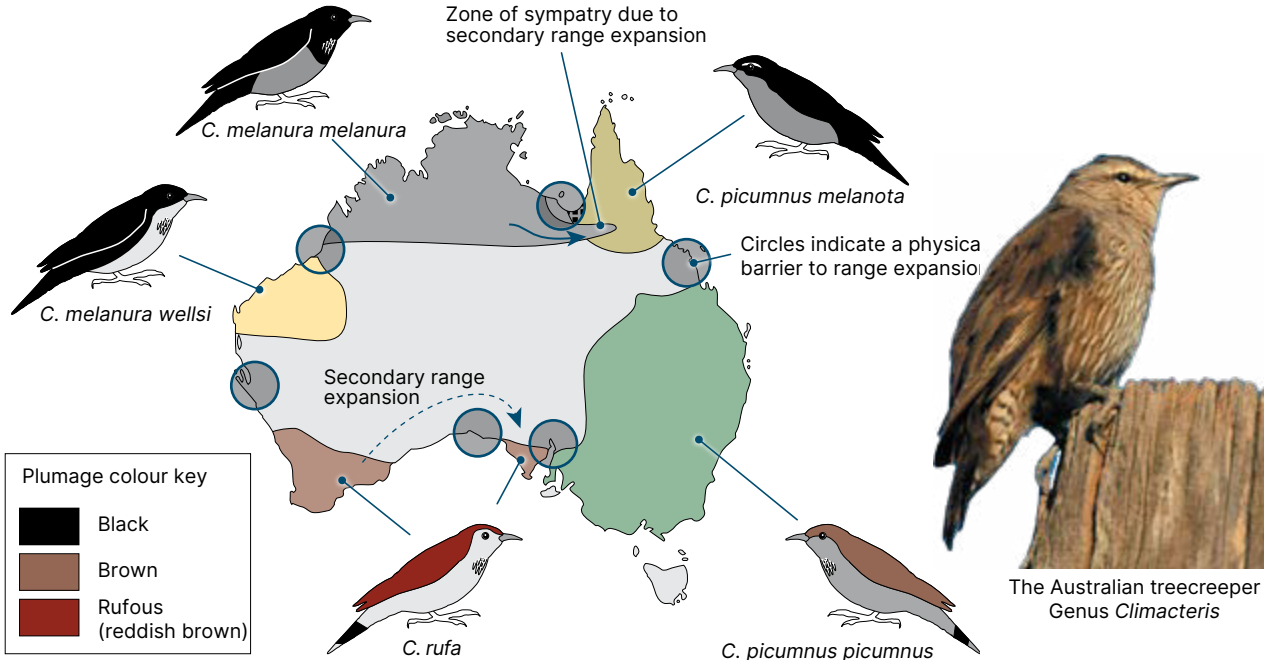
188 Speciation and the Role of Habitat

Key Idea: Geographic barriers presented by inhospitable habitat are contributing to speciation in Australian treecreepers.

The geographical barriers isolating populations on continents are often very different to those isolating island populations. In Australia, geographical barriers exist in the form of regions of inhospitable habitat. These create regions of preferred habitat cut off from one another. The species and subspecies of Australian treecreepers, *Climacteris*, are distinguishable by variations in the colour patterns of their plumage. Their distribution is restricted to savannah woodland and a distinctive form is associated with each of the major woodland areas (below). The populations probably evolved from a single common ancestor, isolated by habitat changes and then unable to expand their individual distributions beyond regions of unsuitable dry habitat. Subsequently, the distribution of two of the treecreeper species has undergone a secondary range expansion (arrows), where they have extended their range beyond their region of origin into new habitat.



1. (a) How many species are illustrated above? Explain your answer: _____

   _____

   (b) Describe the distribution of these treecreeper populations in Australia: _____

   _____

   _____

2. Explain why there are no treecreeper populations in the central region of Australia: _____

   _____

3. Two species in the NE of Australia, *C. melanura melanura* and *C. picumnus melanota*, exhibit sympatric distribution.

   (a) What is meant by the area of sympatry in this context? _____

   _____

   (b) What mechanisms are most likely to prevent interbreeding between these two species? _____

   _____

4. What is meant by secondary range expansion in the two populations above: _____

   _____

5. Describe the physical barriers that have prevented the neighbouring populations from mixing (in all but one case):

   _____

6. Predict a likely outcome to the distribution of these species, should the climate change to produce more coastal rainfall:

   _____

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189 Allopatric Speciation

Key Idea: Allopatric speciation is the genetic divergence of a population after it becomes subdivided and isolated.

Allopatric speciation refers to the genetic divergence of a species after a population becomes split and then isolated geographically. It is probably the most common mechanism by which new species arise and has certainly been important in regions where there have been cycles of geographical fragmentation, e.g. as a result of ice expansion and retreat (and accompanying sea level changes) during glacial and interglacial periods.

Stage 1: Moving into new environments

There are times when the range of a species expands for a variety of different reasons. A single population in a relatively homogeneous environment will move into new regions of their environment if there is intense competition for resources. Competition between members of the same species is the most intense because they are competing for identical resources in the same habitat. In the diagram on the right there is a 'parent population' of a single species with a common gene pool with regular 'gene flow'. Theoretically any individual can mate with any other individual of the opposite sex.

Stage 2: Geographical isolation

Parts of the population may become isolated by physical barriers, such as mountains, deserts, or stretches of water. These barriers may cut off those parts of the population that are at the extremes of the range and gene flow becomes rare or stops altogether. Climate change (e.g. ice ages and a consequent rise and fall in sea level) can leave 'islands' of habitat separated by large inhospitable zones that the species cannot traverse.

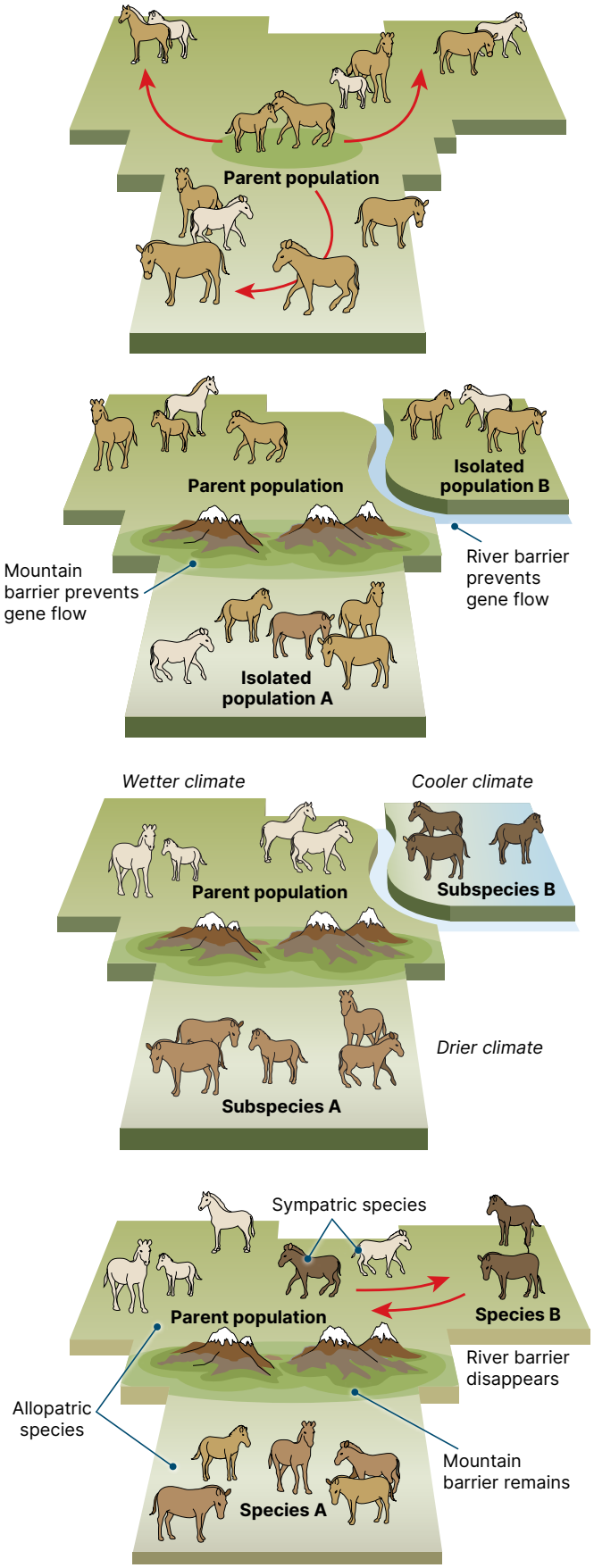
Example: In mountainous regions, alpine species can populate extensive areas of habitat during cool climatic periods. During warmer periods, they may become isolated because their habitat is reduced to 'islands' of high ground surrounded by inhospitable lowland habitat.

Stage 3: Different selection pressures

The isolated populations (A and B) may be subjected to quite different selection pressures. These will favour individuals with traits suited to each particular environment. For example, population A will be subjected to selection pressures found in drier conditions, favouring individuals with phenotypes (and genotypes) suited to dry conditions (e.g. better ability to conserve water). This would result in improved survival and reproductive performance. As allele frequencies for certain genes change, the population takes on the status of a subspecies. **Reproductive isolation** is not yet established but the subspecies are significantly different genetically from related populations.

Stage 4: Reproductive isolation

The separated populations (isolated subspecies) undergo genetic and behavioural changes. These ensure that the gene pool of each population remains isolated and 'undiluted' by genes from other populations, even if the two populations should be able to reunite at a later time (if the geographical barrier is removed). Gene flow does not occur but there is a zone of overlap between two species after species B has moved back into the range of the parent population. Closely-related species with an overlapping distribution like this are called sympatric. Those that remain geographically isolated are called allopatric species.



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1. Why do some animals, given the opportunity, move into new environments? _____

2. Plants are unable to move. How might plants disperse to new environments? _____

3. Describe the amount of gene flow within a parent population prior to and during the expansion of a species' range:

4. Explain how cycles of climate change can cause large changes in sea level (up to 200 m): _____

5. (a) What kinds of physical barriers could isolate different parts of the same population? _____

   (b) How might emigration achieve the same effect as geographical isolation? _____

6. (a) How might selection pressures differ for a population that becomes isolated from the parent population?

   (b) Describe the general effect of the change in selection pressures on the allele frequencies of the isolated gene pool:

7. Distinguish between allopatric and sympatric species: _____

8. Explain how reproductive isolation could develop in geographically separated populations (see previous pages):

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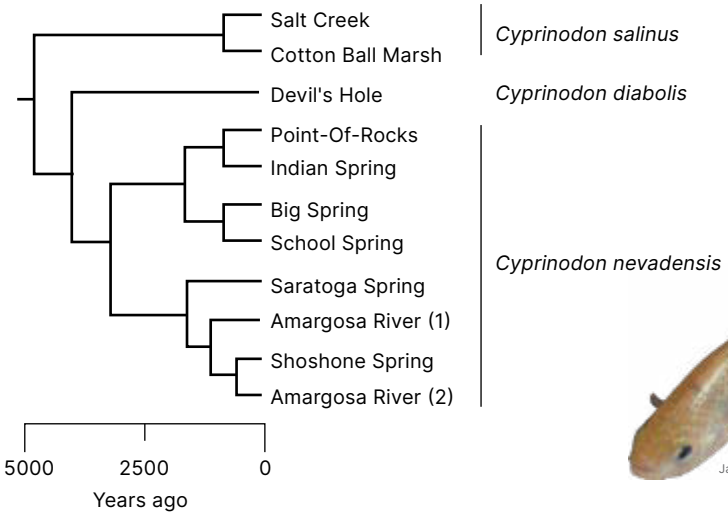
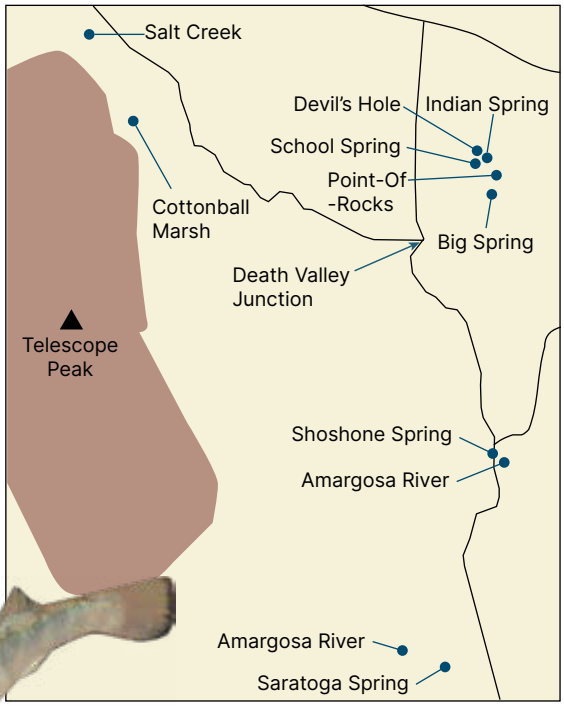
Allopatric speciation in Death Valley pupfish

During the last glacial period, the desert surrounding Death Valley in North America once had a relatively wet climate, with a large lake and numerous rivers. As the lake and rivers dried up, populations of pupfish in it were isolated in several small springs that still exist in the valley area. There are three species of pupfish in the area, each with several subspecies that have diverged in the last few thousand years since their separations.

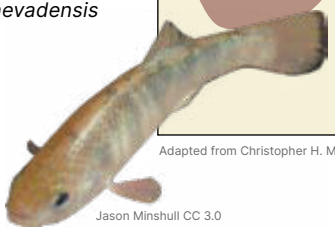
There is still strong debate over the length of time these populations have been separated, with research suggesting the populations have been separated from anywhere between a few hundred years to up to 60,000 years.



Map of Death Valley pupfish locations



Adapted from Christopher H. Martin et al 2016 Royal Society Publishing



Jason Minshull CC 3.0

9. (a) What physical barriers separate the pupfish species? _____

   (b) What environmental event caused these barriers to appear? _____

   _____

   (c) How did this cause the split of the pupfish species? _____

   _____

10. How many subspecies of *Cyprinodon nevadensis* are there? _____

11. (a) Note the locations (above right) and phylogeny (above left) of *Cyprinodon* spp. Are they compatible? Explain:

    _____

    _____

    _____

    _____

    (b) Which species of pupfish appears anomalous in its location and phylogeny? _____

12. Approximately how many years ago did the Devil's Hole pupfish appear? _____

13. The graph on the right shows the difference in escape acceleration in two populations of mosquitofish (*Gambusia*) in the Bahamas. One population is subject to heavy predation, the other is not. Suggest how this difference could lead to speciation over time if the populations remain separate:

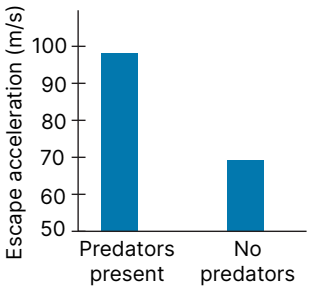
    _____

    _____

    _____

    _____

    _____



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190 Sympatric Speciation

Key Idea: Sympatric speciation is speciation which occurs even when there is no physical barrier separating gene pools. In **sympatric** (same place) **speciation**, a new species evolves from a single ancestral species while inhabiting the same geographic region. Sympatric speciation is rarer than **allopatric speciation**, although it is not uncommon in plants which form polyploids. There are two situations where sympatric speciation is thought to occur. These are described below.

Speciation through niche differentiation

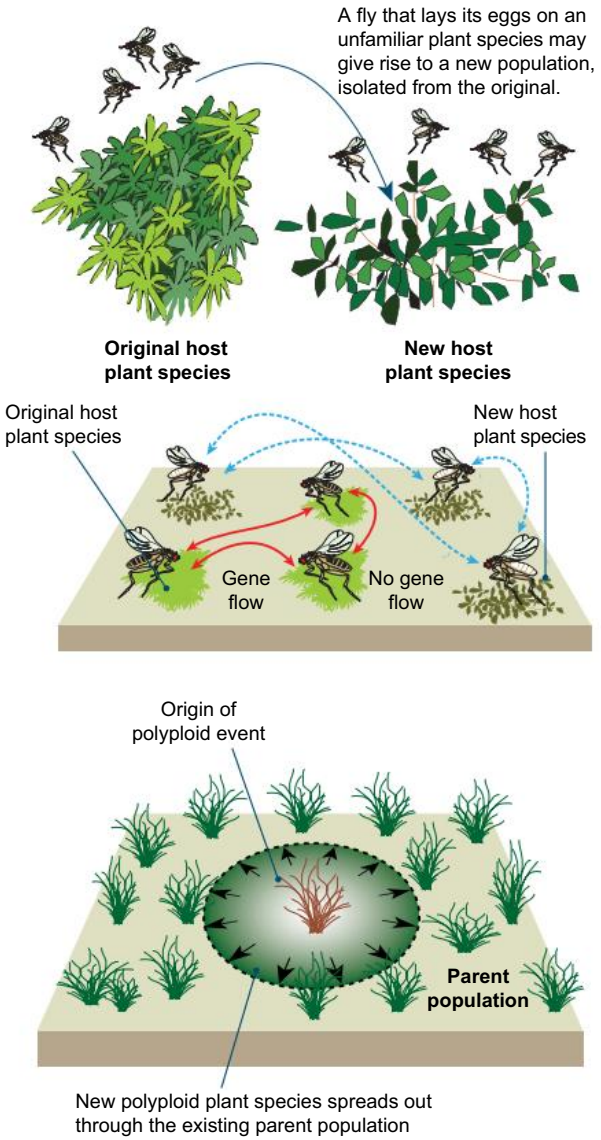
Niche isolation

There are many microhabitats within a heterogeneous environment (one that is not the same everywhere). Some individuals in a population may preferentially occupy to occupy one particular microhabitat, only rarely coming in contact with those that select other microhabitats. Some organisms become so dependent on the resources offered by their particular microhabitat that they never interact with others of their species in different microhabitats.

Reproductive isolation

Sub-populations, which have remained genetically isolated because of their microhabitat preferences, become reproductively isolated. They have become new species with subtle differences in behaviour, structure, and physiology. Gene flow (via sexual reproduction) is limited to organisms that share similar microhabitat preferences (as shown right).

Example: Some host-specific phytophagous insects (insects that feed on plants) lay eggs on plants identical to the species they themselves hatched on. Host plant preference leads to isolation despite the populations being sympatric.



Instant speciation by polyploidy

Polyploidy may result in the formation of a new species without isolation from the parent species. This event, occurring during meiosis, produces sudden **reproductive isolation** for the new group. Because the sex-determining mechanism is disturbed, animals are rarely able to achieve new species status this way (they are sterile). Many plants, on the other hand, are able to reproduce vegetatively, or self pollinate. This ability to reproduce on their own enables such polyploid plants to produce a breeding population.

Speciation by allopolyploidy

This type of polyploidy usually arises from the doubling of chromosomes in a hybrid between two different species. The doubling often makes the hybrid fertile. **Examples**: Modern wheat. Swedes are a polyploid species formed from a hybrid between a type of cabbage and a type of turnip.

1. Explain what is meant by sympatric speciation: _____

_____

2. What is the mechanism for instant speciation? Explain why it is more common in plants than in animals:

_____

_____

_____

3. Explain how niche differentiation could result in the formation of a new species: _____

_____

_____

_____

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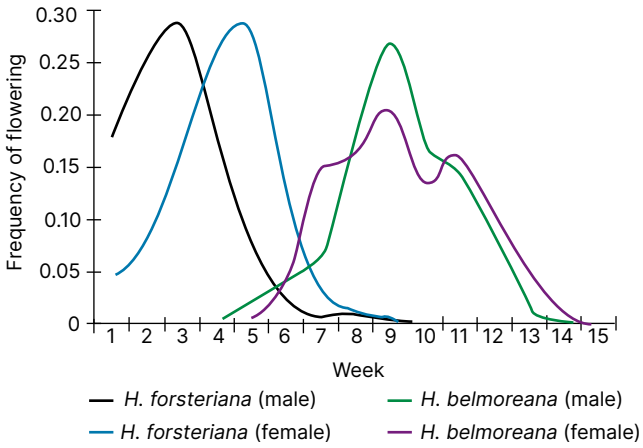
Sympatric speciation in *Howea* palms

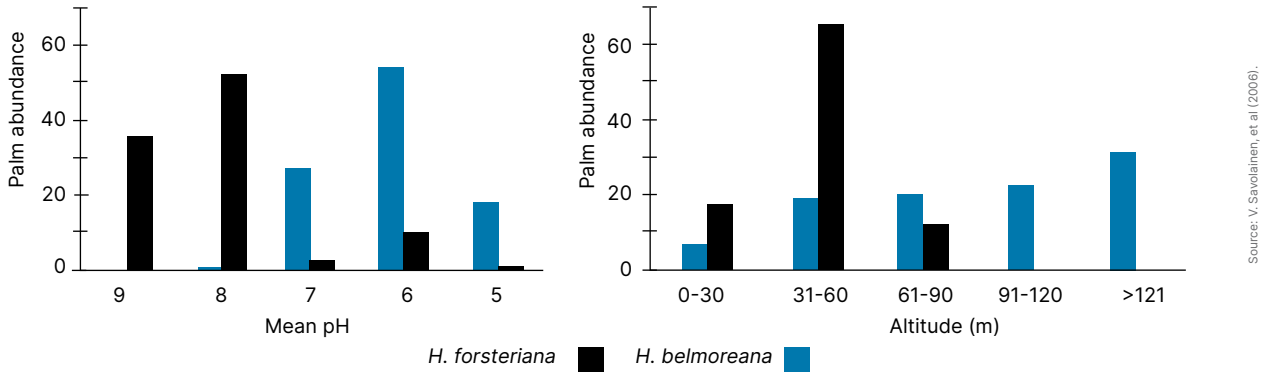
- The palms *Howea forsteriana* (below) and *Howea belmoreana* are endemic to Lord Howe Island. Studies show differences between the species in flowering times, tolerance of soil pH, and altitude preference. Hybrids are rare.

Black Diamond Images CC 2.0

Differences in flowering times



Palm distribution by soil pH and by altitude



Source: V. Savolainen, et al (2006).

David Stanley CC 3.0

- Lord Howe Island is the eroded remains of a 7 million year old volcano. It is located in the Tasman sea about 700 km from Sydney.
- The island is about 10 km long and 2 km wide at its widest point and covers 14.5 km^2. The highest point is 875 m above sea level.
- About half the island's plants are endemic. *Howea* palms are found throughout the island. They are also cultivated and exported.
- As the island is so small, the palms are believed to have evolved by sympatric speciation.

With respect to the palm species *H. forsteriana* and *H. belmoreana:*

4. Approximately how many weeks' difference is there in flowering times between the species? _____

5. Describe the difference in preference for soil pH between the two palm species: _____

_____

_____

6. Describe the difference in altitude preference between the two palm species: _____

_____

_____

7. In what way are the observations above consistent with sympatric speciation? _____

_____

_____

_____

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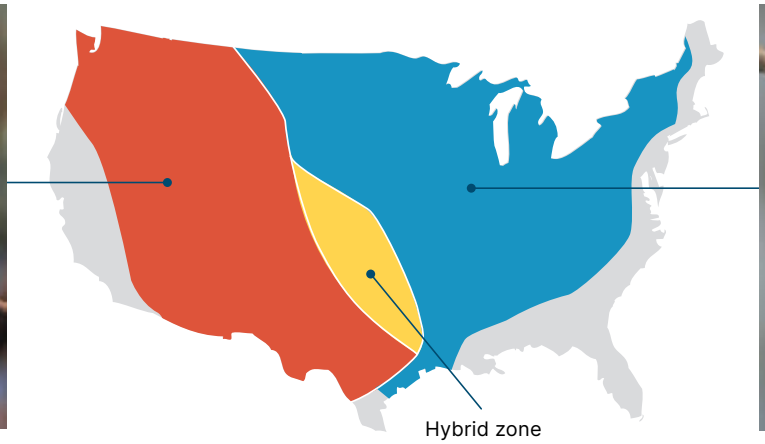
191 Parapatric Speciation

Key Idea: Speciation can occur when a part of a population expands its niche before establishing a separate population.

In **parapatric speciation**, a population enters a new niche and gene flow is reduced between the population in the new niche and parent population. Eventually gene flow ceases, isolating a new species. For this to happen, mating must be non-random, i.e. mates select each other based on niche preference, although a hybrid zone will exist between the two populations. Each population has reduced fitness outside its niche, so gene flow between those in the new niche and those outside it declines. This eventually leads to a difference in characteristics including appearance and behaviour.

Parapatric speciation in orioles

Bullock's oriole



Baltimore oriole

One of the outcomes of parapatric speciation is the formation of a hybrid zone between the parent population in the original environment and the daughter population in the new environment. An example of this hybrid zone can be seen between Bullock's oriole and the Baltimore oriole in North America. Although the birds have very different plumage patterns and songs they can interbreed. The hybrid zone is relatively narrow and appears to remain static because Bullock's oriole has a lower fitness in the east than the Baltimore oriole and vice versa.

Comparison of speciation models

Speciation model	Allopatric	Sympatric	Parapatric
Original population			
Initiating event:	Barrier arises	Genetic change	New niche entered
			
Reproductive isolation occurs:			
New species arise:	In isolation	Within a population	In a new niche
			

1. Explain the difference between parapatric, allopatric, and sympatric speciation: _____

_____

_____

_____

_____

2. Why would a hybrid zone be a feature of parapatric speciation? _____

_____

_____

_____

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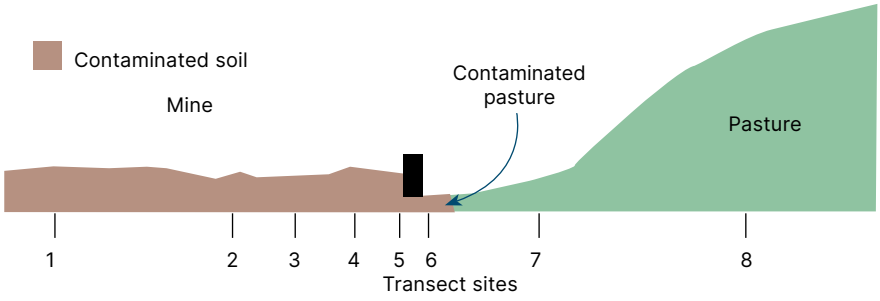
Parapatric speciation in pasture grasses

A well documented example of parapatric speciation is that of the grasses *Agrostis capillaris (tenius)* (browntop) and *Anthoxanthum odoratum* (sweet vernal) growing on pasture and contaminated soil around mine sites.

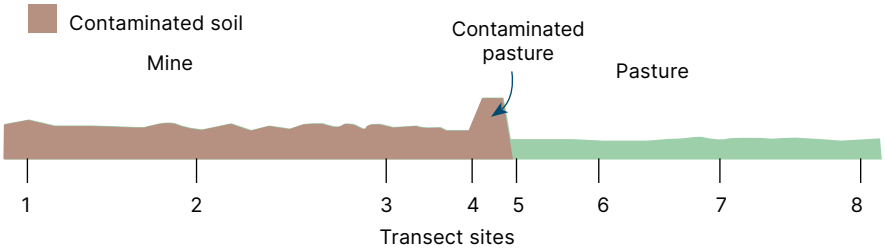
Drws-y-Coed mine (Wales) *Agrostis capillaris*



John M CC 2.0

Dam below Drws-y-Coed copper mine

Trelogan mine (Wales) *Anthoxanthum odoratum*



Thomas McNeilly *et al Heredity* 1968

Maggie Cox CC 2.0

Abandoned mineshaft from Trelogan zinc and lead mine

- Tolerant plants were those able to grow on the contaminated mine soil whereas non-tolerant plants were less able to grow on the mine soil and had reduced fitness. Tolerant plants were less able to grow and had reduced fitness in uncontaminated soil.
- Stages of flowering were used to calculate the number of days the plants in each transect site were reproductively isolated. About a quarter of the tolerant plant population flowered earlier than non-tolerant plants. These flowering differences were verified as genetic by removing plants to a controlled environment where the difference in flowering was still observed.

Flowering isolation in *Agrostis capillaris*

Henri0800 cc 3.0

	Tolerant			Intermediate	Non-tolerant	
Year \ Site	2	3	4	5	6	7
Isolation time (days) 1964	6.09	5.96	12.17	7.95	0	3.23
1965	3.73	4.86	8.49	7.85	0	2.79

Flowering isolation in *Anthoxanthum odoratum*

James Lindsey cc 3.0

	Tolerant				Intermediate	Non-tolerant		
Year \ Site	1	2	3	4	5	6	7	8
Isolation time (days) 1964	4.60	–	7.17	–	2.94	–	0	–
1965	1.85	4.85	4.77	2.62	1.31	1.85	0	0.62

Thomas McNeilly *et al Heredity* 1968

3. What mechanism causes the unequal gene flow between the tolerant and non-tolerant plants at each mine site?

4. How was the difference in flowering time between tolerant and non-tolerant plants confirmed to be genetically influenced rather than environmentally influenced?

5. Explain why the study indicates the speciation of *Agrostis capillaris* and *Anthoxanthum odoratum* is parapatric:

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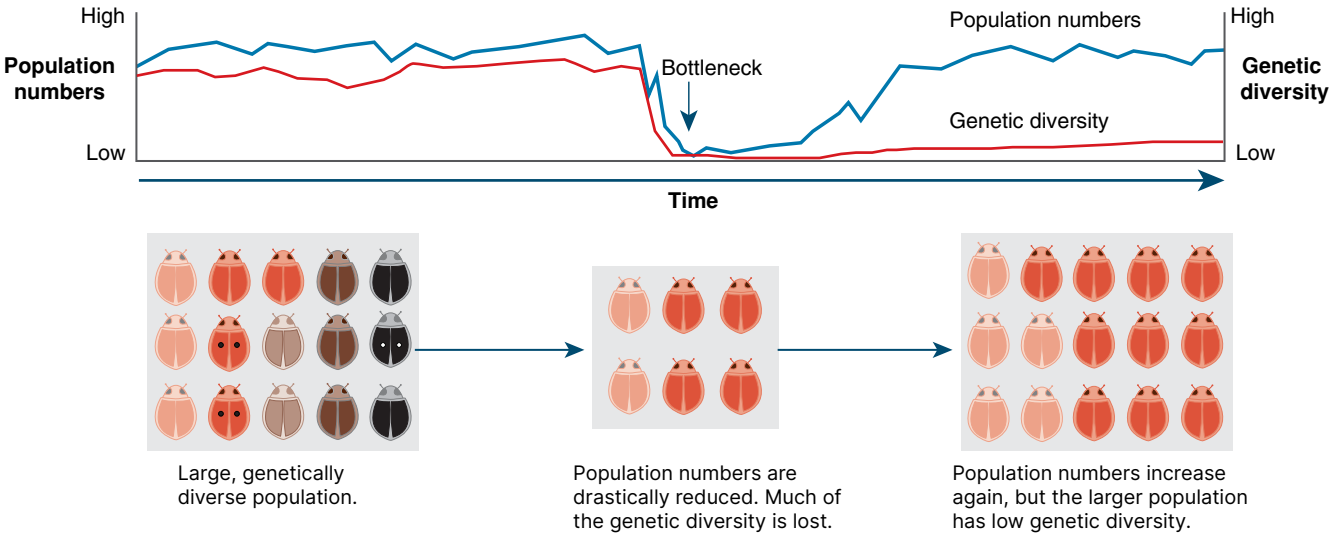
192 Population Bottlenecks: The Role of Diversity

Key Idea: Population bottlenecks occur when population numbers and genetic diversity decline rapidly. The population's numbers may recover, but its genetic diversity often does not.

Populations may sometimes be reduced to low numbers by predation, disease, or periods of climatic change. These large scale reductions are called **population (genetic) bottlenecks**. The sudden population decline is not necessarily selective and it may affect all phenotypes equally. Large scale catastrophic events, such as fire or volcanic eruption, are examples of such non-selective events. Affected populations may later recover, having squeezed through a 'bottleneck' of low numbers. The diagram below illustrates how population numbers may be reduced as a result of a catastrophic event. Following such an event, the gene pool of the surviving remnant population may be markedly different to that of the original gene pool. Genetic drift may cause further changes to allele frequencies. The small population may return to previous levels but with a reduced genetic diversity.

Change in population numbers and diversity



Population bottlenecks and low allelic diversity in Tasmanian devils

- Tasmanian devils are the largest surviving marsupial carnivore. They were once found throughout mainland Australia, but became locally extinct about 3000 years ago and are now restricted to Tasmania. Genetic evidence suggests that devils went through at least two historic population crashes, one about 30,000 years ago and another about 3000 years ago. Added to these historic declines are modern declines (1850 to 1950) as a result of trapping and disease. These population crashes are the likely cause of the very low diversity in the MHC I and II (immune) genes in devils.
- The MHC genes are important in immunity and the body's self recognition system. Low allelic diversity for MHC is implicated in the spread of devil facial tumour disease (DFTD), a contagious cancer that appeared in populations in the mid 1990s and has resulted in the loss of 80% of the devil population. The cancerous cells are transmitted when the devils fight. Ordinarily this foreign material would be recognised and destroyed by the immune system. In Tasmanian devils, the immune diversity is so low that tumours can spread without invoking an immune response.
- Recent evidence also shows that some populations have immunity to DFTD. This may originate in devils with MHC alleles distinctly different from susceptible animals.

Mike Lehmann cc 3/0

1. Define the term population (genetic) bottleneck: _____

2. Explain how a population bottleneck can decrease genetic diversity in a population: _____

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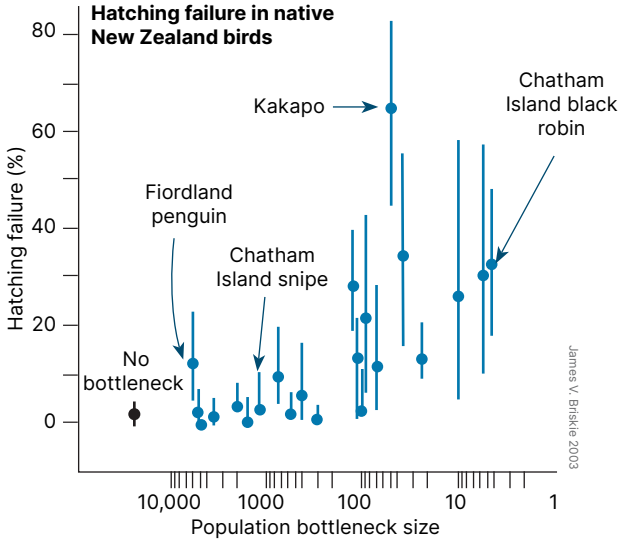
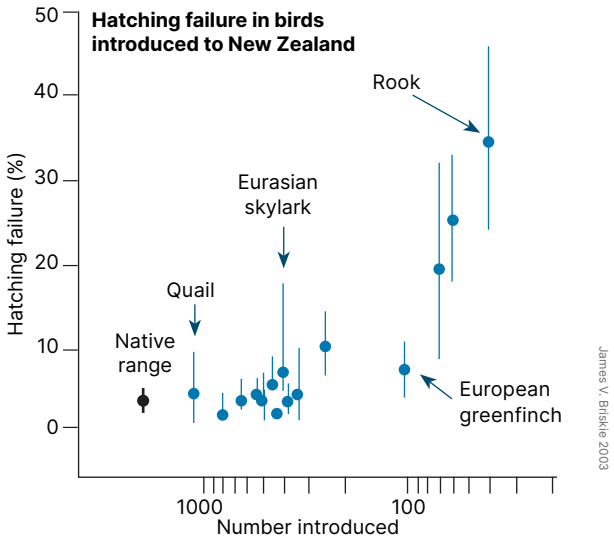
Population bottlenecks affect hatching rates in birds

- Severe bottlenecks reduce genetic diversity but it can be difficult to identify the negative effects of this reduction. New Zealand has many native birds that have gone through recent bottlenecks, and many are still critically endangered.
- The effect of these bottlenecks on egg hatching was investigated in 22 native birds. As a comparison, the hatching rates of introduced birds were also investigated. Many birds were introduced into New Zealand during the 1800s by acclimatisation societies. Some of these introductions were small and so these founder populations also represented population bottlenecks.





Once common throughout New Zealand, by 1995 there were just 51 kakapo left. The population is now around 240.

The Chatham Island black robin population was just 5 in 1980, but has risen to 300. It has very little genetic diversity.

Small numbers of rook were introduced in the 1860s. Its population reached over 60,000 by 1975 before culling reduced it.

3. What events might cause a population (genetic) bottleneck? _____

4. (a) What has been the genetic consequence of bottleneck events in the Tasmanian devil population? _____

   (b) How has this led to increased susceptibility to disease, specifically infectious cancer? _____

5. (a) What was the effect of genetic bottlenecks on hatching failure in native and introduced birds in New Zealand birds?

   (b) Why might this be? _____

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193 Habitat Fragmentation and Speciation

Key Idea: Habitat fragmentation can lead to the evolution of new species or the extinction of them.

Habitat fragmentation occurs when a large area of habitat (e.g. a forest) becomes split up into separate smaller regions (e.g. patches of forest). This may occur naturally (e.g. by forest fire or lava flows) or it may occur because of human influences (e.g. logging large parts of the forest). Habitat fragmentation can lead to **speciation**, especially if a specific type of habitat is isolated or gene flow between populations in different habitat fragments ceases. If an isolated population is too small to breed effectively (or becomes inbred) and gene flow between fragmented areas ceases then that population isolate may die out (a local extinction). If this occurs throughout the fragmented habitats then the species may also die out.

Habitat fragmentation and speciation

Hawai'i, the largest island of the Hawaiian islands (also known as Big Island) is also the youngest of the islands. The island is the tip of a volcano more than 10,000 m tall, which emerged from the ocean less than a million years ago. Hawai'i has since been colonised by many species, with some of these then giving rise to new species in the new island environment. The island is still very volcanically active and lava regularly flows from three active volcanic craters. These lava flows often intersect forests, producing forest fragments separated by black basalt lava. The fragmentation separates organisms and has been shown to produce quite different populations of organisms in each fragment. Two well studied examples are *Drosophila* flies and *Tetragnatha* spiders.

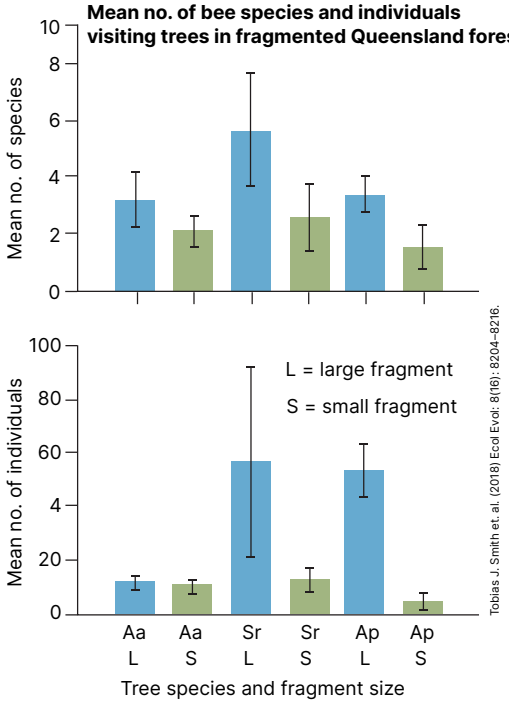
Habitat fragmentation caused by a lava flow from Kilauea volcano.

USGS

- There are at least 12 species of *Tetragnatha* spiders on Hawai'i. Studies of three from forest fragmented by a 160 year old lava flow show genetic differences between isolated populations in two of the species. The third species showed little genetic difference between population isolates. This may be because it is a habitat generalist.
- Forest fragmentation is also important in Hawaiian *Drosophila*. There are 800 species of Drosophilidae in Hawaii, one of the highest concentrations anywhere in the world. *D. silvestris* males have a series of hairs on their forelegs, which they brush against females during courtship. Males in the northeastern part of the island have many more of these hairs than the males on the southwestern side of the island. While still the same species, the two populations are already displaying structural and behavioural isolation.

Habitat fragmentation and species loss

- Often, habitat fragmentation causes a loss of biodiversity, especially in larger animals that require large areas of land to find food. Habitat fragmentation reduces population sizes and can lower migration and therefore gene flow because individuals are unable to move easily between habitat fragments. Fragmentation also affects plants in a similar way. Because plants are immobile, genes are exchanged by the movement of pollen, either by the wind or by pollinators.
- A 2018 study of fragmented tropical forest surrounded by pasture in north Queensland (right) found the diversity of bees pollinating tree flowers was lower in small forest fragments than larger ones as well as reduced numbers of pollinating bees overall.



Tobias J. Smith et. al. (2018) Ecol Evol: 8(16): 8204-8216.

1. What is the difference between the mode of fragmentation in the Hawaiian and Queensland examples?

2. Suggest why was there little genetic difference between fragmented populations of the generalist *Tetragnatha* spider?

3. Why would reduced numbers of pollinators reduce gene flow between plants in small fragmented areas of forest?

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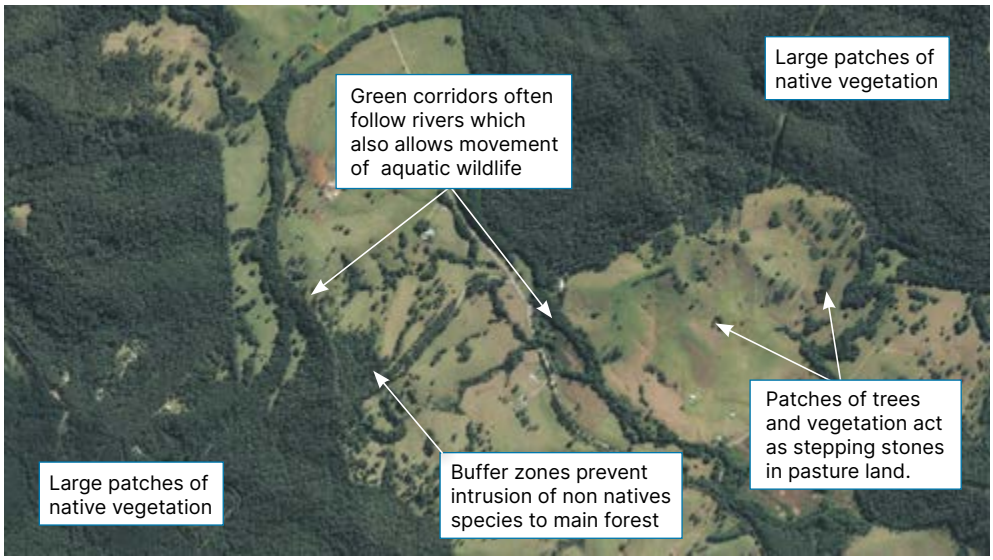
194 Green Corridors and Species Conservation

Key Idea: Green corridors maintain connections between isolated conservation areas, allowing wildlife populations to remain in contact.

Loss of habitat is a major issue in conservation biology. Without the right amount of habitat, organisms cannot forage or find mates adequately. Each organism's requirements are different. Some animals need large ranges to graze or hunt for food. Many of the large conservation areas are isolated, separated from each other by large tracts of farmland or urban areas. By planting and maintaining corridors of forest or riparian areas these conservation areas can be connected, effectively making them larger. Green corridors give isolated populations areas to move about, hunt, and look for mates, increasing gene flow and thus helping to maintain viable populations.

Green corridors

In today's world, with rapidly increasing populations and an increase in land use, it is not always possible to conserve the large areas of land needed for various organisms as single large regions. Instead, smaller land areas can be linked by green corridors. These are strips of land connecting areas of habitat and can include windbreaks, hedgerows, and the riparian zone along waterways. Organisms, especially animals, can use these corridors to travel between reserves, allowing crucial gene flow.



Minimum population and area:

- Connecting areas for native vegetation helps movement and foraging of native animals, but importantly it helps connect populations so that they remain viable. Any population has a minimum viable population (MVP) to maintain genetic diversity and prevent inbreeding. Connecting smaller populations in isolated areas helps avoid any single population falling below the MVP.
- A minimum area for foraging and providing territories is also needed (the minimum area requirement (MAR). This varies in size from species to species. The MAR can be calculated from the MVP and individual's area requirement (IAR):

$$MAR_{mammals} = MVP \times IAR$$

Species	Food	MVP estimate	Body mass (g)	IAR (km^2)
Greater glider	Herbivore	39	1300	0.012
Mahogany glider	Omnivore	271	350	0.014
Leadbeater's possum	Omnivore	537	180	0.008
Brushtail possum	Herbivore	780	1450	0.013
Yellow bellied glider	Omnivore	3214	570	0.020
Koala	Herbivore	3660	5000	0.033

1. What is the importance of green corridors in species conservation? _____

_____

_____

_____

_____

2. How are MAR and MVP linked? _____

_____

_____

3. (a) Use the data in the table to calculate the MAR for the koala: _____

(b) Use the data in the table to calculate the MAR for the brushtail possum: _____

(c) Use the data in the table to calculate the MAR for the yellow bellied glider: _____

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195 Did You Get It?

1. Test your vocabulary by matching each term to its correct definition, as identified by its preceding letter code.

(i) allopatric speciation ☐

(ii) convergent evolution ☐

(iii) divergent evolution ☐

(iv) punctuated equilibrium ☐

(v) reproductive isolation ☐

(vi) sympatric speciation ☐

A The situation in which members of a group of organisms breed with each other but not with members of other such groups.

B A model for the evolution of lineages in which long periods of stasis are interrupted by brief periods of rapid speciation.

C Evolution in unrelated species occupying similar niches that causes them to arrive at similar structural, physiological, and behavioural adaptations.

D Speciation as a result of reproductive isolation without any physical separation of the populations, i.e. populations remain within the same range.

E The division of one species into two or more separate species.

F Speciation in which the populations are physically separated.

2. In the following examples, classify the reproductive isolating mechanism as either prezygotic or postzygotic and describe the mechanisms by which the isolation is achieved (e.g. morphological isolation, hybrid sterility etc.):

(a) Some different cotton species can produce fertile hybrids, but breakdown of the hybrid occurs in the next generation when the offspring of the hybrid die in their seeds or grow into defective plants:

Prezygotic / postzygotic: _____ Mechanism of isolation: _____

(b) Many plants have unique arrangements of their floral parts that stops transfer of pollen between plants:

Prezygotic / postzygotic: _____ Mechanism of isolation: _____

(c) Two skunk species do not mate despite having habitats that overlap because they mate at different times of the year:

Prezygotic / postzygotic: _____ Mechanism of isolation: _____

(d) Several species of the frog genus *Rana* live in the same regions and habitats, where they may occasionally hybridise. The hybrids generally do not complete development, and those that do are weak and do not survive long:

Prezygotic / postzygotic: _____ Mechanism of isolation: _____

3. Consider the diagram (right) showing the evolution of a hypothetical fish species, A, over time. Does the appearance of new species over time resemble phyletic gradualism or punctuated equilibrium? Explain:

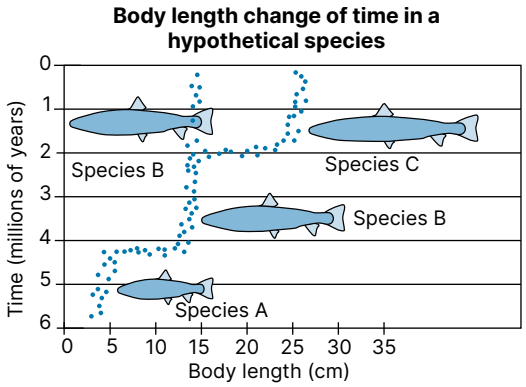
_____

_____

_____

_____

_____



4. The two plants shown right are unrelated. The left hand image shows a cactus from North America, while the right hand image shows a Euphorbia from Africa. Both these plants live in deserts.

(a) Identify the pattern of evolution displayed by these plants:

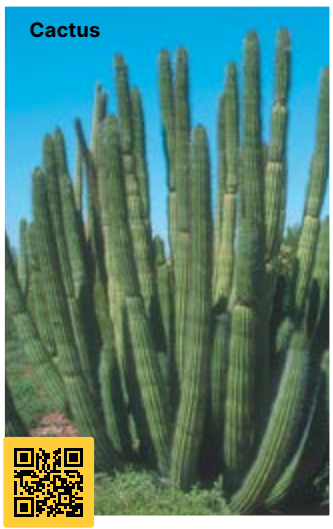
_____

_____

(b) Describe the environments associated with the adaptations.

_____

_____



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196 Synoptic Questions: Unit 4, Topic 2

1. The endemic Hawaiian silverswords form a diverse clade of around 30 distinct species derived from a single ancestor 5.2 ± 0.8 million years ago. The species are phenotypically very different and occupy different niches. Describe the pattern of their evolution and justify your answer:

Geographical isolation as a result of geologic changes has resulted in **adaptive radiation** of cichlid fish species in the rift lakes of East Africa, which is the centre of cichlid diversity. The radiation originated in Lake Tanganyika, where seven lineages diversified to occupy all available freshwater fish niches. Radiations in Lakes Victoria and Malawi began with a single Tanganyikan lineage and diversified in a similar way to occupy the available niches. Within each lake, equivalent ecotypes occupy the same niche and show similar morphology, colouration, and reproductive strategies. Both species pictured right are browsers of benthic algae.

Similarly, in the diverse family of rove beetles, the phenomenon of social parasitism has evolved independently in at least 12 geographically isolated lineages. These beetles mimic different species of army ants in body shape, behaviour, and pheromone chemistry, tricking the ants into accepting the beetles into the colony, where they then consume the ant young.

Rove beetles: Isolated images show the usual morphology of a generalised free living species (left) next to army ant mimics. Photo shows a rove beetle mimic and its host ant.

2 Use the information above and what you have learned during this chapter to explain adaptive radiation and the occurrence of similar life histories, morphologies, and behaviours in geographically separated taxa:

3. The colour of the exoskeleton of a population of bugs is controlled by a single gene with the alleles B (black) and b (brown). The B allele has a frequency of 0.72 in the population. The beetles and their predators are active at night.

(a) What is the frequency of the b allele? _____

(b) Suggest why the frequency of the B allele is much higher than the b allele in the population:

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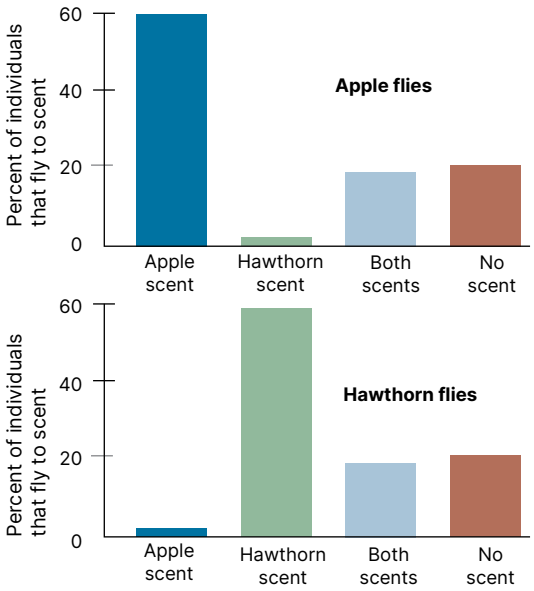
4. Apple maggot flies are native to North America. They infest the fruit of apple trees, laying eggs in the fruit, which develop into maggots that burrow into and eat the fruit. However, apple trees are not native to North America and were introduced less than 300 years ago. The apple maggot fly is also known to infest hawthorn fruit, which is native to North America.

   Some apple maggot flies prefer the scent of apple fruit, while other prefer the scent of hawthorn fruit. This is shown in the graphs right.

   It appears that flies that develop from maggots infesting hawthorns prefer to mate and lay eggs on hawthorns (hawthorn flies). Flies that develop from maggots that infest apples prefer to mate and lay eggs on apples (apple flies). Only 6% of matings take place between flies from different fruits.



   (a) What plant did the apple maggot fly infest before apple trees were introduced to North America?

   _____

   (b) What kind of natural selection is occurring in the apple maggot fly?

   _____

   (c) Explain the mechanisms that are causing this selection to occur: _____

   _____

   _____

   _____

   _____

5. (a) Describe the features of stabilising selection:_____

   _____

   _____

   (b) Using an example, explain what might cause selection to shift from stabilising to directional: _____

   _____

   _____

   _____

   _____

6. The Moreton Bay fig (*Ficus macrophylla*) has an obligate mutualism with the fig wasp *Pleistodontes froggatti*. The fig wasp has an extraordinarily complex life cycle and can only reproduce in fig flowers. The fig is only pollinated by the wasp. Other fig species have similar mutualisms with their own fig wasp species. Describe the evolutionary pattern that has occurred to result in this obligate mutualism and explain how it could have arisen:

   _____

   _____

   _____

   _____

   _____

   _____

   _____

   _____

   _____


Moreton Bay fig (Australian banyan)

Forest and Kim Starr cc 3.0


Pleistodontes froggatti

Sue Thorpe

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Chapter 16 Internal Assessment 3

Guidance on Research Investigation

Resource Hub
bit.ly/3GYTW91

Key Concepts

- Claims or supposed statements of fact need to be critically evaluated using research questions, credible evidence, and scientific reasoning to form justified conclusions and communicate findings effectively.
- Claims should be communicated with clear and accurate information.

Choosing a claim to evaluate

Activity Number

The purpose of this chapter is to provide you with some guidelines for your research and response. These will help you to find and recognise credible sources of information and critically evaluate that information in the context of your research question.

For this assessment task, you will be required to gather secondary evidence related to a research question in order to evaluate a claim. You will develop your research question based on a number of possible claims provided by your teacher. These will be in relation to DNA, genes, and the continuity of life, or the continuity of life on Earth. You must obtain evidence from credible sources and you must work as an individual.

☐	1	To complete the assessment, you must: • select a claim to be evaluated • identify the relevant scientific concepts associated with the claim • pose a research question addressing an aspect of the claim • gather scientific evidence to address the research question and evaluate the claim • identify trends, patterns, or relationships in the evidence • analyse the evidence to identify limitations • interpret the evidence to construct justified scientific arguments • interpret the evidence to form a justified conclusion to the research question • discuss the quality of the evidence • evaluate the claim by extrapolating the findings of the research question to the claim • suggest improvements and extensions to the investigation • communicate your response (your findings) in a an appropriate scientific genre.	197
☐	2	Your response can be a written report up to 2000 words. A multimodal presentation should be up to 11 minutes long. Your response must contain • a claim • a research question • a rationale for the investigation • justified scientific arguments using evidence • a conclusion to the research question based on interpretation of the evidence • evaluation of the claim and suggestions of improvements/extensions • a reference list.	197

The nature of evidence

☐	3	Describe and understand the nature of evidence, including the distinction between opinion, anecdote, and evidence, weak and strong evidence, and scientific and non-scientific ideas	197
☐	4	In your research, evaluate the validity, reliability, and authority of data, including acknowledging any possible errors or bias.	197

Communication

Quantitive reasoning is an essential part of inquiry in biology

☐	5	Understand the characteristics of effective science communication. The biological information you present must be accurate, the biological concepts and models must be clearly explained and key terms defined, it must be clear why the findings are important, and the information presented must be appropriate for purpose and audience.	197
☐	6	Make appropriate use of data, models, and theories when organising and explaining biological phenomena and concepts. Understand and outline the limitations of the data and models used.	197

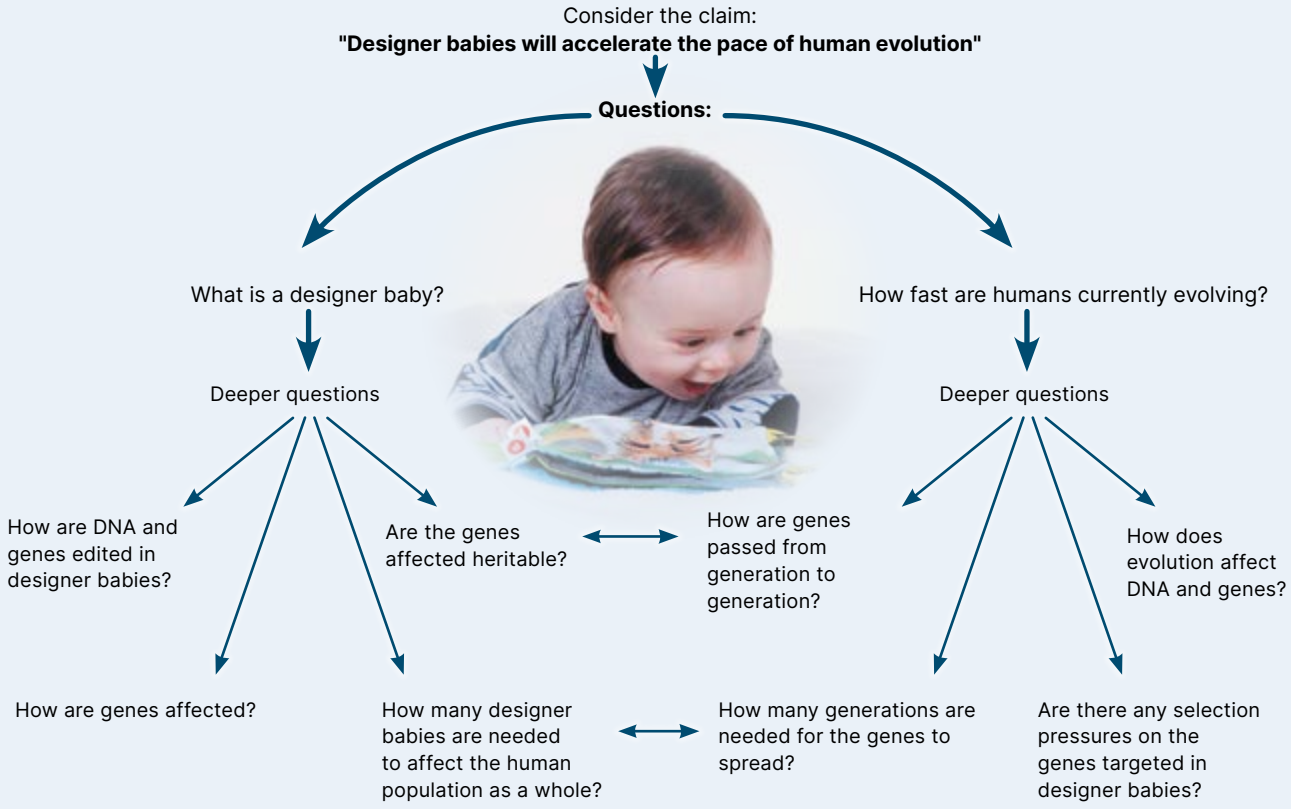
197 IA3: Research Investigation

Key Idea: To evaluate a claim, questions must be asked, research should be done, and the information evaluated to produce a conclusion about the claim.

Research of any kind starts with a claim, hypothesis, or idea. This may be seemingly trivial: e.g. "fans make you feel cooler". Such a claim may seem obvious, but unless you test it you'll never know for sure. Sometimes **evidence** goes against what people claim or "know" to be true. "The Great wall of China can be seen from space" is an often quoted claim. When thinking about that claim, some simple things need to be considered. How wide is the Great Wall of China? At what height will this width become indistinguishable from the background features? Where does space start? What part of space are we taking about? Answering these questions will help evaluate if the claim is correct. Clearly the Great Wall of China can not be seen from the distance of the Moon. At that distance the only features that can be seen are the white, blue, and brown of the clouds, oceans, and continents. What about at the edge of space? What is the smallest feature that can be seen at an altitude of 100 km? Many man-made objects can be seen from 100 km high but these are generally large, such as city suburbs, dams and reservoirs, and large areas of pasture, which are often kilometres across. The Great Wall of China is about 6 metres wide. Using a satellite mapping program such as Google Earth it can be found that something that wide can be seen (with good eyesight) at about 10 km high (about the height a commercial airliner flies). So the Great Wall of China cannot be seen from space, at least not without high powered cameras and telephoto lenses.

The image above is taken from the edge of space, about 100 km. Can you see the Great Wall of China?

Summary internal assessment 3 (IA3) requires you to evaluate a claim. To do this you will need to research and plan, analyse and interpret, conclude and evaluate, and finally communicate your findings. You teacher will provide you with some claims, statements based on DNA, genes, and the continuity of life. The first part of your assessment requires you to develop research questions around the claim.



Next steps

Researching each question will produce a large amount of information and possibly produce new related questions that need to be answered to provide details or supporting information about the claim. An important part of your research is to decide which of these questions are relevant and should be pursued.

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Your evaluation of a claim requires you to investigate biological concepts to produce research questions. In order to do this, you must review a range of information related to your chosen topic. Many scientific processes and ideas can be controversial because they have the potential to affect human social or biological progress. Very quickly, information can be sensationalised or misreported and you must be able to separate relevant facts from hype or propaganda. While evaluating the information, you must use your biological knowledge to evaluate the quality of the information. Some points to consider are presented below.

Finding information

There are many resources that can be used to obtain information about a claim, e.g. journal articles, blogs, news articles, and videos. Most are available on the internet if you use the appropriate wording in your chosen search engine. For example, typing "gene editing" into your search engine will provide some general information on gene editing. Typing "gene editing with CRISPR" will provide information about CRISPR and gene editing. However, because CRISPR is a new and developing technology, there may also be information on the more controversial uses of CRISPR technology.

- Be aware of the site from which you obtain information. Is it reputable or just someone's own website with their own unverifiable ideas? Be cautious with video clips (e.g. YouTube). Again, these may present a personal view with little (or no) basis in fact. Check the comments to see what others have said. Often the comments may point out errors (if any) in the video.
- It is important to verify information about a topic. Information presented on a website should ideally be traced back to its source to see if it is legitimate and has been accurately reported. In doing so you may come across new or more detailed information.
- Journals are peer-reviewed. That is, the information is checked by experts in the topic area of the reported article. This makes the information highly reliable. However, journals are often highly technical and can be difficult to understand, especially for people outside the area of expertise.
- Newspaper articles are a good starting point as a source of generally reliable information but beware of the newspaper's particular leaning. Tabloids often sensationalise stories, while some newspapers may have left or right political leanings which can skew the focus of a story.
- Online sites that are specific for a topic need to be carefully scrutinised for **validity**. Stay away from conspiracy sites as these often dramatise stories and mix them with incorrect science. Government sites often have the most current and reliable **data** based on information from skilled advisers.
- Periodicals or technical magazines, e.g. National Geographic or New Scientist, are useful sources of reliable information. As they are written for the general public, they make understanding the technical information much easier.

Points to consider when evaluating biological information

In order to form an **opinion** about a scientific claim, you must use your biological knowledge to critically evaluate information. Some points to consider include:

- **Validity of the information**
  - The currency of the information. Is it up to date?
  - Is the information peer reviewed?
  - Has the information been accepted by the scientific community?
- **Is the information unbiased?**
  - Is information presented in a fair, unbiased way?
  - Is the information presented clouded by the attitudes, beliefs, or values of the person or group providing the information?
  - Does the information have a political or commercial agenda. Was the supporting research conducted impartially and funded so as not to invite **bias**.
  - The information presented must be based on fact and not emotion.

Keep a log book or portfolio of the information you have reviewed. This can be used by your teacher to verify you have sufficiently researched the topic, and that the work you submit is your own.

Care!

It is important to remember that not all biological information presented to the public is peer reviewed (has been reviewed by experts). Sometimes the information presented may be inaccurate (containing scientific errors) or biased (only one view is presented). It is important to use your own biological knowledge to critically review and analyse information for biological validity.

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Evaluating information analysing information

Balanced reporting provides unbiased information where both the positive and negative aspects are presented without a particular emphasis on either. The reporting of scientific information should always be unbiased and a statement of fact backed by evidence. Unfortunately, a lot of information reported today is highly biased, lacks scientific rigor, or is interpreted incorrectly, resulting in the public being misled about many issues.

- Biological information is presented to the public constantly via print and broadcast media. Some is provided by government organisations, some is compiled and presented by science reporters, and some is provided by individuals or non-governmental organisations with an interest, but not necessarily expertise, in a topic.
- Unlike peer reviewed publications (e.g. journal articles), these sources are not reviewed by experts before being made available to the public. The information presented may be inaccurate (containing scientific errors) or biased (presenting only one view).
- It is important to use your own biological knowledge to critically review and analyse media for biological validity. The decisions made by individuals in a democratic society about biological issues can be heavily dependent on the quality of the information provided. Inaccurate or biased information can lead to poor decision making, whereas accurate information promotes informed debate.

Points to consider when analysing biological information

The following points will help you to critically analyse articles about biological issues and determine whether or not they present a fair, unbiased view, and contain biologically valid information:

- Is there more than one side or view to this issue?
- Are all the views presented?
- Have any compromises been made to reach an outcome?
- What information is presented to the public and is it scientifically correct?
- Is some information more important than other information? If so, how is importance assigned?
- What are the consequences to the public if:
  - the information presented is poor science?
  - the information presented is good science?
  - the information presented is anecdotal (unreliable and based on hearsay?

Student analysis

In order to recognise and validate biological information you have researched, you need to:

- Identify and explain the data presented in the article, report, or paper.
  - Does the information help confirm or explain some aspect of the claim you are researching?
- Recognise whether the information it is accurate or inaccurate. You can determine this by using your own biological knowledge.
- Interpret and discuss the significance of the biological information (e.g. What are the long term effects of gene editing humans?).
  - Does this support or refute the claim being researched?
- Understand that biological validity means the material presented is based on sound biological principles, and the results are logically derived.
- Be able to reference information correctly (by giving the title, publisher or journal, date of publication, and authors).

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Communicating your findings

A report's findings must be communicated in a clear and ordered way. Communicating your findings is as important as the research you have carried out. Poorly presented information cannot be easily understood. Each idea you present must be clearly identified and related to the other information in your report.

Once you have gathered your information and data, use the space on this page to plan your report.

Use bullet points to capture the main points and your ideas. These will provide the scaffold to construct and write your full report or presentation. The list (right) provides key points to think about when planning your report.

Things to think about:

- Who is your report targeting?
- What is the report's main focus (what idea or concept are your trying to explain)?.
- Does your report contain conflicting information (have you said something in one part and said the opposite elsewhere)?
- How are you going to format the report? What tables or graphs are you going to include and what do they show?
- Does the report contain information that is not needed or not obviously related to the main idea? Be concise but precise.
- For written reports, check your spelling and grammar, are key words spelt correctly. Do your sentences make sense? Is your argument presented logically?
- Have you used the correct scientific language?

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Appendix 1

Questioning Terms

The following terms are often used when asking questions in examinations and assessments.

Analyse:	Interpret data to reach stated conclusions.
Annotate:	Add brief notes to a diagram, drawing or graph.
Apply:	Use an idea, equation, principle, theory, or law in a new situation.
Calculate:	Find an answer using mathematical methods. Show the working unless instructed not to.
Compare	Show similarities between two or more items, referring to both (or all) of them throughout.
Construct:	Represent or develop in graphical form.
Contrast:	Show differences. Set in opposition.
Define:	Give the precise meaning of a word or phrase as concisely as possible.
Derive:	Manipulate a mathematical equation to give a new equation or result.
Describe:	Define, name, draw annotated diagrams, give characteristics of, or an account of.
Design:	Produce a plan, object, simulation or model.
Determine:	Find the only possible answer.
Discuss:	Show understanding by linking ideas. Where necessary, justify, relate, evaluate, compare and contrast, or analyse.
Distinguish:	Give the difference(s) between two or more items.
Draw:	Represent by means of pencil lines. Add labels unless told not to do so.
Estimate:	Find an approximate value for an unknown quantity, based on the information provided and application of scientific knowledge.
Evaluate:	Assess the implications and limitations.
Explain:	Provide a reason as to how or why something occurs.
Identify:	Find an answer from a number of possibilities.
Illustrate:	Give concrete examples. Explain clearly by using comparisons or examples.
Interpret:	Comment upon, give examples, describe relationships. Describe, then evaluate.
List:	Give a sequence of answers with no elaboration.
Outline:	Give a brief account or summary. Include essential information only.
Predict:	Give an expected result.
Solve:	Obtain an answer using numerical methods.
State:	Give a specific name, value, or other answer. No supporting argument or calculation is necessary.
Suggest:	Propose a hypothesis or other possible explanation.
Summarise:	Give a brief, condensed account. Include conclusions and avoid unnecessary details.

Birth weight data for Activity 173

The birth weights for 100 babies are displayed below.

3.740	3.510
3.830	3.230
3.530	3.570
3.095	3.620
3.630	3.260
1.560	3.315
3.910	3.230
4.180	3.790
3.570	2.620
2.660	3.030
3.150	3.350
3.400	3.970
3.380	3.915
2.660	2.040
3.375	4.050
3.840	3.105
3.630	3.790
3.810	3.060
2.640	2.770
3.955	3.400
2.980	1.950
3.350	3.800
3.780	2.390
3.260	2.860
4.510	4.110
3.800	1.970
4.170	3.800
4.400	4.490
3.770	2.640
3.400	3.550
3.825	4.050
3.130	4.220
3.400	2.860
3.260	4.060
4.100	3.740
3.220	4.082
3.135	3.000
3.090	3.230
3.830	2.800
3.970	4.050
3.840	4.300
4.710	3.030
4.050	3.160
4.560	3.300
3.350	2.350
3.380	3.970
3.690	2.980
1.495	3.550
3.260	3.070
3.430	2.715

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Appendix 2: Equipment List

1: Biodiversity

INVESTIGATION 1.1
Determining species diversity

Per student/group:

- ☐ Standard pack of cards (minus the jokers)

INVESTIGATION 1.2
Measuring ecosystem diversity

Per student/group:

- ☐ No specific equipment required.

2: Classification Processes

INVESTIGATION 2.1
Develop a dichotomous key

Per student/group:

- ☐ Leaves of various local plants or photos of local animals.

3: Population Ecology

INVESTIGATION 3.1
Modelling yeast growth

Per student/group:

- ☐ 500 mL beaker
- ☐ 10 g sugar (sucrose)
- ☐ 2.5 g yeast
- ☐ Light microscope
- ☐ Microscope slides
- ☐ Coverslips.

7: DNA Structure and Replication

INVESTIGATION 7.1
Extracting DNA

Per student/group:

- ☐ 5 - 6 strawberries
- ☐ 1 large zip-lock bag
- ☐ 100 mL water
- ☐ 5 mL detergent
- ☐ pinch of salt
- ☐ 1 x filter paper
- ☐ 1 x glass filter funnel
- ☐ 1 × 250 mL glass beaker
- ☐ 1 x glass rod
- ☐ ~100 mL ethanol (for rinsing)
- ☐ 2 x centrifuge tubes
- ☐ Centrifuge

INVESTIGATION 7.2
Creating a model of a DNA molecule

Per student/group:

- ☐ Scissors
- ☐ Tape or paste

8: Cell Replication and Variation

INVESTIGATION 8.1
Modelling meiosis using ice-block sticks

Per student/group:

- ☐ 16 x ice block sticks
- ☐ Sticky dots
- ☐ Marker pen

11: Gene Expression

INVESTIGATION 11.1
Measuring continuous variation

Per student/group:

- ☐ Measuring tape or scales
- ☐ Graph paper

14: Natural Selection and Microselection

INVESTIGATION 14.1
Investigating natural selection

Per student/group:

- ☐ Computer
- ☐ Spreadsheet application (e.g. Excel)

INVESTIGATION 14.2
Modelling genetic drift

Per student/group:

- ☐ Computer
- ☐ Spreadsheet application (e.g. Excel)

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Appendix 3: Glossary

A

abiotic factor
Non-living, physical features in an ecosystem, including temperature, humidity, and rainfall.

abundance
The number of individuals of a species.

adaptation
A genetically determined characteristic that improves an organism's ability to survive and reproduce under prevailing environmental conditions.

adaptative radiation
Diversification from an ancestral species into many species occupying many different niches.

adenine
One of the nucleobases in nucleic acids. Pairs with thymine in DNA and uracil in RNA.

allele
Any of the alternative versions of a gene that may produce distinguishable phenotypes.

allele frequency
The incidence of a particular allele relative to all the alleles of a specific gene.

allopatric speciation
Speciation that occurs when biological populations become geographically isolated.

amino acid
Organic molecule that contains an amino group, carboxylate group, and an R group based on a central C atom. Amino acids are the building blocks of proteins. Twenty amino acids appear in the genetic code.

anaphase I
In the first stage of meiosis (meiosis I), replicated homologous chromosomes move to opposite poles of the cell.

anaphase II
In the second stage of meiosis (meiosis II), replicated chromotids are separated and move to opposite poles of the cell.

aneuploidy
A chromosomal aberration in which one or more chromosomes are present in extra copies or are deficient in number.

annealing
The process of joining two pieces of denatured DNA.

analogous structure
A structure present in unrelated species that also has an unrelated mode of origin but carries out the same task, e.g. vertebrate and squid eyes.

anticodon
A sequence of three adjacent nucleotides in tRNA that binds to a corresponding codon in mRNA during protein synthesis (cf. codon).

anti-parallel
Parallel but aligned and running in opposite directions.

autotroph
see producer.

B

base pair rule
The base pairing rule dictates how bases pair up in the DNA double helix: A pairs with T and C pairs with G.

binomial nomenclature
The two part (genus + species) scientific system used to identify organisms.

biodiversity
The amount of biological variation present in a region (includes genetic, species, and habitat diversity).

bioinformatics
A subdiscipline of biology and computer science that is concerned with the acquisition, storage, and analysis of biological data.

biological species
The two part (genus + species) scientific system used to identify organisms.

biomass
The organic material found in living organisms, e.g. wood, crops, animal waste.

biosphere
A combination of all parts of the Earth that support life, from the depth of the ocean to a few km into the atmosphere. Also called the ecosphere.

biotic factor
Relating to the living factors in an ecosystem, including distribution and abundance.

birth rate
Number of individuals born per unit time. Usually given as live births per thousand of population per year.

C

carbon cycle
The process by which carbon is exchanged between living organisms, the Earth and its atmosphere.

carcinogenic
Producing or tending to produce cancer (by a substance, virus, energetic particle etc).

carrying capacity
The maximum number of organisms that can be sustained by a specific environment.

cellular respiration
The series of metabolic reactions that oxidize organic molecules to produce ATP.

chromosome
A cellular structure consisting of one DNA molecule and associated protein molecules.

chromosome mutations
Mutation in which large parts of the chromosome may be deleted, inverted, translocated or duplicated.

clade
A group of organisms all descended from the same common evolutionary ancestor.

cladogram
A phylogenetic tree constructed using cladistic techniques.

classification
The placing of objects or living organisms into groups based on their shared characteristics. In living organisms, this is presumed to show their shared evolutionary relationships.

climax community
A community that has reached an equilibrium with the environment and no longer appears to be changing in composition.

coding strand
The strand of a DNA molecule with the same nucleotide sequence as the mRNA.

codominance
A phenomenon in which two alleles are expressed equally within an organism.

codon
A sequence of three adjacent nucleotides in a DNA or mRNA sequence that is part of the genetic code (cf. anticodon).

coevolution
Evolution that occurs among interdependent species as a result of specific interactions.

comparative genomics
A branch of biology comparing the genomes of different species to establish evolutionary relationships.

competition
Any interaction that is mutually detrimental to both participants, occurring between species that share limited resources.

competitive exclusion principle
The principle that two species with identical niches cannot coexist indefinitely.

complementary base pairing
The pairing of adenine with thymine and cytosine with guanine in the DNA molecule.

consumer (heterotroph)
An organism that feeds on producers, other consumers, or non-living organic material.

convergent evolution
The independent evolution of similar traits or features in unrelated species.

CRISPR-Cas9
A prokaryotic gene sequence used as a tool in the editing of genomes.

cross (genetic cross)
The purposeful mating of two individuals resulting in the combination of genetic material in the offspring.

crossing over
The reciprocal exchange of genetic material between non-sister chromatids during prophase 1 of meiosis.

cytosine
One of the nucleobases in nucleic acids. Pairs with guanine.

D

data logger
Electronic device that records data (e.g. temperature, rainfall, etc.) over time.

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death rate
Number of individual deaths per unit time. Usually given as deaths per thousand of population per year.

degeneracy
A feature of the code whereby several codons code for a single amino acid. This feature creates redundancy.

density
The number of individuals per unit area or volume.

density dependent factor
A factor that affects a population's size, (birth and death rate) and is related to number of individuals per unit area. Includes competition for resources, predation, etc.

density independent factor
A factor that affects population size but acts in the same way regardless of population density, e.g. natural disasters.

dichotomous key
A tool for identifying organisms in which successive choices are made between two features.

directional selection
A mode of natural selection in which an extreme phenotype is favoured over others, causing the allele frequency of a population to shift towards that phenotype.

distribution
The spatial arrangement of organisms.

disruptive selection
A natural selection mechanism in which extreme values for a trait are favoured, creating trait variance that drives divergence.

divergent evolution
The accumulation of differences between closely related populations within a species, leading to the formation of new species.

diversity index
A quantitative measure of the biological diversity (e.g. the number of species) in a given area.

deoxyribose
A monosaccharide pentose ring, similar to ribose, in which a hydroxyl group has been replaced with a hydrogen. It makes up part of the nucleotides found in DNA.

diploid
Having paired sets of chromosomes, one from each parent, in a cell or cell nucleus.

DNA
A large molecule composed of two polynucleotide chains carrying the genetic code and enabling cells to function.

DNA amplification
The production of multiple copies of a sequence of DNA.

DNA helicase
An enzyme that unwinds the DNA helix, separating it into two strands, allowing replication.

DNA ligase
Enzyme that joins DNA fragments toegether into a large molecule.

DNA polymerase
An enzyme that catalyses DNA synthesis from nucleoside triphosphates.

DNA profiling
The process of determining an individual's DNA characteristics.

DNA replication
The process by which DNA is copied to produce an identical version.

DNA sequencing
A technique used to determine the base sequence (As, Ts, Cs, and Gs) in a DNA molecule.

dominant
Relationship in which one animal has priority or seniority over another within a social group.

E

ecoregion
Areas that have similar climate, geology and soils, containing similar natural communities.

ecological niche
The relationship of a species with all the biotic and abiotic factors affecting it. A species' functional role in an ecosystem.

ecological pyramid
A graphical representation of the relationship between different organisms in an ecosystem, and their trophic levels.

ecological succession
The process by which the structure of a biological community evolves over time. May be primary or secondary.

ecosystem
All the organisms in a given area as well as the abiotic factors with which they interact.

emigration
The leaving of a place or country of residence to permanently settle elsewhere.

environmental gradient
The gradual change in the characteristics of an environment from one region to another.

epigenetics
The study of heritable phenotypic changes that do not involve alterations in the DNA sequence.

eukaryote
Organism whose bodies are made up of eukaryotic cells, such as plants, animals, protists, and fungi.

evolution
The change in the heritable characteristics of populations over successive generations.

evolutionary radiation
A increase in the taxonomic diversity (rapid speciation) caused by the appearance of many new niches.

exon
A protein coding region of a gene.

exponential growth
A pattern of population growth where the growth rate is proportional to the size of the population itself. (cf. logistic growth).

extinction
The dying out or extermination of a species.

F

fertilisation
The union of haploid gametes to produce a diploid zygote, initiating the development of a new organism.

flagship species
A species that represents a conservation cause, habitat or campaign, acting as an ambassador for that cause.

food chain
A model that is used to demonstrate the feeding relationships between organisms in an ecosystem.

food web
The combination of all the food chains in a particular ecosystem.

founder effect
The loss of genetic variation that occurs when a new population is established by a very small number of individuals.

forensics
The analysis of body fluids, stains and other bodily materials to help solve a crime.

fossil record
The history of life as documented by fossils.

frameshift
A mutation involving the insertion or deletion of a nucleotide(s) in which the number of nucleotides in not divisible by three, causing the triplet code to shift out of sequence.

G

gamete
A mature sexual reproductive cell, as a sperm or egg, that unites with another cell to form a new organism.

gel electrophoresis
The separation and analysis of protein molecules of varying sizes by moving them through a block of gel using an electric field.

gene
A unit of hereditary information consisting of a specific nucleotide sequence in DNA.

gene expression
The transcription and translation of a gene.

gene flow
The exchange of alleles between two or more populations.

gene modification
The process of making changes to an organism's genes, e.g. to give it new traits.

gene pool
The collective genetic information within a population of interbreeding organisms.

gene mutation
A small, localised change in the DNA sequence of a gene that includes point mutations and changes to a triplet.

genetic code
The set of rules used by living cells to translate information encoded in genetic material into proteins.

genetic drift
The random changes in allele frequency in a population over generations.

genetic equilibrium
Allele frequencies in a population that are static, or unchanging, over time.

genome
The genetic material of an organism, and all the heritable traits encoded in its DNA.

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genotype
The genetic makeup of an organism.

genotypic change
Variation in the DNA sequence of a gene.

GMO
Any organism whose genetic material has been altered using genetic engineering.

gross primary production
The total amount of carbon compounds produced by plants in an ecosystem in a given amount of time. e.g. carbon per square metre per year (C m^{-2} yr^{-1}).

guanine
One of the nucleobases in nucleic acids. Pairs with cytosine.

H

haploid
Having a single set of each chromosome in a cell or cell nucleus, e.g. as in gametes.

herbivore
An animal that feeds exclusively on plant material. A primary consumer.

heterotroph
(see consumer)

heterozygous
Having two different alleles for any hereditary characteristic.

histone
A small basic protein found in the nucleus of eukaryotic cells that organises DNA strands to form chromatin.

homologous pair
Pairs of chromosomes, one inherited from each parent, with the same genes in the same order along their chromosomal arms.

homology
Similarity between two different species of organisms due to shared ancestry.

homozygous
Where both chromosomes possess identical alleles for a gene at a specific locus.

hydrologic cycle
Also known as the water cycle. Describes that way in which water circulates between the earth and its atmosphere.

I-J

immigration
The arrival in a new place or country to permanently live after leaving another country or place.

incomplete dominance
A gene interaction in which both alleles of a gene at a locus are partially expressed, resulting in an intermediate phenotype.

independent assortment
With reference to inheritance, describing how alleles for separate traits are passed to the gametes independently of one another..

interphase
The period in the cell cycle when the cell is not dividing, which accounts for about 90% of the cell cycle. During interphase, cellular metabolic activity is high and cell size may increase.

interspecific competition
Competition for resources between different species.

intron
A segment of DNA that does not code for a protein and is removed before translation.

K

K-selected
A reproductive strategy in which species produce fewer offspring but invest more energy in parental care. They are usually long lived and highly adapted to their (stable) environment.

karyogram
A photograph of the chromosomes of a cell, arranged in homologous pairs and in a numbered sequence.

karyotyping
Investigation of the chromosomal characteristics of an individual or species.

keystone species
A species that occupies an essential role in an ecosystem and on which most or all of the other species in an ecosystem depend, directly or indirectly.

L

limiting factor
Factor or environmental condition that limits the abundance and distribution of an organism.

Lincoln index
A statistical measure of a population's size based on mark, release, and recapture of members of the population.

Linnean classification
A system of hierarchical classification developed by Carl Linnaeus in which living organisms are grouped by their physical similarities into kingdoms (the least specific), phylums, classes, orders, families, genus, and species (the most specific).

locus
A specific place along the length of a chromosome where a given gene is located.

logistic growth
A pattern of population growth that follows a sigmoidal curve in which growth rate declines as the population nears carrying capacity (cf. exponential growth).

M

macroevolution
Large-scale evolution involving the formation of new species and higher taxa.

marker gene
A length of DNA with a known location on a chromosome. It is not necessarily the gene of interest itself, but it is linked to and inherited with the gene of interest.

mass extinction
The extinction of a large number of species within a relatively short period of global time.

meiosis
The process of double nuclear division in sexually reproducing organisms, which results in cells with half the original number of chromosomes (haploid).

metaphase I
The first stage of meiosis (meiosis I), in which pairs of homologous chromosomes line up along the cell's equator.

metaphase II
The second stage of meiosis (meiosis II) in which chromosomes line up along the cell's equator 90° to that of metaphase I.

microclimate
A localised set of atmospheric conditions that differ from the wider surrounding ecosystem climate.

microevolutionary processes
Processes that change allele frequencies in a population over time; includes natural selection and genetic drift.

microhabitat
A small, localised habitat with its own specific conditions surrounded by a wider habitat.

mitosis
The phase of the cell cycle resulting in nuclear division.

mortality
The death rate: the ratio of total number of deaths to the total population.
The ratio of deaths in an area to the population of that area, expressed per 1000 per year.

multiple alleles
The existence of more than two alleles for a gene in the population.

multiple genes (polygenes)
When many genes contribute to a single phenotype (synonym, polygenes).

mutagen
Anything that causes a mutation in the DNA code, including chemicals, and UV radiation.

mutagenic
A substance or agent that has the ability to cause mutations (changes to DNA).

mutation
A change in the nucleotide sequence of an organism's DNA (or RNA).

N

natality
Production of new individuals in a population.

natural selection
The differential survival and reproduction of favourable phenotypes.

net primary production
The rate of energy storage as organic matter after respiration.

nitrogen cycle
The processes by which nitrogen, in different forms, is cycled between living and non-living things in marine, terrestrial and atmospheric ecosystems.

non-disjunction
The failure of homologous chromosomes or sister chromatids to separate properly during cell division.

nucleotide
An organic molecule that is the building block of DNA and RNA. Consists of a sugar molecule (ribose in RNA or deoxyribose in DNA) attached to a phosphate group and a nitrogen-containing base.

nucleic acid
A polymer (poly-nucleotide) consisting of many nucleotide monomers; serves as a blueprint for proteins and, through the actions of proteins, for all cellular activities. The two types are DNA and

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RNA.

nucleus
The organelle of a eukaryotic cell that contains the genetic material in the form of chromosomes, made up of chromatin.

O

omnivore
Animal that eats both plant and animal material. Humans are omnivores.

oogenesis
The process in the female reproductive system in which the primary oocyte matures in the ovum.

P

parallel evolution
Evolution in which the morphologies of closely related lineages change together in a similar fashion. Difficult to distinguish from convergence in practice, but the key is that the lineages should be closely related.

parapatric speciation
Speciation that occurs when two populations evolve reproductive isolation from each while continuing to exchange genes and not being geographically isolated.

pedigree chart
A diagram of a family tree, with conventional symbols, showing the occurrence of heritable characters in parents and offspring over multiple generations.

percentage cover
The percentage of a quadrat or area that is covered by one species.

percentage frequency
A measure of the number of times a plant species is present within a given number of samples.

phenotype
The observable physical and physiological traits of an organism, which are determined by its genetic makeup, environment and epigenetic factors.

phenotypic variation
The variation in phenotype (structural, behavioural, and physiological characteristics) which can be acted upon by environmental pressures.

photosynthesis
A process used by green plants, algae, and some bacteria to convert light energy into chemical energy (carbohydrate).

phyletic gradualism
Evolutionary model proposing that species arise through the gradual and continuous transformation of populations (cf. punctuated equilibrium).

phylogenetics
The study of evolutionary relationships based on their genetic similarities and differences.

phylogenetic classification
System of classification based on evolutionary history, focusing on the production of clades rather than hierarchical ranks.

phylogenetic species
The smallest group of organisms that share an ancestor and can be distinguished from other groups (using DNA , morphologies, etc).

phylogeny
The evolutionary history of a taxon.

phylogram
A phylogenetic tree in which the branch lengths represent time or amount of character change.

pioneer species
A species that is first to colonize areas of bare ground or soil, usually providing shelter for seedlings or other plants that arrive later.

plasmid
A circular extra-chromosomal segment of DNA capable of self replication.

point mutation
A mutation that affects only one base in the DNA, either added, deleted, or substituted.

polymerase chain reaction (PCR)
An in-vitro technique for rapid synthesis of a given DNA sequence.

polypeptide
A chain of amino acids linked together by peptide bonds.

population
A group of interbreeding organisms of the same species, found in the same geographical area.

population bottleneck
An evolutionary event in which the size of a population is sharply reduced, leading to a loss of genetic diversity.

predator
An organism that captures and kills prey for consumption.

primary succession
Vegetational development starting on a new site never before colonized by life.

primer
A short, single-stranded nucleic acid used by all living organisms to initiate DNA synthesis.

probability
The chance or likelihood that a certain event will occur or that a prediction will be correct.

producer
An organism that produces its own food using materials from inorganic sources (also known as an autotroph).

prokaryote
A unicellular organism consisting of a single prokaryotic cell. Prokaryotes lack membrane-bound organelles and a nucleus.

prophase I
In the first stage of meiosis (meiosis I) the chromosomes condense and the nuclear envelope breaks down. Spindle fibres begin to form.

prophase II
In the second stage of meiosis (meiosis II) nuclear envelopes disappear, chromosomes condense, spindle fibres form.

protein
A biologically functional molecule consisting of one or more polypeptides folded into a specific three-dimensional structure.

punctuated equilibrium
Evolutionary model proposing that evolution occurs primarily through short bursts of speciation followed by periods of stasis.

Punnett square
A diagram used in the study of inheritance to show the predicted genotypic results of random fertilization in genetic crosses between individuals of known genotype.

purine
Two-ringed nucleobase in DNA and RNA.

pyrimidine
Single-ringed nucleobase in DNA and RNA.

Q

quadrat
A frame used to outline a standard unit of area for study.

R

r-selected
A form of selection in non-limiting environments favouring short life spans and high reproductive rates.

recognition site
A specific nucleotide sequence in DNA recognised by restriction enzymes.

recombination
The process by which genes are exchanged between different chromosomes to produce new combinations of alleles.

recombinant DNA
Genetically engineered DNA made by recombining DNA from different organisms.

recombinant plasmid
A circular piece of DNA comprising DNA from two sources.

recessive
A trait or disorder that may be passed from one generation to the next, where two copies of an abnormal gene must be present in order for the trait to be expressed.

redundancy
Term used for the presence of many codons for one animo acid.

regulatory gene
A gene that produces a repressor substance to control the expression of other gene(s).

remote sensing
Detecting and monitoring the characteristics of an ecosystem using reflected and emitted radiation at a distance (e.g. photos and radar).

reproductive isolation
A set of mechanisms and conditions that prevent breeding between different species.

restriction enzyme
An enzyme that can cleave DNA strands at recognition sites.

ribose
A monosaccharide pentose ring that forms parts of a nucleotide found in RNA.

ribosome
A complex of rRNA and protein molecules that function as a site of protein synthesis in the cytoplasm.

RNA
A long (generally) single-stranded nucleic acid, essential in various biological roles

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including gene expression.

S

sample
A sub-set of a whole used to estimate the values that might have been obtained if every individual or response was measured.

saprotroph (=decomposer)
An organism that obtains energy from dead material by extracellular digestion.

satellite tracking
The use of satellites and transmitters to track the movement of animals across their environment.

secondary production
The rate of biomass produced by heterotrophs in a given area.

secondary succession
Development of vegetation after a disturbance e.g. fire or minor land slide (seed bank is retained).

semi-conservative
The normal mechanism of DNA replication, where each strand acts as a template for a new double helix.

sex linked gene
A gene located on the X or Y chromosome; inheritance is linked to the sex chromosomes.

sexual reproduction
A type of reproduction in which offspring are created by combining genetic information from two individuals of different sexes.

Simpson's diversity index
A measure of species diversity that takes into account the number of species present as well as their abundance.

speciation
The formation of new biological species through the process of evolution.

species evenness
A measure of how common or rare species are within an ecosystem.

species richness
A measure of the number of species (the biodiversity) in an ecosystem. It does not take into account the abundance of each species.

spermatogenesis
The process in the male reproductive system by which mature sperm cells are produced when spermatogonia develop into mature sperm cells.

stabilising selection
A mode of natural selection that favours retention of the median phenotype.

structural gene
A gene that encodes the amino acid sequence of a protein.

sympatric speciation
The evolution of a new species from an ancestral species while both continue to inhabit the same geographic region.

T

taxonomy
Branch of science based around the classification of living organisms into hierarchical ranks.

telophase I
In the first stage of meiosis (meiosis I) chromosomes decondense and the nuclear envelope begins to form. Cell splits to form two cells.

telophase II
In the second stage of meiosis (meiosis II) chromosomes decondense, nuclear envelope forms and cells split to form a total of four haploid cells.

template strand
The non-coding strand of a DNA molecule, used as a template for RNA synthesis.

thymine
One of the nucleobases in DNA. Pairs with adenine, and is not a component of RNA.

trait
A specific variant of a phenotype, controlled by one or more genes, e.g. flower colour in plants or tongue rolling ability in humans.

transect
A line placed across a community of organisms, used for sampling, to provide information on their distribution.

transcription
The process of copying a segment of DNA into a strand of mRNA.

transcription factor
A protein that binds to specific DNA sequences, controlling the transcription of genetic information from DNA to mRNA.

transgenic organism
An organism whose genome has been altered by the insertion of a novel gene.

translation
The process of decoding a strand of mRNA to produce a sequence of amino acids.

trophic level
A level or position in a food chain, food web or ecological pyramid. An organism's trophic level is determined by its feeding behaviour.

U

umbrella species
A species selected to represent the wider ecosystem in making conservation decisions because the conservation of the species indirectly protects the wider ecosystem and the species in it.

uracil
One of the nucleobases in RNA. Pairs with adenine, and is not a component of DNA.

V W X Y Z

X-linkage
Sex linkage involving the X chromosome.

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