BIOZONE

# QCE | BIOLOGY
## UNITS 3&4

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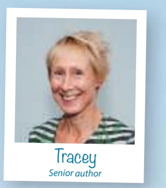
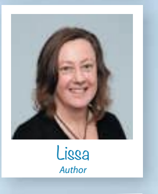
## Meet the Writing Team



**Tracey Greenwood**
I have been writing resources for students since 1993. I have a Ph.D in biology, specialising in lake ecology and I have taught both graduate and undergraduate biology.



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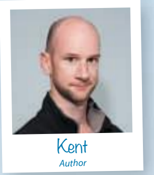

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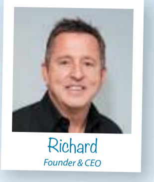
I have a BSc from Massey University majoring in zoology and ecology and taught secondary school biology and chemistry for 9 years before joining BIOZONE as an author in 2009.



**Richard Allan**
I have had 11 years experience teaching senior secondary school biology. I have a Masters degree in biology and founded BIOZONE in the 1980s after developing resources for my own students.

**Thanks to:**
The staff at BIOZONE, including Mike Campbell for design and graphics support, Paolo Curray for IT support, Felix Hicks for illustrations, Anu Chauhan and Allan Young for office handling and logistics, and the BIOZONE sales team.

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## Cover Photograph

The koala (*Phascolarctos cinereus*) is found in coastal regions of Australia's east coast. In Queensland, the koala is listed as vulnerable, meaning it could become endangered unless the circumstances that are threatening its survival and reproduction improve. Climate change, disease, habitat destruction, and habitat fragmentation all contribute to this status.

PHOTO: Eric Isselée
https://stock.adobe.com/nz/images/side-view-of-young-koala-phascolarctos-cinereus-sitting/20948433

**Purchases of this workbook may be made direct from the publisher:**

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### Population Ecology

### Changing Ecosystems

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**CODING**: **Activity** is marked: ☐ to be done ☑ when completed Mandatory practicals in red SHE in orange

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### Cellular Replication and Variation

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**CODING**: **Activity** is marked: ☐ to be done ☑ when completed Mandatory practicals in red SHE in orange

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## TOPIC 2: Continuity of life on Earth

### Evolution

### Natural Selection and Microevolution

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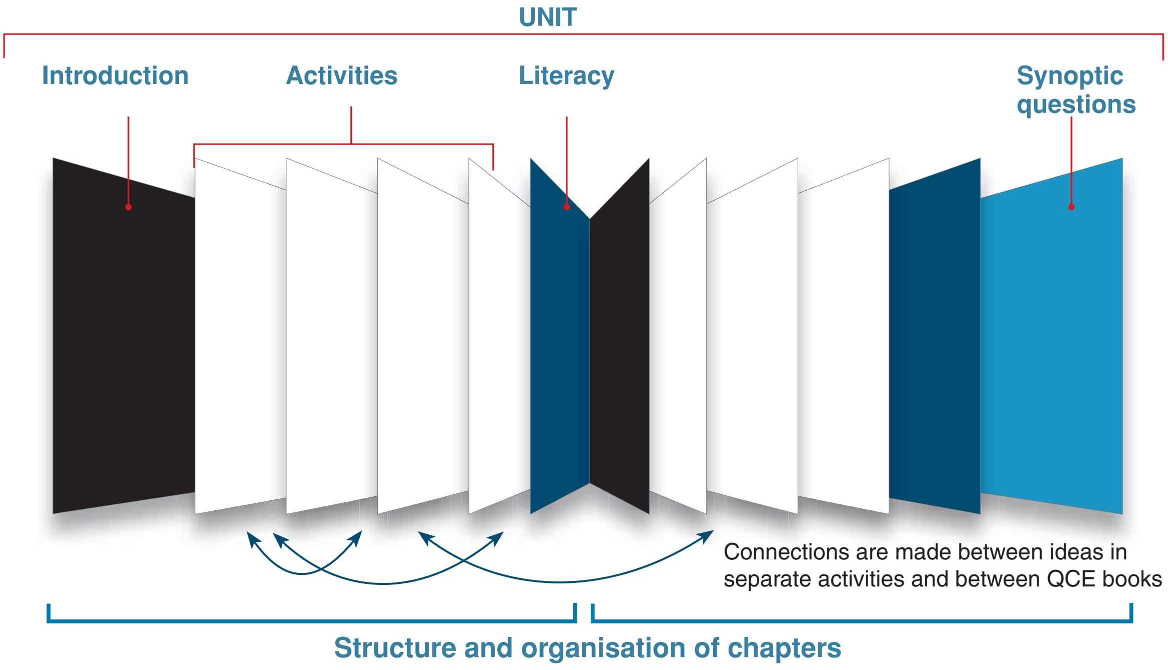
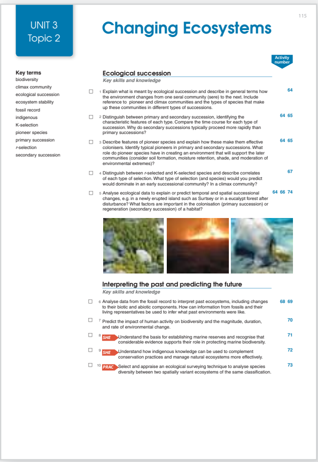
**CODING**: **Activity** is marked: ☐ to be done ☑ when completed Mandatory practicals in red SHE in orange

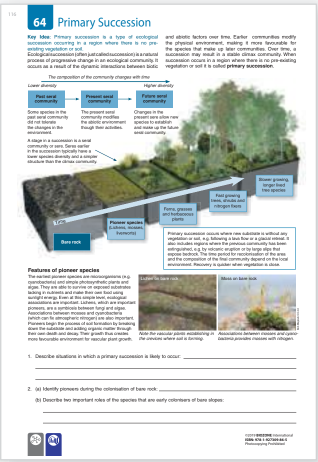
# Using This Book

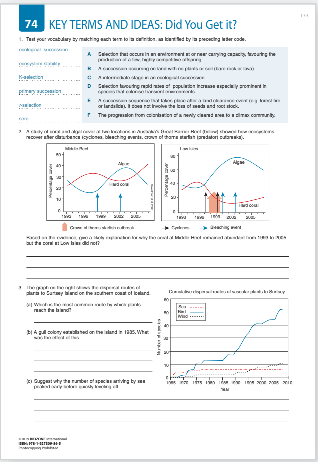
This first edition of Biology for QCE Units 3&4 has been specifically written to meet the content and skills requirements of the Queensland (QCE) Biology general senior syllabus. QCE Biology Units 3&4 consolidates the foundational learning, skills, and knowledge you acquired in QCE Units 1&2 and prepares you for the assessment components of the syllabus. Chapter introductions provide you with a concise guide to the knowledge and skills requirements of each unit of study. A wide range of activities will help you to build on what you already know, explore new topics, work collaboratively, and practise your skills in data handling and analysis. Three chapters specifically addressing the summative internal assessments (IAs) are included. Material for IA1 (data test) is provided and we have provided comprehensive support for your experiment and research investigation. We hope that you find this book valuable and that you make full use of its features.

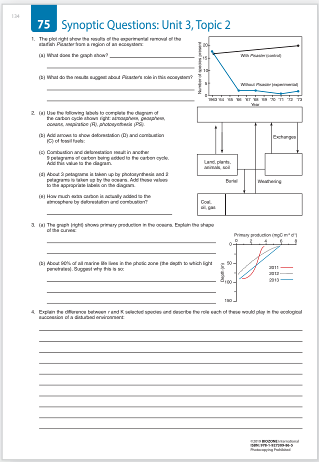
- The outline of the chapter structure below will help you to navigate through the material in each chapter.











### Introduction

- Provides a check list of unit objectives for the chapter.
- Identifies SHEs, mandatory and suggested practicals, and manipulative skills.
- Provides a useful list of important key terms.

### Activities

- The KEY IDEA provides your focus for the activity.
- Annotated diagrams and photographs help you understand the content.
- Questions review the content of the page.

### Key terms and ideas

- All chapters conclude with an activity based on the introductory key terms list and the chapter content.
- These activities test your understanding of biological terms and ideas in the chapter.

### Synoptic questions

- Synoptic questions conclude each topic covered in the book.
- Each unit concludes with a summative assessment (IA1, IA2 in Unit 3 and IA3 in Unit 4).

- The chapter introduction provides you with a summary of the knowledge and skills requirements for the topic, phrased as a set of key skills and knowledge statements.

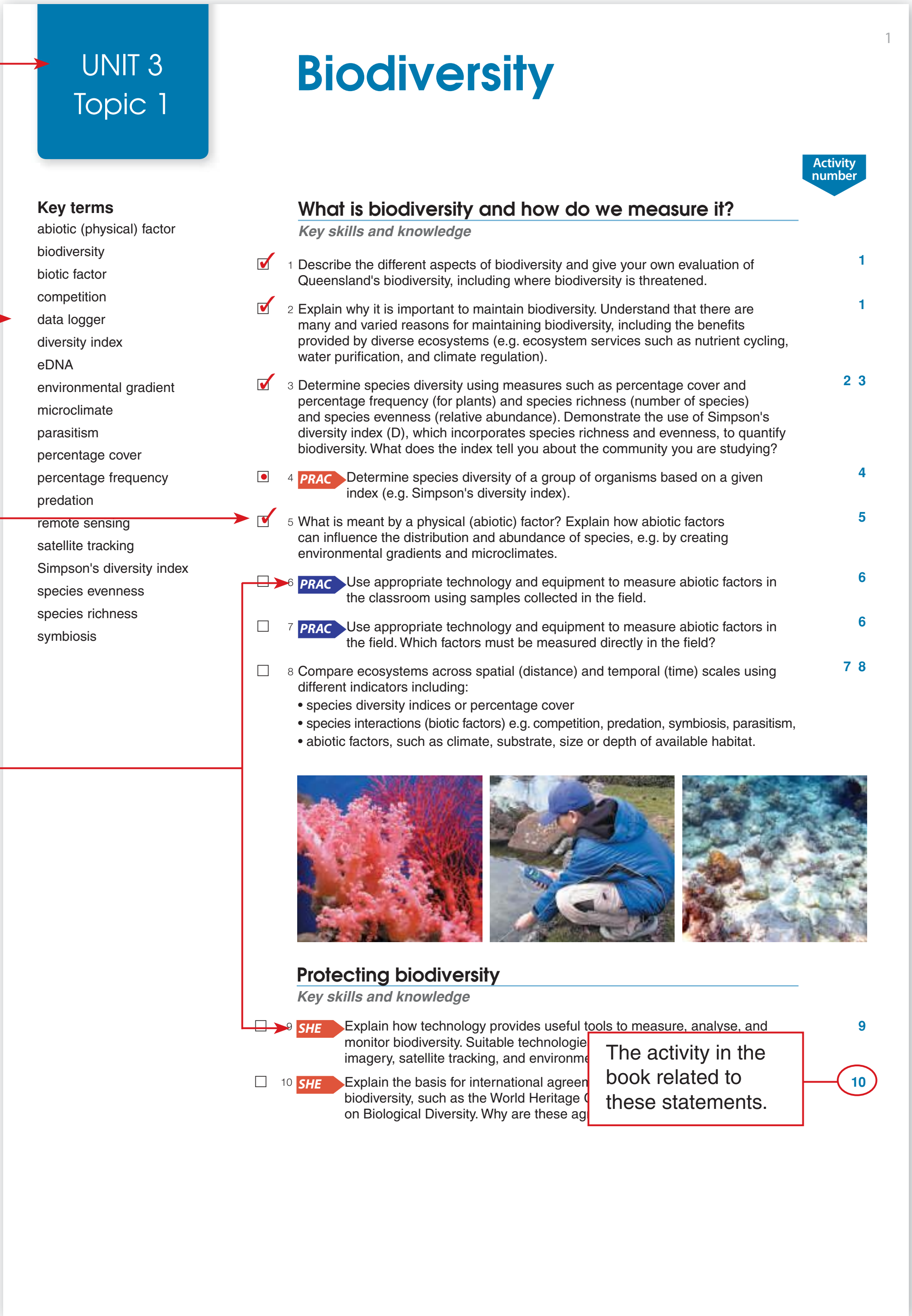
This identifies the unit and topic to which this chapter applies.

A list of key terms for the chapter allows you to construct your own glossary as you work through the activities.

Use the check boxes to identify and mark off the points as you complete them.

Coloured flags identify points related to science as a human endeavour (*SHE*), manipulative skills (*SKILL*), and mandatory (red) and suggested (blue) practicals (*PRAC*)

The activity in the book related to these statements.



UNIT 3
Topic 1

1

# Biodiversity

**Key terms**
abiotic (physical) factor
biodiversity
biotic factor
competition
data logger
diversity index
eDNA
environmental gradient
microclimate
parasitism
percentage cover
percentage frequency
predation
remote sensing
satellite tracking
Simpson's diversity index
species evenness
species richness
symbiosis

Activity number

## What is biodiversity and how do we measure it?

*Key skills and knowledge*

☑ 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. Understand that there are 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 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. What does the index tell you about the community you are studying? 2 3

▣ 4 **PRAC** Determine species diversity of a group of organisms based on a given index (e.g. Simpson's diversity index). 4

☑ 5 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. 5

☐ 6 **PRAC** Use appropriate technology and equipment to measure abiotic factors in the classroom using samples collected in the field. 6

☐ 7 **PRAC** Use appropriate technology and equipment to measure abiotic factors in the field. Which factors must be measured directly in the field? 6

☐ 8 Compare ecosystems across spatial (distance) and temporal (time) scales using different indicators including: 7 8
- species diversity indices or percentage cover
- species interactions (biotic factors) e.g. competition, predation, symbiosis, parasitism,
- abiotic factors, such as climate, substrate, size or depth of available habitat.

## Protecting biodiversity

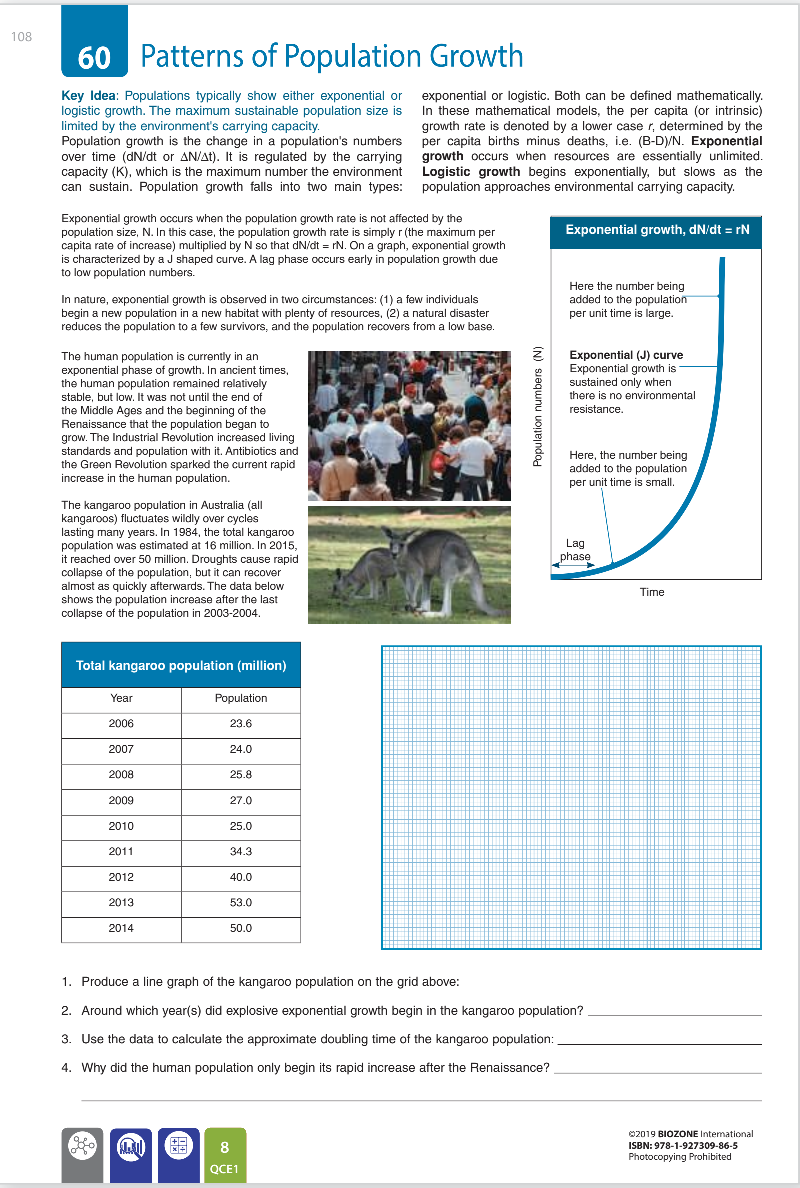
*Key skills and knowledge*

☐ 9 **SHE** Explain how technology provides useful tools to measure, analyse, and monitor biodiversity. Suitable technologie imagery, satellite tracking, and environme 9

☐ 10 **SHE** Explain the basis for international agreen biodiversity, such as the World Heritage C on Biological Diversity. Why are these ag 10

# Using the Tab System

- The tab system is a useful way to identify important parts of the QCE Biology syllabus. These may be suggested or mandatory (required). The tabs also allow you to see at a glance if online support is provided and if there are content links with other activities.



## 60 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.

**Exponential growth, dN/dt = rN**

**Total kangaroo population (million)**

| 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? ___

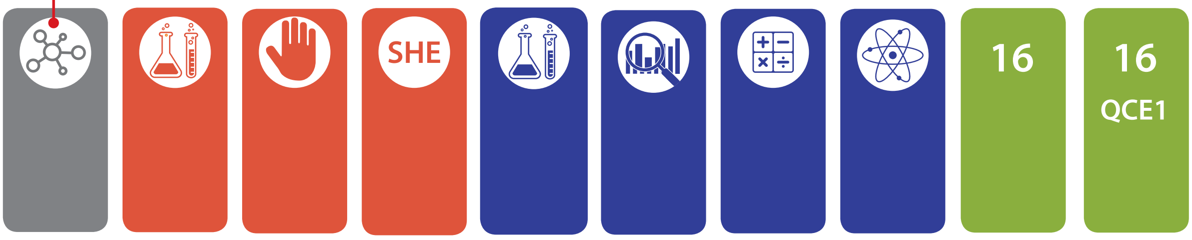
Page tabs show where material addressing science inquiry, practicals, or science as a human endeavour has been incorporated into an activity. They also indicate if there is online support provided and suggest links to activities with related or background content.

### Weblinks

This tab indicates the activity is supported with online content. Bookmark the weblinks page:
www.biozone.com.au/weblink/QCE2-9865
Access the external URL for the activity by clicking the link

### Link

Connections are made between activities in different sections of the syllabus and back to QCE1. These activities may be related conceptually- or they may provide background information.



**Red** tabs indicate that the activity contains the following (L → R):

- Mandatory practical
- Manipulative skill
- Science as a human endeavour

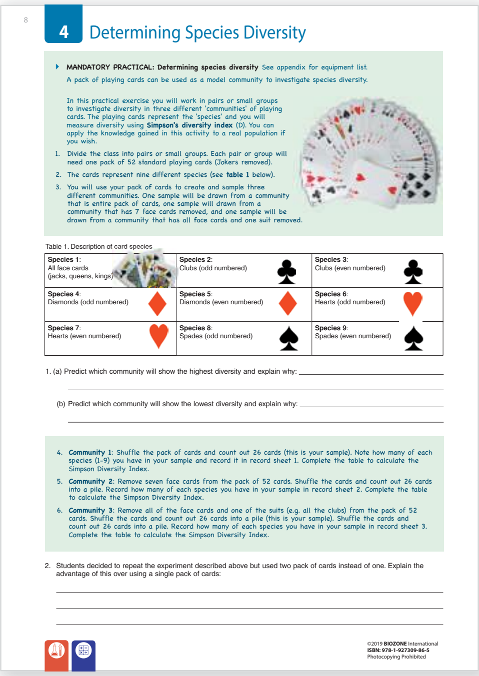
**Blue** tabs indicate the activity contains the following (L → R):

- Suggested practical
- Data analysis and interpretation
- Tasks involving mathematical or numeracy skills
- Modelling

# Practical and Mathematical Skills

## Mandatory and suggested practicals

Practical investigations form an important component of BIOZONE's QCE Biology workbooks. 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. Practical activities fall into two categories, mandatory practicals and suggested practicals (below).



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**4 Determining Species Diversity**

- **MANDATORY PRACTICAL: 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 entire pack of cards, one sample will 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**:<br>All face cards<br>(jacks, queens, kings) | **Species 2**:<br>Clubs (odd numbered) ♣ | **Species 3**:<br>Clubs (even numbered) ♣ |
| **Species 4**:<br>Diamonds (odd numbered) ♦ | **Species 5**:<br>Diamonds (even numbered) ♦ | **Species 6**:<br>Hearts (odd numbered) ♥ |
| **Species 7**:<br>Hearts (even numbered) ♥ | **Species 8**:<br>Spades (odd numbered) ♠ | **Species 9**:<br>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 pack of cards instead of one. Explain the advantage of this over using a single pack of cards:

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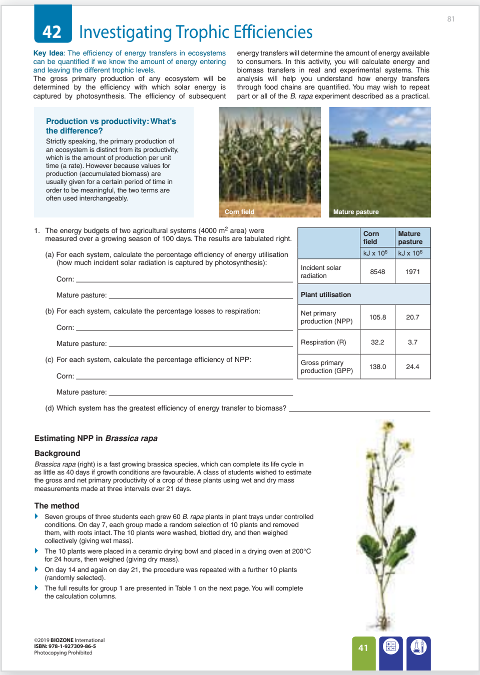

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**42 Investigating Trophic Efficiencies**

**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 analysis 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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### Mandatory practical

Mandatory practicals must be completed to meet the requirements of the QCE Biology general senior syllabus. They are easily identified by the green instruction boxes on the page (above). You will complete the practical activity yourself and, by doing so, meet the learning outcomes associated with the particular mandatory practical.

### Suggested practical

Suggested practicals are optional but provide valuable opportunities for consolidation. BIOZONE's suggested practicals have been designed to provide information and/or data to support the practicals suggested in the syllabus document. They can replace a practical if time is short, or you can adapt the methodology to carry out the practical yourself.

## 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.

1

ALL UNITS
Skills

**Basic Skills for QCE**

**Key terms**
accuracy
bias
chi-squared test
control
controlled variable
dependent variable
estimate
experiment
graph
hypothesis
independent variable
mean
median
model (scientific)
observation
percentage
precision
prediction
proportion
qualitative data
quantitative data
rate
ratio
reliability (of data)
scientific method
significant figures
statistical test
table
trend
variable

Activity number

**Inquiry is the basis of science**

*Key skills and knowledge [points also covered throughout QCE1&2]*

**Inquiry begins with observation**

☐ 1 Describe the role of inquiry-based investigations in science. Show, through your work, your understanding of science as a non-linear process. 1
☐ 2 Use a variety of methods to answer questions you raise as a result of observation. These include field and laboratory-based investigations, simulations and models, and data analysis. 4
☐ 3 Use scientific models to illustrate biological processes and concepts, communicate information, make predictions, and describe systems. 2

**Communication**

*Key skills and knowledge [points also covered throughout QCE1&2]*

**The results of investigations must be communicated to peers to have value**

☐ 4 Demonstrate an ability to communicate the findings of your investigations through oral and written presentations, including lab reports, and through graphs and/or contributions to online resources. 4 11
☐ 5 Use a lab notebook or portfolio to organise your work and provide a record of ideas, methods, results, further questions, and references. 4 11

**Quantitative skills**

*Key skills and knowledge [points also covered throughout QCE1&2]*

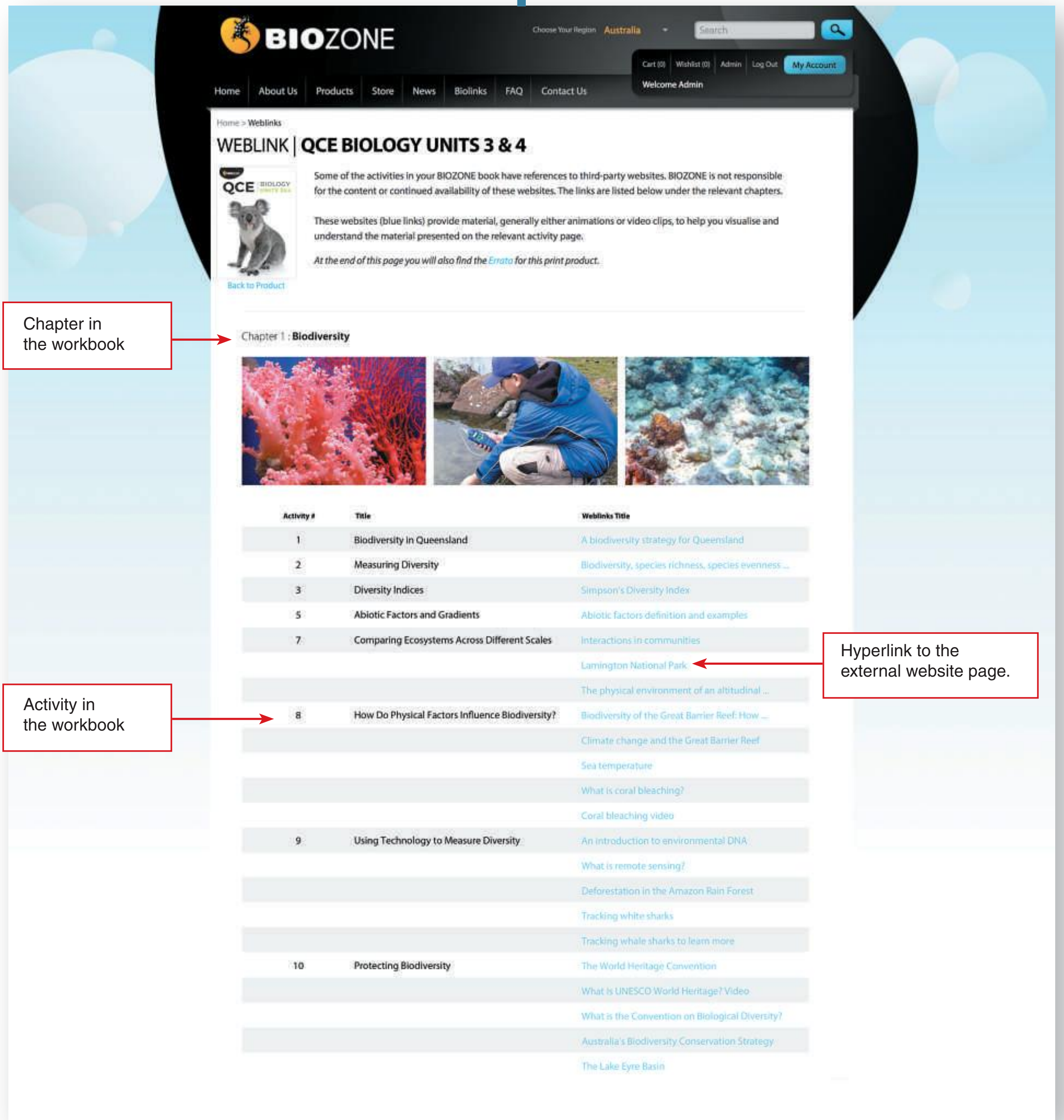
**Quantitative reasoning is an essential part of inquiry in biology**

☐ 6 Demonstrate ability to use basic mathematical skills to collect data. These include making counts and measurements. Distinguish between accuracy and precision (reliability) and understand their importance when collecting quantitative data. 3 4 5
☐ 7 Demonstrate competence in use of ratios and proportions, scientific notation, and significant figures. Use estimation and calculation to analyse data. 6 7
☐ 8 Demonstrate appropriate application of mathematical routines to data, e.g. calculating rates and percentages. Interpret and manipulate mathematical relationships in order to calculate and predict values. 6 7
☐ 9 Use descriptive statistics (e.g. mean and standard deviation) and apply appropriate mathematical tools to analyse data and/or test hypotheses, e.g. linear regression, 95% confidence intervals, and some simple statistical tests such as Student's *t* and chi-squared. 14-21
☐ 10 Use tables or spreadsheets to organise different types of data, including any calculated values (e.g. means and standard deviation). 14-16 19
☐ 11 Construct graphs for different types of data, including logarithmic data and data collected during your investigations. Plot error in calculated values as appropriate (e.g. 95% confidence limits) and understand the value in doing this (in terms of confidence in the data). 11-13 16

# Using BIOZONE's Website

- BIOZONE's Weblinks provides links to online content supporting the activities in the book. From this page, you can also explore BIOZONE's collection of annotated 3D models and check for any errata or clarifications to the book or model answers since printing.
- The external websites are generally narrowly focused animations and video clips relevant to some aspect of the activity on which they are cited. They provide great support to help your understanding.

www.biozone.com.au/weblink/QCE2-9865



WEBLINK | QCE BIOLOGY UNITS 3 & 4

Some of the activities in your BIOZONE book have references to third-party websites. BIOZONE is not responsible for the content or continued availability of these websites. The links are listed below under the relevant chapters.

These websites (blue links) provide material, generally either animations or video clips, to help you visualise and understand the material presented on the relevant activity page.

*At the end of this page you will also find the Errata for this print product.*

Chapter 1 : **Biodiversity**

| Activity # | Title | Weblinks Title |
|---|---|---|
| 1 | Biodiversity in Queensland | A biodiversity strategy for Queensland |
| 2 | Measuring Diversity | Biodiversity, species richness, species evenness ... |
| 3 | Diversity Indices | Simpson's Diversity Index |
| 5 | Abiotic Factors and Gradients | Abiotic factors definition and examples |
| 7 | Comparing Ecosystems Across Different Scales | Interactions in communities |
| | | Lamington National Park |
| | | The physical environment of an altitudinal ... |
| 8 | How Do Physical Factors Influence Biodiversity? | Biodiversity of the Great Barrier Reef: How ... |
| | | Climate change and the Great Barrier Reef |
| | | Sea temperature |
| | | What is coral bleaching? |
| | | Coral bleaching video |
| 9 | Using Technology to Measure Diversity | An introduction to environmental DNA |
| | | What is remote sensing? |
| | | Deforestation in the Amazon Rain Forest |
| | | Tracking white sharks |
| | | Tracking whale sharks to learn more |
| 10 | Protecting Biodiversity | The World Heritage Convention |
| | | What is UNESCO World Heritage? Video |
| | | What is the Convention on Biological Diversity? |
| | | Australia's Biodiversity Conservation Strategy |
| | | The Lake Eyre Basin |

*Bookmark weblinks by typing in the address: it is not accessible directly from BIOZONE's website*

***Corrections and clarifications to current editions are always posted on the weblinks page***

UNIT 3
Topic 1

# Biodiversity

## Key terms

- abiotic (physical) factor
- biodiversity
- biotic factor
- competition
- data logger
- diversity index
- eDNA
- environmental gradient
- microclimate
- parasitism
- percentage cover
- percentage frequency
- predation
- remote sensing
- satellite tracking
- Simpson's diversity index
- species evenness
- species richness
- symbiosis

## What is biodiversity and how do we measure it?

*Key skills and knowledge*

| | | | 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. Understand that there are 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 | 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. What does the index tell you about the community you are studying? | 2 3 |
| ☐ | 4 | **PRAC** Determine species diversity of a group of organisms based on a given index (e.g. Simpson's diversity index). | 4 |
| ☐ | 5 | 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. | 5 |
| ☐ | 6 | **PRAC** Use appropriate technology and equipment to measure abiotic factors in the classroom using samples collected in the field. | 6 |
| ☐ | 7 | **PRAC** Use appropriate technology and equipment to measure abiotic factors in the field. Which factors must be measured directly in the field? | 6 |
| ☐ | 8 | **SKILL** Use appropriate technology, such as data loggers chemical tests, turbidity tubes and other equipment to measure abiotic factors. | 6 |
| ☐ | 9 | Compare ecosystems across spatial (distance) and temporal (time) scales using different indicators including:<br>• species diversity indices or percentage cover.<br>• species interactions (biotic factors) e.g. competition, predation, symbiosis, parasitism.<br>• abiotic factors, such as climate, substrate, size or depth of available habitat. | 7 8 |

Bruno de Giusti

## Protecting biodiversity

*Key skills and knowledge*

| | | | Activity number |
|---|---|---|---|
| ☐ | 10 | **SHE** Explain how technology provides useful tools to measure, analyse, and monitor biodiversity. Suitable technologies include remote sensing imagery, satellite tracking, and environmental DNA analysis (eDNA). | 9 |
| ☐ | 11 | **SHE** Explain the basis for international agreements about protection of biodiversity, such as the World Heritage Convention and the Convention on Biological Diversity. Why are these agreements necessary? | 10 |

# 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 24 million tourists visited Queensland in 2017, 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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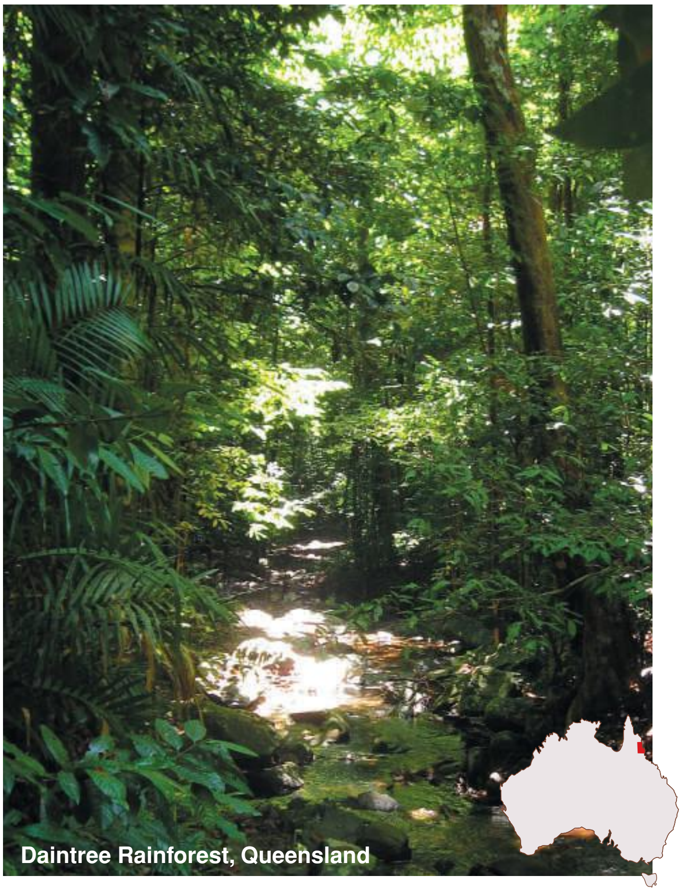
The wet forest of Queensland and the Brigalow Belt described below are two examples of important Queensland bioregions. Human activity has affected the biodiversity of both these biologically distinctive regions to different degrees.

### High biodiversity: Wet tropics of Queensland


Daintree Rainforest, Queensland

Killerscene Public Domain

The wet tropics of Queensland stretch along the north-east Queensland portion of the Great Dividing Range and cover an area of around 8,940 km$^2$. 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 (not found anywhere else) and many are endangered (at very 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 forest (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


Remnant brigalow tree, QLD

Ethel Aardvark cc3.0

The Brigalow Belt is named after the Brigalow (*Acacia harpophylla*) which once dominated this bioregion. The band of acacia wooded grassland 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 woodland. 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 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 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 a 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 | × | × | × | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | 7/10 | 70% |
| Species B | × | × | × | × | ✓ | ✓ | ✓ | × | × | × | | |
| Species C | ✓ | × | ✓ | ✓ | × | × | × | × | × | × | | |
| Species D | × | × | × | × | ✓ | × | ✓ | ✓ | ✓ | ✓ | | |
| Species E | × | × | × | × | ✓ | ✓ | ✓ | ✓ | × | × | | |

### 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

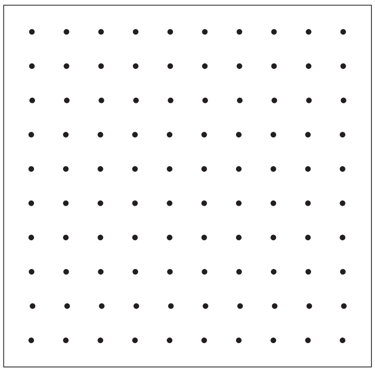

Table 2. Percentage cover of five species of plants.

| 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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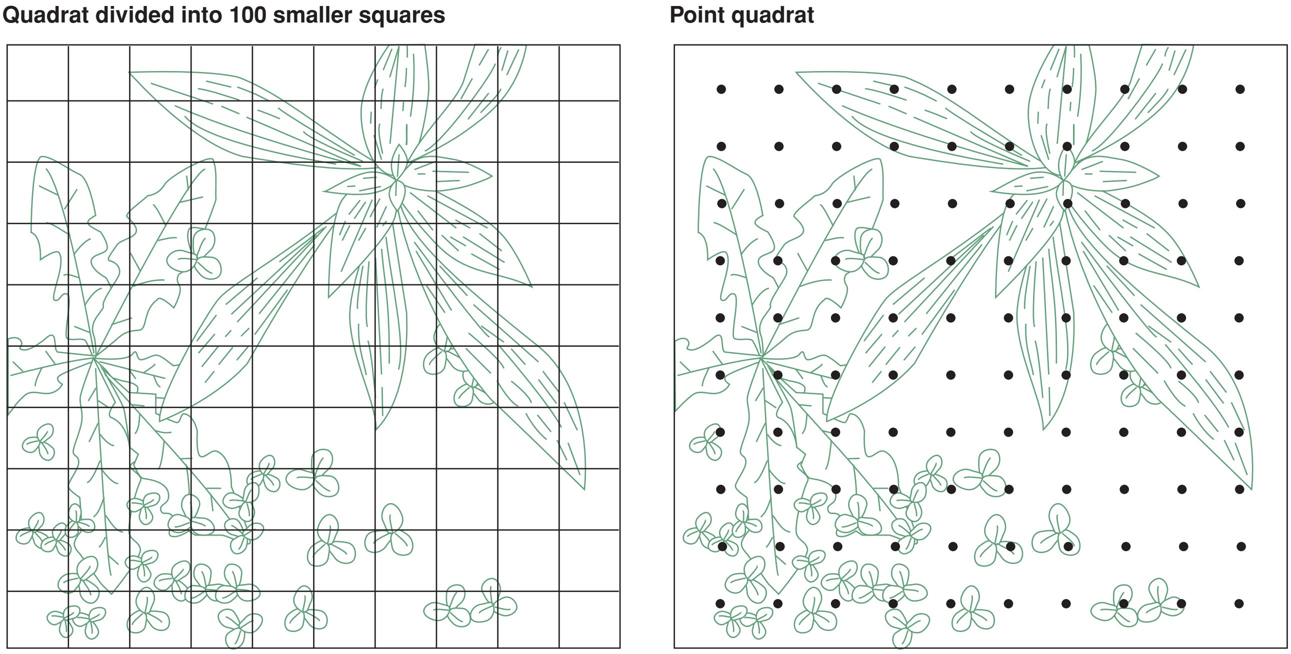
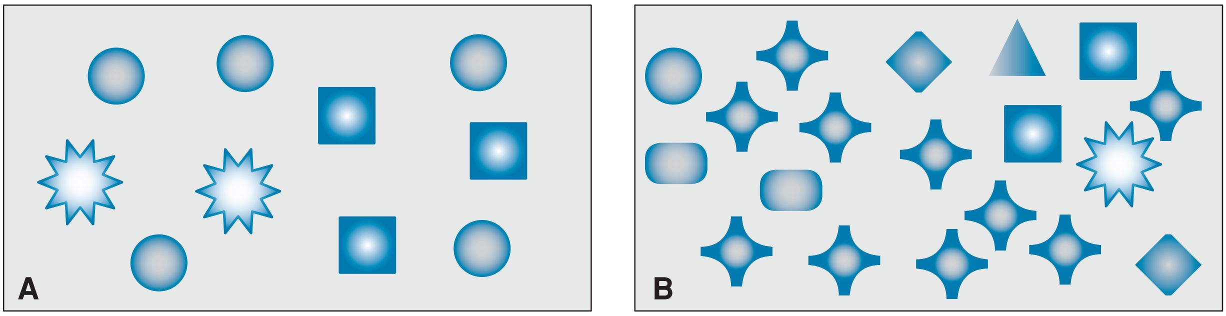


## Measuring diversity in animal populations

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 500 of species A and 3 of species B has the same species richness as a sample area with 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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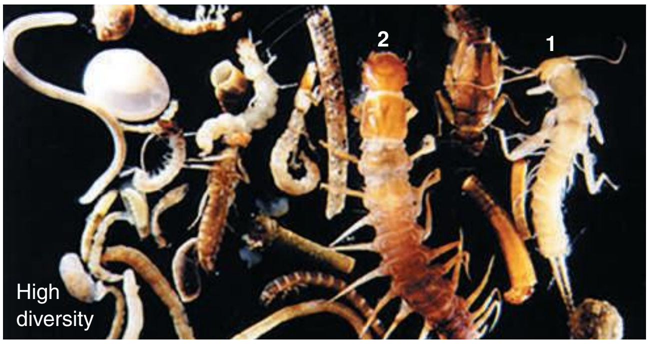
# 3 Diversity Indices

**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, included degraded environments.

### Simpson's index of diversity

Simpson's Index of Diversity (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 Index of Diversity (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 Index of Diversity using D = 1 – (Σn(n–1)÷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) = 1560 | Σn = 40 | Σn(n–1) = 282 |
| | Σn(n–1)÷ N(N–1) = | 282 ÷ 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 different 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) = | Σn = 98 | Σn(n–1) = |
| Σn(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) = | Σn = 101 | Σn(n–1) = |
| Σn(n–1)÷ N(N–1) = | | D = |


Species 1
Mite

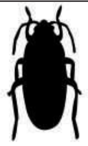

Species 2
Ant


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 Σn(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 and suggest any reasons for it: ____________________

____________________

____________________

____________________

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

____________________

   (b) Why would measuring species richness not be as informative as measuring species diversity? ____________________

____________________

____________________

____________________

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# 4 Determining Species Diversity

**MANDATORY PRACTICAL: Determining species diversity**

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**:<br>All face cards<br>(jacks, queens, kings)  | **Species 2**:<br>Clubs (odd numbered) ♣ | **Species 3**:<br>Clubs (even numbered) ♣ |
| **Species 4**:<br>Diamonds (odd numbered) ♦ | **Species 5**:<br>Diamonds (even numbered) ♦ | **Species 6**:<br>Hearts (odd numbered) ♥ |
| **Species 7**:<br>Hearts (even numbered) ♥ | **Species 8**:<br>Spades (odd numbered) ♠ | **Species 9**:<br>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:<br>Face cards | | | | | |
| Species 2:<br>Clubs (odds) | ♣ | | | | |
| Species 3:<br>Clubs (evens) | | | | | |
| Species 4:<br>Diamonds (odds) | ♦ | | | | |
| Species 5:<br>Diamonds (evens) | | | | | |
| Species 6:<br>Hearts (odds) | ♥ | | | | |
| Species 7:<br>Hearts (evens) | | | | | |
| Species 8:<br>Spades (odds) | ♠ | | | | |
| Species 9:<br>Spades (evens) | | | | | |
| N =<br>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:<br>Face cards | | | | | |
| Species 2:<br>Clubs (odds) | ♣ | | | | |
| Species 3:<br>Clubs (evens) | | | | | |
| Species 4:<br>Diamonds (odds) | ♦ | | | | |
| Species 5:<br>Diamonds (evens) | | | | | |
| Species 6:<br>Hearts (odds) | ♥ | | | | |
| Species 7:<br>Hearts (evens) | | | | | |
| Species 8:<br>Spades (odds) | ♠ | | | | |
| Species 9:<br>Spades (evens) | | | | | |
| N =<br>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:<br>Face cards |  | | | | |
| Species 2:<br>Clubs (odds) | ♣ | | | | |
| Species 3:<br>Clubs (evens) | | | | | |
| Species 4:<br>Diamonds (odds) | ♦ | | | | |
| Species 5:<br>Diamonds (evens) | | | | | |
| Species 6:<br>Hearts (odds) | ♥ | | | | |
| Species 7:<br>Hearts (evens) | | | | | |
| Species 8:<br>Spades (odds) | ♠ | | | | |
| Species 9:<br>Spades (evens) | | | | | |
| N =<br>N(N–1) = | | | Σn = | | Σn(n–1) = |
| Σn(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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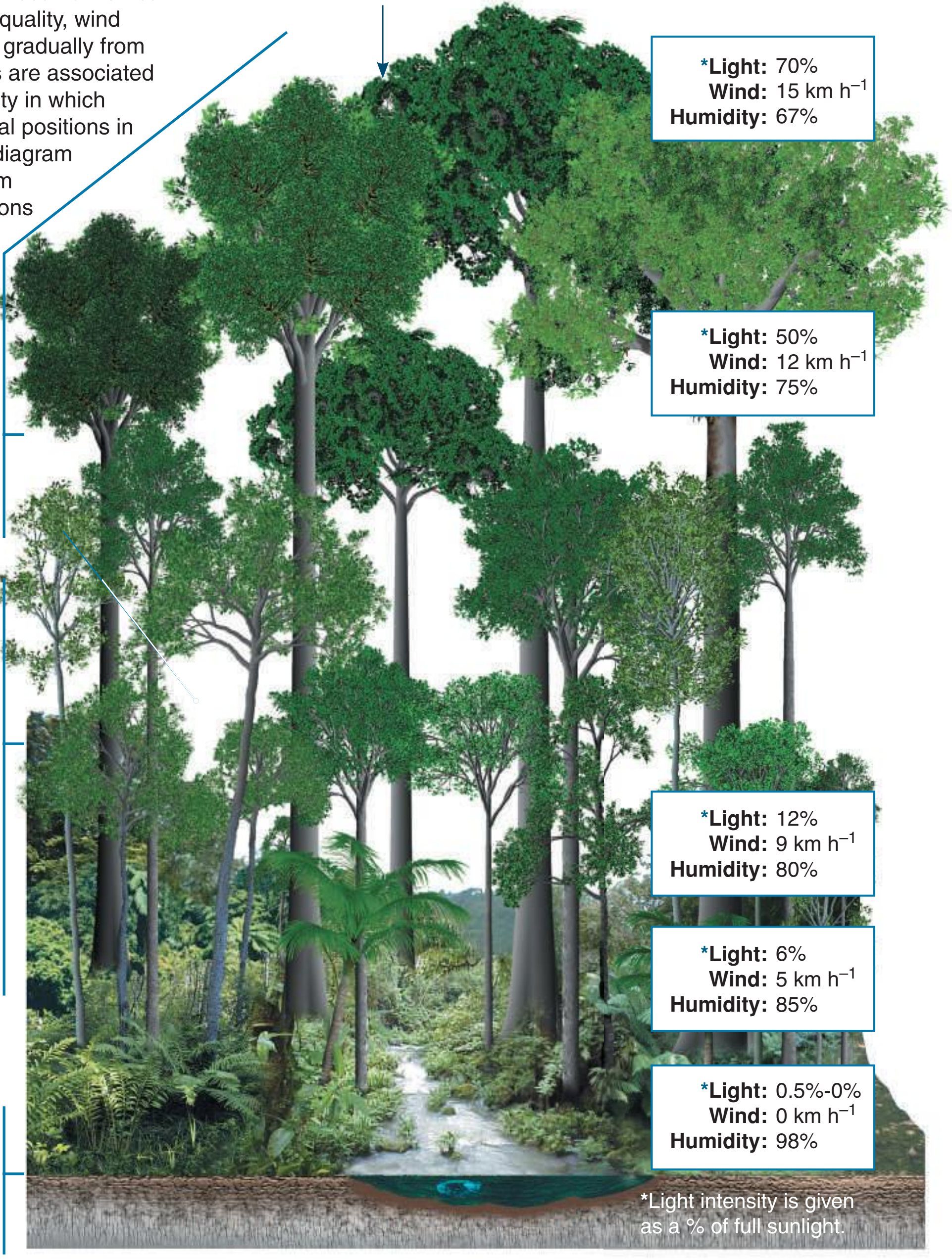
# 5 Abiotic Factors and Gradients

**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:

# 6 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 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.

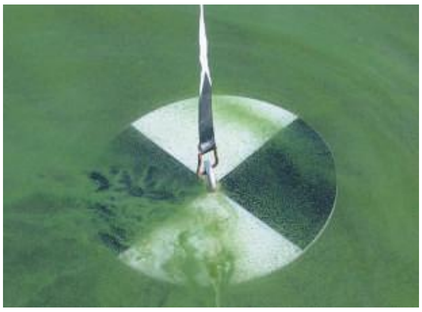
A data logger can be fitted with specific probes to gather and record physical measurements (e.g. wind speed, pH, humidity, temperature).

Pasco

### 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

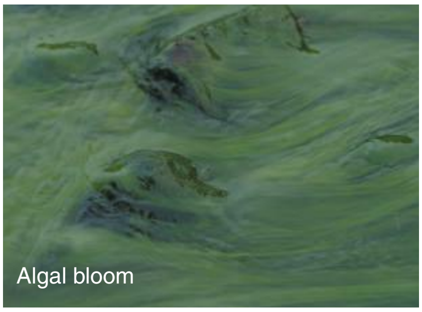
Salinity, the dissolved inorganic salt content of water or soil, is measured by passing an electric current between two electrodes. The conductivity is influenced by the concentration and composition of dissolved salts. Organisms have specific salinity preferences although many intertidal and estuarine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

Menindee ponds on the Murray-Darling River system

Tim Keegan cc 2.0

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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# 7 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.

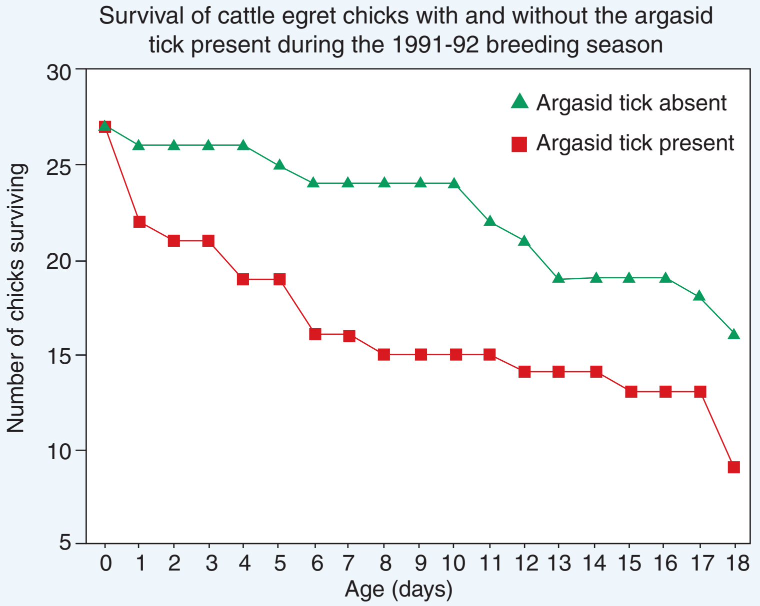
## Biotic factors and community change over time

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

Adapted from McKilligan (1996), Australian Journal of Ecology 21, 442-9.

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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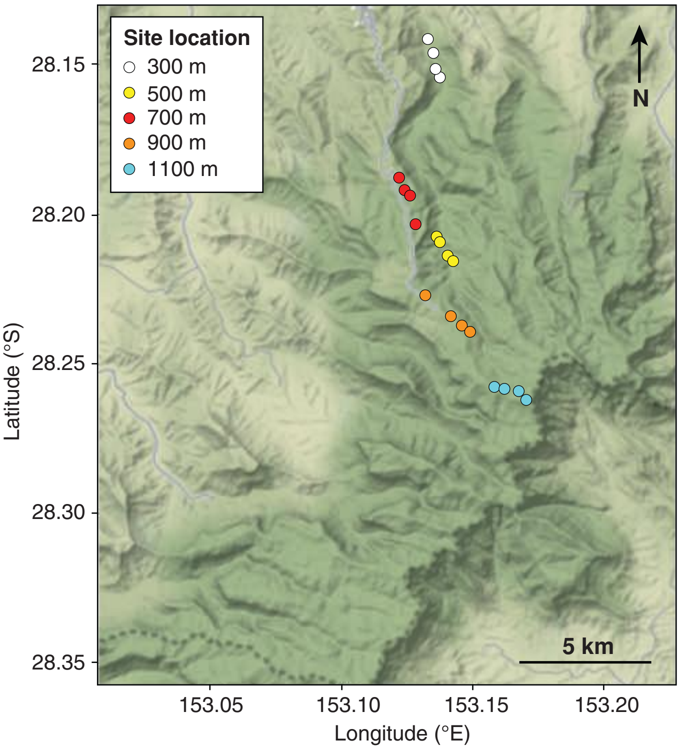
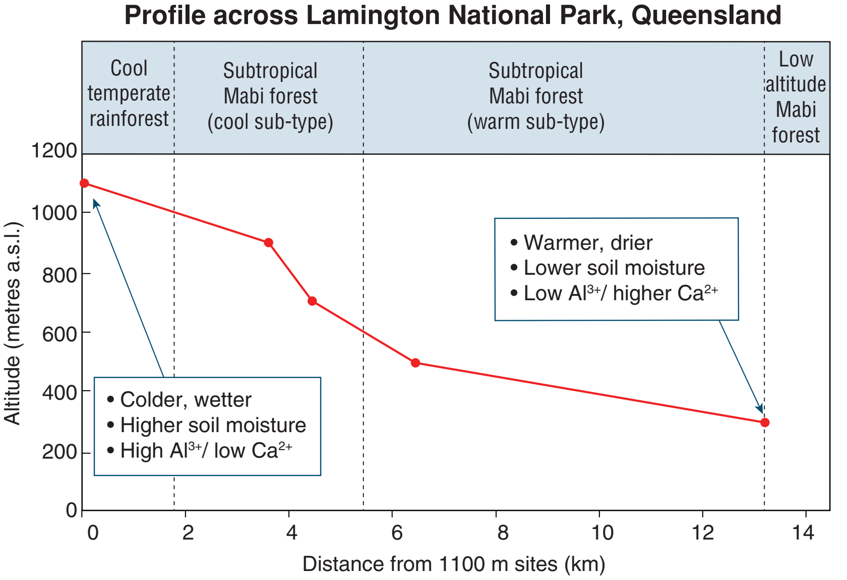
## Abiotic factors and community change over distance

- 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 **Weblinks** 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 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 Mabi forest (also called Complex Notophyll Vine Forest or CNVF). The distribution of the rainforest types is correlated with features of topography, climate, and soil properties.





| | 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 |


Malcolm Jacobson cc 3.0

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


Johncatsoulis Public Domain

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

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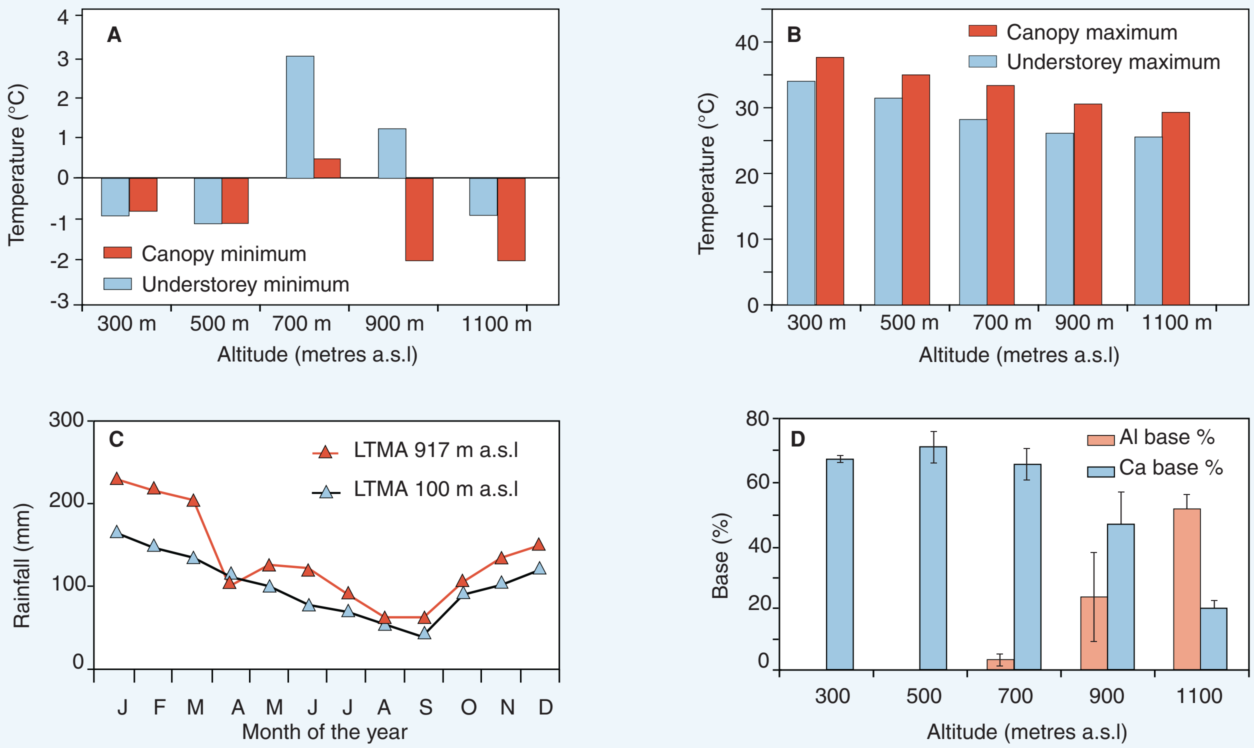
## Trends in some of the abiotic factors determining rainforest type at different altitudes, Lamington National Park, south-east Queensland



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 long term monthly average rainfall (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 long term rainfall data from nearby stations was used instead.

   (a) Describe the long term 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 Mabi forest 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 alys cc 3.0

Antarctic beech is a Gondwanan relict (survivor from the Gondwana). It is part of a species assemblage found only above 1000 m. Plants here 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 microclimates 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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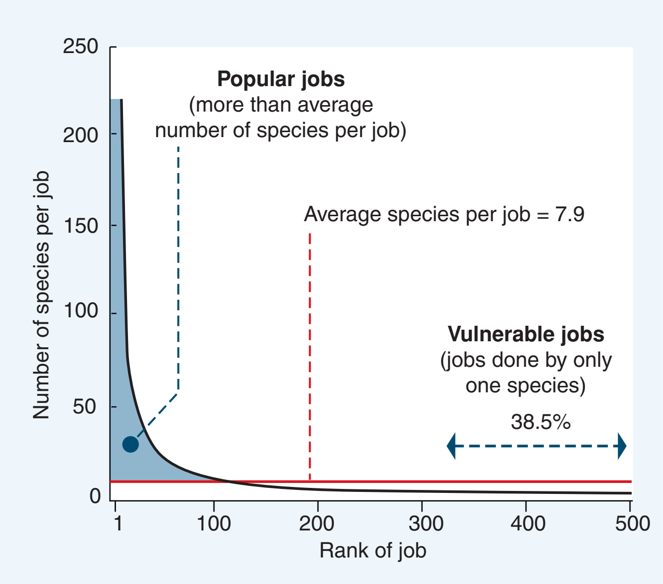
# 8 How Do Physical Factors Influence Biodiversity?

**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.



### DID YOU KNOW?

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.

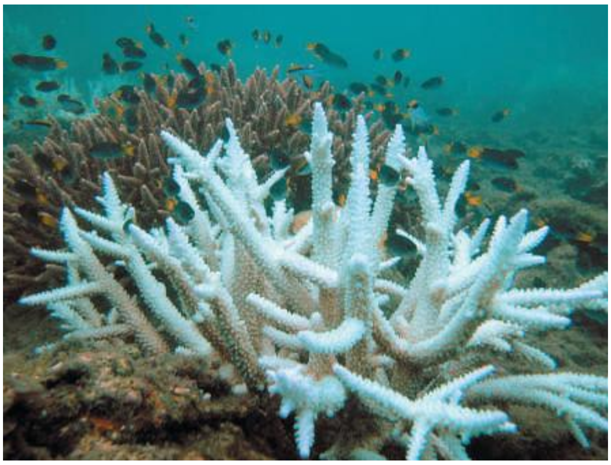
## Changing environments and the long term health of the Great Barrier Reef

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 and 2002 and again in 2016 and 2017. The two most recent major bleaching events, in 2016 and 2017, coincided with the highest sea surface temperatures experienced since 1900. An estimated 50% of the reef was lost as a result. The 2016 event affected 1100 km of reef and was the largest die-off of corals ever recorded. After the subsequent 2017 event and the effects of tropical cyclone Debbie, an estimated two thirds of the reef's corals were damaged.
- 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?

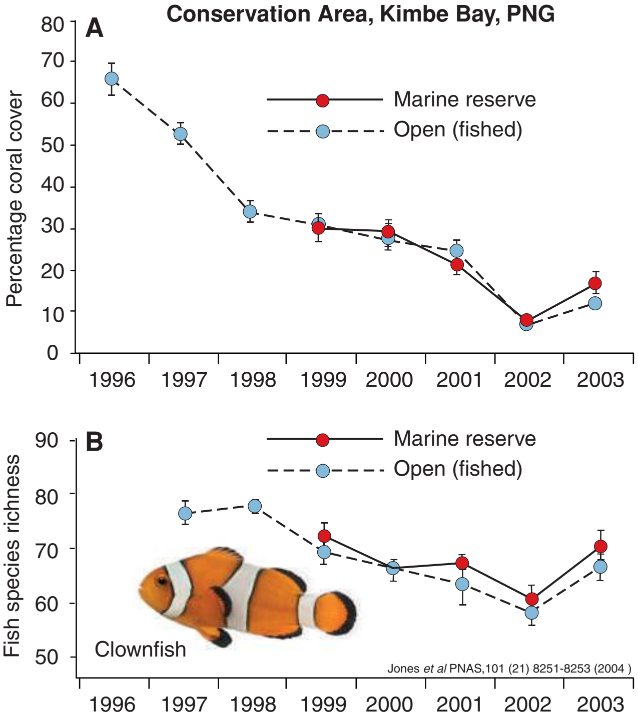
Thousand of species shelter, find food, reproduce, and raise their young in coral reefs. When irreversible coral bleaching occurs the coral dies and begins to break down. Any species reliant on the coral now become vulnerable themselves. For example, with no coral to hide in, prey species will be found 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).

**Coral cover and fish diversity, Tamane Puli Conservation Area, Kimbe Bay, PNG**



Jones *et al* PNAS,101 (21) 8251-8253 (2004 )

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.

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 (see **Weblinks**) 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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# 9 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.

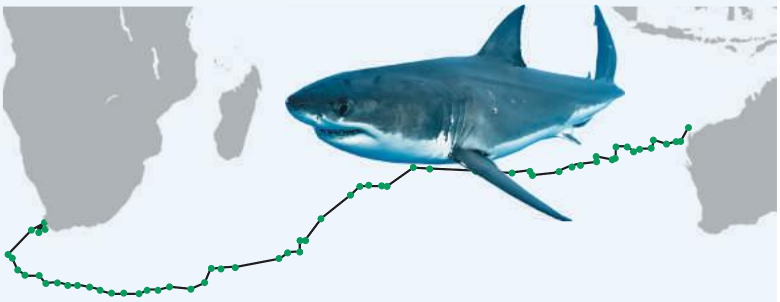
It is not always possible or practical to directly measure diversity within an ecosystem by traditional count methods. For example, some ecosystems are too large or too difficult to access, or the populations being studied may be too difficult or dangerous to monitor. In these instances, technology provides a useful way to measure, analyse, and monitor changes in biodiversity. A number of different 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.

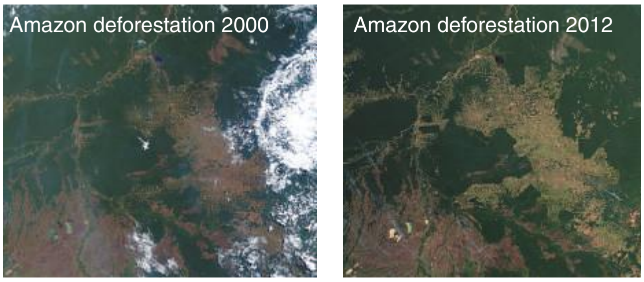
Radio-tracking is useful for studying threatened species. The information gathered can be used to manage an endangered species effectively.



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.

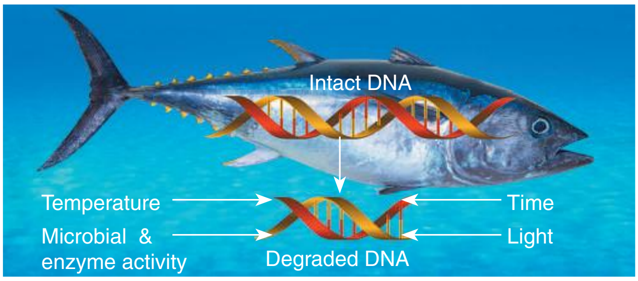
## Remote sensing



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:

SHE

# 10 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:
    1. The conservation of biological diversity.
    2. The sustainable use of the Earth's resources.
    3. 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.

CBD

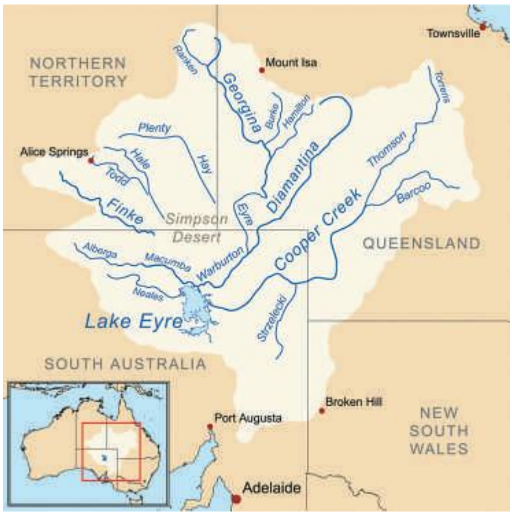
**Strategic Goal C**:
To improve the status of biodiversity by safeguarding ecosystems, species, and genetic diversity.

**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.



Kmusser CC3.5

# 11 KEY TERMS AND IDEAS: Did You Get It?

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

abiotic factor ..........

biodiversity ..........

diversity index ..........

microclimate ..........

percentage cover ..........

species richness ..........

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.

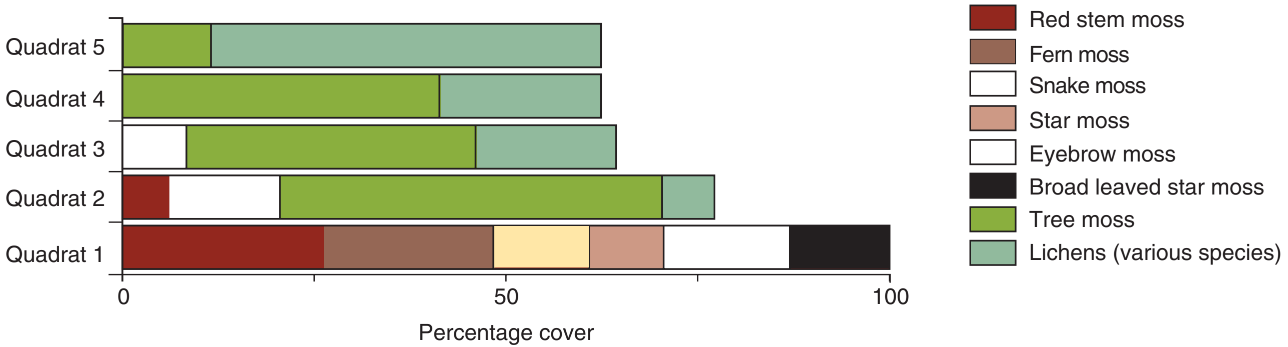
**F** A term for any non-living part of the environment, e.g. rainfall or temperature.

**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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UNIT 3
Topic 1

# Classification Processes

### Key terms

bias
biological species
clade
cladistics
cladogram
classification
common ancestry
density
distribution
DNA barcoding
ecoregion
ecosystem
Linnean classification
microhabitat
molecular phylogenetics
monophyletic
paraphyletic
phylogenetic classification
phylogenetic species
phylogeny
polyphyletic
quadrat
shared derived characteristics
stratified sampling
taxonomy
transect

**Activity number**

## The classification and phylogeny of organisms

*Key skills and knowledge*

☐ 1 What is the purpose of classification? Understand that classification can be hierarchical and based on different levels of similarity of physical features, molecular sequences, and methods of reproduction. **12**

☐ 2 Describe classification systems based on 1) similarity of physical features (the Linnaean system), 2) modes of reproduction (asexual, sexual, K-selected, r-selected), and 3) molecular sequences (molecular phylogenetics). **12 17**

☐ 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. **13**

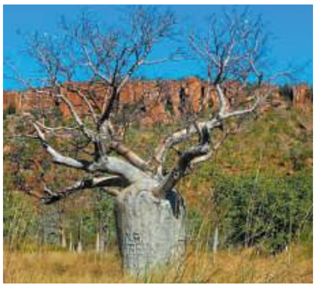
☐ 4 Explain what is meant by a phylogenetic tree. Distinguish between monophyletic, polyphyletic, and paraphyletic taxa in phylogenetic trees. **14**

☐ 5 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. **15**

☐ 6 Construct cladograms based on tables of characteristics. **15 16**

☐ 7 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. **17**

☐ 8 Explain how species can be classified according to their interactions with other species, e.g. predation, parasitism, mutualism, competition, commensalism. **18**



## Classifying communities and ecosystems

*Key skills and knowledge*

☐ 9 Define: ecosystem. Using examples, explain that ecosystems are composed of varied habitats from the very small (microhabitats) to the much larger (ecoregions). **19**

☐ 10 Interpret data to classify and name an ecosystem. Classification systems include Specht's vegetation classification, the ANAE system for aquatic ecosystems, and the Regional Ecosystems classification. **20 21**

☐ 11 Interpret data to classify and name an ecosystem. Classification systems include Specht's vegetation classification, the ANAE system for aquatic ecosystems, and the Regional Ecosystems classification. **21**

☐ 12 Explain how classifying ecosystems helps in their effective management. **22**

☐ 13 Describe the process of stratified sampling in terms of: **23-29**
- 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)

☐ 14 **PRAC** Use the process of stratified sampling to collect and anlyse primary biotic and abiotic field data to classify an ecosystem. **30**

# 12 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.

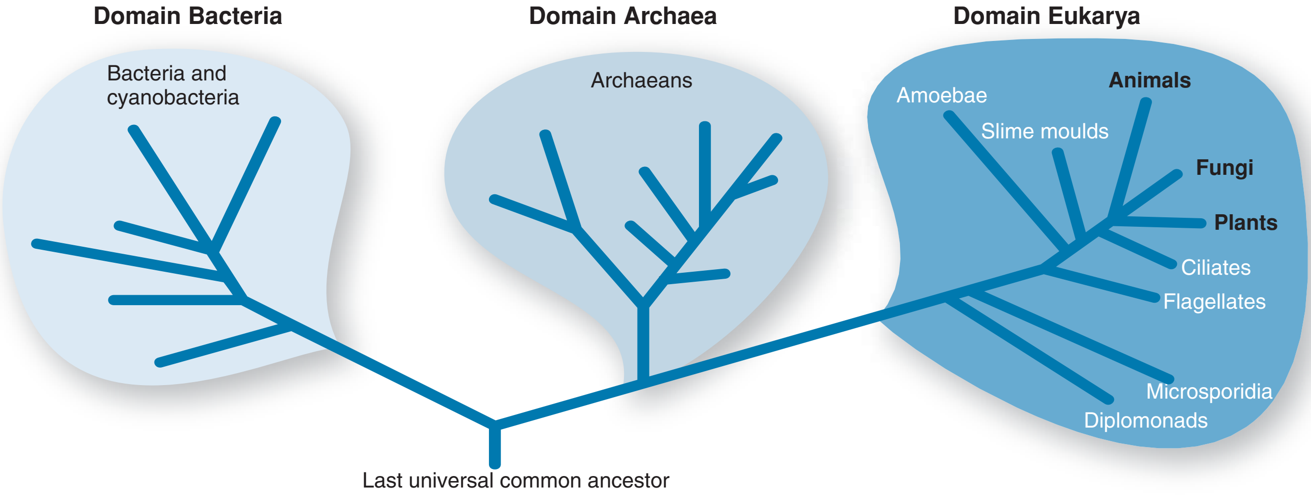
## A changing view of classification

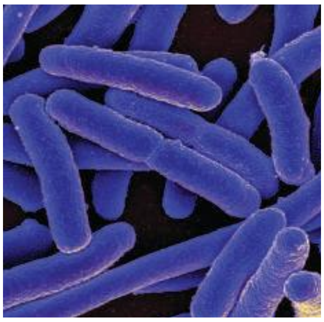
- Before DNA sequencing, taxonomists divided life into five kingdoms, classifying organisms based mainly on visible characteristics (**morphology**). The five kingdom system places all prokaryotes in one kingdom, with protists, fungi, plants, and animals being the other four.
- This system conflicted 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

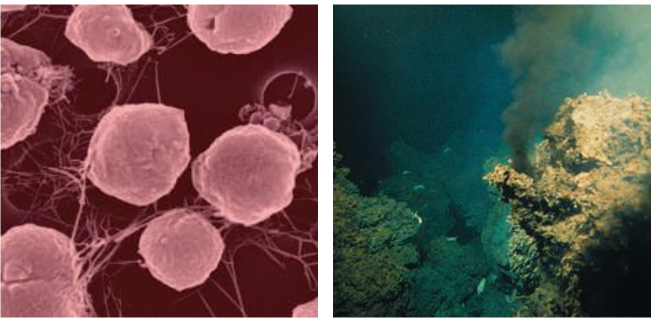
- In 1996, scientists deciphered the full DNA sequence of the thermophilic bacterium *Methanococcus jannaschii*. The data supported the hypothesis of three major evolutionary lineages and gave rise to a modified six kingdom classification.
- This was further revised to the current three domain system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

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




NIAID

**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).


UC Berkeley

**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 posses several metabolic pathways that are more similar to eukaryotes. Other aspects of their structure and metabolism, such 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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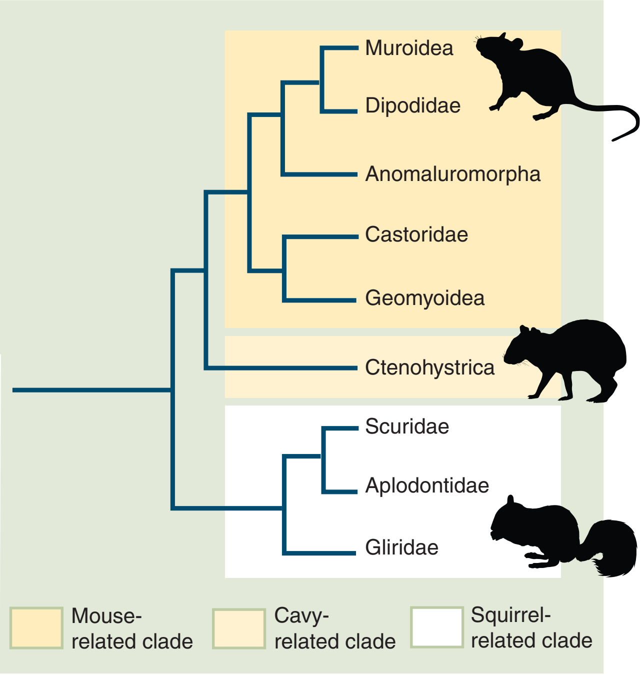
## Traditional classification

Based on the Linnaean system (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.

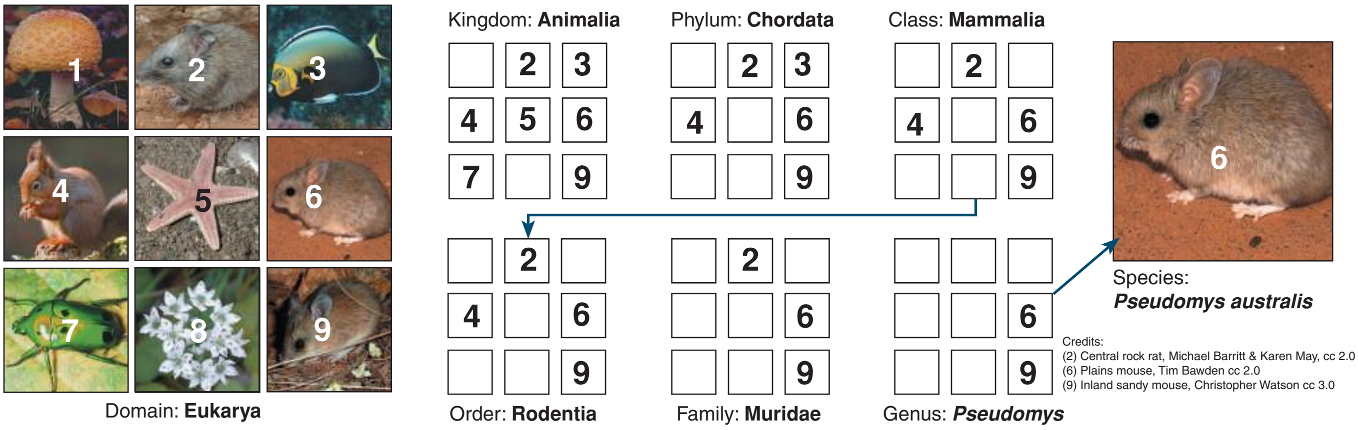
## Phylogenetic classification

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*.



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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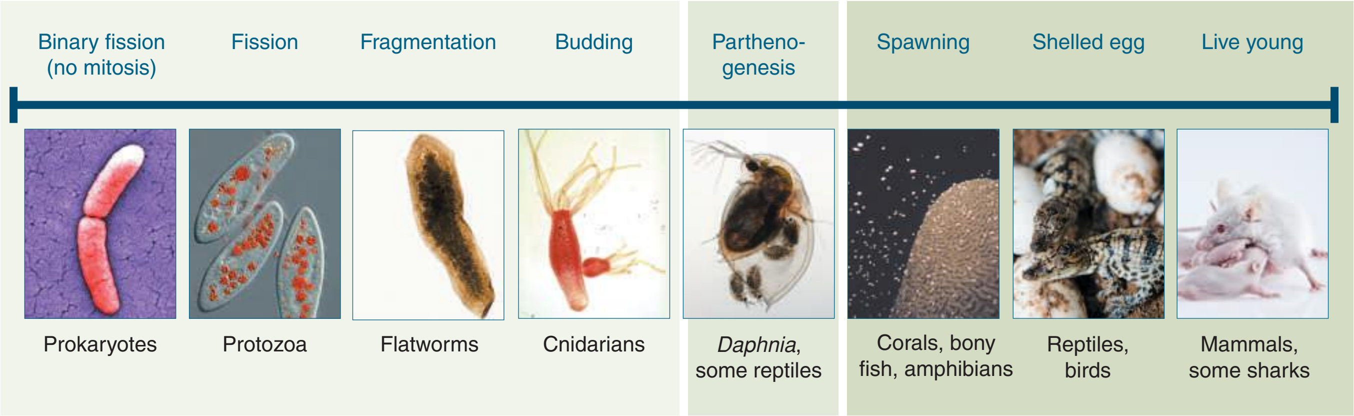
## Less formal ways to organise species

- Classification is a way to group organisms so that we can make sense of their characteristics. The best classification schemes attempt to reflect the true evolutionary history of a species (its **phylogeny**). Traditional and phylogenetic schemes are like this.
- However, organisms can also be grouped according to their mode of reproduction (e.g. asexual versus sexual) or their life history strategy (r versus K selected). These groupings are do not necessarily reflect evolutionary history although they may do so.
- Within related groups, reproductive and life history strategies are typically a continuum.

### Classification by mode of reproduction

Note that there is great variation in the reproductive strategies of eukaryotes. Only a few examples are given.



☐ Asexual reproduction ☐ Cycles of sexual and asexual reproduction ☐ Exclusively sexual reproduction

### Classification by life history strategy

Organisms can be grouped according to how they allocate their resources to growth and reproduction. A suite of characteristics are correlated with species that are either "r-selected" or K-selected. Where K = the carrying capacity of the environment (the number of organisms that the environment can support indefinitely) and *r* = biotic potential (the potential of the species to increase in number).

| | ***r*-selected** | **K-selected** |
|---|---|---|
| **Climate** | Variable and/or unpredictable | Fairly constant and/or predictable |
| **Mortality** | Density independent | Density dependent |
| **Survivorship** | Often large early losses | Types I or II (late or constant loss) |
| **Population size** | Highly variable. Often below K | Fairly constant in time. Close to K. |
| **Competition** | Variable, often lax. Generalist niche. | Usually keen. Specialist niche. |
| **Selection favors** | Rapid development, early reproduction, small body size, single reproduction (annual). | Longer development, delayed reproduction, larger body size, repeated reproduction. |
| **Length of life** | Short (often less than one year) | Longer (greater than one year) |
| **Examples** | Rodents, annual plants, bacteria | Elephants, humans, beech trees, tortoises |

3. Compare and contrast the basic features of traditional and phylogenetic classifications. In your answer, identify some of the advantages and drawbacks of each system:

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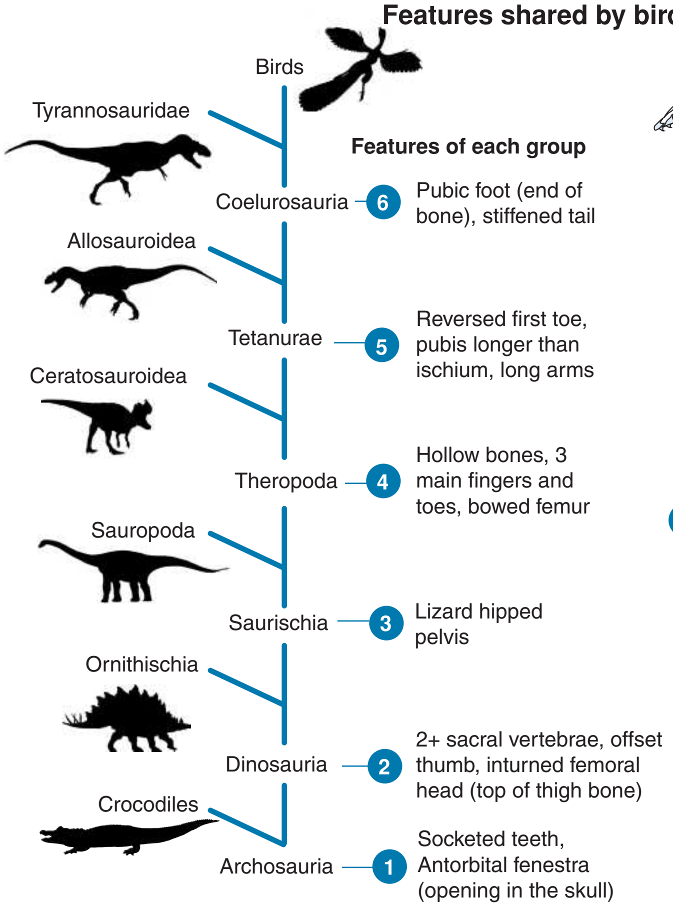
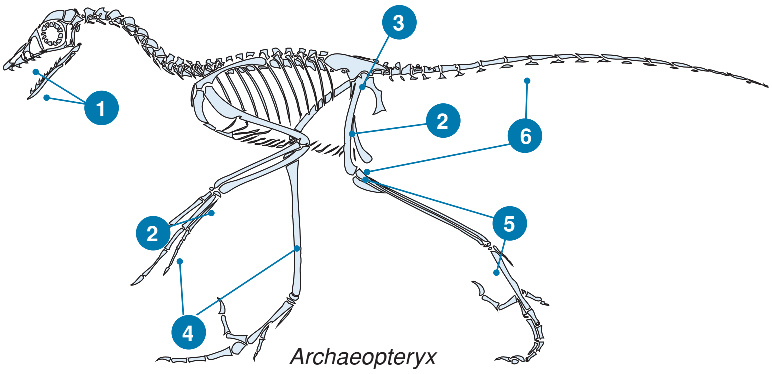
## Why are birds dinosaurs?

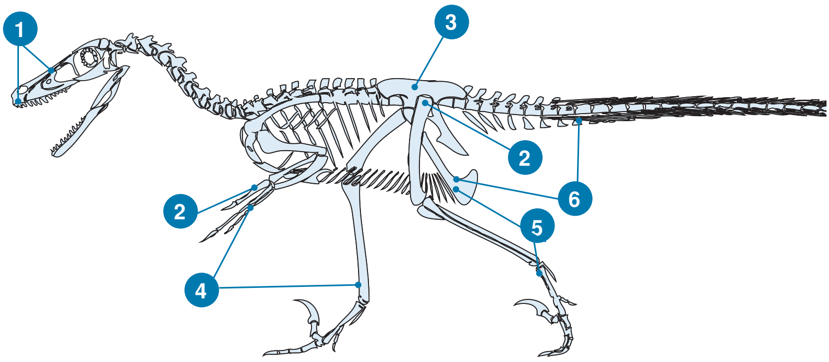
Defining groups of organisms and evaluating their ancestry using morphological features alone can be problematic because similarities in structure may not necessarily be the result of shared ancestry. This problem can be overcome by only considering the shared derived characteristics, i.e. the characteristics of two of more taxa that are present in their most recent common ancestor but not in older ancestors. Tracing the evolution of derived character states is the basis of cladistics and more accurately identifies the evolutionary history of a taxon. The ancestry of birds below illustrates this. Although birds are commonly regarded as a single taxon in traditional classification schemes (and in modern terms they are) birds are simply the last in the lineage of theropod dinosaurs (dinosaurs characterised by hollow bones and three-toed limbs). Recent analysis of the protein structure of fossil collagen from fossils puts birds and theropod dinosaurs firmly in the same taxon.

### Features shared by birds and theropod dinosaurs





*Archaeopteryx*
(transitional between birds and dinosaurs)



*Velociraptor*
(a late Cretaceous theropod dinosaur)

4. Why do you think classifications based on molecular evidence provide a more likely phylogeny than one based on appearance alone:

5. (a) Are classifications based on life history strategy or mode of reproduction useful for determining phylogeny? Explain:

(b) Can you think of when you might use such classifications?

6. Are dinosaurs extinct (gone forever)? Use phylogenetic classification to defend your answer:

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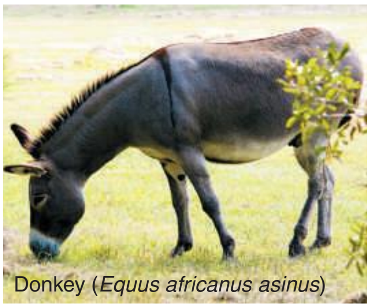
# 13 What is a Species?

**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.<br>Cannot successfully interbreed with other species. | Must be distinguishable from other such groups.<br>Does not rely on reproductive isolation. |
| **Works well for…** | Sexually reproducing organisms. | Asexual organisms. Detecting recent divergences. |
| **Difficulties** | Difficult to apply to asexual organisms.<br>Difficult to apply to extinct organisms. | Can require enough genomic diversity to evaluate (enough loci to analyse).<br>Can result in a proliferation of species. |

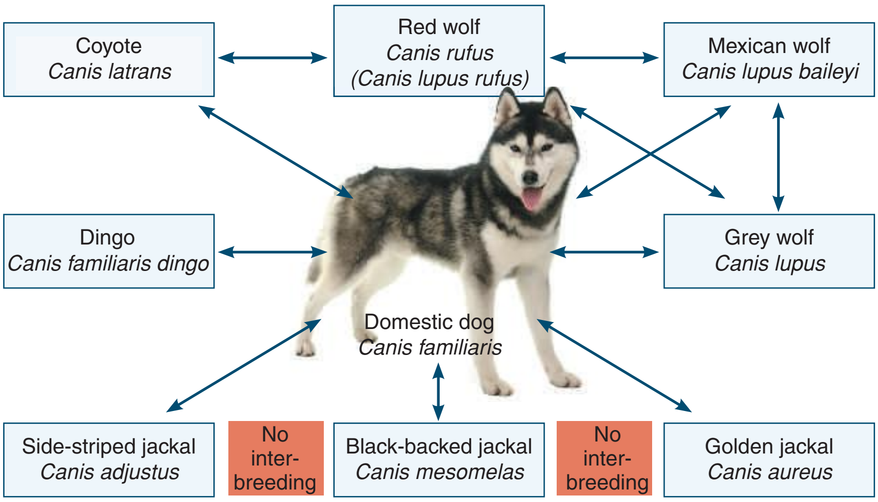

Donkey (*Equus africanus asinus*)


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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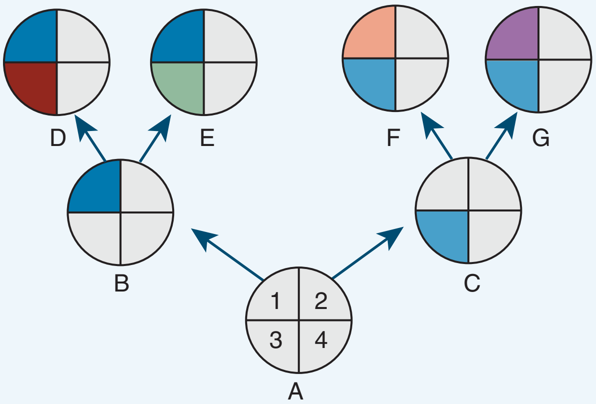
## The phylogenetic species concept (PSC)

- 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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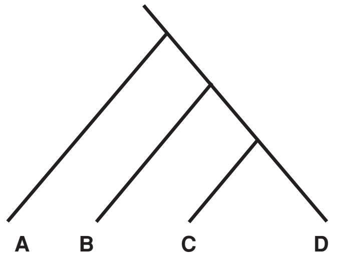
# 14 What is a Phylogenetic Tree?

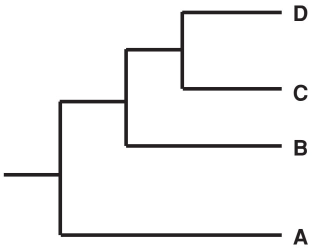
**Key Idea**: Phylogenetic trees represent possible evolutionary relationships among organisms. They can be constructed based on appearance or molecular data.

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 through the length of the branches (lines). Phylogenetic trees based on cladistics (cladograms) do not represent evolutionary time.



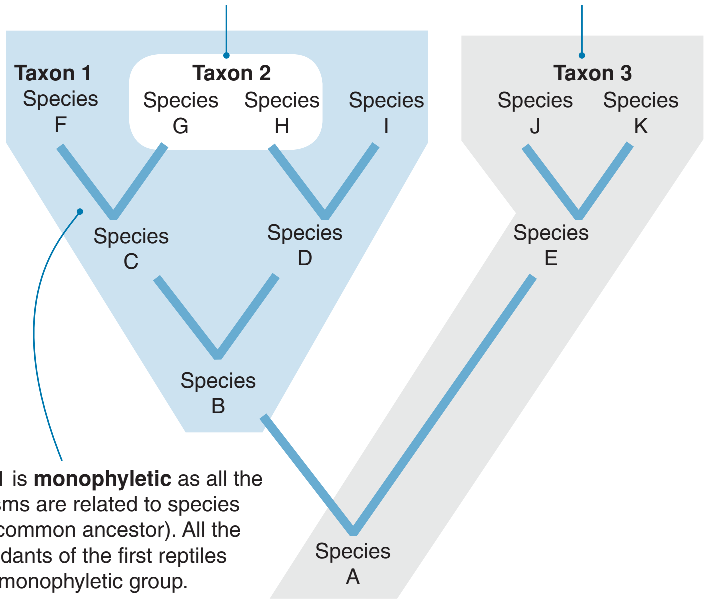


## Determining phylogenetic relationships

- 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 characters 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 whereever 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** as 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** as 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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# 15 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

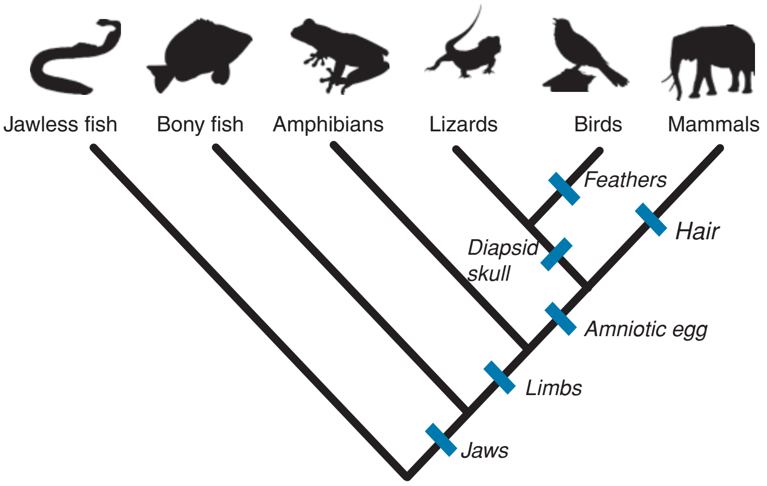
A table listing the features for comparison allows us to identify where we should make branches in the cladogram. An outgroup (one which is known to have no or little relationship to the other organisms) is used as a basis for comparison. The table (right) lists features shared by selected taxa. The 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.

| | Taxa | | | | | |
|---|---|---|---|---|---|---|
| **Comparative features** | Jawless fish (outgroup) | Bony fish | Amphibians | Lizards | Birds | Mammals |
| Vertebral column | ✔ | ✔ | ✔ | ✔ | ✔ | ✔ |
| Jaws | ✘ | ✔ | ✔ | ✔ | ✔ | ✔ |
| Four supporting limbs | ✘ | ✘ | ✔ | ✔ | ✔ | ✔ |
| Amniotic egg | ✘ | ✘ | ✘ | ✔ | ✔ | ✔ |
| Diapsid skull | ✘ | ✘ | ✘ | ✔ | ✔ | ✘ |
| Feathers | ✘ | ✘ | ✘ | ✘ | ✔ | ✘ |
| Hair | ✘ | ✘ | ✘ | ✘ | ✘ | ✔ |



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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?

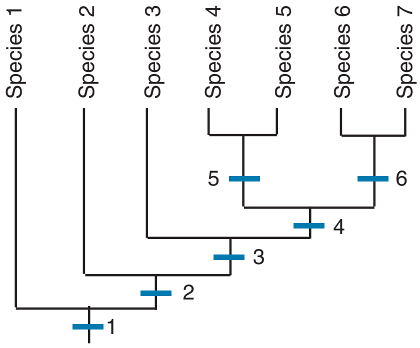
2. What assumption is made when applying the rule of parsimony in constructing a cladogram?

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.

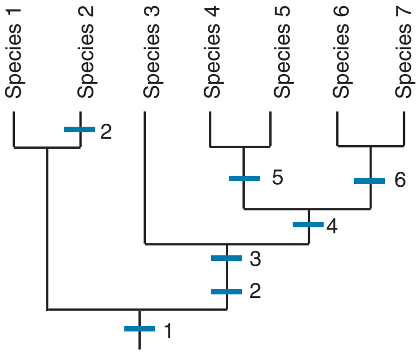
   (a) Which tree is more likely to be correct?

   (b) State your reason:

**Phylogenetic tree 1**



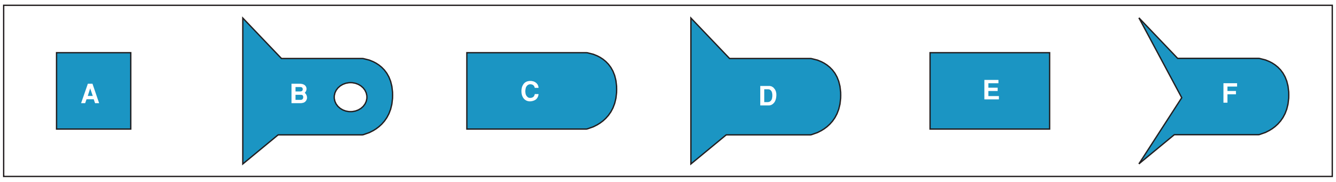
**Phylogenetic tree 2**



   (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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# 16 Constructing a Cladogram

**Key Idea**: A table of selected characteristics can be organised systematically as a matrix and used to construct a cladogram.

| | Character | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Taxon | **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 characters (below, left) relate to adaptations of the male for internal fertilisation. Others relate to deterring or detecting predators. In the matrix, characters 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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# 17 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).

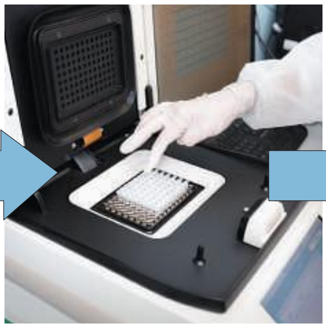
Fungal barcoding uses the nuclear ribosomal internal transcribed spacer (ITS).

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.

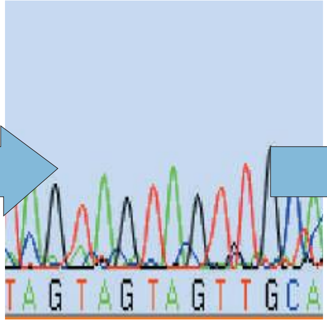
## Barcoding and molecular phylogenetics

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.

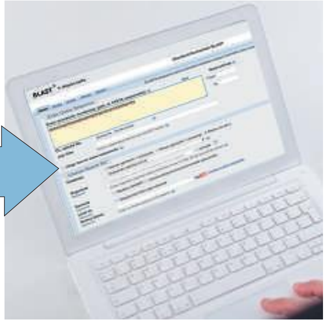
Isolate DNA from sample.



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.
- **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 **Phylogeny.fr** at **http://www.phylogeny.fr/index.cgi** developed by Sebastien Santini.

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 in the **Weblinks** below 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.

```
>1
AGATGATCTCGCTGATAGCTCGATGATCGTCGATAGAGACAGATACAGTCG
>2
AAATGATCTCGCTGATAGCTCGATGATCGTCGATAGAGACAGATACAGTCG
>3
AAATGATCTCGTTGATAGCTCGATGATCGTCGATAGAGACAGATACAGTCG
>4
AAATGATCTCGTTGATAGCTCGATGATCGTCGATACAGTCAGATACAGTCG
>5
AGATGATCTCGCTGATAGCTCGATGATCGTCGATAGAGACTTATACAGTCG
>6
AGATGATCTCGCTGATAGCTCGATGATCGTCGATAGAGACTTATACACTCG
>7
AGATGACTCGCTGATAGCTCGATGATCGTCAGATAGACTTATACACTCGGC
```

3. Draw the phylogenetic tree produced by Phylogeny.fr in the box below:

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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# 18 Classification by 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<br>Benefits Benefits | A → B<br>Benefits Unharmed | A → B<br>Unaffected Harmed | A → B<br>Benefits Harmed | A → B<br>Benefits Harmed |
| Both species benefit from the association.<br>**Examples**: Tick bird on zebra removes parasites and alerts zebra to danger, while tick bird gains access to food.<br>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.<br>**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.<br>**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.<br>**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.<br>**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. |
|  |  |  |  Luc Viatour www.Lucnix.be |  |

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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# 19 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).

**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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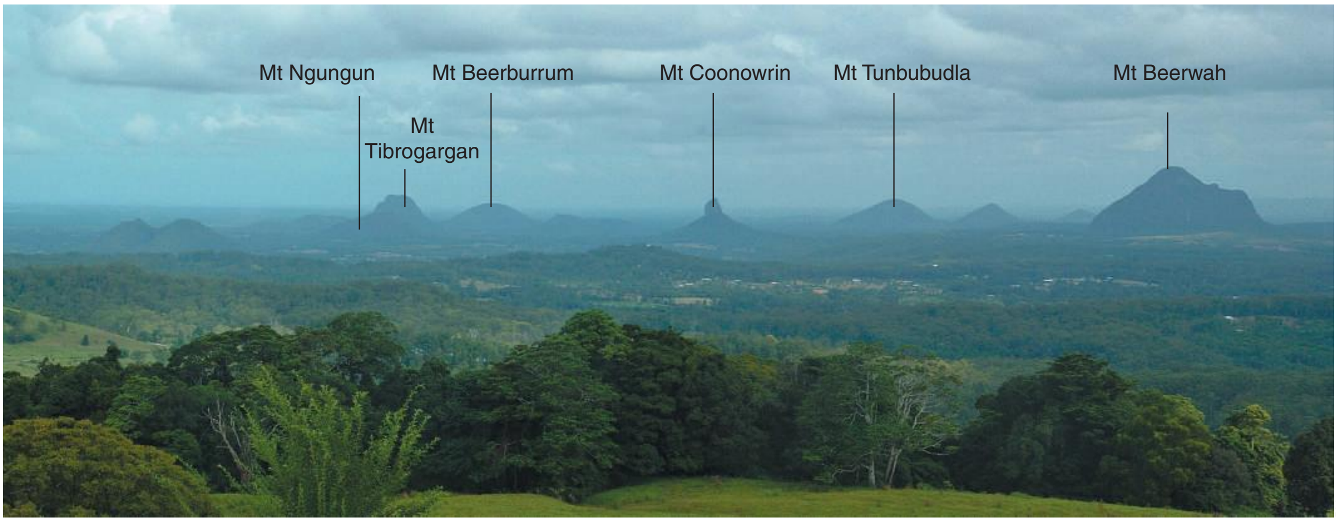

Bidgee cc 3.0

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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# 20 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.

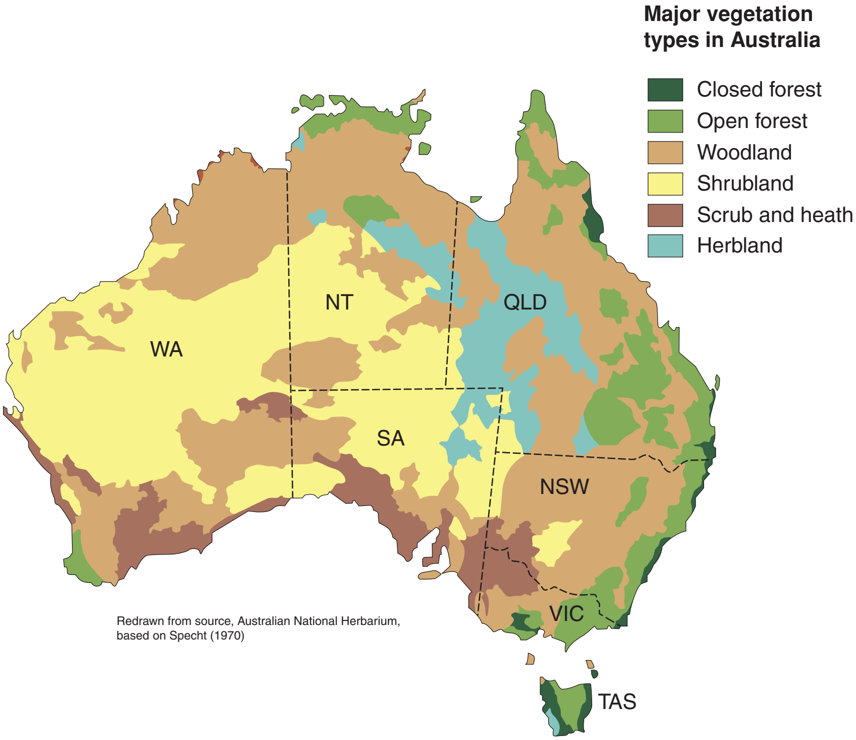
The ability to classify ecosystems allows us to recognise them and determine their extent. Broad classifications for ecosystem types can be applied globally (e.g. the Holdridge life zone classification scheme) or on a regional basis. Australia has a number of different classification schemes for its 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 is a vast country with highly variable climatic, topographical, and edaphic (soil) factors influencing vegetation type and distribution.

## 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.


**Major vegetation types in Australia**

Redrawn from source, Australian National Herbarium, based on Specht (1970)

| | 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 |

1. 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**<br>(Attributes: hydrology, climate, landform) | | | | | | | | | |
| **Level 2** | | **Landscape scale**<br>(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**<br>(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.

2. 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?

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

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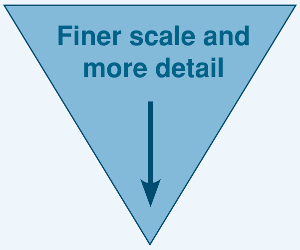
# 21 Classifying Queensland's Terrestrial Ecosystems

**Key Idea**: Bioregions are a 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 the Weblinks, 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. In note form, 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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# 22 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.

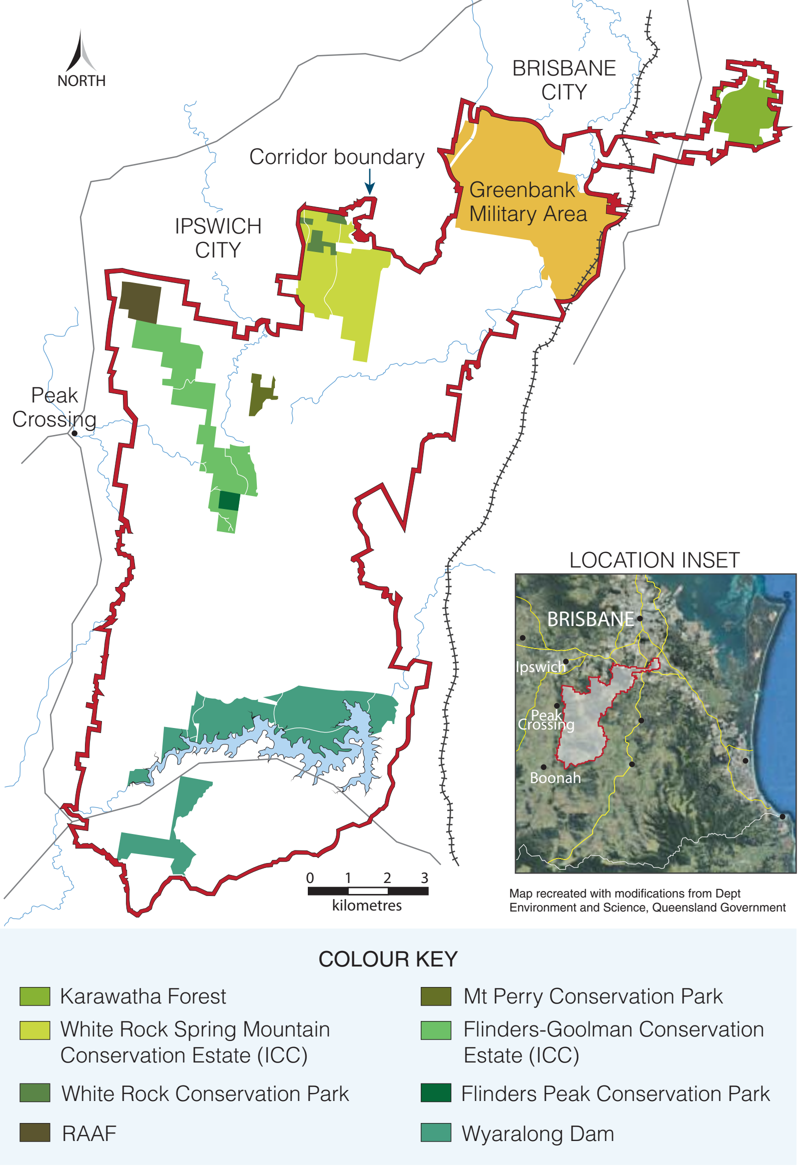
In 2011, the Queensland Government, in partnership with local government and other stakeholders developed the Flinders Karawatha Corridor Management Strategy. This 5-year management plan identified actions to maintain and enhance the environmental, recreational and cultural heritage values of the corridor. 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 Qeensland. 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 for 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 • reporting, research, and monitoring. Each area has its own overall objective and key actions to achieve this.


Illaweena Lagoon, Kaawatha 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 the **Weblinks** 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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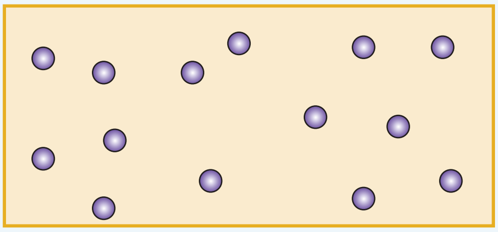
# 23 Population Density and Distribution

**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.

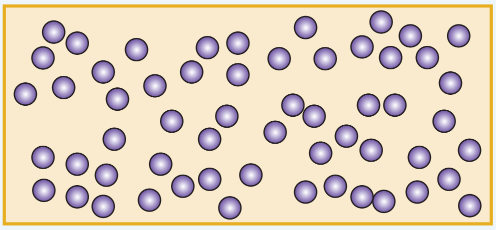
A population is defined as all the members of the same species in a particular geographical area (and therefore capable of interbreeding). Populations have characteristics, such as density, distribution, and age structure, not shown by individuals. Population density is the number of individuals per 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



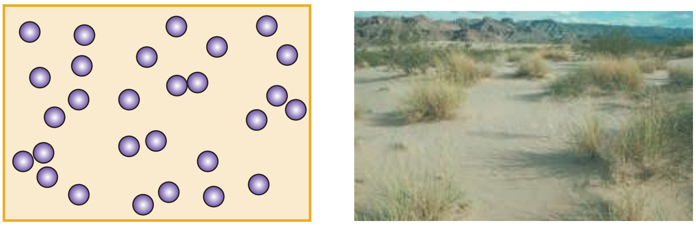
In high density populations, individuals are crowded together. There are many individuals per unit area or volume (e.g. colonial organisms, such as many corals).

Michael J Fromholtz cc 4.0

Quolls are mostly solitary, meeting up for mating.

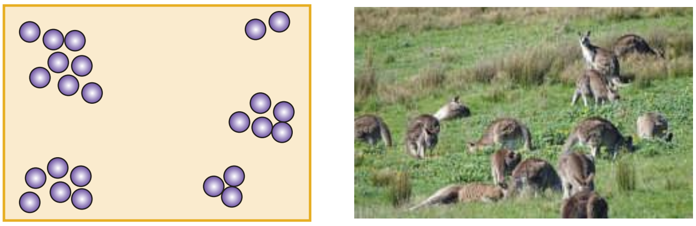
Termites form well organised, high density colonies.

### Random distribution



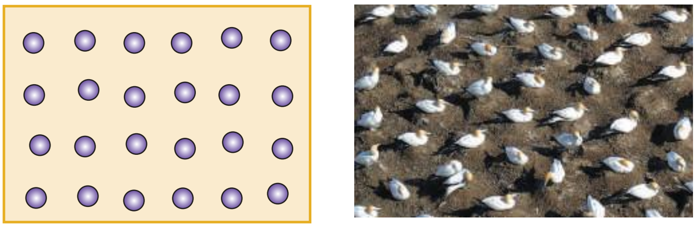
A random distribution describes an irregular spacing between individuals. The presence of one individual does not directly affect the location of any other. Random distributions are uncommon in animals but are often seen in plants.

### Clumped distribution



Clumped distributions occur when individuals are grouped in patches (often around a resource). The presence of one individual increases the probability 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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# 24 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. Why do you think 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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# 25 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.

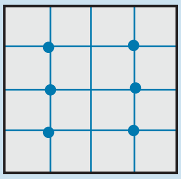
Most practical exercises in ecology involve collecting data about the distribution and abundance of one or more species in a community. Most studies also measure the physical factors in the environment as these may help to explain the patterns of distribution and abundance observed. There are many sampling 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.

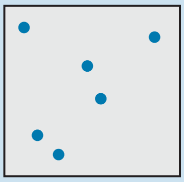
## Sampling designs and techniques

### 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.

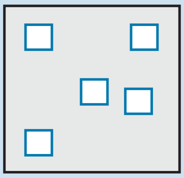
**Pros**: Point sampling is efficient if time is limited. It is a good method for determining species abundance and community composition.
**Cons**: May miss organisms in low abundance.


Systematic (grid)


Random

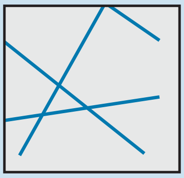
### Area sampling using quadrats

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.

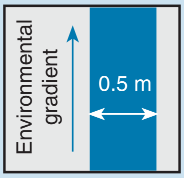


### Line and belt transects

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.



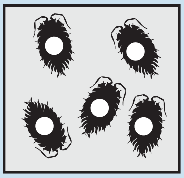
In a **belt transect**, quadrats are used to sample the plants and/or animals at regular intervals along a measured strip.
**Pros**: Provide a lot of information on abundance and distribution as well as presence/absence. **Cons**: Can be time consuming to carry out properly.

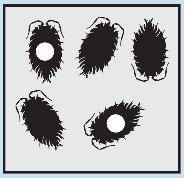


### Mark and recapture sampling

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:

   ______________________________

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

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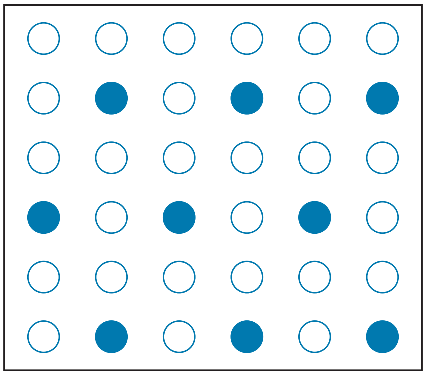
## Sampling strategies

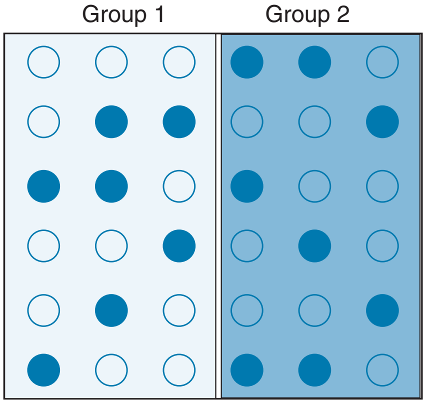
In most ecological studies, it is not possible to measure or count all the members of a population. Instead, information is obtained through sampling in a manner that provides a fair (unbiased) representation of the organisms present and their distribution. This is usually achieved through **random sampling**. 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.

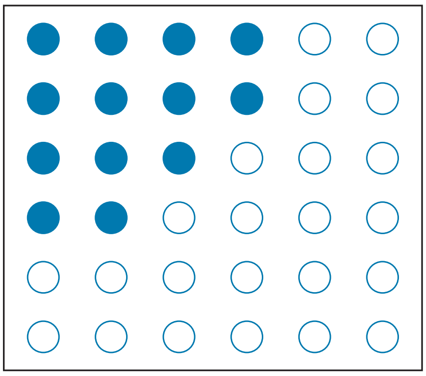
**Example**: Selecting individuals from a patient list.



### 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.



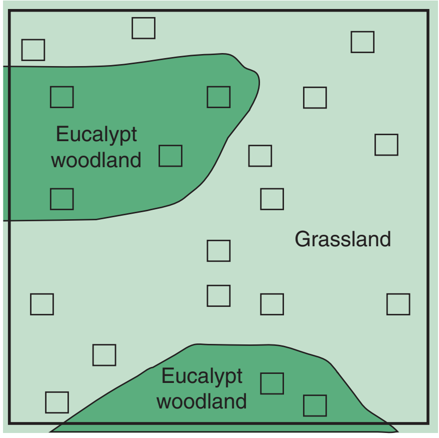
### Opportunistic sampling

A non-random sampling technique in which subjects are selected because of 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.

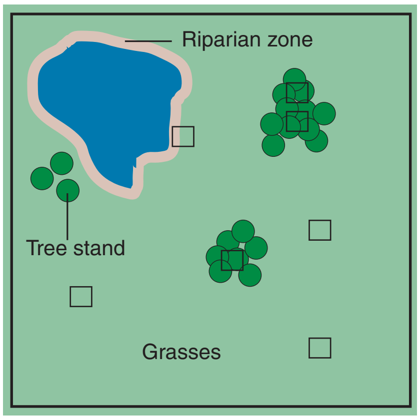

Pooter being used to collect insects from a collection net.

Fritz Geller-Grimm CC3.0

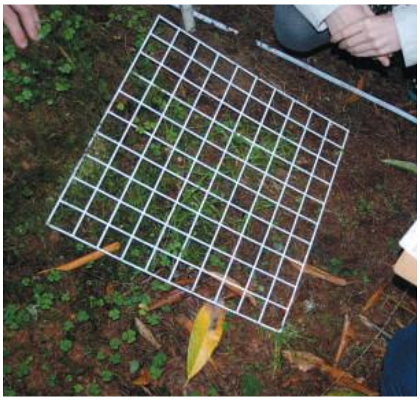
Quadrats are excellent for collecting data on plants but it is not so useful for highly mobile species. Researchers use a variety of collection methods, including pooters (aspirators) to collect insects and other mobile species.

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

5. Study the diagram on the right, it 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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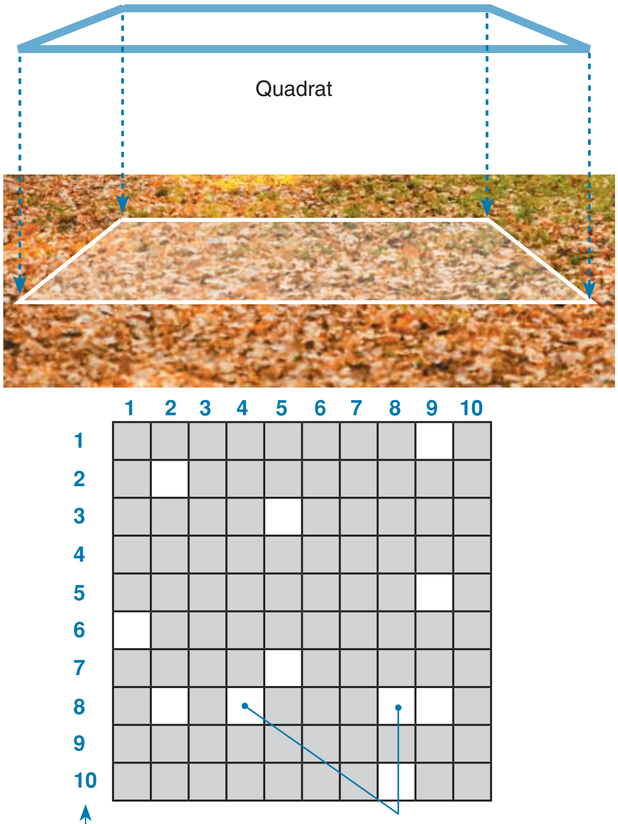
# 26 Quadrat Sampling

**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.



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.

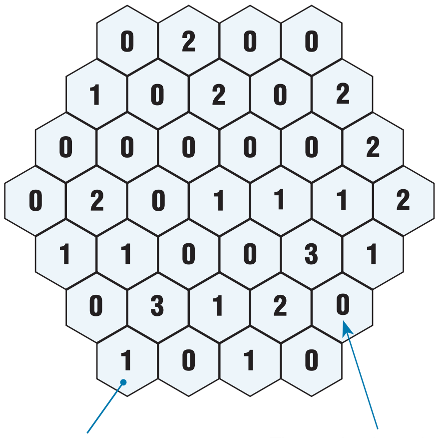
$$\text{Estimated average density} = \frac{\text{Total number of individuals counted}}{\text{Number of quadrats} \times \text{area of each quadrat}}$$

### 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).

## 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:

_______________

_______________

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# 27 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 x 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.

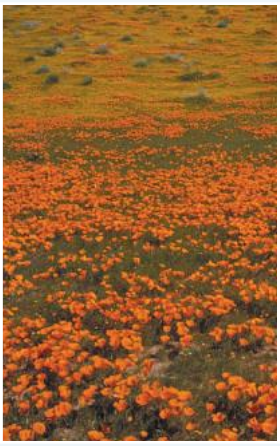
## Describing vegetation

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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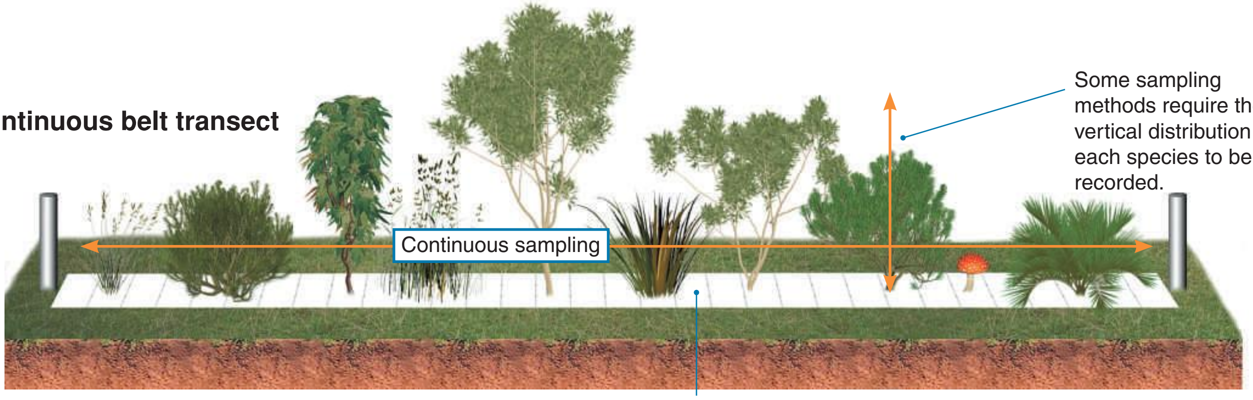
# 28 Transect Sampling

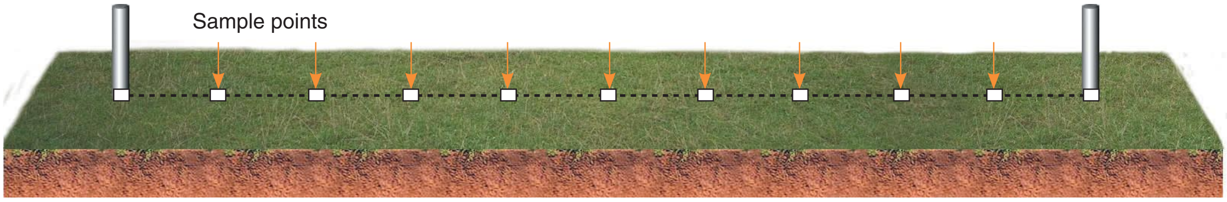
**Key Idea**: Transect sampling is useful for providing information about species distribution along an environmental gradient.

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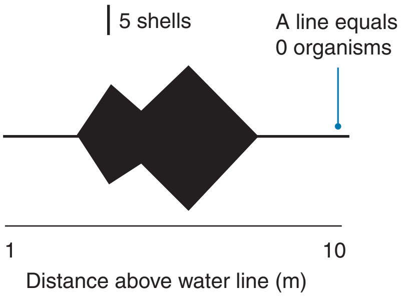
A **kite graph** is a good way to show the distribution of organisms sampled using a belt transect. Dat may be expressed as abundance or percentage cover along an environmental gradient. Sever species can be shown together on the same plot so that the distributions can be easily compared.

3. The data on the right were collected from a rocky shore field trip. Four common species of bar were sampled in a continuous belt transect from the low water mark, to a height of 10 m above 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 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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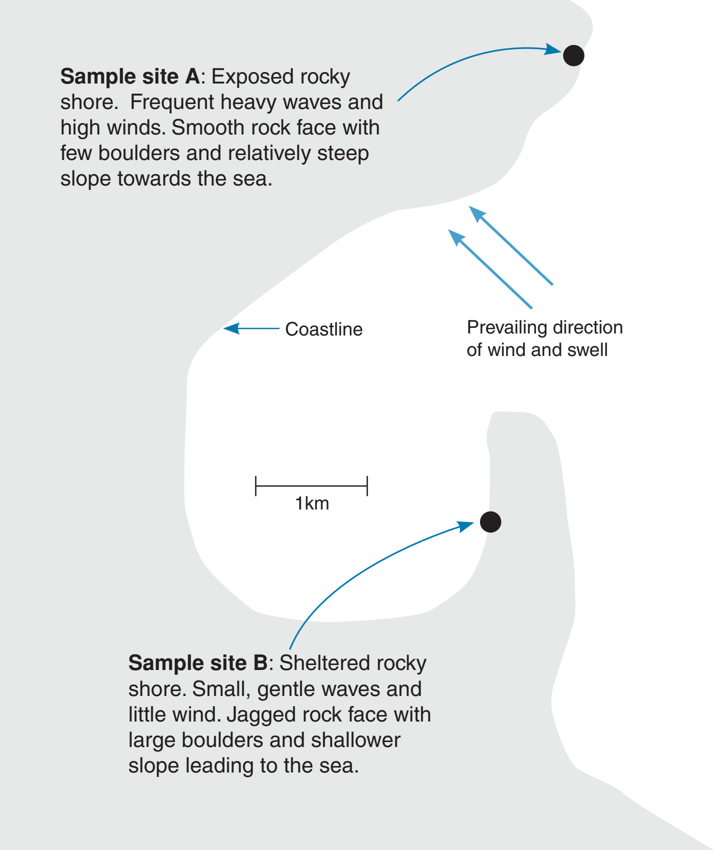
# 29 Stratified Sampling in a Variable Ecosystem

**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 within 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.



**Sample site A**: Exposed rocky shore. Frequent heavy waves and high winds. Smooth rock face with few boulders and relatively steep slope towards the sea.

**Sample site B**: Sheltered rocky shore. Small, gentle waves and little wind. Jagged rock face with large boulders and shallower slope leading to the sea.

### 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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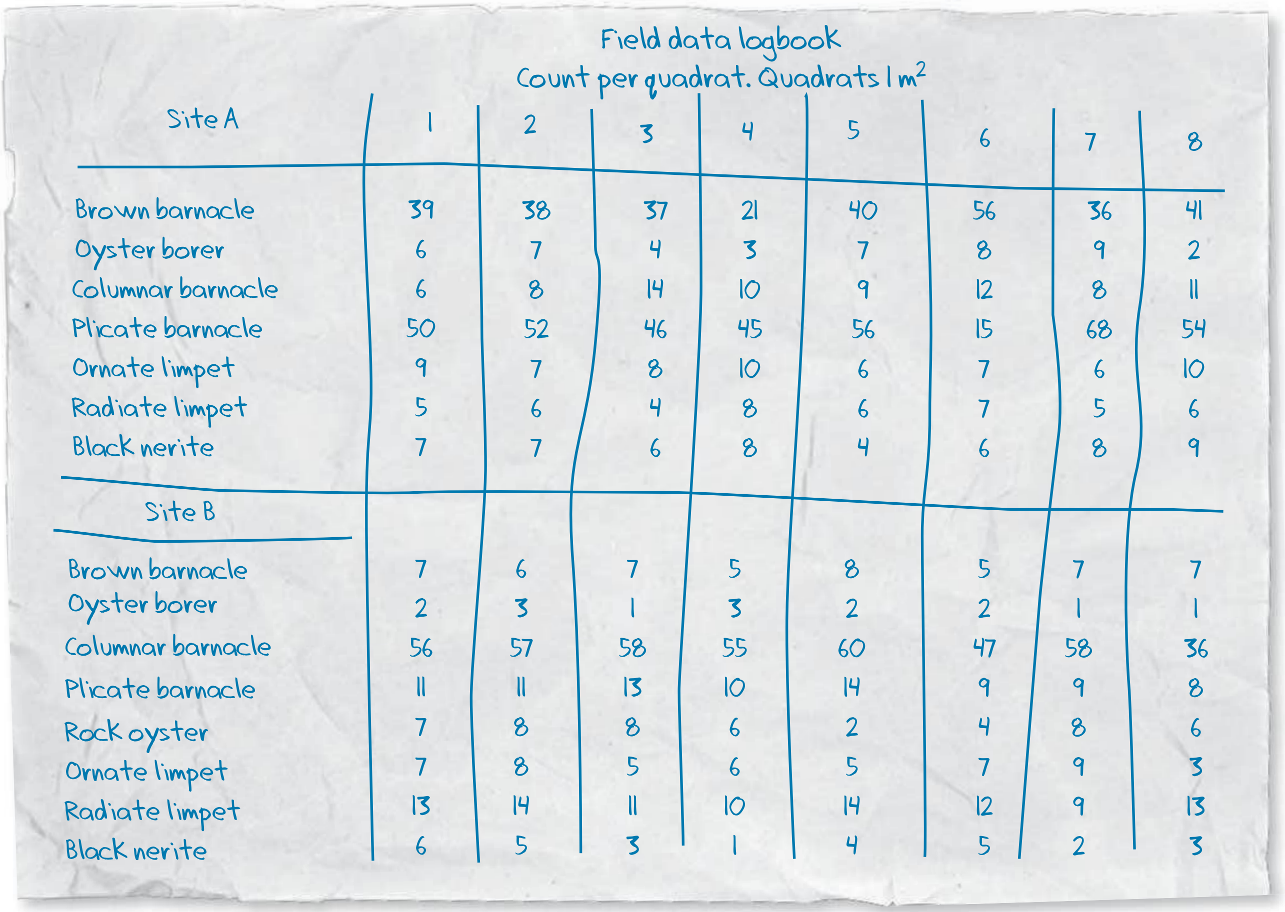
1. During the field study, students counted the number of animals in each quadrat and recorded them in a logbook (below). Complete the table below the raw data with the total number of each species at each site, the mean number of animals per quadrat, and the median and mode for each set of samples per 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 $m^2$ 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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# 30 Classifying Ecosystems 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 you 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 21) what code will you give your sample area? Use the website (see Weblinks or Activity 21) 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 KEY TERMS AND IDEAS: Did You Get it?

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

biological species ..........

cladogram ..........

phylogeny ..........

quadrat ..........

transect ..........

**A** A measured and marked region used to isolate a sample area.

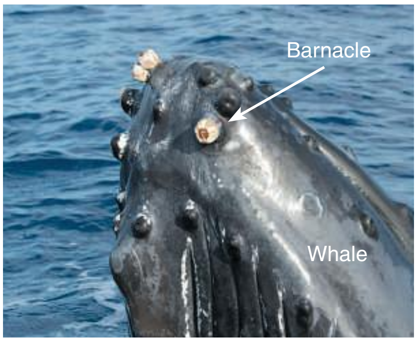
**B** The evolutionary history of a species or group in terms of lines of descent.

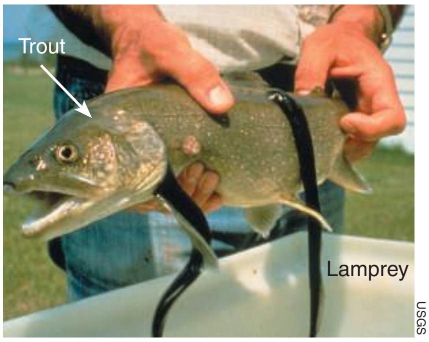
**C** A line across a habitat along which organisms are sampled at set intervals to determine changes in community composition.

**D** A phylogenetic tree constructed using a cladistic approach.

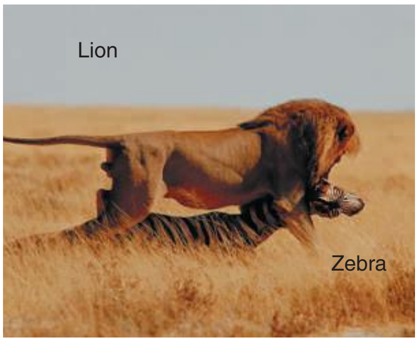
**E** A group of organisms that are capable of interbreeding to produce fertile offspring.

2. Describe the species interactions below as mutualism, commensalism, amensalism, predation, or parasitism, and note which species benefits and which is harmed (if any).





USGS

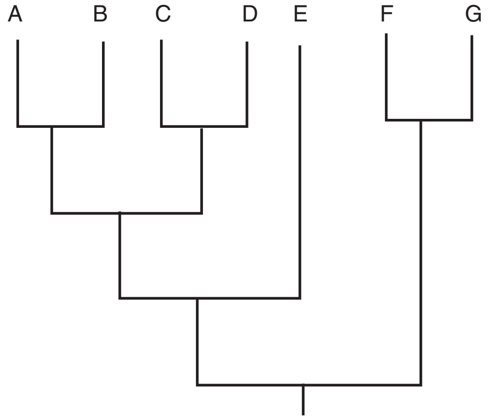


(a) ____________________

(b) ____________________

(c) ____________________

3. Study the phylogenetic relationship below:



(a) Circle and label a monophyletic group. Write the letters of the species included here: ____________________

(b) Circle and label paraphyletic group. Write the letters of the species included here and explain why its paraphyletic:

____________________

(c) Circle a polyphyletic group and explain why it is polyphyletic: ____________________

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# 32 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. Carry out a method to find the biodiversity of this community.

3. Produce a cladogram for species relatedness from the table of comparative features below:

Species

| Comparative features | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|---|---|---|---|---|---|---|---|
| A | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| B | ✗ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| C | ✗ | ✗ | ✓ | ✓ | ✓ | ✓ | ✓ |
| D | ✗ | ✗ | ✗ | ✓ | ✓ | ✓ | ✓ |
| E | ✗ | ✗ | ✗ | ✓ | ✓ | ✓ | ✗ |
| F | ✗ | ✗ | ✗ | ✗ | ✗ | ✗ | ✓ |
| G | ✗ | ✗ | ✗ | ✗ | ✓ | ✓ | ✗ |
| H | ✗ | ✗ | ✗ | ✗ | ✓ | ✗ | ✗ |

(a) Which feature is common to all species 1 to 7? ____________________

(b) Which species is the outgroup? ____________________

(c) Which species is most closely related to 4? ____________________

(d) Which species is most closely related to 6? ____________________

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UNIT 3
Topic 2

# Functioning Ecosystems

**Key terms**

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

**Activity number**

## Energy transfers and nutrient cycling in ecosystems

*Key skills and knowledge*

☐ 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. **33 34 45**

☐ 2 Describe energy transfer through ecosystems in food chains and food webs. Identify trophic levels including producers, primary consumers, and secondary and subsequent consumers. What limits the number of links in a food chain? **34**

☐ 3 Analyse data and calculate energy transfers through ecosystems to include: **35-42**
- loss of energy through radiation, reflection, and absorption,
- efficiencies of energy transfer from one trophic level to another,
- biomass at successive trophic levels.

☐ 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. **35**

☐ 5 Understand the terms gross primary production, net primary production, and secondary production. What is meant by trophic efficiency and how is it determined? Explain how productivity and efficiency are increased in managed monoculture (as opposed to natural) systems. **41 42**

☐ 6 **PRAC** Measure the wet biomass of producer samples as part of an analysis of energy transfers between trophic levels. **42**

☐ 7 Interpret a general model of nutrient cycling between the abiotic and biotic components of an ecosystem. Identify processes involved in the cycling of matter and factors that affect the rate of nutrient recycling. **43**

☐ 8 In more detail than above, 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. **44-46**

## Niche, competition, and keystone species

*Key skills and knowledge*

☐ 9 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. Understand what is meant by the competitive exclusion principle and what it means for the distribution of species with overlapping niches. **47 48**

☐ 10 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). **48 49 50**

☐ 11 Using examples, explain the role of keystone species in the stability of community structure and function. **51**

☐ 12 Analyse data from an Australian ecosystem to identify a keystone species and predict the outcomes of removing the species from an ecosystem. **52**

☐ 13 **SHE** Suggest why conserving keystone species might be a better conservation strategy than other strategies (such as conservation of flagship species). **53**

# 33 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.

Cellular respiration generates ATP, an 'energy carrier', which provides the usable energy for essential life processes in **all organisms**, including growth and production of biomass.

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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# 34 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.

**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.

**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).

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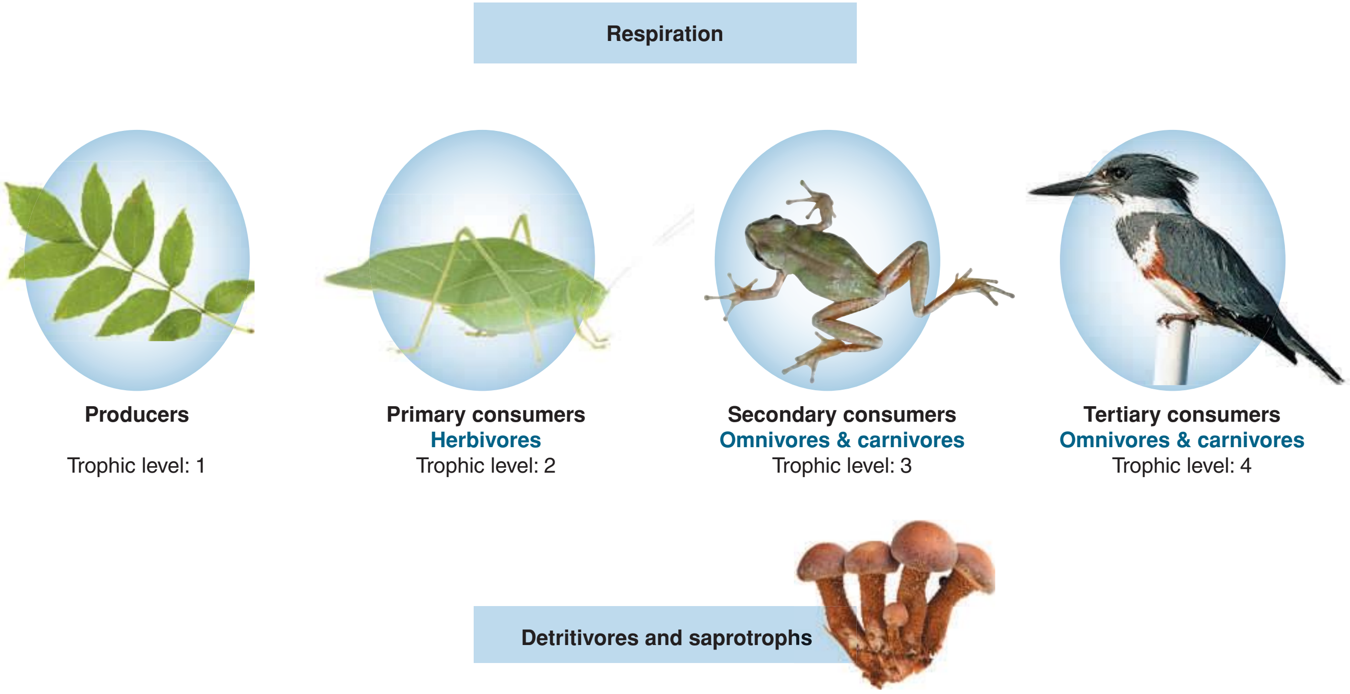
Detritivores and saprotrophs (decomposers) are consumers that obtain nutrients from dead organic matter (DOM). **Detritivores** ingest DOM (e.g. earthworms, millipedes) whereas **saprotrophs** (fungi, soil bacteria) secrete enzymes to digest the DOM extracellularly and absorb the nutrients released.

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



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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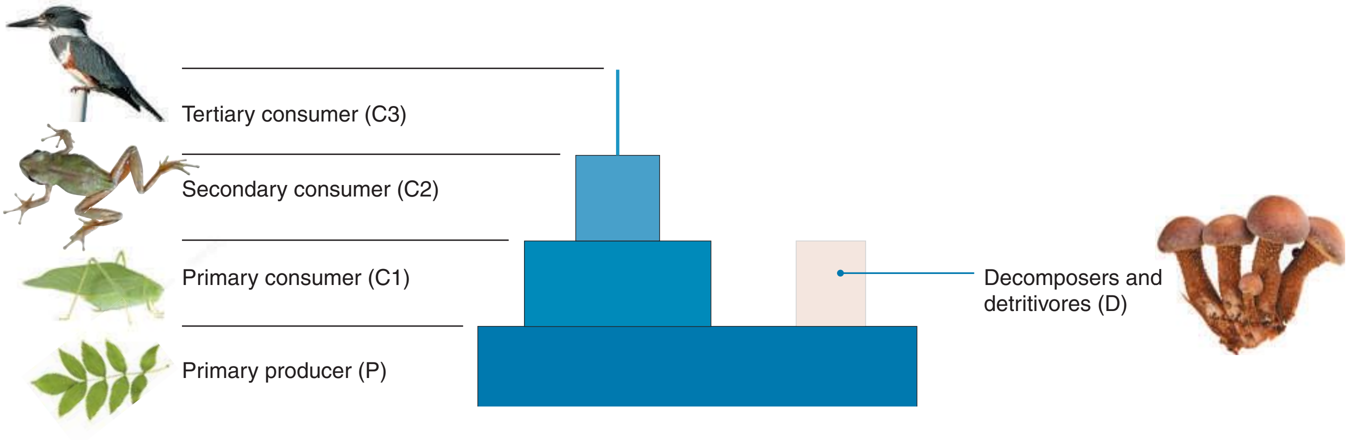
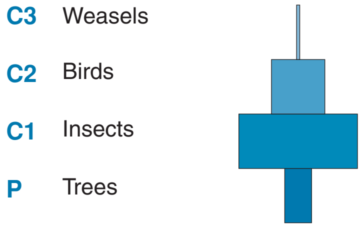
# 35 Ecological Pyramids

**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.

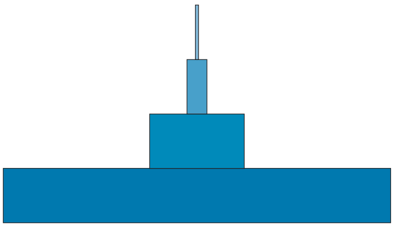


- The generalised ecological pyramid pictured above shows a conventional pyramid shape, with a large number (or biomass) of producers forming the base for an increasingly smaller number (or biomass) of consumers.
- Decomposers are placed at the level of the primary consumers and off to the side. They 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.



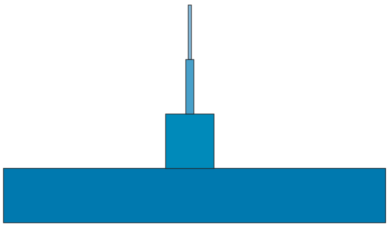
### Numbers in a forest community

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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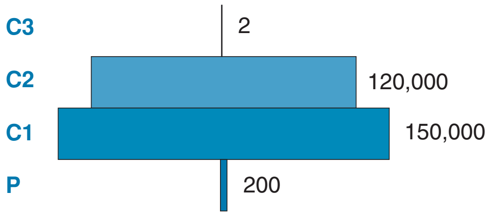
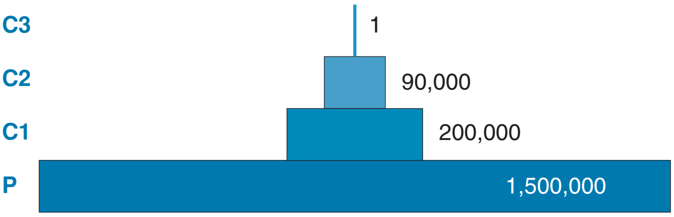


### Pyramid of numbers: forest community

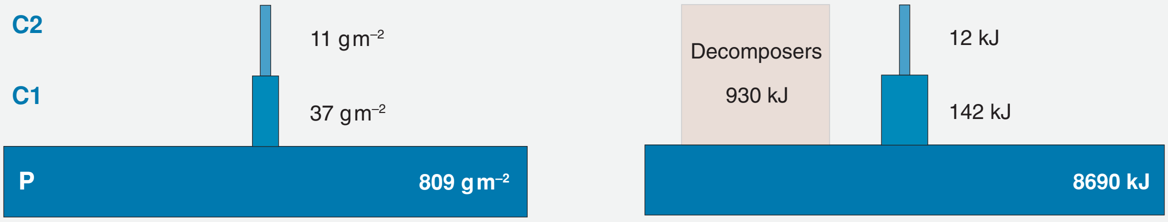
In a forest community, a few producers may support a large number of consumers. This is due to the large size of the producers; large trees can support many individual consumer organisms. The example above shows the numbers at each trophic level for an oak forest in England, in an area of 10 $m^2$.



### 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



**Biomass** **Energy**

- 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:

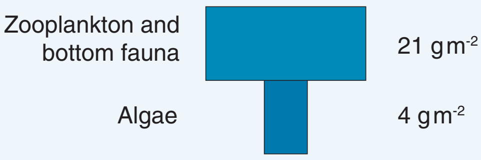
(c) Why is the amount of energy transferred from the producer level to primary consumers considerably less than the approximate 10% that commonly occurs in many other communities?

(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.



**Biomass**

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

# 36 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.

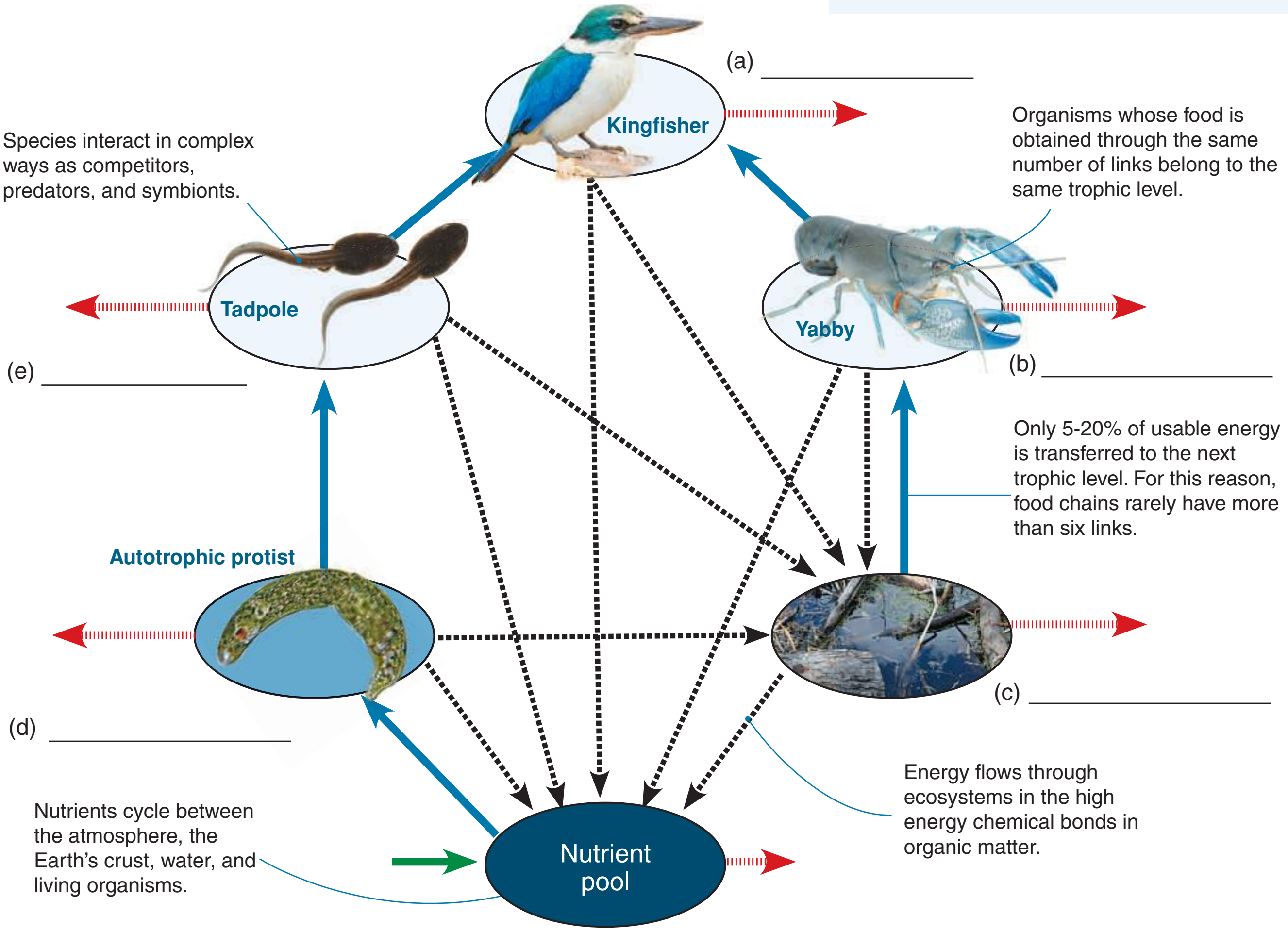
## The complexity of food webs varies

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



Species interact in complex ways as competitors, predators, and symbionts.

Organisms whose food is obtained through the same number of links belong to the same trophic level.

Only 5-20% of usable energy is transferred to the next trophic level. For this reason, food chains rarely have more than six links.

Energy flows through ecosystems in the high energy chemical bonds in organic matter.

Nutrients cycle between the atmosphere, the Earth's crust, water, and living organisms.

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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# 37 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.

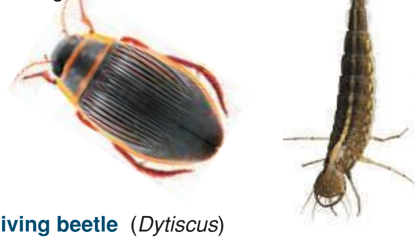
**Autotrophic protists**
e.g. *Chlamydomonas* (left), *Euglena* (right)
Microscopic, autotrophic protists. Two of many species that form the phytoplankton.

**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.

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**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.

**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.

**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.

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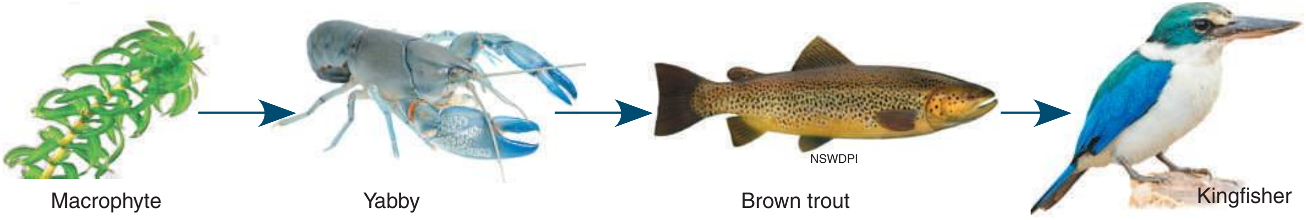
1. From the information provided for the lake food web components on the previous page, construct ten different food chains (using their names only) to show the feeding relationships between the organisms. Some food chains may be shorter than others and most species will appear in more than one food chain. An example has been completed for you.

Example 1:



(a) ______________________________

(b) ______________________________

(c) ______________________________

(d) ______________________________

(e) ______________________________

(f) ______________________________

(g) ______________________________

(h) ______________________________

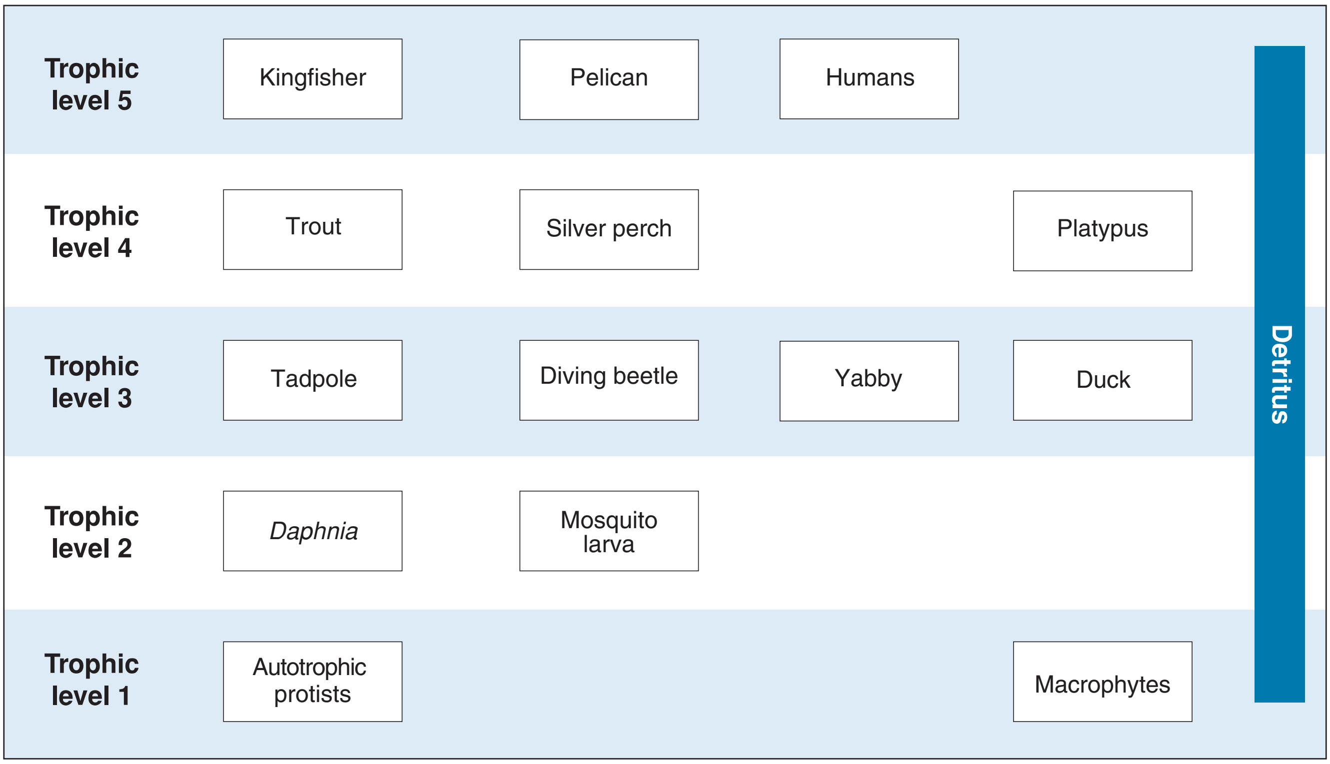
(i) ______________________________

(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 | |

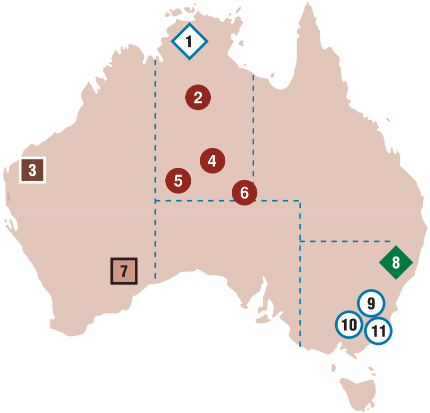
# 38 Dingo Food Webs

**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 | ● **Arid & semi-arid central Australia** | 1480 stomachs | □ **Arid south-west Australia** | 131 faeces/ stomachs |
|---|---|---|---|---|---|
| Dusky rat | 33.8 | Rabbit | 37.9 | Rabbit | 63.4 |
| Magpie goose | 32.5 | Cattle | 23.3 | Red kangaroo | 32.1 |
| Agile wallaby | 15.1 | Long-haired rat | 17.6 | Cattle | 7.6 |
| Northern ringtailed possum | 9.7 | Red kangaroo | 10.2 | Red fox | 3.8 |
| Grass species | 7.1 | Central netted dragon | 7.8 | Little crow | 2.3 |
| Feral water buffalo | 5.8 | Small mammal (undetermined sp.) | 3.8 | Bobtail skink | 1.5 |
| Feral pig | 3.5 | House mouse | 3.6 | Feral cat | 1.5 |
| Unidentified matter | 2.6 | Grasshopper | 2.7 | Centipede/millipede | 0.8 |
| Antilopine wallaroo | 1.8 | Bearded dragon | 2.2 | Dingo | 0.8 |
| Northern brown bandicoot | 1.4 | Zebra finch | 2.1 | Grasshopper | 0.8 |
| Feral cattle | 1.3 | Bird (undetermined species) | 2.0 | | |
| Bird (undetermined species) | 0.7 | Feral cat | 1.8 | | |
| Insect (undetermined species) | 0.7 | Galah | 1.8 | | |
| Beetle | 0.4 | Budgerigar | 1.5 | | |

| ■ **Semi-arid north-west Australia** | 413 faeces/ stomachs | ○ **Cool coastal mountains SE Australia** | 2063 faeces/ stomachs | ◆ **Humid coastal mountains E Australia** | 1993 faeces |
|---|---|---|---|---|---|
| Red kangaroo/euro | 80.6 | Swamp wallaby | 17.9 | Swamp wallaby | 30.5 |
| Cattle | 11.4 | Wallaby (undetermined spp.) | 15.8 | Bush rat | 12.2 |
| Sheep | 8.0 | Wombat | 15.0 | Red-necked wallaby | 11.1 |
| Bird (undetermined species) | 5.6 | Animal remains (unidentified) | 11.5 | Brushtail possums | 6.9 |
| Reptile (undetermined species) | 3.4 | Rabbit | 10.5 | Bandicoots (long-nosed, Southern brown) | 6.8 |
| Insects (undetermined species) | 2.9 | Common ringtail possum | 8.0 | Rabbit | 6.4 |
| Echidna | 2.2 | Waterbird (undetermined sp.) | 7.7 | Antichinuses (brown, dusky) | 5.8 |
| Dingo | 1.7 | Red-neck wallaby | 5.3 | Parma wallaby | 4.6 |
| Feral cat | 0.5 | Possum (undetermined species) | 5.1 | Common ringtail possum | 4.4 |
| Bat (undetermined species) | 0.2 | Rat (undetermined species) | 5.0 | Ring-necked pademelon | 3.8 |
| Fish (undetermined species) | 0.2 | Little penguin | 4.4 | Echidna | 3.5 |
| Red fox | 0.2 | Fish (undetermined species) | 3.7 | Long-nosed potoroo | 1.7 |
| Rothschild's rock wallaby | 0.2 | Mutton bird | 3.6 | Greater glider | 1.5 |
| | | Echidna | 3.3 | | |

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):

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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# 39 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 x $10^{-12}$ 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).

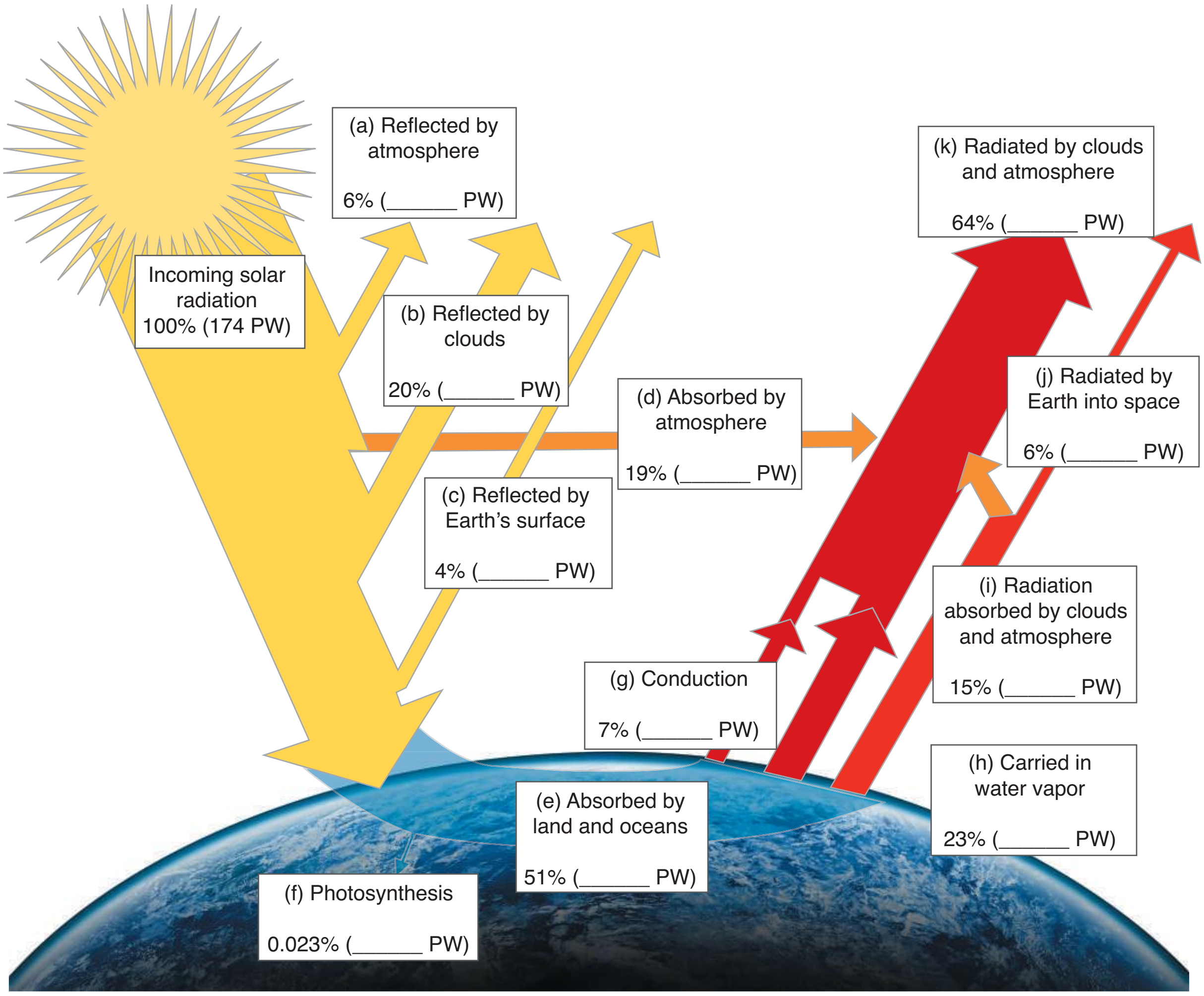
The tropics receive the full amount of sunlight and energy available. This causes heating, which carries water into the air, creating a hot, wet climate.

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 reaches the Earth's surface. Some (0.023%) of this 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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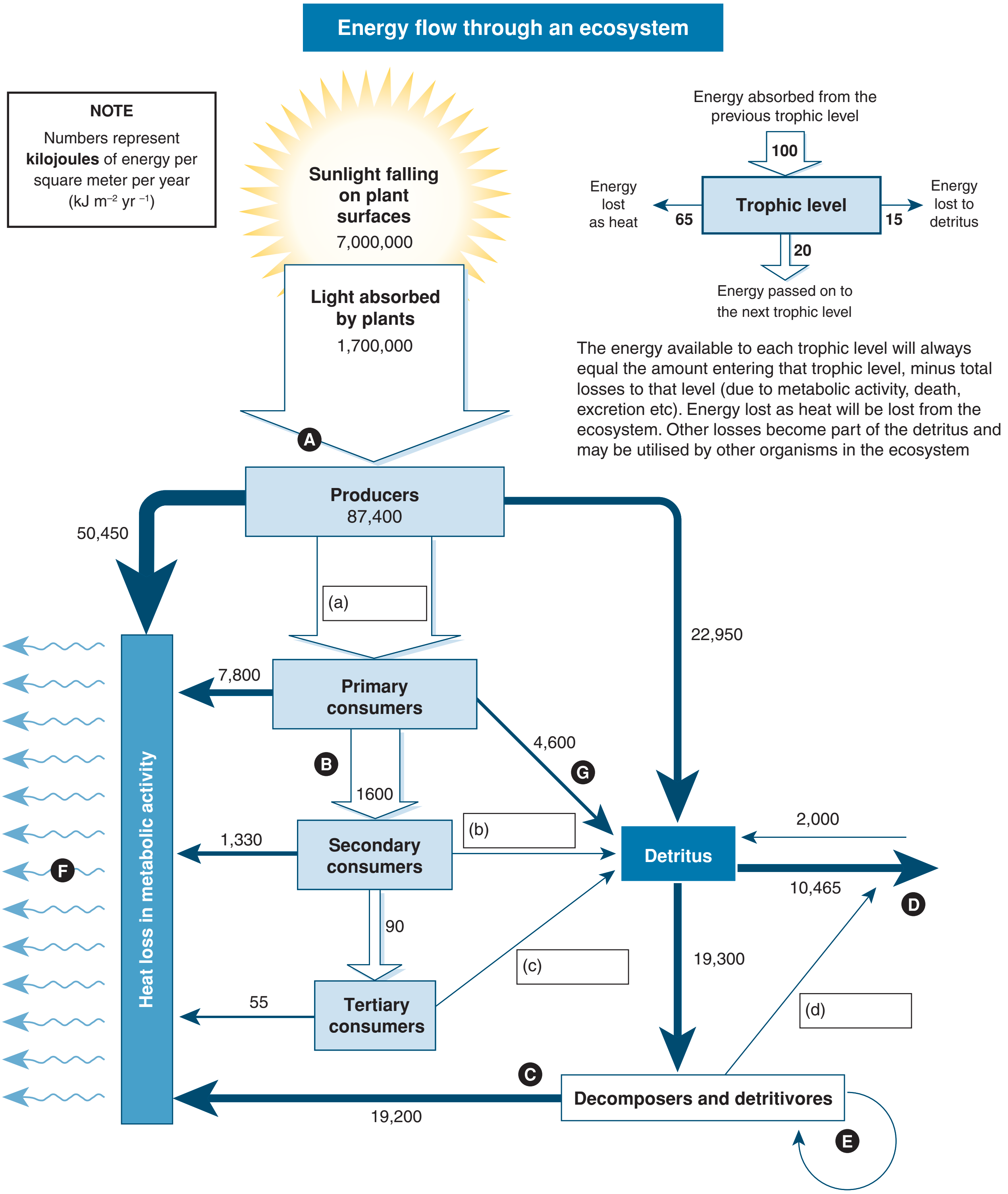
# 40 Quantifying Energy Flow in an Ecosystem

**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**

**NOTE**

Numbers represent **kilojoules** of energy per square meter per year (kJ m$^{-2}$ yr$^{-1}$)

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.

B.

C.

D.

E.

F.

G.

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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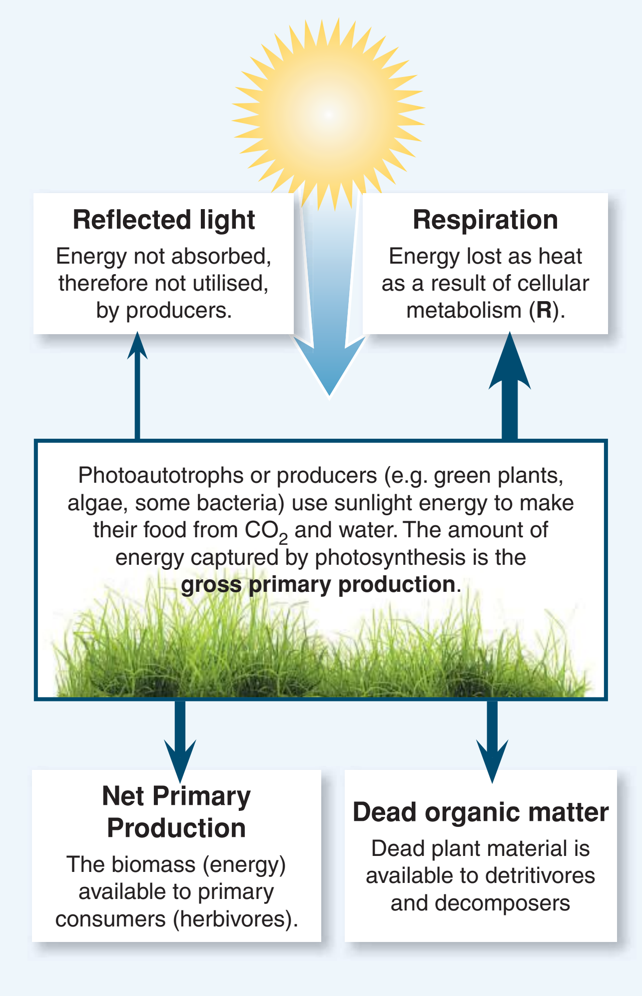
# 41 Productivity and Efficiency

**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.



**Reflected light**

Energy not absorbed, therefore not utilised, by producers.

**Respiration**

Energy lost as heat as a result of cellular metabolism (**R**).

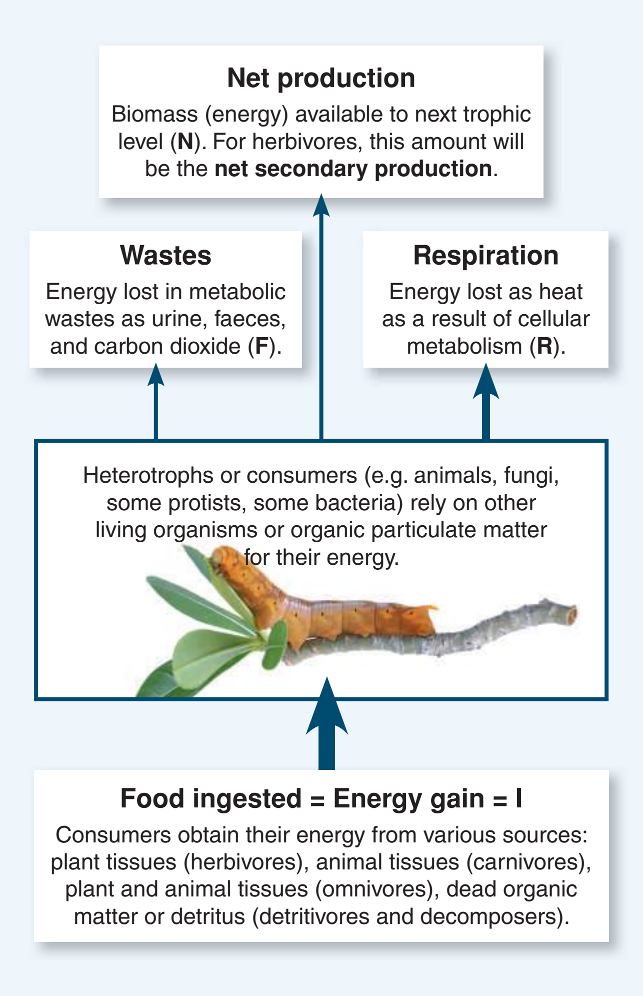
Photoautotrophs or producers (e.g. green plants, algae, some bacteria) use sunlight energy to make their food from $CO_2$ and water. The amount of energy captured by photosynthesis is the **gross primary production**.

**Net Primary Production**

The biomass (energy) available to primary consumers (herbivores).

**Dead organic matter**

Dead plant material is available to detritivores and decomposers



**Net production**

Biomass (energy) available to next trophic level (**N**). For herbivores, this amount will be the **net secondary production**.

**Wastes**

Energy lost in metabolic wastes as urine, faeces, and carbon dioxide (**F**).

**Respiration**

Energy lost as heat as a result of cellular metabolism (**R**).

Heterotrophs or consumers (e.g. animals, fungi, some protists, some bacteria) rely on other living organisms or organic particulate matter for their energy.

**Food ingested = Energy gain = I**

Consumers obtain their energy from various sources: plant tissues (herbivores), animal tissues (carnivores), plant and animal tissues (omnivores), dead organic matter or detritus (detritivores and decomposers).

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

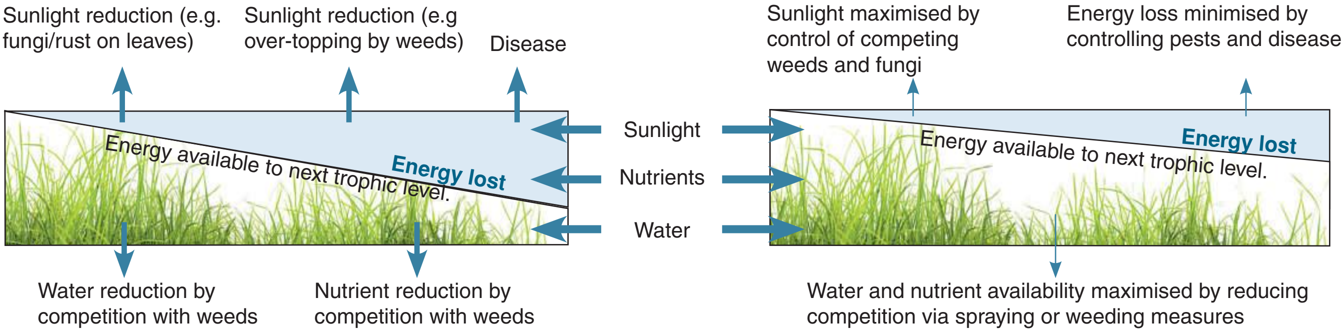
- The energy entering ecosystems is fixed by producers at a rate that depends on limiting factors such as temperature and the availability of light, water, and nutrients such as nitrogen.
- This energy is converted to biomass by anabolic reactions. The rate of biomass production (net primary productivity), 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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# 42 Investigating Trophic Efficiencies

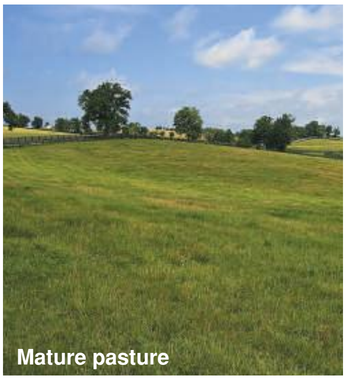
**Key Idea**: The efficiency of energy transfers in ecosystems can be quantified if we know the amount of energy entering and leaving the different trophic levels.

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 analysis 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

| | 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 |

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.

   (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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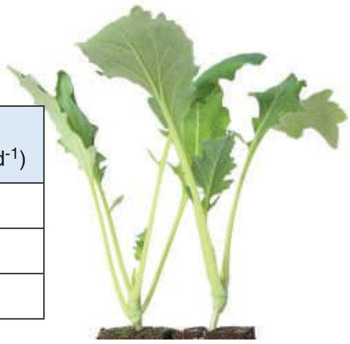
**Table 1: Group 1's results for growth of 10 *B. rapa* plants over 21 days**

| 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*.

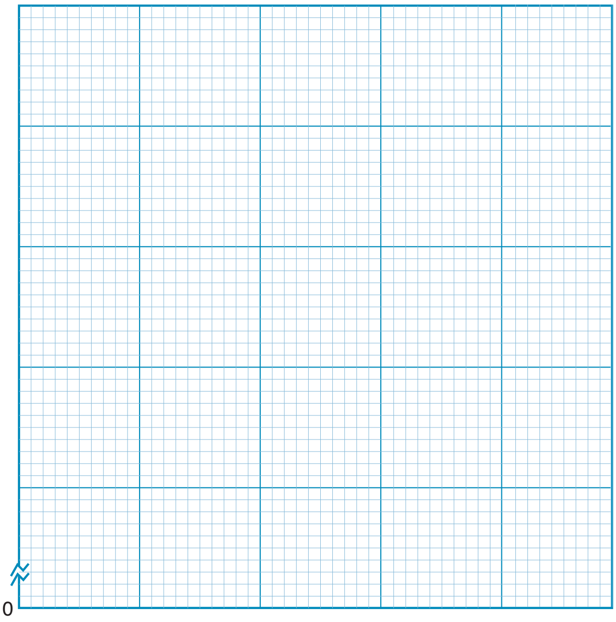
**Table 2: Class results for NPP of *B. rapa* over 21 days**

| 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?

## 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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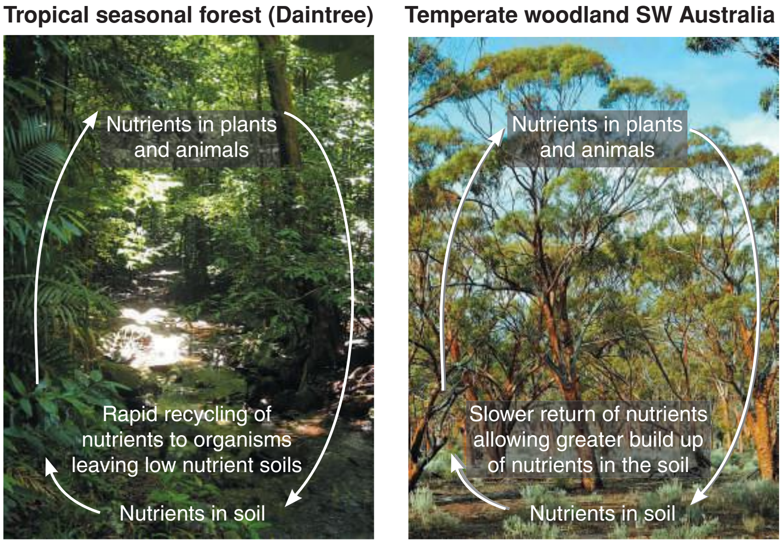
# 43 Nutrient Cycles

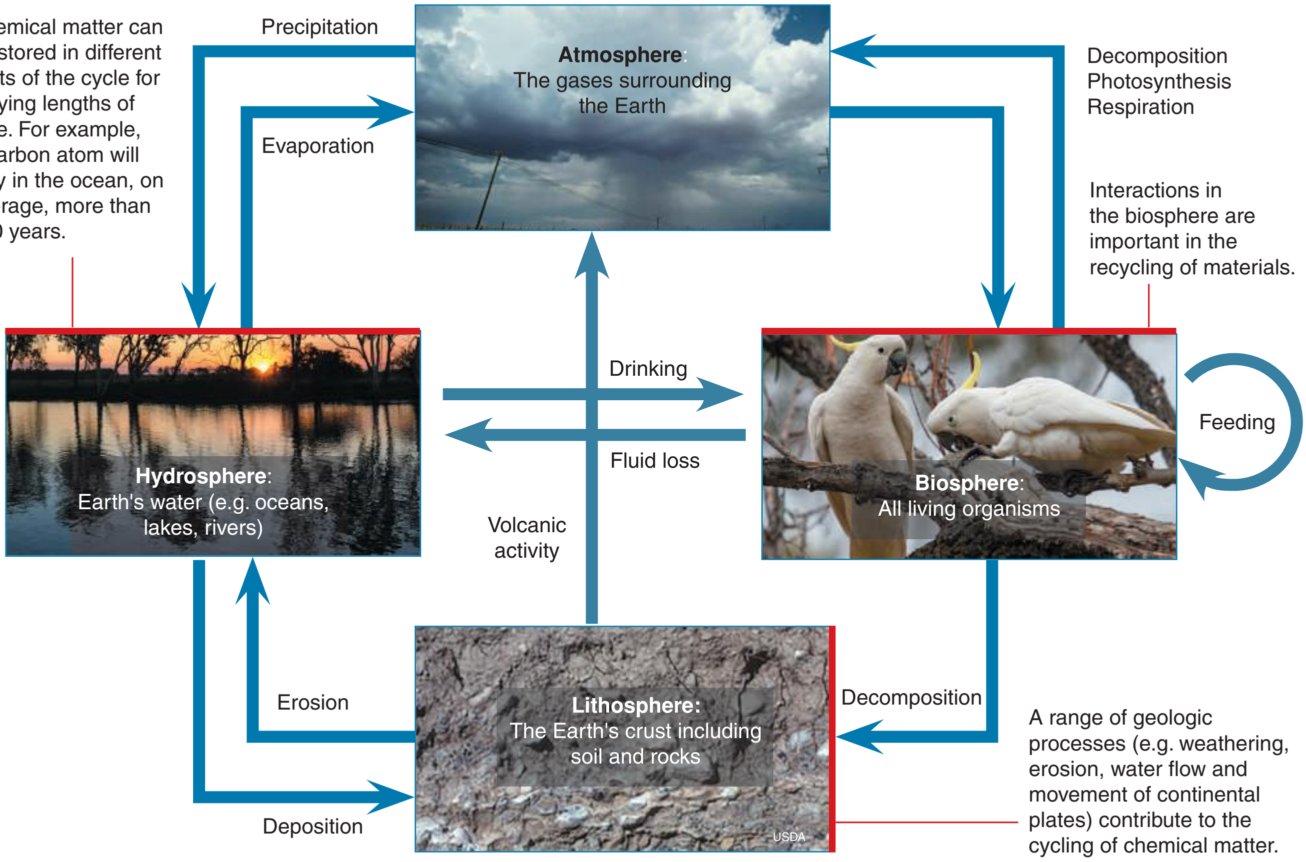
**Key Idea**: Matter cycles through the biotic and abiotic compartments of Earth's ecosystems. These cycles are called nutrient cycles or biogeochemical cycles.

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 **bio**logical, **geo**logical, 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



Chemical matter can be stored in different parts of the cycle for varying lengths of time. For example, a carbon atom will stay in the ocean, on average, more than 500 years.

Interactions in the biosphere are important in the recycling of materials.

A range of geologic processes (e.g. weathering, erosion, water flow and movement of continental plates) contribute to the cycling of chemical matter.

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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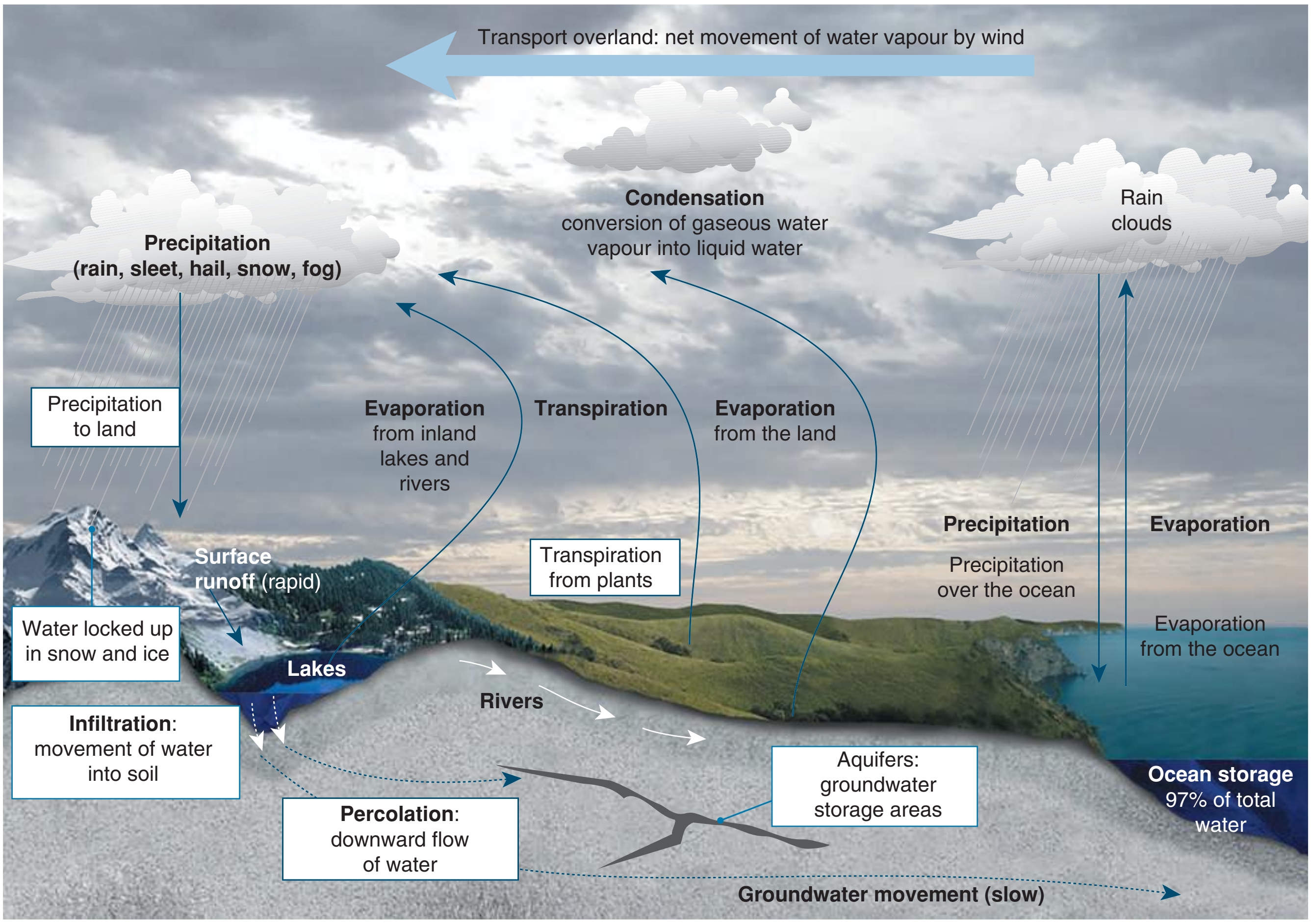
# 44 The Water Cycle

**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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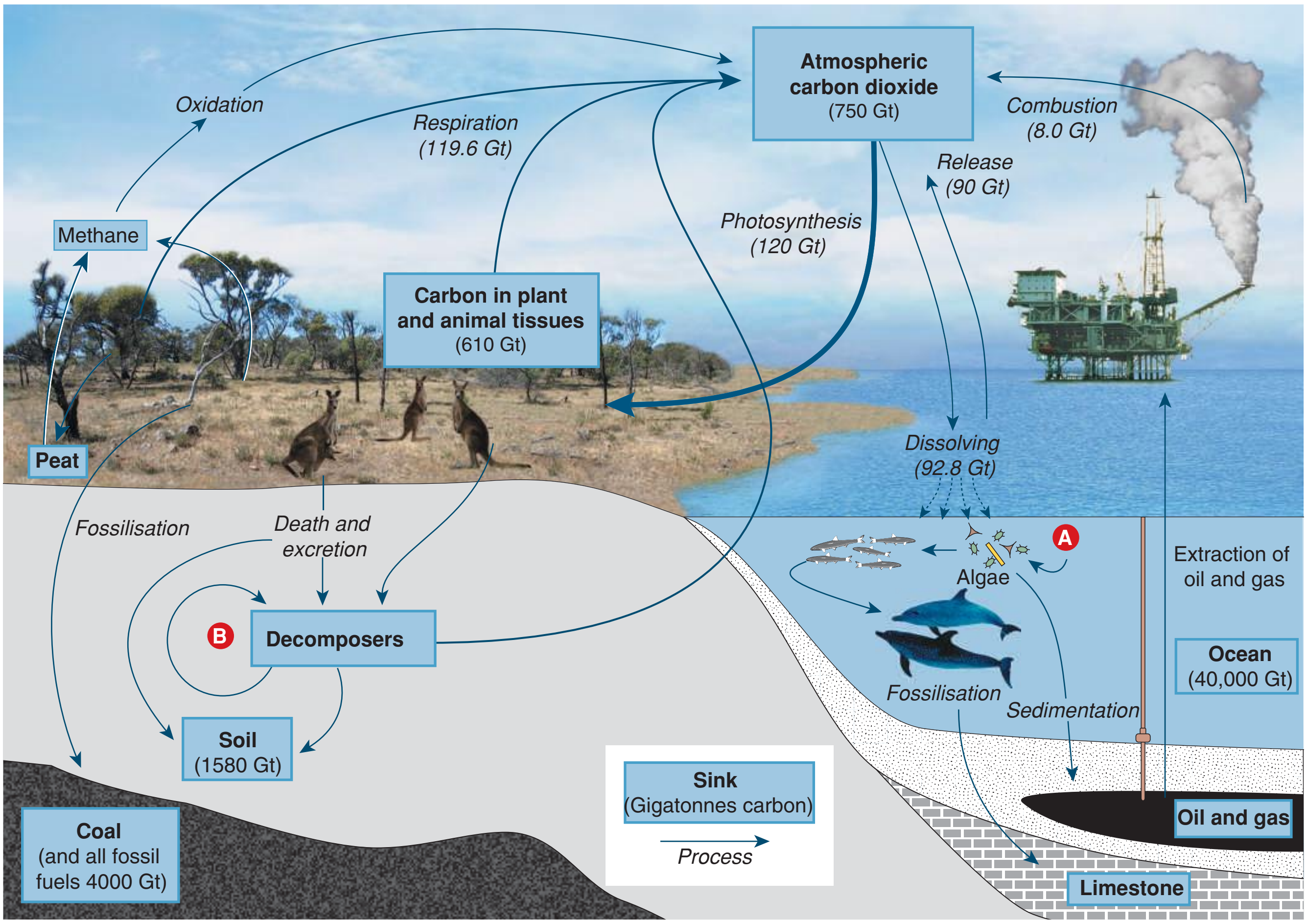
# 45 The Carbon Cycle

**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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**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 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.

**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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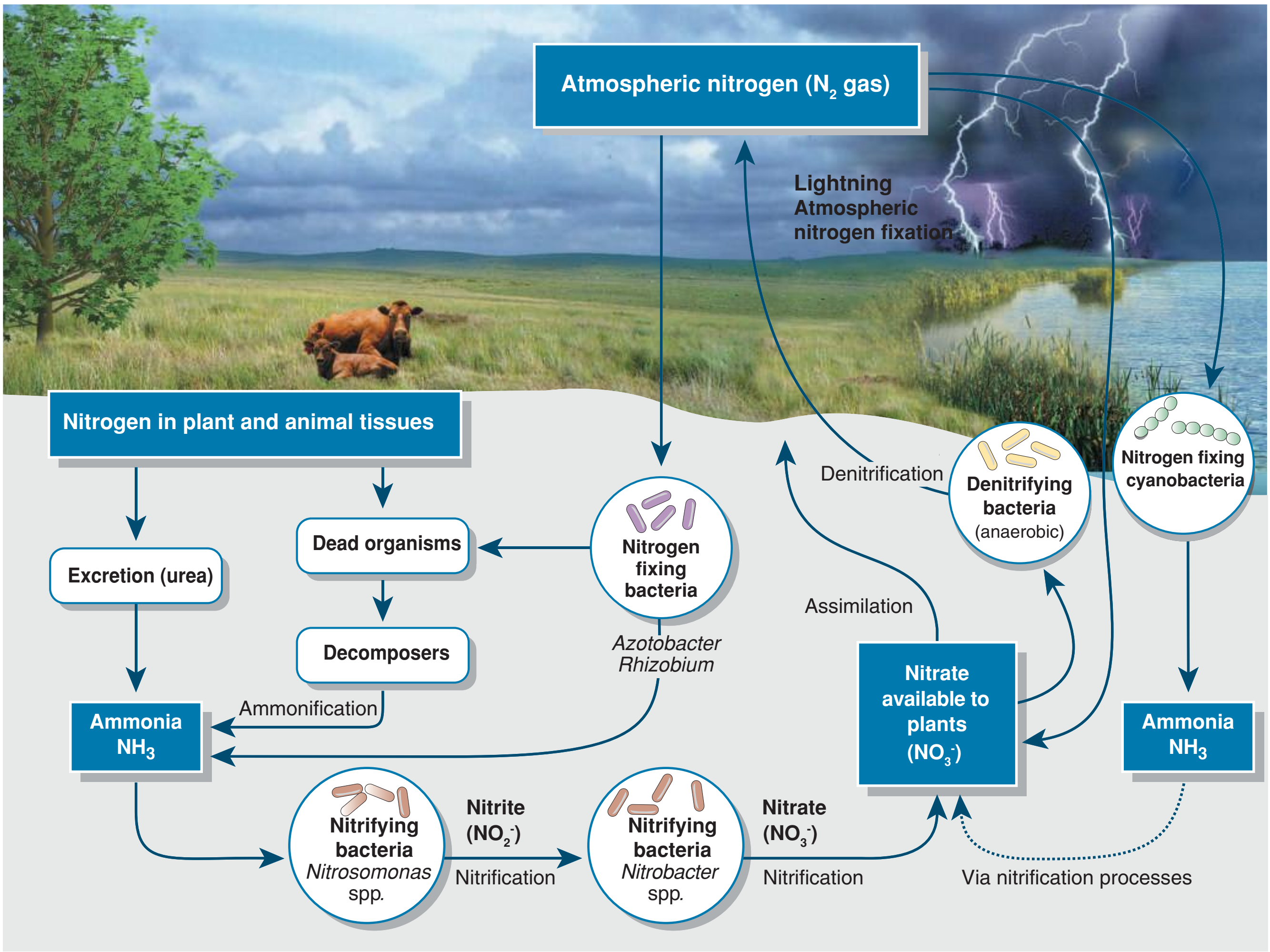
# 46 The Nitrogen Cycle

**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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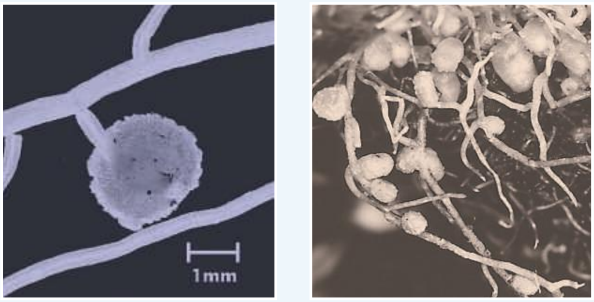
## Nitrogen fixation in root nodules

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.



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) ______________________

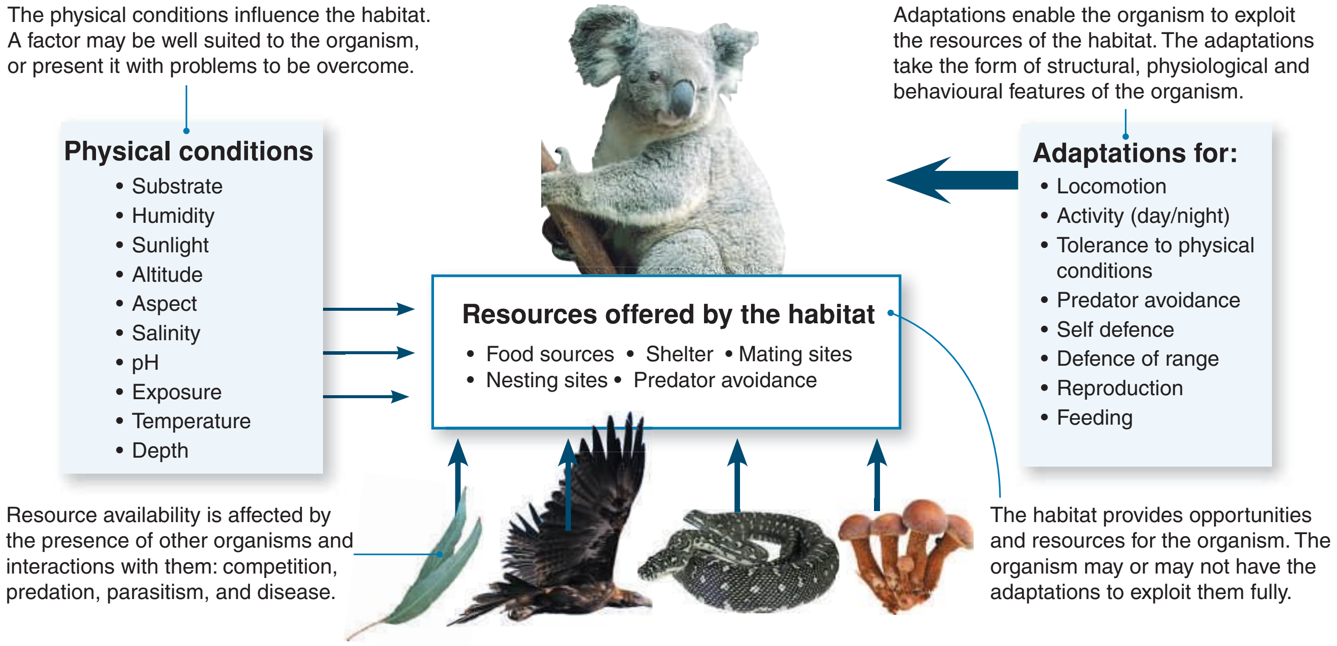
______________________

**ISBN: 978-1-927309-86-5**

# 47 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

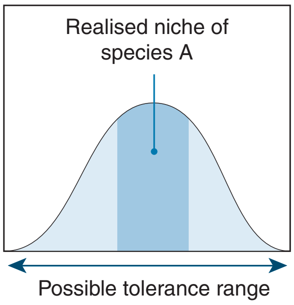
**Resources offered by the habitat**

- 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.

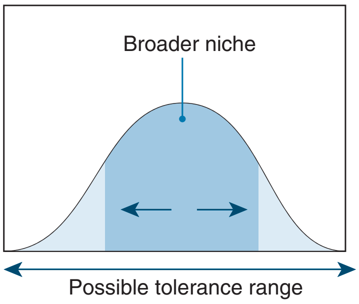
The habitat provides opportunities and resources for the organism. The organism may or may not have the adaptations to exploit them fully.

### The realised niche



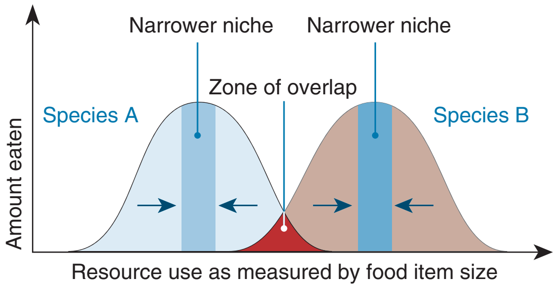
The tolerance range represents the **fundamental niche** of a species. The **realised niche** of a species is narrower than this because of competition with other species.

### 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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# 48 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 you think 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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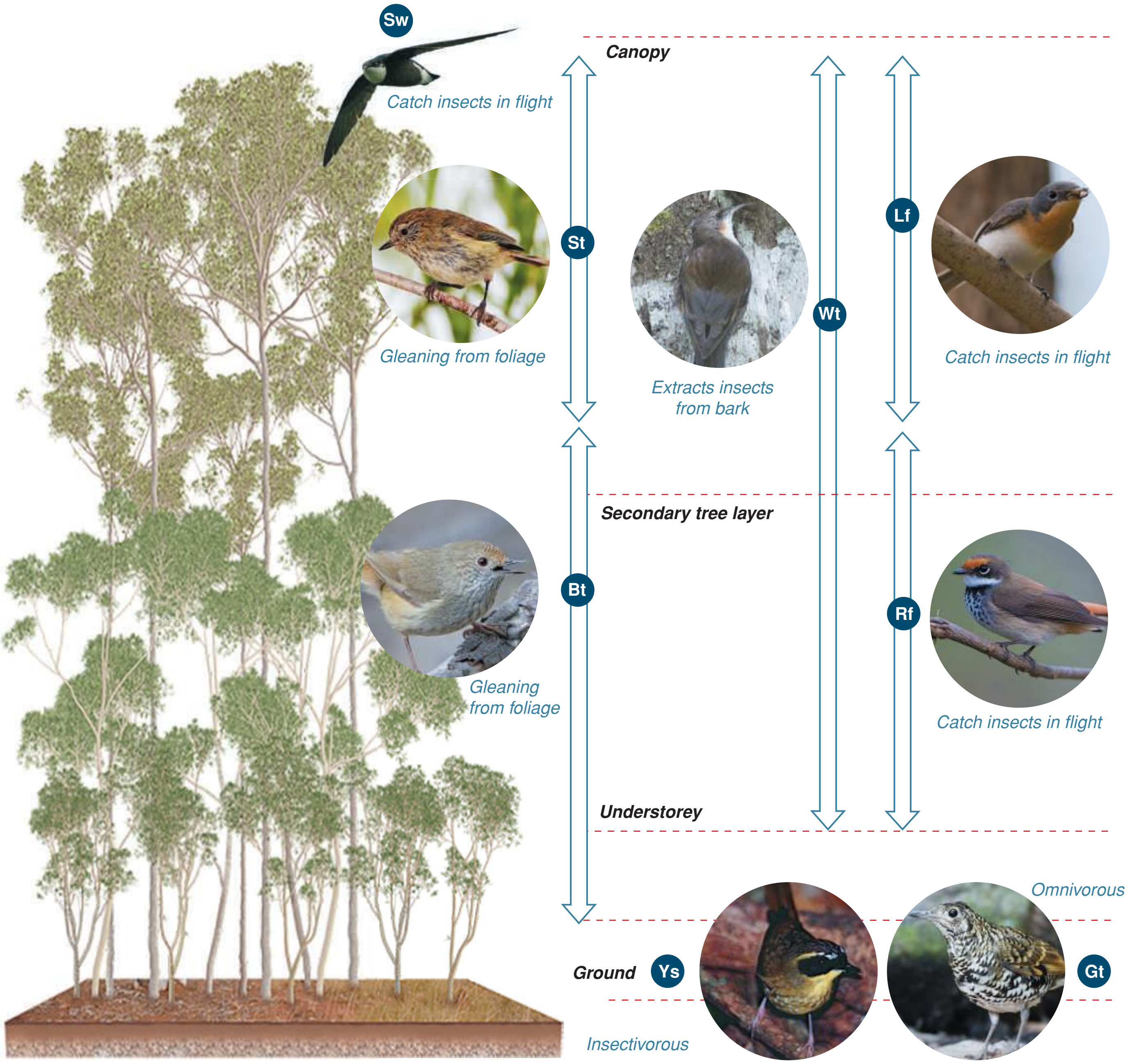
# 49 Competition and Species Distribution

**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

**Bt** Brown thornbill
PHOTO: JJ Harrison cc 3.0

**Sw** Spine-tailed swift
PHOTO: Ron Knight cc 2.0

**St** Striated thornbill
PHOTO: JJ Harrison cc 3.0

**Lf** Leaden flycatcher
PHOTO: Jim Bendon cc 2.0

**Gt** Ground thrush
PHOTO: JJ Harrison cc 3.0

**Wt** White-throated treecreeper
PHOTO: Lip Kee cc 2.0

**Ys** Yellow-throated scrubwren
PHOTO: Bernard Dupont cc 2.0

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Photocopying Prohibited

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?

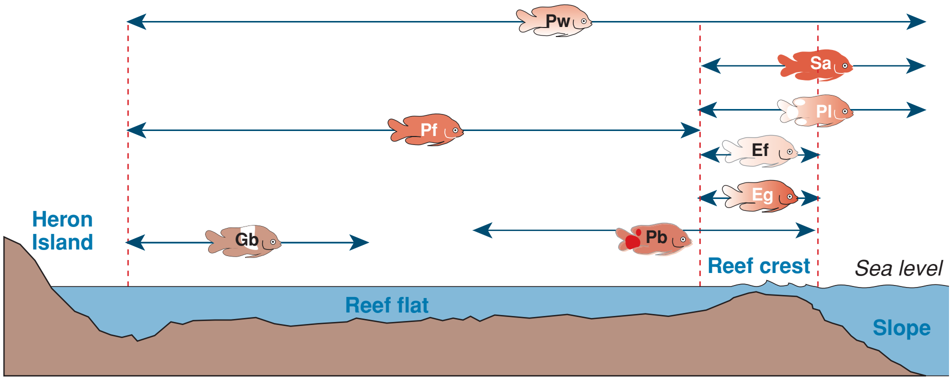
3. The yellow-throated scrubwren (Ys) and ground thrush (Gt) are both ground feeders. Explain why both species are able to inhabit the ground layer in eucalypt forest:

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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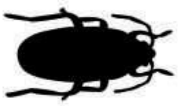
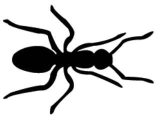
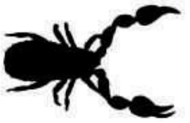
# 50 Identifying Species in a Eucalypt Forest

**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 |
|---|---|---|---|---|
| <br>**Hard wing covers**<br>BEETLES<br>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. | <br>**Membranous wings**<br>BUGS<br>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. | <br>**Narrow waist**<br>ANTS<br>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). | <br>**Tail nippers**<br>EARWIGS<br>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. | <br>**Spiky legs**<br>COCKROACHES<br>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** |
| <br>**4-10 false legs**<br>CATERPILLARS<br>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. | <br>**Very small and slender**<br>THRIPS<br>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. | <br>**Often long wings**<br>BOOKLICE (BARKFLY)<br>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. | <br>**Have a folded tail-like furcula for jumping**<br>SPRINGTAILS<br>Important detritivores. Abundant in soil and leaf litter, especially after rain (prefer moist conditions). Omnivorous, mainly eating bacteria and fungi, and dead organic matter. | <br>**Obvious fangs**<br>SPIDERS<br>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** |
| <br>**Small size, simple unsegmented body**<br>MITES<br>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. | <br>**Flat pear-shaped body**<br>PSEUDOSCORPIONS<br>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). | <br>**Body segmented**<br>WOODLICE (SLATERS)<br>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. | <br>**Body flattened**<br>CENTIPEDES<br>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. | <br>**Body rounded**<br>MILLIPEDES<br>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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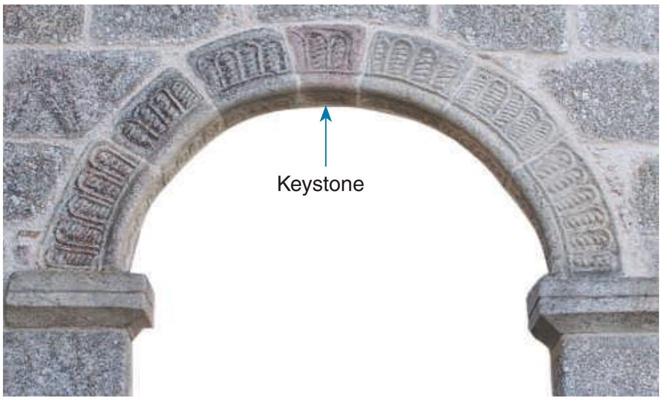
# 51 Keystone Species

**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.

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.

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.

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? ____________________

____________________

____________________

____________________

____________________

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## Australian keystone species


Tiger shark

Albert kok cc3.0


Cockatoo grass

Marjorie Lundgren cc3.0


Grey-headed flying fox

Andrew Mercer cc 4.0

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.

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.

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: ______________________________

______________________________

______________________________

**ISBN: 978-1-927309-86-5**

# 52 How Do We Recognise Keystone Species?

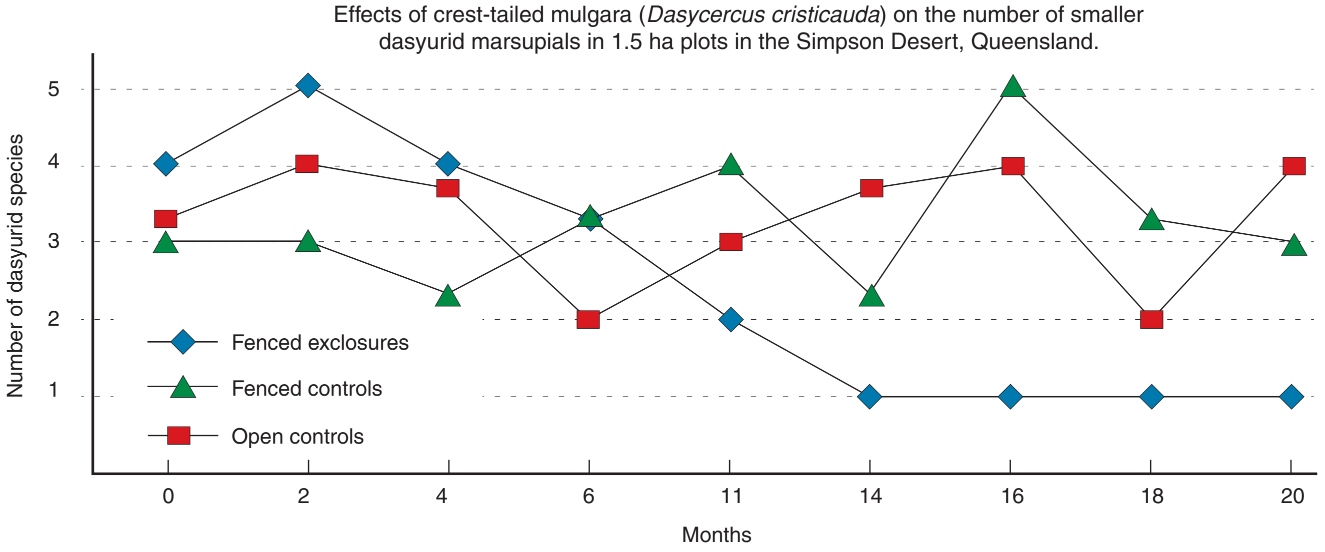
**Key Idea**: When mulgara were excluded from a fenced area, the number of smaller dasyurid species present reduced.

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.

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.



Data source: Dickman in Attiwell, 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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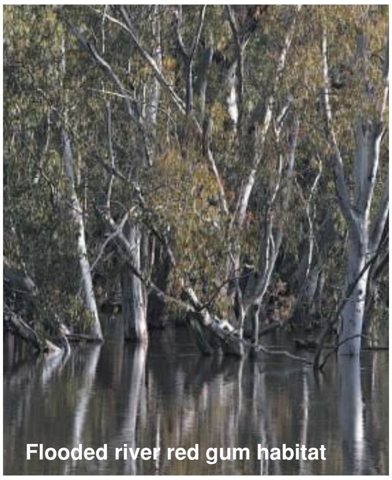
# 53 Keystone Species and Conservation

**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

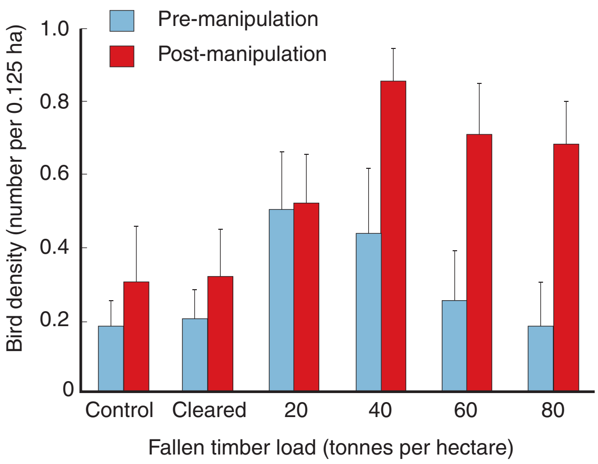
MargaretRDonald CC 4.0

## 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 habitat 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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# 54 KEY TERMS AND IDEAS: Did You Get It?

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

consumer ..............................

food chain ..............................

food web ..............................

keystone species ..............................

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.

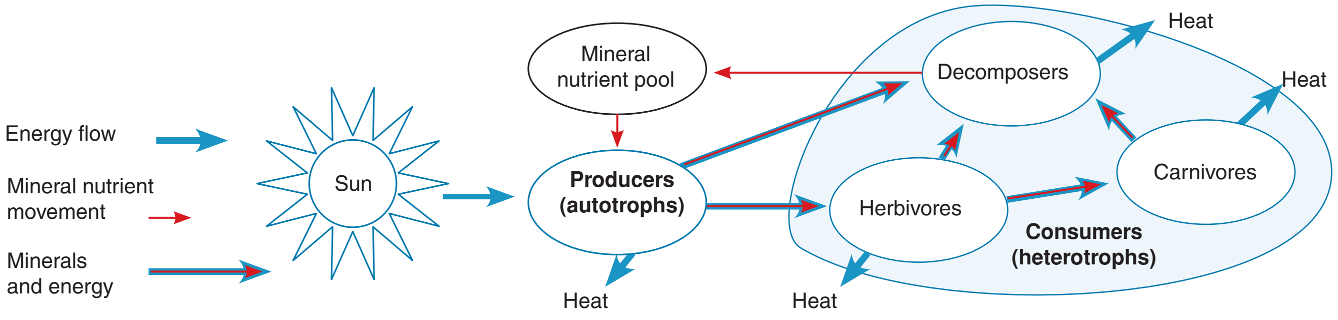
**C** An organism that obtains its carbon and energy from other organisms.

**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.

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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UNIT 3
Topic 2

# Population Ecology

### 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

**Activity number**

## Carrying capacity and limiting factors

*Key skills and knowledge*

☐ 1 Define the term carrying capacity. Explain how limiting factors determine the carrying capacity of environment. Discuss how changes in limiting factors can alter carrying capacity over time. What might cause changes in limiting factors? **55**

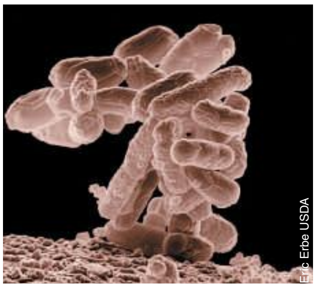
☐ 2 Identify biotic and abiotic limiting factors in the environment. Abiotic factors are density independent whereas biotic factors are density dependent. Understand that both types of factors may operate to create the fluctuations we see in natural populations. For example, a population may be regulated at near carrying capacity by density dependent factors, but be reduced to a low level by a natural disaster (density independent). **55**

☐ 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. **56**

☐ 4 Describe an example of how a biotic factor, e.g. level of available food/prey, can regulate population growth and size. How do predator-prey relationships result in cycles of population growth in both predator and prey populations? **57**

☐ 5 Describe an example of how an abiotic factor, e.g. rainfall, can regulate population growth and size over the long term. What abiotic factors are particularly important in the Australian environment and how do they operate? **58**

☐ 6 Use the Lincoln Index (N = M x n ÷ m) to estimate population size from primary and/or secondary data. **59**



Eric Erbe USDA

USFWS

## Exponential and logistic growth

*Key skills and knowledge*

☐ 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). **60**

☐ 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. **60**

☐ 9 **PRAC** Measure a population of microorganisms in a closed system (e.g. petri dish) to observe carrying capacity. **61**

☐ 10 Use a computer simulation to model continuous density-independent (exponential) and density-dependent (logistic) population growth. What is the effect of changing *r* (biotic potential or intrinsic rate of increase)? What happens if you introduce a lag into the logistic model. How does introducing a lag make the model more realistic? **62**

# 55 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.

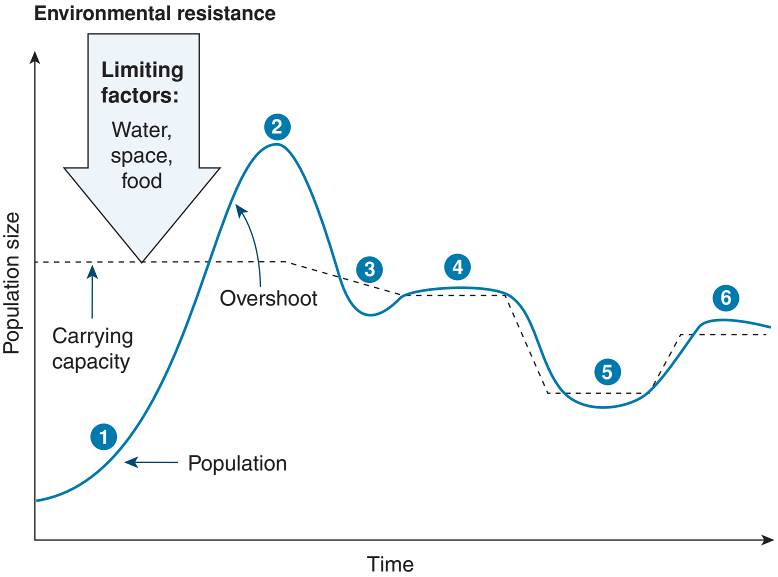
② The population overshoots the carrying capacity.

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:

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# 56 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:

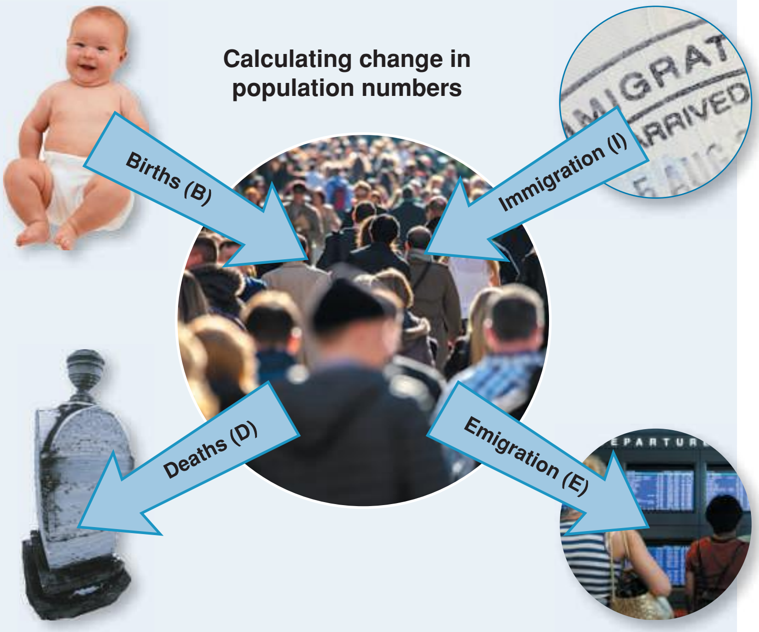
**Population growth =**
**Births – Deaths + Immigration – Emigration**
**(B) (D) (I) (E)**

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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# 57 Predation and Population Cycles

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

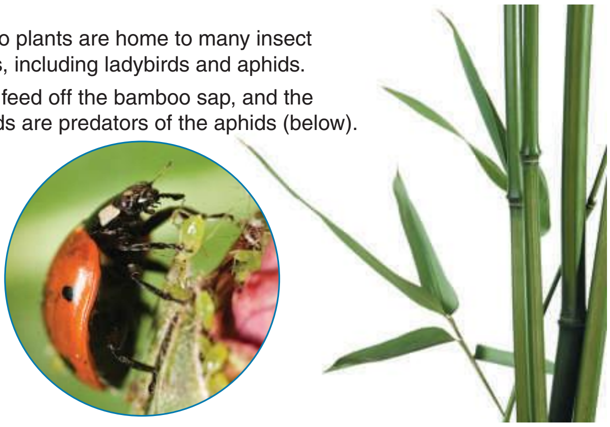
It was once thought that predators regulated the population numbers of their prey. However, we now know that this is not usually the case. Prey species are more likely to be regulated by other factors such as the availability of food. However, predator population cycles are often regulated by the availability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

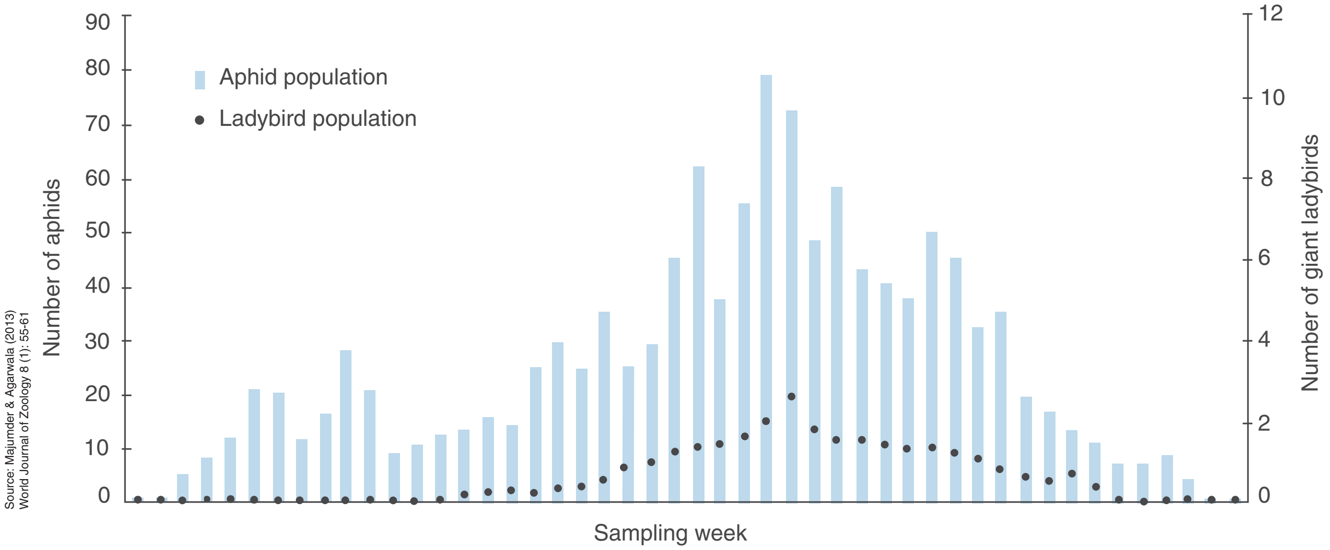
Giant ladybird beetles (*Anisolemnia dilatata*) feed exclusively on the woolly aphids of bamboo plants. There is some interest in using them as biological control agents to reduce woolly aphid numbers, and limit the damage woolly aphids do to bamboo plants.

The graph below shows the relationship between the giant lady bird 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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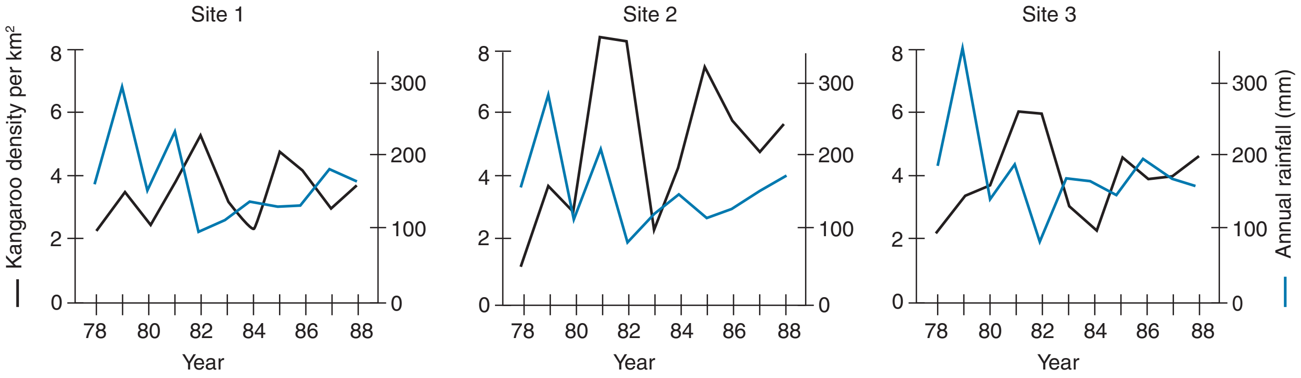
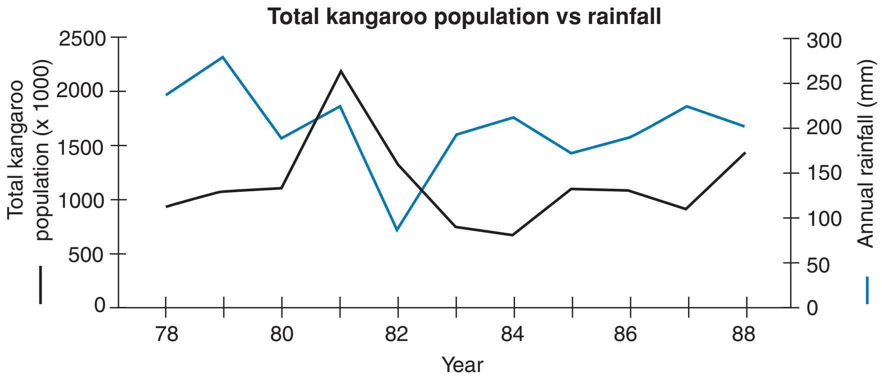
# 58 Abiotic Factors and Population Size

**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


Total kangaroo population vs 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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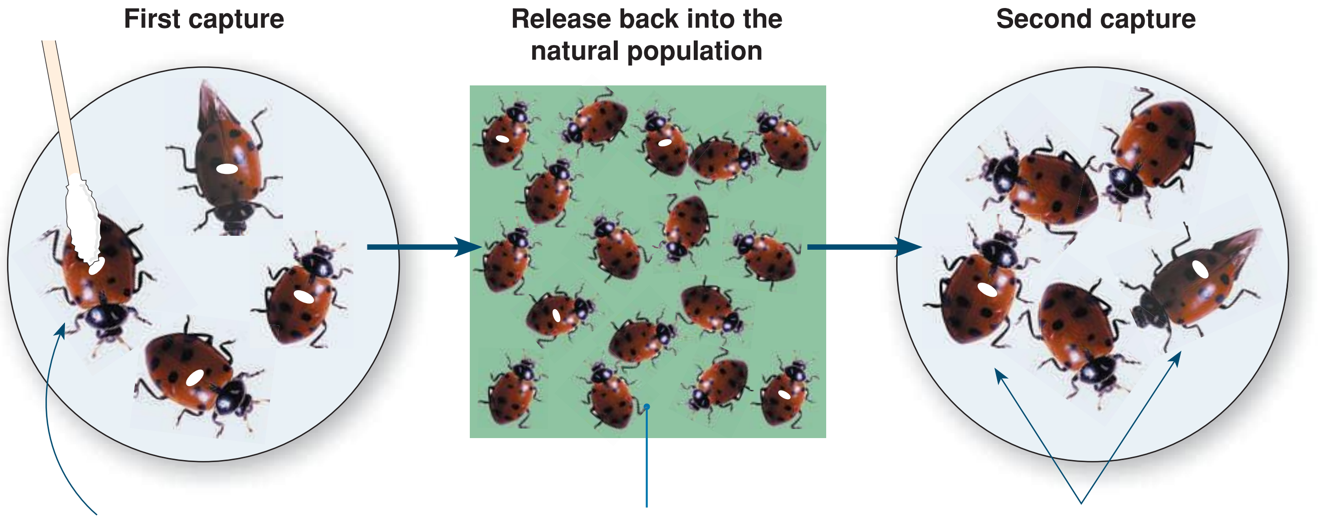
# 59 Estimating Population Size

**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.



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**

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

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.

Animals may be marked or tagged

USFWS

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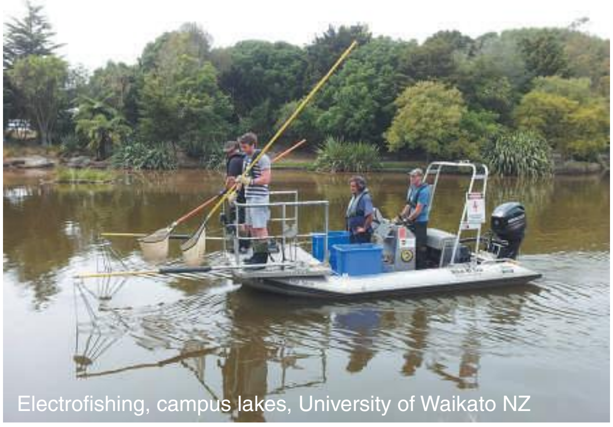
Researchers at New Zealand's University of Waikato used mark and recapture to obtain estimates of population number and biomass of four fish species and one hybrid in one of the campus lakes. Fish were sampled using electrofishing (right), which temporarily stuns the fish so that they can be netted.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



Electrofishing, campus lakes, University of Waikato NZ

Prof. Brendan Hicks, UOW

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:

| 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 method of sampling 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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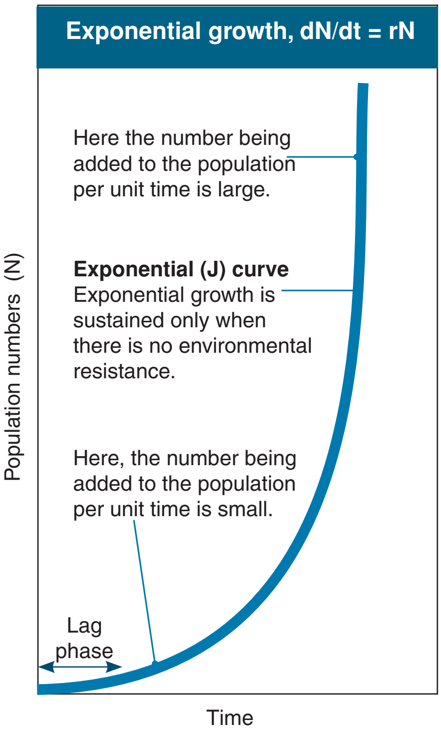
# 60 Patterns of Population Growth

**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? ______________________

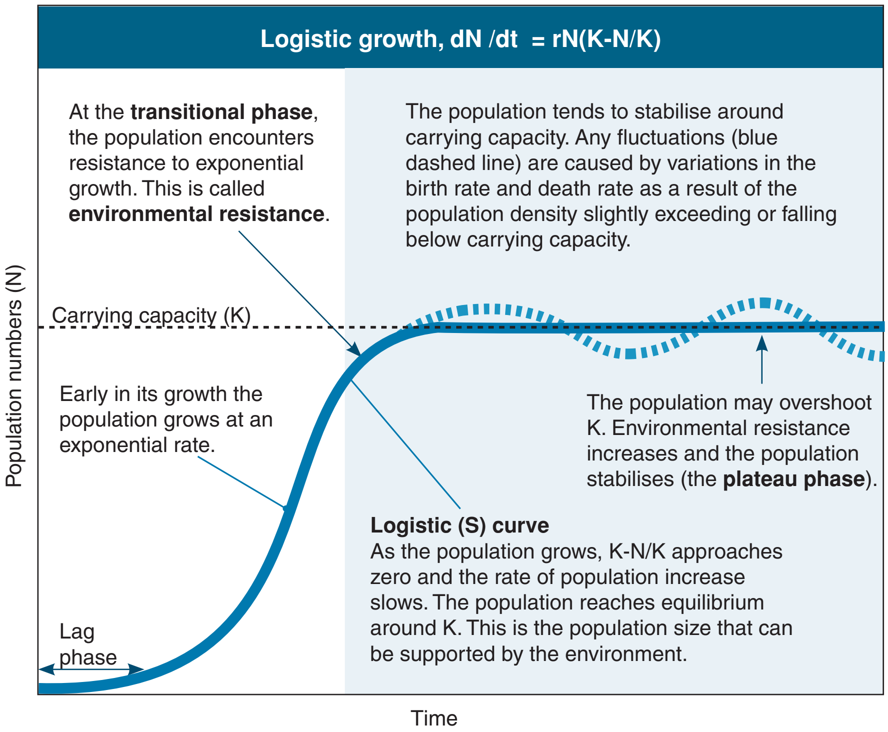
______________________________________________

**ISBN: 978-1-927309-86-5**

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, dN /dt = rN(K-N/K)**

At the **transitional phase**, the population encounters resistance to exponential growth. This is called **environmental resistance**.

The population tends to stabilise around carrying capacity. Any fluctuations (blue dashed line) are caused by variations in the birth rate and death rate as a result of the population density slightly exceeding or falling below carrying capacity.

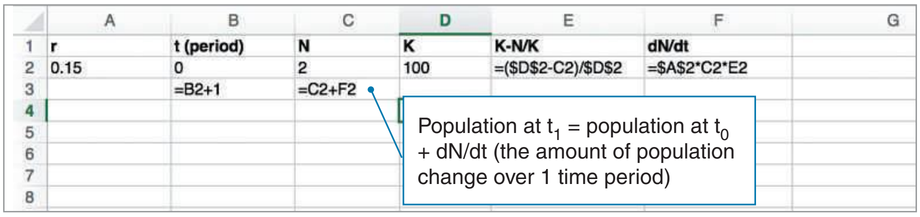
Early in its growth the population grows at an exponential rate.

The population may overshoot K. Environmental resistance increases and the population stabilises (the **plateau phase**).

**Logistic (S) curve**
As the population grows, K-N/K approaches zero and the rate of population increase slows. The population reaches equilibrium around K. This is the population size that can be supported by the environment.

## Logistic growth curve on a spreadsheet.

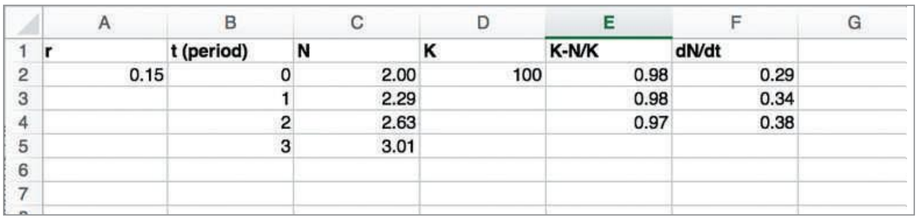
Plotting a logistic growth curve on a spreadsheet can help in understanding the effect of population size on the population growth rate and how the logistic equation describes this. For a hypothetical population of 2, r is 0.15 and K 100. The following formulae can be entered into the spreadsheet:



| | 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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# 61 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).

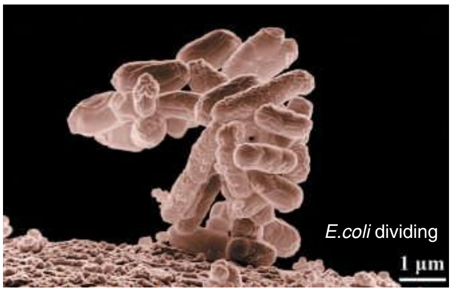
A spectrophotometer (left) is an instrument used to measure transmittance of a solution and so can be used to quantify bacterial growth where an increase in cell numbers results in an increase in turbidity.

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 |



*E.coli* dividing

USDA

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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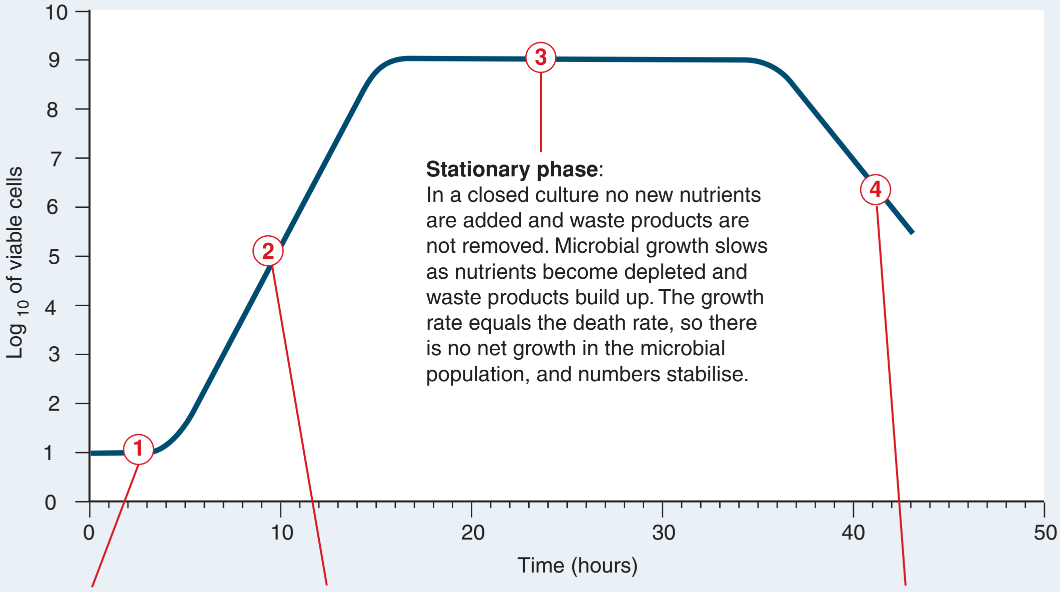
- When a population reaches the carrying capacity of an environment its growth rate slows to zero as deaths and emigration equal births and immigration. This reduction in growth is partially because resources are being replaced at the same rate they are being used, and there are no spare resources available 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)**



**Stationary phase**: In a closed culture no new nutrients are added and waste products are not removed. Microbial growth slows as nutrients become depleted and waste products build up. The growth rate equals the death rate, so there is no net growth in the microbial population, and numbers stabilise.

**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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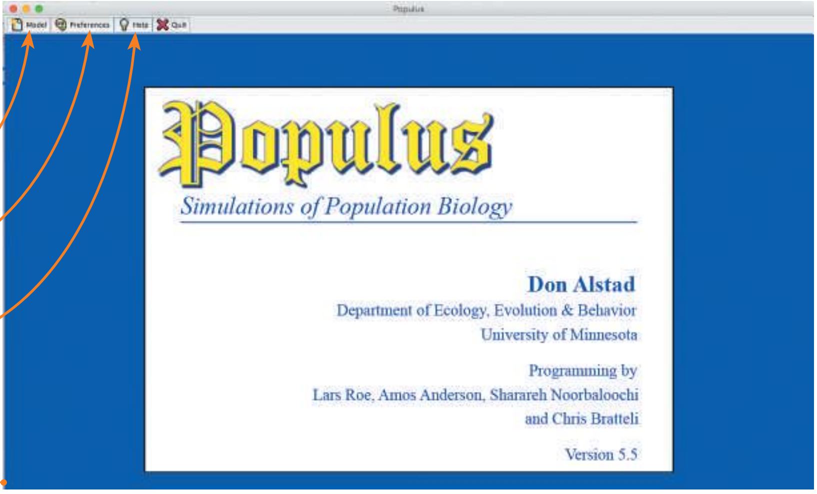
# 62 Modelling Population Growth

**Key Idea**: Computer programs can be used to model population growth. This activity uses Populus 5.5.

Population growth can be simulated using spreadsheets or computer programs. This activity uses Populus 5.5, 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 from **https://cbs.umn.edu/populus/overview**

(you can also download via Weblinks)



Populus

*Simulations of Population Biology*

**Don Alstad**

Department of Ecology, Evolution & Behavior

University of Minnesota

Programming by

Lars Roe, Amos Anderson, Sharareh Noorbaloochi and Chris Bratteli

Version 5.5

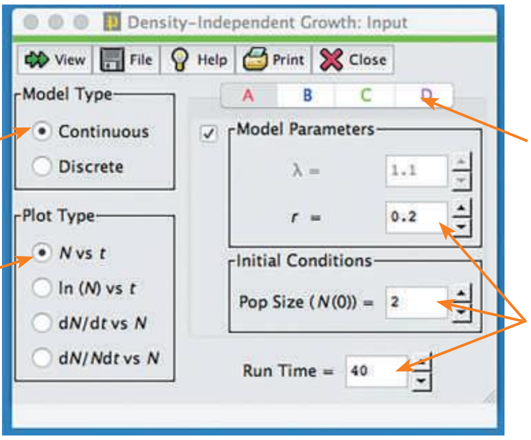
The opening screen looks like this.

- **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



Model Type
● Continuous
○ Discrete

Plot Type
● *N* vs *t*
○ ln (*N*) vs *t*
○ d*N*/d*t* vs *N*
○ d*N*/*N*d*t* vs *N*

☑ Model Parameters
λ = 1.1
*r* = 0.2

Initial Conditions
Pop Size (*N*(0)) = 2

Run Time = 40

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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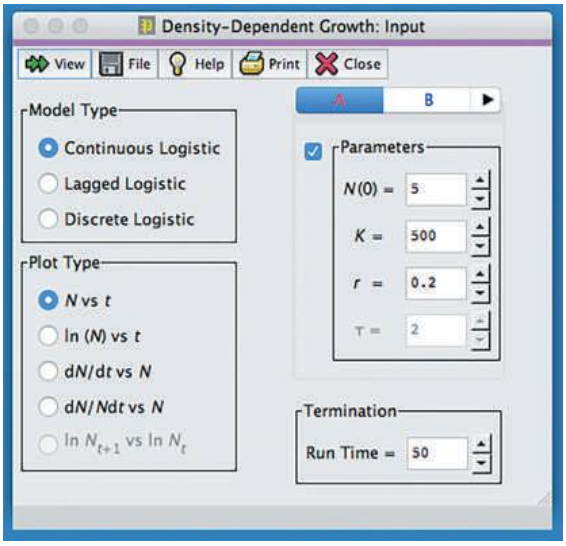
## Density dependent growth

- 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.



Model Type
● Continuous Logistic
○ Lagged Logistic
○ Discrete Logistic

Plot Type
● $N$ vs $t$
○ ln ($N$) vs $t$
○ dN/dt vs $N$
○ dN/Ndt vs $N$
○ ln $N_{t+1}$ vs ln $N_t$

☑ Parameters
$N(0)$ = 5
$K$ = 500
$r$ = 0.2
T = 2

Termination
Run Time = 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?

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

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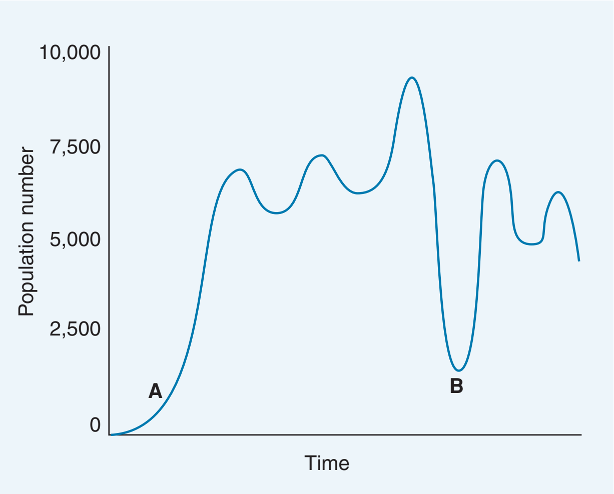
# 63 KEY TERMS AND IDEAS: Did You Get It?

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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## UNIT 3
## Topic 2

# Changing Ecosystems

### Key terms

biodiversity
climax community
ecological succession
ecosystem stability
fossil record
indigenous
K-selection
pioneer species
primary succession
*r*-selection
secondary succession

**Activity number**

## Ecological succession

*Key skills and knowledge*

☐ 1 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. **64**

☐ 2 Distinguish between primary and secondary succession, identifying the characteristic features of each type. Compare the time course for each type of succession. Why do secondary successions typically proceed more rapidly than primary successions? **64 65**

☐ 3 Describe features of pioneer species and explain how these make them effective colonisers. Identify typical pioneers in primary and secondary successions. What role do pioneer species have in creating an environment that will support the later communities (consider soil formation, moisture retention, shade, and moderation of environmental extremes)? **64 65**

☐ 4 Distinguish between *r*-selected and K-selected species and describe features correlated with each type. What type of selection (and species) would you predict would dominate in an early successional community? In a climax community? **67**

☐ 5 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. What factors are important in the colonisation (primary succession) or regeneration (secondary succession) of a habitat? **64 66 74**


Mikrolit' FAL


Julien Willem CC 3.0

## Interpreting the past and predicting the future

*Key skills and knowledge*

☐ 6 Analyse data from the fossil record to interpret past ecosystems, including changes to their biotic and abiotic components. How can information from fossils and their living representatives be used to infer what past environments were like. **68 69**

☐ 7 Predict the impact of human activity on biodiversity and the magnitude, duration, and rate of environmental change. **70**

☐ 8 **SHE** Understand the basis for establishing marine reserves and recognise that considerable evidence supports their role in protecting marine biodiversity. **71**

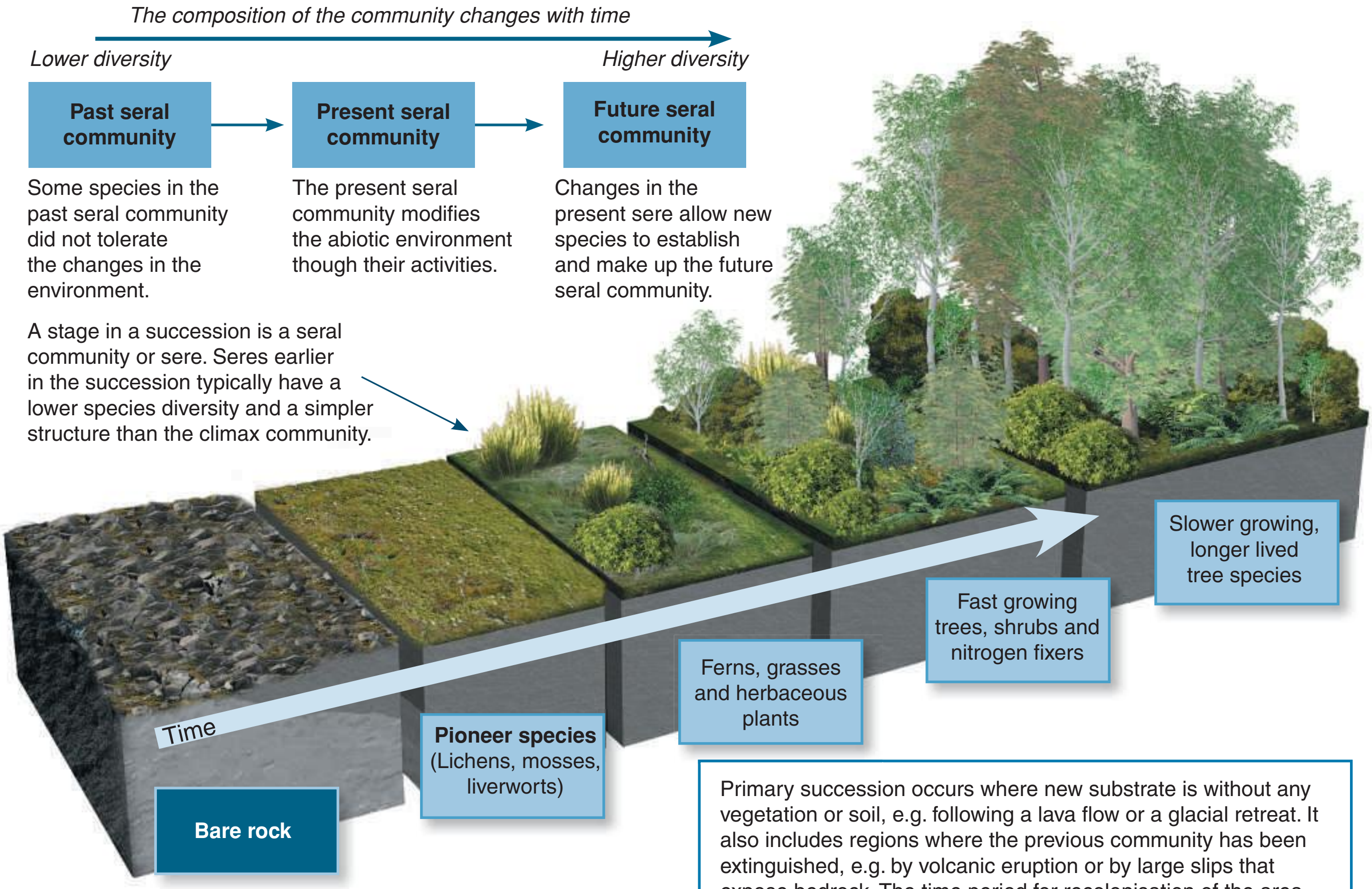
☐ 9 **SHE** Understand how indigenous knowledge can be used to complement conservation practices and manage natural ecosystems more effectively. **72**

☐ 10 **PRAC** Select and appraise an ecological surveying technique to analyse species diversity between two spatially variant ecosystems of the same classification. **73**

# 64 Primary Succession

**Key Idea**: Primary succession is a type of ecological succession occurring 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**.



Some species in the past seral community did not tolerate the changes in the environment.

The present seral community modifies the abiotic environment though their activities.

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.

*Note the vascular plants establishing in the crevices where soil is forming.*

Bob Blaylock CC 4.0

*Associations between mosses and cyanobacteria provides mosses with nitrogen.*

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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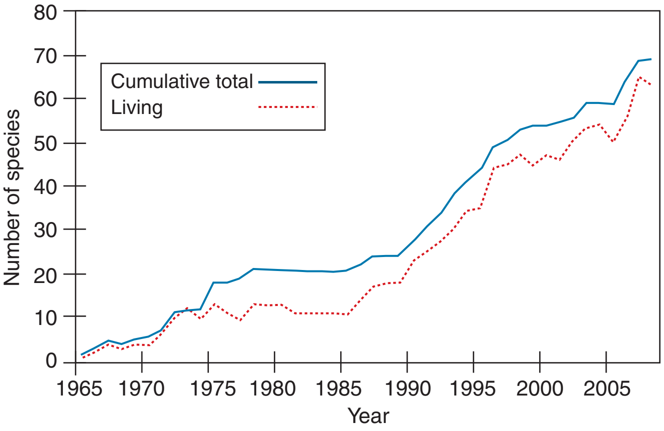
# Surtsey: A case study in primary succession

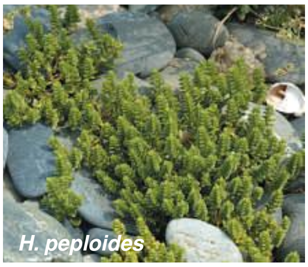
Surtsey Island is a volcanic island lying 33 km off the southern coast of Iceland. The island was formed over four years from 1963 to 1967 when a submarine volcano 130 m below the ocean surface built up an island that initially reached 174 m above sea level and covered 2.7 km$^2$. Erosion has since reduced 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



Daderot

Rasbak

Mikrolit

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.

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 on 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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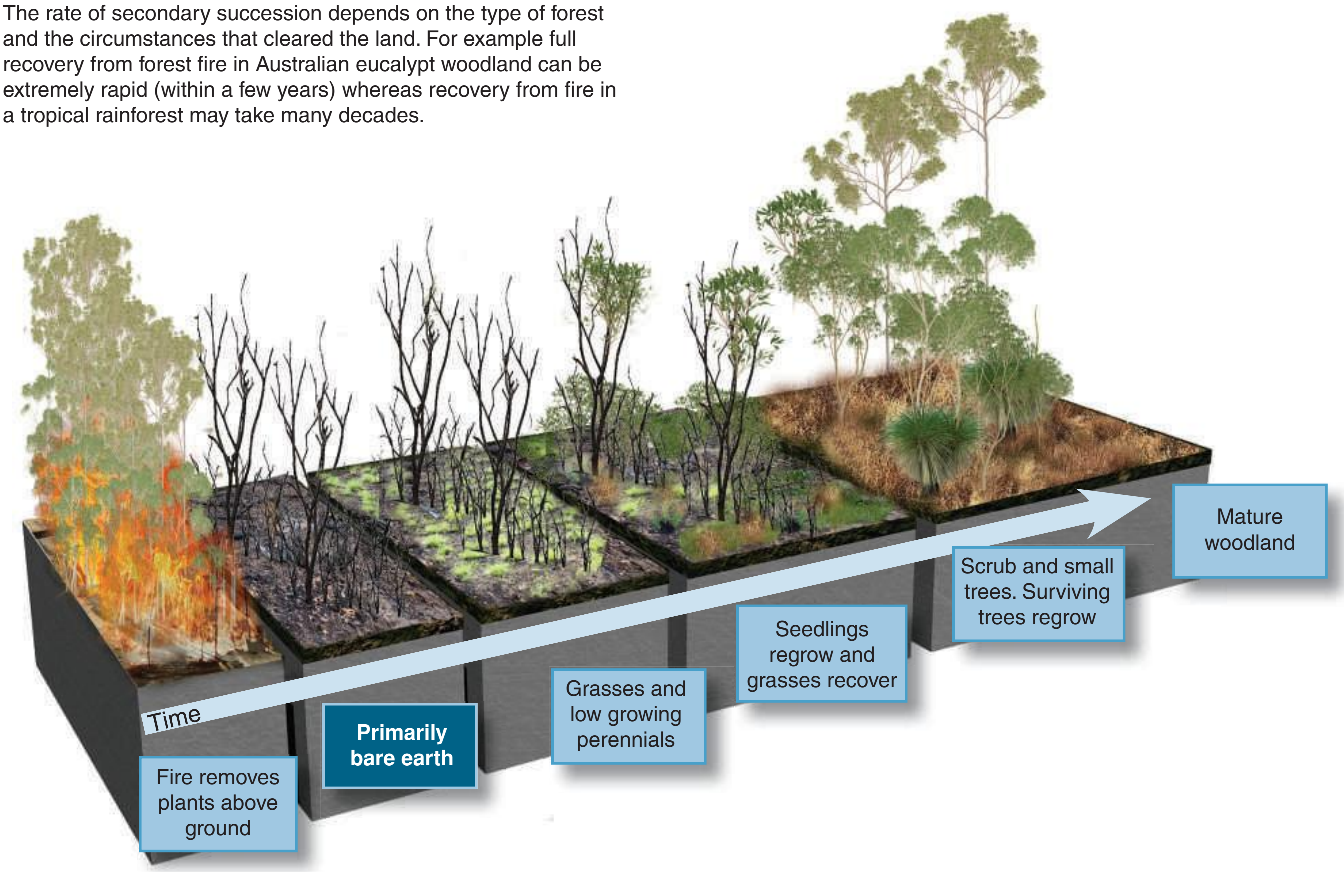
# 65 Secondary Succession

**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 community 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: ______________________

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# 66 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

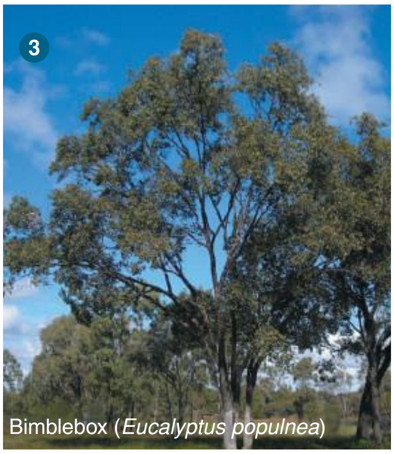
1. Bush fires (above) are more common in some types of forest (e.g. dry sclerophyll forests) than cool, temperate forests. Fire adapted vegetation types in Queensland include eucalypt forests, woodlands, paperbark forests, grasslands, and heathlands.

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.



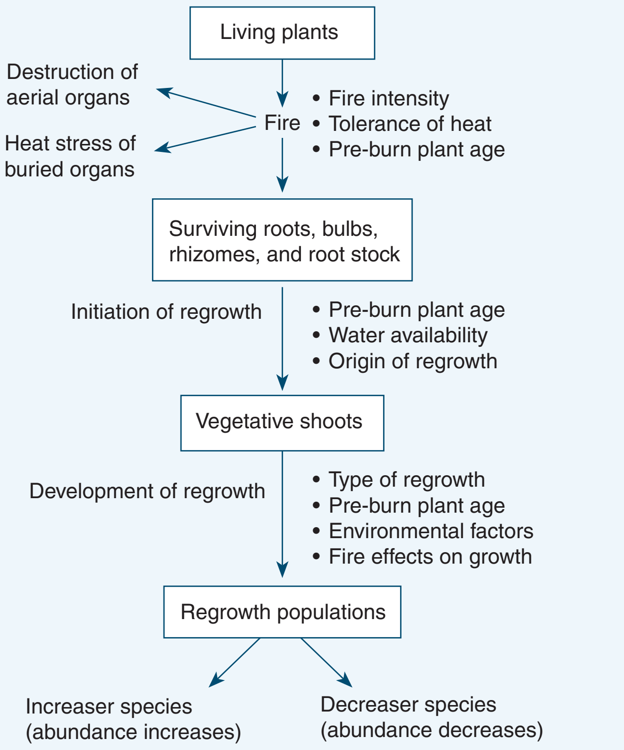
Bimblebox (*Eucalyptus populnea*)

Ethel Aardvark cc 3.0

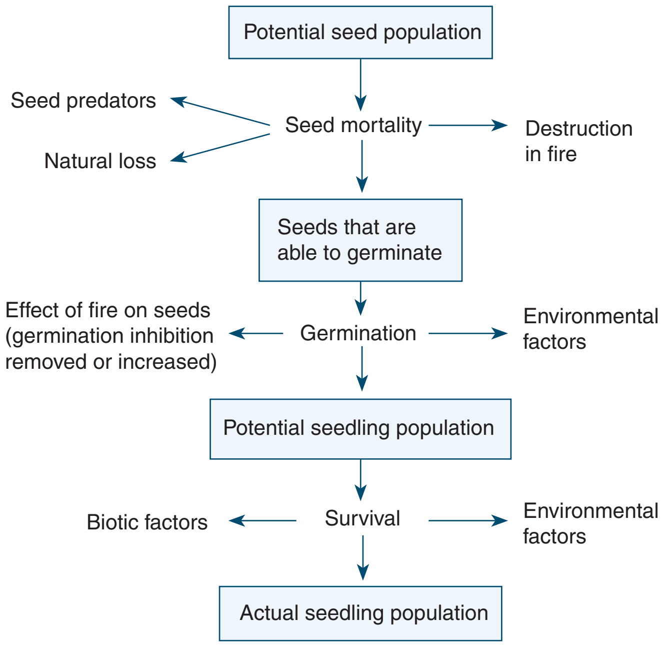
The bimblebox is found associated with acacia species in semi-arid woodlands.

The diagrams below show how various factors affect the recovery of forests after fire:

**Factors affecting regeneration by vegetative means**



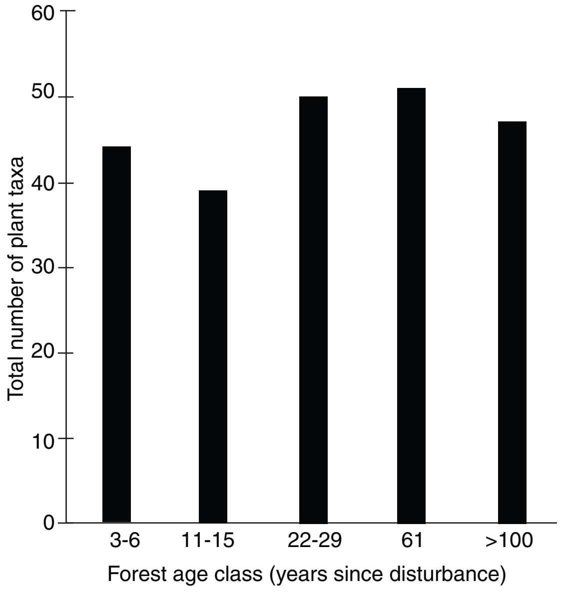
**Factors affecting regeneration by residual seeds**

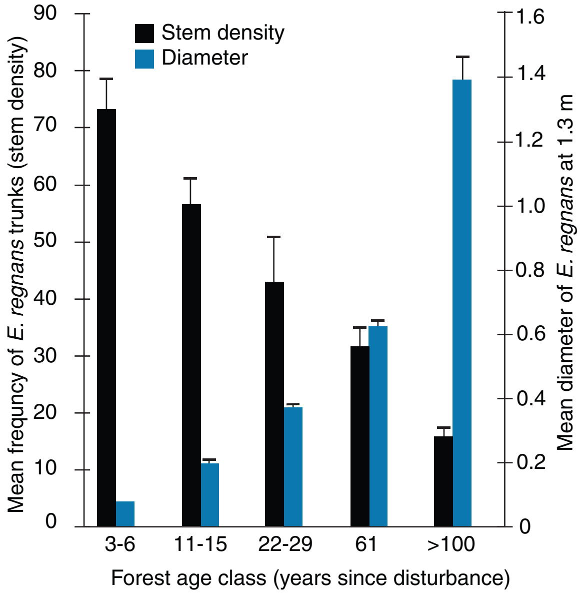


Modified from Vegetation succession after fire in sclerophyll woodland communities in south-eastern Australia Rosemary W. Prudie & R.O. Slayter, Australian Journal of Ecology (1976), I, 223-236

**ISBN: 978-1-927309-86-5**

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:


**Total plant taxa vs time since disturbance**


***E. regnans* characteristics**

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 plant 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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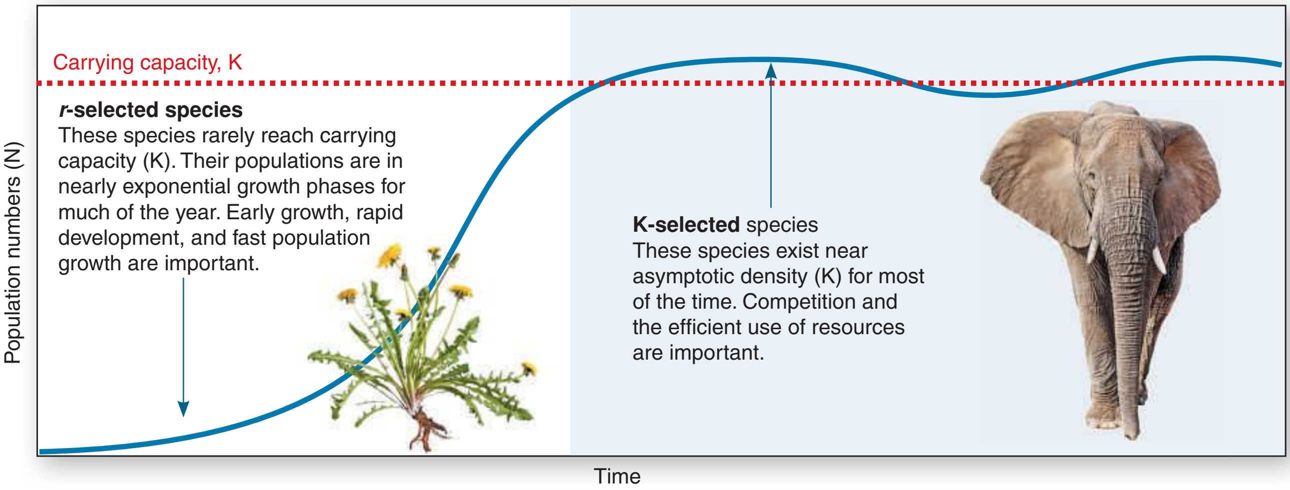
# 67 *r* and K Selection

**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 are 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.



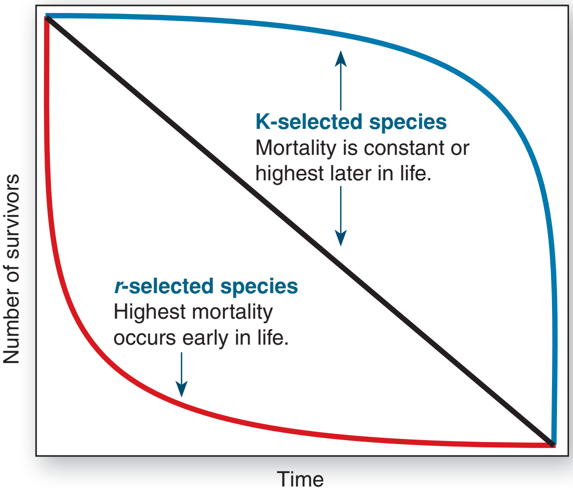
***r*-selected species**
These species rarely reach carrying capacity (K). Their populations are in nearly exponential growth phases for much of the year. Early growth, rapid development, and fast population growth are important.

**K-selected** species
These species exist near asymptotic density (K) for most of the time. Competition and the efficient use of resources are important.

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.



**K-selected species**
Mortality is constant or highest later in life.

***r*-selected species**
Highest mortality occurs early in life.

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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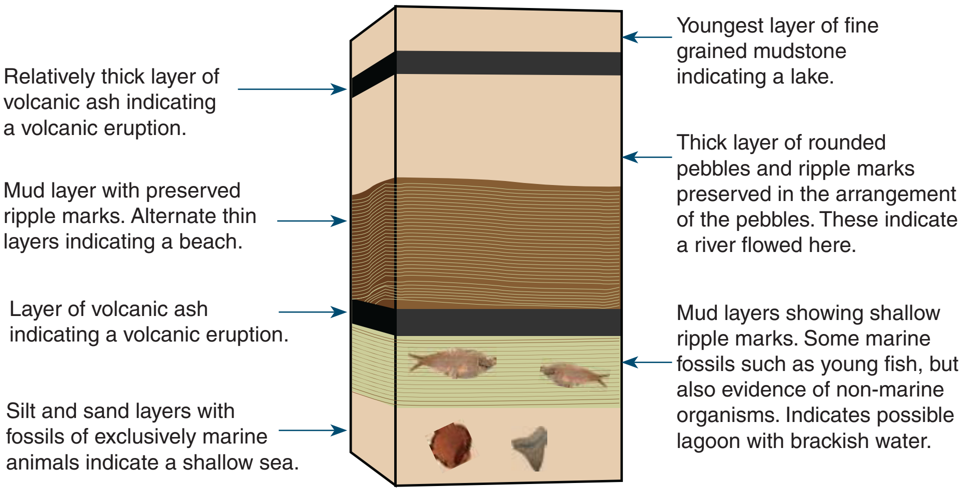
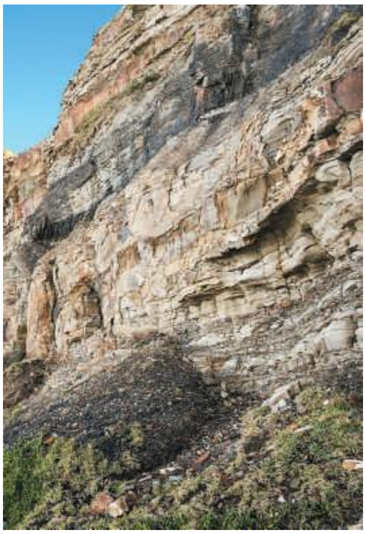
# 68 Interpreting Past Environments

**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.

Fossil stromatolites

Rygel, M.C. CC 3.0 via wikipedia

**Locations of Australian stromatolite fossils**

Stromatolites at Shark Bay, WA

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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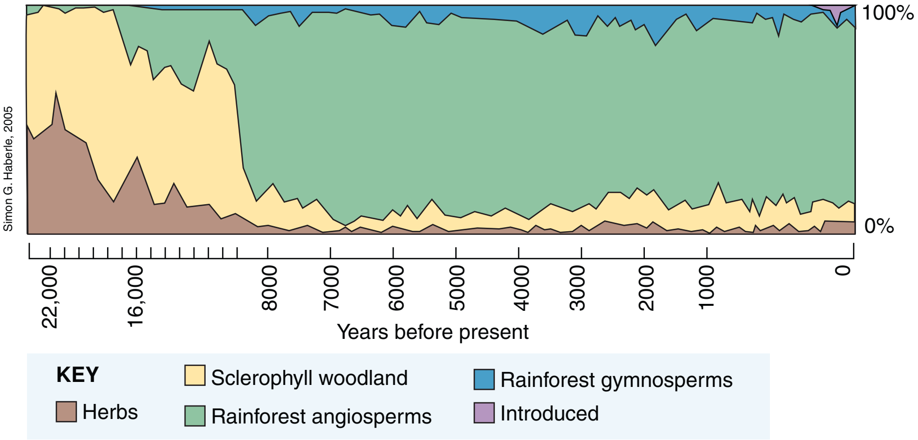
# 69 Analysing Ecosystem Change

**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

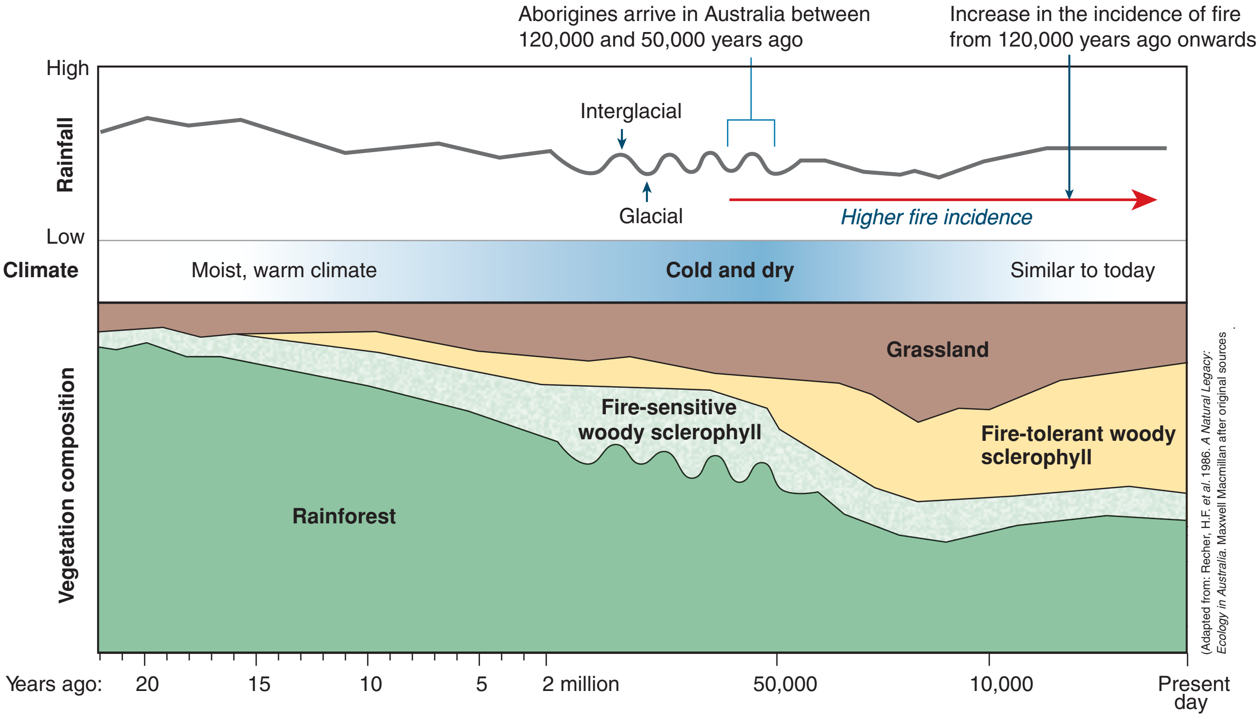


Simon G. Haberle, 2005

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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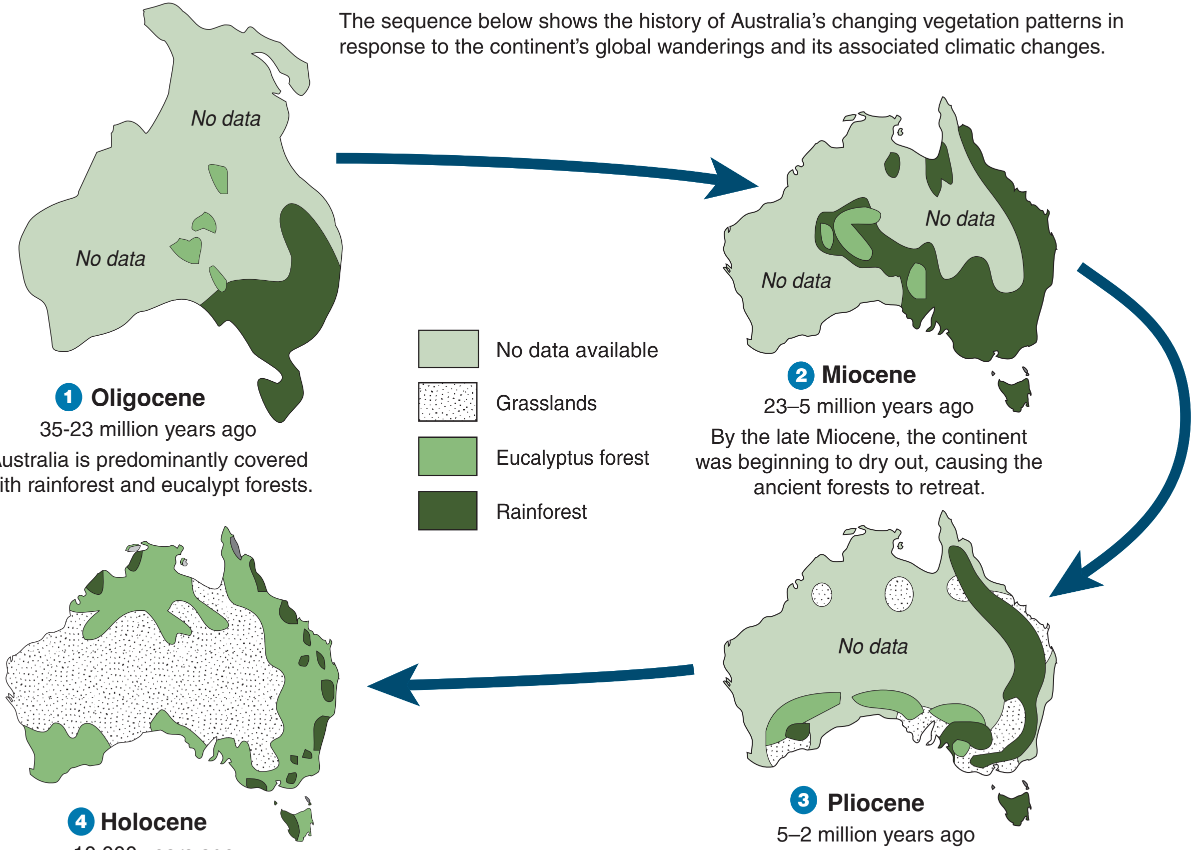
## Australia's changing vegetation patterns

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.



**① Oligocene**
35-23 million years ago
Australia is predominantly covered with rainforest and eucalypt forests.

**② Miocene**
23–5 million years ago
By the late Miocene, the continent was beginning to dry out, causing the ancient forests to retreat.

**③ Pliocene**
5–2 million years ago
By the early Pliocene, Australia was cooling as the world headed for a ice age. Much of Australia was covered by grasslands.

**④ Holocene**
10,000 years ago
The ancient rainforests are just a green rim to the edge of the continent.

*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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# 70 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.

## How humans affect the environment

Projections of current human population growth predict the human population will reach between 9 and 11 billion by 2050. This growth will create an increasing demand on natural resources, particularly water, arable land, and minerals.

As the human population increases, cities expand, fragmenting or destroying the natural ecosystems surrounding them. Careful management of urban development and resource use will be needed to prevent local extinctions and loss of biodiversity.

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.

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.

Eighty percent of Earth's documented species are found in tropical rainforests. These rainforests are being destroyed rapidly as land is cleared for agriculture or cattle ranching, to supply logs, for mining, or to build dams. Deforestation places a majority of the Earth's biodiversity at risk and threatens the stability of important ecosystems.

Demand for food increases as the population grows. Modern farming techniques favour **monocultures** to maximise yield and profit. However monocultures, in which a single crop type is grown year after year, are low diversity systems and food supplies are vulnerable if the crop fails. The UN estimates that 12 plant species provide 75% of our total food supply.

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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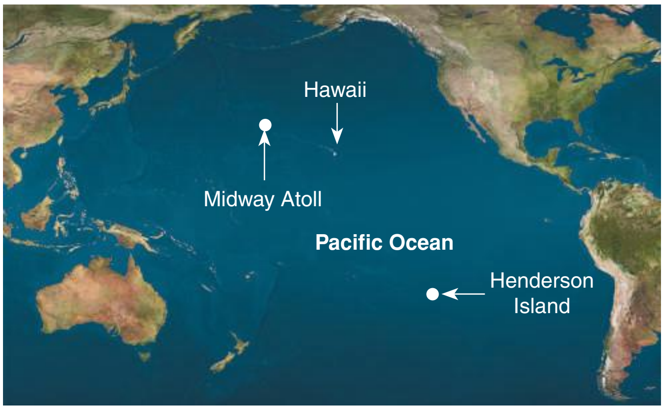
## Plastic in the Pacific

Human activity is global. There is no part of the planet that is not affected in some way by human activity. Even remote parts of the world are affected by activities thousands of kilometres away.

It is estimated 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, which 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 and Midway Atoll are two of these islands.



## 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 (below).

| | Mean density on beach (items per m$^2$) | Rate of accumulation (items km$^{-1}$ d$^{-1}$) | 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 | 13,316 | 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

## Midway Atoll

Midway Atoll (land area 6.2 km$^2$) is in the North Pacific Ocean, 2,400 km west of Hawaii (the nearest significant land) and near the centre of the North Pacific Gyre. As with Henderson Island, the circulation of the ocean washes vast quantities of plastic onto the beaches. NOAA regularly removes plastic debris from the beaches. Since 1999 they have removed 125 tonnes of plastic.

On both these islands, and many others, plastic is mistaken by seabirds for food and they eat it or feed it to their young. Every year on Midway Island, thousands of albatross young die from ingesting plastic products. The proportion of plastic deposited in the ocean is expected to increase at a rate of 4.8% each year until 2025 and at a rate of 3% from 2025 to 2050. At this rate, the ratio of plastic mass to fish mass could be roughly 1:1 by 2050. Microplastic and nanoplastic, tiny pieces of plastic including microbeads, enters the food chain and has been demonstrated to concentrate toxins, and so increase toxins in the fish that eat them. Nanoplastic can enter cells and affect their functioning.


Duncan Wright

Plastic in dead albatross chick, Midway Atoll


Plastic debris on beach, Henderson Island


Discarded nets can trap and drown marine mammals, reptiles, and birds (above).

2. Explain how plastic thrown away in a city on the west coast of North America can end up in a Laysan albatross chick on Midway Atoll:

3. What effect do micro and nanoplastics have on the animals that ingest them:

# 71 Marine Parks and Their Effects

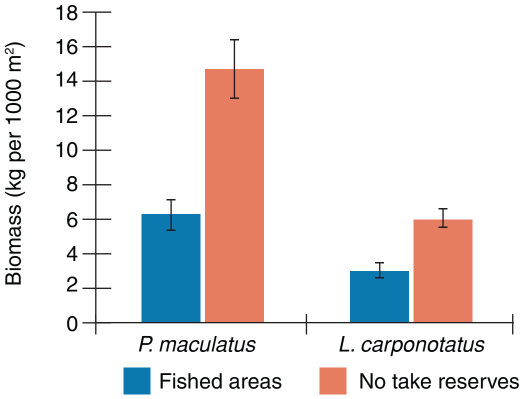
**Key Idea**: Marine parks deliver both direct and indirect protection to marine organisms.

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, and is 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), but they are exporters of juvenile fish to other areas. A study in 2012 focussed on popular fisheries species, the coral trout, *Plectropomus maculatus*, and the 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.

No take reserves vs fished areas: Keppel Islands

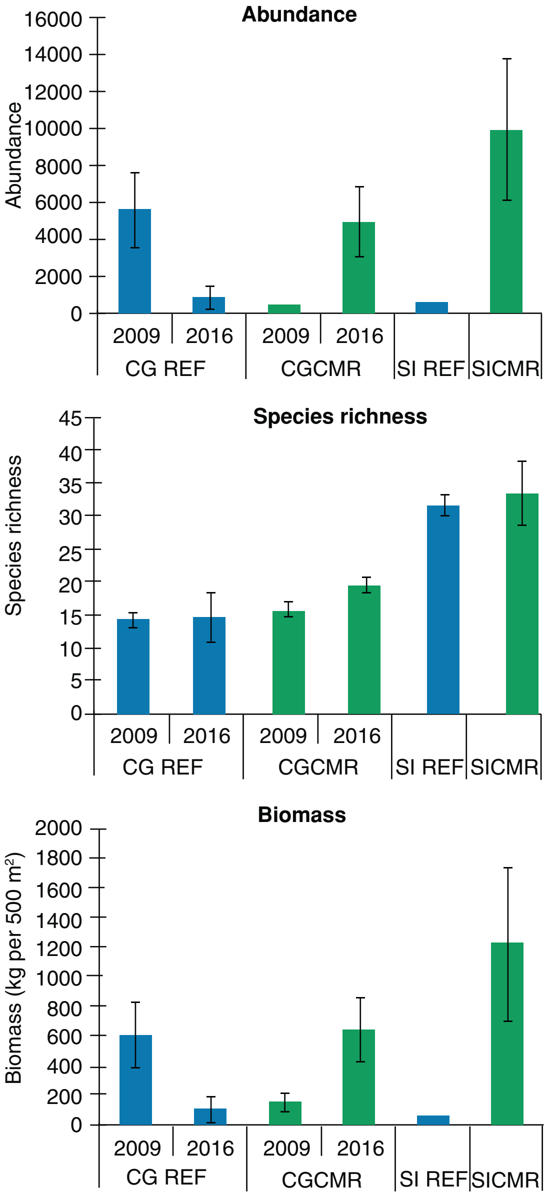


Hugo B. Harrison *et al.*/Current Biology 22, 1023–1028, June 5, 2012

## 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.

No take reserves vs fished areas



2016 biodiversity surveys of the Cod Grounds and Pimpernel Rocks Commonwealth Marine Reserves, Rick D Stuart-Smith *et al*

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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# 72 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?

SHE

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# 73 Measuring Ecosystem Diversity

**Key Idea**: Different sampling techniques can produce different results for the same survey area.

This practical is designed for you to appraise different sampling techniques and how those techniques quantify the diversity of plants in a forest community. Here you will examine two plots of hypothetical wet sclerophyll forest, one that has been undisturbed for many decades and the other that has been affected by fire. Each plot shown on the following pages represents a hectare of forest with sides of 100 m x 100 m.

▸ **MANDATORY PRACTICAL: 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 area into a grid 10 squares by 10 squares. This will split the area up into 100 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 10 on each axis.

### Quadrat sampling (random and systematic 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 10 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**
   Examine each selected quadrat and count the number of individuals of each species present. Record your data in the spaces provided in the table 'Random quadrat count'.
6. **Choose quadrats systematically**
   Again using 10 quadrats, this time place them in a systematic way around the sample area, e.g. in a diagonal, or every fourth square from the top left. Record your systematic methodology in your logbook. Record your data in the spaces provided in the table 'Systematic quadrat count'.

### Transect sampling

7. **Line transect**
   Draw 10 transect lines across the sampling area from side to side or top to bottom. Use the random number table to work out where the transect line should go. For example, using the numbers in column A (5, 5) the first line should start in the middle of column 5 in the top row and go to the middle of column 5 in the bottom row. Count and record every plant the line touches. Record the results in the table 'Line transect count'.
8. Repeat steps 3-7 of this procedure with the fire disturbed sample area. Your systematic methodology should be the same.
9. Calculate a diversity index for each sampling type and each ecosystem.

**Table of random numbers**

| A | | B | | C | | D | |
|---|---|---|---|---|---|---|---|
| 5 | 5 | 2 | 10 | 5 | 4 | 4 | 6 |
| 7 | 7 | 9 | 1 | 6 | 4 | 1 | 2 |
| 7 | 6 | 1 | 3 | 7 | 6 | 4 | 9 |
| 7 | 5 | 8 | 6 | 9 | 3 | 6 | 7 |
| 2 | 5 | 2 | 3 | 3 | 9 | 1 | 10 |
| 1 | 9 | 6 | 2 | 9 | 8 | 10 | 3 |
| 3 | 1 | 8 | 8 | 7 | 9 | 10 | 1 |
| 5 | 9 | 9 | 5 | 10 | 7 | 6 | 1 |
| 6 | 6 | 1 | 5 | 5 | 3 | 9 | 3 |
| 8 | 8 | 5 | 4 | 4 | 9 | 3 | 7 |

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

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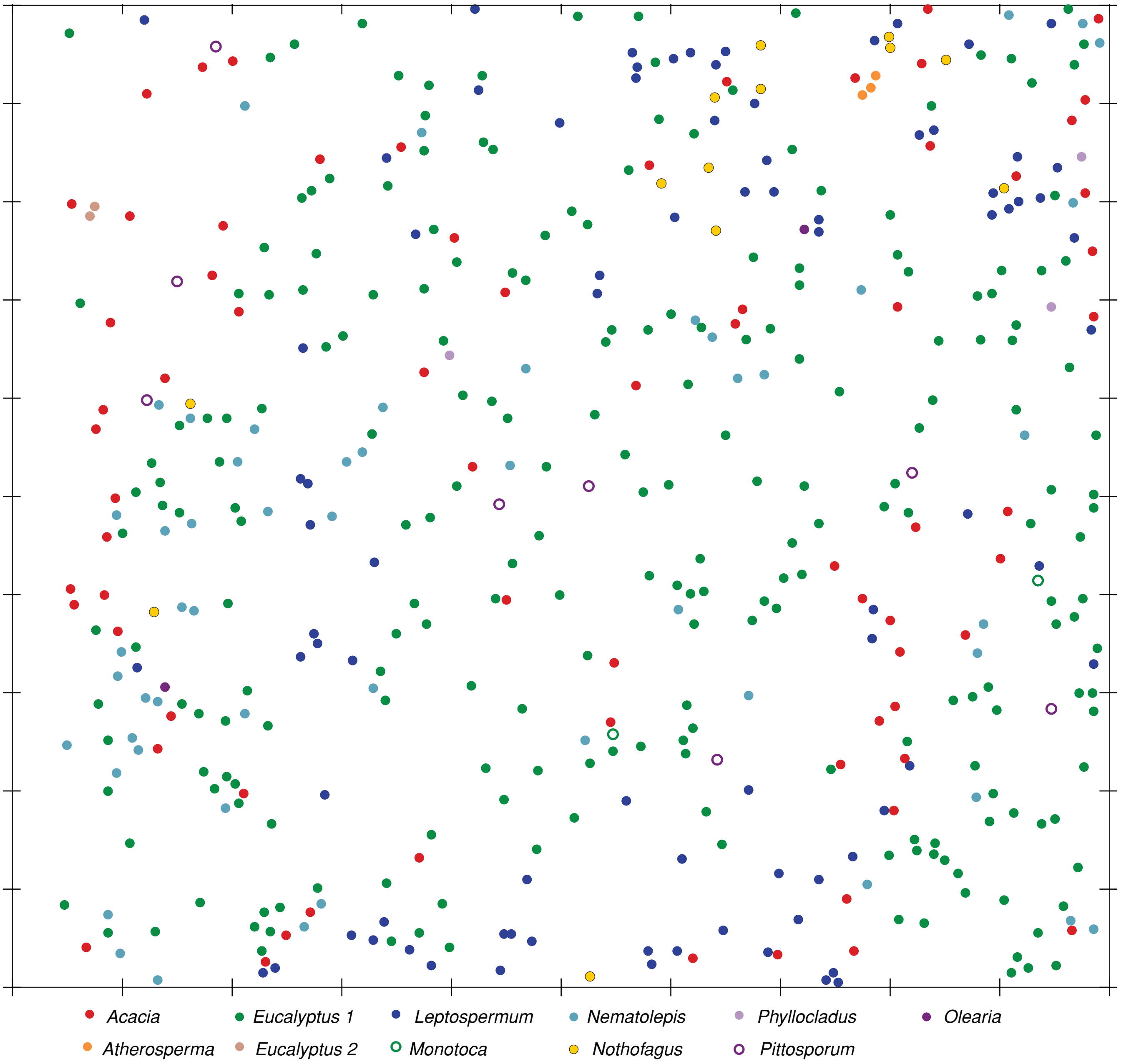
## Undisturbed wet sclerophyll forest



## Random quadrat count:

| | |
|---|---|
| *Acacia* | |
| *Atherosperma* | |
| *Eucalyptus 1* | |
| *Eucalyptus 2* | |
| *Leptospermum* | |
| *Monotoca* | |
| *Nematolepis* | |
| *Nothofagus* | |
| *Olearia* | |
| *Pittosporum* | |
| *Phyllocladus* | |
| Total individuals | |

## Systematic quadrat count:

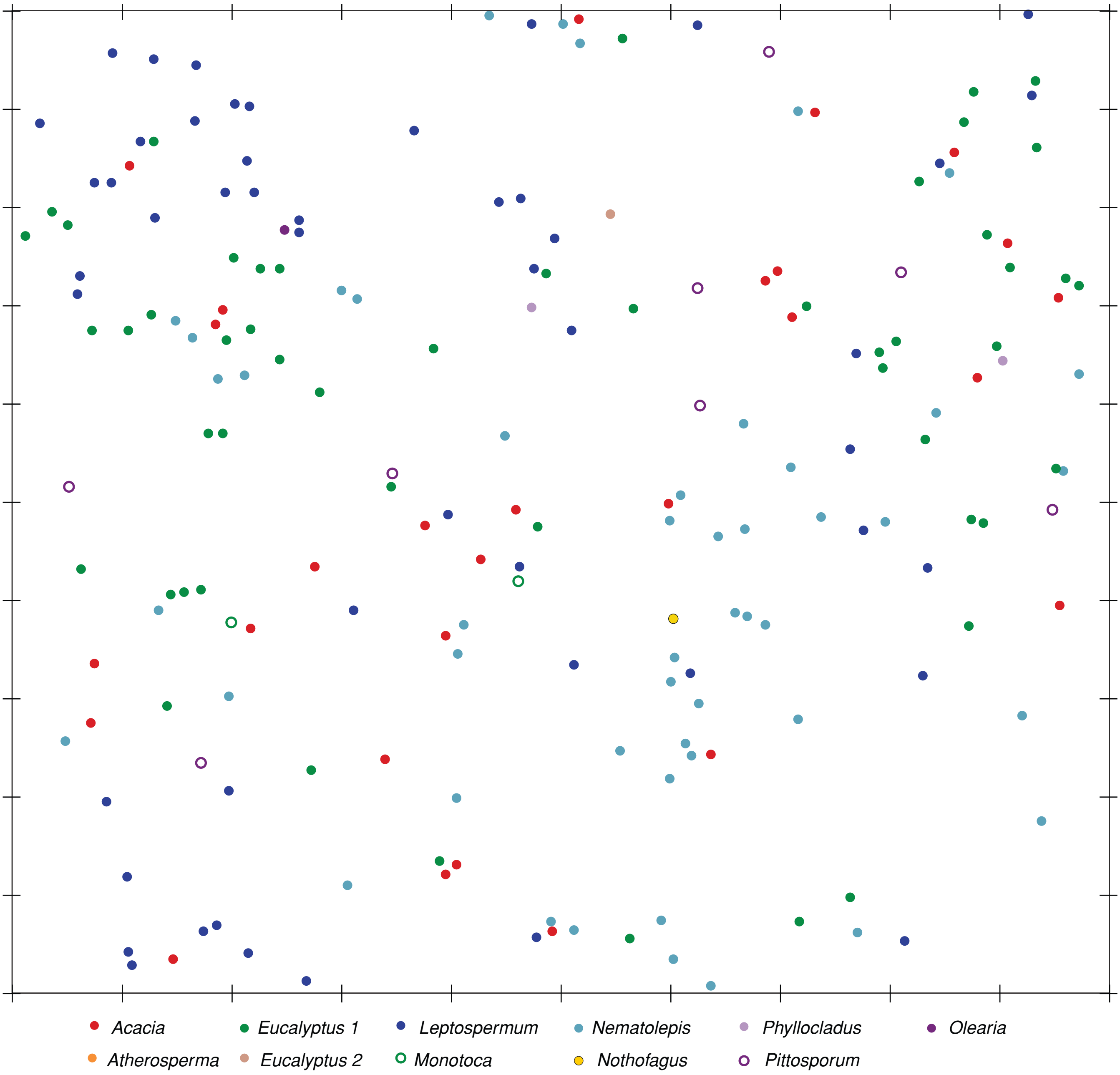
| | |
|---|---|
| *Acacia* | |
| *Atherosperma* | |
| *Eucalyptus 1* | |
| *Eucalyptus 2* | |
| *Leptospermum* | |
| *Monotoca* | |
| *Nematolepis* | |
| *Nothofagus* | |
| *Olearia* | |
| *Pittosporum* | |
| *Phyllocladus* | |
| Total individuals | |

## Transect count:

| | |
|---|---|
| *Acacia* | |
| *Atherosperma* | |
| *Eucalyptus 1* | |
| *Eucalyptus 2* | |
| *Leptospermum* | |
| *Monotoca* | |
| *Nematolepis* | |
| *Nothofagus* | |
| *Olearia* | |
| *Pittosporum* | |
| *Phyllocladus* | |
| Total individuals | |

**ISBN: 978-1-927309-86-5**

## Disturbed (by fire) wet sclerophyll forest



### Random quadrat count:

| | |
|---|---|
| *Acacia* | |
| *Atherosperma* | |
| *Eucalyptus 1* | |
| *Eucalyptus 2* | |
| *Leptospermum* | |
| *Monotoca* | |
| *Nematolepis* | |
| *Nothofagus* | |
| *Olearia* | |
| *Pittosporum* | |
| *Phyllocladus* | |
| Total individuals | |

### Systematic quadrat count:

| | |
|---|---|
| *Acacia* | |
| *Atherosperma* | |
| *Eucalyptus 1* | |
| *Eucalyptus 2* | |
| *Leptospermum* | |
| *Monotoca* | |
| *Nematolepis* | |
| *Nothofagus* | |
| *Olearia* | |
| *Pittosporum* | |
| *Phyllocladus* | |
| Total individuals | |

### Transect count:

| | |
|---|---|
| *Acacia* | |
| *Atherosperma* | |
| *Eucalyptus 1* | |
| *Eucalyptus 2* | |
| *Leptospermum* | |
| *Monotoca* | |
| *Nematolepis* | |
| *Nothofagus* | |
| *Olearia* | |
| *Pittosporum* | |
| *Phyllocladus* | |
| Total individuals | |

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1. Recall the calculation of Simpson's diversity index you learned about earlier in chapter 1. Use the space below to calculate the diversity for each of the sampling types and for each of the sampling areas (six calculations in total).

Simpson's index diversity results for undisturbed ecosystem:

Random quadrats: ________________ Systematic quadrats: __________________ Transect: ____________________

Simpson's index diversity results for fire disturbed ecosystem:

Random quadrats: ________________ Systematic quadrats: __________________ Transect: ____________________

2. The diversity of the undisturbed area is actually 0.692 and the diversity of the fire disturbed area is 0.789. Compare the diversity calculations you obtained to these known indexes. Compare the picture of the community provided by the different sampling methods. Which method provided the more accurate result?

3. (a) The disturbed ecosystem actually had a higher biodiversity. Can you explain why?

   (b) What other methods of analysing the data could be used to obtain a clearer picture of the difference between the ecosystems?

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# 74 KEY TERMS AND IDEAS: Did You Get it?

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

ecological succession ..........

sere ..........

K-selection ..........

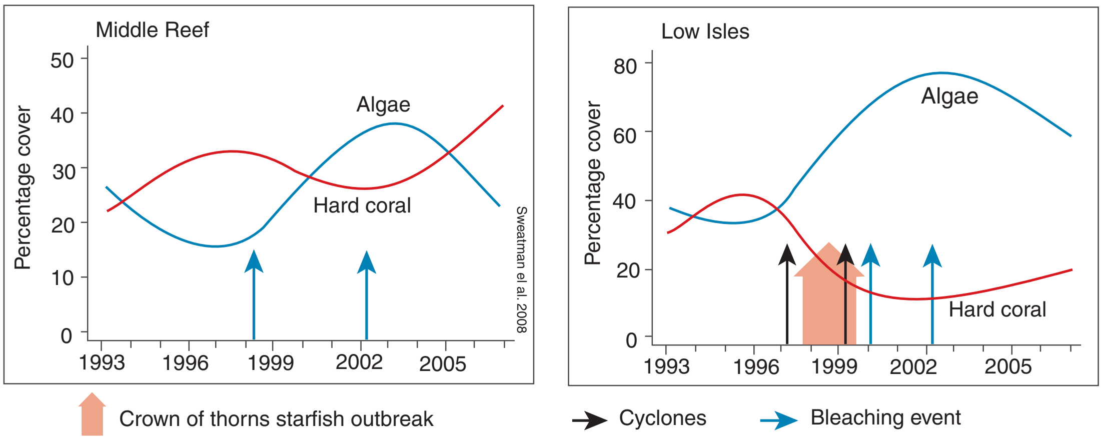
primary succession ..........

*r*-selection ..........

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** | A 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.

______________________________

______________________________

______________________________

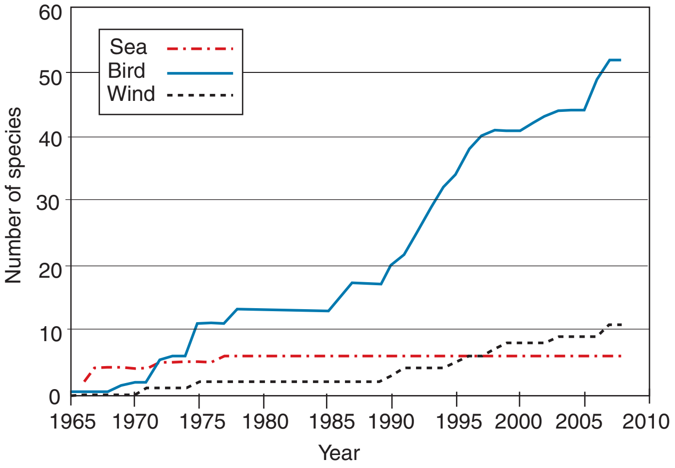
(c) Suggest why the number of species arriving by sea peaked early before quickly leveling off:

______________________________

______________________________

______________________________

Cumulative dispersal routes of vascular plants to Surtsey



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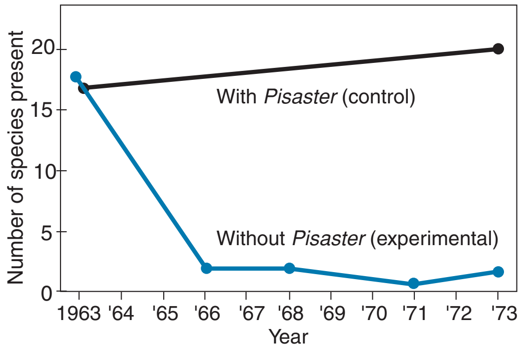
# 75 Synoptic Questions: Unit 3, Topic 2

1. The plot right show 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?



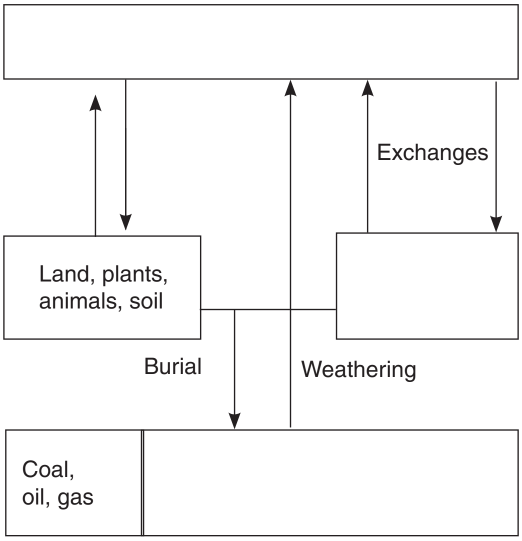
2. (a) Use the following labels to complete the diagram of the carbon cycle shown right: a*tmosphere, geosphere, oceans, respiration (R), photosynthesis (PS)*.

   (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.

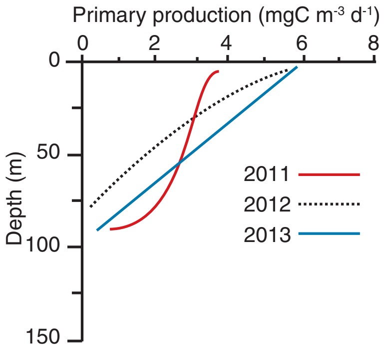
   (d) About 3 petagrams is taken up by photosynthesis and 2 petagrams is taken up by the oceans. Add these values to the appropriate labels on the diagram.

   (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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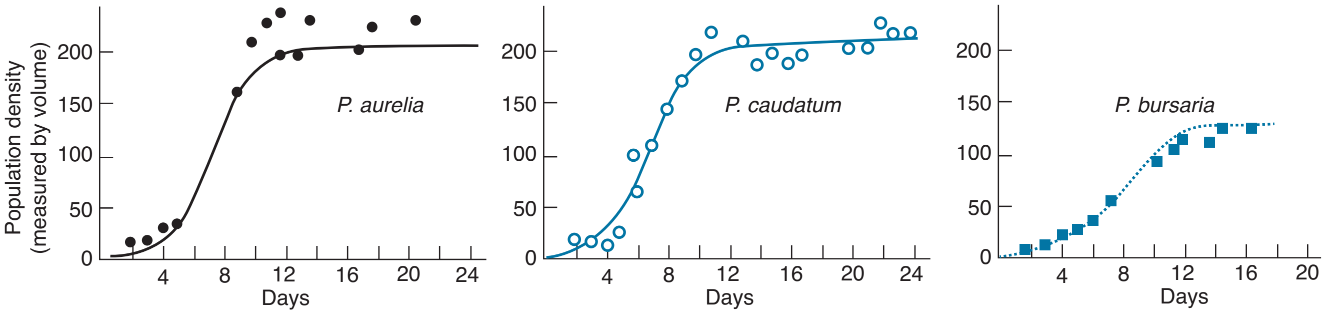
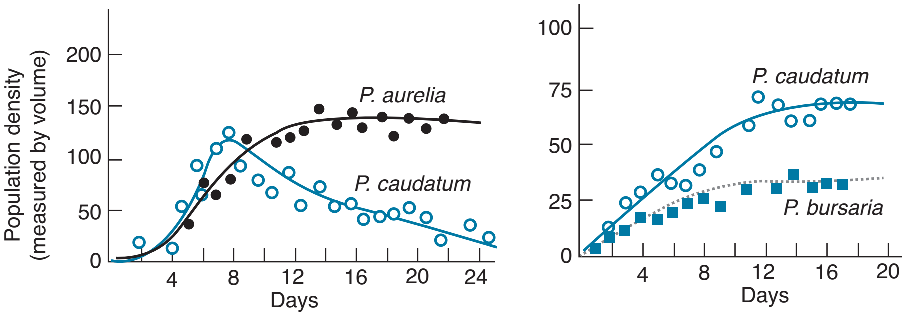
5. In 1934, Georgii Gause, a Russian biologist, carried out a series of experiments on *Paramecium*. The results led him to propose the **competitive exclusion principle**, a fundamental idea in ecology. In the first stage of the experiments, he grew three species of *Paramecium* in isolation in a nutritive 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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# 76 IA1: Data Test

This summative internal assessment requires you to work individually. In this assessment you will:

- Apply your understanding of biodiversity or ecosystem dynamics to determine unknown scientific quantities or features.
- Analyse evidence about biodiversity or ecosystem dynamics to identify trends, patterns, relationships, limitations or uncertainty in data.
- Interpret evidence about biodiversity or ecosystem dynamics to draw conclusions based on the analysis of data.

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 | Σn(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 | Σn(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 $\mathbf{D} = 1 - \left(\frac{\Sigma n(n-1)}{N(N-1)}\right)$ 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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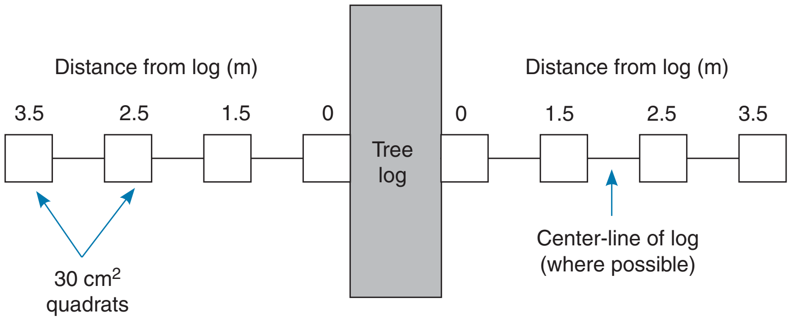
A field study was carried out to investigate the distribution of millipedes around fallen logs in a small forest reserve. Millipedes consume decaying vegetation and live in the moist conditions beneath logs and in the leaf litter of forest floors. The moist environment protects them from drying out as their cuticle is not a barrier to water loss.

Six logs of similar size were chosen from similar but separate regions of the forest. Logs with the same or similar surrounding environment (e.g. leaf litter depth, moisture levels) were selected. For each log, eight samples of leaf litter at varying distances from the fallen tree log were taken using 30 $cm^2$ quadrats. Samples were taken from two transects, one each side of the log. The sample distances were: directly below the log (0 m), 1.5 m, 2.5 m, and 3.5 m from the log. It was assumed that the conditions on each side of the log would be essentially the same. The leaf litter was placed in Tullgren funnels and the invertebrates extracted. The number of millipedes in each sample was counted. The raw data are shown below.

**Experimental setup**



Environmental conditions on either side of the log were assumed to be equal.

Marshal Hedin CC 2.0

Giant pill millipede

| | | Distance from log (m) | | | |
|---|---|---|---|---|---|
| **Tree log** | **Transect** | **0** | **1.5** | **2.5** | **3.5** |
| 1 | 1 | 12 | 11 | 3 | 2 |
| | 2 | 10 | 12 | 2 | 1 |
| 2 | 1 | 8 | 3 | 4 | 4 |
| | 2 | 9 | 5 | 2 | 1 |
| 3 | 1 | 14 | 6 | 3 | 3 |
| | 2 | 3 | 8 | 7 | 2 |

| | | Distance from log (m) | | | |
|---|---|---|---|---|---|
| **Tree log** | **Transect** | **0** | **1.5** | **2.5** | **3.5** |
| 4 | 1 | 2 | 4 | 1 | 6 |
| | 2 | 4 | 5 | 2 | 2 |
| 5 | 1 | 12 | 10 | 16 | 10 |
| | 2 | 6 | 3 | 2 | 5 |
| 6 | 1 | 10 | 9 | 7 | 2 |
| | 2 | 11 | 11 | 8 | 1 |

3. Plot column graphs on the grids below to show the distribution of millipedes at each log. Plot transect 1 and 2 data separately (double columns) for each graph:

Log 1

Log 2

Log 3

Log 4

Log 5

Log 6

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4. Study the graphs and answer the following questions:

(a) Is there a relationship between distance from the tree log and the number of millipedes found?

(b) What physical factors might account for this?

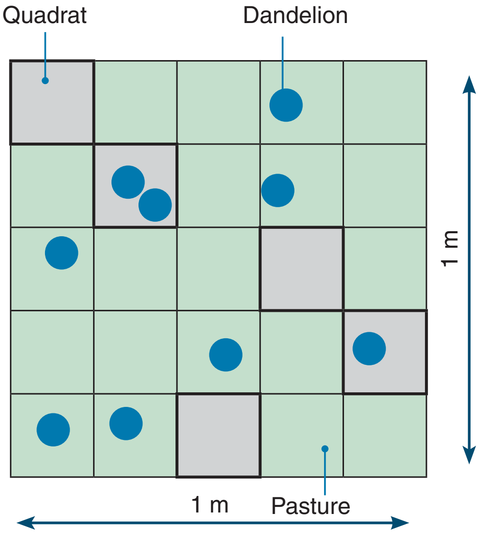
5. During this investigation, the assumption was made that the abiotic factors were the same on each side of the log.

(a) Do you think this assumption is valid?

(b) Explain the reason you have given in (a):

(c) How could you test the assumption?

6. 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:



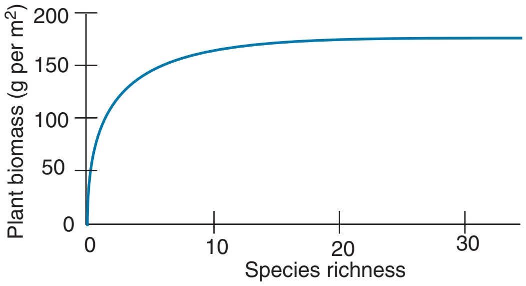
(a) From the quadrat based sample, what is the density of dandelions? Use the formula:

$$\text{Density} = \frac{\text{Total number in all quadrats sampled}}{\text{No. of quadrats sampled x area of quadrat}}$$

(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?

7. Study the graph right. What can be said about the relationship between species richness and plant biomass in a grassland ecosystem?



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8. Study the ecosystem NPP graph on the right:

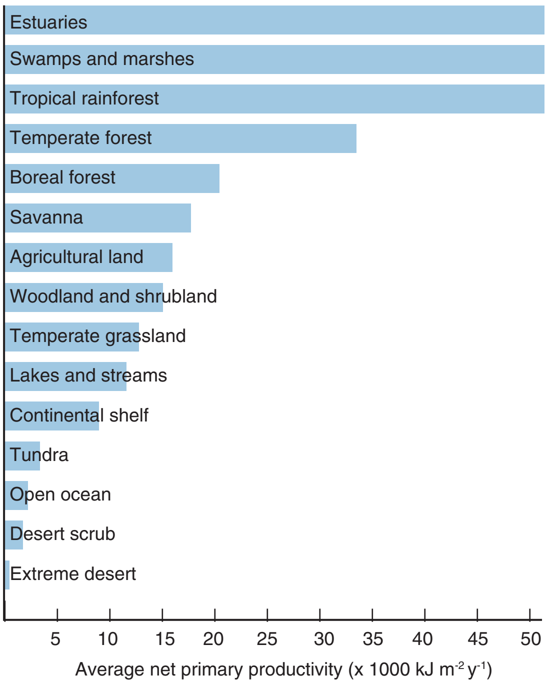
(a) Identify the three most productive ecosystems:

(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?

Net primary productivity of various ecosystems



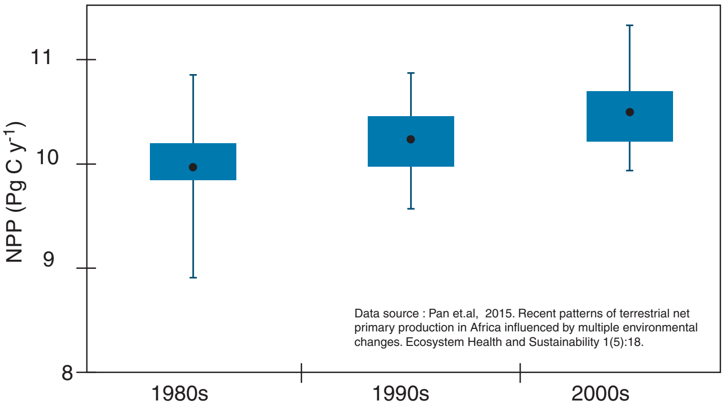
9. Study the information and graph of NPP in Africa below:

## 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).

Decadal means of terrestrial NPP in Africa (1980-2009)



Data source : Pan et.al, 2015. Recent patterns of terrestrial net primary production in Africa influenced by multiple environmental changes. Ecosystem Health and Sustainability 1(5):18.

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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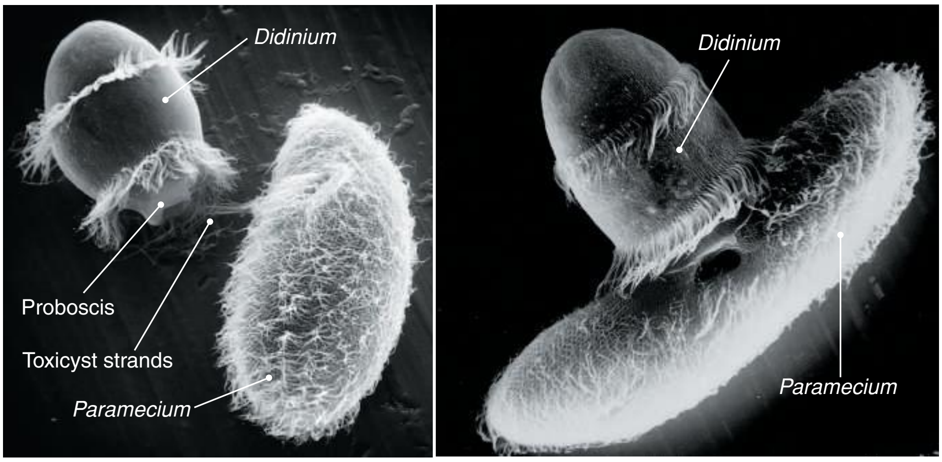
## Predator-prey experiments

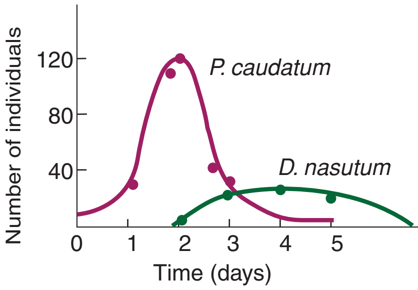
Gause studied predator-prey interactions in two protists, *Paramecium* and its predator *Didinium,* in simple test tube 'microcosms'. The results are shown in the graphs below. In the first and third experiments, there was no sediment in the test tube. In the second experiment, sediment was added to the test tube.



SEM images: Gregory Antipa (San Francisco State University), H. S. Wessenberg

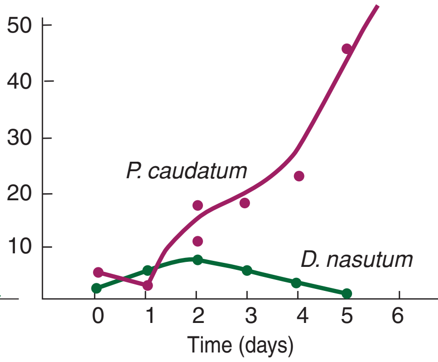
*Didinium*, a unicellular ciliate, feeds almost exclusively on *Paramecium*. It captures *Paramecium* by shooting toxicysts into the *Paramecium* (left). It then reels the *Paramecium* in to its proboscis.

**① Without sediment**



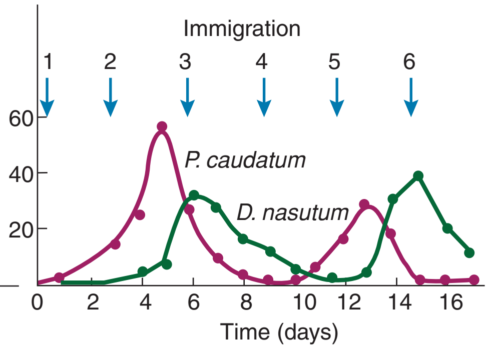
Five *Paramecium* were added to the medium and three *Didinium* added after two days.

**② With sediment**



Same regime as experiment 1 but the medium included sediment.

**③ Without 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?

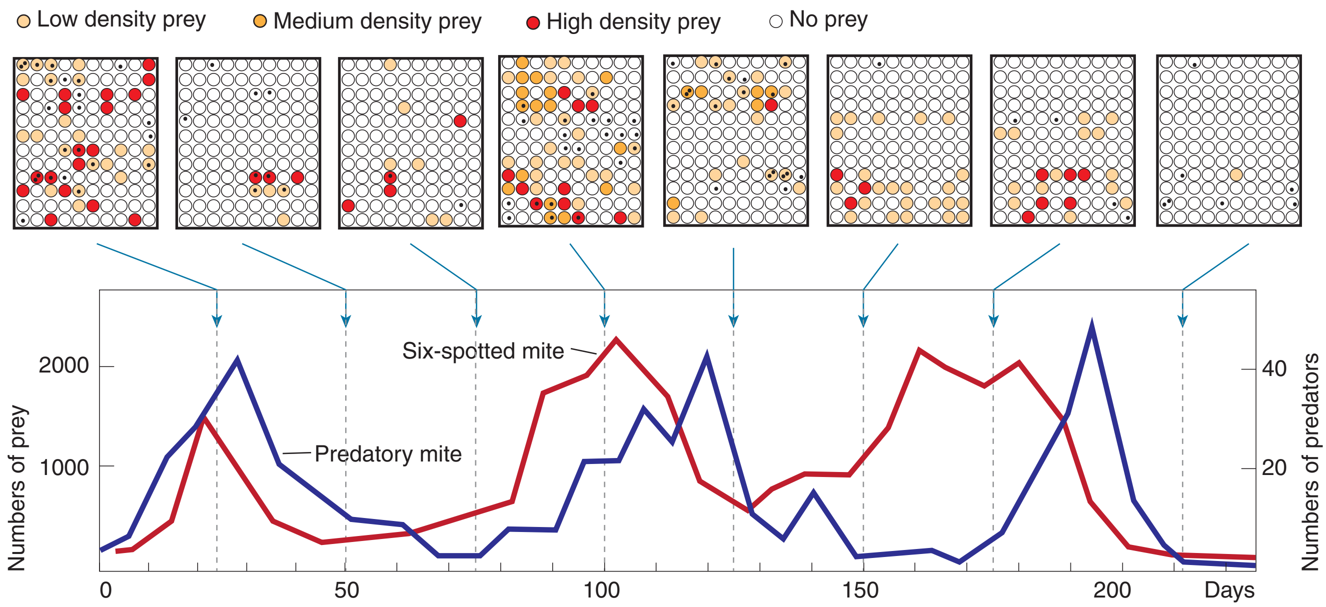
11. Why did the *Paramecium* survive in the second experiment?

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?

- 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. Indications were by 1961 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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# Internal Assessment 2: Student Experiment

Activity number

### Key terms

accuracy
aim
assumption
control
controlled variable
dependent variable
ethics
hypothesis
independent variable
observation
precision
prediction
primary data
quantitative data
qualitative data
reliability
sample
validity (of data)
variable

## Assessment objectives

*Key skills and knowledge*

☐ 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:

- Apply understanding of biodiversity or ecosystem dynamics to modify an experimental method and process primary data.
- Analyse experimental evidence about biodiversity or ecosystem dynamics.
- Interpret experimental evidence about biodiversity or ecosystem dynamics.
- Investigate phenomena associated with biodiversity or ecosystem dynamics by experiment.
- Evaluate experimental processes and conclusions about biodiversity or ecosystem dynamics.
- Communicate understandings and experimental findings, arguments, and conclusions about biodiversity and ecosystem dynamics.

Habitat News

Yohan euan o4

## Key considerations

*Key skills and knowledge*

☐ 1 Show an understanding of the biological concepts and terms as relevant to your investigation.

☐ 2 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.

☐ 3 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.

☐ 4 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.

☐ 5 Demonstrate an ability to carry out an investigation safely and ethically.

☐ 6 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.

☐ 7 Make clear, accurate scientific drawings as appropriate to your investigation.

☐ 8 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.

# 77 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.

## Heath 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.

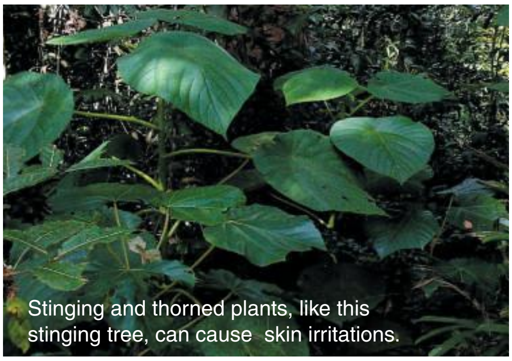
Make sure you know the hazards and look out for them.

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 heath and safety



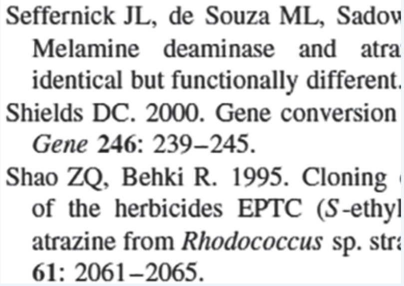
Stinging and thorned plants, like this stinging tree, can cause skin irritations.

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.



Seffernick JL, de Souza ML, Sadov
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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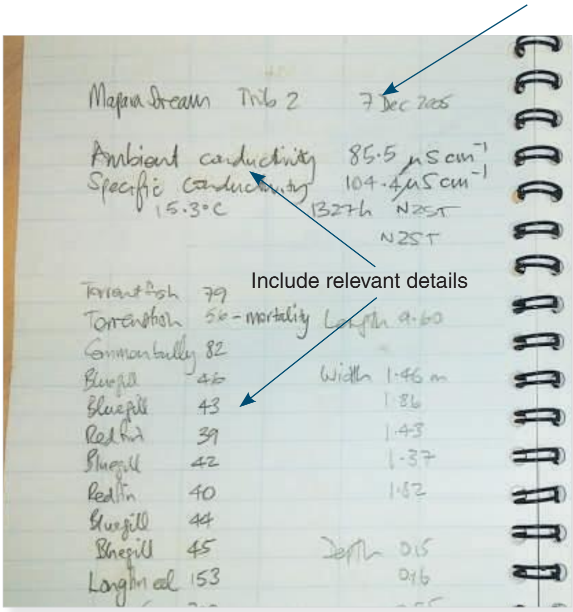
## Logbooks

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 a 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 planing 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.

Date your entries



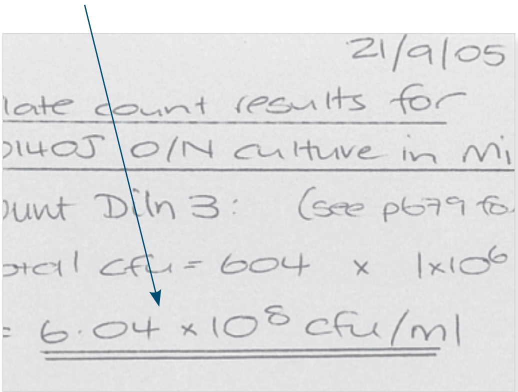
Mapara Stream Trib 2 7 Dec 2005

Ambient conductivity 85.5 $\mu S\,cm^{-1}$
Specific conductivity 104.4 $\mu S\,cm^{-1}$
15.3°C 1327h ~~N25T~~
N25T

Torrentfish 79
Torrentfish 56 – mortality Length 9.60
Common bully 82
Bluegill 46 Width 1.46 m
Bluegill 43 1.86
Redfin 39 1.43
Bluegill 42 1.37
Redfin 40 1.62
Bluegill 44
Bluegill 45 Depth 0.15
Longfin eel 153 0.16

Include relevant details

Calculations
should be included



21/9/05
late count results for
0140J O/N culture in Mi
unt Diln 3: (see p679 fo
otal cfu = 604 × $1 \times 10^6$
= $6.04 \times 10^8$ cfu/ml

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?

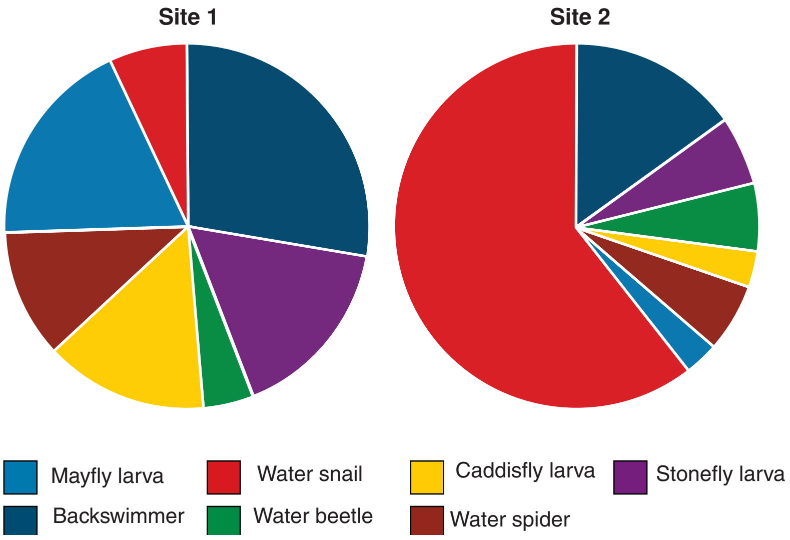
- Check your data to see that it makes sense. Do the results seem logical? Are there any outliers? If so, you must decided whether to include them in your analysis.
- Raw data may need to be transformed to see trends and patterns. Recall that these transformations are often quite simple (e.g. percentages, 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**
*Cyliosoma*

Pill millipede: Marshal Hedin CC 2.0

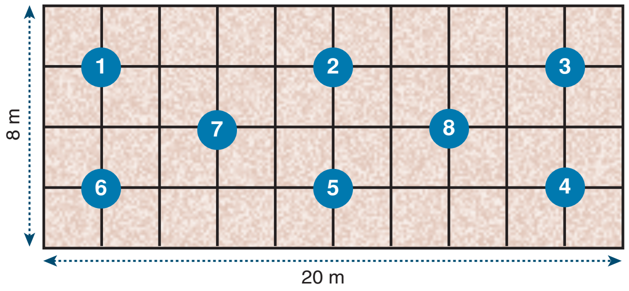
### Observation

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

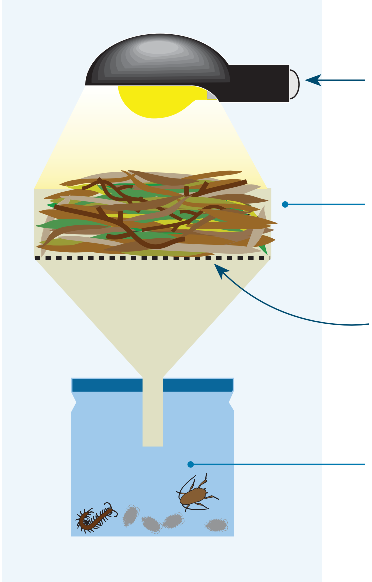
This millipede species is adapted to a niche in the leaf litter of humid forests and is abundant there. However, it is rare in the litter of drier plantation forests. The **null hypothesis** is that there is no difference between the abundance of this millipede species in wet sclerophyll and plantation forests.

### Wet sclerophyll or plantation forest



① Sampling sites numbered 1-8 at evenly spaced intervals on a 2 x 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 x 8 m was chosen and marked out in 2 x 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 x 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 x 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 o4

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

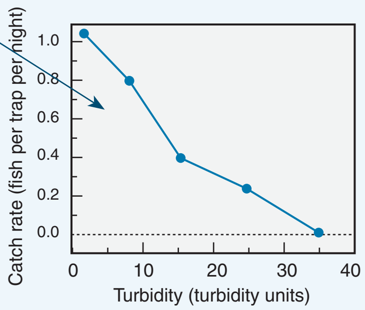
The results section is arguably the most important part of any research report; it is the place where you can bring together and present your findings. When properly constructed, this section will present your results clearly and in a way that shows you have organised your data and carefully considered 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.**

er water depth, m
etween sites wit
Table 5). Mean summer water depth was only 2.1 cm at t
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 dissolved solids, dissolved oxygen at the water surface, humic concentration, pH, an est, $P > 0.153$:
Table 5). Catch rates at sites with mudfish ometric mean
0.70: Table 5).

**Fig. 2 Catch rates in turbid water**



**Label figures and tables clearly and in sequence so that they can be referred to easily in the text.**

**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 y described for predictive purposes by four variables that are
easy to measure: summer w tent of disturbance (as indicated by vegetation), and turbidity.
Catch rates of black mudfish sent 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 h rate in our
study, 8.4 mudfish per trap per night, was at Site 24 (Table 1, Figure 1). The sec o per night)
was at Site 32, in a drain about 4 km east of Hamilton. Black mudfish in the Wa nly found at
sites in wetlands with absence of water in summer, moderate depth of water in w vegetation
(low DSR), and low turbidity (Fig. 2). There are similarities between the habitat requirements of black mudfish and those of
bro galaxias (*Galaxias vulgaris*). Brown mudfish inhabited shallow water, sometimes at the
edg e usually absent from water deeper than about 30-50 cm (Eldon 1978). The common
rive r shallow water, occupying river margins < 20 cm deep (Jowett and Richardson 1995).

**State any limitations of your approach in carrying out the investigation and what further studies might be appropriate.**

**Reference is made to the work of others.**

**Further research is suggested**

**A clear conclusion is made towards the end of the discussion.**

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 s corded (Ogle & Cheyne 1981).
Cover is also important for brown mudfish (Eldon 1978). Black mudfi h the predatory mosquitofish
and juvenile eels, and the seasonal drying of their habitats may be a key to the successful coexistence of mudfish with their
predators. M f 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 clas dfish in future. The adaptability
of black mudfish allows them to survive in some alter rains. From this study, we can
conclude that the continued existence of suitable habit k mudfish than the presence of
predators and competitors. This study has also improved methods of identifying suitable mudfish habitats in the Waikato region.

### 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<br>Book titles in italics<br>Publisher<br>Davis, P. (1996). Cellular factories. *New Scientist* 2057: Inside science supplement.<br>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.<br>Article title<br>Volume (Issue number), Pages |
| Last name and initials of authors. | Indge, B. (2002). Experiments. *Biological Sciences Review*, 14(3), 11-13. |
| Internet sites change often so the date accessed is included. The person or organization in charge of the site is also included. | Kingsland, J. (2000). Border control. *New Scientist* 2247: Inside science supplement.<br>Publication date<br>http://www.cbc.umn.edu/~mwd/cell_intro.html (Dalton, M. "Introduction to cell biology" 12.02.03) |

## 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

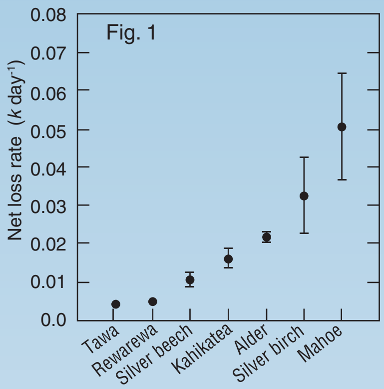
Mayfly larva, *Deleatidium* *(collector-browser)*

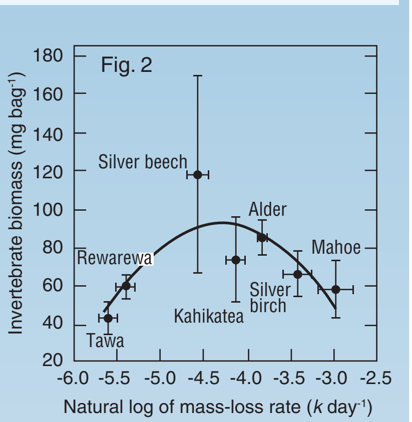
Beetle larva (Elmidae) *(collector-browser)*

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.

- 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**<br>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<br>☐ Includes species scientific and common name if this is appropriate |
| **Introduction**<br>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<br>☐ Provides relevant background and a logical rationale for the study<br>☐ Explains specialised terminology |
| **Methods**<br>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.<br>☐ Provides the information to enable the procedures to be repeated<br>☐ The reason for each step in the methodology is evident or explained<br>☐ Factors important in the outcome are mentioned and explained<br>☐ Includes relevant details of data collection and analysis (e.g. preparation of materials, controls, sample sizes, methods of measurement) |
| **Results**<br>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<br>☐ Clearly presents the findings of the study or experiment. General statements are supported with reference to the data.<br>☐ Major results are presented in tables and figures and briefly described<br>☐ Each figure or table is self-sufficient and includes title and caption<br>☐ Figures and tables are numbered sequentially |
| **Conclusion**<br>A clear statement describing whether or not the results of the investigation support the hypothesis. | ☐ The conclusions are clearly stated<br>☐ You can discuss continuing research (if applicable) |
| **Acknowledgments**<br>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<br>☐ Allows your work to be assessed in the light of other work in the area.<br>☐ Full citations are provided for every reference cited in the report<br>☐ There are no references included that are not cited in the report.<br>☐ Each citation is correctly and consistently formatted. |

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UNIT 4
Topic 1

# DNA Structure and Replication

## Key terms

3'

5'

adenine

anti-parallel

base pair rule

chromosome

complementary base pairing

cytosine

deoxyribose

DNA

DNA helicase

DNA polymerase

DNA replication

eukaryote

guanine

histone

nucelotide

nucleic acid

nucleus

prokaryote

purine

pyrimidine

ribose

RNA

semi-conservative

thymine

uracil

Activity number

## The structure of DNA

*Key skills and knowledge*

☐ 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. Where is most of the DNA found in prokaryotes and in eukaryotes? Contrast the structure and organisation of the DNA in prokaryotes and eukaryotes. Is there DNA outside the main chromosome in prokaryotes? What about outside the nucleus in eukaryotes? **78**

☐ 2 In more detail than above, describe how the DNA in eukaryotic chromosomes is associated with histone proteins, which package and organise the DNA. What is the purpose of this highly ordered organisation? **79**

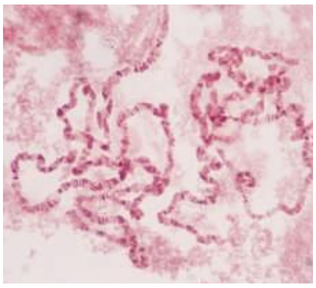
☐ 3 Recall the structure of the nucleic acid DNA, including the composition of nucleotides, the complementary base pairing (base pairing rule) and the base-specific hydrogen bonding between anti-parallel strands. Explain how nucleotides and nucleic acids are both formed by condensation reactions. **80 81**

☐ 4 Compare and contrast the structure of the nucleic acids DNA and RNA and recognise the various roles of different types of RNAs. **81**

☐ 5 ***SHE*** Understand how the contributions of Rosalind Franklin, James Watson, and Francis Crick led to the development of the double-helix model of DNA. **82**

☐ 6 ***PRAC*** Extract DNA from strawberries, kiwifruit or wheatgerm. **82**

☐ 7 Explore the structure of DNA further by building a physical model to illustrate the characteristics of the DNA molecule. How realistic is your model? **83**



DNA helicase unwinding DNA

## DNA replication

*Key skills and knowledge*

☐ 8 Describe the semi-conservative replication of DNA, including reference to: **84**

- the role of the enzyme DNA helicase,
- the role of DNA polymerase,
- the direction of synthesis and its significance.

☐ 9 Explain what semi-conservative replication means. What are the consequences for the newly formed DNA molecules? **84**

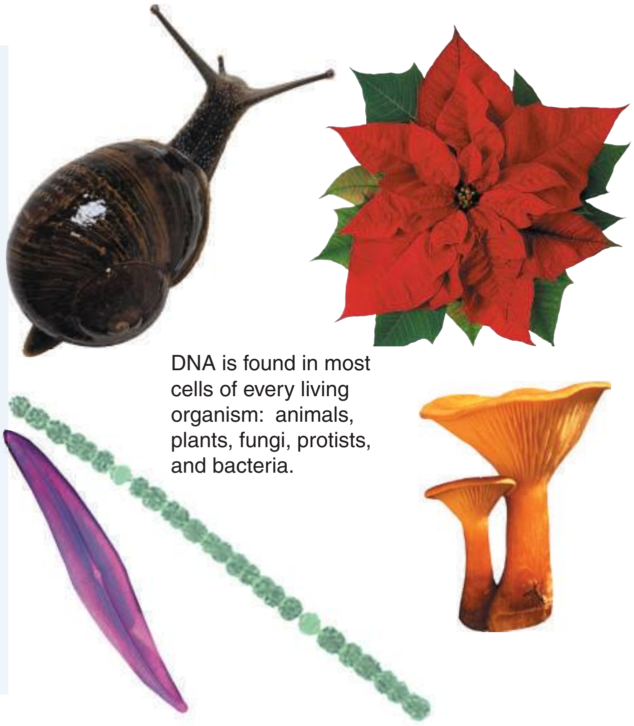
# 78 What is DNA?

**Key Idea**: DNA carries the cell's genetic information. It is organised differently in prokaryotes and eukaryotes.

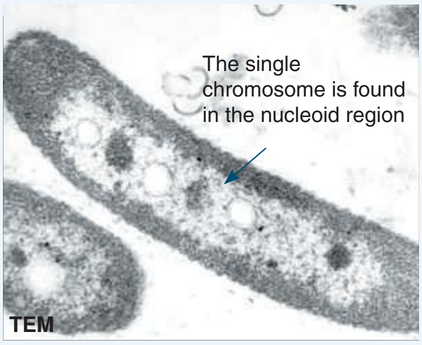
DNA is found in all living organisms. It stores the information using units called bases. There are only four types of bases but the combinations of millions of bases together stores the information that controls all the functions in a cell.

### About DNA

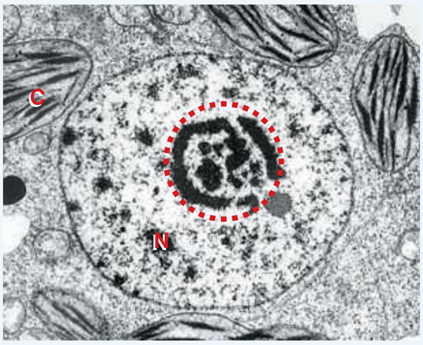
- **DNA** stands for **d**eoxyribo**n**ucleic **a**cid.
- DNA has a double-helix structure with two anti-parallel strands held together by hydrogen bonds (left). It stores and transmits genetic information.
- DNA carries all the information an organism needs to develop, function, and reproduce.
- DNA 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).



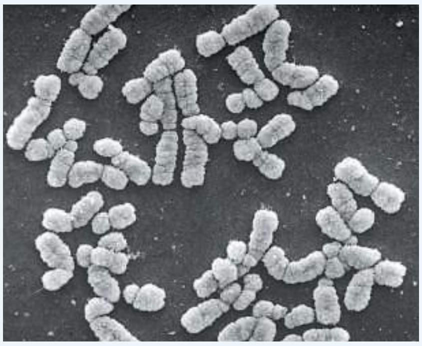
DNA is found in most cells of every living organism: animals, plants, fungi, protists, and bacteria.



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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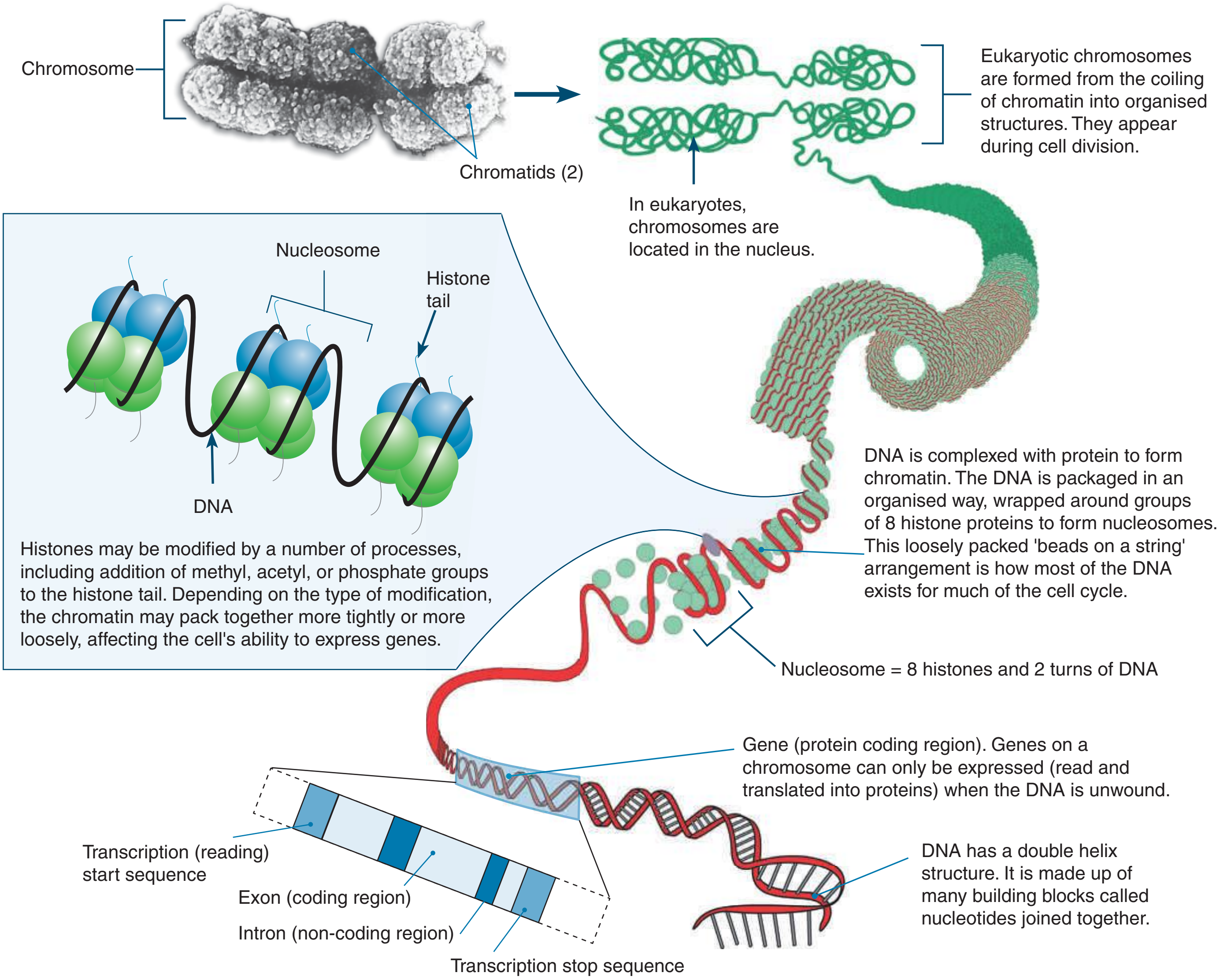
# 79 Eukaryotic Chromosome Structure

**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.



Eukaryotic chromosomes are formed from the coiling of chromatin into organised structures. They appear during cell division.

In eukaryotes, chromosomes are located in the nucleus.

Histones may be modified by a number of processes, including addition of methyl, acetyl, or phosphate groups to the histone tail. Depending on the type of modification, the chromatin may pack together more tightly or more loosely, affecting the cell's ability to express genes.

DNA is complexed with protein to form chromatin. The DNA is packaged in an organised way, wrapped around groups of 8 histone proteins to form nucleosomes. This loosely packed 'beads on a string' arrangement is how most of the DNA exists for much of the cell cycle.

Nucleosome = 8 histones and 2 turns of DNA

Gene (protein coding region). Genes on a chromosome can only be expressed (read and translated into proteins) when the DNA is unwound.

DNA has a double helix structure. It is made up of many building blocks called nucleotides joined together.

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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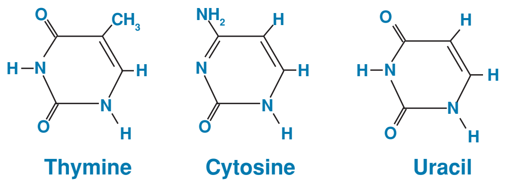
# 80 Nucleotides

**Key Idea**: Nucleotides make up nucleic acids. A nucleotide is made up of a base, a sugar, and a phosphate group.

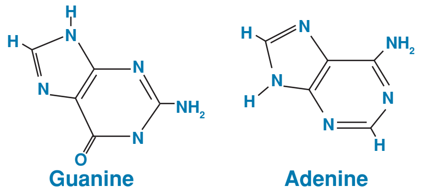
Nucleotides are the building blocks of the nucleic acids DNA and RNA, which are involved in the transmission of inherited information. Nucleotide derivatives, such as ATP and GTP, are involved in energy transfers in cells. A nucleotide has three components: a base, a sugar, and a phosphate group. Nucleotides 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



Pyrimidines are single ringed bases. DNA contains the pyrimidines cytosine (C) and thymine (T). RNA contains the pyrimidines cytosine and uracil (U).

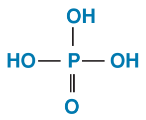
## Purines

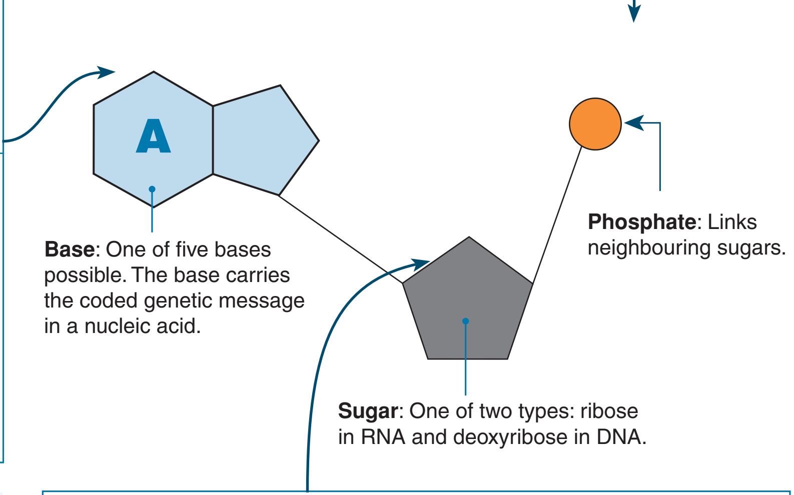


Purines are double ringed bases. Both DNA and RNA contain the purines adenine (A) and guanine (G).

## Phosphate

Phosphate groups are represented by circles. Along with the pentose sugar they form the "backbone" of the DNA or RNA molecule.



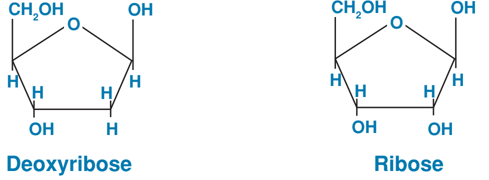


**Base**: One of five bases possible. The base carries the coded genetic message in a nucleic acid.

**Phosphate**: Links neighbouring sugars.

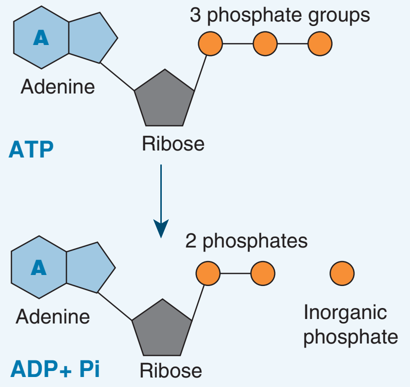
**Sugar**: One of two types: ribose in RNA and deoxyribose in DNA.

## Sugars



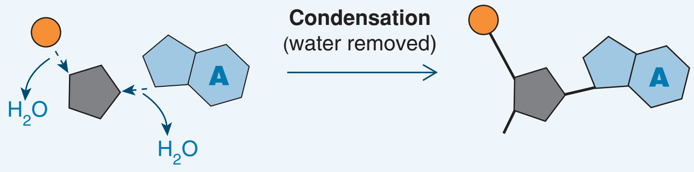
Nucleotides contain one of two different sorts of sugars. **Deoxyribose** sugar is only found in DNA. **Ribose** sugar is found in RNA.

## 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.

## 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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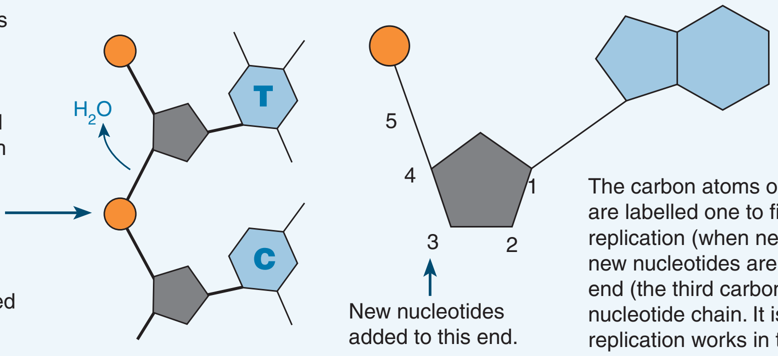
# 81 Nucleic Acids

**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.

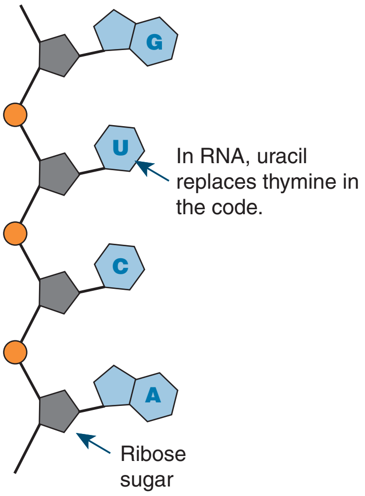
## Nucleotides are joined by condensation polymerisation

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**.

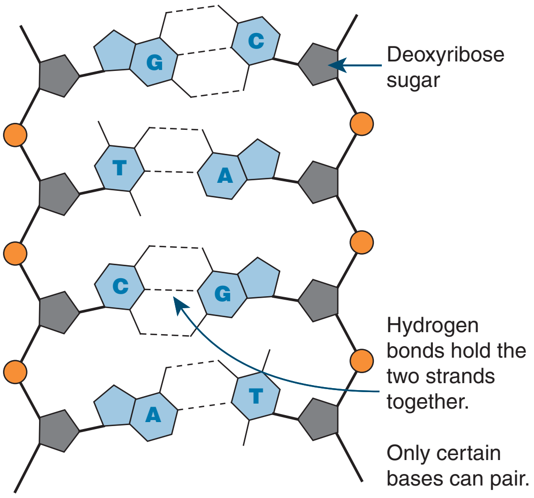


The carbon atoms on the pentose sugar are labelled one to five. During DNA replication (when new DNA is made) new nucleotides are added to the 3' end (the third carbon) of the existing nucleotide chain. It is therefore said DNA replication works in the 5' to 3' direction.

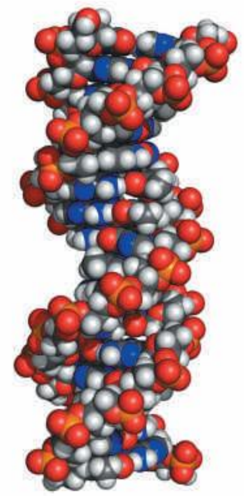
## RNA molecule



## DNA molecule



Symbolic representation



Space filling model

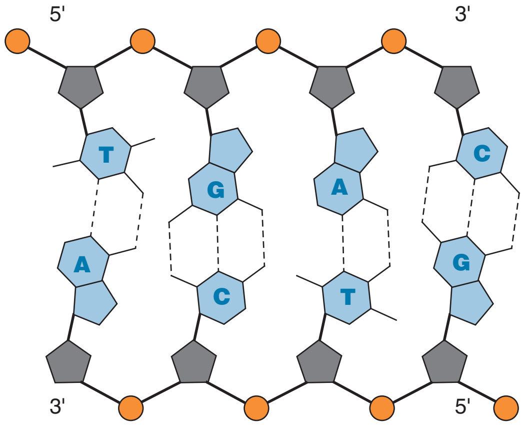
**Ribonucleic acid** (RNA) consists of a single strand of linked nucleotides. Although it is single stranded, it is often folded back on itself, with complementary bases joined by hydrogen bonds.

**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).
- 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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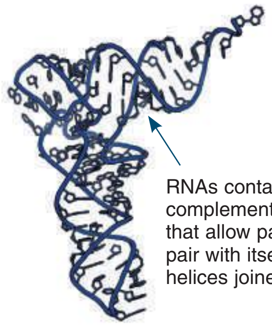
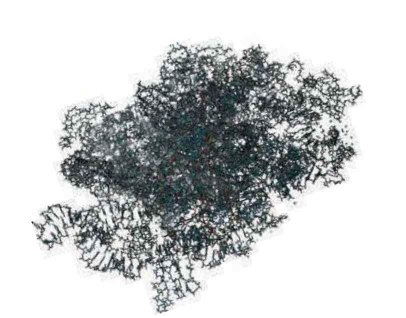
**RNA**s are involved in decoding the genetic information in DNA, as messenger RNA (mRNA), transfer RNA (tRNA), and ribosomal RNA (rRNA). RNA is also involved in modifying mRNA after transcription and in regulating translation.

**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 opposite 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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# 82 The Evidence for DNA Structure

**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.

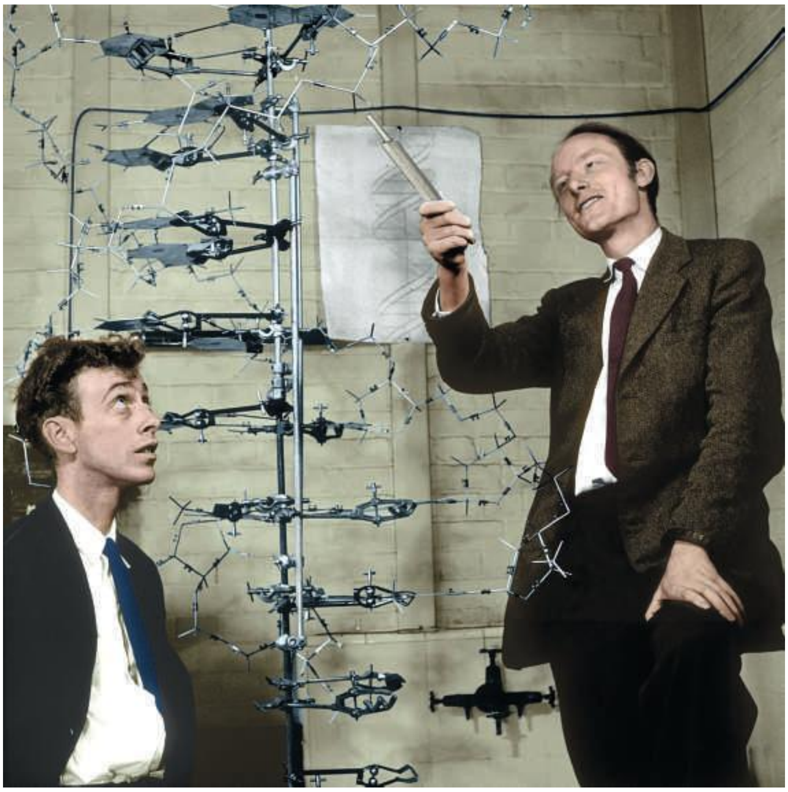


IMAGE: A. Barrington-Brown, © Gonville and Caius College, Cambridge / Coloured by Science Photo Library

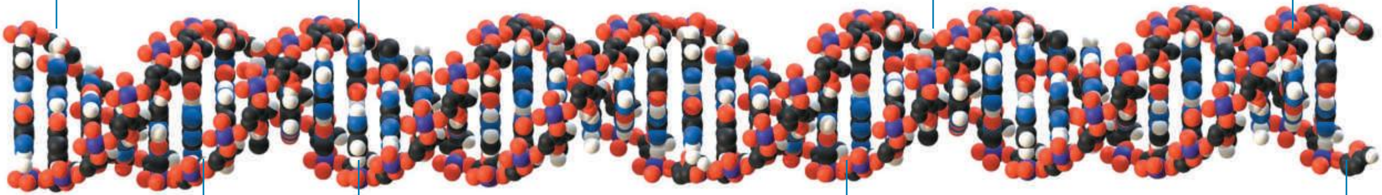
James Watson (left) and Francis Crick (right) in 1953 with their DNA model.

**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. You can use the information presented in this activity, as well as any information provided on **Weblinks**. 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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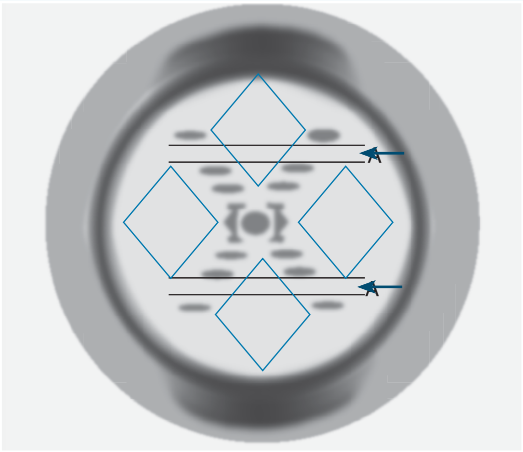
### Photo 51

Photo 51 is famous in the history of DNA research, not only because it provided the crucial evidence for DNA's structure, but also because of controversy surrounding how it was obtained and used by Watson and Crick.

The numerous distinct parts of the x-ray image indicate specific qualities of the DNA. The distinct X pattern indicates a helix structure, but Watson and Crick realised that the apparent gaps in the X (labelled **A**) were due to the repeating pattern of a *double* helix. The diamond shapes (in blue) indicate the helix is continuous and of constant dimensions and that the sugar-phosphate backbone is on the outside of the helix. The distance between the dark horizontal bands allows the calculation of the length of one full turn of the helix.



### DNA extraction by ethanol precipitation

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.

**You will need**: Strawberries, beaker, funnel, teaspoon, glass stirring rod, large zip lock bag, iced (or cold) water, salt, detergent, ethanol (on ice).

**Method**:

- 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.
- 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.
- 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).
- 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.
- 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.
- The DNA strands can be centrifuged with ethanol to isolate the DNA as a pellet.

Yaminchhipa10 CC 4.0

2. Describe two features on photo 51 that show DNA is a double helix:

3. In the extraction and isolation of DNA:

   (a) Why is it necessary to dissolve 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?

4. 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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# 83 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: the available space within the DNA double helix and 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 antiparallel (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.

**DNA base pairing rule**

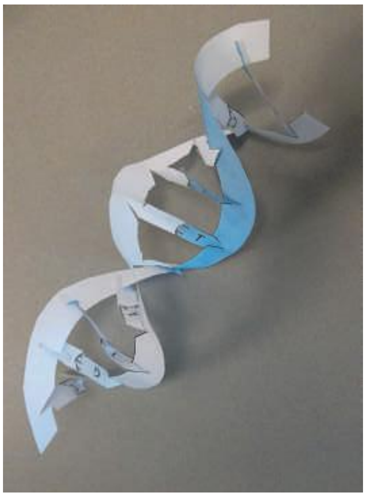
| | | | |
|---|---|---|---|
| **Adenine** | is always attracted to | **Thymine** | A ⟷ T |
| **Thymine** | is always attracted to | **Adenine** | T ⟷ A |
| **Cytosine** | is always attracted to | **Guanine** | C ⟷ G |
| **Guanine** | is always attracted to | **Cytosine** | G ⟷ C |

1. Cut out the opposite page. Cut out the template strand. Dark black lines should be cut. Fold on the blue dotted lines so that the grey surfaces are facing (a valley fold).

2. Cut out the complementary strand. The first base (G) is already in position as a guide. Again fold on the blue line so that the blue surfaces are facing each other.

3. (a) Fill in the table below to help you place the remaining bases in the correct order on the complementary strand:

| Template strand | Complementary strand |
|---|---|
| Cytosine (C) | Guanine (G) |
| Guanine (G) | |
| Thymine (T) | |
| Adenine (A) | |
| Thymine (T) | |
| Adenine (A) | |
| Thymine (T) | |
| Thymine (T) | |
| Cytosine (C) | |
| Guanine (G) | |



A finished model

(b) 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).

4. Line up the first base pairs (C and G) and stick them together with tape. Note that the bases are facing in opposite directions.

5. Continue sticking base pairs together, working your way around the helix, to complete the DNA molecule.

6. What does anti-parallel mean? ________________________________________

7. How is your model similar to other DNA models such as the ones on page 158? What differences you have noticed?

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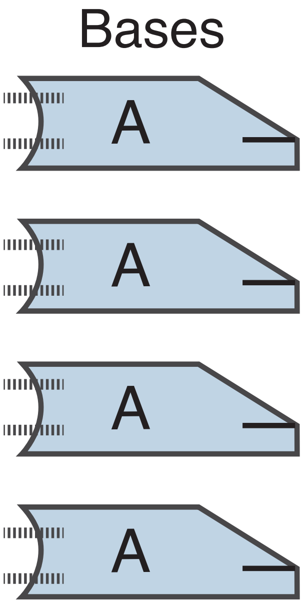

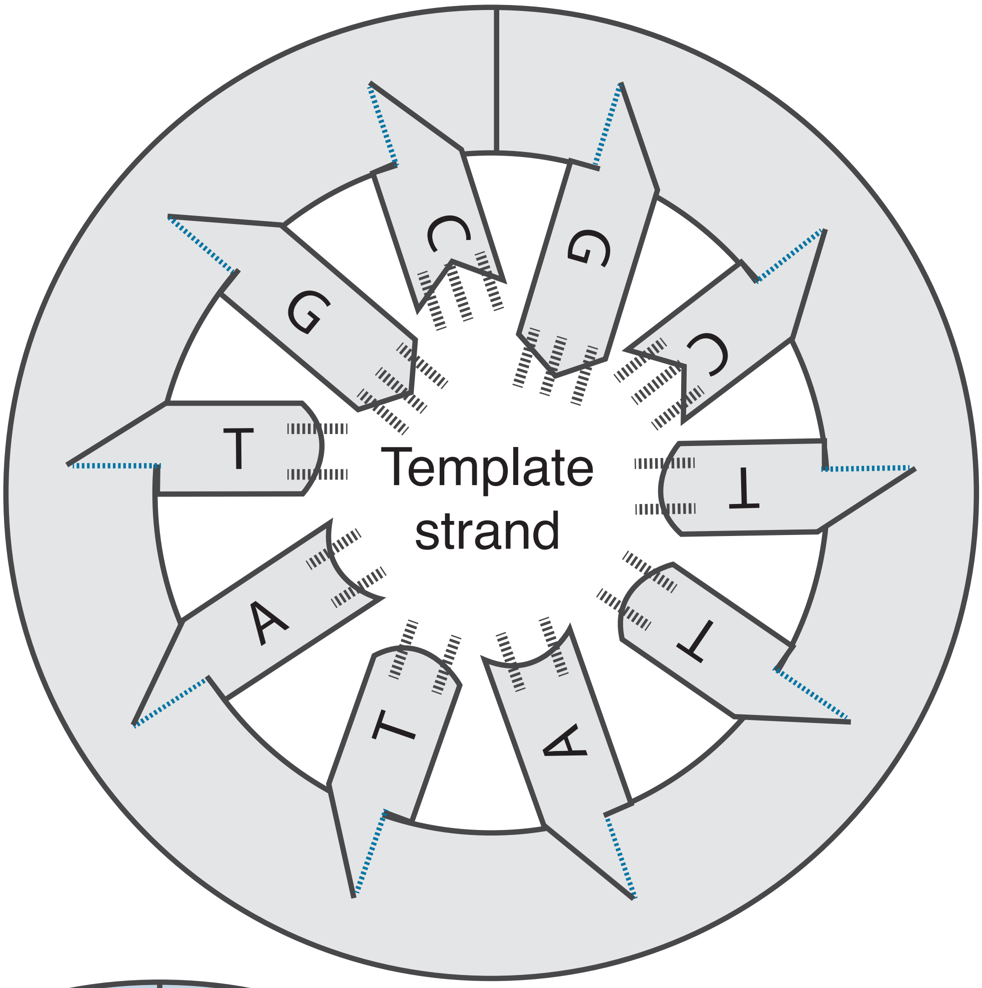

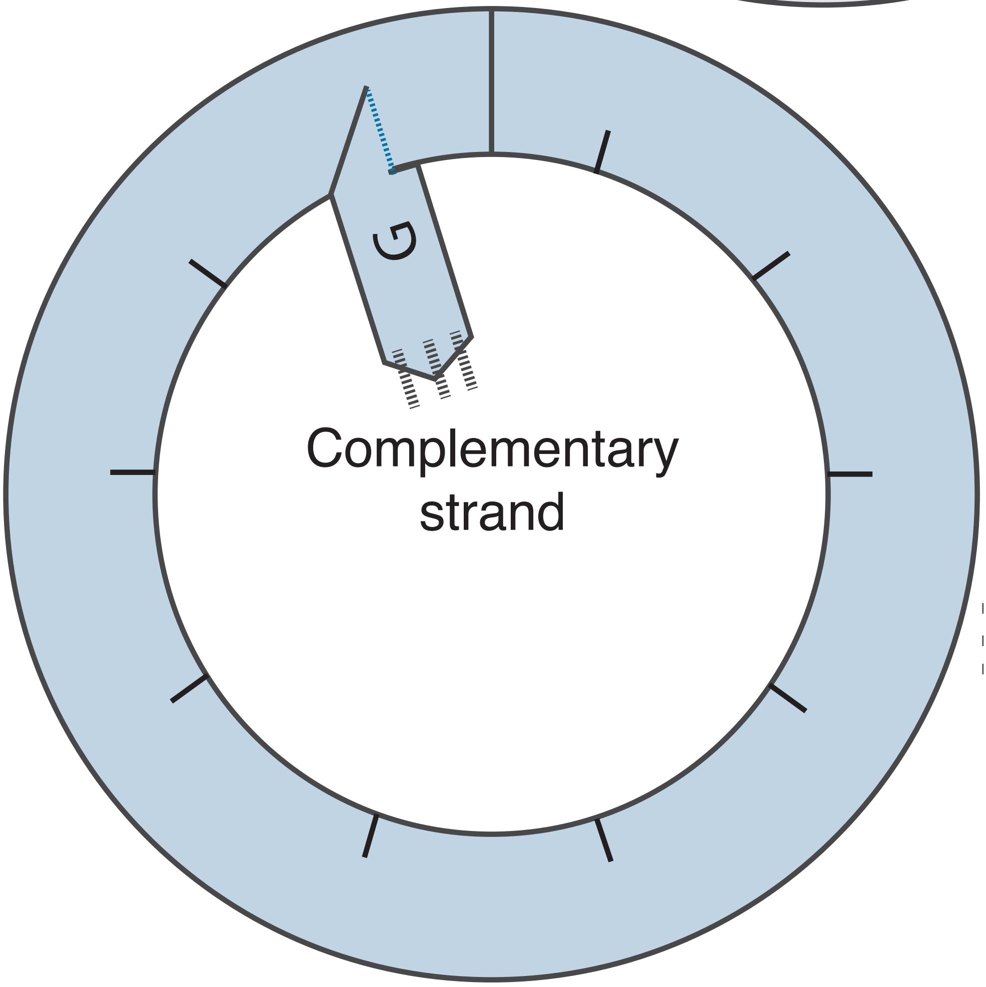

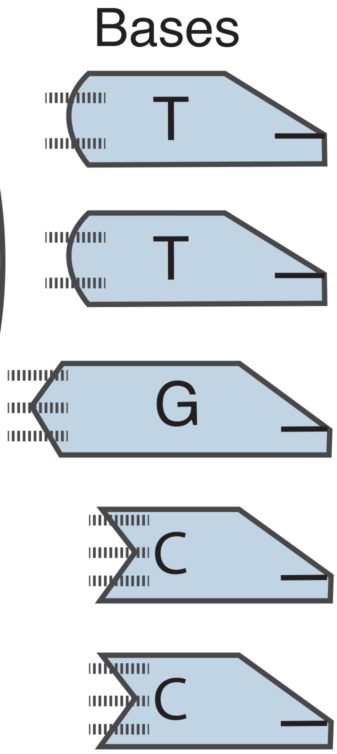

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# 84 How Does DNA Replicate?

**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 **helicase**. Another enzyme relieves the strain that this generates by cutting, winding and rejoining the DNA strands.

### Step 2
### Making new DNA strands

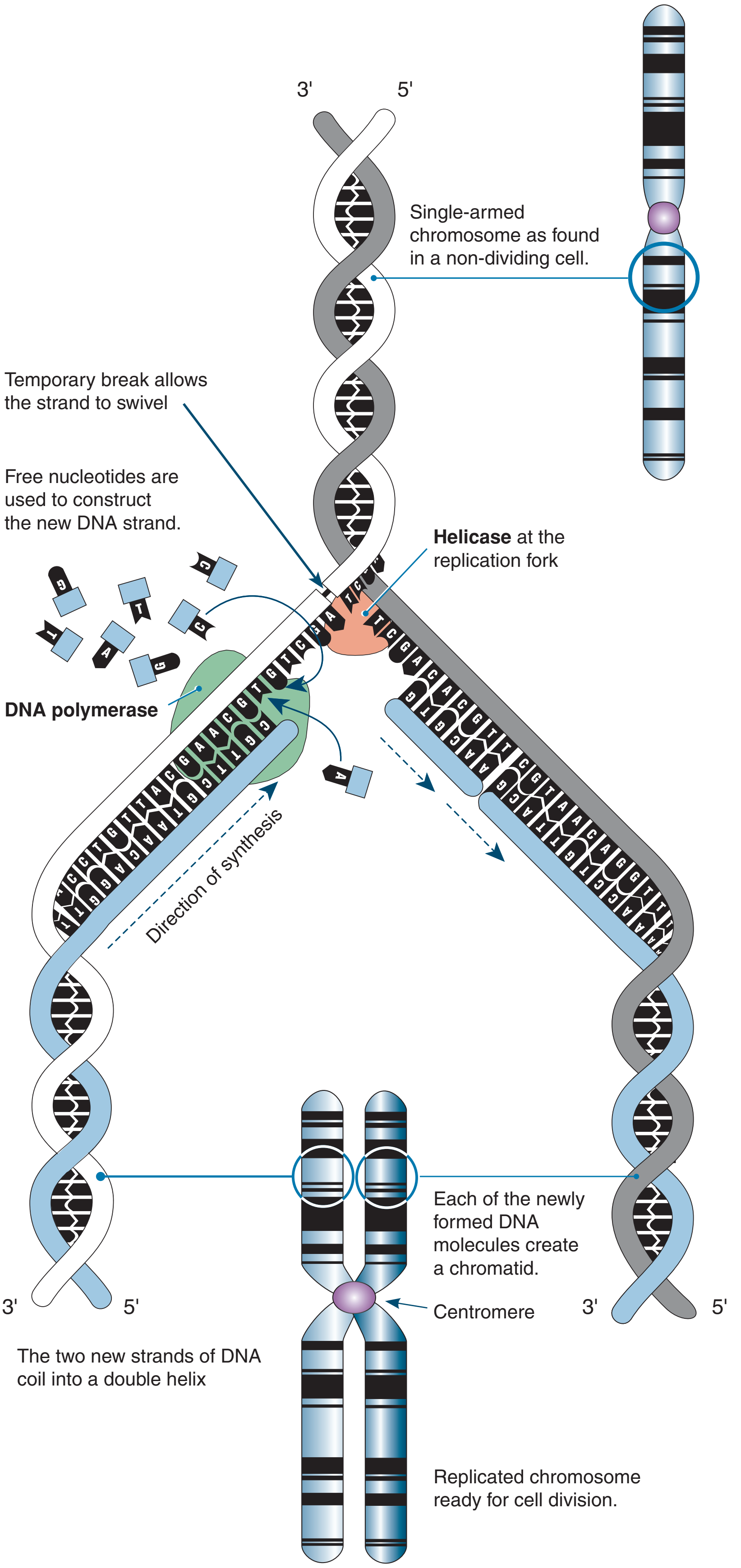
The formation of new DNA is carried out mostly by an enzyme complex called **DNA polymerase**.

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.



Single-armed chromosome as found in a non-dividing cell.

Temporary break allows the strand to swivel

Free nucleotides are used to construct the new DNA strand.

**Helicase** at the replication fork

**DNA polymerase**

Each of the newly formed DNA molecules create a chromatid.

Centromere

The two new strands of DNA coil into a double helix

Replicated chromosome ready for cell division.

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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...
DNA replication is the process by which the DNA molecule...
Replication is tightly controlled...
After replication, the chromosome...
DNA replication...
The chromatids separate...
A chromatid contains half original ...

...is required before mitosis or meiosis can occur.
...by enzymes.
...to correct any mistakes.
...and half new DNA.
...during mitosis.
...is copied to produce two identical DNA strands.
...is made up of two chromatids.

Write the complete paragraph here:

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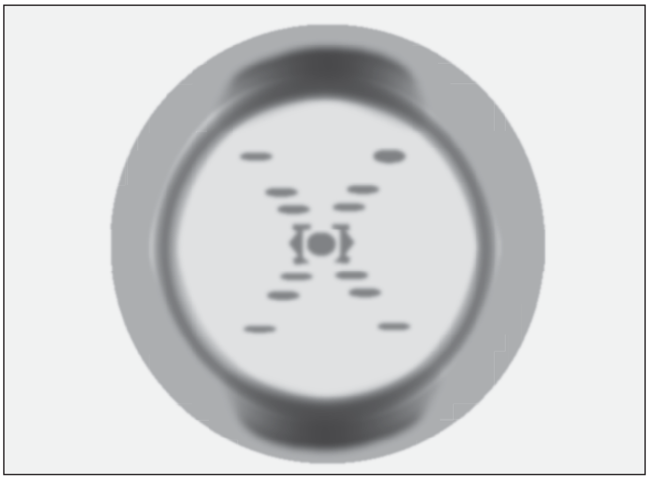
# 85 KEY TERMS AND IDEAS: Did You Get It?



1. (a) On the diagram shown right, highlight the region of the image that indicates a DNA helix.

   (b) Circle the regions that indicates there is a double helix.

   (c) What do the blank diamond shaped areas in the diagram indicate?

2. 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

3. (a) Which base does the base thymine (T) pair with in DNA?

   (b) Which base does the base cytosine (C) pair with in DNA?

4. What is the difference between a chromosome, a chromatid, and chromatin?

5. Under the headings Unwind, Replicate, Rewind, describe the stages of DNA replication:

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UNIT 4
Topic 1

# Cellular Replication and Variation

### Key terms

anaphase I
anaphase II
CRISPR
crossing over
diploid
fertilisation
gamete
haploid
homologous pair
independent assortment
interphase
meiosis
metaphase I
metaphase II
mitosis
oogenesis
pre-implanation genetic diagnosis
prophase I
prophase II
recombination
sexual reproduction
spermatogenesis
telophase I
telophase II

Activity number

## Cell division

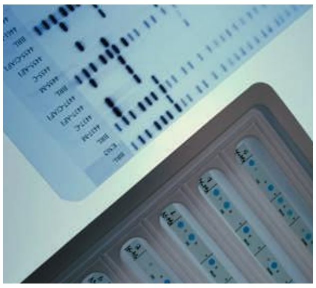
*Key skills and knowledge*

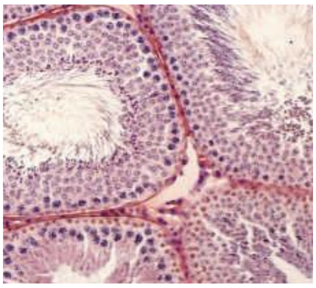
☐ 1 Recall that cells replicate by cell division, which is preceded by duplication of the genetic material by DNA replication. Distinguish between mitotic and meiotic division in terms of their genetic outcome and biological role. **86**

☐ 2 Recall how gametes produced by meiosis are brought together in fertilisation to restore the diploid number of the organism. **86**

☐ 3 Compare and contrast the behaviour of homologous chromosomes in mitosis and meiosis. What events are unique to meiosis? **86**

Thomas Splettstoesser cc4.0





## Meiosis

*Key skills and knowledge*

☐ 4 Understand the key events in the two divisions of meiosis, including the behaviour and role of homologous chromosomes: **87**

- **Meiosis I**: prophase I, metaphase I, anaphase I, and telophase I
- **Meiosis II**: prophase II, metaphase II, anaphase II, and telophase II

☐ 5 Describe the processes of crossing over and recombination between non-sister chromatids of homologous chromosomes

☐ 6 Explain the significance of the following events in meiosis: **87**

- 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.

☐ 7 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. **88**

☐ 8 Compare and contrast the processes of spermatogenesis and oogenesis with reference to haploid and diploid cells. **89**

## Genetic technologies and reproduction

*Key skills and knowledge*

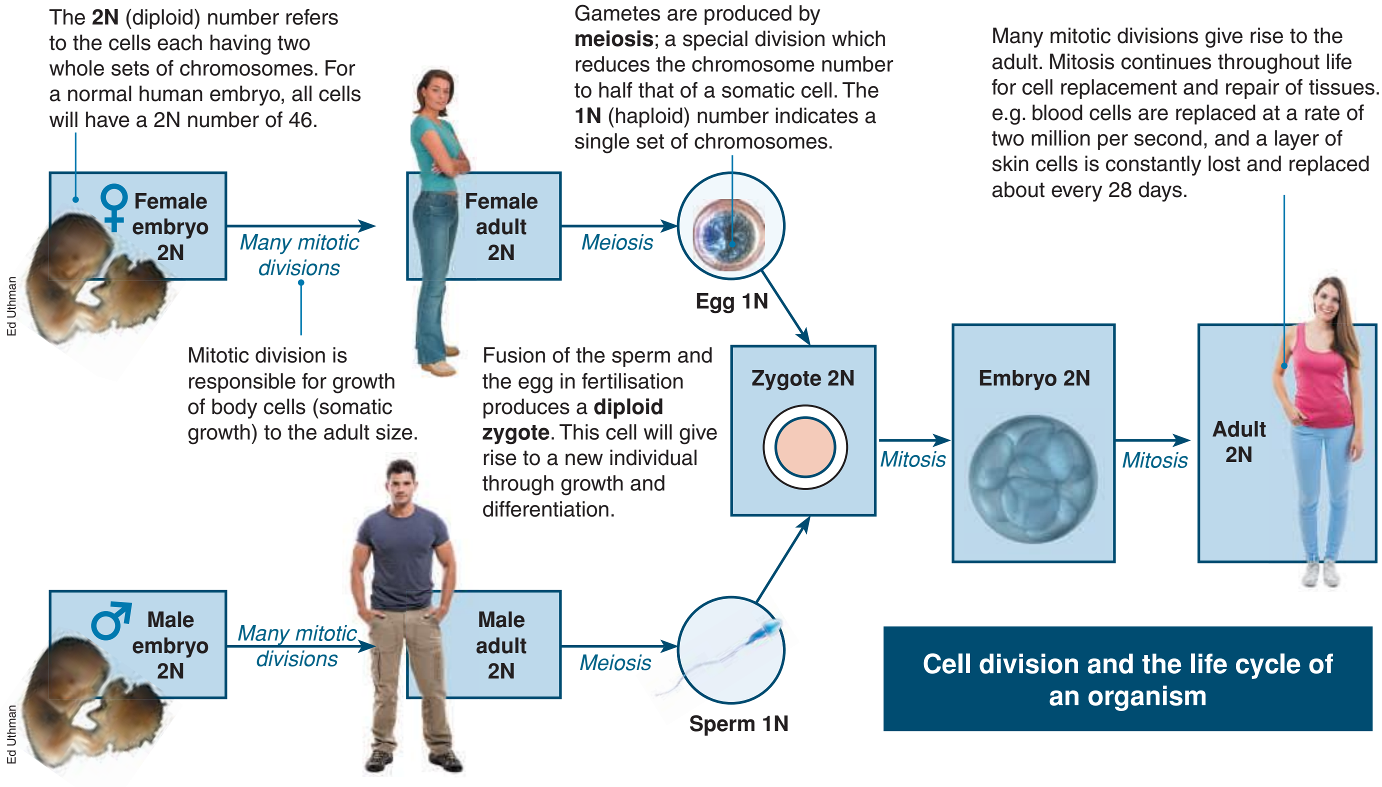
☐ 9 **SHE** Discuss the implications of preimplantation genetic diagnosis and CRISPR gene editing techniques on reproductive technology. **90**

☐ 10 **SHE** How have gene probes and CRISPR changed the options for therapeutic and non-therapeutic gene editing? What are the ethical issues involved? **91**

# 86 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.



The **2N** (diploid) number refers to the cells each having two whole sets of chromosomes. For a normal human embryo, all cells will have a 2N number of 46.

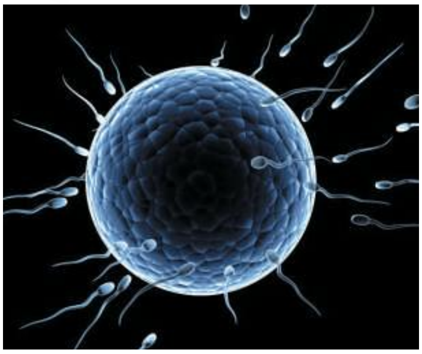
Gametes are produced by **meiosis**; a special division which reduces the chromosome number to half that of a somatic cell. The **1N** (haploid) number indicates a single set of chromosomes.

Many mitotic divisions give rise to the adult. Mitosis continues throughout life for cell replacement and repair of tissues. e.g. blood cells are replaced at a rate of two million per second, and a layer of skin cells is constantly lost and replaced about every 28 days.

Mitotic division is responsible for growth of body cells (somatic growth) to the adult size.

Fusion of the sperm and the egg in fertilisation produces a **diploid zygote**. This cell will give rise to a new individual through growth and differentiation.

**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).

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 (delete one)

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 (delete one)

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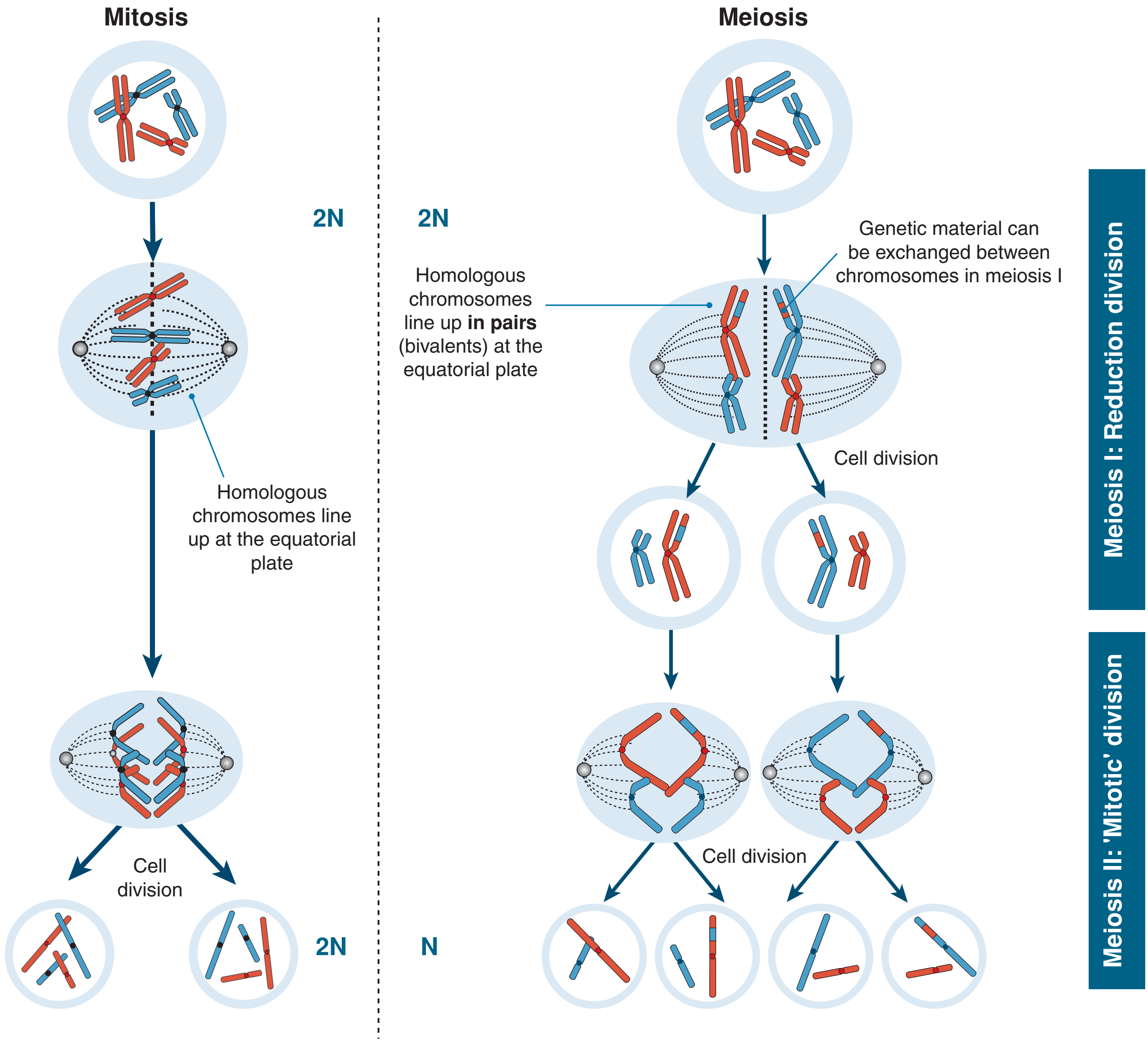
- **Mitosis** and **meiosis** have quite different purposes and genetic outcomes.
- Mitosis is the simpler process and produces two identical daughter cells from each parent cell. It is responsible for growth and repair in multicellular organisms and reproduction in single-celled and asexual eukaryotes.
- 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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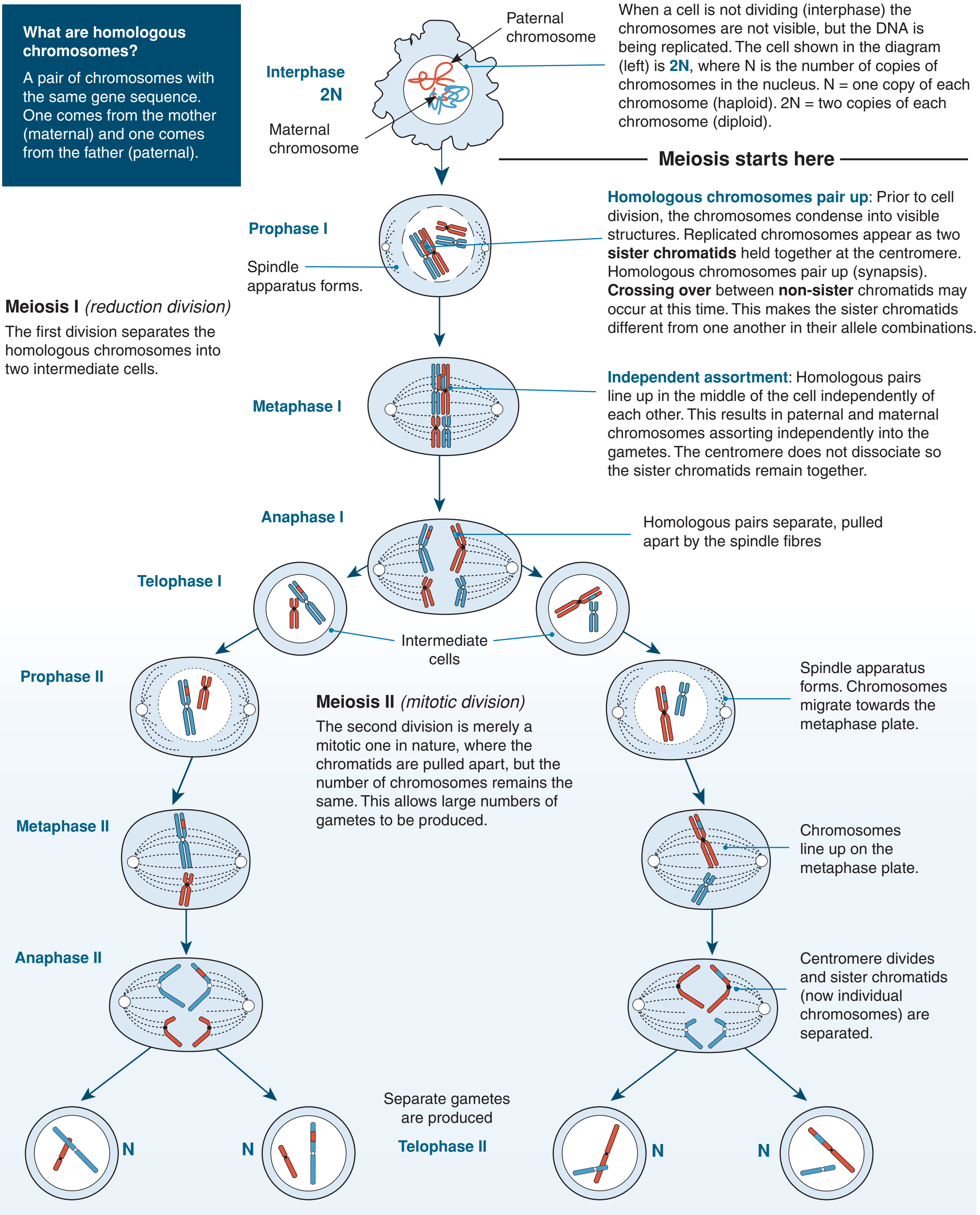
# 87 Meiosis

**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).



When a cell is not dividing (interphase) the chromosomes are not visible, but the DNA is being replicated. The cell shown in the diagram (left) is **2N**, where N is the number of copies of chromosomes in the nucleus. N = one copy of each chromosome (haploid). 2N = two copies of each chromosome (diploid).

**Meiosis starts here**

**Homologous chromosomes pair up**: Prior to cell division, the chromosomes condense into visible structures. Replicated chromosomes appear as two **sister chromatids** held together at the centromere. Homologous chromosomes pair up (synapsis). **Crossing over** between **non-sister** chromatids may occur at this time. This makes the sister chromatids different from one another in their allele combinations.

**Meiosis I** *(reduction division)*

The first division separates the homologous chromosomes into two intermediate cells.

**Independent assortment**: Homologous pairs line up in the middle of the cell independently of each other. This results in paternal and maternal chromosomes assorting independently into the gametes. The centromere does not dissociate so the sister chromatids remain together.

Homologous pairs separate, pulled apart by the spindle fibres

**Meiosis II** *(mitotic division)*

The second division is merely a mitotic one in nature, where the chromatids are pulled apart, but the number of chromosomes remains the same. This allows large numbers of gametes to be produced.

Spindle apparatus forms. Chromosomes migrate towards the metaphase plate.

Chromosomes line up on the metaphase plate.

Centromere divides and sister chromatids (now individual chromosomes) are separated.

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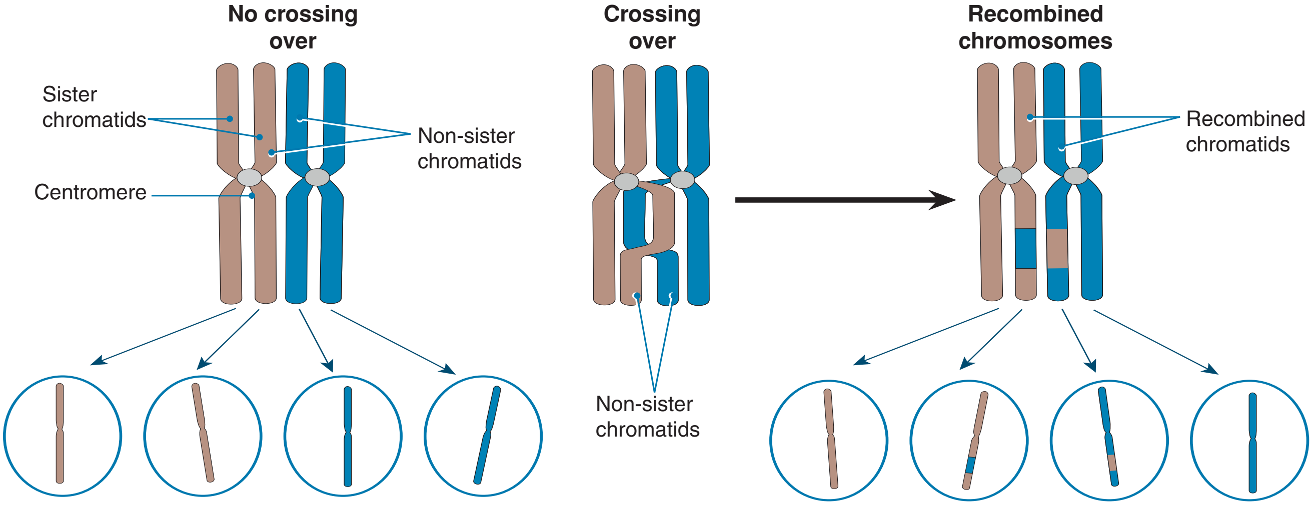
## Crossing over and recombination

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.

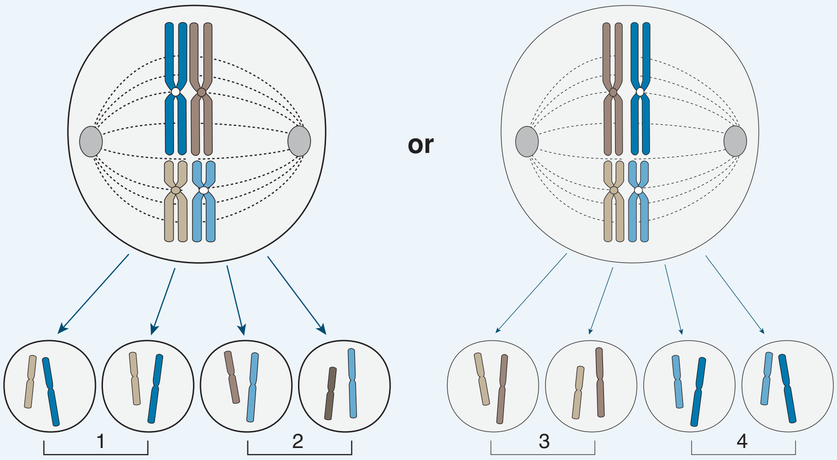


Possible gametes with no crossing over

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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# 88 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 meiosis. It will take 25-45 minutes.

## Background

Each of your somatic cells contain 46 chromosomes. You received 23 chromosomes from your mother (**maternal chromosomes**), and 23 chromosomes from your father (**paternal chromosomes**). Therefore, you have 23 homologous (same) pairs. For simplicity, the number of chromosomes studied in this exercise has been reduced to four (two homologous pairs). To study the effect of crossing over on genetic variability, you will look at the inheritance of two of your own traits: the ability to **tongue roll** and **handedness**.

| Chromosome # | Phenotype | Genotype |
|---|---|---|
| 10 | Tongue roller | TT, Tt |
| 10 | Non-tongue roller | tt |
| 2 | Right handed | RR, Rr |
| 2 | Left handed | rr |

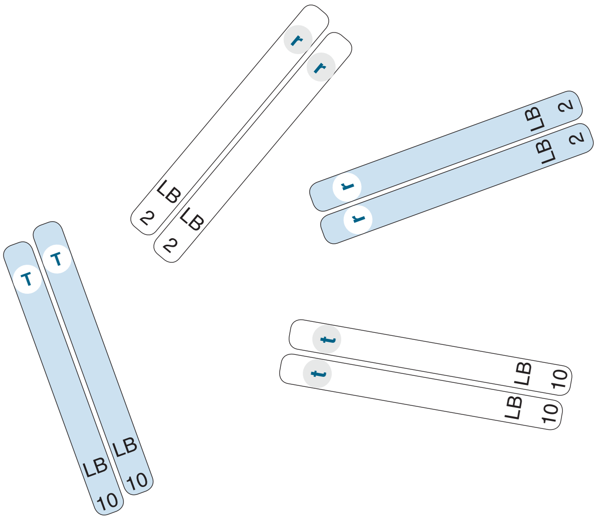
Record your phenotype and genotype for each trait in the table (right). **NOTE:** If you have a dominant trait, you will not know if you are heterozygous or homozygous for that trait, so you can choose either genotype for this activity.

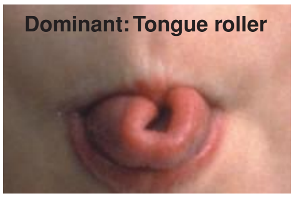
**BEFORE YOU START THE SIMULATION:** Partner up with a classmate. Your gametes will combine with theirs (fertilisation) at the end of the activity to produce a child. Decide who will be the female, and who will be the male. You will need to work with this person again at step 6.

1. Collect four ice-blocks 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 initial on each of the four sticks. Label each chromosome with their chromosome number (right).

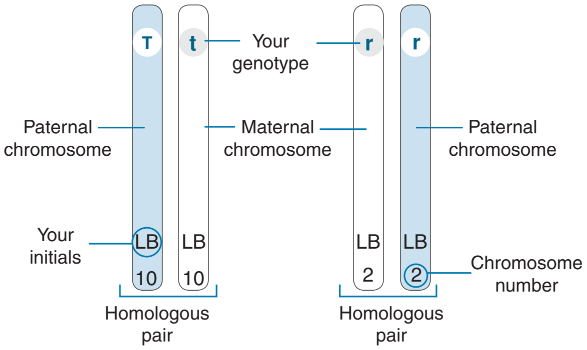
   Label four sticky dots with the alleles for each of your phenotypic traits, and stick it onto the appropriate chromosome. For example, if you are heterozygous for tongue rolling, the sticky dots with have the alleles **T** and **t**, and they will be placed on chromosome 10. If you are left handed, the alleles will be **r** and **r** and be placed on chromosome 2 (right).

2. Randomly drop the chromosomes onto a table. This represents a cell in either the testes or ovaries. **Duplicate** your chromosomes (to simulate DNA replication) by adding four more identical ice-block sticks to the table (below). This represents **interphase**.



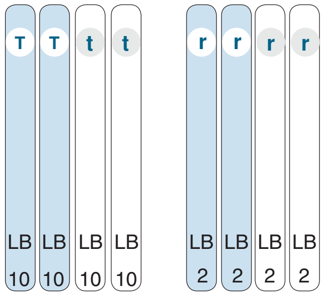


| Trait | Phenotype | Genotype |
|---|---|---|
| **Handedness** | | |
| **Tongue rolling** | | |

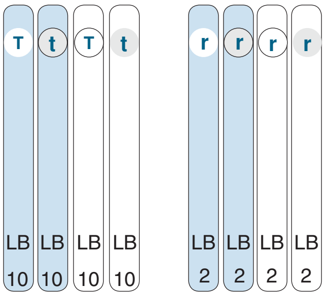


3. Simulate **prophase I** by lining the duplicated chromosome pair with their homologous pair (below). For each chromosome number, you will have four sticks touching side-by-side (A). At this stage **crossing over** occurs. Simulate this by swapping sticky dots from adjoining homologs (B).

(A)



(B)



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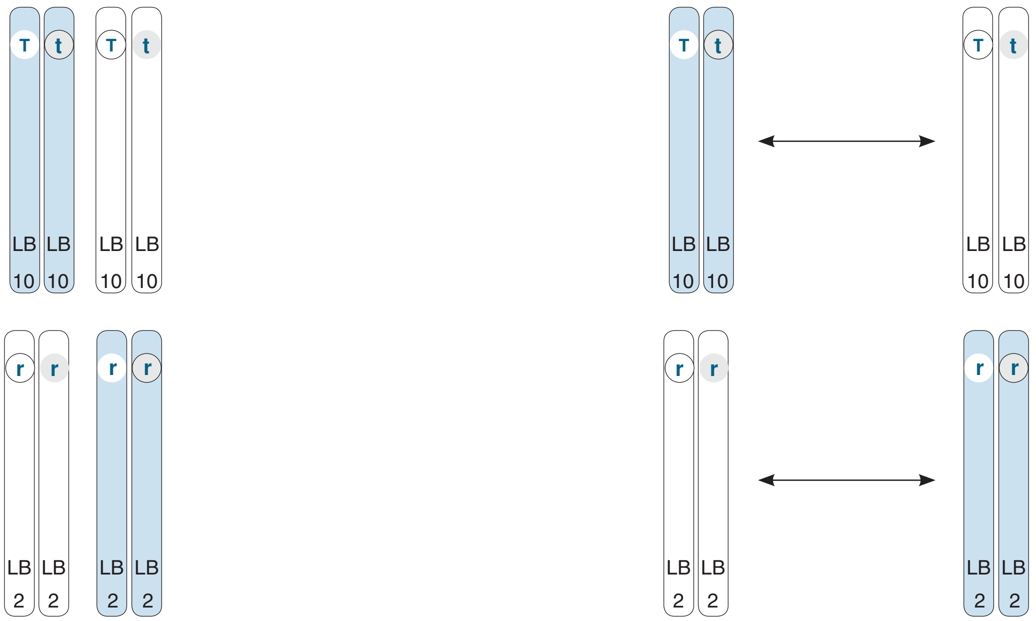
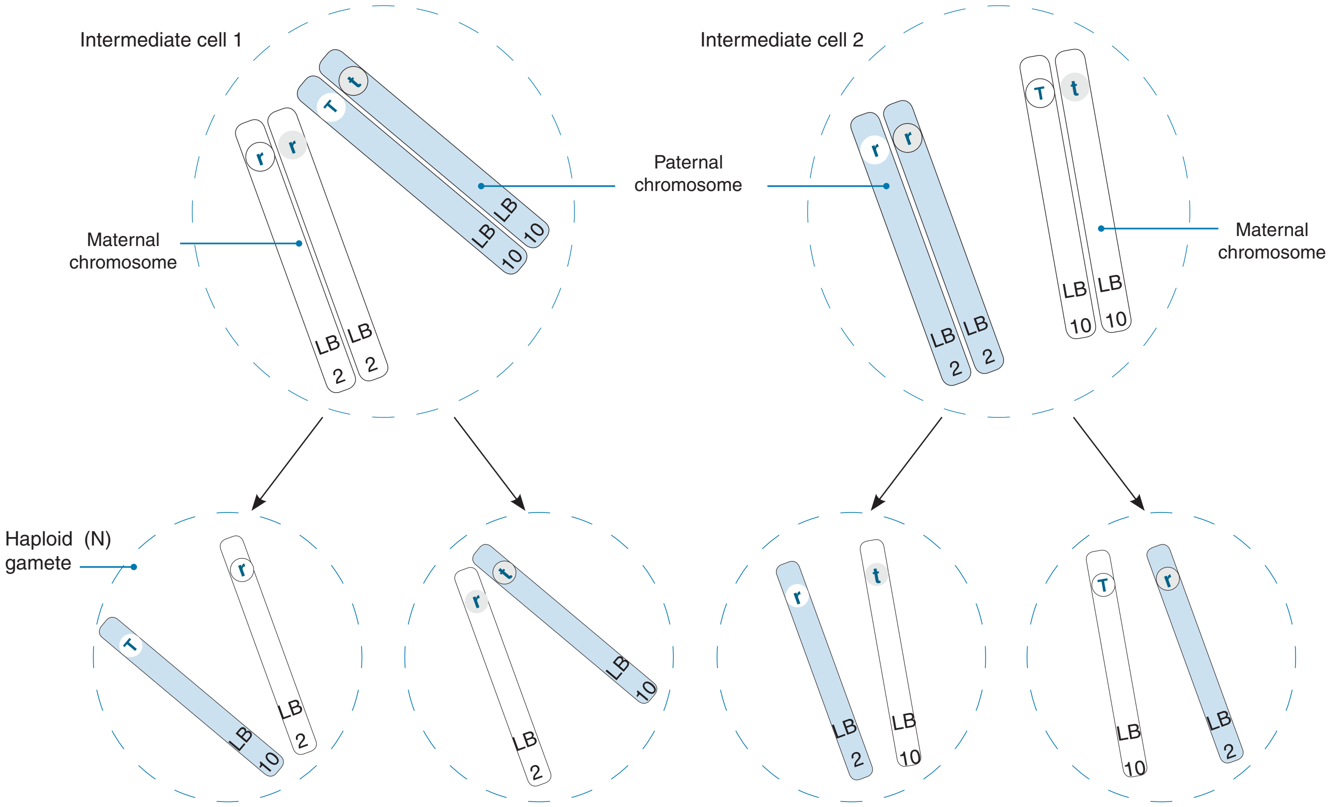
4. Randomly align the homologous chromosome pairs to simulate alignment on the metaphase plate (as occurs in **metaphase I**). Simulate **anaphase I** by separating chromosome pairs. For each group of four sticks, two are pulled to each pole.



5. **Telophase I:** Two intermediate cells are formed. If you have been random in the previous step, each intermediate cell will contain a mixture of maternal and paternal chromosomes. This is the end of **meiosis 1**.

   Now that meiosis 1 is completed, your cells need to undergo **meiosis 2.** Carry out prophase II, metaphase II, anaphase II, and telophase II. Remember, there is no crossing over in meiosis II. At the end of the process each intermediate cell will have produced two haploid gametes (below).



6. 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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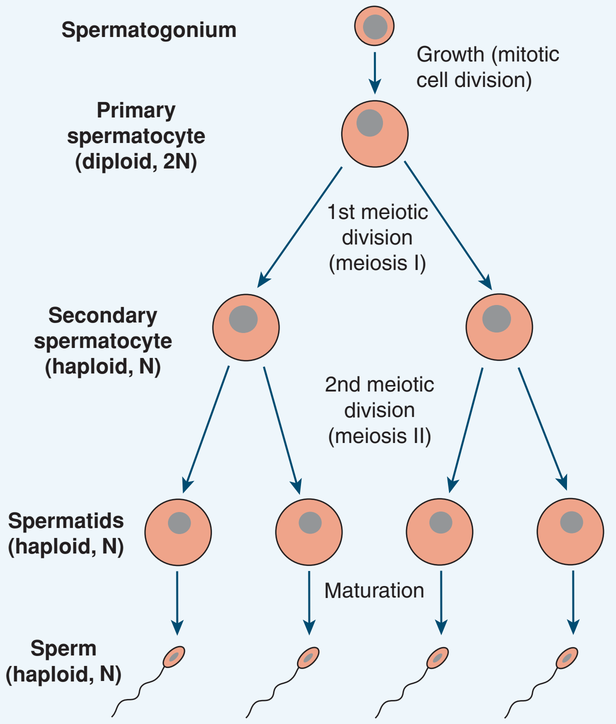
# 89 Producing Sex Cells

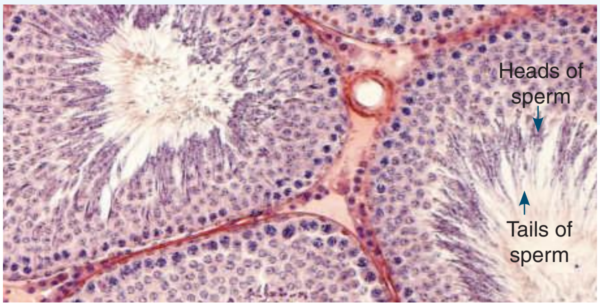
**Key Idea**: Sperm are the male gametes. They are produced in the testes by spermatogenesis. Eggs are the female gametes. They are produced by oogenesis in the ovaries.

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.

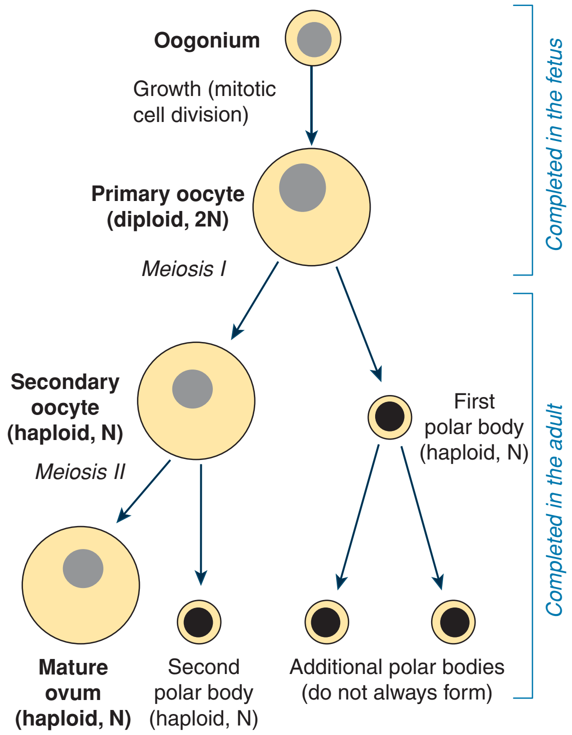
## Spermatogenesis



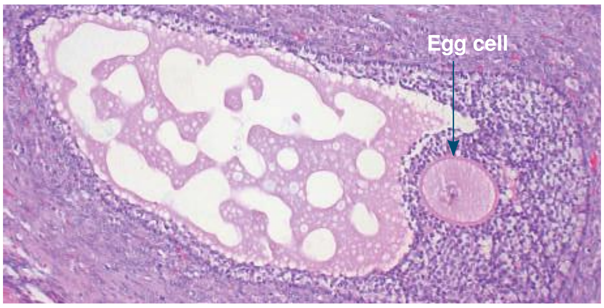
Spermatogenesis is the process by which mature sperm are produced in the testes. In humans, they are produced at the rate of about 120 million per day. Spermatogonia, in the outer layer of the seminiferous tubules, multiply throughout reproductive life. Some of them divide by meiosis into spermatocytes, 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.



Ed Uhlman

1. How are diploid (2N) cells maintained during sexual reproduction: ______________________________

______________________________

2. What are the main differences between spermatogenesis and oogenesis? ______________________________

______________________________

______________________________

______________________________

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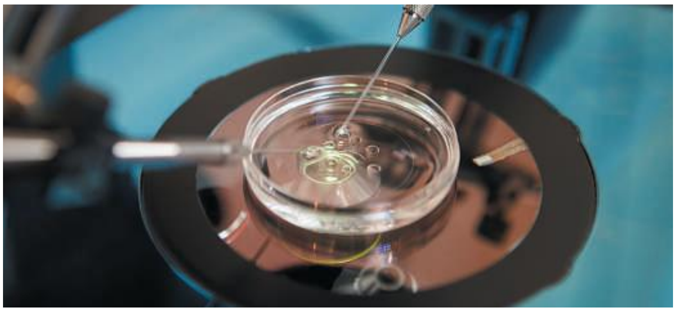
# 90 Genetic Screening

**Key Idea**: Genetic screening is used to identify specific (often harmful) genes in embryos, children, and adults. It raises a number of ethical issues, especially for embryo testing.

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).

## 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.



**Preimplantation genetic diagnosis (PGD)**: In this procedure (right) a cell is taken for screening from an embryo produced by *in vitro* fertilisation. Only suitable, healthy embryos will be implanted.

Thomas Splettstoesser CC4.0

**CRISPR-Cas9**: CRISPRs are specialised sequences of DNA. The sequences are associated with the Cas9 enzyme and together the complex can be used to locate and cut specific DNA sequences. This tool is now being widely used to edit genes, including the gene sequences of embryos before implantation.

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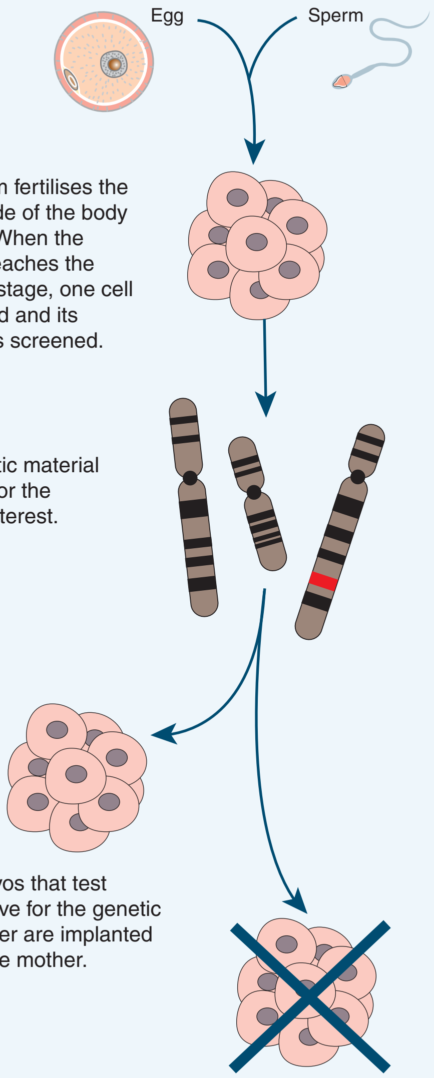
**Newborn screening**: Newborn babies are screened for a range of metabolic disorders (e.g. phenylketonuria). If a disease is detected, treatment (e.g. dietary modification) can begin immediately and the child's prognosis is greatly improved.

## Preimplantation genetic diagnosis



The sperm fertilises the egg outside of the body (*in vitro*). When the embryo reaches the eight cell stage, one cell is removed and its genome is screened.

The genetic material is tested for the gene of interest.

Embryos that test negative for the genetic disorder are implanted into the mother.

Embryos that test positive for the genetic disorder are not implanted into the mother.

- Embryos produced by *in vitro* fertilisation (IVF) are tested for genetic abnormalities to ensure only healthy embryos are transplanted into the mother. This is called pre-implantation genetic diagnosis (PGD).
- Sometimes PGD is used to select embryos *with* a genetic disorder. This most often occurs when parents have a particular disorder (e.g. genetic deafness) and they want their child to have it too.
- Embryos can also be screened *in vivo* (inside the mother) for genetic disorders. For example, Down syndrome is often first detected by ultrasound, and then confirmed by genetic testing.

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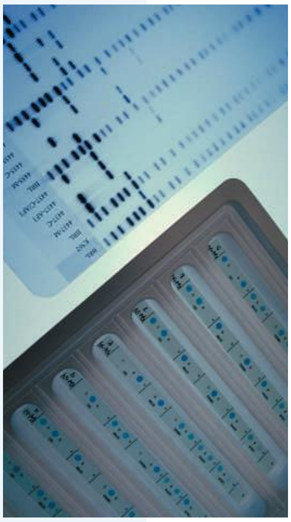
## Arguments for genetic screening

- 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 developing 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 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. Why would carrier testing be useful before deciding to have children? ______________________

2. Explain how preimplantation genetic diagnosis works: ______________________

3. CRISPR-cas9 can be used to edit specific genes or parts of a gene. By cutting out a part of a gene, that gene may be rendered inoperative or a new piece of DNA can be added in to change the operation of a gene. How would this technology be useful if an *in vitro* embryo was found to have a genetic defect?

4. PGD is controversially used to produce 'saviour siblings'. Saviour siblings are created using IVF to provide an organ or stem cells for an existing child with a certain disease. During the process, the embryos are tested to make sure that they are healthy and that they are compatible with the existing sibling. Any undesirable embryos are destroyed. Using saviour siblings as an example, discuss the ethics of genetic screening:

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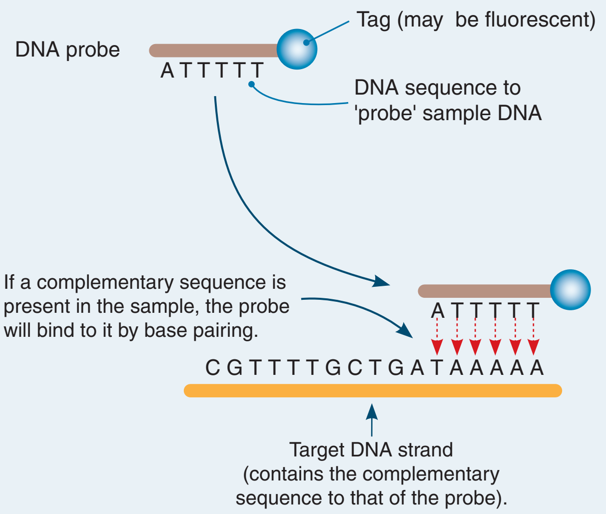
# 91 Designer Babies

**Key Idea**: The combination of preimplantation genetic diagnosis and gene editing means designer babies are a very real possibility. The possibility is very controversial.

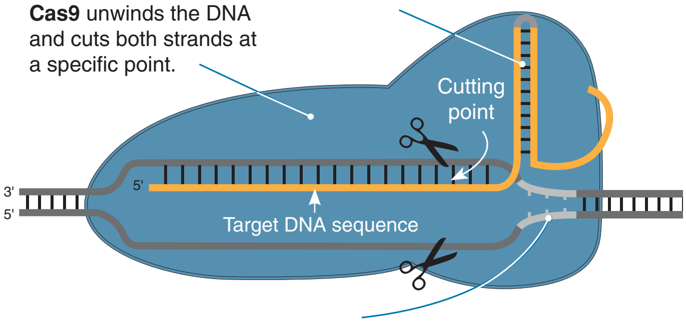
Assisted reproduction, such as *in vitro* fertilisation (IVF), was first developed to help infertile couples have children. Since the first IVF baby was born in 1978, technology has developed significantly and scientists can now edit an embryo's DNA before proceeding with the IVF process. Embryos whose genetic make-up has been selected or altered in some way are called 'designer babies'. The changes could involve removing genes associated with disease, but could also involve selecting for desirable traits (e.g. hair colour).

## DNA probes locate specific DNA



Specific DNA sequences can be located using DNA probes (above). These are single stranded sequences of DNA with a molecular tag added. When introduced to a prepared DNA sample, the probe binds to its complementary DNA sequence. The attached molecular tag indicates the presence of the specific DNA sequence. This can be used to identify the DNA sequences specific to certain genetic disorders.

## CRISPR-Cas9 is a powerful gene editing tool



**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 which is complementary to the DNA of interest.

**Cas9** unwinds the DNA and cuts both strands at a specific point.

Cas9 recognises a specific DNA sequence downstream of the target site. It destabilises the DNA allowing the sgRNA to be inserted.

CRISPR is an enzyme complex that is able to find specific stretches of DNA and edit it at very precise locations (by adding or removing DNA). CRISPR requires an RNA guide, which locates and binds to the target piece of DNA, and the Cas9 enzyme, which unwinds and cuts the DNA. If genes are edited in the gametes or the early embryo the edits will be passed to developing individual. This leads to two possible gene editing pathways: therapeutic and non-therapeutic genetic editing (opposite).

## Designer babies may be here, ready or not!

The Australian government recently announced it will not regulate the use of gene-editing techniques in plants, animals and human cell lines that do not introduce new genetic material. However, the use of gene editing in human embryos for reproduction is banned.

Recently the world was stunned when a Chinese scientist announced he had edited the genes of twin babies Lulu and Nana who were born in 2018. The scientist said he modified the gene CCR5 in the embryos using CRISPR technology. The CCR5 mutation may provide resistance against HIV (the girls' father is HIV positive). The claim has not been validated, and has been met with widespread criticism from the scientific community. The announcement has fuelled the fear that widespread use of gene editing technology in humans will make designer babies a common occurrence.

A Russian scientist has announced he has five couples who want their embryos modified so they do not inherit a gene for deafness. Each of the couples are deaf due to mutations to the GJB2 gene. Without intervention, their babies would be born deaf. By editing one copy of the GJB2 gene, the scientist believes the babies will be born being able to hear. However, there are several ethical issues raised by genetic editing:

- **Safety**: Are there any health issues that could occur later? How do we know that altering one gene does not affect something else too?
- **Cost**: Treatment is costly, so available only to those who can afford it.
- **Informed consent**: An embryo cannot give consent for the procedure.
- **Embryo destruction**: Unsuccessfully edited embryos are destroyed.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A hearing test being performed on a newborn

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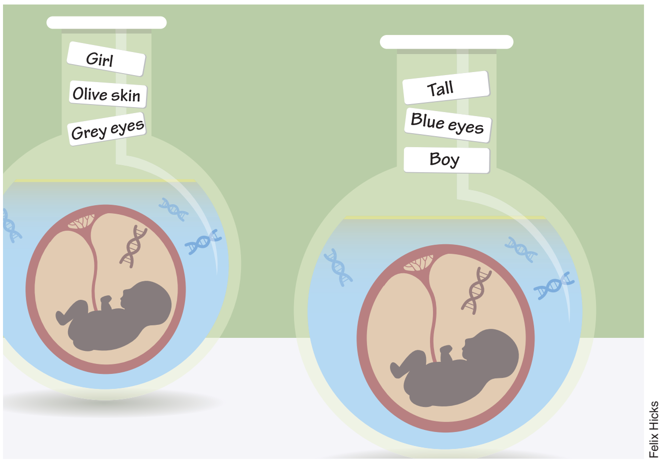

**Therapeutic genetic editing**
Thousands of diseases are caused by gene mutations. Some diseases such as cystic fibrosis (CF), alpha-1-antitrypsin deficiency, and thalassemia mutations have the potential to be corrected using therapeutic genetic editing. The technique aims to improve the a person's quality of life or to eradicate diseases.

**Non-therapeutic genetic editing**
Non-therapeutic gene editing is used to enhance human intelligence or physiology. In other words the technology could be used to "make a person the best they can be". This use is more controversial than therapeutic genetic editing because it is seen as crossing an ethical line associated with modifying nature.

1. Explain how DNA probes and CRISPR could be used to produce designer babies: ______________________________

2. Describe the difference between therapeutic and non-therapeutic genetic editing: ______________________________

3. (a) In groups, discuss the implications of genetic screening and gene editing technologies. Research and present an argument for or against the use of gene editing on humans. Arguments could include technological, medical, or ethical reasons. Present your argument to your class as a group. Use the space below to organise your ideas:

(b) After all the groups have presented their arguments, discuss as a class whether therapeutic or non-therapeutic gene editing of embryos should be allowed in future. Summarise the main points of the discussion below:

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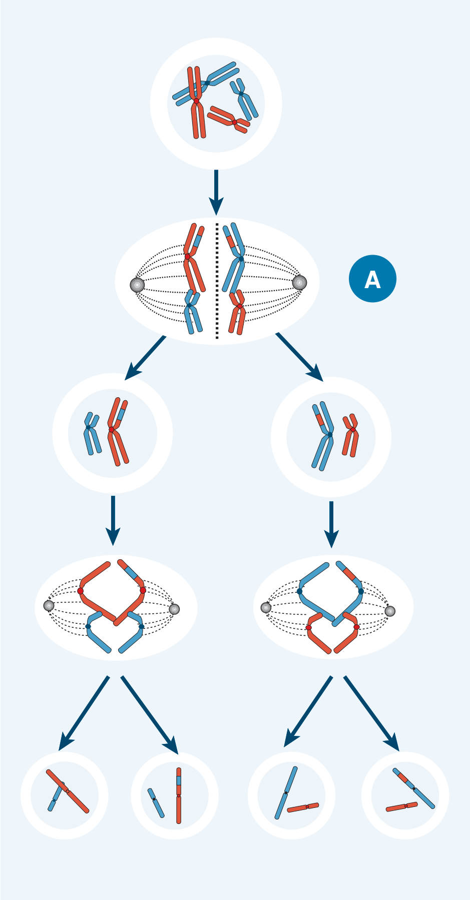
# 92 KEY TERMS AND IDEAS: Did You Get It?



1. Identify the process shown on the right: ____________________

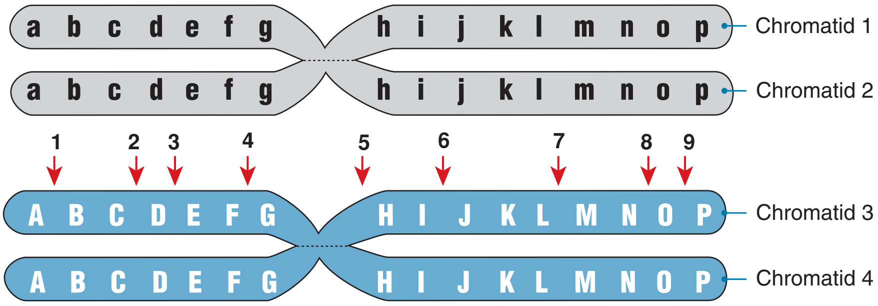
2. What is the purpose of this process? ____________________

3. (a) Describe the two events that have occurred at point A on the diagram:

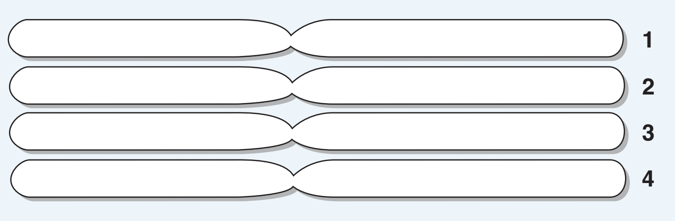
   (b) How do these events increase genetic variation in the offspring?

   (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.

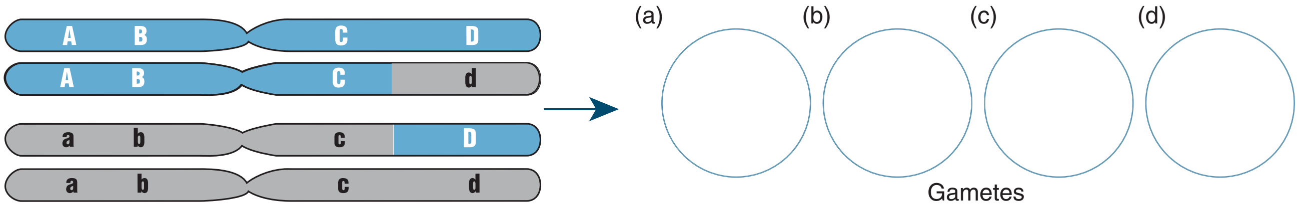


   (a) Draw the gene sequences for the four chromatids (above), after crossing over has occurred at **crossover point 2**:



   (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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UNIT 4
Topic 1

# Gene Expression

## Key terms

- adenine
- amino acid
- anticodon
- base-pairing rule
- coding strand
- cytosine
- epigenetics
- exons
- gene
- gene expression
- genetic code
- genome
- guanine
- introns
- peptide bond
- polypeptide
- proteome
- regulatory gene
- ribosome
- RNA (mRNA, rRNA, tRNA)
- structural gene
- template strand
- terminator sequence
- thymine
- transcription
- transcription factors
- translation
- uracil

**Activity number**

## Eukaryotic gene structure and protein synthesis

*Key skills and knowledge*

☐ 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. **93 94**

☐ 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. **94 95**

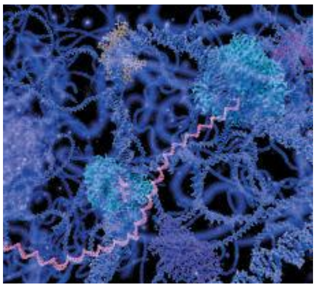
☐ 3 Describe the features of the genetic code, including: **95**
- The 4-letter alphabet and the 3-letter triplet code (codon) of base sequences.
- The non-overlapping, linear nature of the code, which is read from start to finish in one direction. The specific punctuation codons and their significance.
- The universal nature and degeneracy of the code.

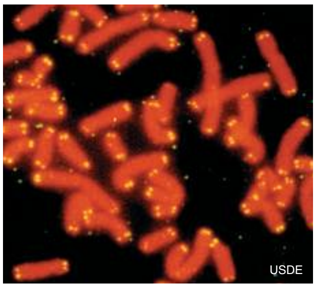
☐ 4 Recall that the purpose of gene expression is to synthesise a functional gene product and that the process can be regulated and is common to all life. **95**

☐ 5 Describe transcription in eukaryotes, including reference to the start and end points, the direction of transcription, and the role of RNA polymerase. **96 98**

☐ 6 Describe translation of mRNA into an amino acid sequence (polypeptide) at the ribosome, including reference to the role of transfer RNA, codons, and anticodons. **97 98**

☐ 7 Understand how gene expression profiles allow us to recognise which genes are being expressed in different cells and tissues. How can this information be applied? **97**

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## Regulating gene expression

*Key skills and knowledge*

☐ 8 Identify factors regulating the phenotypic expression of genes, including: **99 - 103**
- control of transcription via transcription factors encoded by regulatory genes
- post transcriptional modification (mRNA editing and exon splicing)
- post translational modification of proteins (e.g. attachment of carbohydrate)
- environment, including the epigenetic environment

☐ 9 Explain how transcription in eukaryotes involves the interaction of transcription factors with specific DNA sequences so that RNA polymerase can transcribe (rewrite) the protein-coding gene into a primary RNA transcript. **99**

☐ 10 Describe how mRNA is processed after transcription, including reference to intron removal and exon splicing. How does alternative exon splicing account for the difference in the size of the proteome relative to the number of identified genes in the human genome? **100**

☐ 11 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. **101**

☐ 12 Explain how epigenetic factors can influence the level of gene expression. Describe some of the evidence for epigenetic regulation, including from twin studies. **102**

☐ 13 Describe an example of a regulatory (transcription factor) gene that regulates morphology (e.g. HOX gene family) and cell differentiation (SRY). **103**

# 93

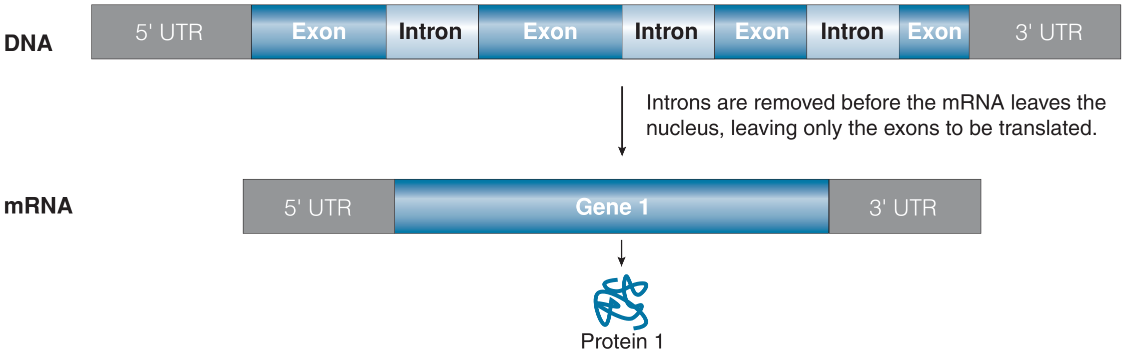
# Eukaryotic Gene Structure

**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.

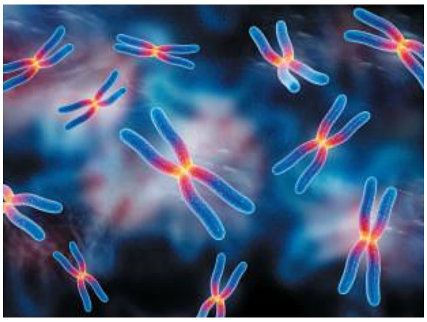
## Eukaryotic gene structure

- 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).

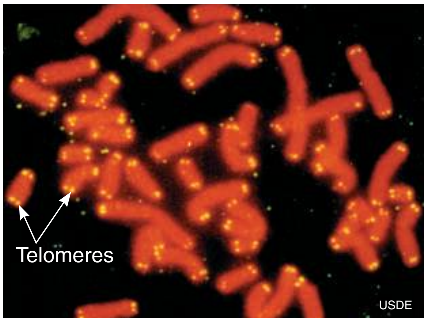


Introns are removed before the mRNA leaves the nucleus, leaving only the exons to be translated.

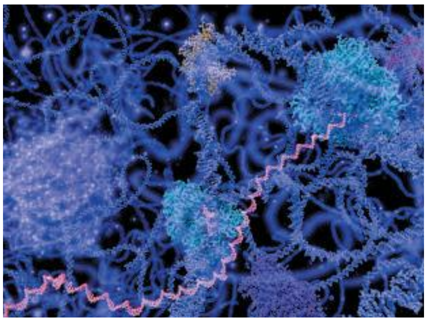
## Structures outside the gene



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:

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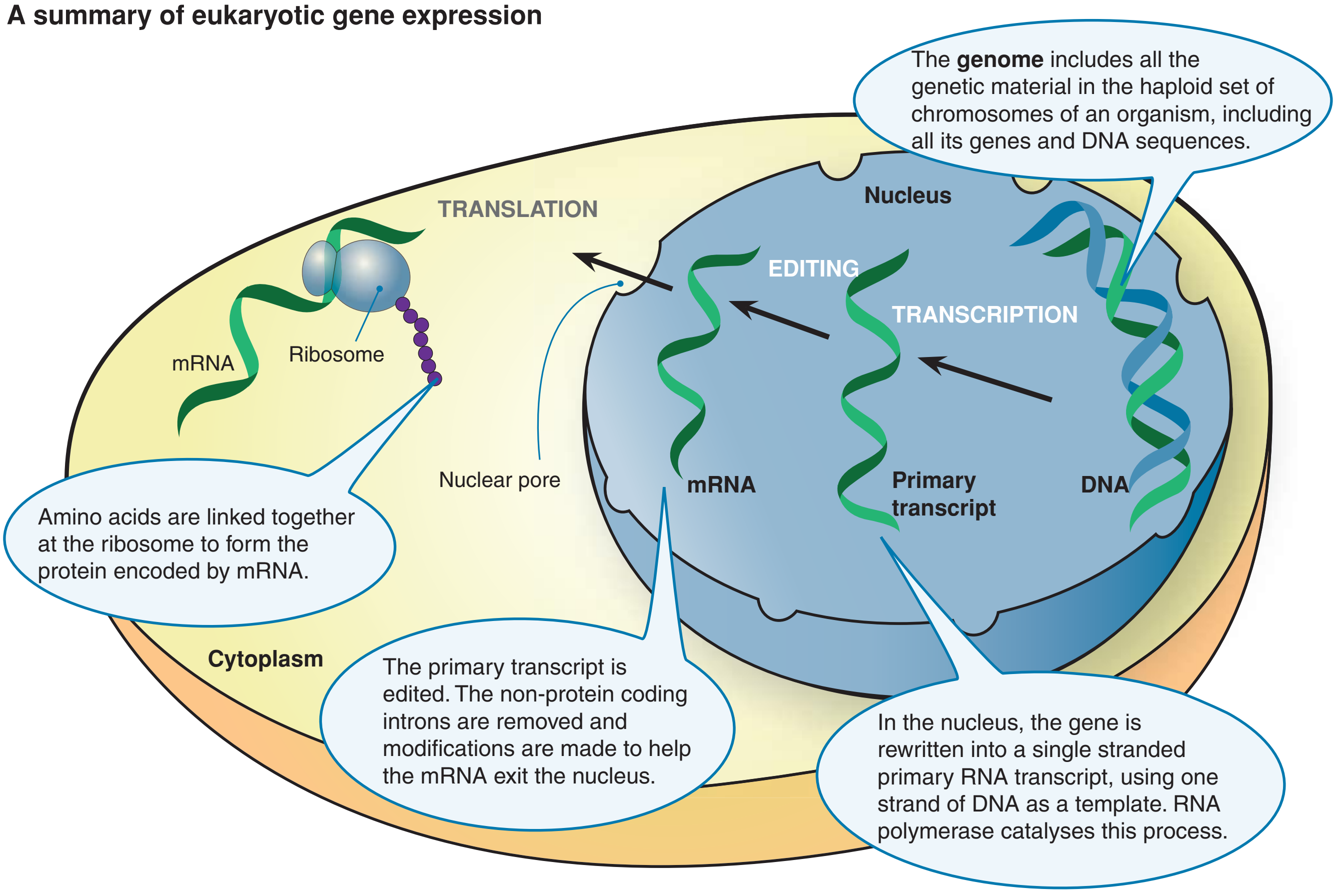
# 94 What is Gene Expression?

**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



The **genome** includes all the genetic material in the haploid set of chromosomes of an organism, including all its genes and DNA sequences.

Amino acids are linked together at the ribosome to form the protein encoded by mRNA.

The primary transcript is edited. The non-protein coding introns are removed and modifications are made to help the mRNA exit the nucleus.

In the nucleus, the gene is rewritten into a single stranded primary RNA transcript, using one strand of DNA as a template. RNA polymerase catalyses this process.

1. What is a gene? ____________________

____________________

2. (a) What does gene expression mean? ____________________

____________________

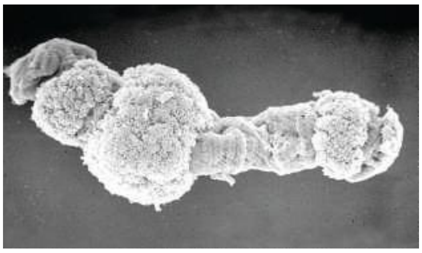
(b) What are the three stages in gene expression in eukaryotes and what happens in each stage?

(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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# 95 What is 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 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

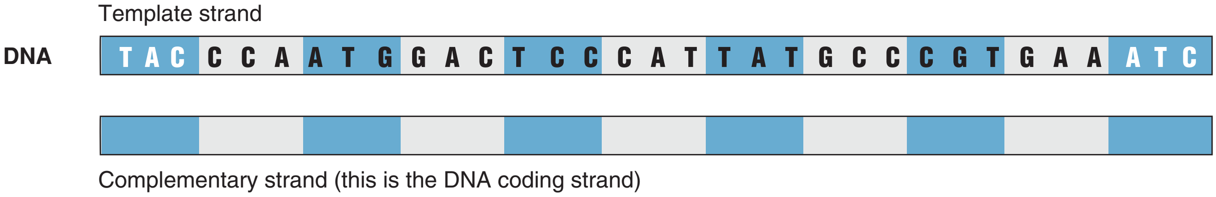
| First letter | Second letter | | | | Third letter |
|---|---|---|---|---|---|
| | U | C | A | G | |
| U | UUU Phe | UCU Ser | UAU Tyr | UGU Cys | U |
| | UUC Phe | UCC Ser | UAC Tyr | UGC Cys | C |
| | UUA Leu | UCA Ser | UAA STOP | UGA STOP | A |
| | UUG Leu | UCG Ser | UAG STOP | UGG Trp | G |
| 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

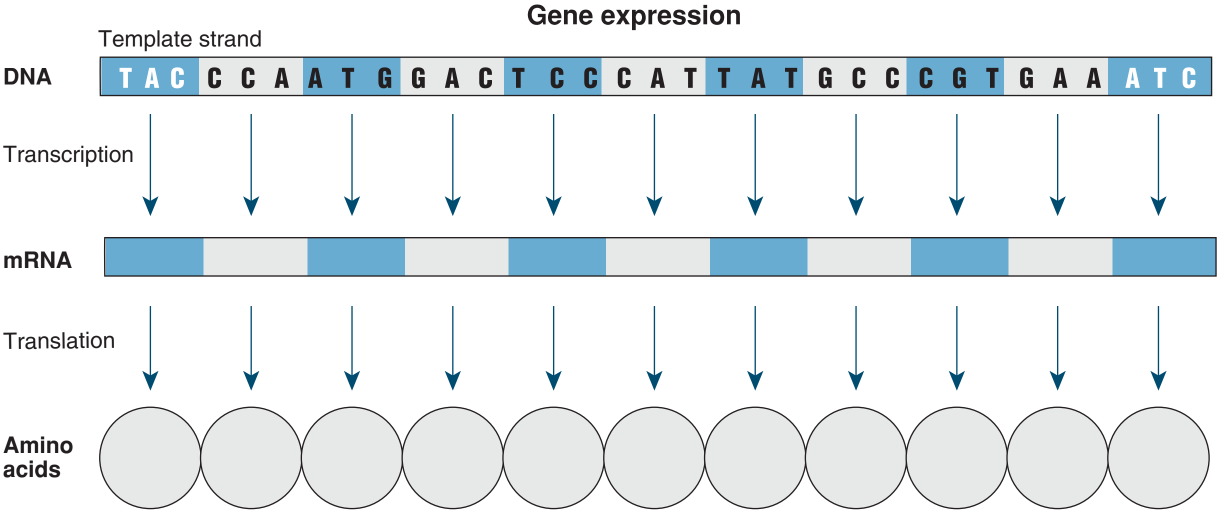
Read third letter here

1. (a) Use the base-pairing rule for to create the complementary strand for the DNA template strand shown below.

(b) For the same DNA template strand, then determine the mRNA sequence and use the mRNA-amino acid table to determine the amino acid sequence. Note that in mRNA, uracil (U) replaces thymine (T) and pairs with adenine.



### Gene expression



2. What do you notice about the sequence on the DNA coding strand and the mRNA strand? ______________________________

______________________________________________________________

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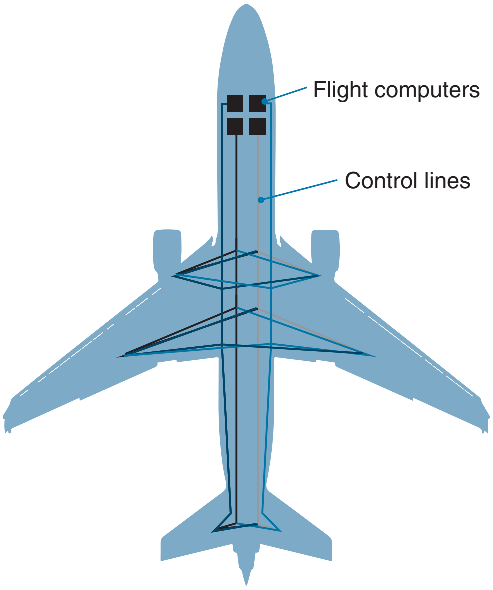
## Redundancy and degeneracy

Redundancy and degeneracy are important concepts in understanding the **genetic code.**

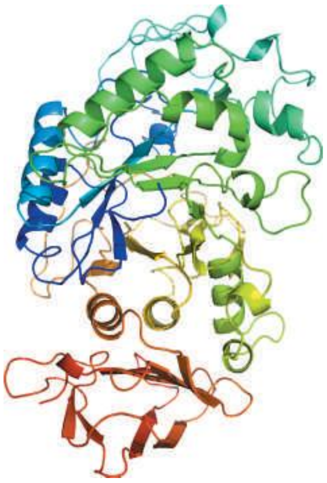
- **Redundancy** is when several situations code for or control the actions of one specific thing.
- **Degeneracy** is when a particular output can be produced by several different pathways.

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.



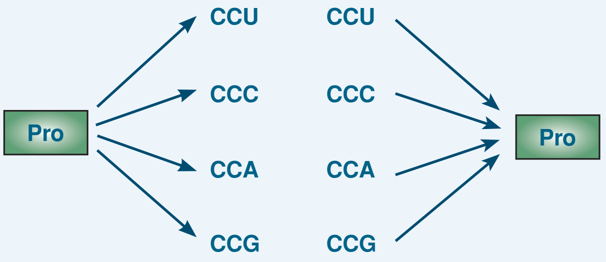
Modern aircraft (left) have multiple redundant features for safety. Often there are three or four flight computers linked independently to the flight surfaces and other input/output devices. If one computer or control line fails the others can continue to fly the plane normally.

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?

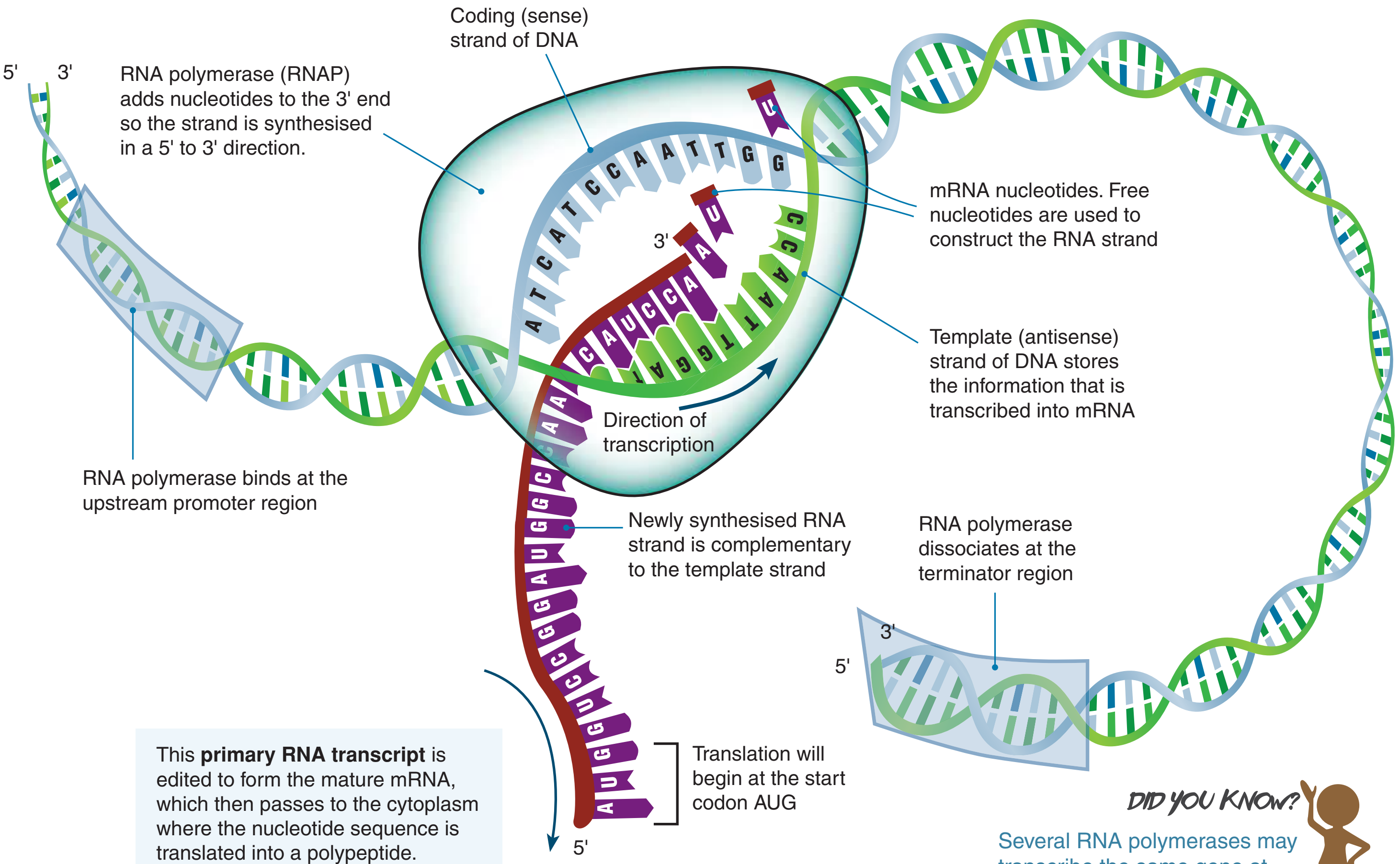
   (c) Which amino acid(s) are encoded in only one way?

# 96 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.

**DID YOU KNOW?**

Several RNA polymerases may transcribe the same gene at any one time, allowing a high rate of mRNA synthesis.

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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# 97 Translation

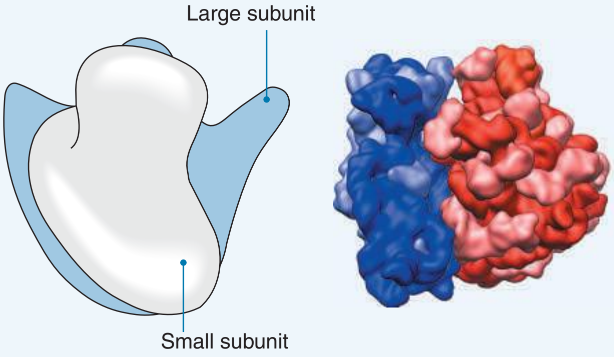
**Key Idea**: Translation is the final stage of gene expression in which ribosomes read the mRNA and decode (translate) it to synthesise a protein. This occurs in the cytoplasm.

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

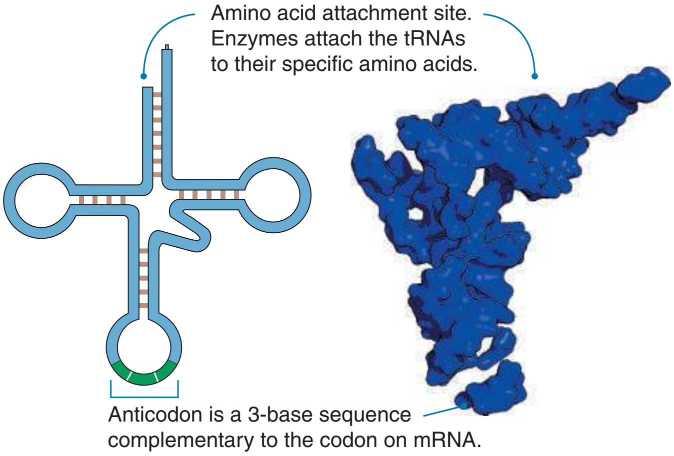
Ribosomes are made up of a complex of ribosomal RNA (rRNA) and ribosomal proteins. These small cellular structures direct the catalytic steps required for protein synthesis and have specific regions that accommodate transfer RNA (tRNA) molecules loaded with amino acids.

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: UAC UAG CCG CGA UUU

   Codons on the mRNA:

   Amino acids encoded:

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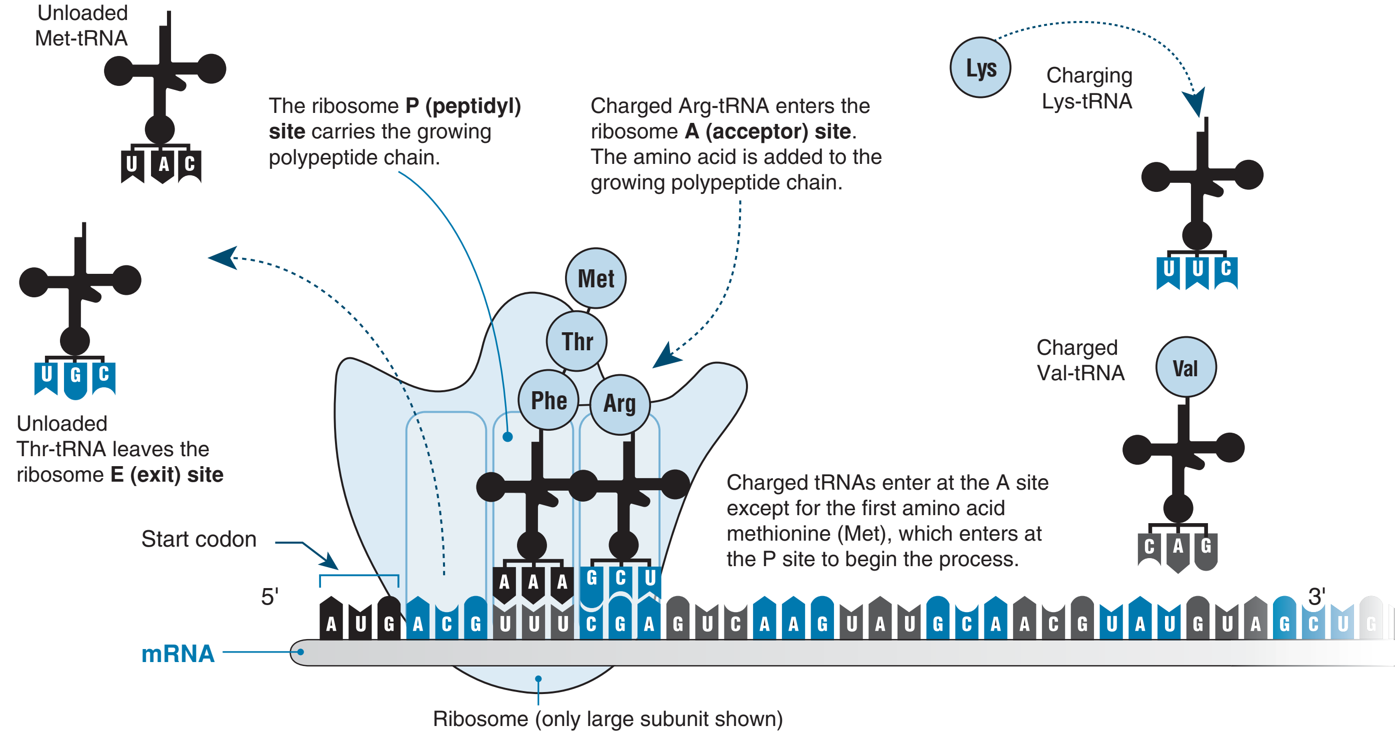
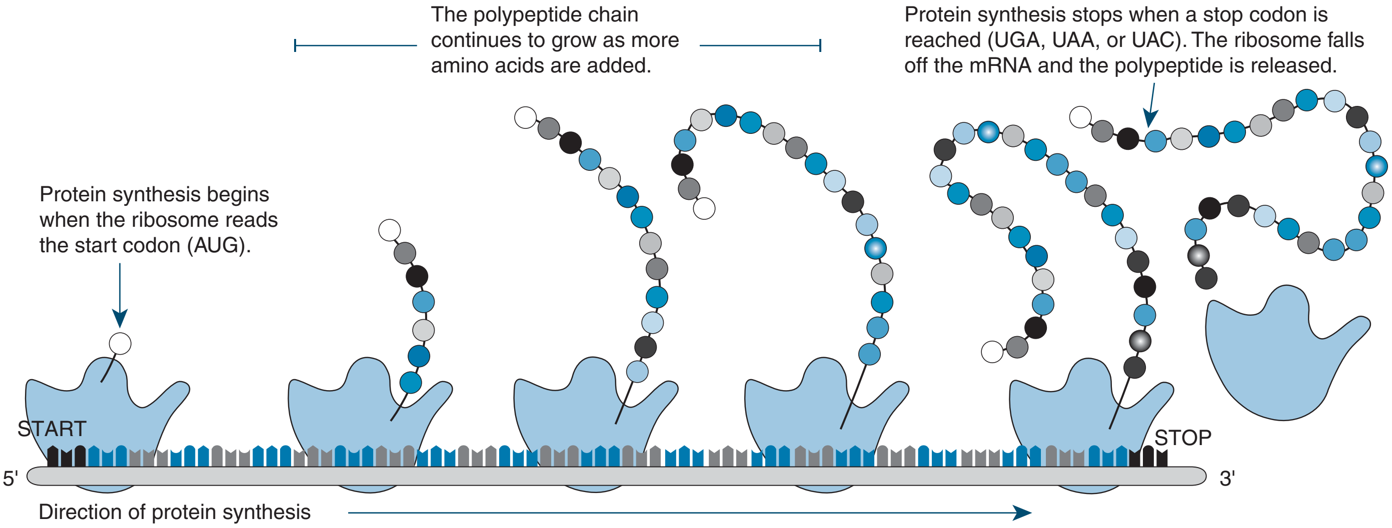
## tRNA molecules deliver amino acids to ribosomes

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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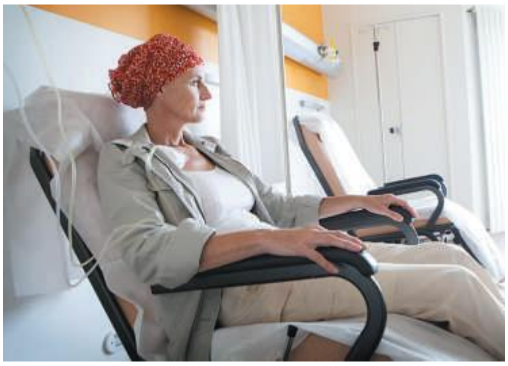
## Gene expression in cancer cells

- Every cell in an organism has the same DNA and therefore the same complement of genes. Different types of cells look and behave differently because they express different genes in different sequences for different lengths of time. Thus a skin cell expresses different genes and therefore different types of proteins, structures, and behaviours than a muscle cell.
- It is now possible to quantify the genes being expressed by looking for and measuring the different types and amounts of mRNAs and proteins found in a cell. This is called **gene expression profiling**. Using this technique, it is possible to identify the genes that are behaving incorrectly in cancer cells by comparing their gene expression profiles to the gene expression profiles of non-cancerous cells.
- The table right shows the top ten genes that are expressed more than normal (up regulated) and the top nine that are expressed less than normal (down regulated) in breast cancer patients. Most of the up regulated genes are involved in the cell cycle, whereas most of the down regulated genes are involved in lipid metabolism.

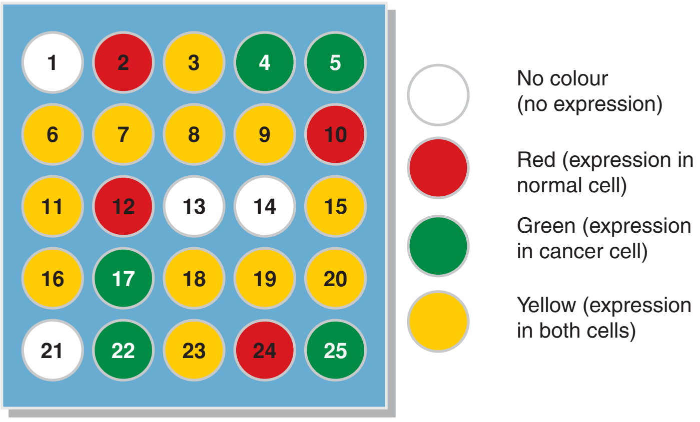
| Over-expressed genes | Under-expressed genes |
|---|---|
| COL10A1 | C7 |
| MMP11 | FABP4 |
| GJB2 | TIMP4 |
| CST1 | GPD1 |
| KIAA1199 | THRSP |
| MMP1 | CIDEC |
| MMP13 | ADH1B |
| CEACAM6 | ADH1A |
| BUB1 | KIAA1881 |
| ASPM | |



## Using gene expression profiles

- Many drugs act on biochemical pathways in cells to alter some part of the cell's activity. Some people respond to these drugs better than other people, often because their cells have more of a crucial receptor. The receptor is produced by a biochemical pathway regulated by proteins, which are a product of gene expression. Thus variations in gene expression can determine the way a drug affects a person.
- Gene expression profiling can be used to identify suitable drugs for different patients. It can be especially useful in developing a chemotherapy regime for cancer treatment and identifying any side effects. This makes it possible to develop treatments that more effective and more tolerable for the patient.

6. DNA chips (microarrays) can be used to determine which genes are being expressed in a cell. In one type of microarray, genes expressed in a normal cell turn the dot red while genes expressed in a cancer cell turn the dot green. Gene expression in both cells turns the dot yellow (the DNA chips are normally read by a laser). Each dot represents a different gene. Thus it can be seen which genes are being over or under expressed in a cancerous cell: green is being over expressed, red is being under expressed and yellow is being expressed normally.



| | | | | |
|---|---|---|---|---|
| ○ 1 | 🔴 2 | 🟡 3 | 🟢 4 | 🟢 5 |
| 🟡 6 | 🟡 7 | 🟡 8 | 🟡 9 | 🔴 10 |
| 🟡 11 | 🔴 12 | ○ 13 | ○ 14 | 🟡 15 |
| 🟡 16 | 🟢 17 | 🟡 18 | 🟡 19 | 🟡 20 |
| ○ 21 | 🟢 22 | 🟡 23 | 🔴 24 | 🟢 25 |

○ No colour (no expression)

🔴 Red (expression in normal cell)

🟢 Green (expression in cancer cell)

🟡 Yellow (expression in both cells)

(a) From the DNA chip above, which genes in the cell being tested are: over-expressed, under-expressed and being expressed normally:

(b) Suggest how this information could be used to design medical treatment for a cancer patient:

7. Why would the over-expression of genes associated with the cell cycle be a major factor in causing cancer?

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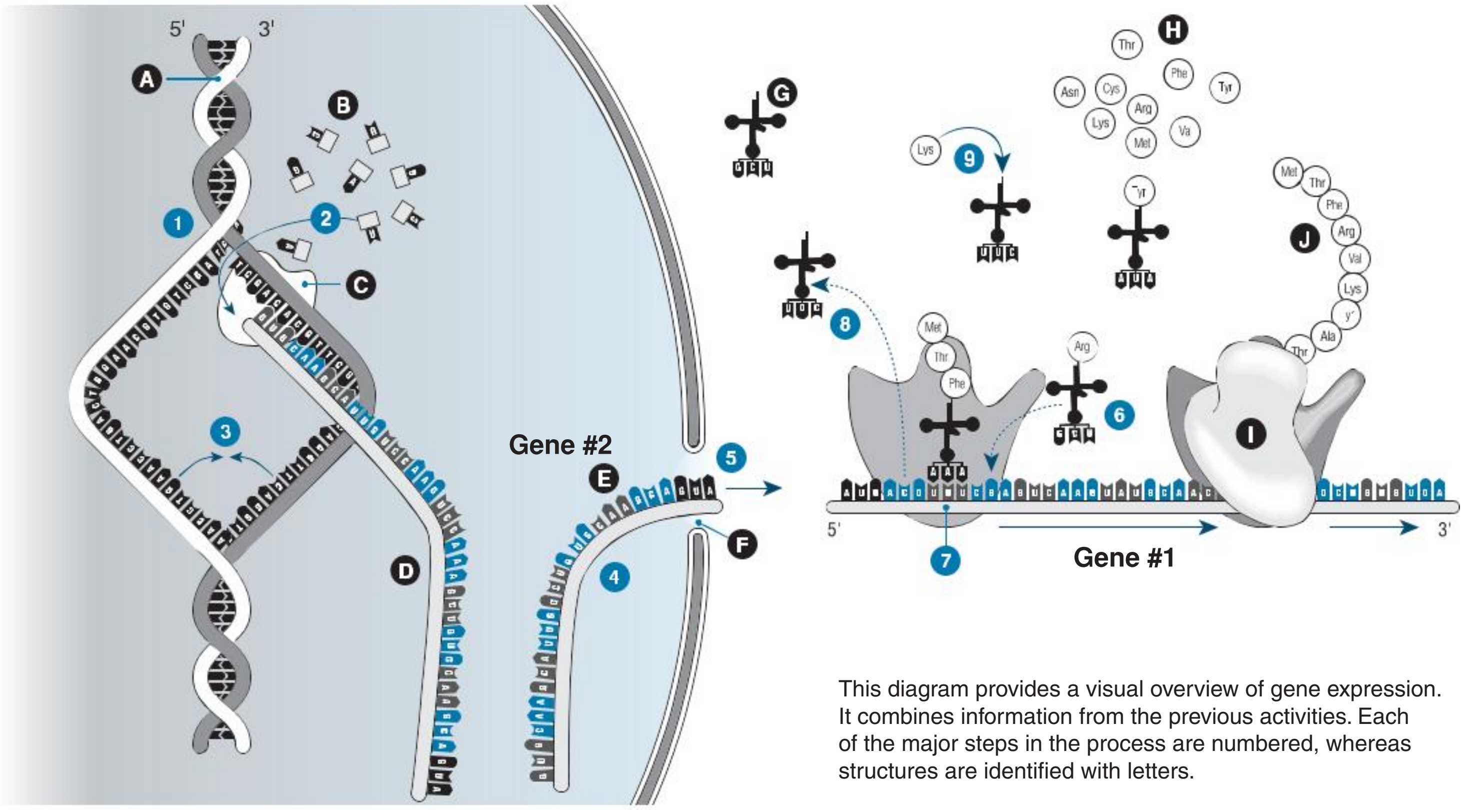
# 98 Gene Expression Summary



This diagram provides a visual overview of gene expression. It combines information from the previous activities. Each of the major steps in the process are 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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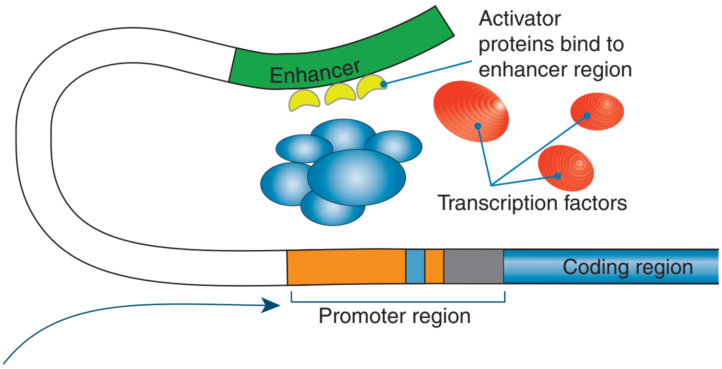
# 99 Transcriptional Control of Gene Expression

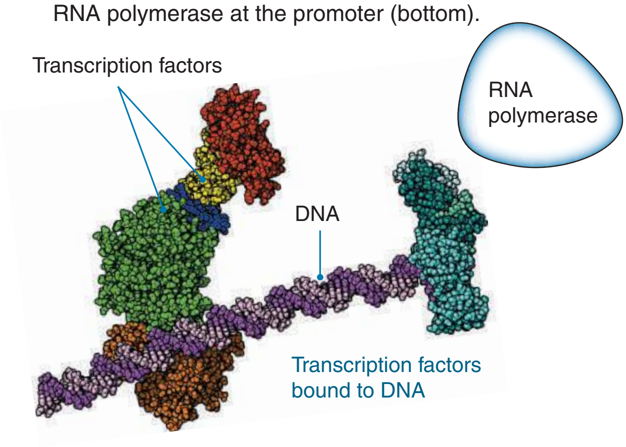
**Key Idea**: In eukaryotes, transcription is initiated by proteins called transcription factors.

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'.

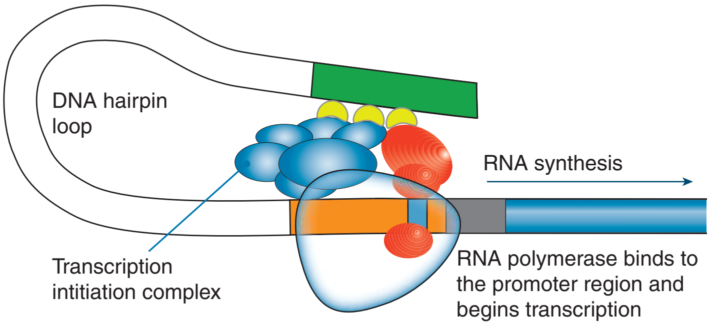
- Transcription factors bind to distinct regions of the DNA, including the promoter and upstream enhancers. They will act as a guide to indicate to RNA polymerase where transcription should start.
- Once bound to the promoter sequence, the transcription factors capture RNA polymerase, which can then 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**



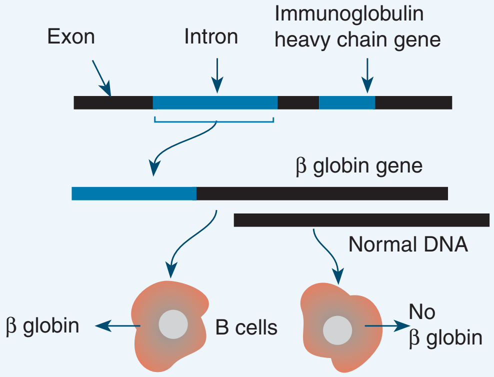


**RNA polymerase binds and transcription begins**



## Parts of the DNA act as enhancers

- In the early 1980s, Julian Banaerji 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 sort of genes encode transcription factors? ______________________

(b) How are transcription factors involved in regulating gene expression? ______________________

2. What evidence is there that introns can be involved in regulating gene expression? ______________________

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# 100 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.

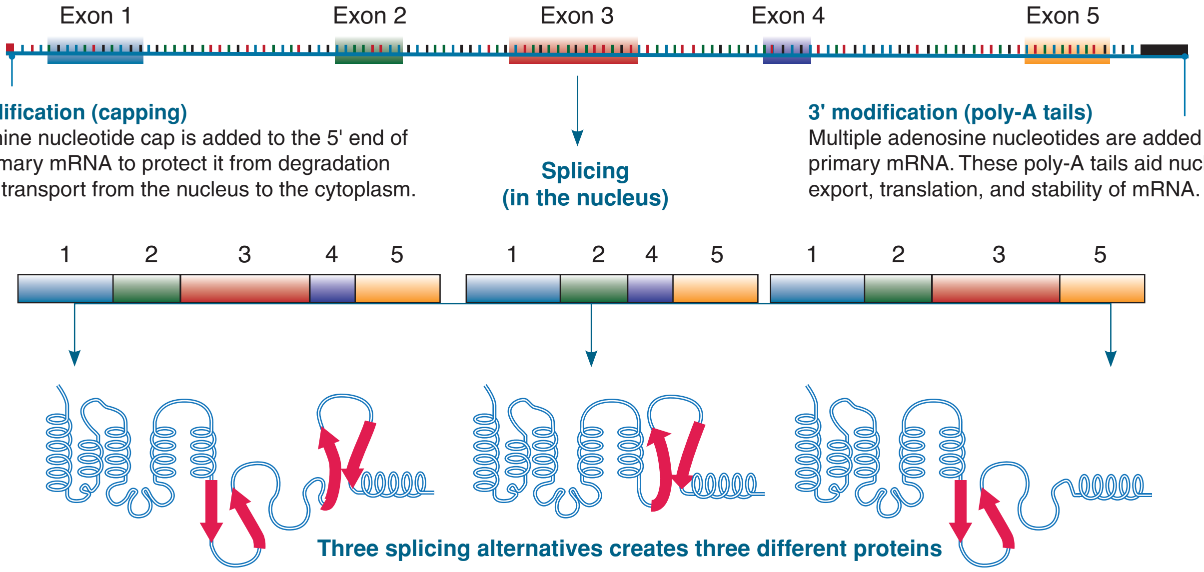
Once a gene is transcribed, the primary transcript is modified to produce the mRNA strand that will be translated in the cytoplasm. Caps and tails assist transport of the mRNA from the nucleus and increase its stability in the cytoplasm. Exon splicing produces exon combinations that result in different protein products. Modification of proteins after translation further increases the variety of proteins produced.

## Post transcriptional modification

- As you have seen earlier, introns are removed from the primary mRNA transcript and the exons are spliced together. However, exons can be sliced 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).

DID YOU KNOW?

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.



**5' modification (capping)**
A guanine nucleotide cap is added to the 5' end of the primary mRNA to protect it from degradation during transport from the nucleus to the cytoplasm.

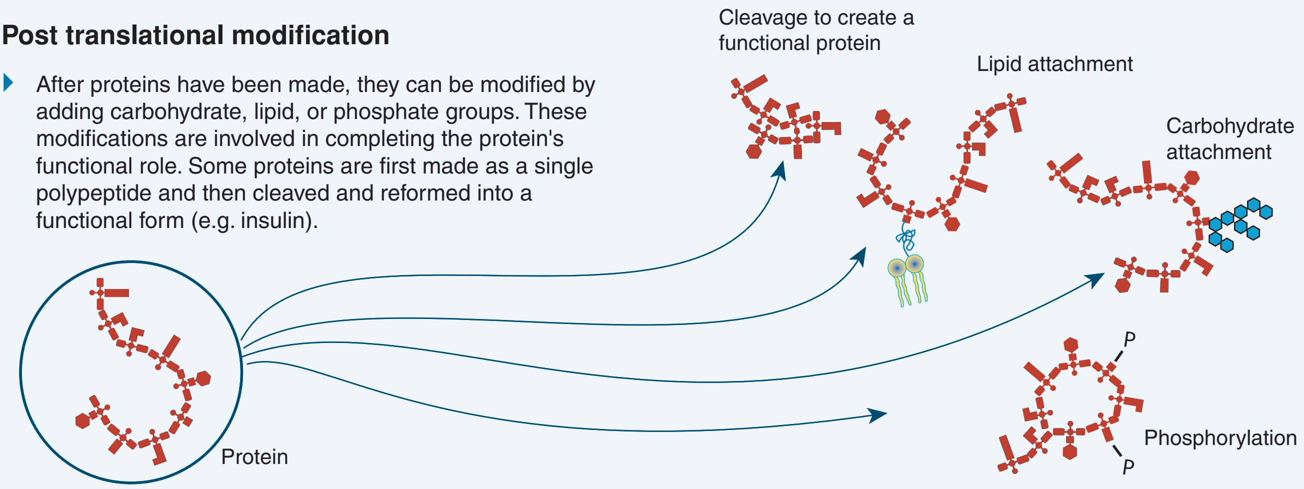
**Splicing (in the nucleus)**

**3' modification (poly-A tails)**
Multiple adenosine nucleotides are added to the primary mRNA. These poly-A tails aid nuclear export, translation, and stability of mRNA.

**Three splicing alternatives creates three different proteins**

## 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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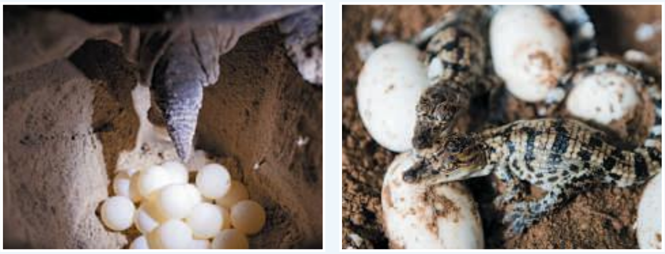
# 101 Gene Expression and Environment

**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 the environment of gene expression

### The effect of temperature



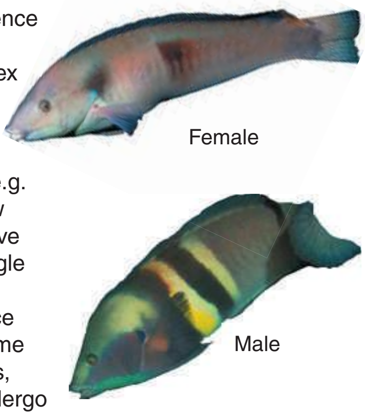
The sex of some animals is determined by incubation temperature during embryonic development. Examples include turtles, crocodiles, and the American alligator. In some species, high incubation temperatures produce males and low temperatures produce females. In other species, the opposite is true. Temperature 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.

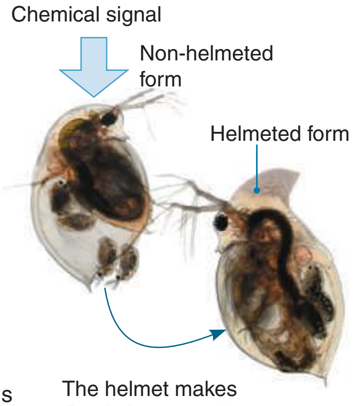
### The effect of other organisms

For some animals, the presence of other individuals of the same species may control sex determination.

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.



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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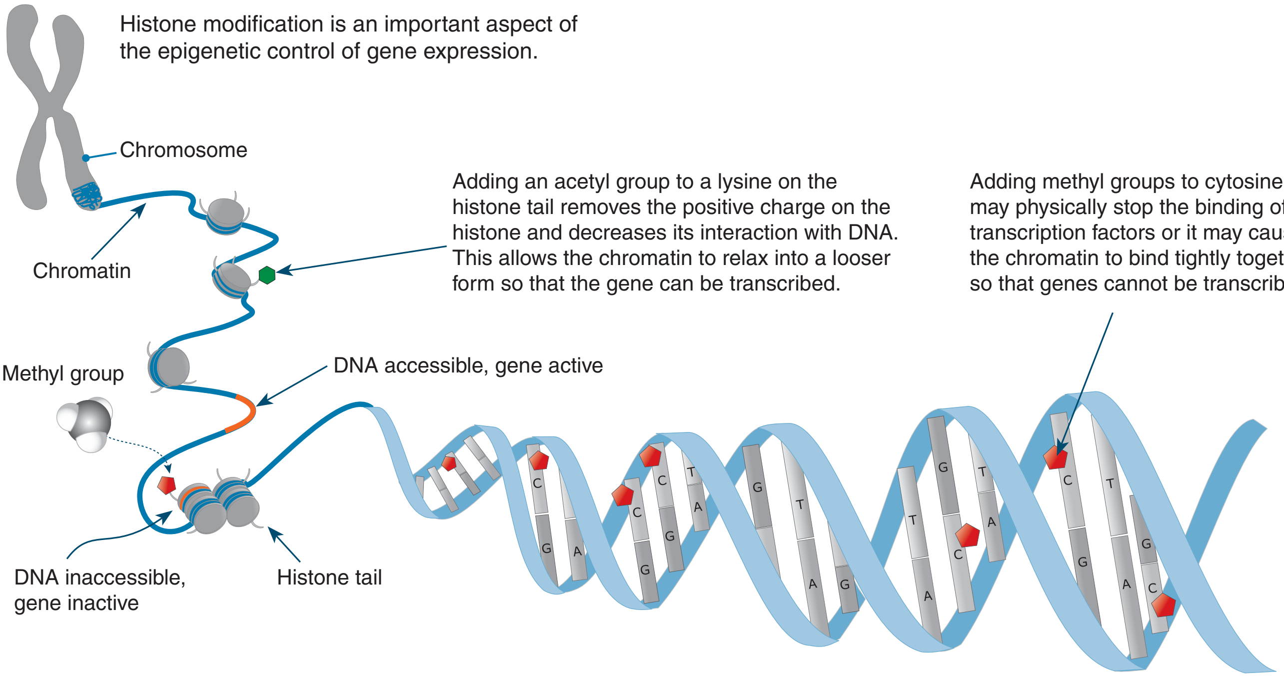
# 102 Epigenetic Regulation of Gene Expression

**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.


Histone modification is an important aspect of the epigenetic control of gene expression.

Adding an acetyl group to a lysine on the histone tail removes the positive charge on the histone and decreases its interaction with DNA. This allows the chromatin to relax into a looser form so that the gene can be transcribed.

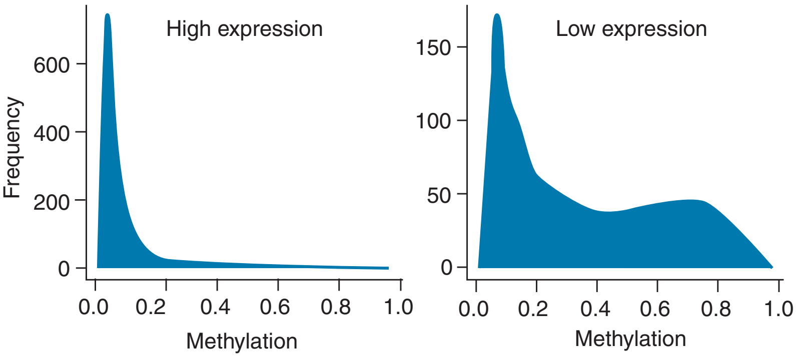
Adding methyl groups to cytosine may physically stop the binding of transcription factors or it may cause the chromatin to bind tightly together so that genes cannot be transcribed.

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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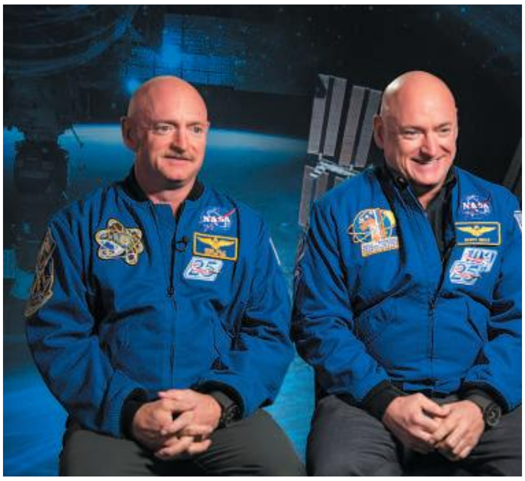
## Epigenetics and gene expression

### 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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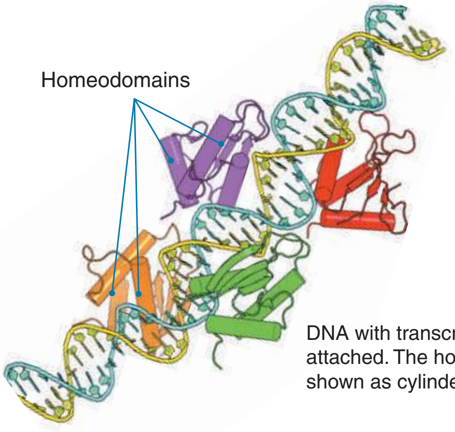
# 103 Regulating Morphology and Cell Differentiation

**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 are the *Hox* genes and the *SRY* gene. *Hox* genes play a major part in determining morphology because they regulate genes that then regulate networks of other genes. The *SRY* gene is responsible for the initiation of sex determination in humans and other mammals.

## Homeobox genes

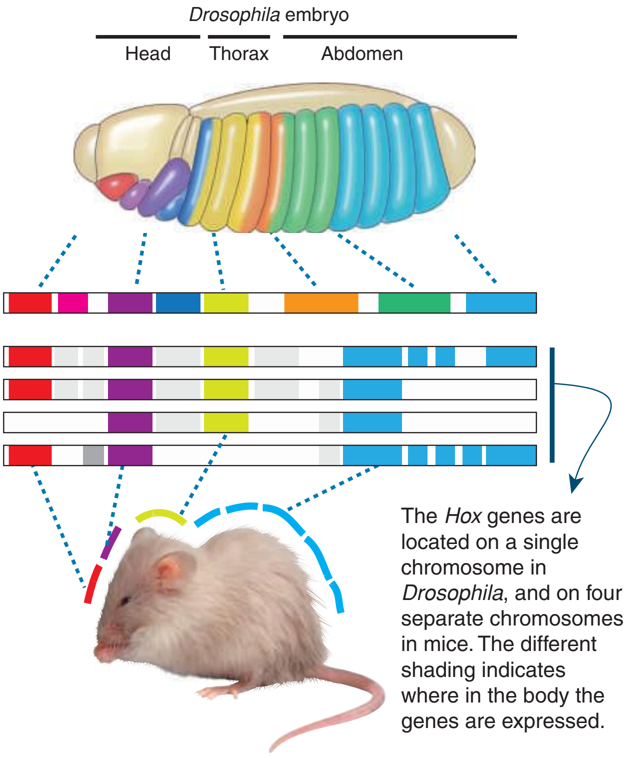
- Homeobox genes are genes containing a highly conserved (unchanging) sequence called the **homeobox**. The homeobox is about 180 base pairs long and encodes a string of about 60 amino acids called a **homeodomain**, which can bind to DNA.
- Proteins containing the homeodomain act as transcription factors 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.

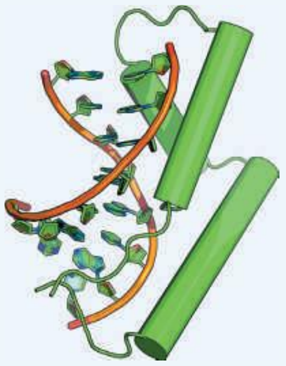


The *Hox* genes are located on a single chromosome in *Drosophila*, and on four separate chromosomes in mice. The different shading indicates where in the body the genes are expressed.

## 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 developed 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.

1. Why would a XY person without an SRY gene on the Y chromosome appear female? ______________________________

______________________________________________________________________

______________________________________________________________________

______________________________________________________________________

2. What are *Hox* genes and how do they function? ______________________________

______________________________________________________________________

______________________________________________________________________

______________________________________________________________________

**ISBN: 978-1-927309-86-5**

# 104 KEY TERMS AND IDEAS: 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: ______________________________

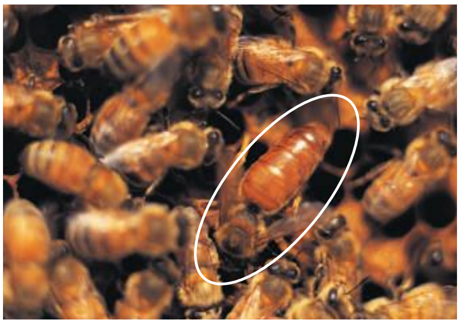
   Amino acids: ______________________________

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:



   ______________________________

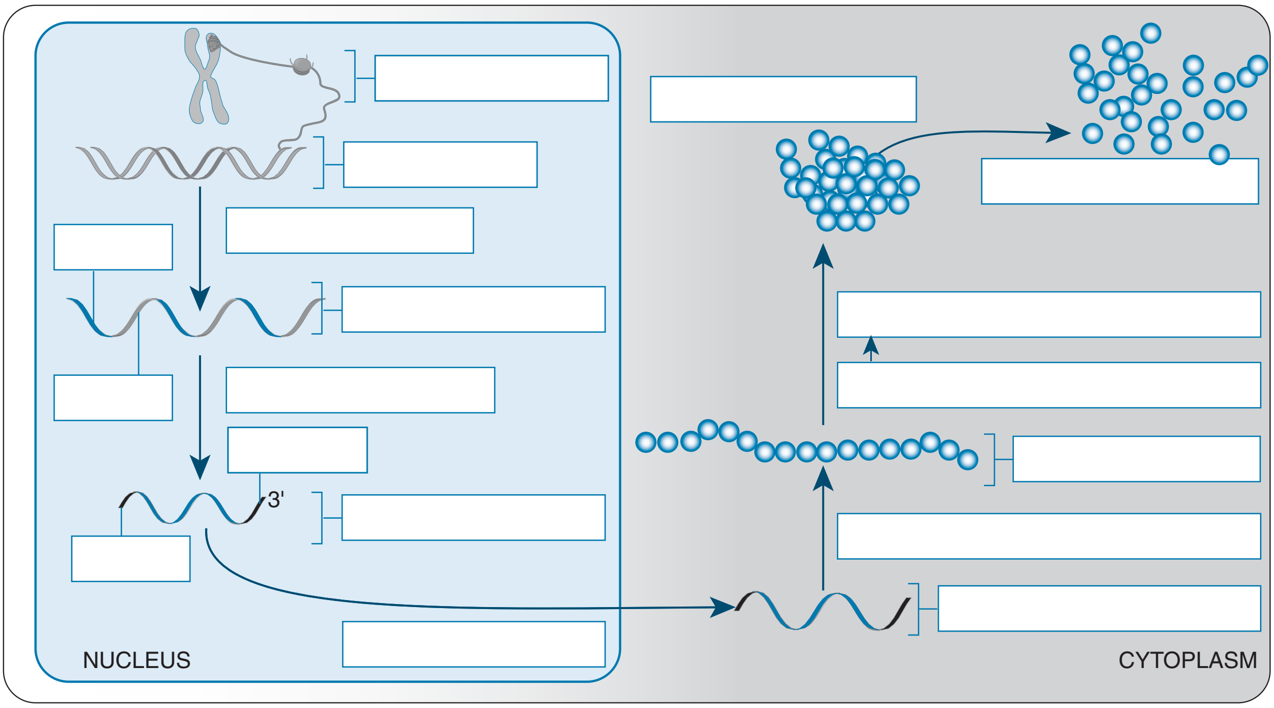
   ______________________________

   ______________________________

   ______________________________

4. (a) 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. **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.*

   (b) Use a highlighter or different colored pens to distinguish processes (in red or black) and structures (in blue).



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UNIT 4
Topic 1

# Mutations

### Key terms

allele
aneuploidy
carcinogenic
frameshift
gene
gene mutation
karyogram
karyotyping
mutagen
mutagenic
mutation
non-disjunction
point mutation

**Activity number**

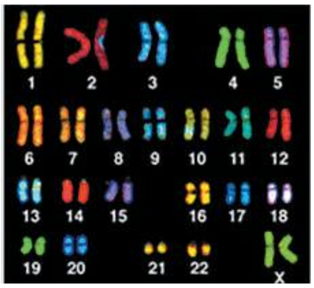
## Causes of mutations

*Key skills and knowledge*

☐ 1 Identify how mutations in genes and chromosomes can arise as a result of: **105-107**
- errors in DNA replication prior to cell division (point and frameshift mutations)
- non-disjunction during cell division
- damage to DNA by mutagens

☐ 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. If you can, identify some examples of point mutations. **105 106**

☐ 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. **107**



## Karyotypes and chromosome abnormalities

*Key skills and knowledge*

☐ 4 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. **108**

☐ 5 Explain what is meant by a karyogram. Describe the use of karyotyping in the identification of chromosomal abnormalities such as aneuploidy. **109**

☐ 6 Use a human karyotype to identify ploidy changes and predict a genetic disorder from given data. **110**

☐ 7 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. **106**

# 105 Gene Mutations

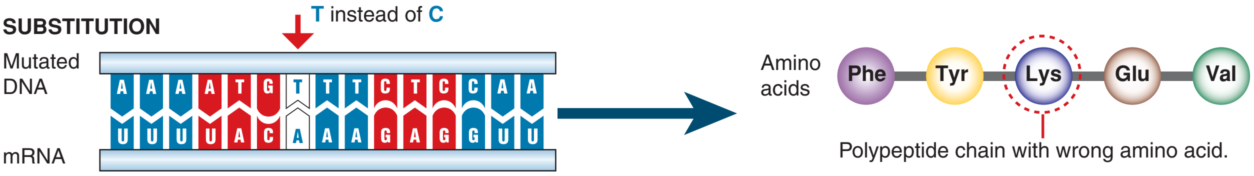
**Key Idea**: Gene mutations are localised changes to the DNA base sequence. The effects can be minimal or large.

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.

**NO MUTATION**

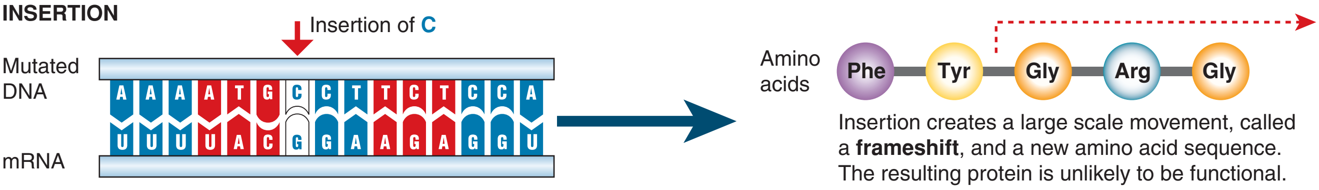
Amino acid sequence forms a normal polypeptide chain.

**SUBSTITUTION**



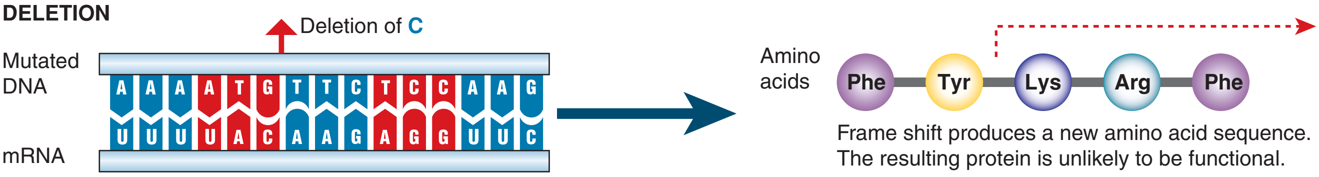
Polypeptide chain with wrong amino acid.

**INSERTION**



Insertion creates a large scale movement, called a **frameshift**, and a new amino acid sequence. The resulting protein is unlikely to be functional.

**DELETION**



Frame shift produces a new amino acid sequence. The resulting protein is unlikely to be functional.

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 AT$\boxed{G}$ 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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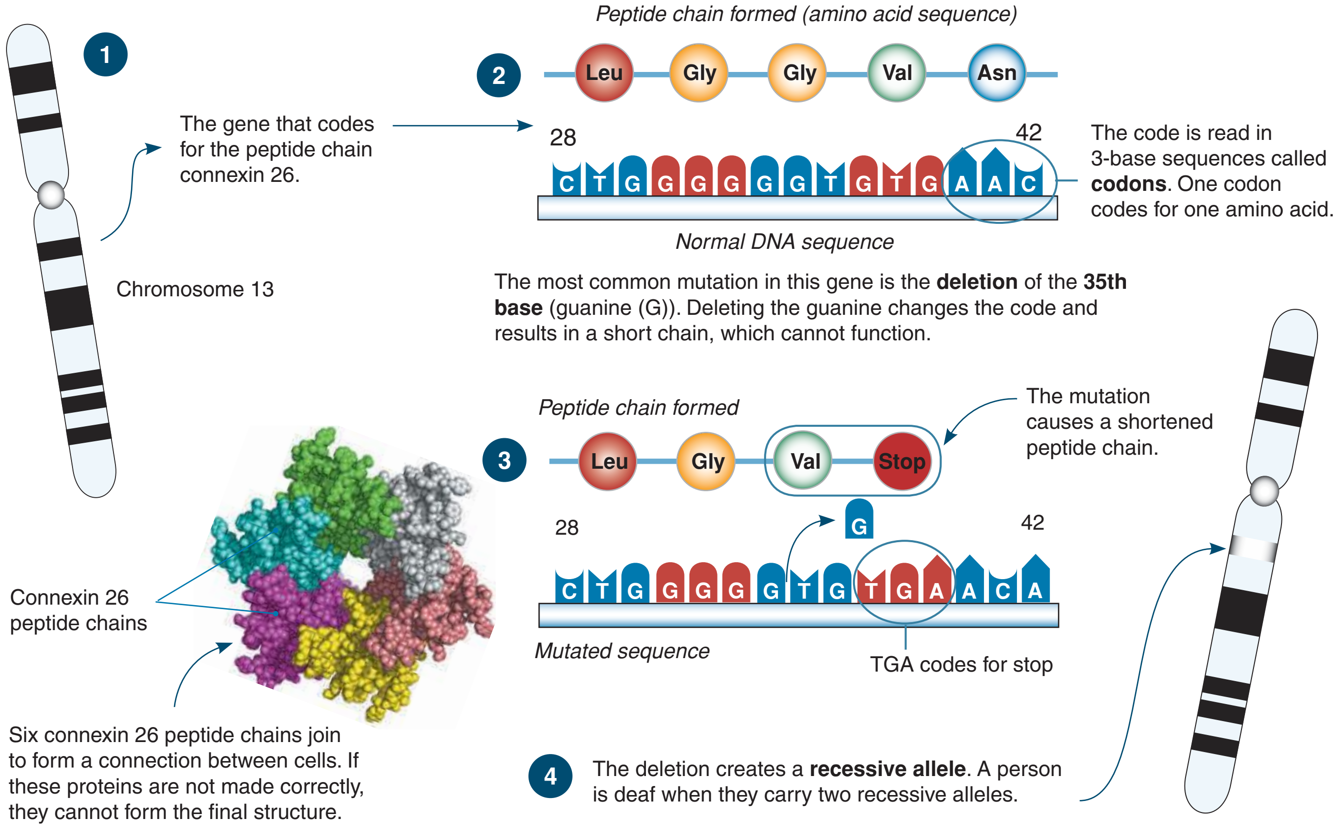
# 106 Mutations Can Alter Phenotype

**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)**



The gene that codes for the peptide chain connexin 26.

The code is read in 3-base sequences called **codons**. One codon codes for one amino acid.

The most common mutation in this gene is the **deletion** of the **35th base** (guanine (G)). Deleting the guanine changes the code and results in a short chain, which cannot function.

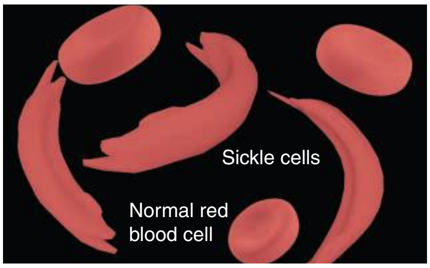
The mutation causes a shortened peptide chain.

Six connexin 26 peptide chains join to form a connection between cells. If these proteins are not made correctly, they cannot form the final structure.

The deletion creates a **recessive allele**. A person is deaf when they carry two recessive alleles.

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? ______________________________

______________________________

______________________________

**ISBN: 978-1-927309-86-5**

# 107 Mutagens

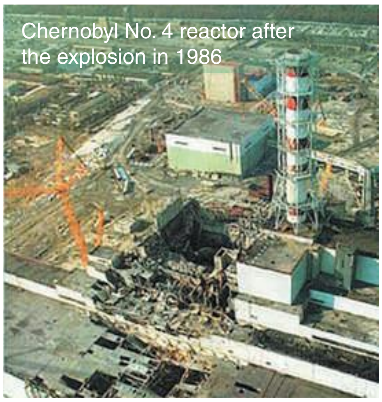
**Key Idea**: Mutagens are chemical or physical agents that cause a change in the DNA sequence.

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).



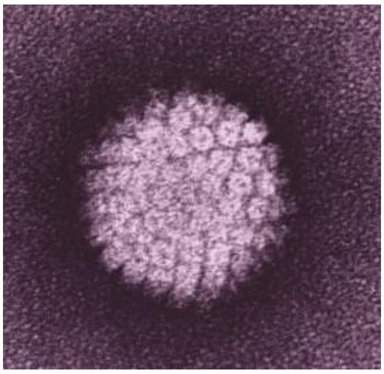
Chernobyl No. 4 reactor after the explosion in 1986

Soviet Authorities Fair Use

### 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, petrol pump attendants, 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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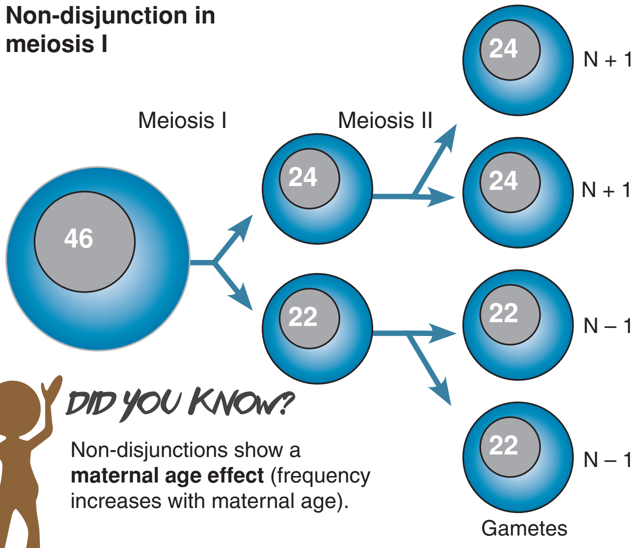
# 108 Non-Disjunction Can Produce Aneuploidies

**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**.

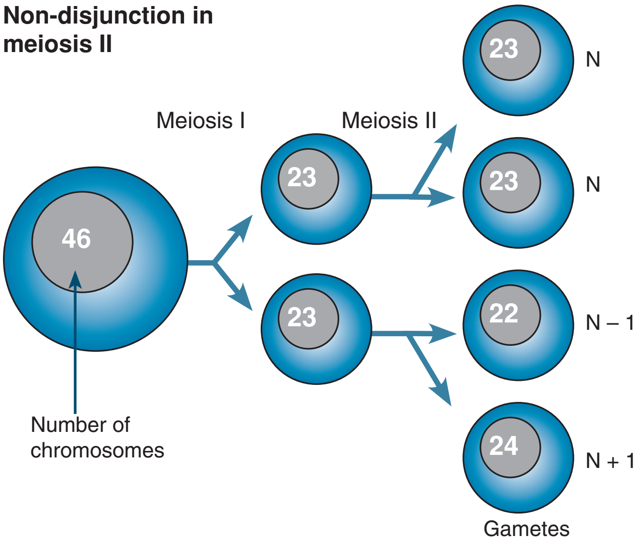
### Non-disjunction in meiosis I



**DID YOU KNOW?**

Non-disjunctions show a **maternal age effect** (frequency increases with maternal age).

### Non-disjunction in meiosis II



### Down syndrome (trisomy 21)

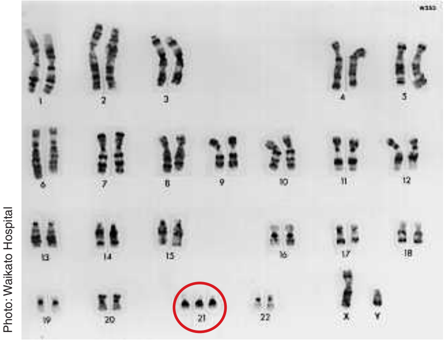


Photo: Waikato Hospital

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? ______

**ISBN: 978-1-927309-86-5**

# 109 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).

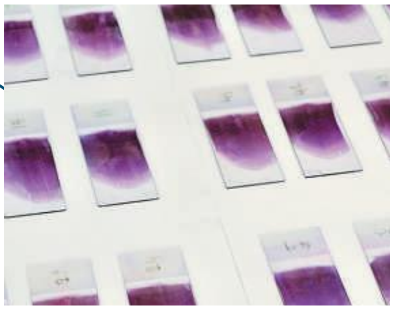
## Preparing a karyotype

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.

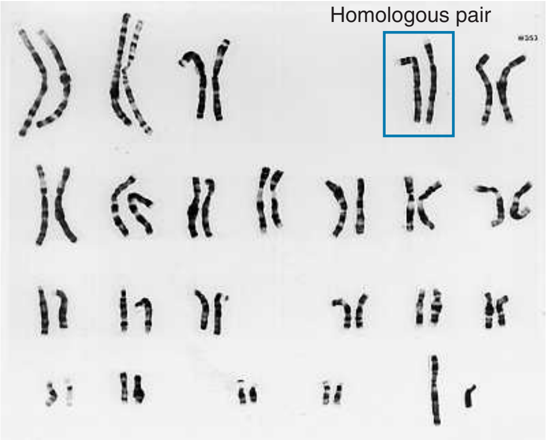


Microscope slides with stained smears

④ The stained white blood cells are viewed under a microscope and a clearly arranged spread of chromosomes is photographed.

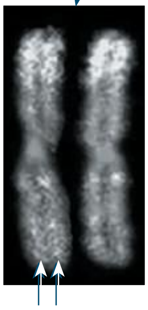
Newer techniques use fluorescent probes to color-code chromosomes and provide a spectral karyogram (left).

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).



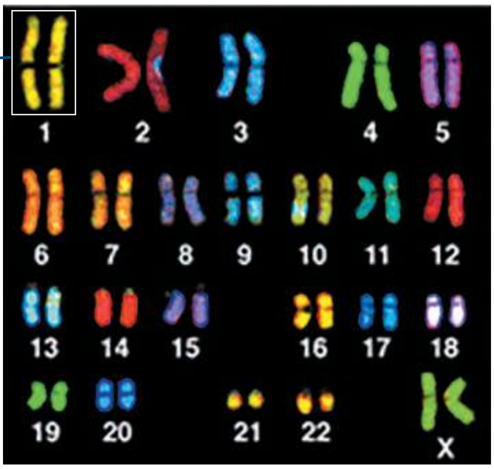
Karyotypes: Cytogenetics Dept, Waikato Hospital

**Conventional karyogram (male)**: 44 + XY



PLOS cc 2.5

Close up reveals two chromatids



**Spectral karyogram (female)**: 44 + XX

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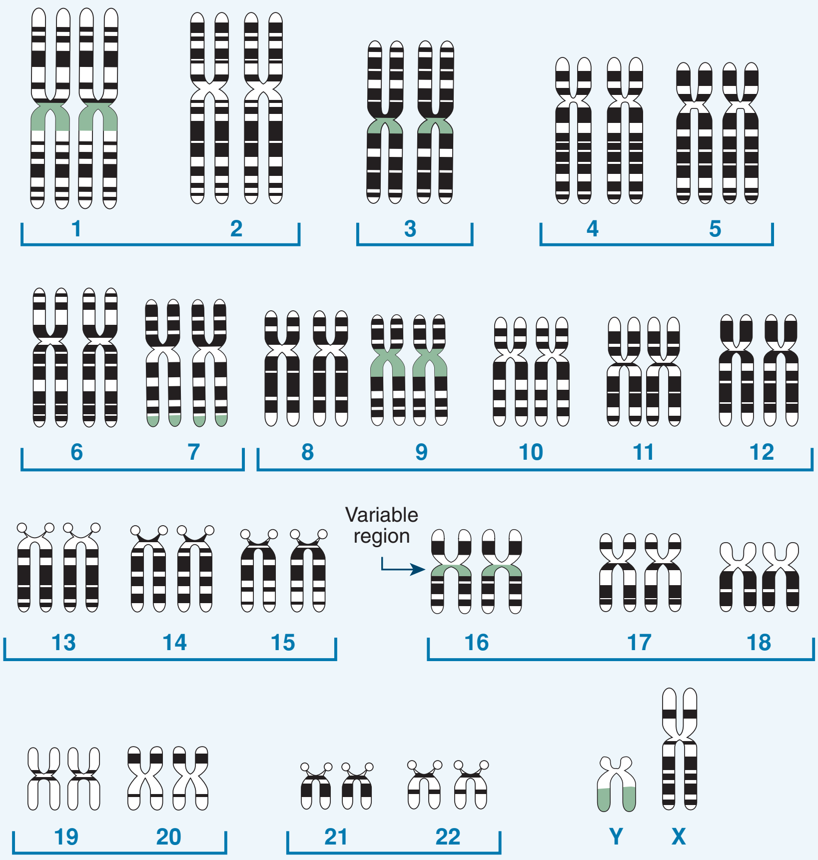
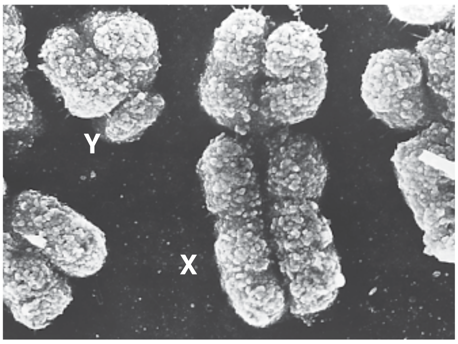
## Typical layout of a human karyogram





EII

SEM showing human X and Y chromosomes. Although these two are the sex chromosomes, they are not homologous.

EII

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? ______

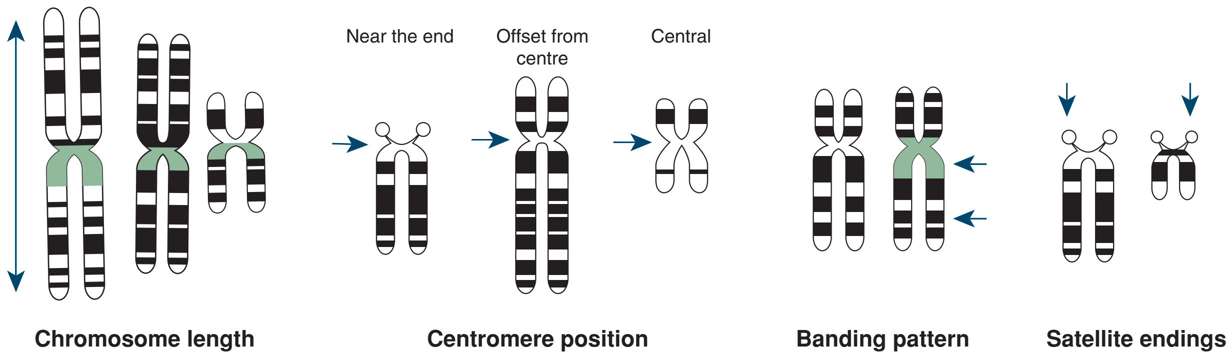
# 110 Making a Karyogram

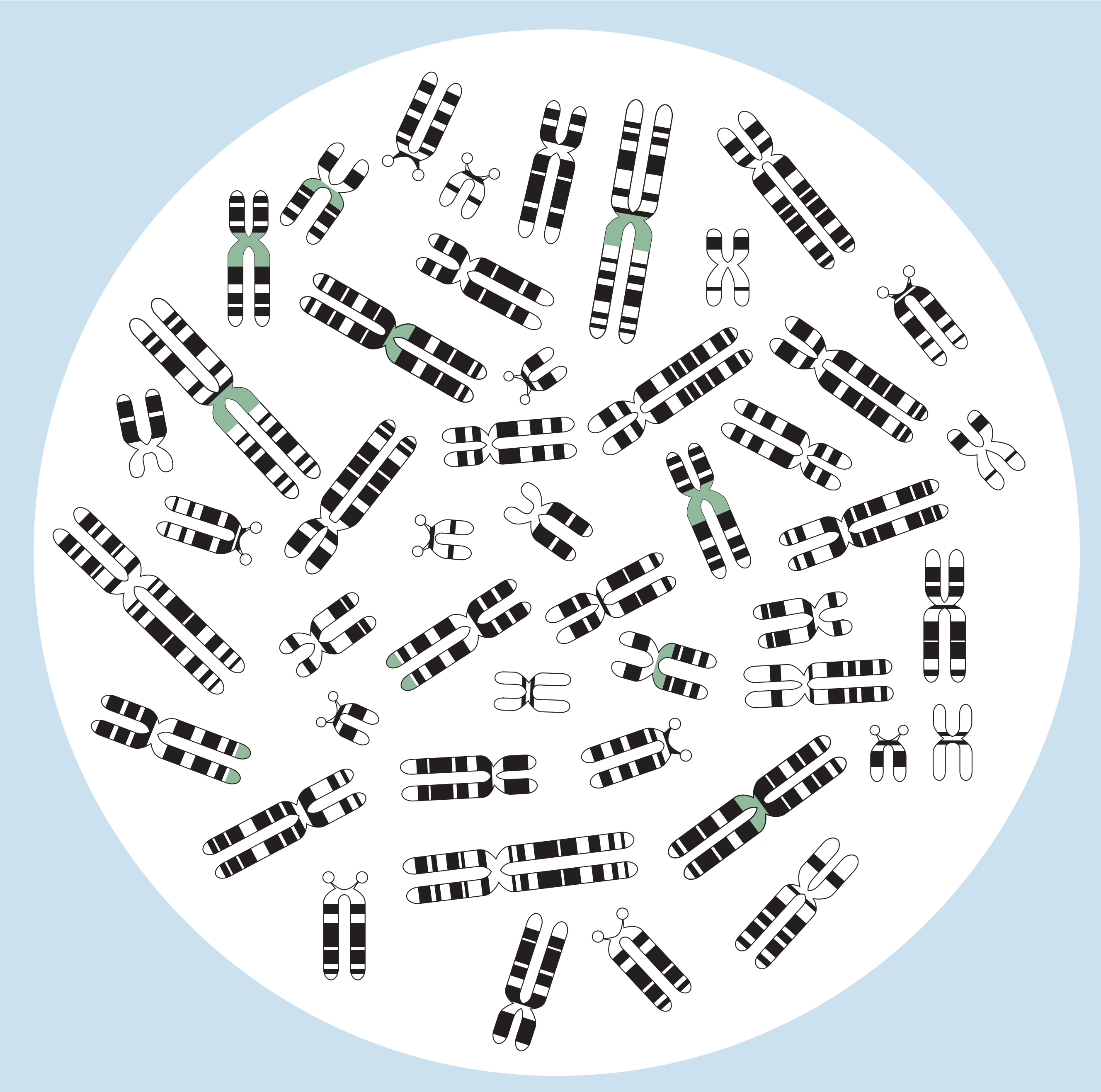
**Key Idea**: A karyogram can be created by matching the size and banding pattern of individual chromosomes.

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 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**





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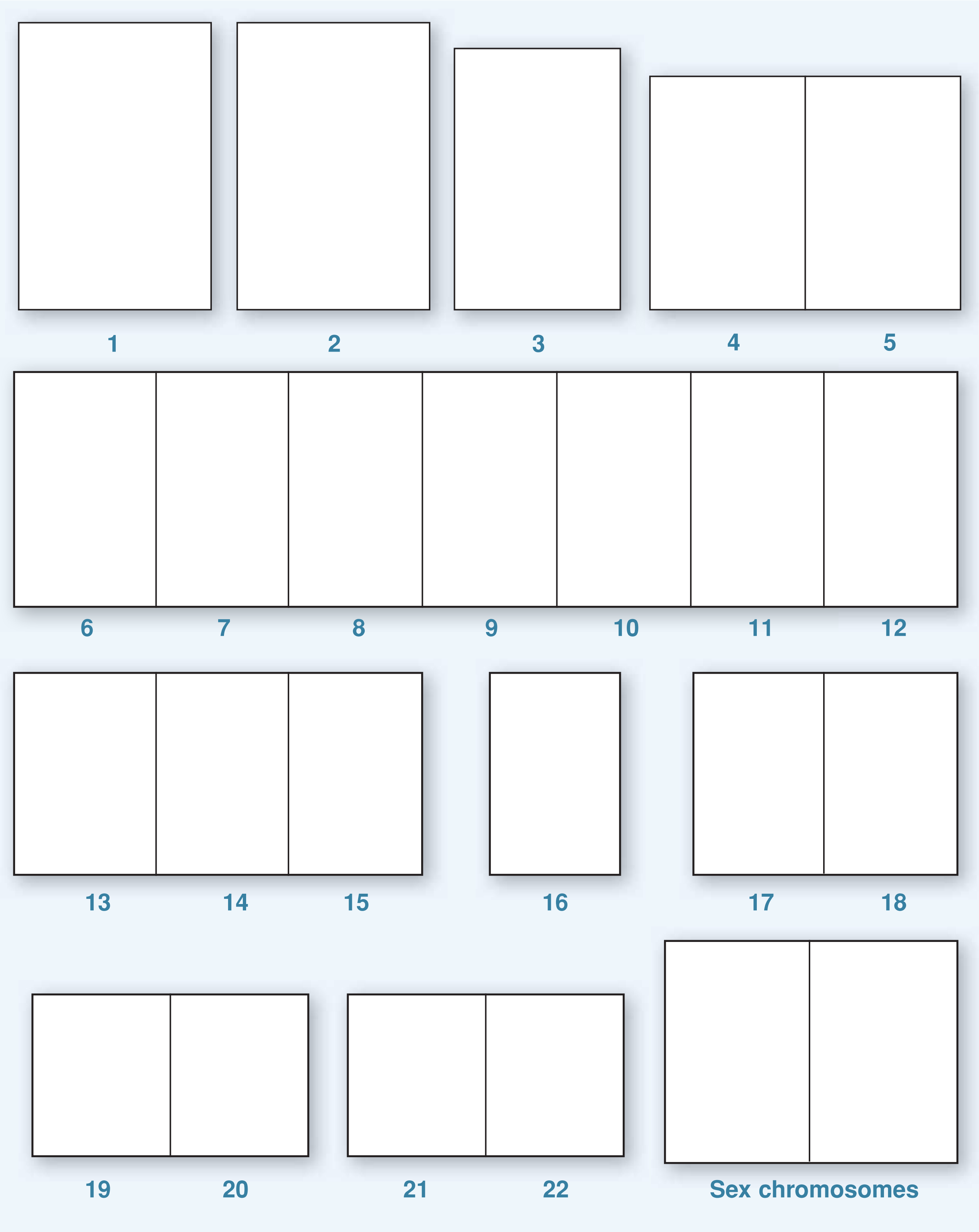
1. Cut out the chromosomes on page 205 and arrange them on the record sheet below in their homologous pairs.
2. (a) Determine the sex of this individual: **male** or **female** (circle one)

   (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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# 111 KEY TERMS AND IDEAS: Did You Get It?

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

aneuploidy ..........

karyogram ..........

karyotype ..........

non-disjunction ..........

trisomy ..........

**A** The number and appearance of chromosomes in the nucleus of a eukaryotic cell.

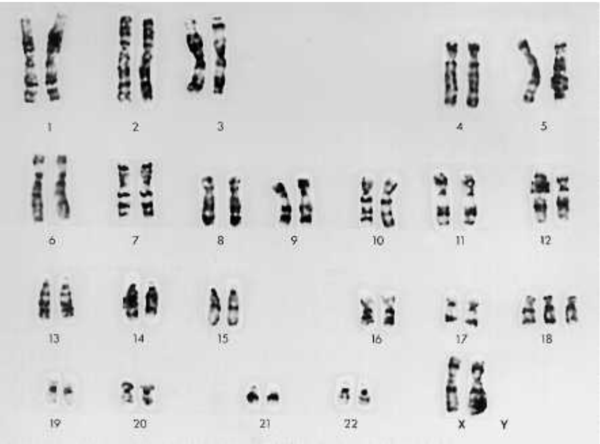
**B** Condition in which there is one extra chromosome in the body's cells.

**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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UNIT 4
Topic 1

# Inheritance

## Key terms

- allele
- codominance
- cross (genetic cross)
- genetype
- heterozygous
- homozygous
- incomplete dominance
- locus
- Mendelian inheritance
- multiple alleles
- multiple genes (=polygenes)
- probability
- Punnett square
- sex linked gene
- trait
- X-linkage

## Alleles and dominance patterns

*Key skills and knowledge*

| | | | 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. | 112-114 |
| ☐ | 2 | Giving examples, distinguish between recessive and dominant traits. | 112 113 |
| ☐ | 3 | Understand the rules for calculating probability and apply them to predictions of the genotype and phenotype ratios of genetic crosses. | |
| ☐ | 4 | 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. What are its characteristics? | 115 119 |
| ☐ | 5 | Use Punnett squares to predict the frequencies of genotypes and phenotypes in crosses involving incomplete dominance. What are the characteristics of this type of inheritance? | 116 |
| ☐ | 6 | Use Punnett squares to predict the frequencies of genotypes and phenotypes in crosses involving codominance. What are the characteristics of this type of inheritance? | 117 |
| ☐ | 7 | 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. | 117 |
| ☐ | 8 | Using an example, explain what is meant by a sex-linked gene. Use Punnett squares to predict the frequencies of genotypes and phenotypes in crosses involving sex linkage. What are the characteristics of X-linked inheritance of dominant traits? Of recessive traits? How would you distinguish X-lined from Y-linked inheritance? | 118 119 |

Bill Ebbesen cc 3.0

## Polygenic inheritance

*Key skills and knowledge*

| | | | Activity number |
|---|---|---|---|
| ☐ | 9 | Explain what is meant by polygenic inheritance. | 120 |
| ☐ | 10 | Predict the frequencies of genotypes and phenotypes for polygenic inheritance involving three genes. How many phenotypes are expected in an $F_1$ cross involving a three-gene polygenic system? | 120 |

# 112 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

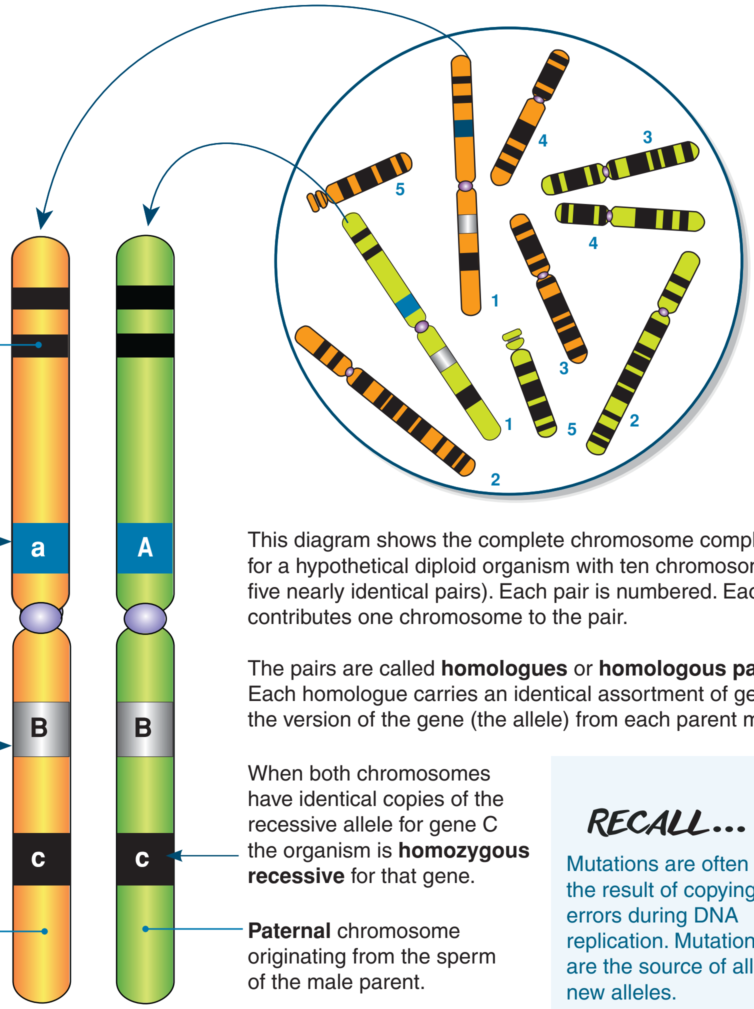
Most cells in sexually reproducing organisms have a homologous pair of chromosomes (one from each parent). Chromosomes are formed from DNA tightly wound around special proteins. This diagram shows the position of three different genes on the same chromosome that control three different traits (A, B and 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 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.

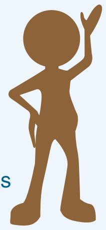
The pairs are called **homologues** or **homologous pairs**. Each homologue carries an identical assortment of genes, but the version of the gene (the allele) from each parent may differ.

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.

**RECALL...**

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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# 113 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.

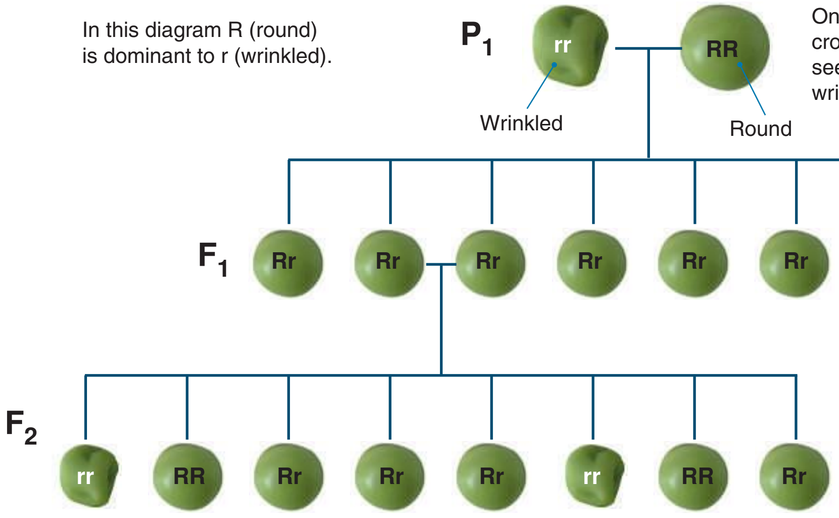
Traits are particular variants of phenotypic (observed physical) characters. For example, a phenotypic character is eye colour, a trait is blue eye colour. Traits may be controlled by one gene or many genes and can show continuous variation, e.g. height in humans, or discontinuous variation, e.g. flower 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 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)



In this diagram R (round) is dominant to r (wrinkled).

One of the experiments crossed true breeding round seed plants with true breeding wrinkled seed plants.

Out of the thousands of seeds produced, all were round, none were wrinkled.

Mendel then crossed the $F_1$ offspring together. The wrinkled seed reappeared in the second generation. He saw similar results with all the other phenotypic characters he studied.

### 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.

$$\textbf{Probability of an event happening} = \frac{\textbf{Number of ways it can happen}}{\textbf{Total number of outcomes}}$$

- 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):


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### 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 x 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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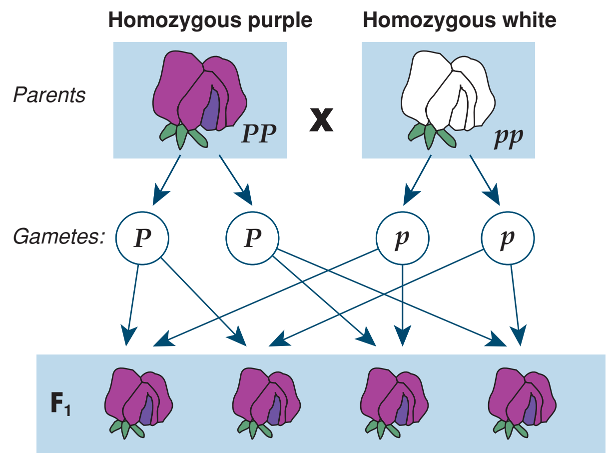
# 114 Basic Genetic Crosses

**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 $F_1$ 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.

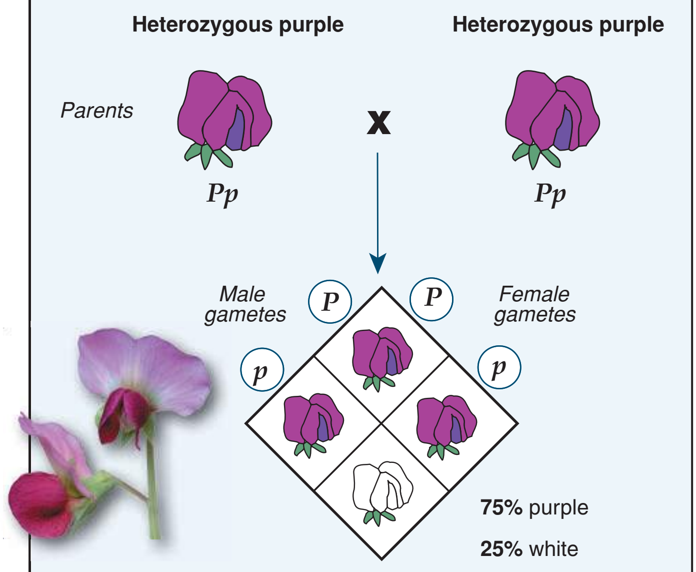
**Monohybrid cross $F_1$**



**Genotypes:** All *Pp* **Phenotypes:** All purple

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*).

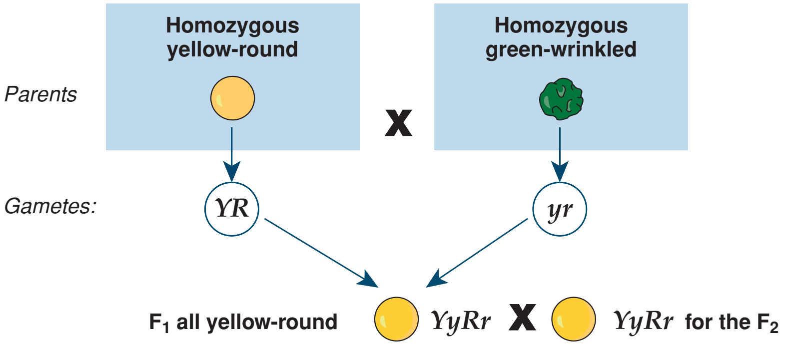
**Monohybrid cross $F_2$**



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.

| | | |
|---|---|---|
| ● | Yellow-round | ☐ |
| ● | Green-round | ☐ |
| ● | Yellow-wrinkled | ☐ |
| ● | Green-wrinkled | ☐ |

3. Express these numbers as a ratio:

______________________________

**Offspring ($F_2$)**

**Female gametes**

*Possible fertilisations*

**Male gametes**

| | *YR* | *Yr* | *yR* | *yr* |
|---|---|---|---|---|
| *YR* | | | | |
| *Yr* | | | | |
| *yR* | | | | |
| *yr* | | | | |

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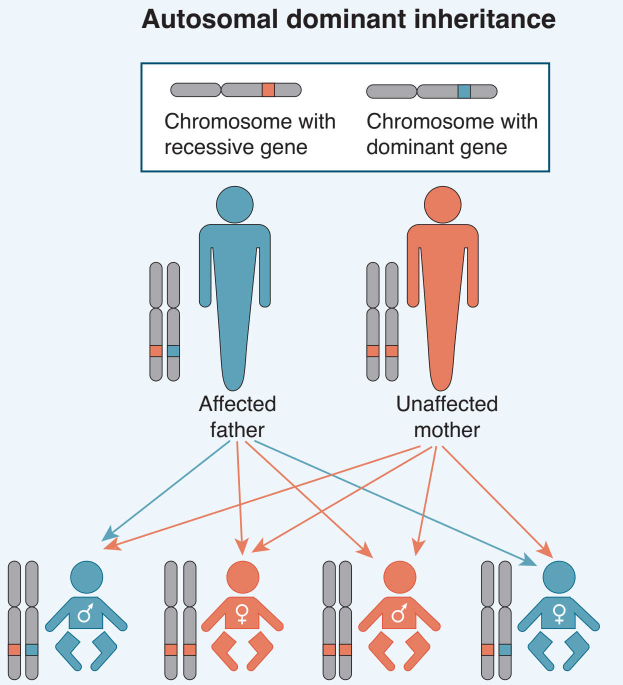
# 115 Autosomal Dominant Inheritance

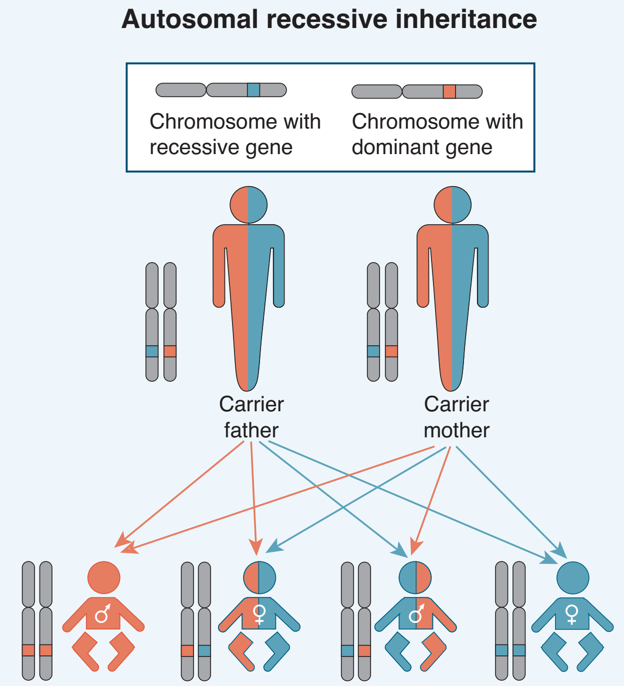
**Key Idea**: Autosomal dominant traits are always expressed regardless of whether there is one or two copies of the allele.

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).



i ____________ ii ____________ iii ____________ iv ____________

**Example**: Autosomal Dominant PKD (ADPKD) Mutation to PKD1 or PKD2 genes.



v ____________ vi ____________ vii ____________ viii ____________

**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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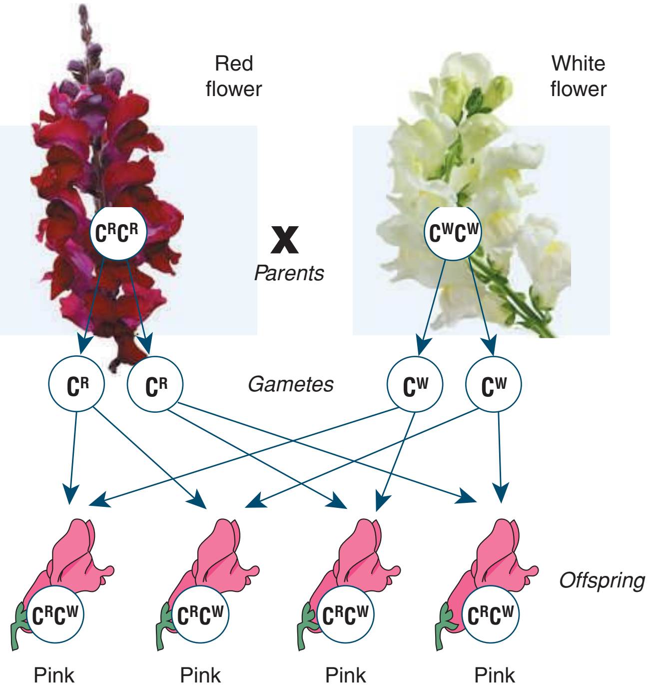
# 116 Incomplete Dominance

**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:

______________________

______________________

______________________

Gametes from male

Gametes from female

| | | |
|---|---|---|
| | | |
| | | |

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.

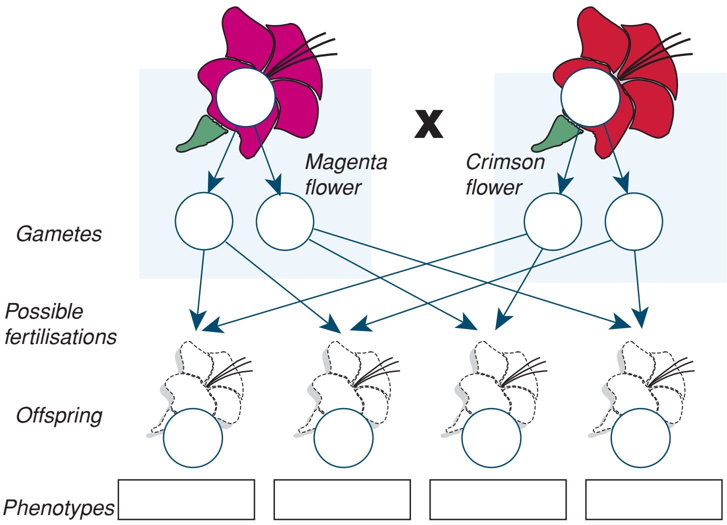
   (b) State the phenotype ratio:

   ______________________

   ______________________

   ______________________

   ______________________



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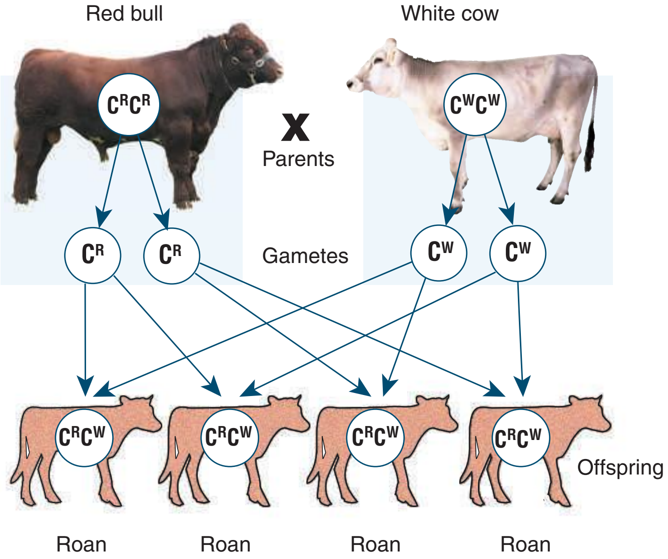
# 117 Codominance

**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).




A roan shorthorn heifer

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.

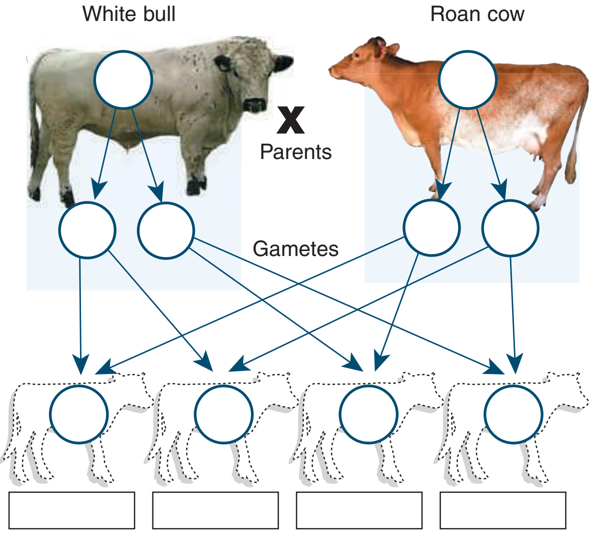
1. Explain how codominance of alleles can result in offspring with a phenotype that is different from either parent:

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:

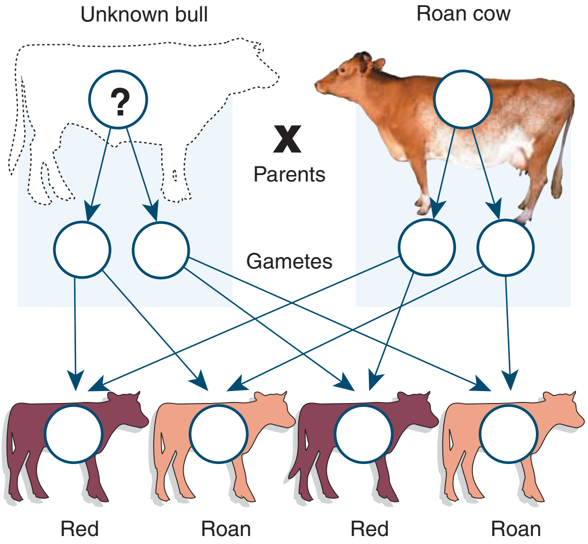


3. A farmer has only roan cattle on his farm. He suspects that one of the neighbours' bulls may have jumped the fence to mate with his cows earlier in the year because half the calves born were red and half were roan. One neighbour has a red bull, the other has a roan.

   (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 (*delete one*)

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.

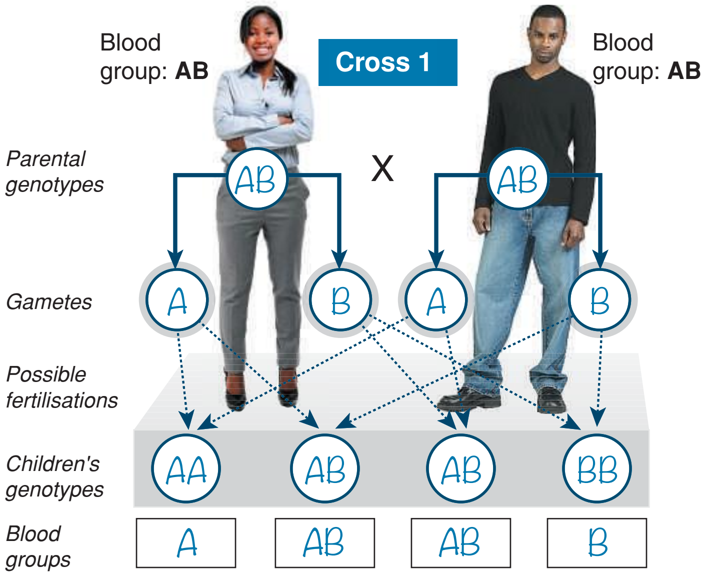
Recessive allele: *O* produces a non-functioning protein
Dominant allele: *A* produces an enzyme which forms **A antigen**
Dominant allele: *B* produces an enzyme which forms **B antigen**

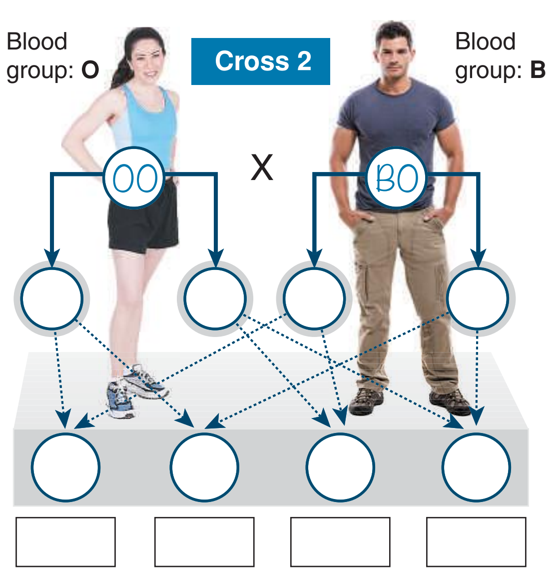
| Blood group (phenotype) | Possible genotypes | Frequency in Australia |
|---|---|---|
| **O** | OO | 49% |
| **A** | AA AO | 38% |
| **B** | | 10% |
| **AB** | | 3% |

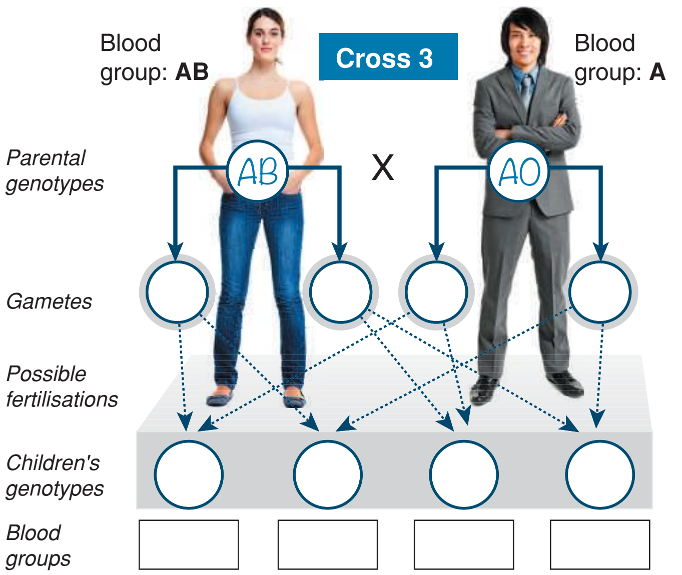
If a person has the ***AO*** allele combination then their blood group will be group **A**. The presence of the recessive allele has no effect on the blood group in the presence of a dominant allele. Another possible allele combination that can create the same blood group is ***AA***.

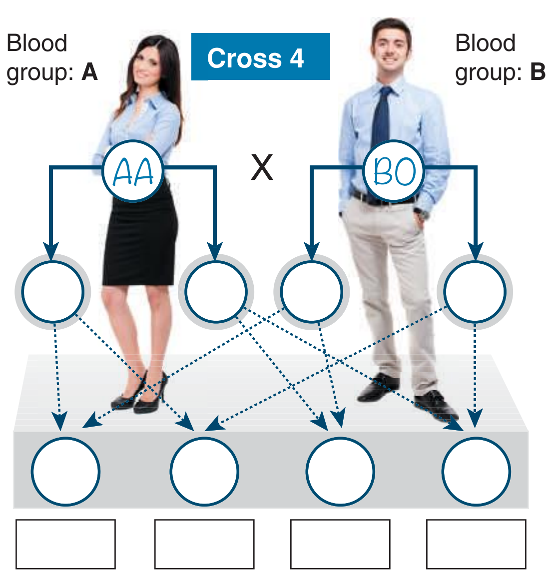
5. Use the information above to complete the table for the possible genotypes for blood group B and group AB.

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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# 118 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.

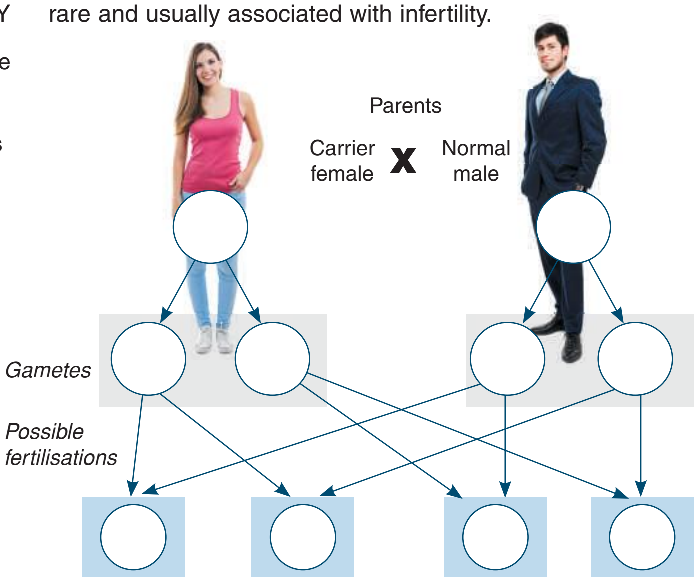
Sex linkage refers to the way genes on the sex chromosomes are inherited and expressed. In humans, the sex chromosomes are X and Y, but sex linkage usually involves genes on the X chromosome, which has many more genes than the Y chromosome. X-linked recessive traits are usually seen only in males (XY) 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.

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.

1. A couple wish 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 | | |
| | | |



2. (a) A second couple also wish 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:

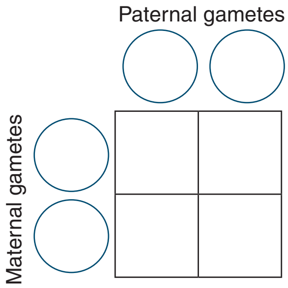
_______________________________________________

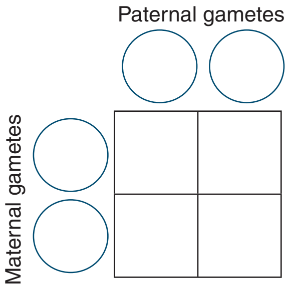
_______________________________________________

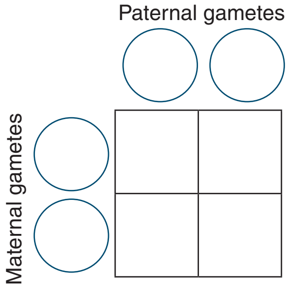
(b) The man is not a haemophiliac. Determine the probability that their first male child will have haemophilia. Use the Punnett squares to help you:

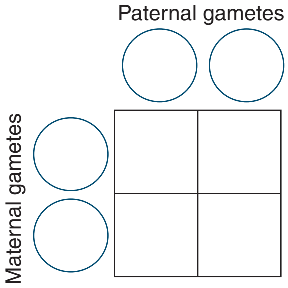
_______________________________________________

_______________________________________________









3. The gene for red-green colour vision is carried on the X chromosome. If the gene is faulty, colour blindness ($X^b$) will occur in males. Red-green colour blindness occurs in about 8% of males but in fewer than 1% of females.

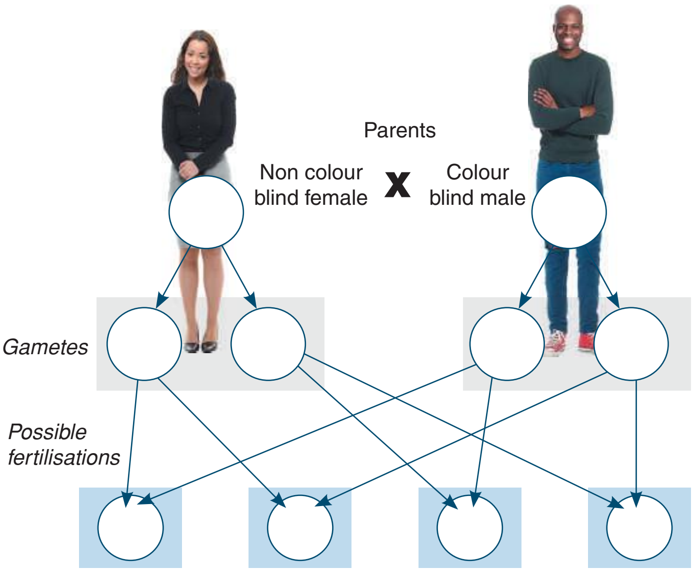
A colour blind man has children with a woman who is not colour blind. The couple have four children: 1 non colour blind son, 1 colour blind son, 2 non colour blind daughters. Describe the mother's:

(a) Genotype: _______________________________

(b) Phenotype: _______________________________

(c) Identify the genotype not possessed by any of the children:

_______________________________________________



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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:

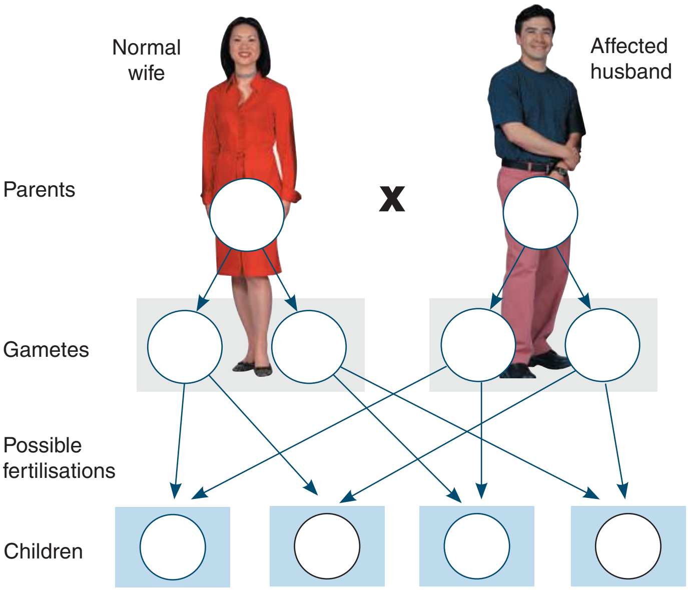
**Allele types**

**$X^R$** = affected by rickets
**X** = normal

**Genotypes** **Phenotypes**

**$X^RX^R$, $X^RX$** = Affected female
**$X^RY$** = Affected male
**XX, XY** = Normal 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 normal. 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).



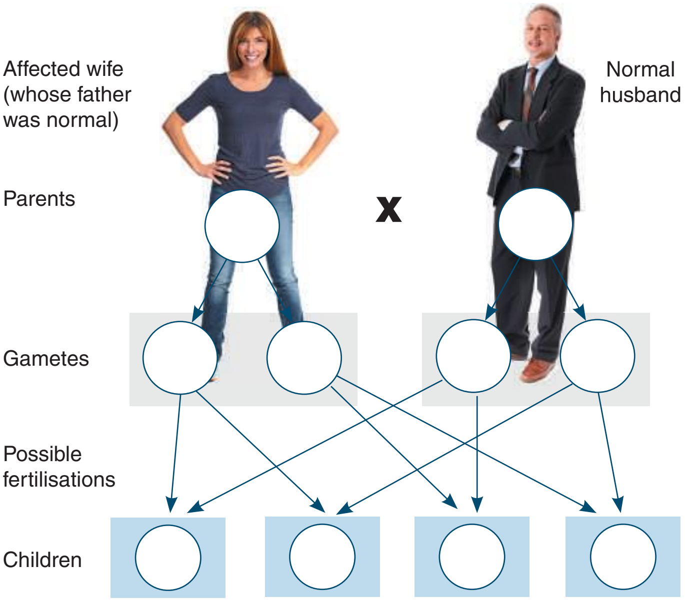
4. Determine the probability of having:

   (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 normal 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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# 119 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).

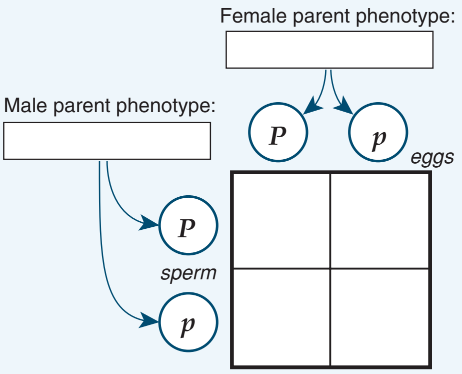
Using the codes: **PP** (normal) **Pp** (carrier)
**pp** (albino)

(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.

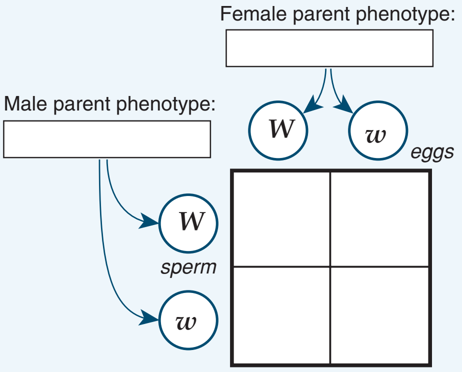
Using the codes: **WW** (woolly hair)
**Ww** (woolly hair, heterozygous)
**ww** (normal hair)

(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.

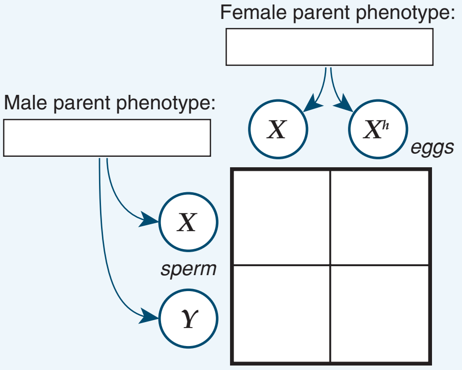
Using the codes: **XX** (normal female)
**$XX^h$** (carrier female)
**$X^hX^h$** (haemophiliac female)
**XY** (normal male)
**$X^hY$** (haemophiliac male)

(a) Enter the parent phenotypes and complete the Punnett square for a cross between a normal 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.

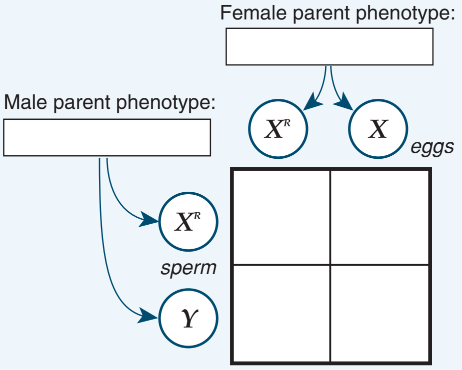
Using the codes: **XX** (normal female); **XY** (normal male)
**$X^RX$** (affected heterozygote female)
**$X^RX^R$** (affected female)
**$X^RY$** (affected male)

(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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# 120 Polygenes

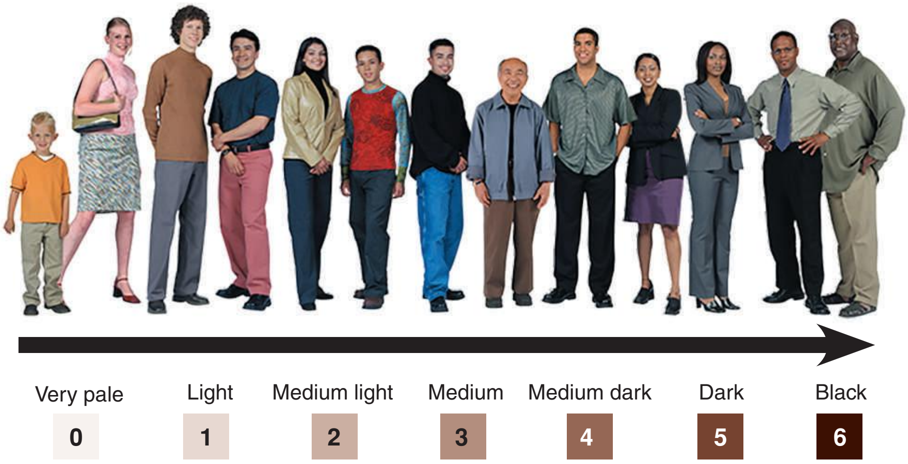
**Key Idea**: Many phenotypes are determined by multiple genes. Many phenotypes are controlled by more than one gene, a situation known as polygeny or polygenic inheritance. As there are many genes and therefore many alleles controlling the phenotype, there are a large range of possible phenotypes. Combined with environmental effects, this produces **continuous variation** within the population. Two examples in humans are skin colour and height.

## Polygenic traits

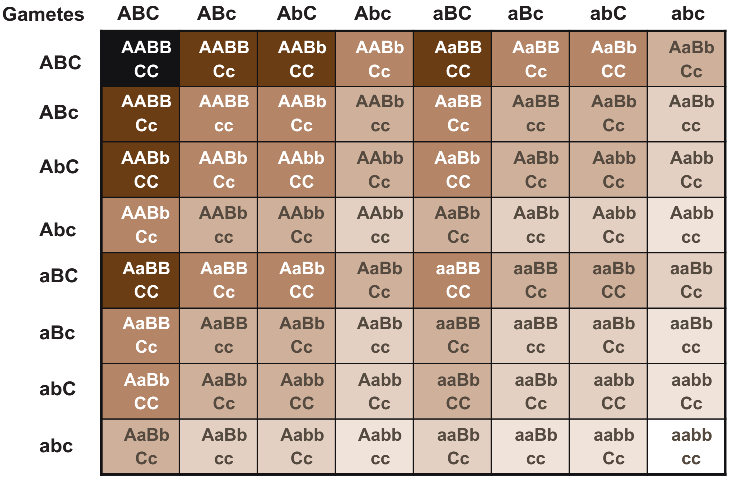
Polygenic traits are usually identified by

- 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.

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 right, in which there are seven shades ranging from very pale to very dark. Most individuals are somewhat intermediate in skin colour.



The table below shows the results of an $F_1$ cross involving three genes for 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. How many would there be if eight genes were included in the table?



| 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 |

### A dark knight to rescue the fair maiden?

Read a fairy tale and inevitably the princess is fair-complexioned and light of hair. The knight sent to save her is darker or tanned, with wild black or dark hair. Really? It's just a fairy tale, isn't it?... Well, not entirely.

Research shows that, in any human population, women on average have a lighter skin colour than men. In European populations, women have skin 15.2% lighter than men while, in African populations, women have skin 11.1% lighter than men. The same research shows men are generally attracted to women with lighter skin, whereas women are attracted to men with darker skin.

Why? Although preference is undoubtedly linked to cultural values, there is an evolutionary advantage for women to have lighter skin. It enables them to absorb more UV light, which helps manufacture the vitamin D needed to absorb calcium from the diet. High calcium levels are needed for strong pelvic development, development of the fetal skeleton, and to produce milk to feed the growing infant.

So, is there something in those old fairy tales after all?

1. (a) What is polygeny?

(b) How does polygeny contribute to continuous variation?

2. Identify two continuous phenotypes in humans and explain why the traits are continuous:

3. 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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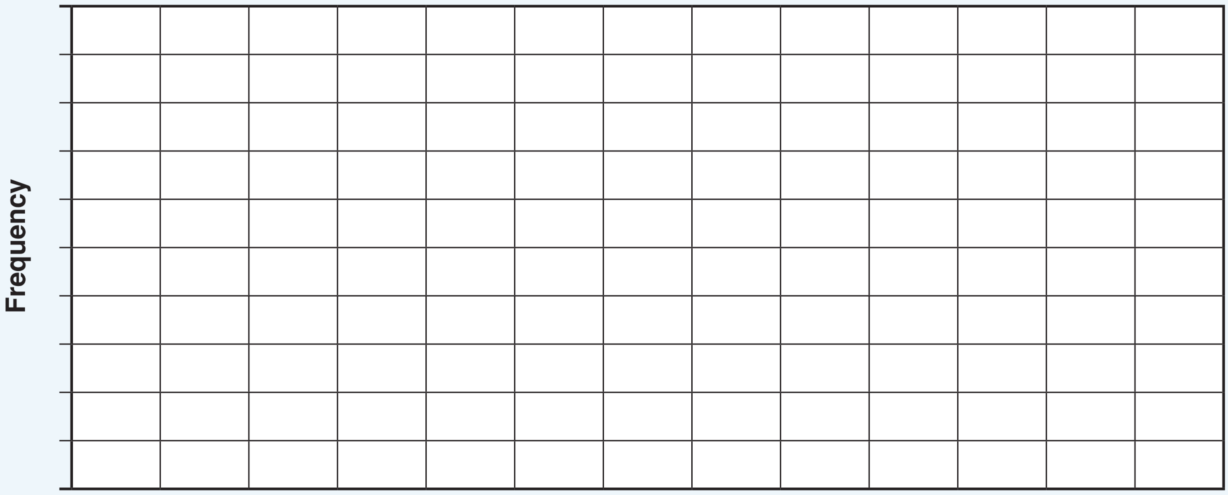
4. Explain the differences between continuous and discontinuous variation, giving examples to illustrate your answer:

5. From a sample of no less than 30 adults (or similar aged teenagers), collect data (by request or measurement) for one continuous variable (e.g. height, weight, shoe size, or hand span). Record and tabulate your results in the space below, and then plot a frequency histogram of the data on the grid below:

**Raw data**

**Tally chart (frequency table)**

**Variable:** ……………………………………………



(a) Calculate the following for your data and attach your working:

**Mean**: ____________ **Mode**: ____________ **Median**: ____________

**Standard deviation**: ____________

(b) Describe the pattern of distribution shown by the graph, giving a reason for your answer:

(c) What is the genetic basis of this distribution?

(d) What is the importance of a large sample size when gathering data relating to a continuous variable?

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# 121 KEY TERMS AND IDEAS: Did You Get It?

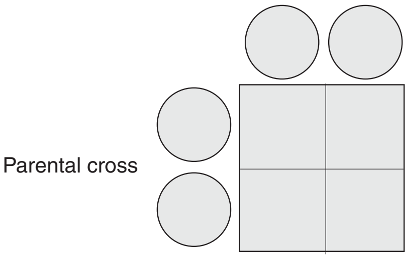
1. Test your vocabulary by matching each term to its correct definition, as identified by its preceding letter code.

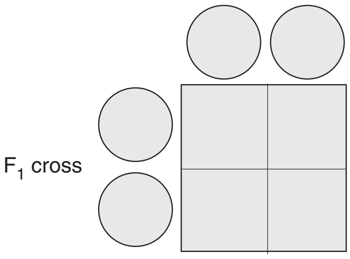
allele
dominant
heterozygous
homozygous
phenotype
recessive

**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:





(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?

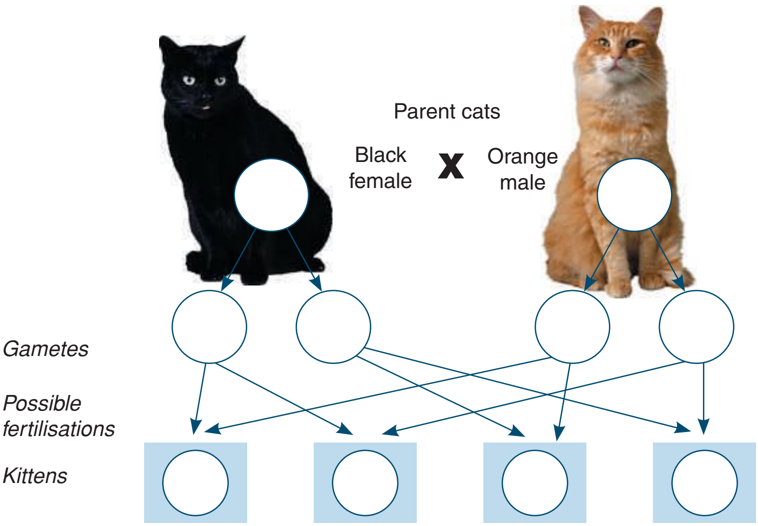
(b) Which phenotypic trait is dominant?

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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UNIT 4
Topic 1

# Biotechnology

### Key terms

annealing
bioinformatics
CRISPR-Cas9
DNA amplification
DNA ligase
DNA ligation
DNA polymerase
DNA profiling
forensics
gel electrophoresis
gene technology
genetic modification
GMO
marker gene
plasmid
polymerase chain reaction (PCR)
primer
recognition site
recombinant DNA
recombinant plasmid
restriction enzyme
transgenic organism

Activity number

## Recombinant DNA

*Key skills and knowledge*

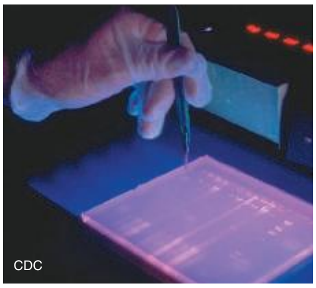
☐ 1 Understand what is meant by genetic modification and briefly describe the ways in which organisms can be genetically modified. Know that genetic modification may involve adding novel genes to an organism to create a transgenic organism. **122**

☐ 2 Describe the process of making recombinant DNA Including: **123**
- 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)

☐ 3 Explain how transformed bacteria are identified and isolated. Understand that these transformed bacteria are transgenic organisms. **124**

☐ 4 **PRAC** Perform a bacterial transformation. Determine the success of the transformation by calculating its efficiency. **125**

☐ 5 **SHE** Discuss the potential of GMOs (including transgenic organisms) for advancing agriculture and pharmaceutical development. **126**


CDC

## DNA sequencing, genome mapping and DNA profiling

*Key skills and knowledge*

☐ 6 Describe DNA amplification using the polymerase chain reaction (PCR). Explain the role of PCR in DNA analyses such as sequencing and profiling. **127**

☐ 7 Explain the basis for separation of DNA fragments using gel electrophoresis. Describe how gel electrophoresis is used in older DNA sequencing technologies and in DNA profiling. **128**

☐ 8 **PRAC** Interpret DNA profiles from gel electrophoresis. **128 133**

☐ 9 Distinguish between DNA sequencing and DNA profiling. Recognise the applications of DNA sequencing in genome mapping and DNA profiling to identify unique genetic information. **129**

☐ 10 **SHE** Explain how genome sequencing projects (e.g. the Human Genome Project or HGP) can advance our understanding of genes and gene function. **130**

☐ 11 **SHE** Explain the use of bioinformatics in analysing biological data, such as DNA sequences (e.g. the HGP). What are the applications of this information? **131**

☐ 12 **SHE** Describe the applications of low cost genome sequencing. What are the implications of this knowledge. How can it be used or misused? **132**

☐ 13 Describe how DNA profiling is used in forensic analysis and paternity testing. **133**

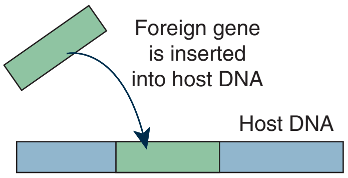
☐ 14 Appraise forensic DNA profiling data to determine its success rate. How are successful DNA matches determined and what factors determine success?

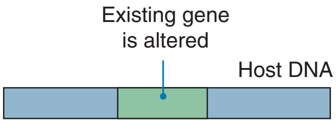
# 122 What is DNA Manipulation?

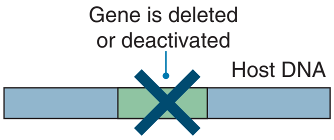
**Key Idea**: DNA manipulation alters an organism's DNA either by adding new DNA or editing the existing DNA.

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 (GMOs).

## 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**.

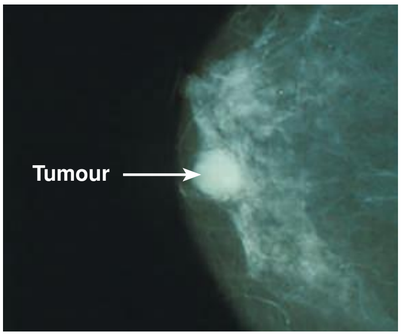
### Alter an existing gene

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.



NIH

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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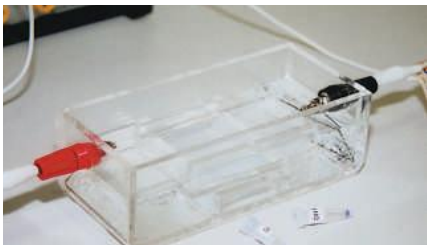
# 123 Making Recombinant DNA

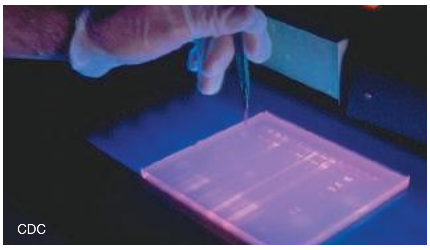
**Key Idea**: Recombinant DNA (rDNA) is produced by first isolating (or synthesising) a DNA sequence, then inserting it into the genome of a different organism, e.g. a bacterium.

**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.

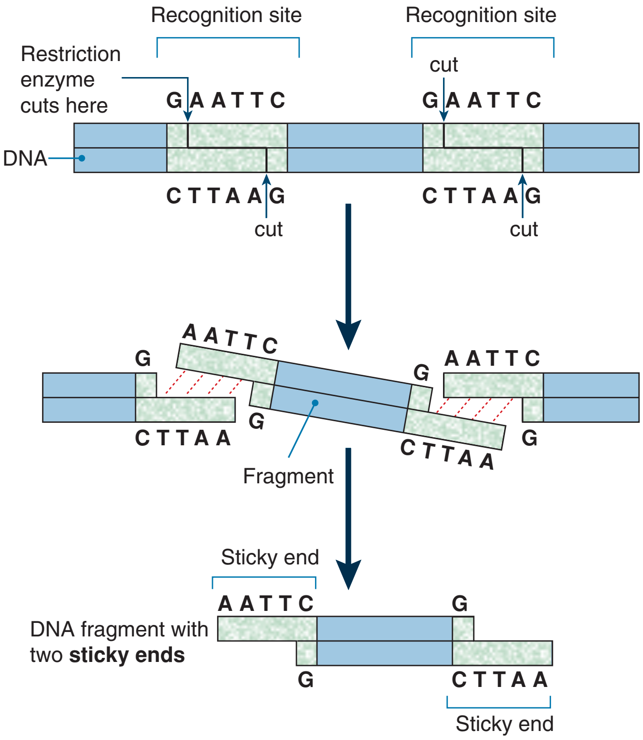


Once the DNA fragments are separated, the gel is placed on a UV viewing platform. The area of the gel containing the DNA fragments of the correct length is cut out and placed in a solution that dissolves the gel. This releases the DNA into the solution.

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, 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 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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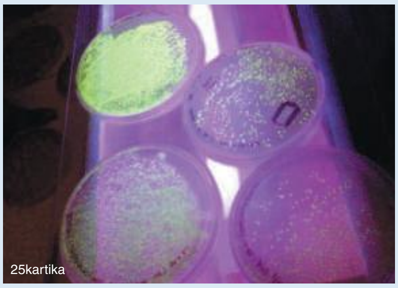
## Creating a recombinant DNA plasmid

1. Two pieces of DNA are cut by the same restriction enzyme (they will produce fragments with matching sticky ends).

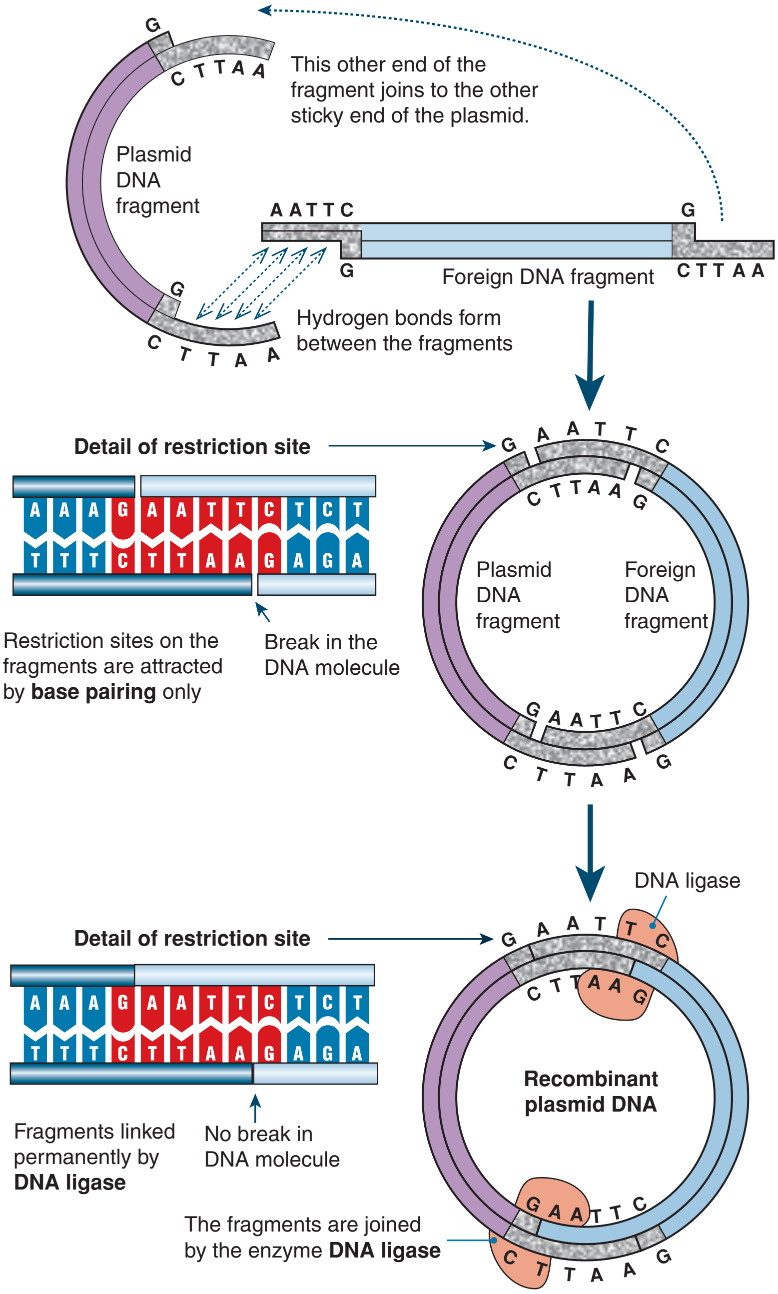
2. Fragments with matching sticky ends can be joined by base-pairing. This process is called **annealing.** This allows DNA fragments from different sources to be joined.

   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.


25kartika

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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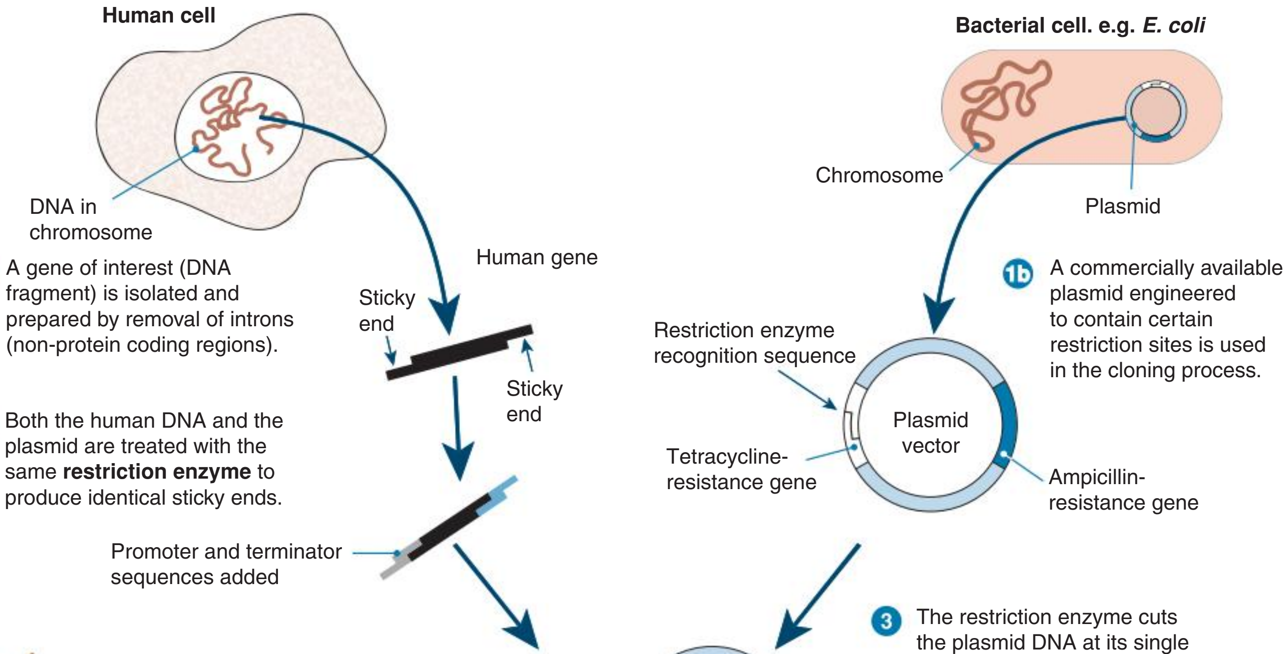
# 124 DNA Amplification By Bacterial Transformation

**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.

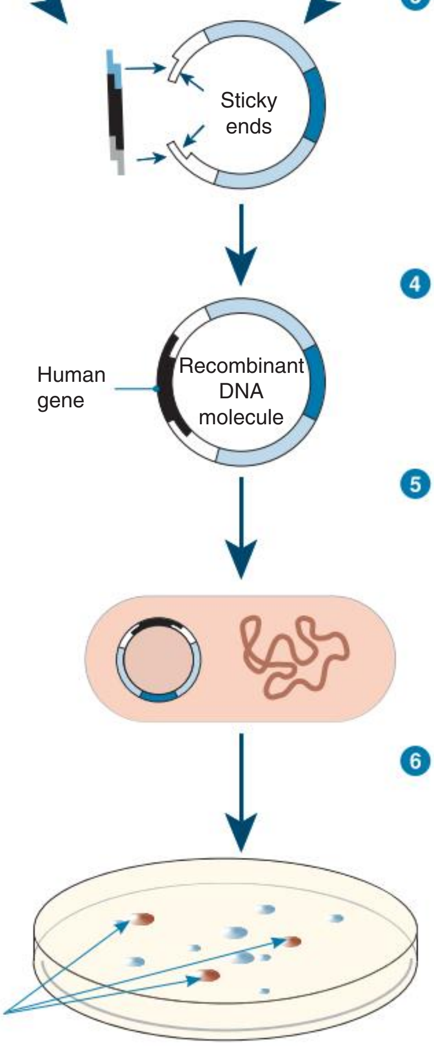
We have already seen that recombinant DNA techniques can be used to insert a gene into a plasmid. The plasmid can then be used to transmit the gene to another organism (e.g. *E. coli* bacteria). Once inside *E. coli*, the gene is replicated along with the host DNA. This technique is called **gene cloning** 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.



1a A gene of interest (DNA fragment) is isolated and prepared by removal of introns (non-protein coding regions).

1b A commercially available plasmid engineered to contain certain restriction sites is used in the cloning process.

2 Both the human DNA and the plasmid are treated with the same **restriction enzyme** to produce identical sticky ends.



3 The restriction enzyme cuts the plasmid DNA at its single **recognition sequence**, disrupting the tetracycline resistance gene.

4 The DNA fragments are mixed together and the enzyme DNA ligase is used to anneal (join) the complementary sticky ends.

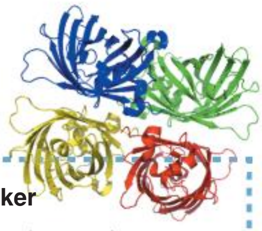
5 The recombinant plasmid is introduced into a bacterial cell by adding the DNA to a bacterial culture. Under the right conditions, some bacteria will take up the plasmid from solution by the process of **transformation**. These bacteria are transgenic organisms.

6 **Replica plating** can be used to identify colonies of bacteria that carry the recombinant plasmid. Recombinant bacteria are resistant to ampicillin but sensitive to tetracycline. These colonies can be isolated and grown in culture.

Agar plate with bacterial colonies. Only some have the plasmid with the human gene.

**DID YOU KNOW?**

Several types of vectors are used in bacterial transformation, but bacterial plasmids are commonly used because they are easy to manipulate, their restriction sites are well known, and they are readily taken up by cells in culture.



### *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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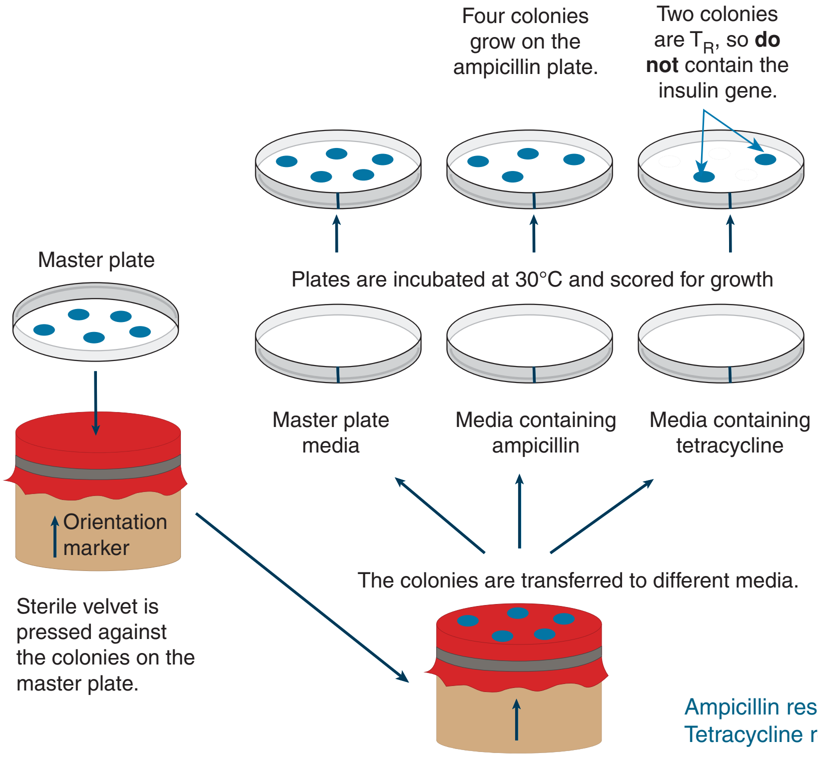
## Replica plating identifies colonies with desirable qualities

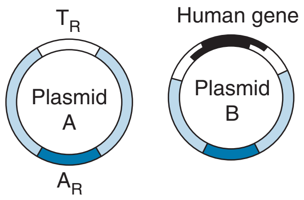
After gene cloning, it is important to be able to identify the colonies in which transformation has occurred. This is achieved by **replica plating**.

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.



Sterile velvet is pressed against the colonies on the master plate.



| | Plasmid A | Plasmid B |
|---|---|---|
| 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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# 125 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 $\mu L^{-1}$ 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:

● Transformed *E.coli*

● Untransformed *E.coli*

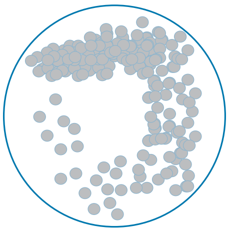

Plate 1: Nutrient agar only (no ampicillin) -plasmid

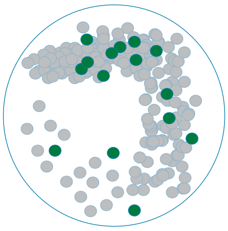

Plate 2: Nutrient agar only (no ampicillin) +plasmid

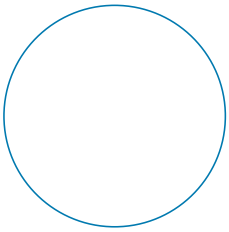

Plate 3: Nutrient agar + ampicillin -plasmid

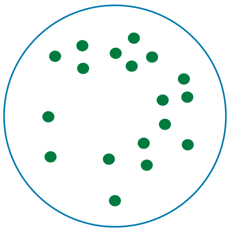

Plate 4: Nutrient agar + ampicillin +plasmid

1. (a) Determine the mass of plasmid pipetted into the microcentrifuge tubes.
   Use the formula mass (µg) (of plasmid) = concentration (µg $\mu L^{-1}$) 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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# 126 Applications of Genetically Modified Organisms

**Key Idea**: GMOs are widely used to increase yields or quality in agricultural, or to produce pharmaceutical products.

Recall that organisms that have had their DNA altered are called genetically modified organisms (GMOs). 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?

Three GM crops are currently grown in Australia, canola (right), cotton, and safflower. There are a number of experimental field trials also in progress. These include bananas, 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.

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**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).

Scott Bauer, USDA ARS

**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. Choose one of the following topics to research:

   (a) Choose one genetically modified crop grown in Australia (canola, cotton, or safflower) and research the advantages and disadvantages of its use compared to a non-GMO crop. Summarise you 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.

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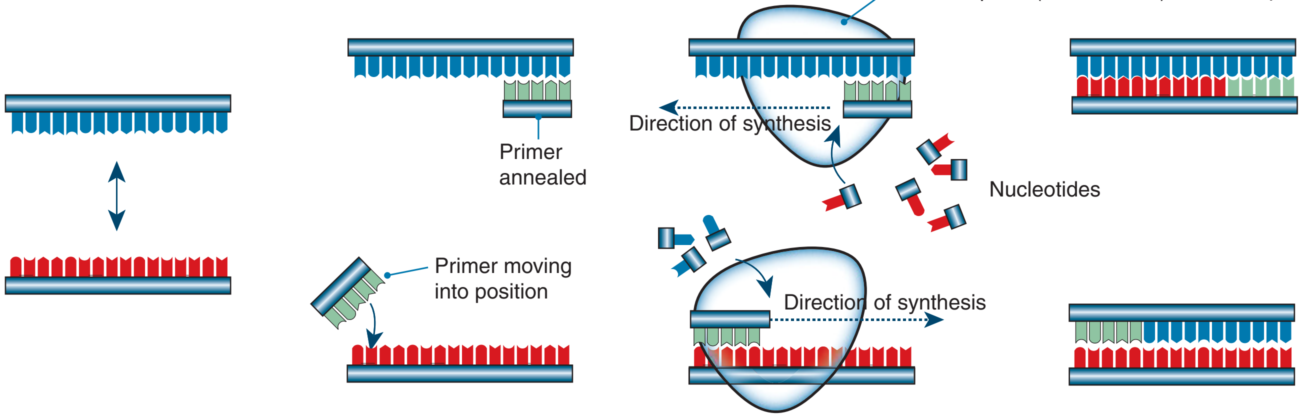
# 127 DNA Amplification Using PCR

**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, 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 given below.

### A single cycle of PCR

**DNA polymerase**: A thermally stable form of the enzyme is used (e.g. ***Taq* polymerase**). This is extracted from thermophilic (heat tolerant) bacteria.



**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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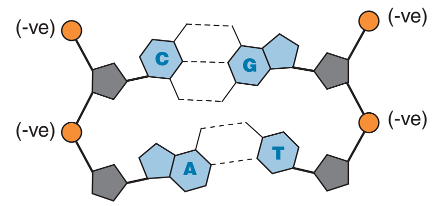
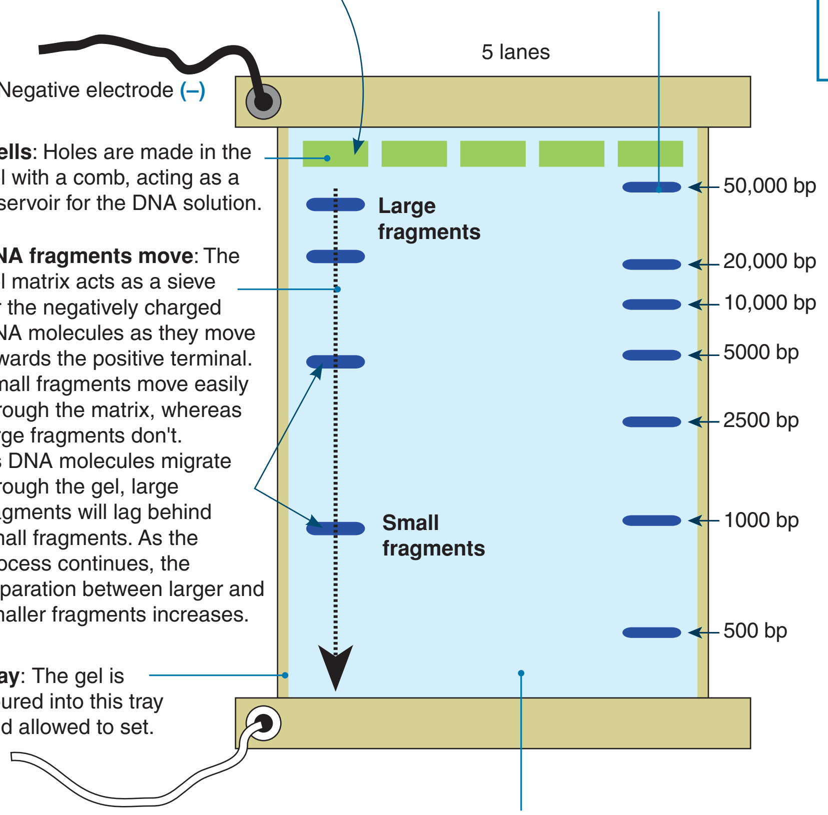
# 128 Gel Electrophoresis

**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).

**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 will 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.

**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 the electric current from electrodes at either end of the gel to flow through the gel.
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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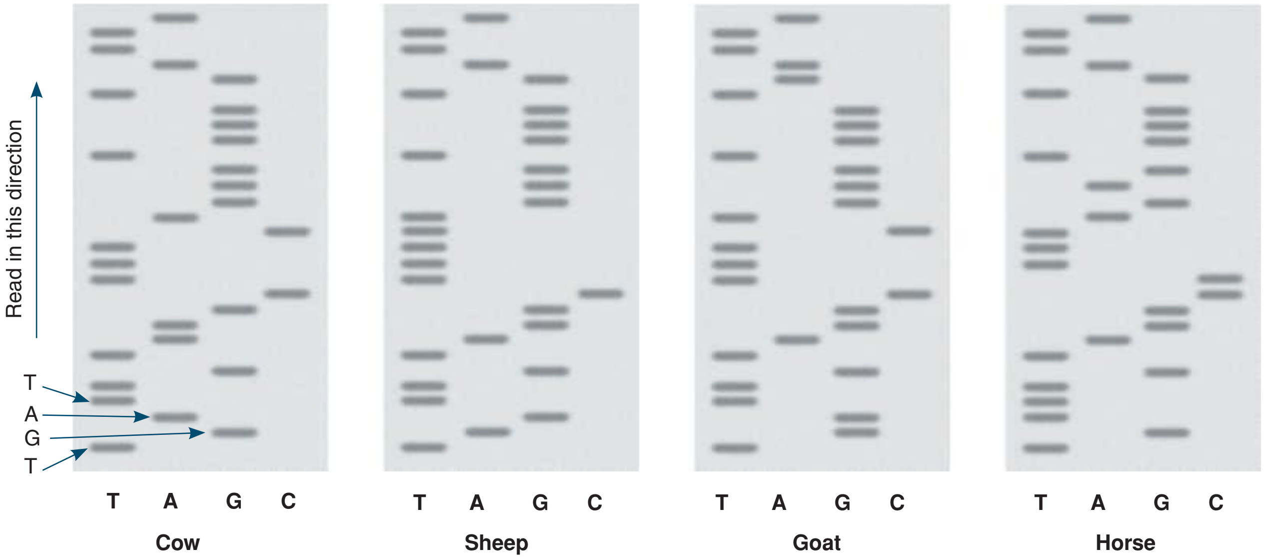
Once made, an electrophoresis gel must be interpreted. If a specific DNA base sequence was being investigated, then the band pattern can be used to determine the DNA sequence and the protein that it encoded. Alternatively, depending on how the original DNA was treated, the banding pattern may be used as a profile for a species or individual. Commonly, the gene for cytochrome oxidase I (COXI), a mitochondrial protein, is used to distinguish animal species. The genetic information from this gene is both large enough to measure differences between species and small enough to have the differences make sense (i.e. the differences occur in small regions and aren't hugely varied).



4. The photographs above show gel electrophoresis results for four species.

   (a) For each of the species determine the sequence of DNA:

   Cow DNA sequence: ____________________

   Sheep DNA sequence: ____________________

   Goat DNA sequence: ____________________

   Horse DNA sequence: ____________________

   Based on the number of differences in the DNA sequences:

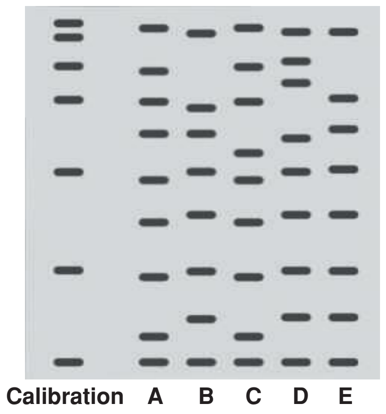
   (b) Identify the two species that are most closely related: ____________________

   (c) Identify the two species that are the least closely related: ____________________

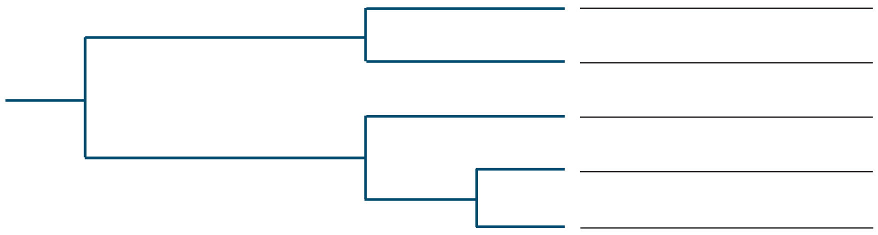
5. What makes COXI useful for comparing species by gel electrophoresis? ____________________

____________________

____________________



6. 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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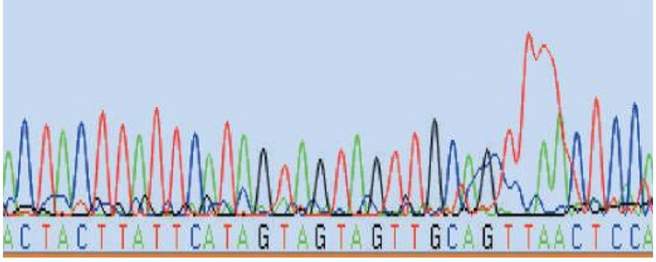
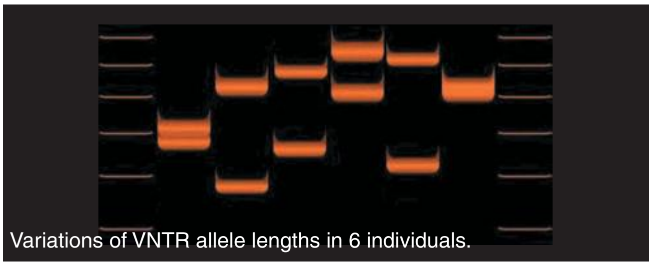
# 129 Applications of DNA Analysis

**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.




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). Large genomes must be broken down into small pieces and amplified using PCR first. In chain termination methods (Sanger technology), the terminator end of the DNA fragments have fluorescent labels attached and the fragments are separated using gel electrophoresis. Each type of nucleotide base fluoresces a different colour so when the gel is scanned the DNA sequence can be obtained (above). Current high throughput sequencing technologies have automated this basic process, running systems in parallel and producing thousands or millions of sequences concurrently.

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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# 130 The Human Genome Project

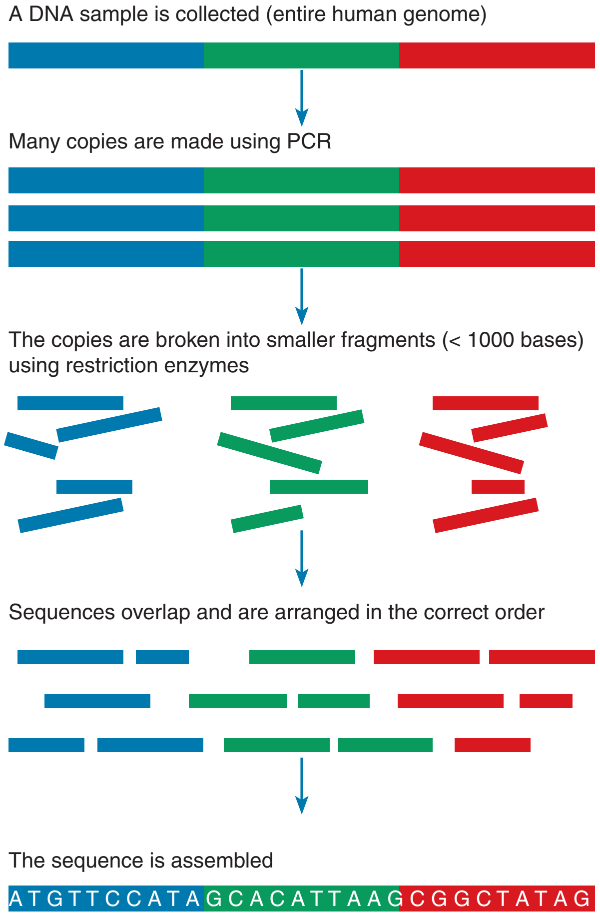
**Key Idea**: The Human Genome Project (HGP) sequenced the entire human genome. The information is used in many fields of science and medicine.

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.

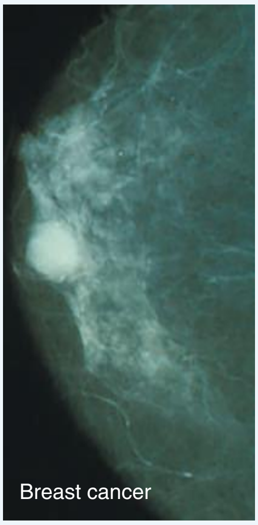
## A hierarchical shotgun method was used to sequence the human genome

**DID YOU KNOW?**

Shotgun sequencing resembles the process of physical mapping (a map of genes and their positions) because it shatters the genome into fragments, 'describes' each fragment, and then reassembles the fragments. This provides all the information of a traditional physical map.



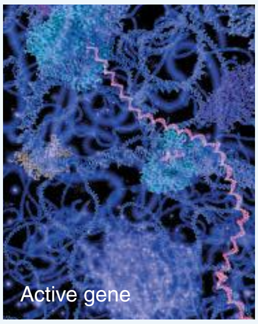
## How is the information from the HGP used?


Breast cancer

NIH

**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.


Active gene

**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.


Mutated gene

**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?

SHE 129

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# 131 Bioinformatics

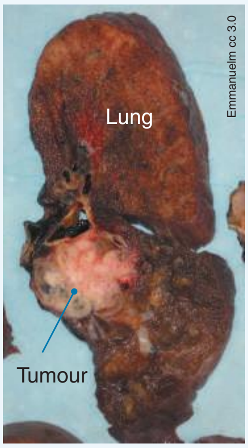
**Key Idea**: Bioinformatics uses powerful computing and mathematical tools to collect, store, and analyse large amounts of biological information, such as data from the HGP.

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**) is a project with the aim of improving the diagnosis, treatment, and prevention of cancer. During the 12 years the project has been running it has:

- 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).



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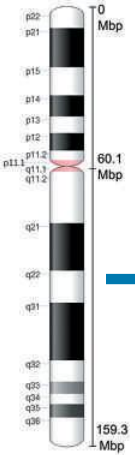
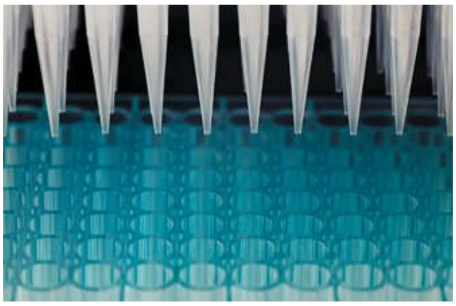


The EGFR gene is located between 55 and 55.2 Mbp on the p arm of chromosome 7.

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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# 132 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. 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?

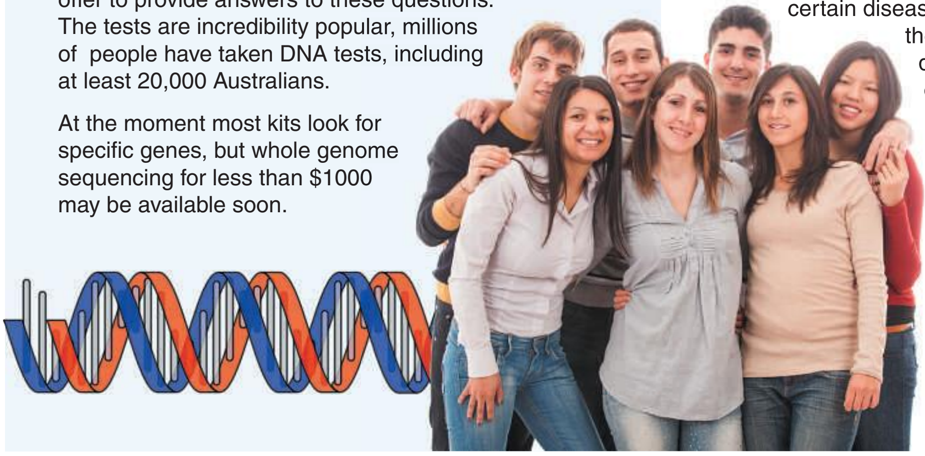
## What does my DNA tell me?

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 incredibility 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?

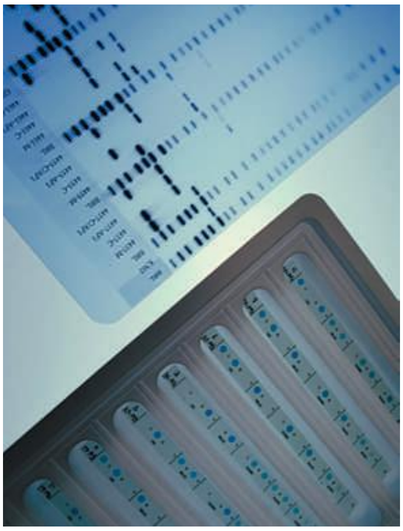
No, not always. Some companies have very rigourous testing procedures while others do not. Recently a customer sent a sample of his dog's DNA to a laboratory and they didn't notice it wasn't human DNA! There are many examples when people have had their ancestry analysed using different companies and 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.

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 if there is no cure for the disease (e.g. Huntington's). What impact would that have on a person's wellbeing and outlook on life?

## 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 a this is not always the case. 23andMe is one of the world's most popular DNA testing companies. In 2018, they 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 state the data was being on-sold to the pharmaceutical company so that new drugs could be developed. More recently 23andMe has added an opt out option for its customers, but many other companies haven't. So what does this mean for you?

- The testing company is making money by selling customer data, but the customer gets no money.
- Your personal information is being shared with other parties. Your unique genetic information 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.
- In Australia, life insurance companies can ask if you have had a DNA test, or if you are considering having a test. They can refuse to give you cover if there are any concerning health markers present. This is called genetic discrimination.



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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# 133 Applications of Profiling

**Key Idea**: DNA profiling has many forensic applications, from identifying criminal offenders to saving endangered species.

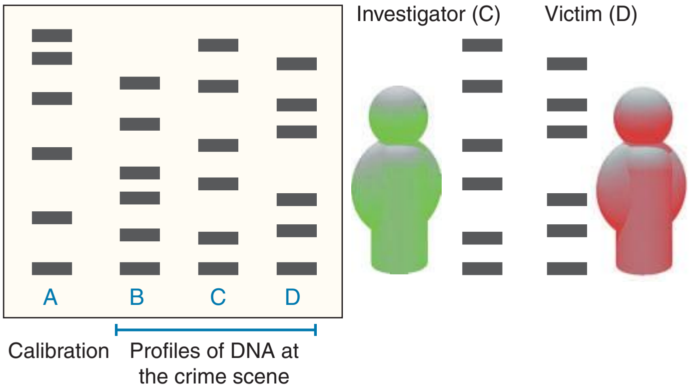
The use of DNA as a tool for solving crimes such as homicide is well known, but it can also has several other applications. DNA evidence has been used to identify body parts, solve cases of industrial sabotage and contamination, for paternity testing, and even in identifying animal products illegally made from endangered species.

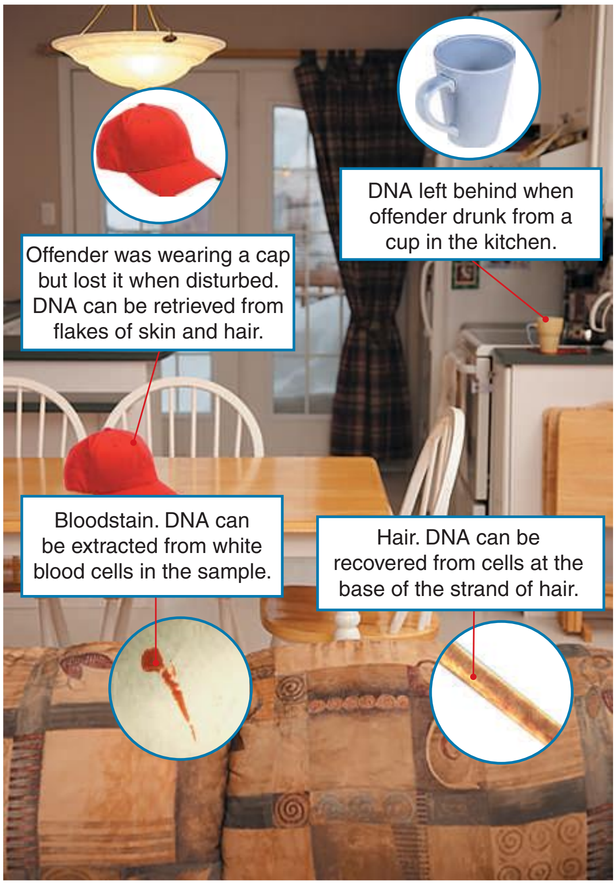
## Using DNA to solve crimes

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 their profiles can be eliminated. A calibration or standard is run so the technician knows the profile has run correctly.




Offender was wearing a cap but lost it when disturbed. DNA can be retrieved from flakes of skin and hair.

DNA left behind when offender drunk from a cup in the kitchen.

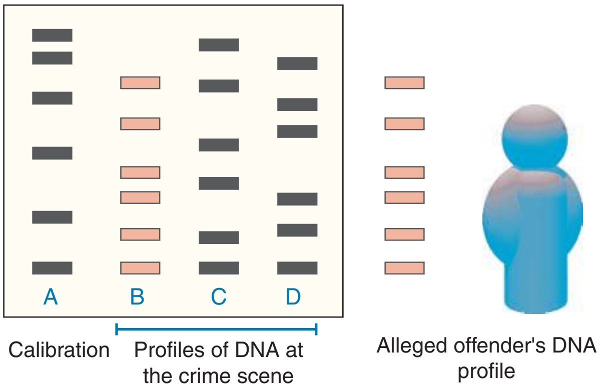
Bloodstain. DNA can be extracted from white blood cells in the sample.

Hair. DNA can be recovered from cells at the base of the strand of hair.

There are two different ways an offender can be identified through DNA profiling.

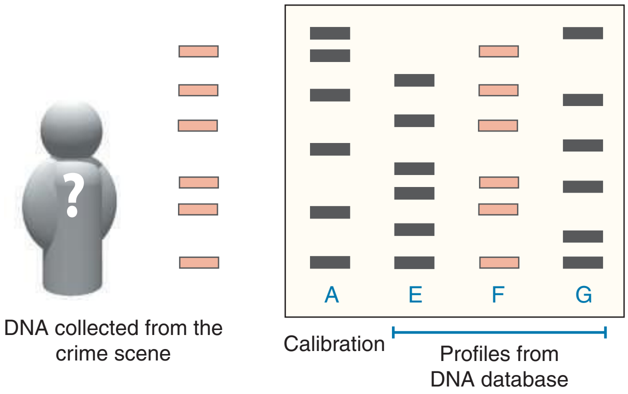
1. If a person is suspected of a crime, a sample of their DNA can be taken (e.g. blood sample) and compared to DNA evidence collected at the crime scene. A match indicates they are the offender. If there is no match, the person can be cleared as a suspect.
2. In cases where the suspect is unknown, biological 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.

### ① A person is suspected of the crime



**Match**! The alleged offender's profile matches the DNA collected at the crime scene.

### ② The offender is unknown



**Match**! The DNA collected from the crime scene matches the profile of a known offender in the database.

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## Paternity testing

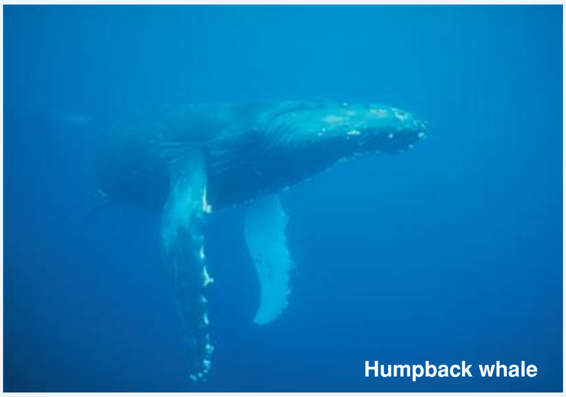
DNA profiling can be used to determine paternity (and maternity) by looking for matches in alleles between parents and children. It is used in cases such as child support or inheritance. DNA profiling can establish the certainty of paternity (and maternity) to a 99.99% probability of parentage.

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


Humpback whale

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.

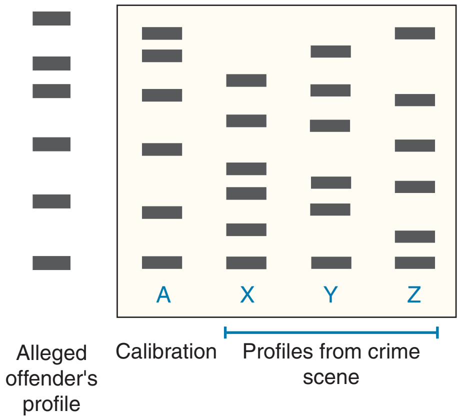
Between 1999 and 2003, researchers used DNA profiling to investigate whale meat sold in markets in Japan and South Korea. They found 10% of the samples tested were from fully protected whales including western grey whales and humpbacks. They also found that many more whales were being killed than were being officially reported.

1. Why are DNA profiles obtained for both the victim and investigator? ____________________

2. Study the profile on the right.

   (a) Is the alleged offender innocent or guilty? ____________________

   (b) Explain your decision: ____________________



3. For the STR D10S1248 in the example above, what possible allele combinations could the child have?

4 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 |

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# 134 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.


Palewhalegail CC 3.0

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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# 135 KEY TERMS AND IDEAS: Did You Get It?

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

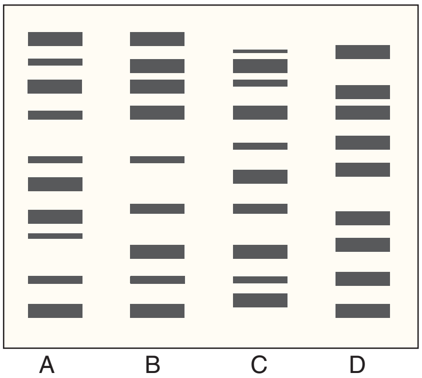
DNA profiling ..............
forensics ..............
gel electrophoresis ..............
genetic modification ..............
GMO ..............
marker gene ..............
PCR ..............
plasmid ..............
recombinant DNA ..............
transgenic organism ..............

| | |
|---|---|
| **A** | The manipulation of DNA in order to modify the characteristics of organisms. |
| **B** | A reaction that is used to amplify fragments of DNA using cycles of heating and cooling. |
| **C** | The process of identifying and visualising regions of a DNA sequence that are variable between individuals in order to distinguish between individuals. |
| **D** | An organism that has had part of its DNA sequence altered either by the removal or insertion of a piece of DNA. |
| **E** | An organism that has had its genome modified to carry genes that are not usually found in that species (acronym). |
| **F** | A small circular piece of DNA commonly found in bacteria. |
| **G** | The application of scientific methods to the investigation of matters involving criminal and civil laws. |
| **H** | DNA that has had a new sequence added so that the sequence has been altered. |
| **I** | A gene, with an identifiable effect, used to determine if a piece of DNA has been successfully inserted into the target organism. |
| **J** | A process that is used to separate different lengths of DNA by placing them in a gel matrix placed in a buffered solution through which an electric current is passed. |

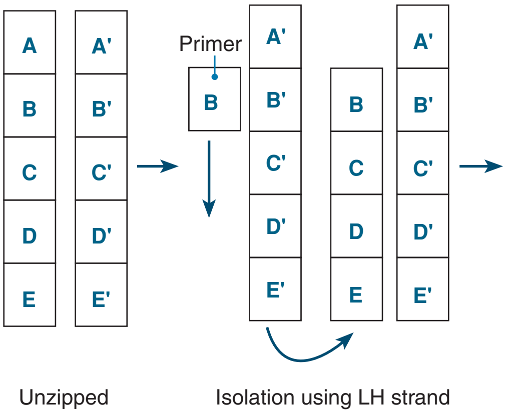
2. The electrophoresis gel (below, right) shows four profiles containing five STR sites: the mother (A) her daughter (B) and two possible fathers (C and D). Which of the possible fathers is the biological father?

(a) The biological father is: ______________________________

(b) Why do profiles B and D only have 9 bands?



3. Below is a DNA sequence of sections, A, B, C, D, and E and A', B', C', D', and E'. A scientist wants to isolate sections B, C, and D as a continuous group by PCR. Primers are B and D'. Complete the PCR process, using the right hand (') strand to show how B, C, and D are isolated. The first step is done for you. Note that the process could be shown for the left hand strand also but the sequence of events would be different.



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# 136 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

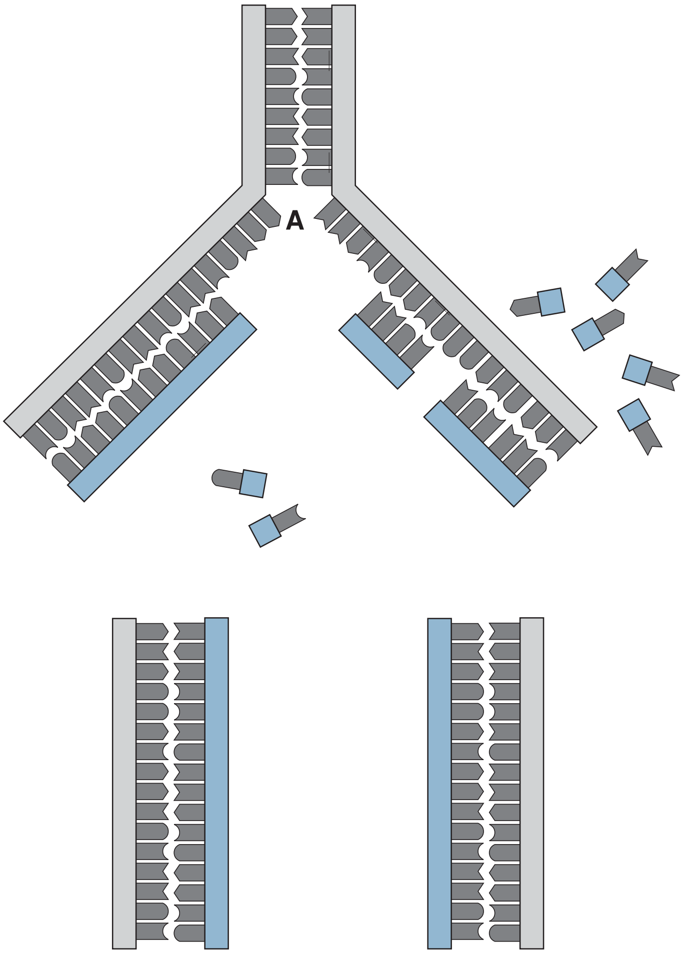
   (c) Draw in the likely positions of:

      (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.



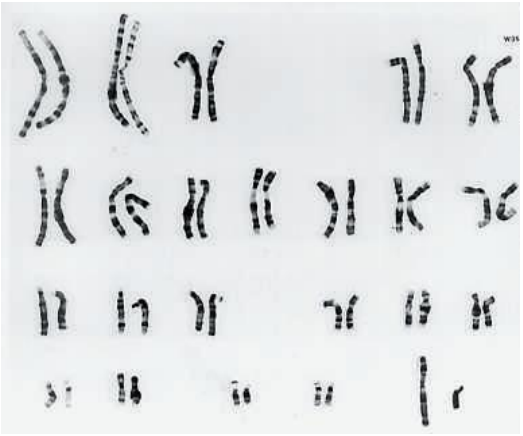
2. The preparation of a karyogram involves arranging the chromosomes of an individual into homologous pairs in order.

   (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):



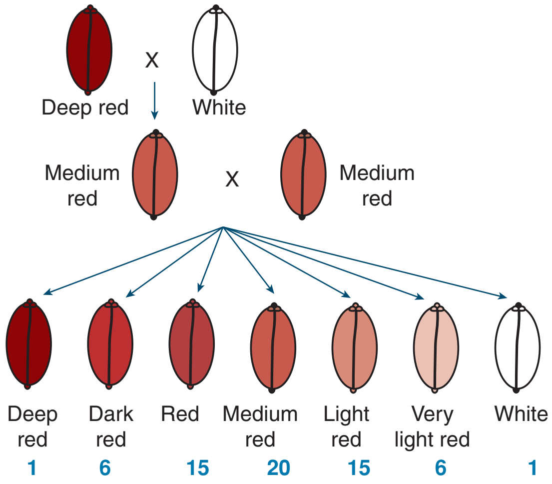
Cytogenetics Dept, Waikato Hospital

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:

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:

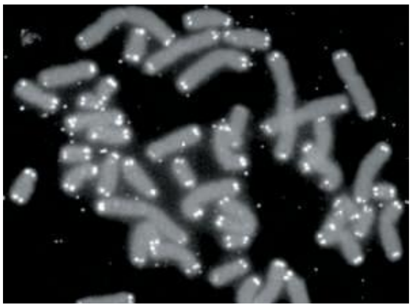
5. The diagram below shows a simplified eukaryotic gene.

(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:

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UNIT 4
Topic 2

# Evolution

**Key terms**

- comparative genomics
- evolution
- evolutionary radiation
- extinction
- homology
- macroevolution
- mass extinction
- microevolution
- phylogeny

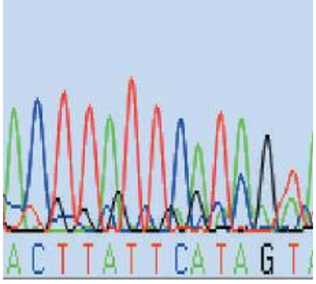
Activity number

## What is evolution?

*Key skills and knowledge*

☐ 1 What do you understand by the term evolution. Distinguish between microevolution and macroevolution and give examples of each. **137**

☐ 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. **138 139**



## Comparative genomics and phylogeny

*Key skills and knowledge*

☐ 3 Understand that the evidence for evolution comes from many disciplines, including morphological comparisons, but increasingly from comparative genomics. **140-143**

☐ 4 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): **140-144**

- 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

☐ 5 Interpret data to show how similarities in proteins are used to determine the relatedness of different organisms. **140 141**

☐ 6 How are highly conserved genes and proteins used as molecular clocks to determine when two species last shared a common ancestor? What are the problems with molecular clocks and how can they be overcome? **141**

☐ 7 What types of genes are useful in revealing evolutionary relationships? Explain how studying genes that have been duplicated and modified provides evidence for how new body forms arise during the diversification of lineages (e.g. arthropods). **142**

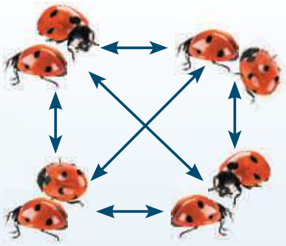
☐ 8 Interpret data to show how the DNA sequences of different organisms can be compared and the comparisons used to determine relatedness among different taxa. Do the phylogenies established using different methods (e.g. DNA and proteins) agree? Why? **143**

☐ 9 **SHE** Explain how developments in comparative genomics and bioinformatics provide evidence of evolutionary relationships among organisms. **144**

# 137 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.

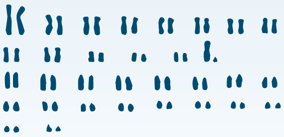
**Gene flow**
Genetic information flowing into or out of the population affects the population over time. As populations diverge, gene flow is reduced.

**Genetic drift**
Random changes in gene frequencies between generations affect the genes available for recombining in later generations.

**MICROEVOLUTION**

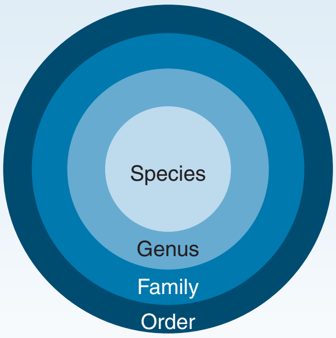
**MACROEVOLUTION**

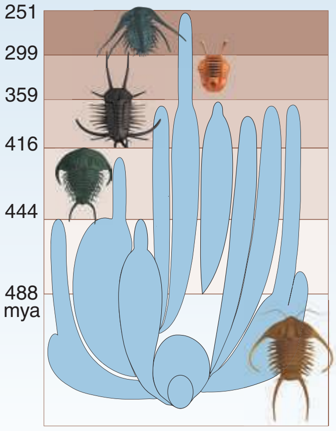
Zebra karyogram



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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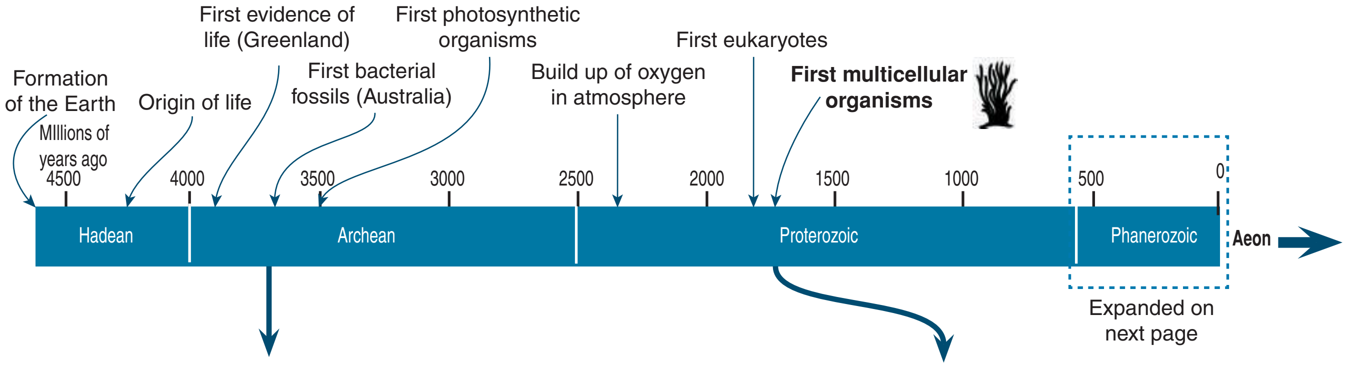
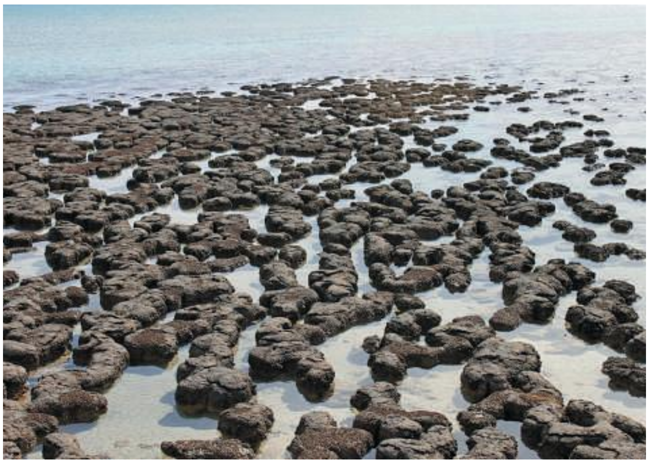
# 138 Earth's Evolutionary History

**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.

**Time line of Earth's biodiversity**





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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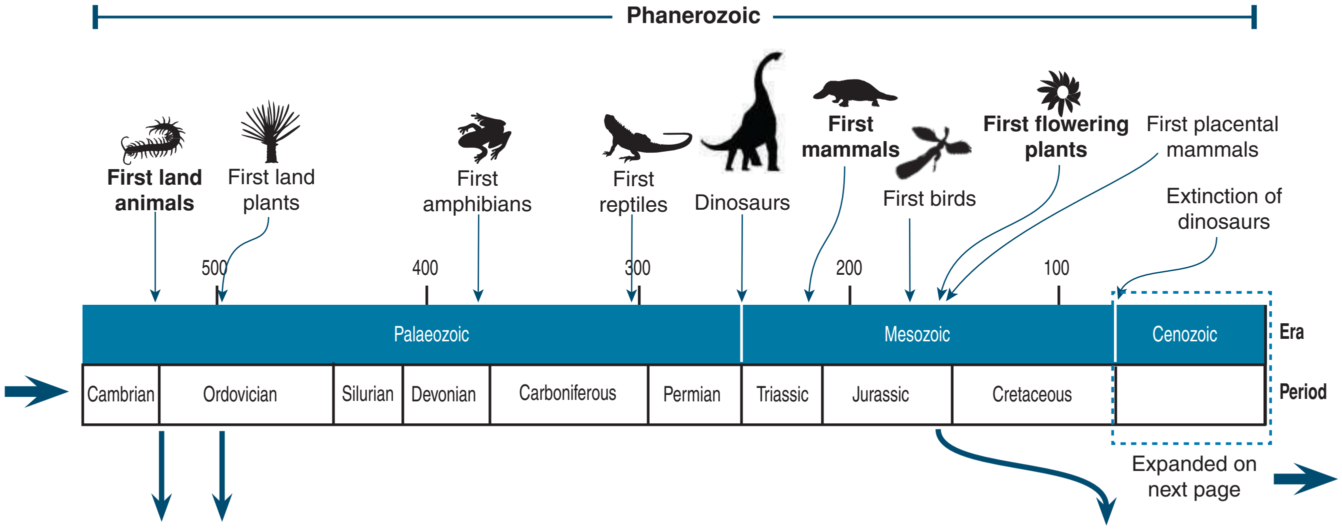

*Arthropleura* (extinct millipede) tracks

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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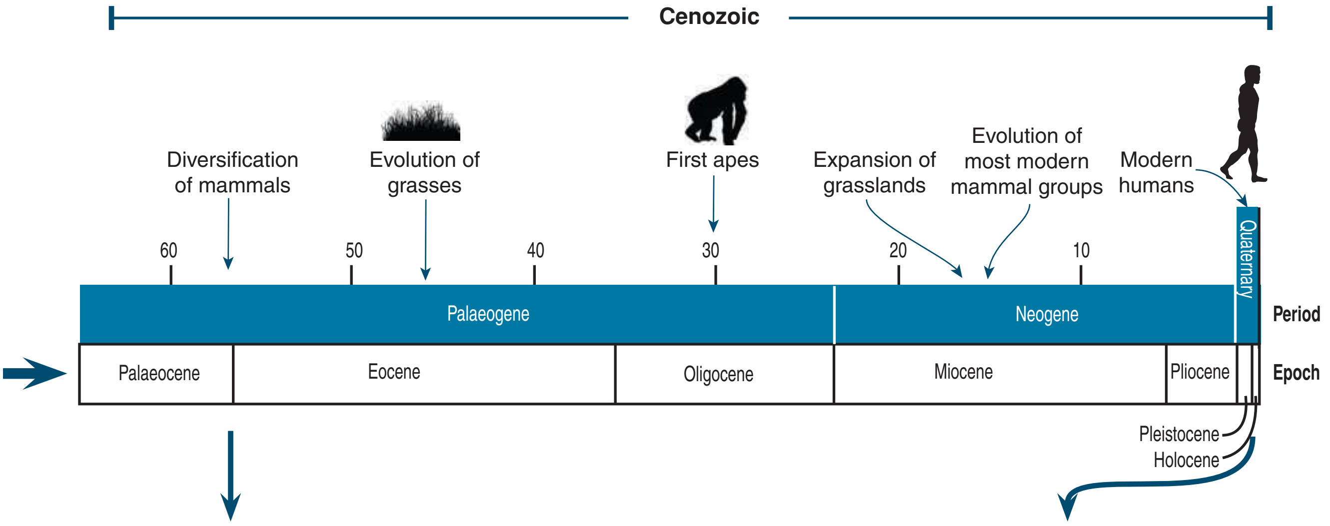

NASA

**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.

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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# 139 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.

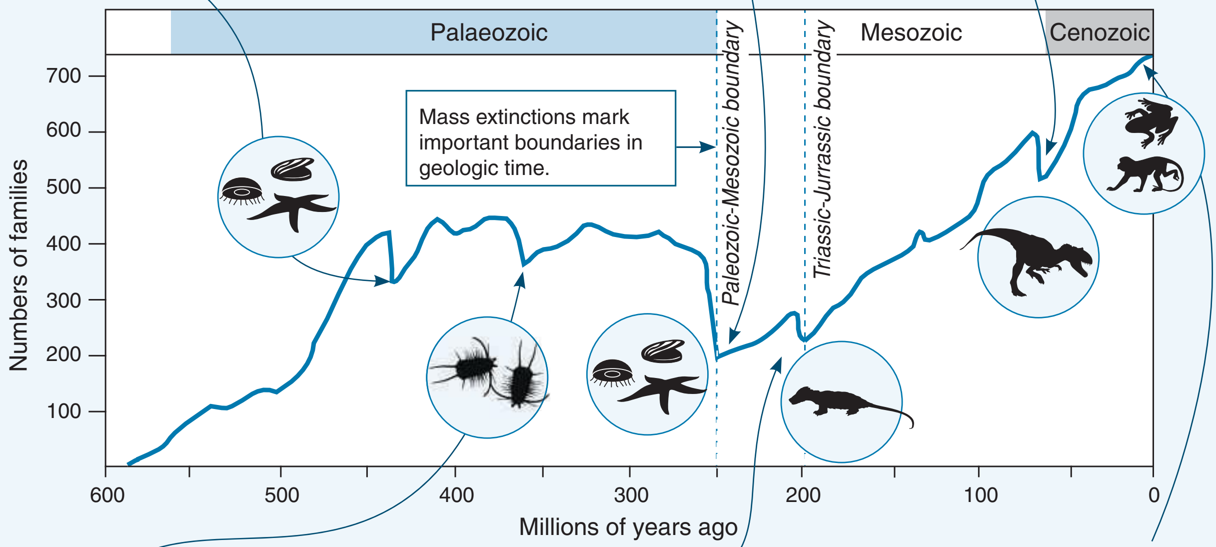
Extinction is important in evolution because it provides opportunities, in the form of vacant niches, for the evolution of new species. The species alive today make up only a fraction of the total list of species that have lived on Earth throughout its history. The duration of a species is thought to 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.



Mass extinctions mark important boundaries in geologic time.

**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 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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# 140 Protein Homology and Phylogeny

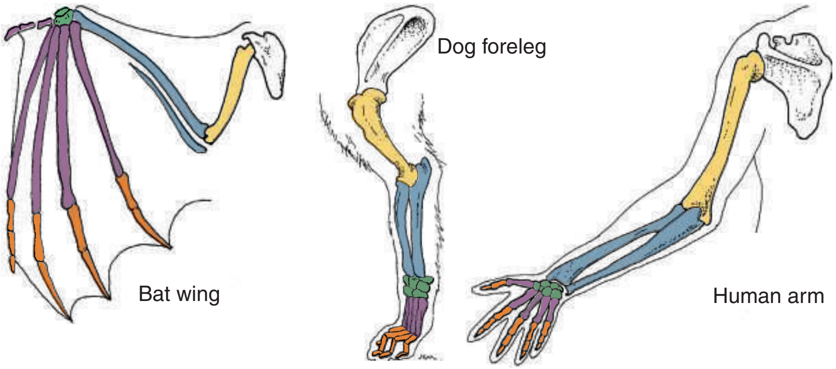
**Key Idea**: Proteins are the product of gene expression, so an analysis of the differences between the same protein in different taxa gives an indication of species relatedness.

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?

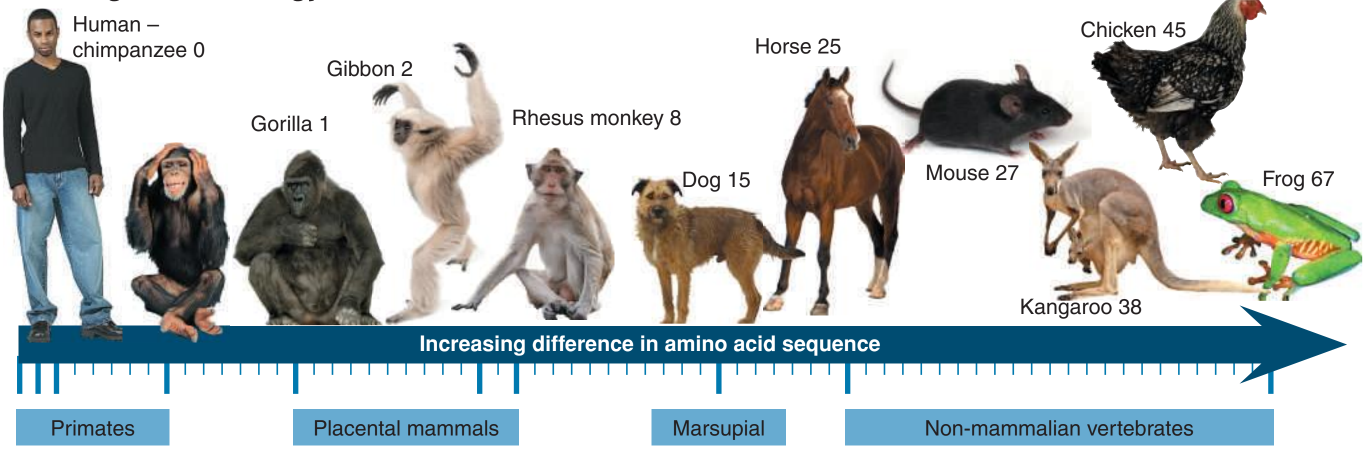
Homology is the similarity between structures, genes, or proteins arising as a result of shared ancestry. In vertebrates, homology can be seen in the bones of the forelimbs (right). It can also be seen in the wings of different insects.

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 dog's foreleg, a human arm and a bat's wing 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.

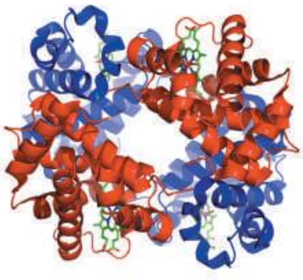


Image: Zephyris CC 3.0

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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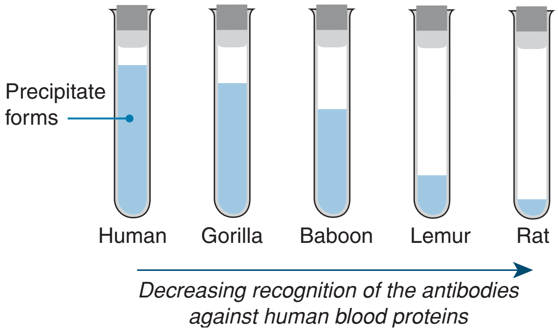
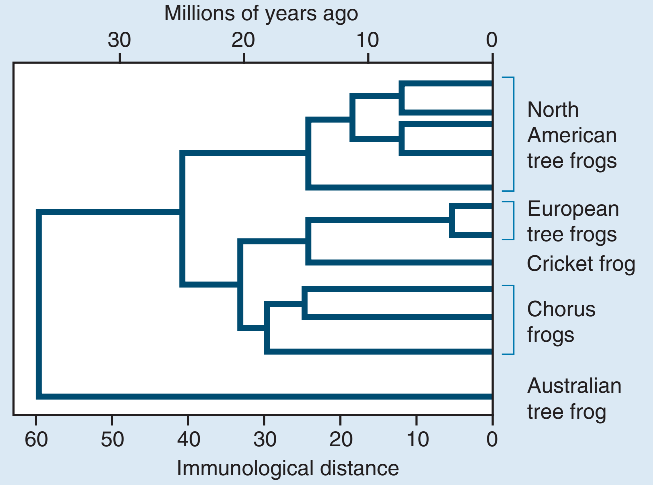
## Using immunology to determine phylogeny

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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# 141 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

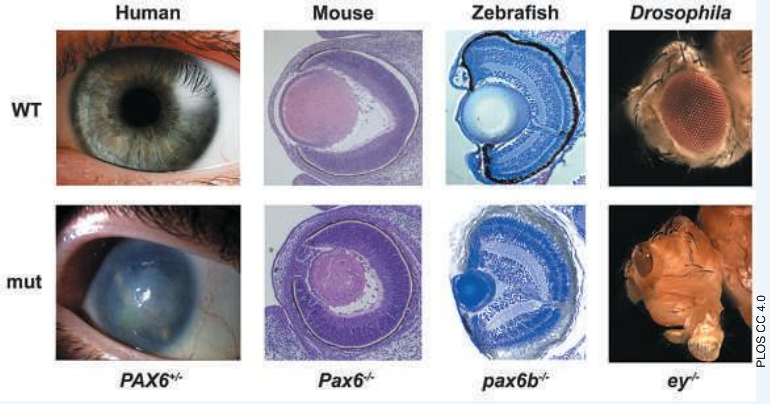
| Human | | Gly | Asp | Val | Glu | Lys | Gly | Lys | Lys | Ile | Phe | Ile | Met | Lys | Cys | Ser | Gln | Cys | His | Thr | Val | Glu | Lys |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Pig | | | | | | | | | | | | Val | Gln | | | Ala | | | | | | | |
| 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 (left) 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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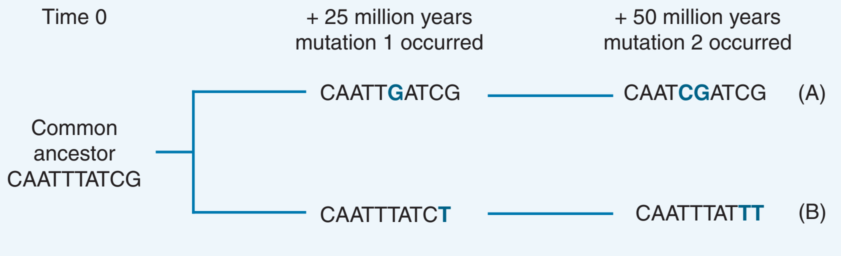
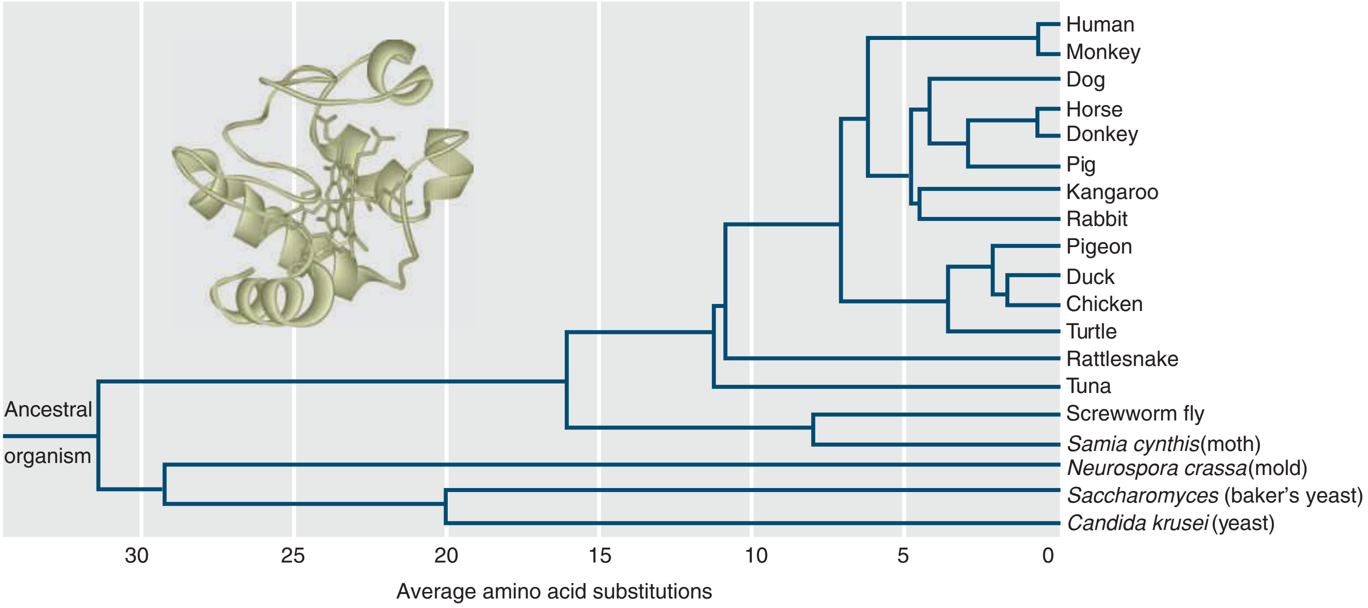
## Cytochrome *c* and phylogeny

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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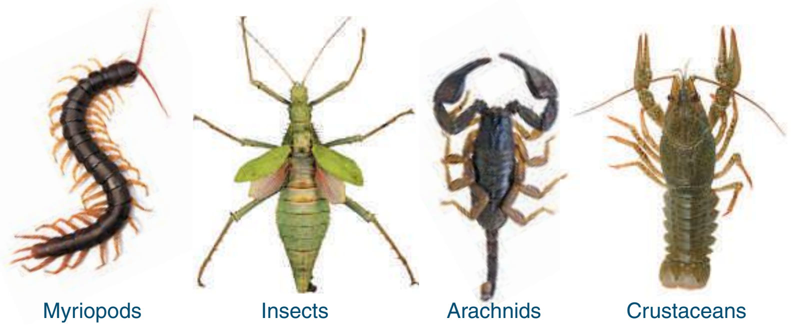
# 142 Gene Duplication and Animal Diversification

**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 particularly, it explains how new characteristics can appear with apparent suddenness.

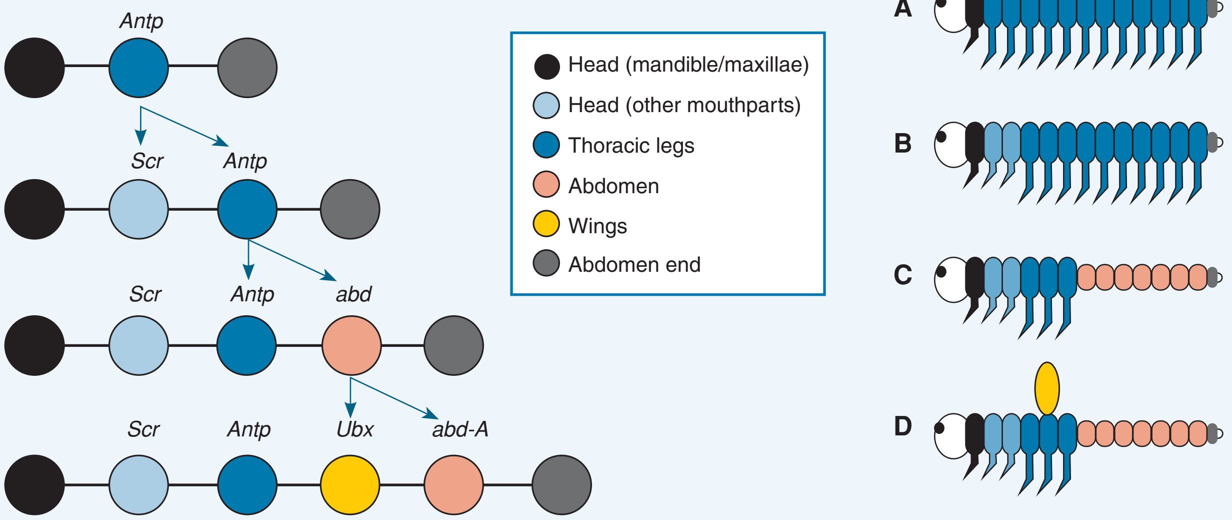
## Evolution: you work with what you've got!

- 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.



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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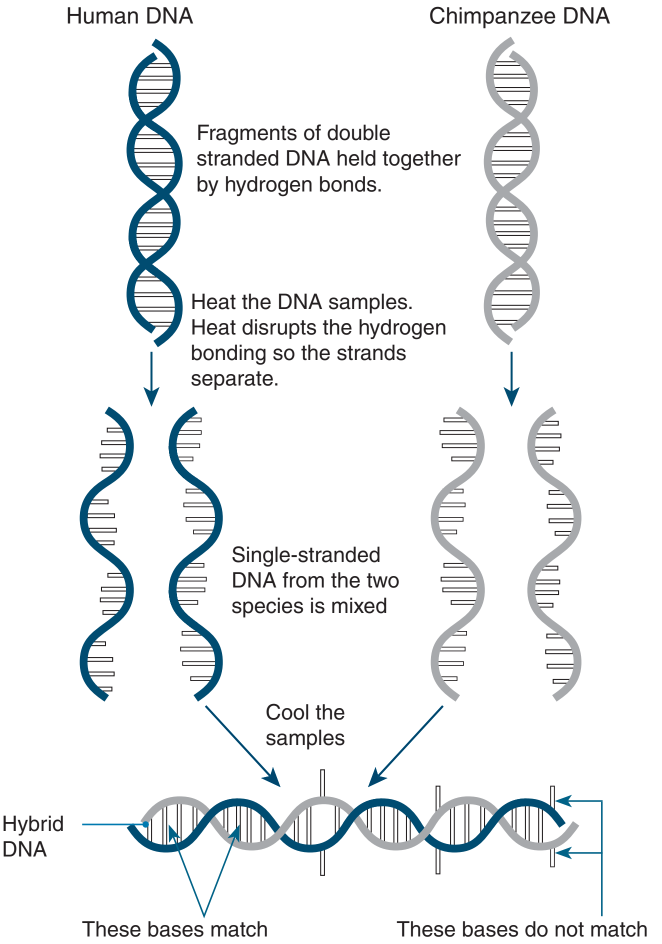
# 143 Genomic Comparisons and Relatedness

**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 that is required to break the hybrid DNA apart.

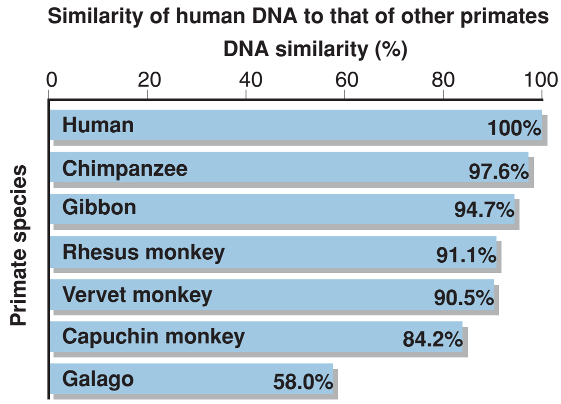


1. How can DNA hybridisation give a measure of genetic relatedness between species?

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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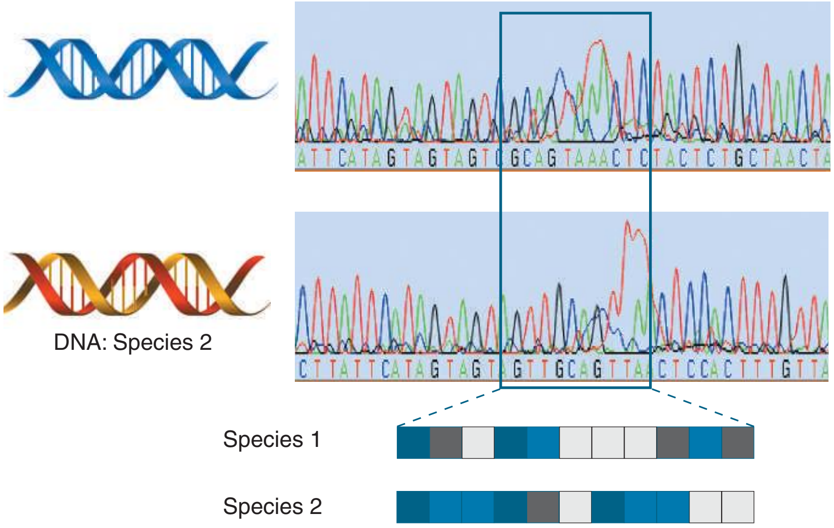
## DNA sequencing

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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# 144 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

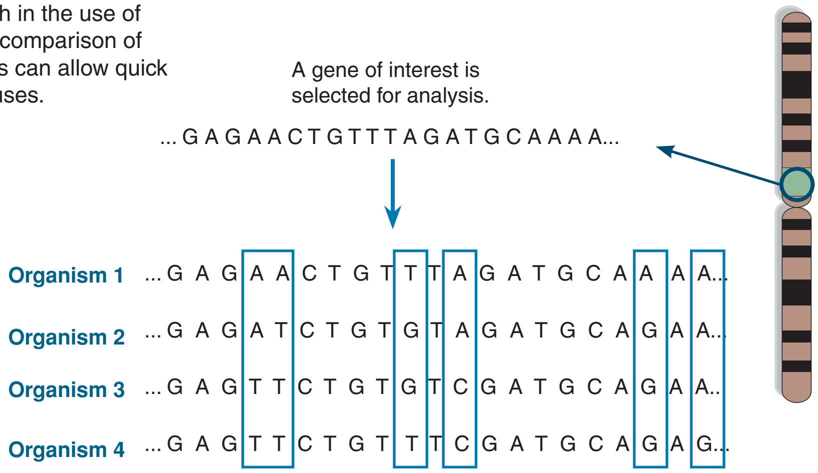
- Early DNA sequencing technologies, such as the Sanger method, required that the sample sequence was copied using modified DNA, producing various lengths of DNA. These then had to be separated on a gel and read on a UV bed or as they passed by a laser.
- High throughput sequencers read the DNA as it 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.

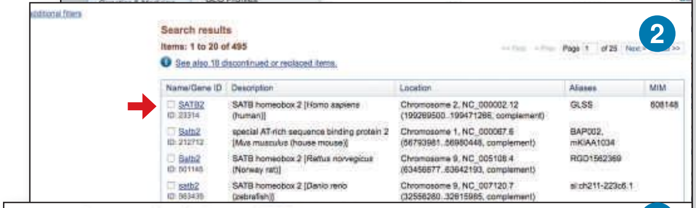
## Online data bases

There are many easily accessible online data bases where DNA sequences can be studied. The example below uses NCBI data base at **www.ncbi.nlm.nih.gov**.

- 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).
- 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.
- Click **search** and a new window appears showing the results.
- Click the first SATB2 on the list (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.
- 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.
- Click the first on the list **(NM_001172509.2**).
- This brings up information on the transcript. Scroll to the bottom and the DNA sequence for the mRNA is shown.
- Highlight and copy this sequence.

NCBI

...r for Biotechnology Information advances science and health by providing access to ...omic information.



Search results

Items: 1 to 20 of 495

| Name/Gene ID | Description | Location | Aliases | MIM |
|---|---|---|---|---|
| ☐ SATB2<br>ID: 23314 | SATB homeobox 2 [Homo sapiens (human)] | Chromosome 2, NC_000002.12 (199269500..199471266, complement) | GLSS | 608148 |
| ☐ Satb2<br>ID: 212712 | special AT-rich sequence binding protein 2 [Mus musculus (house mouse)] | Chromosome 1, NC_000067.6 (56793981..56980448, complement) | BAP002, mKIAA1034 | |
| ☐ Satb2<br>ID: 501145 | SATB homeobox 2 [Rattus norvegicus (Norway rat)] | Chromosome 9, NC_005108.4 (63456677..63642193, complement) | RGD1562369 | |
| ☐ satb2<br>ID: 563435 | SATB homeobox 2 [Danio rerio (zebrafish)] | Chromosome 9, NC_007120.7 (32556280..32615985, complement) | si:ch211-223c6.1 | |

Genomic

1. NG_016976.2 RefSeqGene

Range 5001..206767

Download GenBank, FASTA, Sequence Viewer (Graphics)

mRNA and Protein(s)

1. NM_001172509.2 → NP_001165980.1 DNA-binding protein SATB2

See identical proteins and their annotated locations for NP_001165980.1

Status: REVIEWED

| | |
|---|---|
| Description | Transcript Variant: This variant (1) represents the longest transcript. Variants 1, 2 and 3 encode the same protein. |
| Source sequence(s) | AC016746, AK056838 |
| Consensus CDS | CCDS2327.1 |
| UniProtKB/Swiss-Prot | Q9UPW6 |
| UniProtKB/TrEMBL | A0A024R3U8, B3KPQ8 |
| Related | ENSP00000401112.1, ENST00000417098.6 |

Conserved Domains (4) summary

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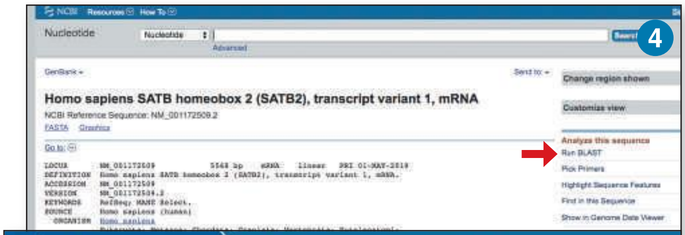
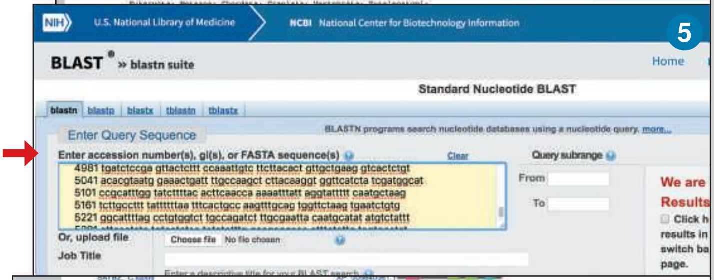
- Scroll back to the top of the page. On the right is the heading **Analyze this sequence** (image 4). Under this, click the heading **Run BLAST**. This opens a search box where you can compare the SATB2 sequence from the previous website to other sequences.
- Paste the SATB2 DNA sequence in your paste 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.
- 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.
- Once you are familiar with this process go back to the opening page **www.ncbi.nlm.nih.gov**. Find **HomoloGene** in the drop down menu beside the search box and click it. This is the homologous gene database. Type SATB2 in the search box and click **search**.
- A new page comparing the SATB2 proteins in other species appears (image 6). Under the heading **Protein alignments** is a pair of drop down boxes. Here you can compare any two species' SATB2 proteins.
- Compare humans and dogs (*Canis lupus familiaris*).
- Click **BLAST** under the drop down boxes. After a minute all the amino acids coded for by the SATB2 gene will appear compared as a query (what you are comparing to) and a subject (what is being compared). Any differences are shown in the middle line of text.


4

Homo sapiens SATB homeobox 2 (SATB2), transcript variant 1, mRNA

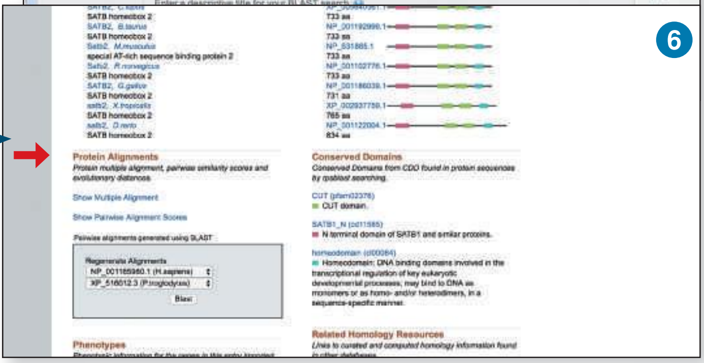
NCBI Reference Sequence: NM_001172509.2


5

BLASTN programs search nucleotide databases using a nucleotide query. more...

Enter accession number(s), gi(s), or FASTA sequence(s)

```
4981 tgatctccga gttactcttt ccaaattgtc ttcttacact gttgctgaag gtcactctgt
5041 acacgtaatg gaaactgatt ttgccaagct cttacaaggt ggttcatcta tcgatggcat
5101 ccgcatttgg tatcttttac acttcaacca aaaatttatt aggtattttt caatgctaag
5161 tcttgccttt tatttttaa tttcactgcc aagtttgcag tggttctaag tgaatctgtg
5221 ggcattttag cctgtggtct tgccagatct ttgcgaatta caatgcatat atgtctattt
```


6

| | |
|---|---|
| SATB homeobox 2 | 733 aa |
| SATB2, B.taurus | NP_001192999.1 |
| SATB homeobox 2 | 733 aa |
| Satb2, M.musculus | NP_631885.1 |
| special AT-rich sequence binding protein 2 | 733 aa |
| Satb2, R.norvegicus | NP_001102776.1 |
| SATB homeobox 2 | 733 aa |
| SATB2, G.gallus | NP_001186039.1 |
| SATB homeobox 2 | 731 aa |
| satb2, X.tropicalis | XP_002937759.1 |
| SATB homeobox 2 | 765 aa |
| satb2, D.rerio | NP_001122004.1 |
| SATB homeobox 2 | 834 aa |

Protein Alignments

*Protein multiple alignment, pairwise similarity scores and evolutionary distances*

Show Multiple Alignment

Show Pairwise Alignment Scores

Pairwise alignments generated using BLAST

Regenerate Alignments

NP_001165980.1 (H.sapiens)

XP_516012.3 (P.troglodytes)

Conserved Domains

*Conserved Domains from CDD found in protein sequences by rpsblast searching.*

CUT (pfam02376)

CUT domain.

SATB1_N (cd11585)

N-terminal domain of SATB1 and similar proteins.

homeodomain (cd00086)

Homeodomain; DNA binding domains involved in the transcriptional regulation of key eukaryotic developmental processes; may bind to DNA as monomers or as homo- and/or heterodimers, in a sequence-specific manner.

Related Homology Resources

*Links to curated and computed homology information found in other databases.*

Phenotypes

The steps above are a highly simplified step-through of the database. It is 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 wolf and human DNA begin to align?

   ________________________________________________

3. Using the Homologene search for the gene SATB2 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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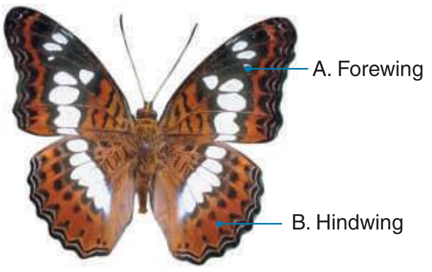
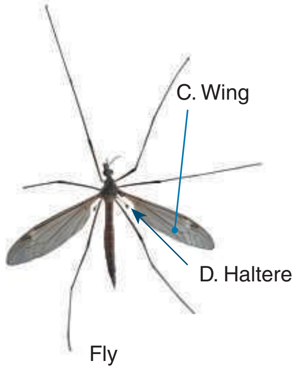
# 145 KEY TERMS AND IDEAS: Did You Get It?

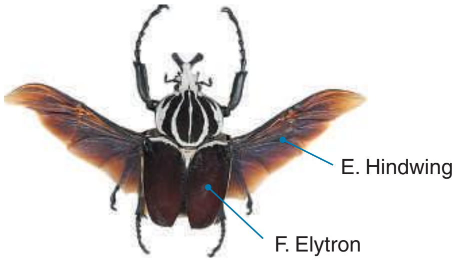
1. Insects are extremely adaptable and have a wide range of body forms. Consider the wing structure of the insects below:



Butterfly



Fly



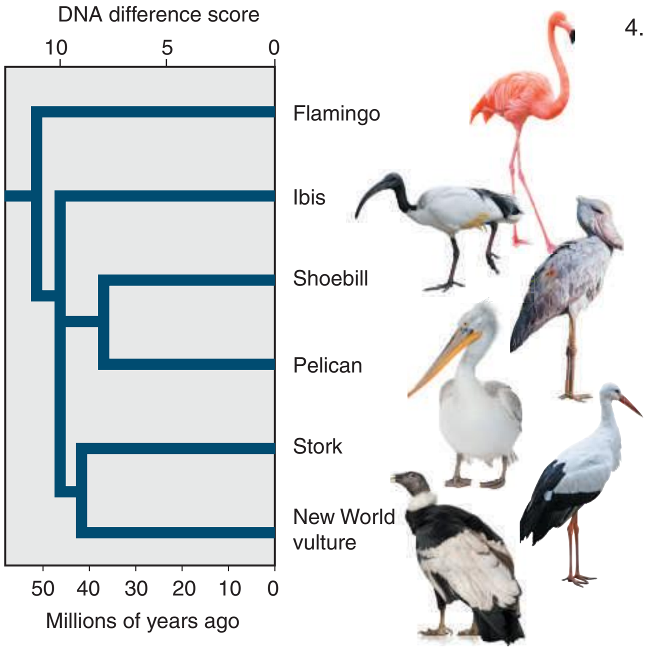
Beetle

   (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. How is the diversity of life linked to mass extinctions?



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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UNIT 4
Topic 2

# Natural Selection and Microevolution

### Key terms

adaptation
allele frequency
directional selection
disruptive selection
founder effect
gene flow
gene pool
genetic drift
genetic equilibrium
genotypic change
microevolution
mutation
natural selection
phenotypic change
stabilising selection

**Activity number**

## Natural selection and changes in gene pools

*Key skills and knowledge*

☐ 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. **146 147**

☐ 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. **147 148**

☐ 3 **PRAC** Use a computer simulation to analyse genotypic changes for a selective pressure in a gene pool. **148**

☐ 4 What is meant by an adaptation and what is 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).

☐ 5 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. **150-154**

☐ 6 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. **155**
- Antibiotic resistance in bacteria (including horizontal gene transmission)
- Pesticide resistance in insects

J. Podos

## Other processes in microevolution

*Key skills and knowledge*

☐ 7 Recall that natural selection, which has been our focus so far, is one just 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. **147**

☐ 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. You may include reference to the role of genetic drift. **156**

☐ 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. **157**

# 146 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.


#1

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.


#2

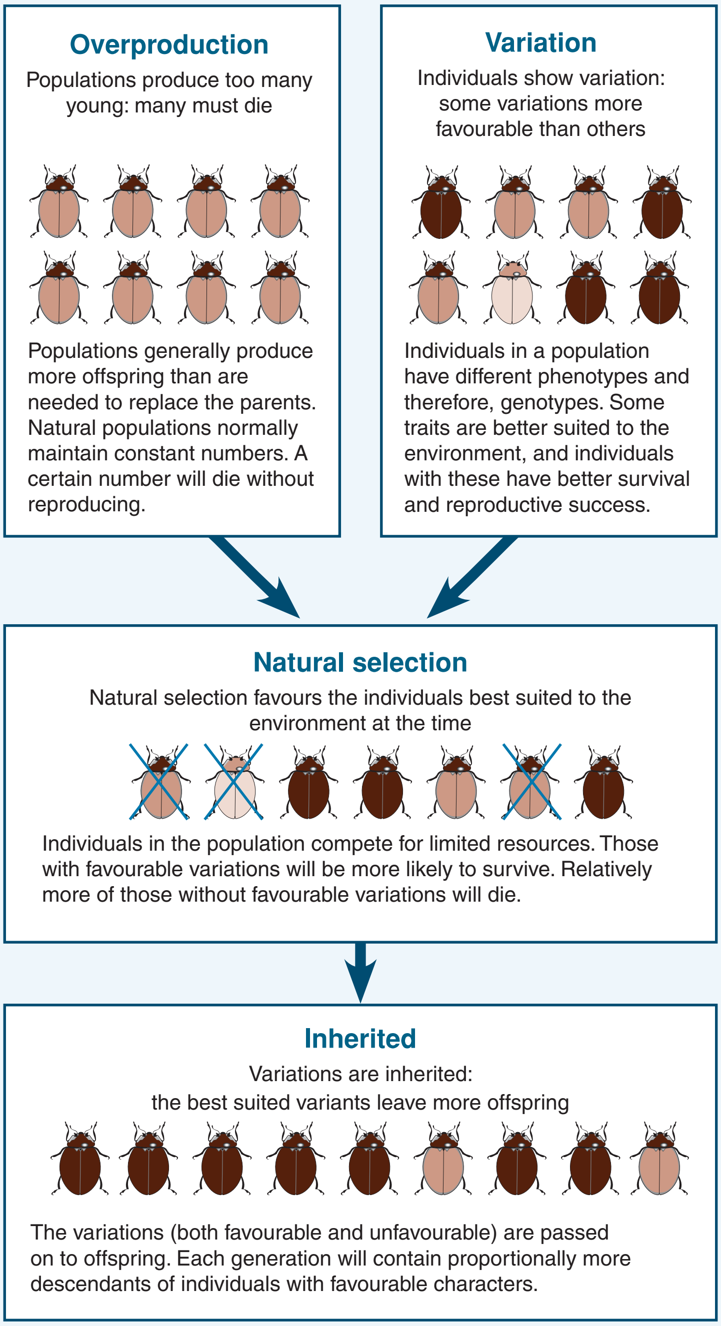
The blue candy becomes more common...


#3

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 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 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: ____________________

____________________

____________________

____________________

87 137

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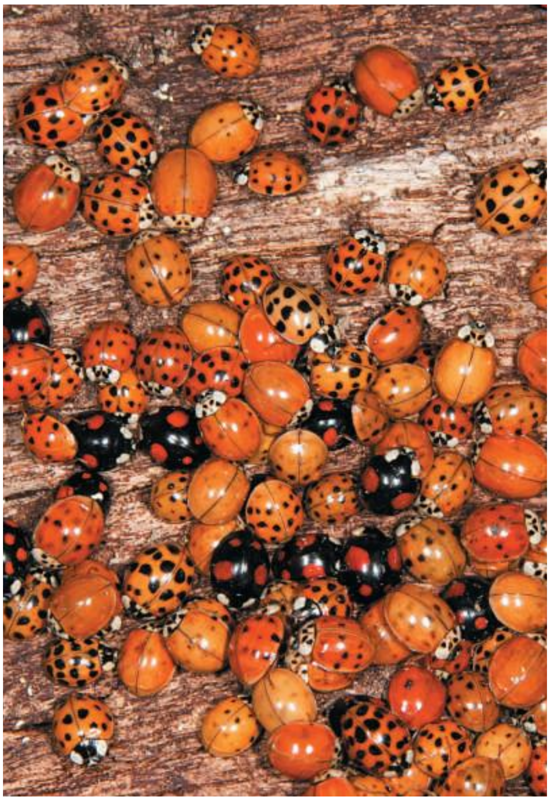
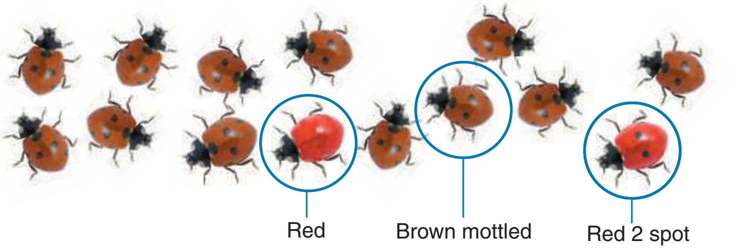
## Variation, selection, and population change



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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# 147 Microevolutionary Processes in Gene Pools

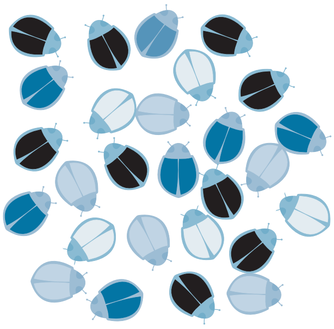
**Key Idea**: Mutations, gene flow, genetic drift, and natural selection all contribute to changes in the genetic makeup (frequency of different alleles) of a population.

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

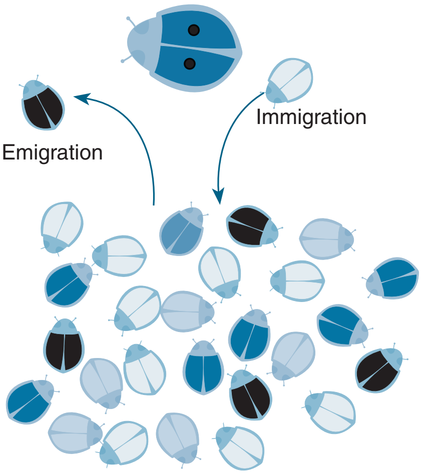
**Genetic variation** refers to the number of different types of alleles in a population. Genetic variation produces **phenotypic variation** (e.g. colour of ladybirds). It is this phenotypic variation that is the raw material for natural selection.

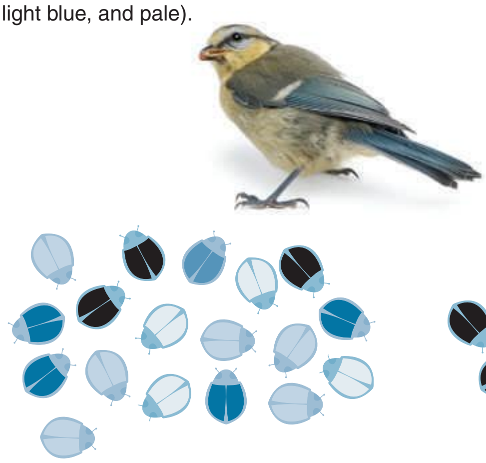
This ladybird population has five different phenotypes (black, dark blue, medium blue, light blue, and pale).

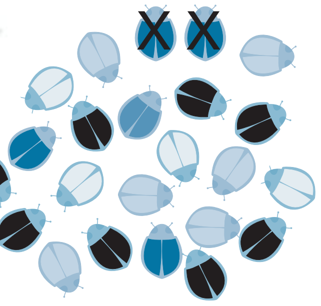


As we have seen in earlier activities, genetic variation arises through mutations and the recombination of alleles through sexual reproduction.

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 blue ladybirds are crushed than any other phenotype. The proportion of dark blue 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 lady birds have left and some very pale lady birds 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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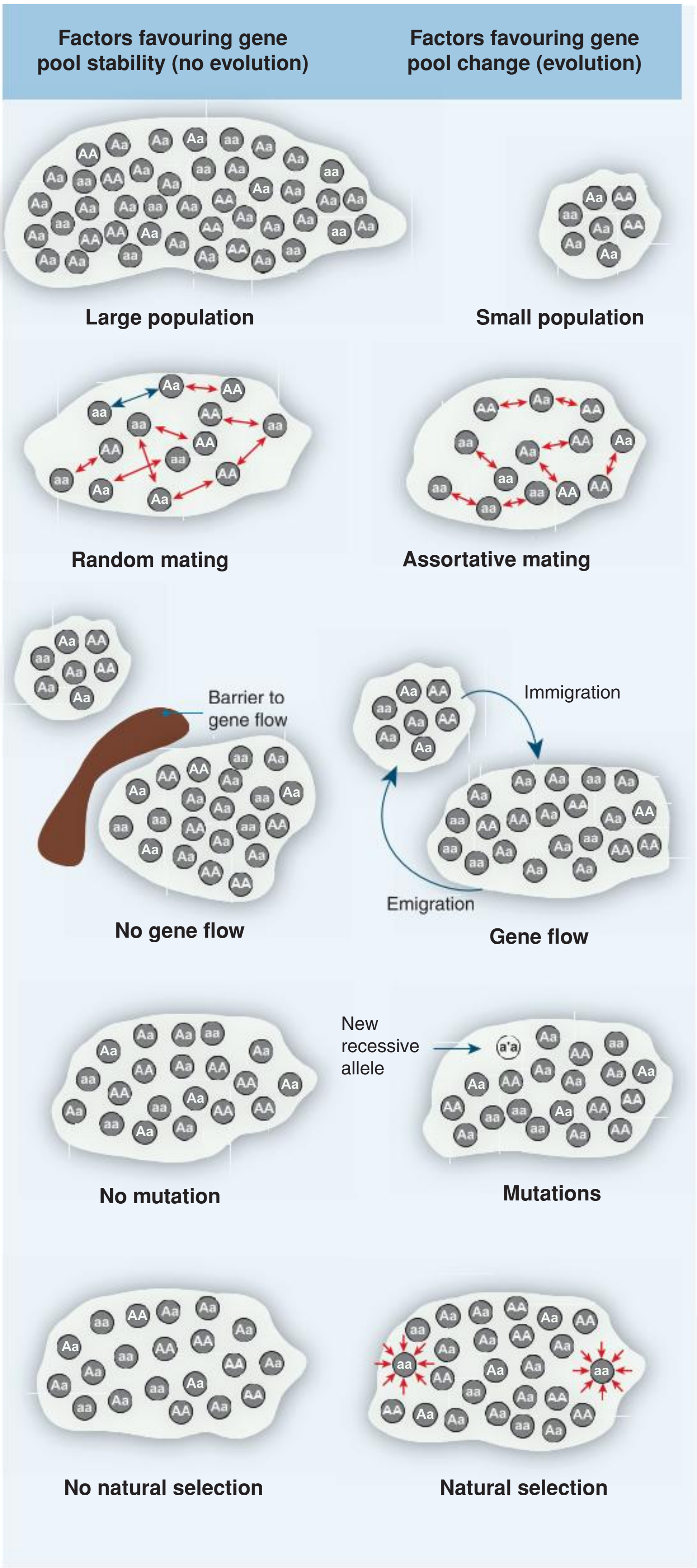
2. One of the important theoretical concepts in population genetics is that of **genetic equilibrium**, which states that "***for a large, randomly mating population, allele frequencies do not change from generation to generation***". If allele frequencies in a population are to remain unchanged, all 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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# 148 Changes in a Gene Pool

**Key Idea**: Natural selection and migration can alter the allele frequencies in gene pools.

The diagram below shows an 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 (black 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):

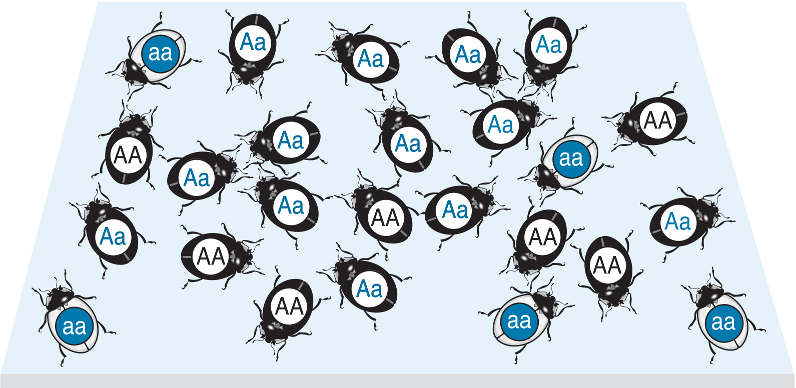
   (a) Count the number of A and a alleles separately. Enter the count into the top row of the table (left hand columns).
   (b) Count the number of each type of allele combination (AA, Aa and aa) in the gene pool. Enter the count into the top row of the table (right hand columns).
   (c) For each of the 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*

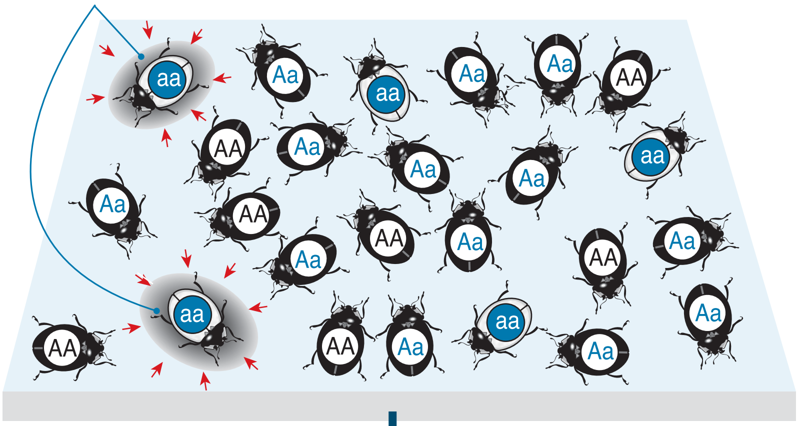


Two pale individuals died. Their alleles are removed from the gene pool.

### 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 white arrows) are not counted for allele frequencies; they are dead!



| | A | a | AA | Aa | aa |
|---|---|---|---|---|---|
| No. | | | | | |
| % | | | | | |

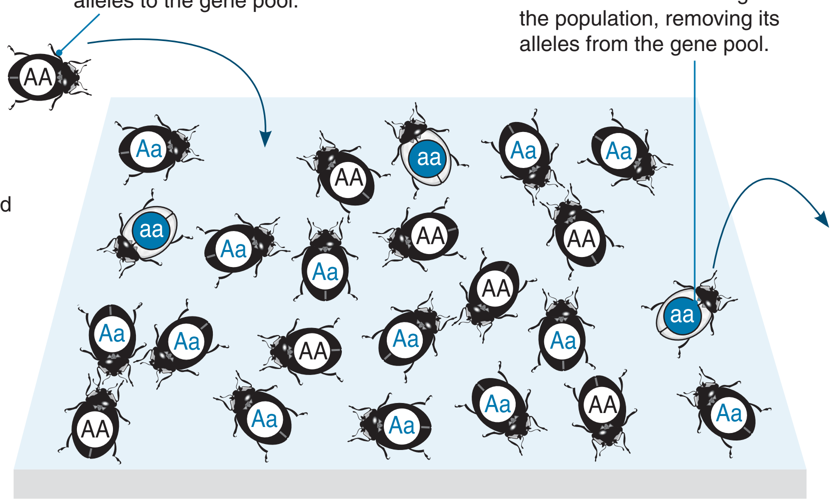
This individual is entering the population and will add its alleles to the gene pool.

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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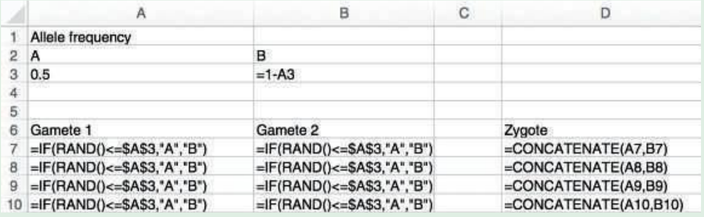
### MANDATORY PRACTICAL: Analyse genotypic changes for a selection pressure

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 157.

### 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. In cell **A1**, type the heading **Allele frequency.** Then in cell **A2** type the heading **A** and in cell **B2** type the heading **B**. These 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. In cell **A3**, type **0.5**. This is the frequency of the A allele in the population (generation 0). In cell **B3**, type the formula **=1-A3**. This is the frequency of the B allele in the population. In our initial population, 50% of the alleles will be A and 50% will be B (A and a in the population).
4. In cell **A6**, type the heading **Gamete 1** and **B6** type the heading **Gamete 2**. In the columns underneath we will use a formula to randomly produce A and B alleles from potential mates.
5. In cell **A7**, type the formula **=IF(RAND()<=$A$3,"A","B")**. This 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.
6. Copy the formula and paste it into cell **B7**. **Highlight** both cells **A7** and **B7** and **copy down** to **row 57** to produce 100 random gametes containing alleles.
7. You now need to unite the gametes to produce the zygote containing both alleles. In cell **D6**, type the heading **Zygote**. In cell **D7** enter the formula **=CONCATENATE(A7,B7)**. This takes the letters in cell A7 and B7 and puts them together in cell D7. **Highlight** the cell and **copy** this down to cell **D57**.



| | 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) |

8. At this point it is useful to test the spreadsheet so far. Click the **Calculate Now** button and you should see the gametes and zygotes change randomly. Continue clicking Calculate Now to produce more random gametes.
9. You now need to count up the number of AA, AB, and BB genotypes. In cell **F1** type the heading **AA**, in **G1** type **AB**, and in **H1** type **BB**. In cell **F2**, type the formula **=COUNTIF($D$7:$D$56,"AA")**. This counts all the AA genotypes in cells D7 to D57 and displays the number in F2. **Copy** the formula and paste it into **H2**. Change the **AA** in the formula to **BB**.
10. In cell **G2**, you need a formula that will look for and count the number of AB and BA genotypes. Enter the formula **=COUNTIF($D$7:$D$56,"AB")+COUNTIF($D$7:$D$56,"BA")**.
11. In cell **J1**, type the heading **Total Genotypes**. In cell **J2**, type the formula **=SUM(F2:H2)**. This adds all the genotypes together and produces a total. Click **Calculate Now** and the number 50 should appear. This provide a check that the rest of the spreadsheet is working as this number will always equal the number of zygotes produced in column D.

| | 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 | | | | | |

12. 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**.
13. In cell **F5**, type the formula **=(F2*2)+G2**. This adds up all the alleles from the AA genotype and the A alleles from the AB genotype. In cell **G5** type the formula **=(H2*2)+G2**. This adds up all the B alleles. In cell **I5** type the formula **=F5+G5**. This adds up all the alleles. Click **Calculate Now** and you should see the number 100 appear. This is expected because if there are 50 genotypes then 50 x 2 = 100 alleles.
14. You now need to calculate the frequency of As and Bs in Generation 1. In cell **F8**, type the heading **Frequency A** and in cell **G8** type the heading **Frequency B**. In Cell **I8**, type the heading **Frequency A + B**.

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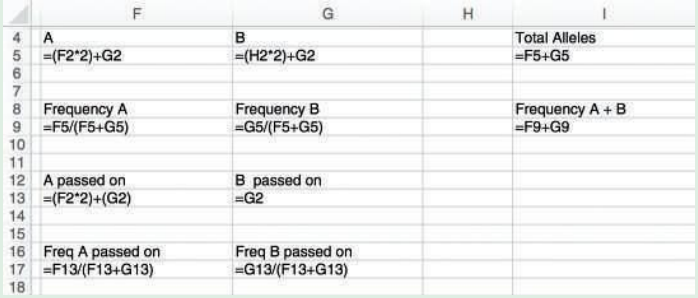
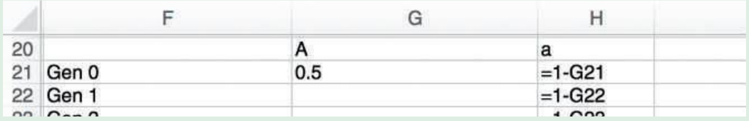


|  | F | G | H | I |
|---|---|---|---|---|
| 4 | A | B |  | Total Alleles |
| 5 | =(F2*2)+G2 | =(H2*2)+G2 |  | =F5+G5 |
| 6 |  |  |  |  |
| 7 |  |  |  |  |
| 8 | Frequency A | Frequency B |  | Frequency A + B |
| 9 | =F5/(F5+G5) | =G5/(F5+G5) |  | =F9+G9 |
| 10 |  |  |  |  |
| 11 |  |  |  |  |
| 12 | A passed on | B passed on |  |  |
| 13 | =(F2*2)+(G2) | =G2 |  |  |
| 14 |  |  |  |  |
| 15 |  |  |  |  |
| 16 | Freq A passed on | Freq B passed on |  |  |
| 17 | =F13/(F13+G13) | =G13/(F13+G13) |  |  |
| 18 |  |  |  |  |

15. In cell **F9**, type the formula **=F5/(F5+G5)** and in cell **G9**, type the formula **=G5/(F5+G5)**. These formulae simply divide the number of A or B alleles by the total number of A and B alleles. In cell **I9**, type the formula **=F9+G9**.
    Click **Calculate Now** and the number 1 should appear in I9 because the total frequency of alleles must always be 1.
16. Our **selection pressure** here will be 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. In cell **F12**, type the heading **A passed on** and in cell **G12** type the heading **B passed on**. In cell **F13**, type the formula **=(F2*2)+(G2)** and in cell **G13**, type the formula **=G2**. This calculates the number of alleles that will be passed on (excluding those in genotype BB).
17. In cell F16, type the heading **Freq A passed on** and in cell **G16** type the heading **Freq B passed on**. In cell **F17**, type the formula **=F13/(F13+G13)** and in **G17** type the formula **=G13/(F13+G13)**. This calculates the frequency of alleles that will be available to the next generation.
18. Finally you must keep a record of each generation's allele frequencies before mating (i.e. before BB is excluded). In cell **G20**, type the heading **A** and in cell **H20**, type the heading **a** (which has so far been represented by B in your spreadsheet).
19. In cell **F21** type **Gen 0**. This was your starting population Now highlight the cell and copy down to cell **F25** to get ten generations. In cell **G21**, type 0.5. In cell **H21**, type **=1-G21**. **Highlight H21** and copy it down to **H31**. 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.



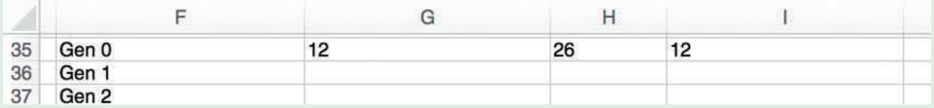
|  | F | G | H |
|---|---|---|---|
| 20 |  | A | a |
| 21 | Gen 0 | 0.5 | =1-G21 |
| 22 | Gen 1 |  | =1-G22 |

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 **G2** 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 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.

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**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.

**PART 4: Changing the number of aa genotypes that can breed**

1. What about if some of the aa genotype get to breed (i.e their fitness is not 0)? You can modify the spreadsheet to account for this. Instead of cell **G13** using just the number from the Aa genotype, you can add in a specific proportion of the aa genotype by entering the formula **=G2+((H2*2)*0.4)** into G13 (or you can use any other proportion of aa you want to pass to the next generation e.g. 0.7).
   This calculates the total number of aa alleles, then reduces the number by a predetermined proportion and adds to it to the a alleles from the genotype Aa.
2. Produce ten generations of alleles starting at frequencies of 0.5 for each allele A and a as in part 2. Produce graphs for allele frequencies and genotypes as in part 3 print them and attach them to this page.

2. (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) What difference occurs when some of the aa genotype is able to pass a proportion of alleles to the next generation?

(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)?

3. Imagine a change happens in the environment so that now the dominant phenotype instead of the recessive phenotype is excluded from breeding. What would happen to the proportion and A and a alleles in the population (assuming the aa hadn't become extinct before then)?

4. Describe a situation or situations where this kind of selection occurs in the real world and what the effect of the selection could be:

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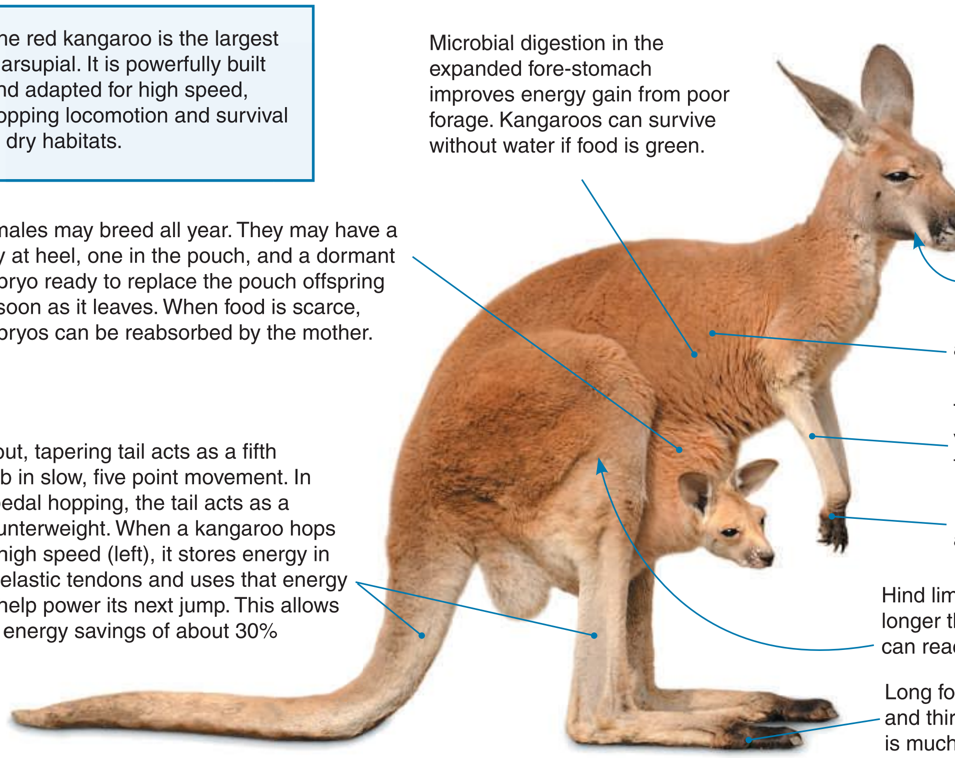
# 149 Adaptation and Fitness

**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 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:

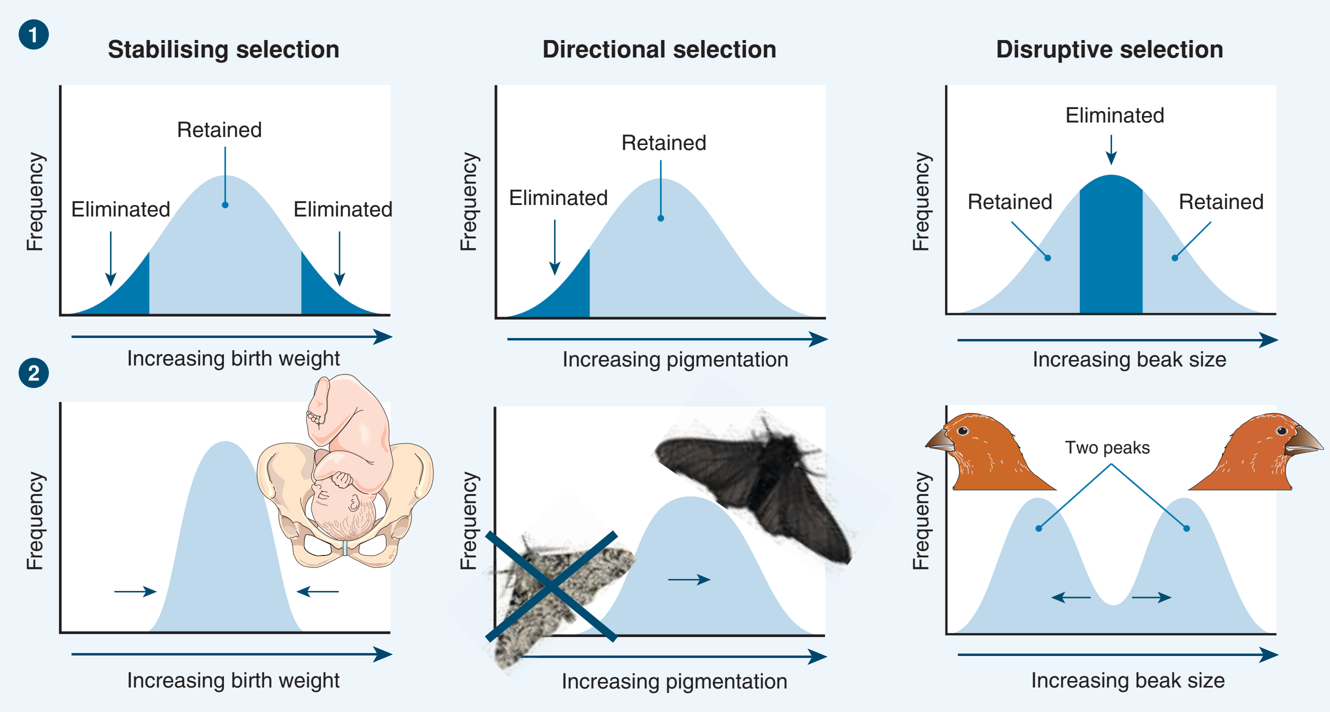
Paste cc 3.0

**ISBN: 978-1-927309-86-5**

# 150 Types of Natural Selection

**Key Idea**: Natural selection is responsible for the differential survival of some phenotypes (and genotypes) over others. It is an important cause of genetic change in populations.

Natural selection operates on the phenotypes of individuals, produced by their particular combinations of alleles. It results in the differential survival of some phenotypes over others. As a result, organisms with phenotypes most suited to the environment at the time are more likely to survive and breed than those phenotypes that are less suited. Favourable phenotypes will become relatively more numerous and than unfavourable phenotypes. Over time, natural selection may lead to a permanent change in the genetic makeup of a population. Natural selection is always linked to phenotypic suitability in the prevailing environment so it is a dynamic process. It may favour existing phenotypes or shift the phenotypic median, as is shown below. The top row of diagrams below represents the population phenotypic spread before selection, and the bottom row the spread afterwards.



Extreme variations are selected against and the middle range (most common) phenotypes are retained in greater numbers. Stabilising selection results in decreased variation for the phenotypic character involved. This type of 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. Stabilising selection predominates when environments are stable.

The adaptive phenotype is shifted in one direction and one phenotype is favoured over others. 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. Selection will be directional when there is a trend in environmental conditions, e.g. warm to cold.

Disruptive selection favours two phenotypic extremes at the expense of intermediate forms. During a prolonged drought on Santa Cruz Island in the Galápagos, it 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. Disruptive selection may occur when environments or resources are fluctuating or distinctly divergent.

1. Define the following, including a statement about the type of environment that favours each:

   (a) Stabilising selection: ____________________

   (b) Directional selection: ____________________

   (c) Disruptive selection: ____________________

2. Explain why fluctuating (as opposed to stable) environments favour disruptive (diversifying) selection: ____________________

**ISBN: 978-1-927309-86-5**

# 151 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.

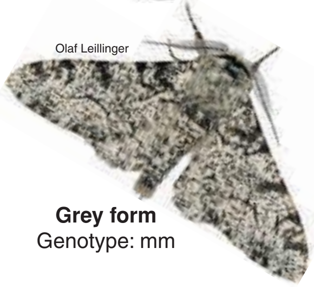
Genetically determined melanism is a common polymorphism in animals (meaning different forms exist in the population). In the **peppered moth** (*Biston betularia*) during the Industrial Revolution, selection favoured the proliferation of dark (melanic) forms over the pale (non-melanic) forms. Intensive 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**).

Olaf Leillinger

**Melanic form**
Genotype: MM or 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.

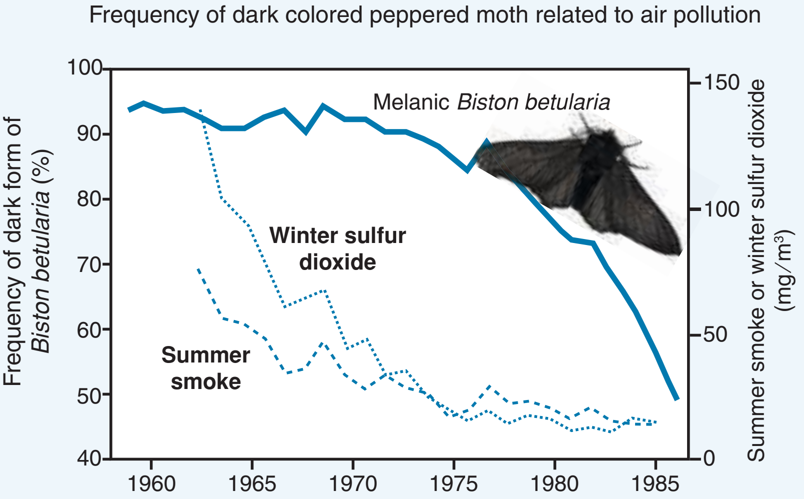


Olaf Leillinger

**Grey form**
Genotype: mm

**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. 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).



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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# 152 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 beaks 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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# 153 Disruptive Selection in Darwin's Finches

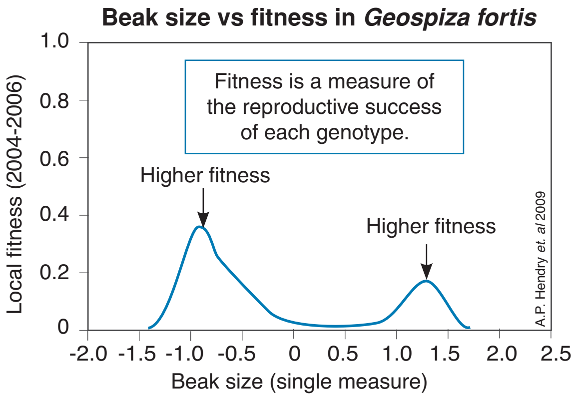
**Key Idea**: Disruptive selection in the finch *Geospiza fortis* produces a bimodal distribution for beak size.

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.



Fitness is a measure of the reproductive success of each genotype.

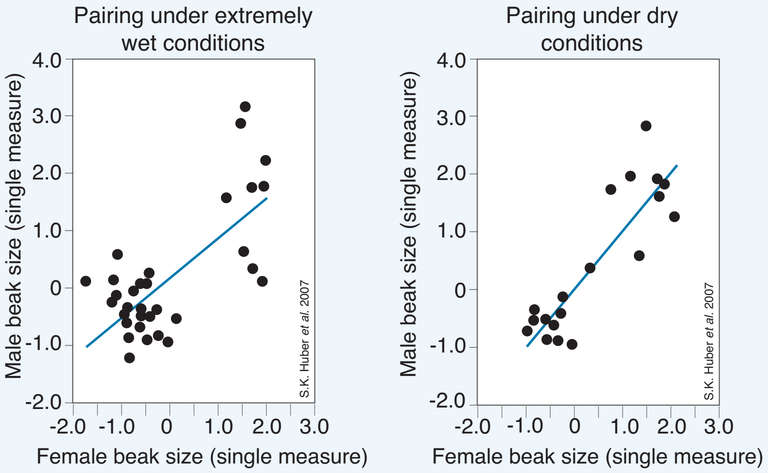
A.P. Hendry *et. al* 2009

*Fitness showed a bimodal distribution (arrowed) being highest for smaller and larger beak sizes.*

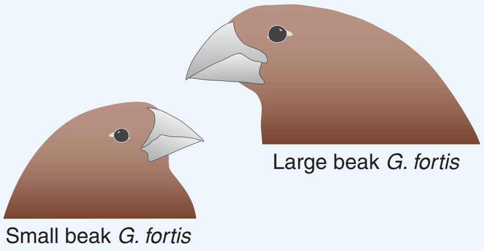
Measurements of the beak length, width, and depth were combined into one **single measure**.

Jeff Podos

**Beak size pairing in *Geospiza fortis***



S.K. Huber *et al.* 2007



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? (delete one)

   (b) Give reasons for your answer: ____________________

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# 154 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.

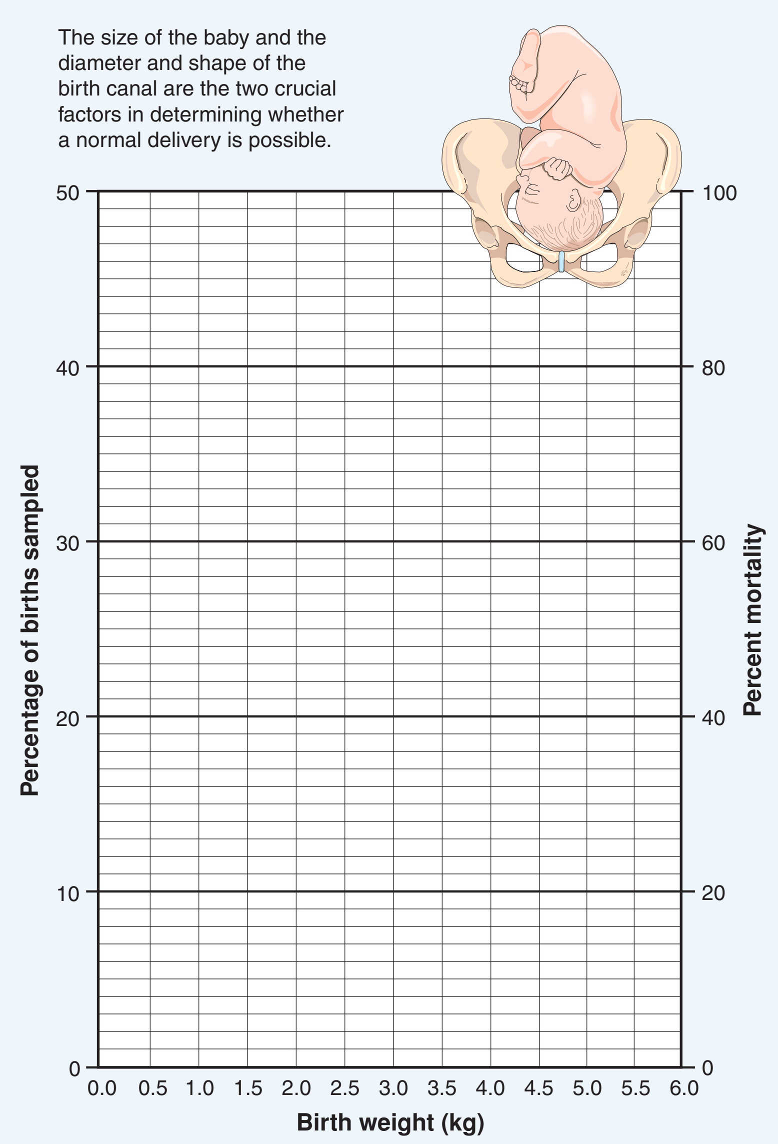
**Step 1**: For this activity, you will need a sample of 100 birth weights. You can search birth records online or use the data provided in the appendix at the back of this book.

**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 |



The size of the baby and the diameter and shape of the birth canal are the two crucial factors in determining whether a normal delivery is possible.

**DID YOU KNOW?**

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 narrow pelves 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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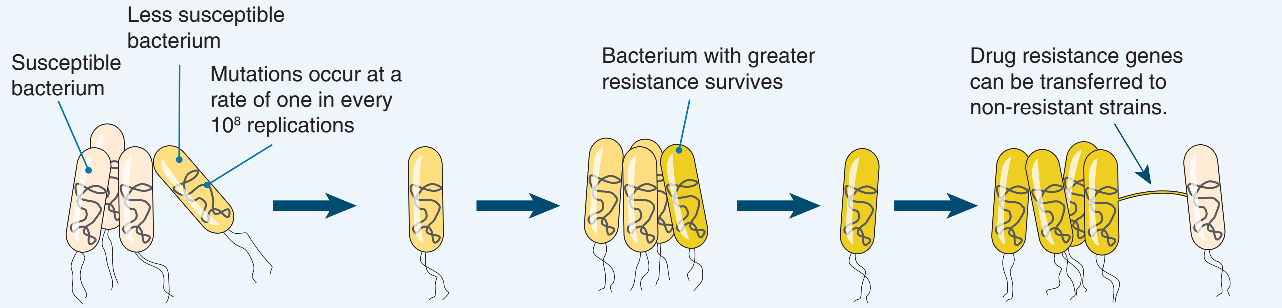
# 155 Modern Drivers in Evolution

**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.

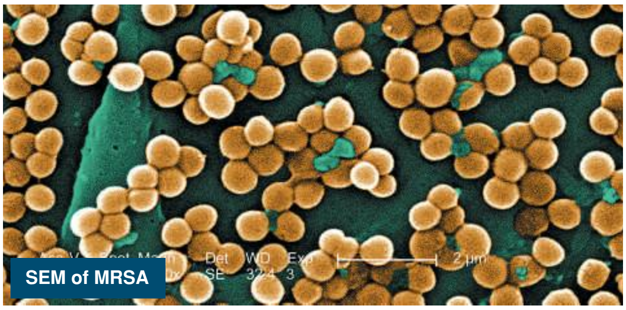


Any population, including bacterial populations, includes variants with unusual traits, in this case reduced sensitivity to an antibiotic. These variants arise as a result of mutations in the bacterial chromosome.

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.

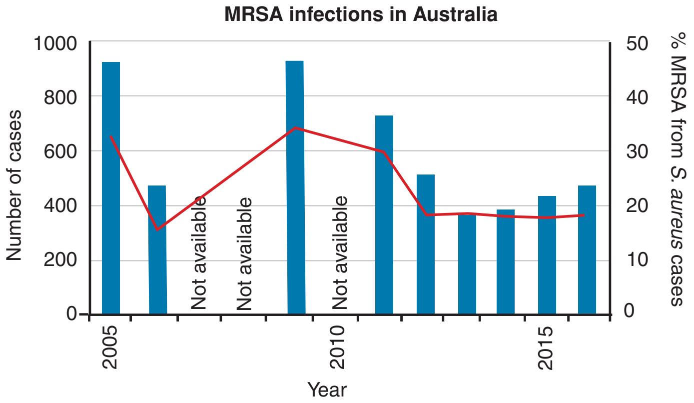
If the amount of antibiotic delivered is too low, or the course of antibiotics is not completed, a population of resistant bacteria develops. Within this population too, there will be variation in susceptibility. Some will survive higher antibiotic levels than others.

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.



CDC

*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.



In Australia MRSA cases have remained relatively steady since 2012. Greater reporting measures and cleaning standards have reduced the number of cases since the early 2000s.

1. Describe how resistance develops in a population: ______________________________

______________________________

______________________________

______________________________

2. How can antibiotic resistance be transferred between strains of bacteria? ______________________________

______________________________

______________________________

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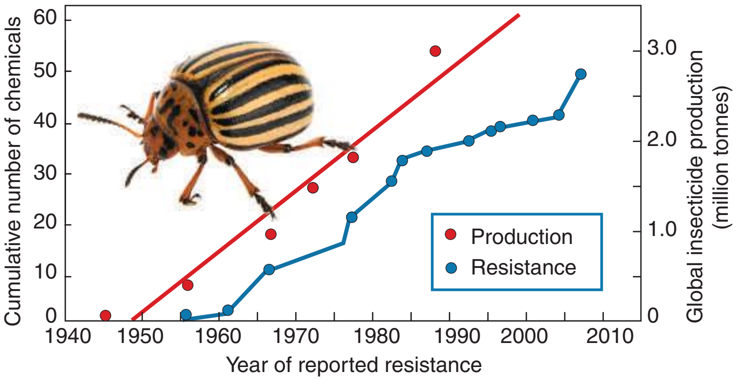
ISBN: 978-1-927309-86-5

## 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.

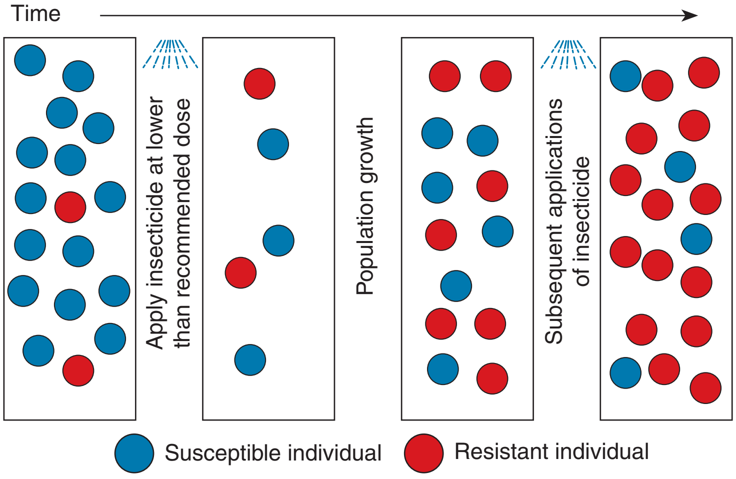


The Colorado potato beetle is a major potato pest that was originally found living on buffalo-bur (*Solanum rostratum* ) in the Rocky mountains. Since synthetic insecticides began to be produced, it has become resistant to more than 50 different types.

## 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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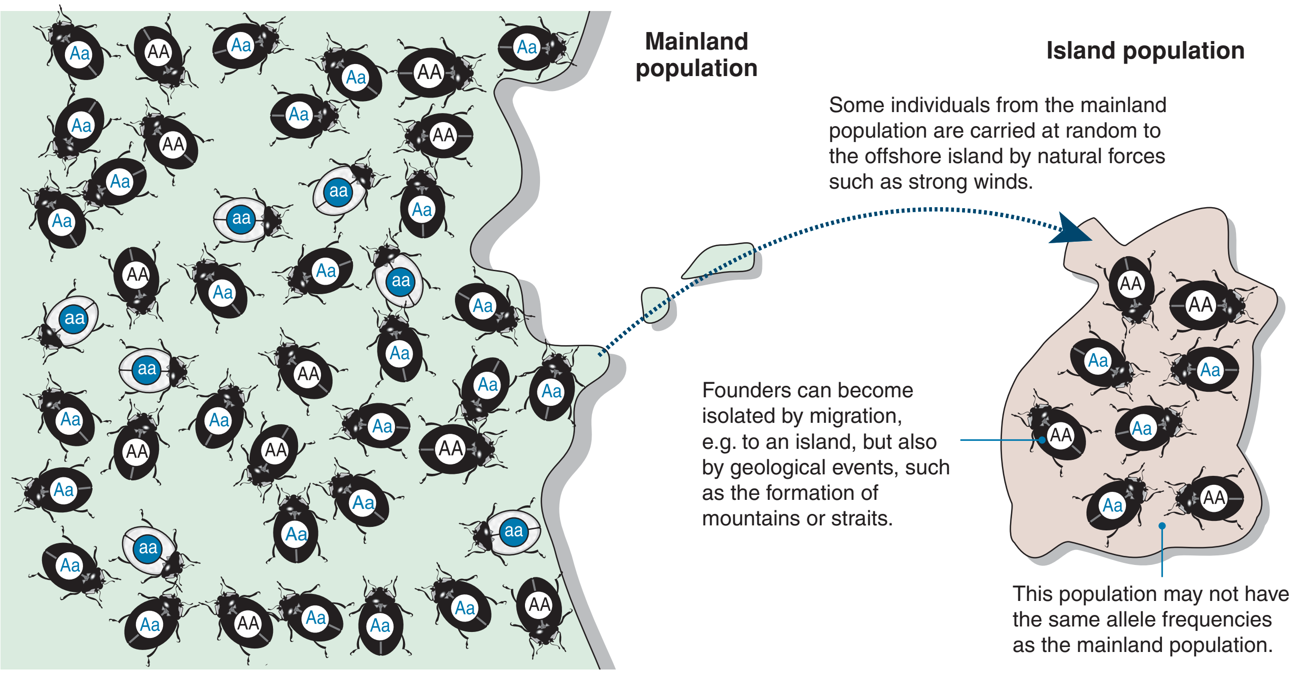
# 156 The Founder Effect

**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**

**Island population**

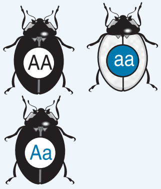
Some individuals from the mainland population are carried at random to the offshore island by natural forces such as strong winds.

Founders can become isolated by migration, e.g. to an island, but also by geological events, such as the formation of mountains or straits.

This population may not have the same allele frequencies as the mainland population.

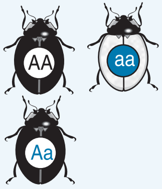
## Mainland population

| | Allele frequencies | | Phenotype frequencies | |
|---|---|---|---|---|
| | Actual numbers | Calculate % | Black | Pale |
| **Allele A** | | | | |
| **Allele a** | | | | |
| Total | | | | |



## Colonising island population

| | Allele frequencies | | Phenotype frequencies | |
|---|---|---|---|---|
| | Actual numbers | Calculate % | Black | 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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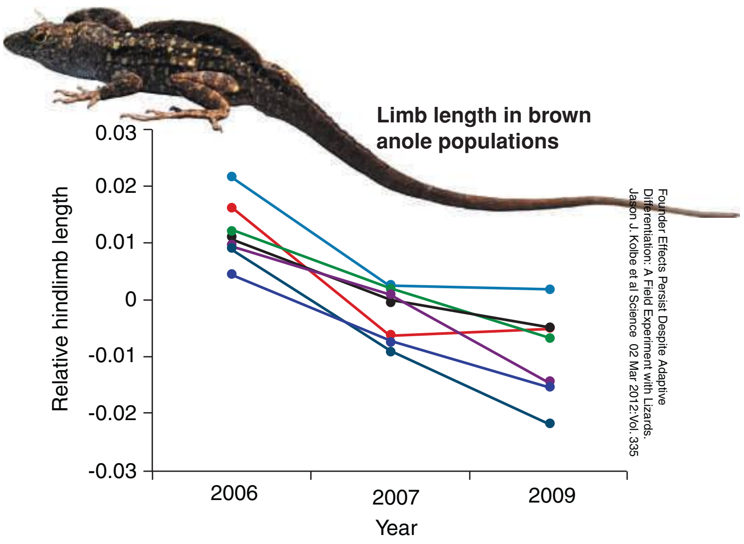
## Founder effect in brown anole lizards

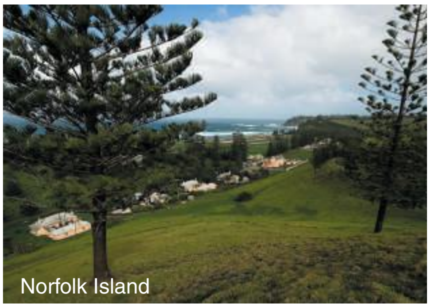
- In 2004 Hurricane Francis wiped out the brown anole lizard (*Anolis sagrei*) populations on several cays (small sandy islands) around the Bahamas. Scientists used this as a chance to study the founder effect. They took pairs of lizards from the mainland and placed them on different cays.
- The vegetation 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 Effects Persist Despite Adaptive Differentiation: A Field Experiment with Lizards. Jason J. Kolbe et al Science 02 Mar 2012:Vol. 335

## Founder effect in human populations

thinboyfatter CC 2.0



Brian Gratwicke 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.

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. From 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 Cunha?

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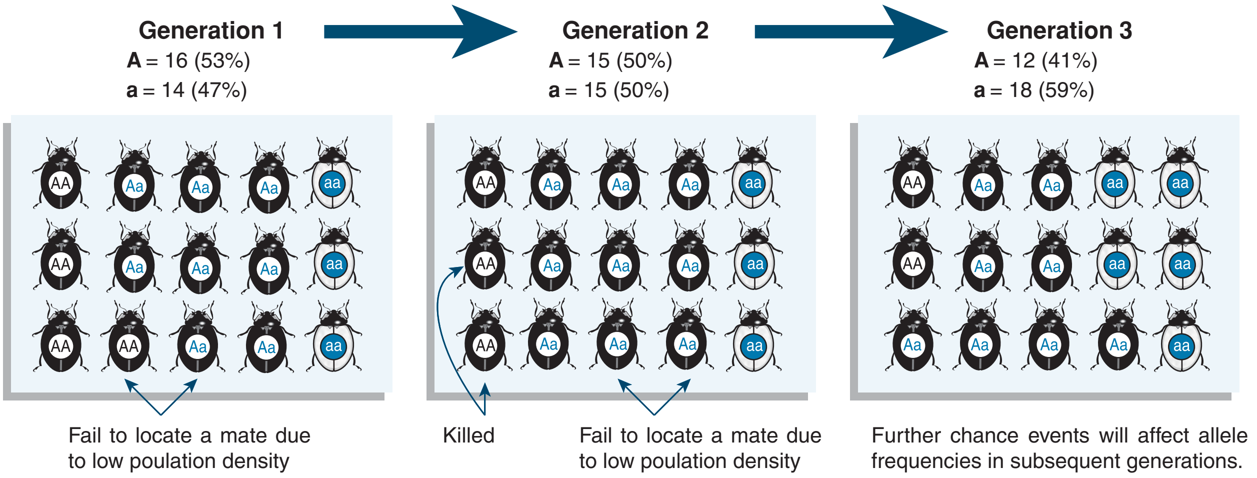
# 157 Genetic Drift

**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**. In a small population, its effects on the gene pool are more pronounced (a consequence of sampling error). Alleles may become **lost** from the gene pool altogether (frequency = 0%) or **fixed** as the only allele present for the gene (frequency = 100%).

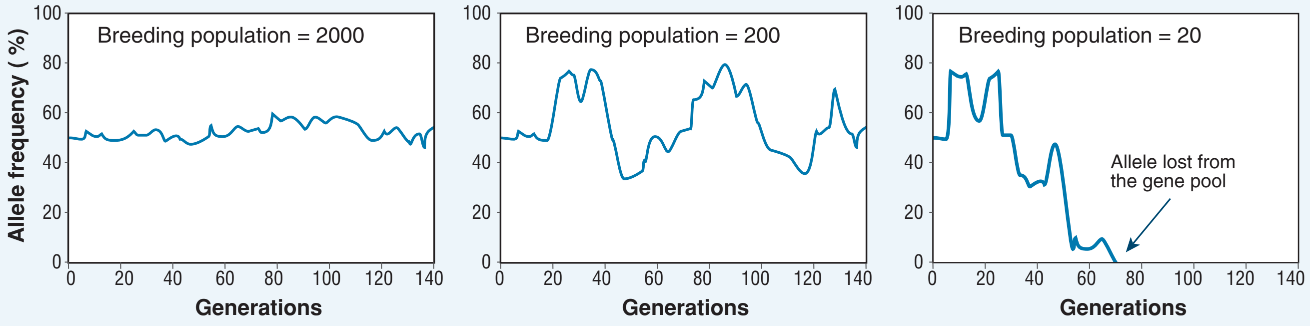
*The genetic makeup (allele frequencies) of the population changes randomly over a period of time*



This diagram shows the gene pool of a hypothetical small population over three generations. For various reasons, not all individuals contribute alleles to the next generation. With the random loss of the alleles carried by these individuals, the allele frequency changes from one generation to the next. The change in frequency is directionless as there is no selecting force. The allele combinations for each successive generation are determined by how many alleles of each type are passed on from the preceding one.

### Computer simulation of genetic drift

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%).

1. What is genetic drift? ______________________________

______________________________

2. 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:

______________________________

______________________________

______________________________

______________________________

**ISBN: 978-1-927309-86-5**

## 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 animals are likely to have low resistance to new diseases and environmental change.

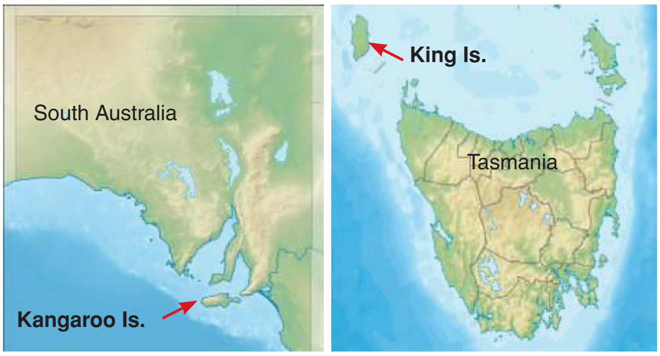
The study found that populations on the Australian mainland and in Tasmania have high levels of genetic diversity within their populations, with 57 DZB alleles identified in 70 individuals. However platypuses on King Island and Kangaroo Island (see maps), had very low levels of genetic diversity. For 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. 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.


Platypus, Tasmanian mainland

Klaus cc 2.0



Tentotwo cc 3.0

Nzeemin cc 3.0

Source: Diversity at the Major Histocompatibility Complex Class II in he Platypus, *Ornithorhynchus anatinus* Mette Lillie *et. al.* Journal of Heredity 2012:103(4):467–478

### COMPUTER SIMULATION: Modelling genetic drift

You can use the spreadsheet you made in Activity 148 to investigate the effect of population size on allele frequency changes due genetic drift. 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). **Attach all the graphs you plot to this page**.

1. 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. In cell **G13**, change the formula to **=(H2*2*RAND())+(G2*RAND())**. This randomly selects B alleles.
2. 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 ten generations.
3. 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. 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.
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 ten generations. Note Gen 0 AA = 5, Aa = 10 and aa = 5.
5. 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.
6. 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 ten generations. Note Gen 0 AA = 25, Aa = 50 and aa = 25.

3. (a) What factors have contributed to the low genetic diversity of the platypus populations on King Island and Kangaroo Island and explain their effect(s)?

(b) Why would genetic drift have more impact on the genetic diversity of these populations than those on the mainland?

# 158 KEY TERMS AND IDEAS: Did You Get it?

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

founder effect

gene pool

genetic drift

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:

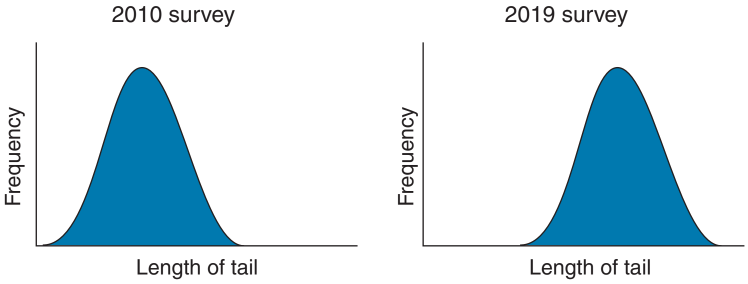
(c) Natural selection:

(d) Genetic drift:

3. Study the graphs below right.

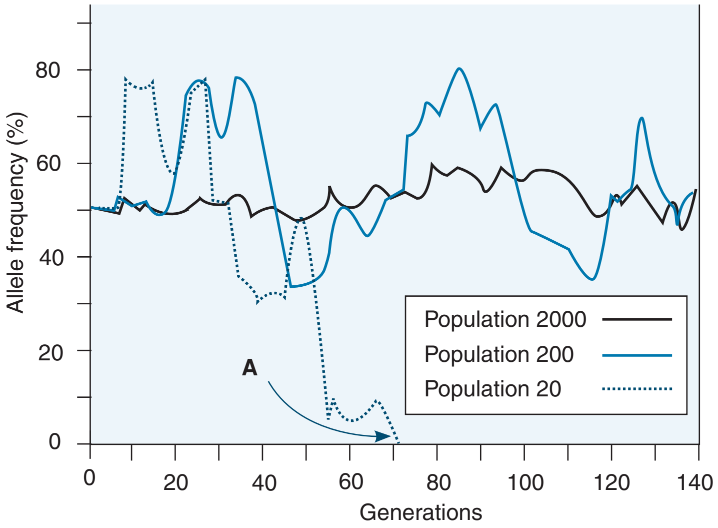
(a) What kind of selection is occurring?

(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?

UNIT 4
Topic 2

# Speciation and Macroevolution

### 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

Activity number

## Macroevolutionary patterns

*Key skills and knowledge*

☐ 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: **159**
- divergent evolution (including radiations)
- convergent evolution (including analogous structures)
- parallel evolution (including the significance of degree of relatedness)
- coevolution

☐ 2 Understand that the pace of macroevolutionary change can vary, as described by the punctuated equilibrium and the phyletic gradualism models. **159 168**

☐ 3 Recognise and describe examples of divergent evolution, including evolutionary radiations such as the adaptive radiation of the mammals. What distinguishes adaptive radiation from other types of evolutionary divergence? **160 - 162**

☐ 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). **163**

☐ 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. **164**

☐ 6 Recognise and describe examples of coevolution, including between competitors, plants and their pollinators, predators and prey, and hosts and parasites. **165**

Mike Lehmann cc3.0

## Patterns of speciation

*Key skills and knowledge*

☐ 7 Identify the different mechanisms of isolation that operate to restrict or stop gene flow between populations, prior to and after, speciation events. These include geographic isolation (including habitat fragmentation) and reproductive isolation. **166 - 169 174**

☐ 8 In more detail than above, 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 mechanisms prior to reproductive isolation (which is part of the species biology). **166 169**

☐ 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. **167**

☐ 10 Identify and describe different modes of speciation: allopatric, sympatric, and parapatric. Interpret data from different populations as evidence for speciation. **168 - 172**

☐ 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 describe some examples. **173**

☐ 12 ***SHE*** Explain the importance of minimum reserve size and minimum population size for target conservation species. How is such information applied? **175**

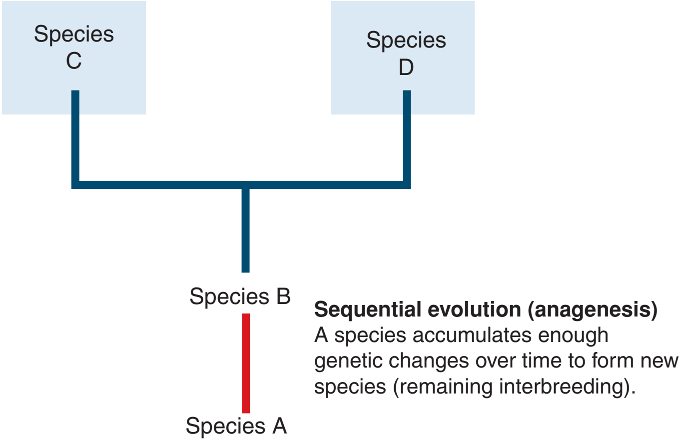
☐ 13 ***SHE*** Explain how technology, e.g. in agriculture and medicine, has influenced (and continues to influence) human evolution. **176**

# 159 Patterns of Evolution

**Key Idea**: Populations moving into a new environment may follow particular patterns of evolution.

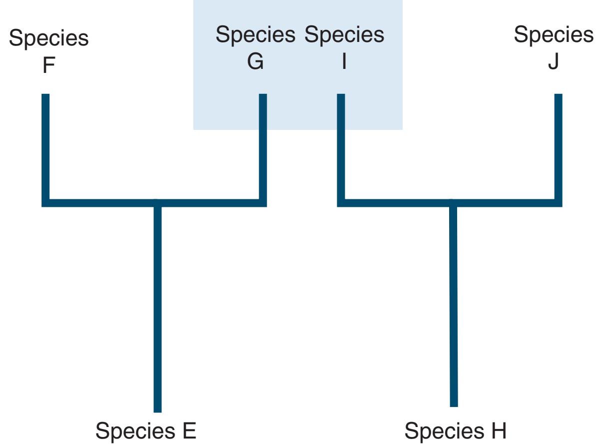
The diversification of one species into one or more separate species can follow one of four main patterns. **Divergent evolution** occurs when two species diverge from a common ancestor. Divergence is common in evolution and responsible for evolutionary radiations. When unrelated species evolve similar 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*).

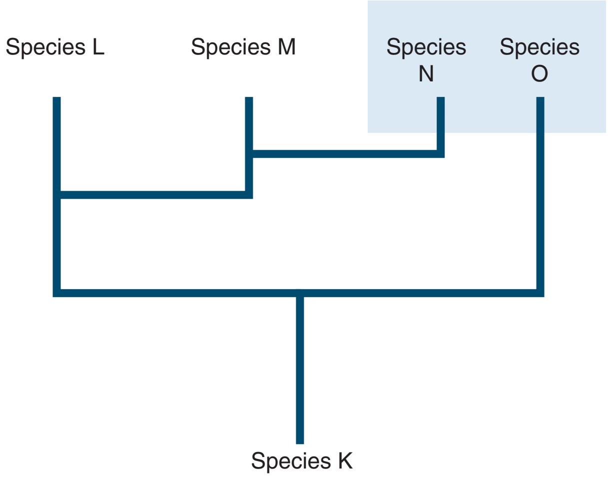


**Sequential evolution (anagenesis)**
A species accumulates enough genetic changes over time to form new species (remaining interbreeding).

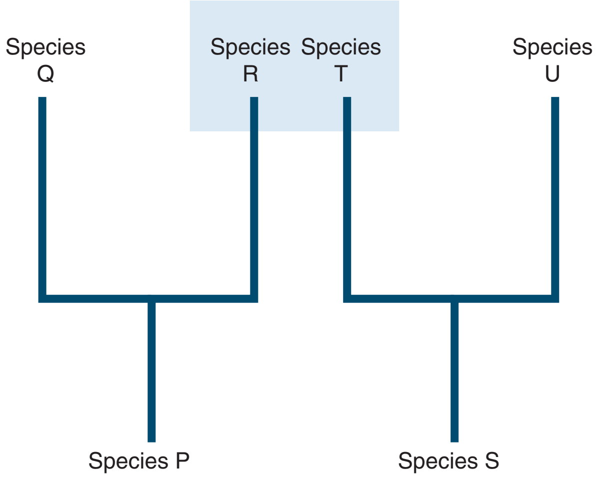
**Convergent evolution**. Unrelated or distantly related species in similar environments and under similar selection pressures evolve similar features, e.g. streamlined swimming form in aquatic birds and mammals.



**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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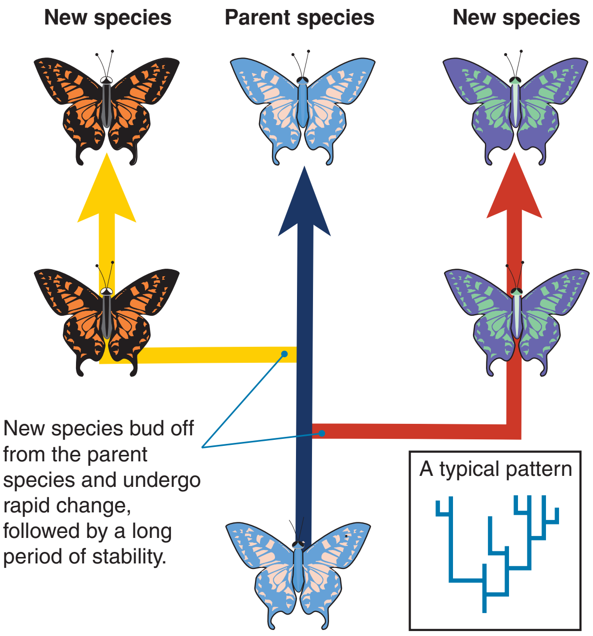
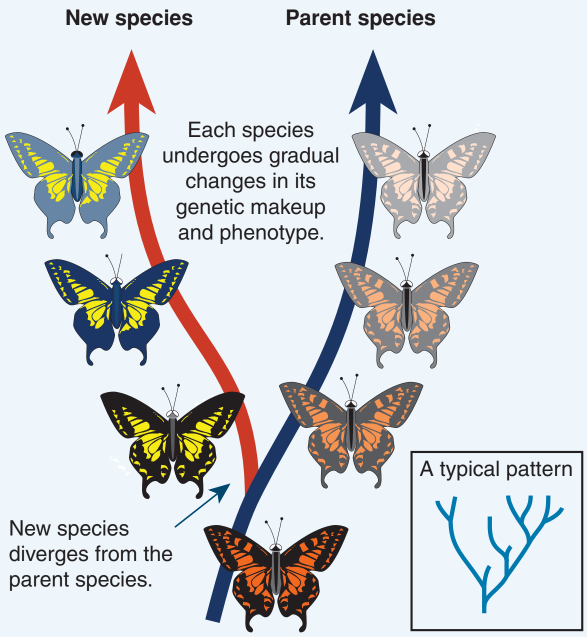
There are two basic models for the pace of evolutionary change: phyletic gradualism and punctuated equilibrium. It is likely that both mechanisms operate at different times and in different situations. Interpretations of the fossil record vary depending on the time scales involved. During its formative 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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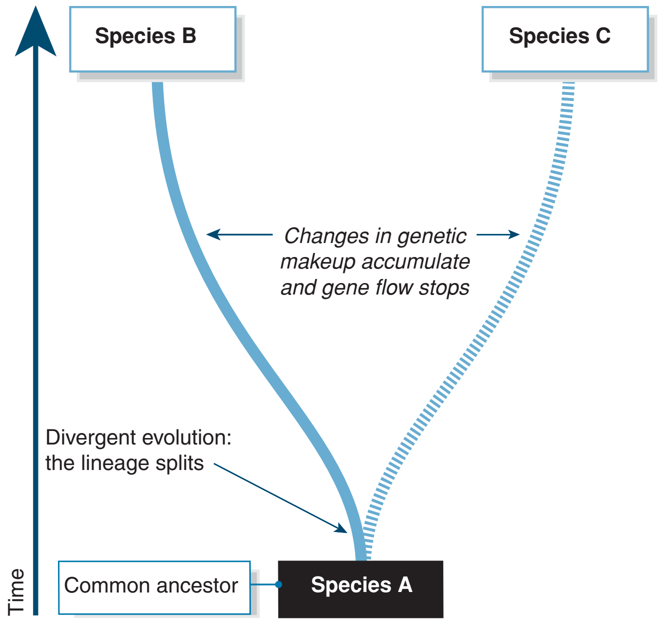
# 160 Divergence is an Evolutionary Pattern

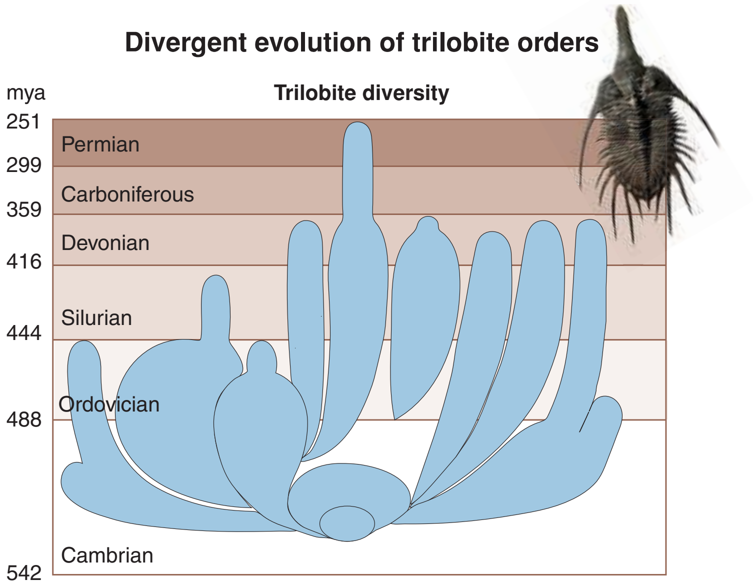
**Key Idea**: Divergent evolution describes the accumulation of differences between initially more similar lineages so that new species arise from a common ancestor.

**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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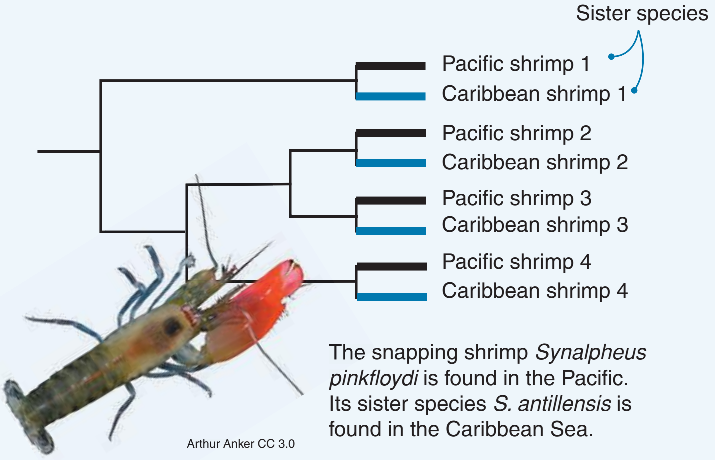
## Divergent evolution: snapping shrimp

- 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.



Arthur Anker CC 3.0

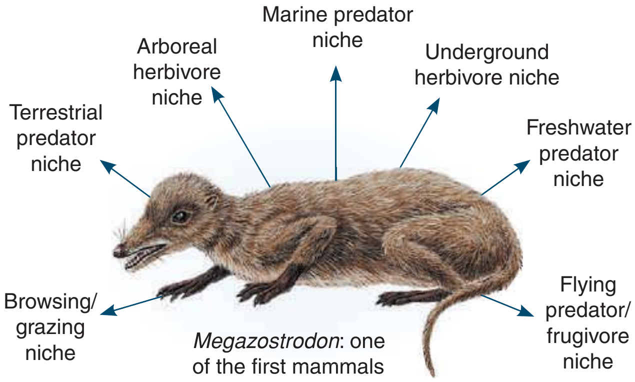
The snapping shrimp *Synalpheus pinkfloydi* is found in the Pacific. Its sister species *S. antillensis* is found in the Caribbean Sea.

## 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.



*Megazostrodon*: one of the first mammals

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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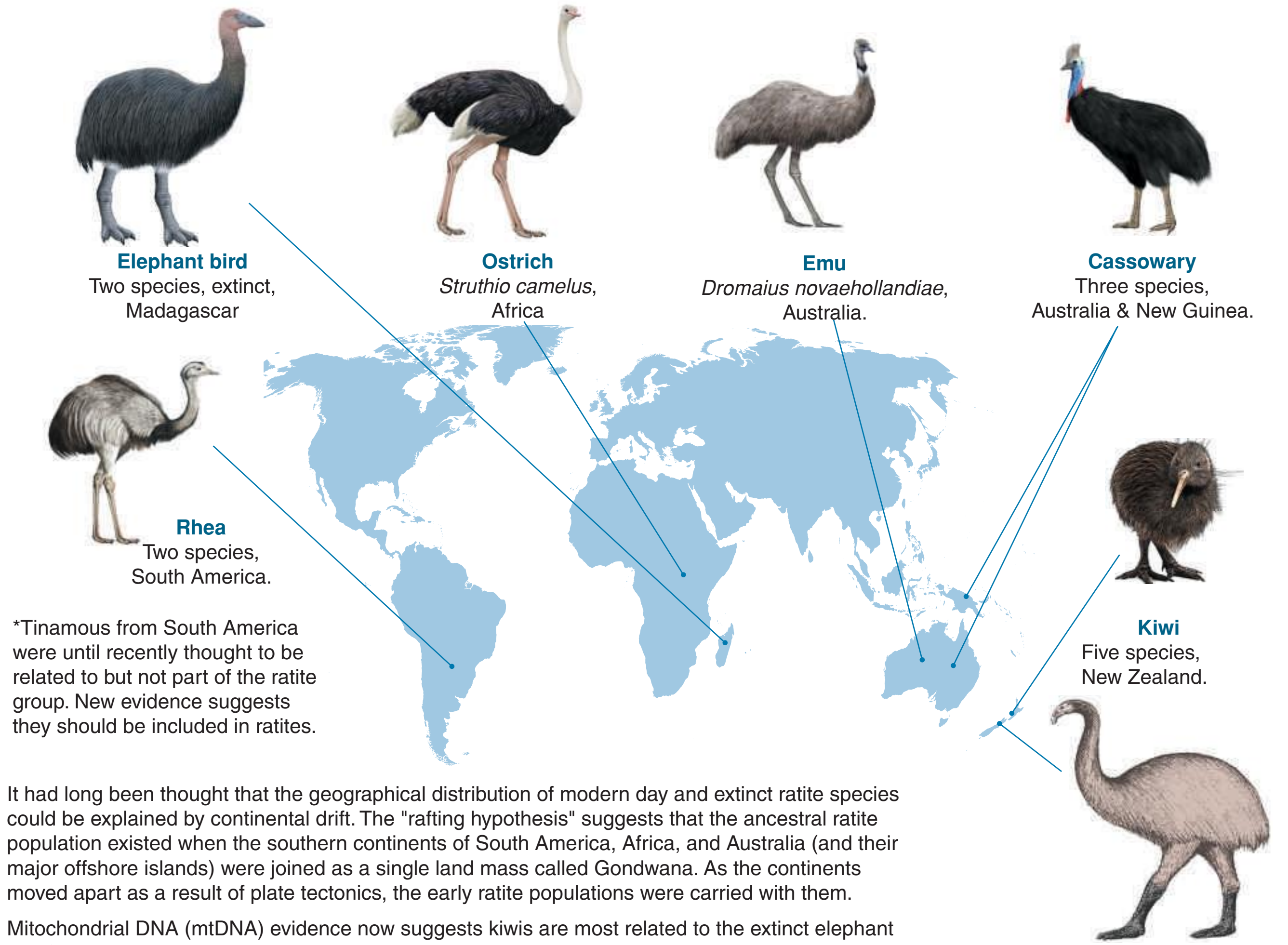
# 161 Divergent Evolution in Ratites

**Key Idea**: The ratites are 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.



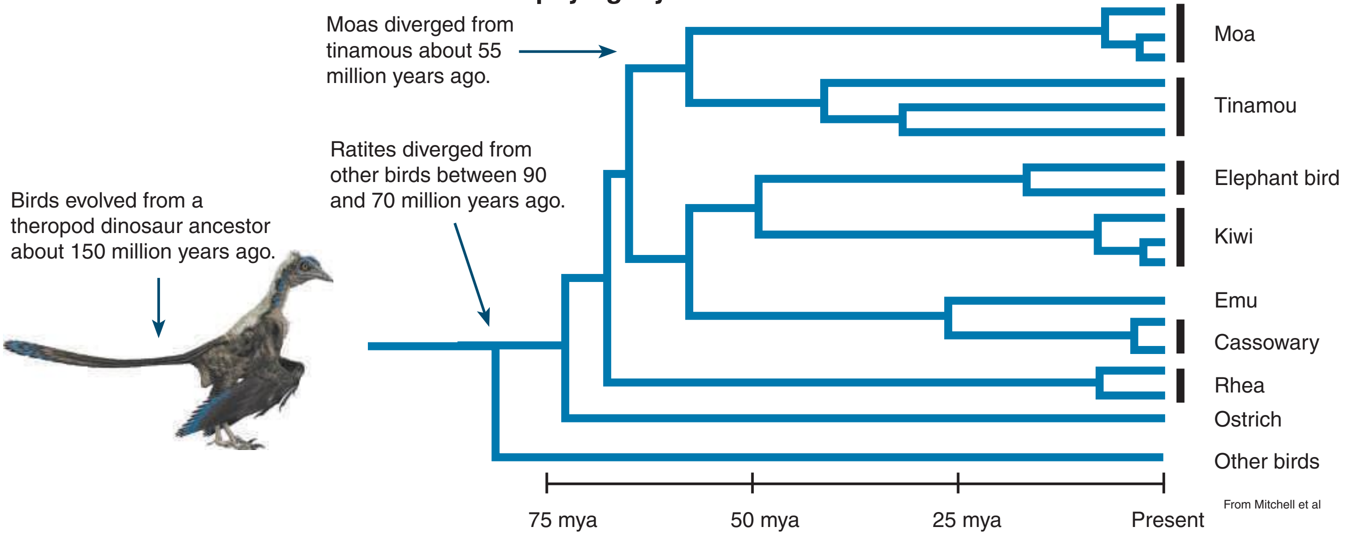
*Tinamous from South America were until recently thought to be related to but not part of the ratite group. New evidence suggests they should be included in ratites.

**Moa**
Eleven species (Lambert *et al.* 2004*), all extinct, New Zealand.

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 opposite, circle the branching marking the common ancestor of moa and kiwi.

   (b) On the phylogenetic tree opposite, 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 opposite to suggest a possible sequence of events for the distribution of ratites, assuming the phylogeny is accurate:

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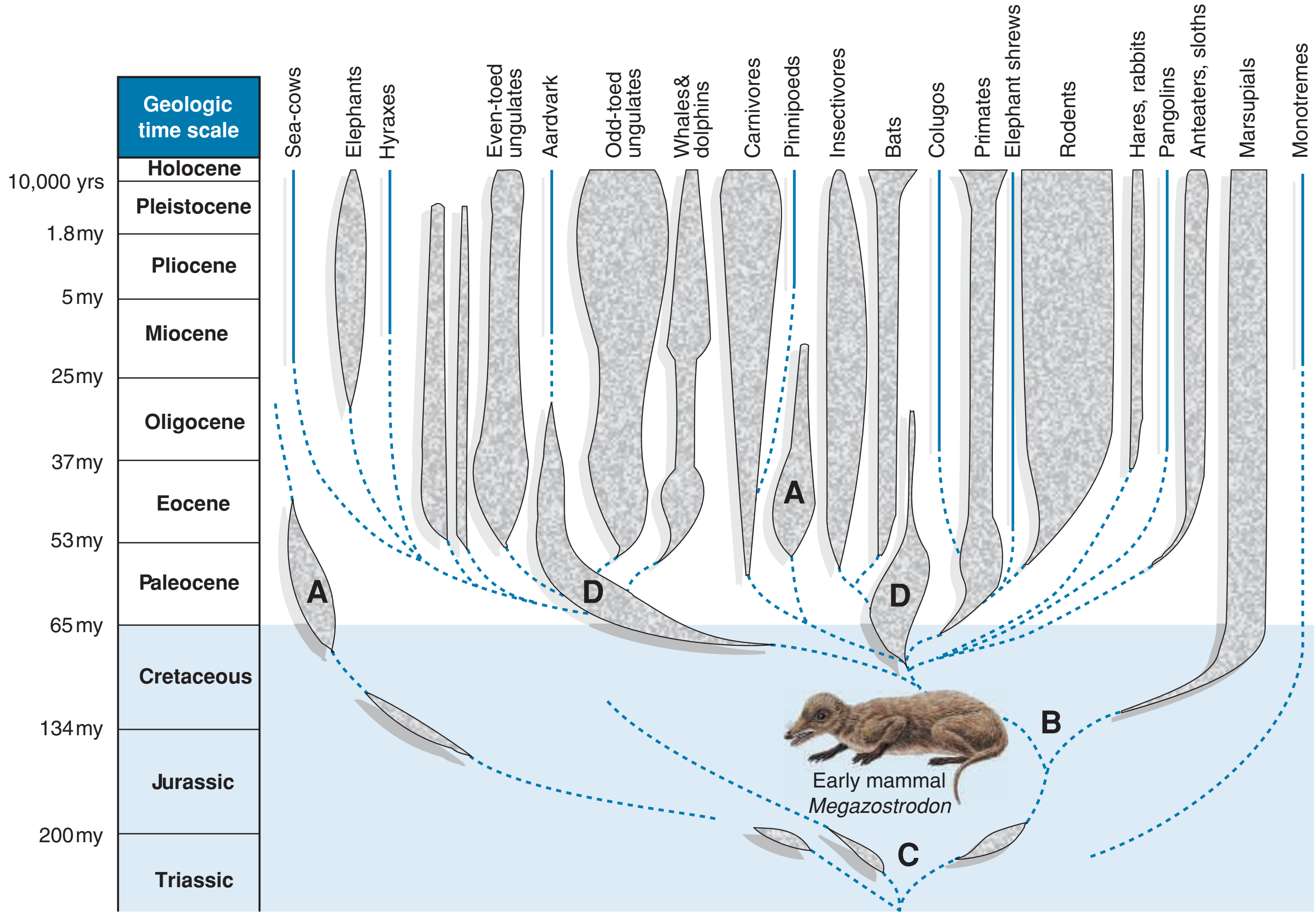
# 162 Adaptive Radiation in Mammals

**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 grey 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 grey 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: ________________

137 149

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## Rodent diversity

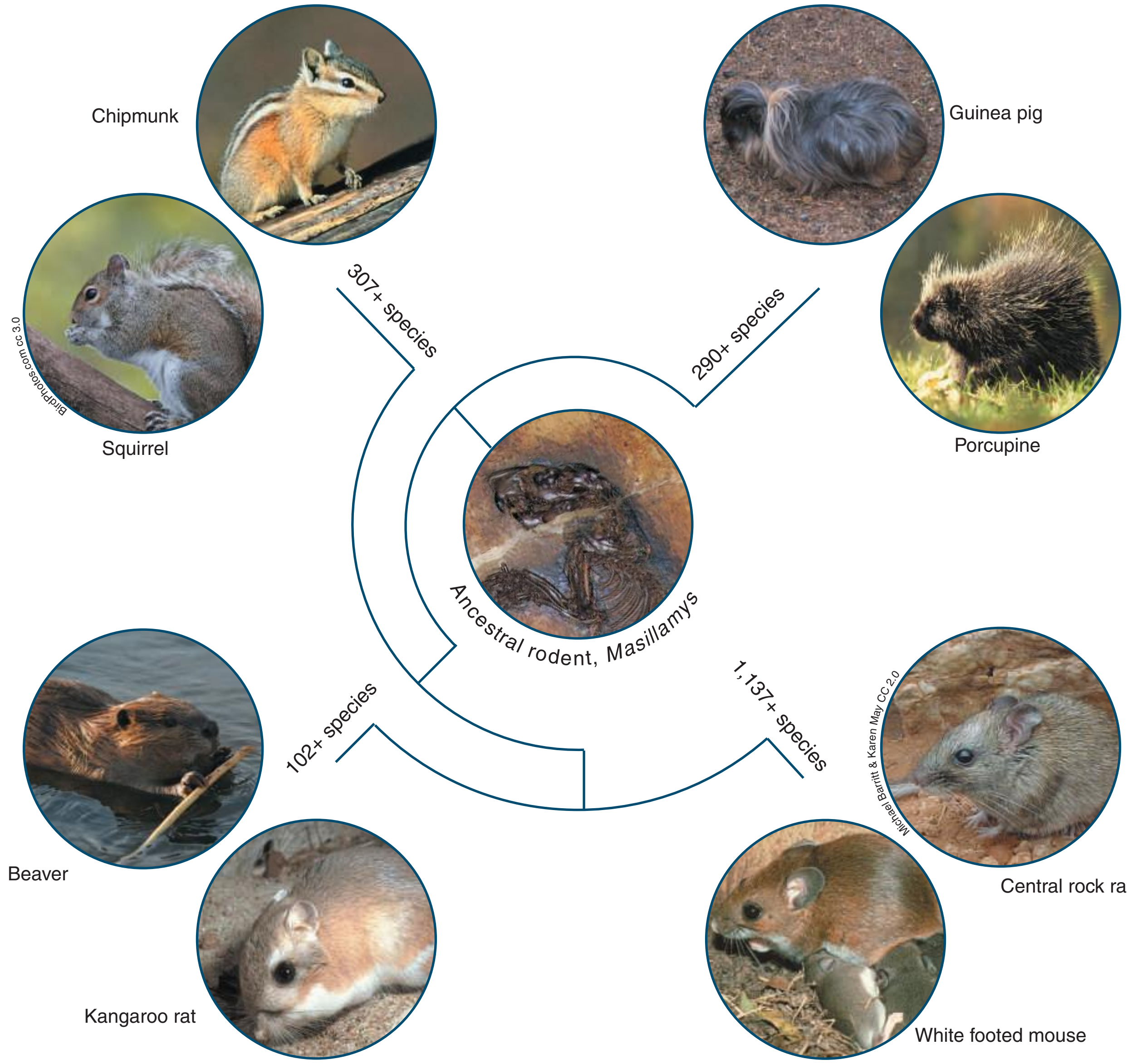
Rodents make up 40% of mammalian species, making them easily the most successful of the mammalian groups. Fossils with distinctive rodent features first appeared about 66 million years ago. All rodents have upper and lower incisor teeth that grow continuously. They are morphologically quite generalised 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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# 163 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).

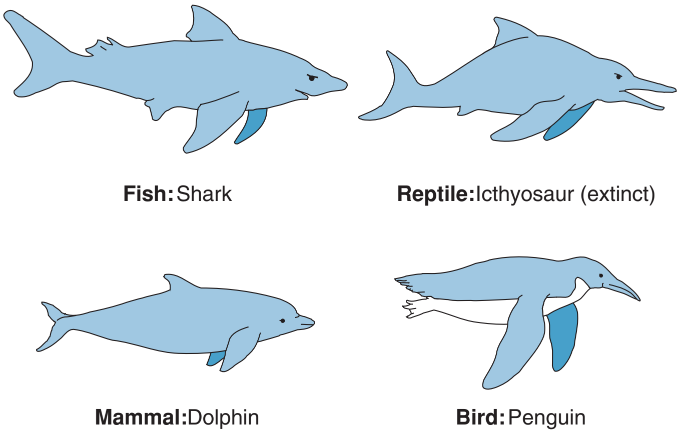
### Convergence: same look, different origins

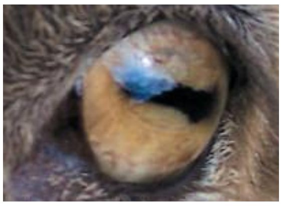
Not all similarities between species are the result of common ancestry. Selection pressures to solve similar problems in particular environments may result in similarity of form and function in unrelated (or distantly related) species. The evolution of succulence in unrelated plant groups (*Euphorbia* 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. Icthyosaurs, 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

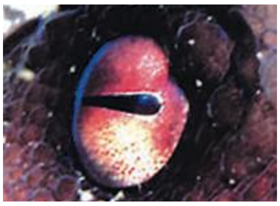
Analogous structures have the same function and often the same appearance, but different origins. The example (right) shows the structure of the **eye** in two unrelated taxa (mammals and cephalopod molluscs). The eye appears similar, but has evolved independently.

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).

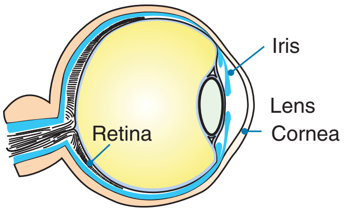


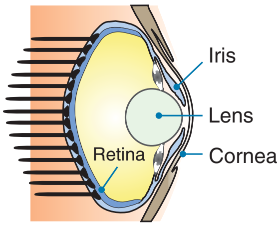

Jo Naylor cc2.0

**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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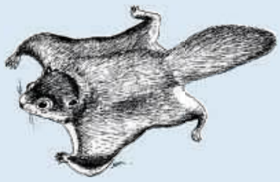
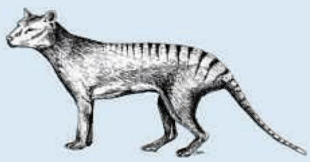
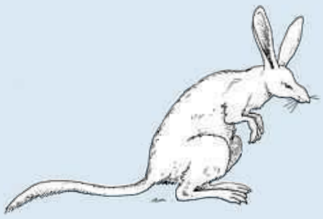
4. For each of the paired examples, briefly describe the adaptations of body shape, diet and locomotion that appear to be similar in both forms, and the likely selection pressures that are acting on these mammals to produce similar body forms:

## 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** | | **Placental mammals** |
|---|---|---|
| Wombat<br> | (a) Adaptations: Rodent-like teeth, eat roots and above ground plants, and can excavate burrows.<br>Selection pressures: Diet requires chisel-like teeth for gnawing. The need to seek safety from predators on open grassland. | Woodchuck<br> |
| Flying phalanger<br> | (b) Adaptations:<br>Selection pressures: | Flying squirrel<br> |
| Marsupial mole<br> | (c) Adaptations:<br>Selection pressures: | Mole<br> |
| Marsupial mouse<br> | (d) Adaptations:<br>Selection pressures: | Mouse<br> |
| Tasmanian wolf (tiger)<br> | (e) Adaptations:<br>Selection pressures: | Wolf<br> |
| Long-eared bandicoot<br> | (f) Adaptations:<br>Selection pressures: | Jack rabbit<br> |

# 164 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 idea of parallel evolution assumed that if a similar phenotype evolved independently in related species then it must have been because the same genetic pathway was involved in each case (parallelism). If a similar phenotype evolved in unrelated organisms then it was due to different genetic pathways (convergence). However there is now much evidence to show this is a flawed argument and there is no real distinction between parallel evolution and convergent evolution. At the very least, is it debatable as to when organisms become "unrelated", e.g. is placental and marsupial convergence in fact parallelism because both groups are mammals? Because of its difficulties, the term parallel evolution has tended to fall out of favour in recent times and all cases of convergent morphologies are now called convergent evolution.

## 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

## Convergent or parallel?

- *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 along the Gulf coast form one genetically distinct population (monophyletic), whereas the mainland mice and the mice along the Atlantic coast form a separate less defined paraphyletic group. From this we can see that light coloured fur must have evolved independently in the Gulf coast and Atlantic coast populations. Genetic analysis also shows that the genes responsible for the light fur are different in the two groups. Thus the light phenotype has been arrived at by different genetic mechanisms in the different subspecies of mouse.
- The light fur colouration in Florida beach mice is caused by a mutation in the MC1R gene. This gene is found in all mammals and in many cases is responsible for changes in skin or hair/fur colouration. Thus many more distantly related mammals arrive at lighter coloured skin or hair via the same genetic mechanism.

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. Why are parallel and convergent evolution usually now just grouped under convergent evolution?

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# 165 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 color 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.

Bats are nocturnal and color-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 colors 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.

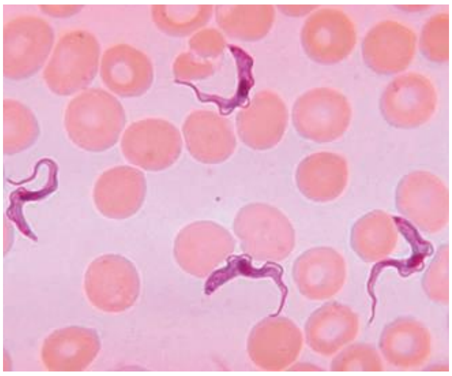
## Predator/prey relationships

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

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



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 Niolu 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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# 166 Prezygotic Isolating Mechanisms

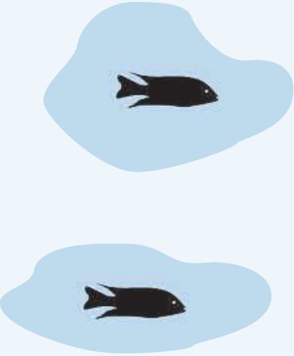
**Key Idea**: Reproductive isolating mechanisms prevent interbreeding between different species. Prezygotic isolating mechanisms occur before fertilisation can take place.

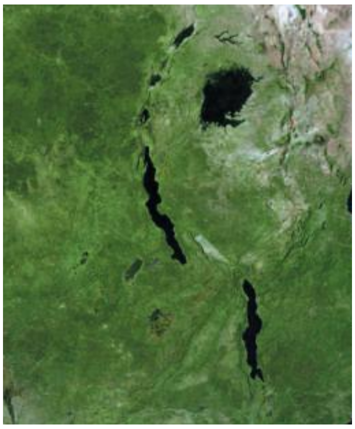
Reproductive isolation prevents successful interbreeding between species and is crucial to maintaining species' integrity. Prezygotic isolating mechanisms operate before fertilisation can occur and prevent "gamete wastage". They are the most common type of isolating mechanism and may be associated with 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.

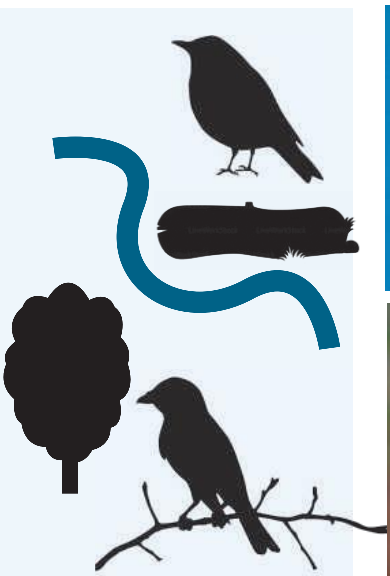



NASA Earth Observatory

## 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.




Aviceda


Aviceda

## 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.


Bruce Marlin


Lorax

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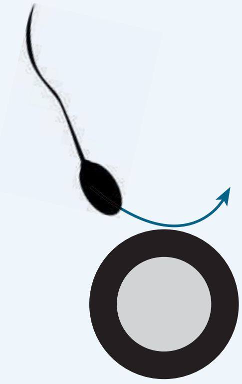
## Gamete Isolation

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.



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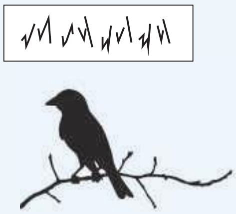
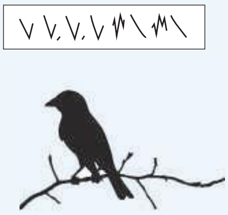
Taollan82; Kirt L. Onthank cc3.0

## 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.



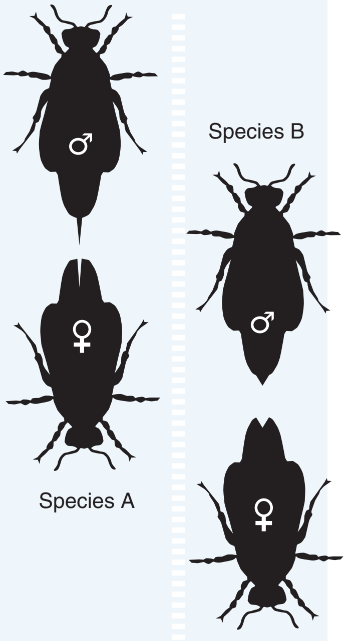


## Mechanical (morphological) isolation

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?

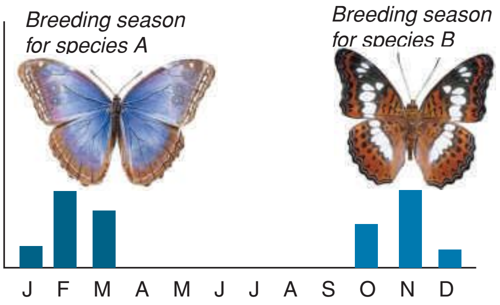
3. (a) Why is geographical isolation not regarded as a reproductive isolating mechanism?

   (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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# 167 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

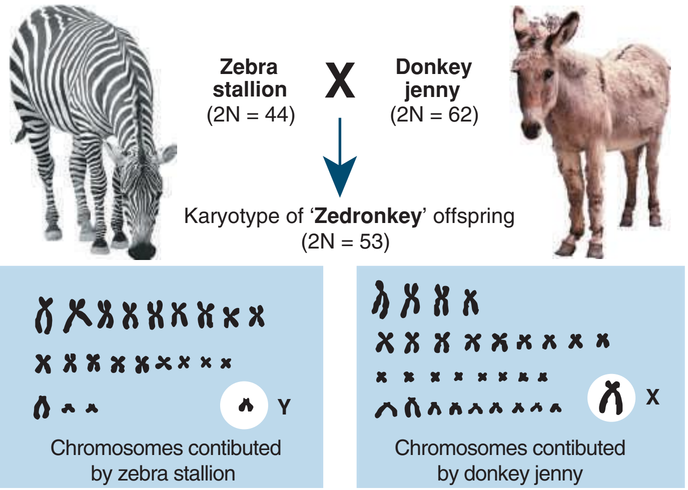
Mating between individuals of two species may produce a zygote (fertilised egg), but genetic incompatibility may stop development of the zygote. Fertilised eggs often fail to divide because of mis-matched chromosome numbers from each gamete. Very occasionally, the hybrid zygote will complete embryonic 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.

## 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.



AKA

## 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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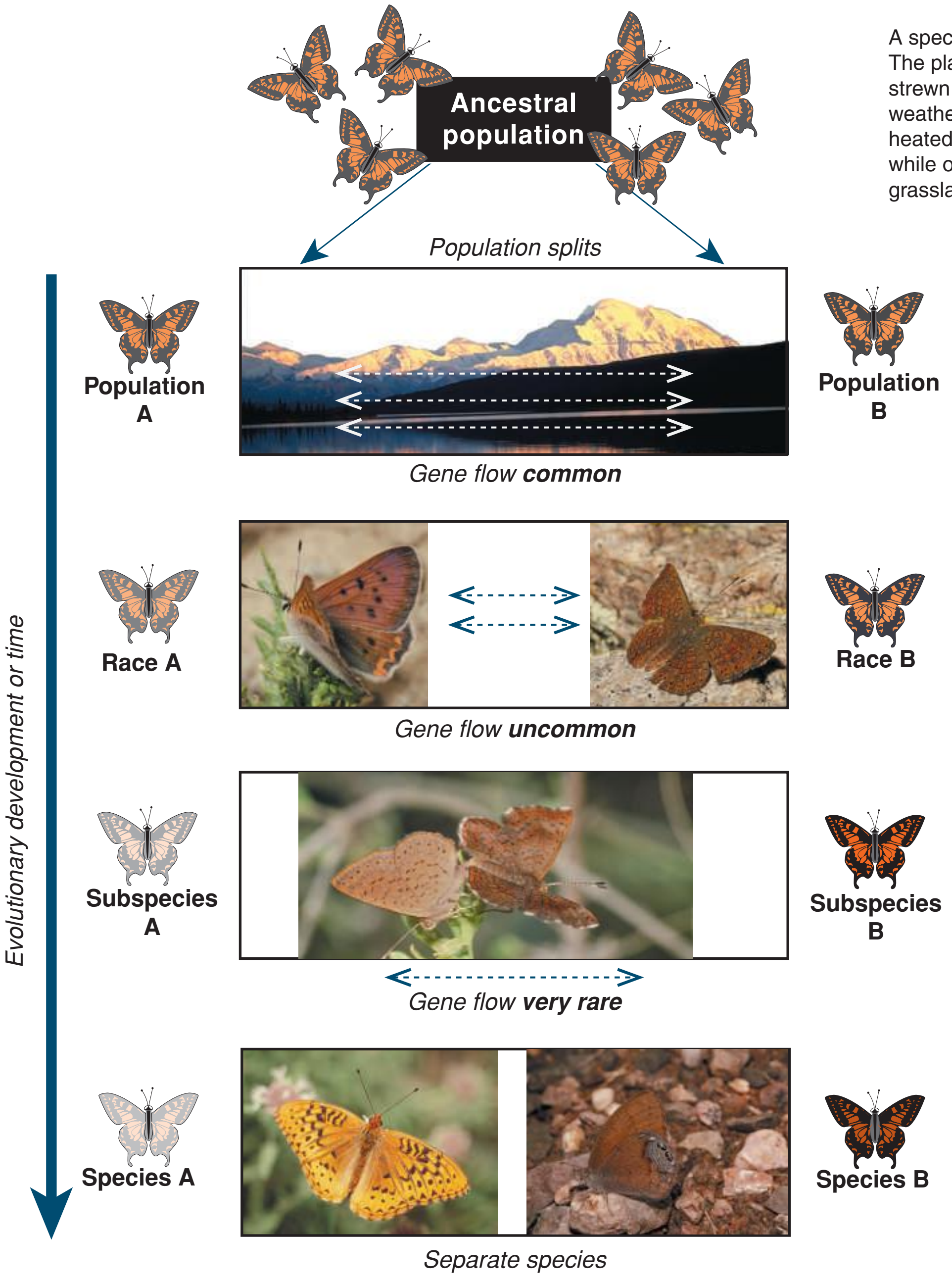
# 168 Stages in Species Formation

**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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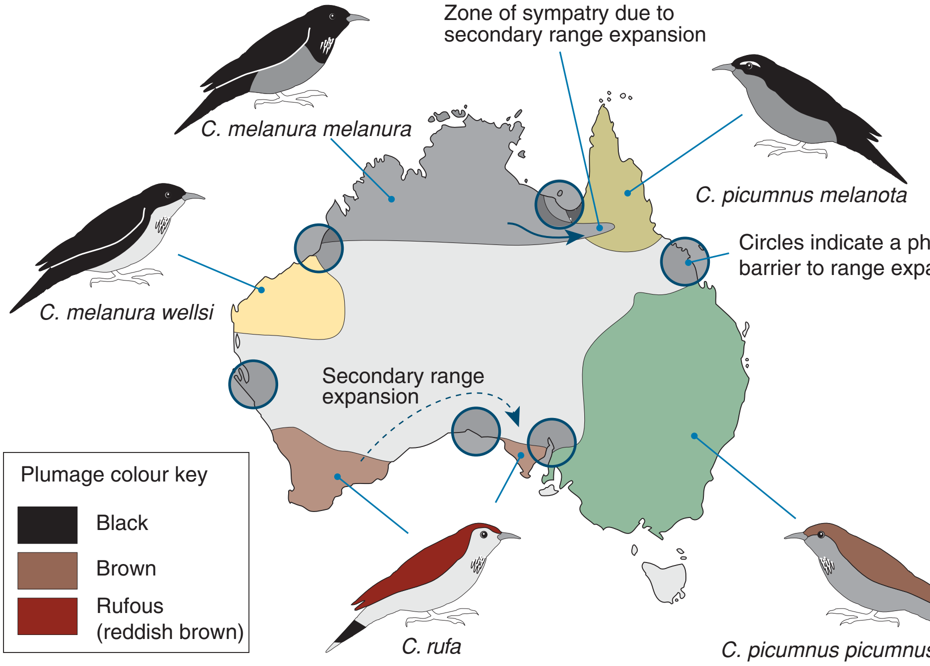
# 169 Speciation and the Role of Habitat

**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.



The Australian treecreeper
Genus *Climacteris*

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:

**ISBN: 978-1-927309-86-5**

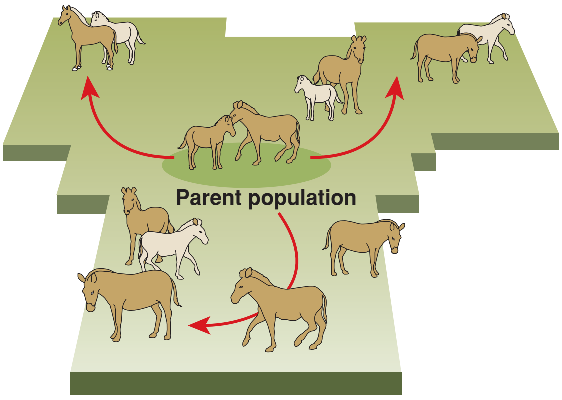
# 170 Allopatric Speciation

**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

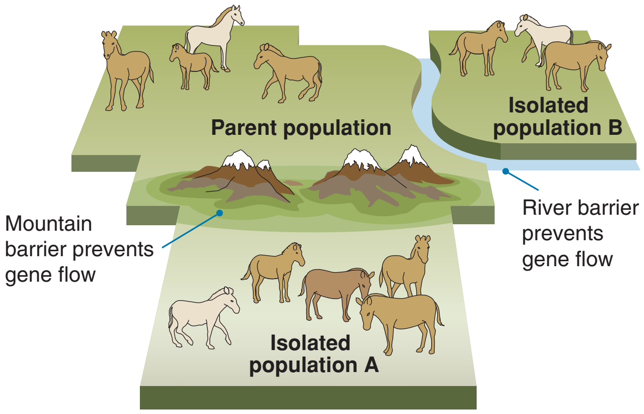
There are times when the range of a species expands for a variety of different reasons. A single population in a relatively homogeneous environment will move into new regions of their environment if there is intense competition for resources. Competition between members of the same species is the most 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

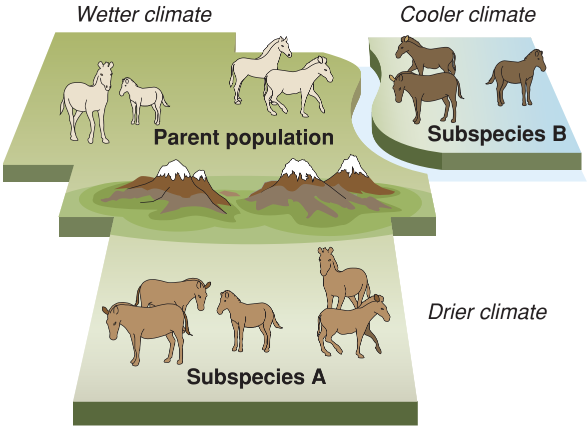
Parts of the population may become isolated by **physical barriers**, such as mountains, deserts, or stretches of water. These barriers may cut off those parts of the population that are at the extremes of the range and gene flow becomes rare or stops altogether. Climate change (e.g. ice ages and a consequent 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.



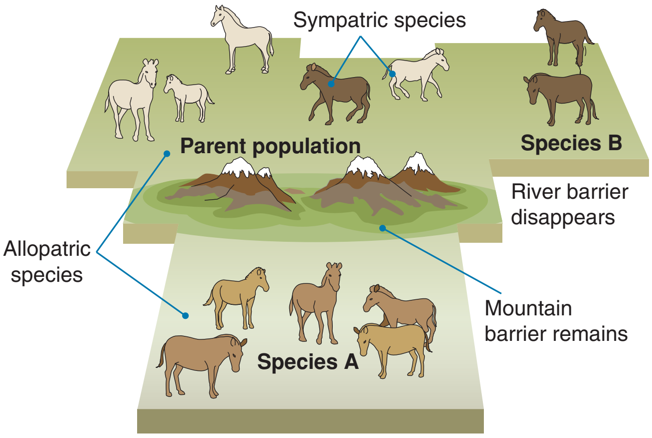
### Stage 3: Different selection pressures

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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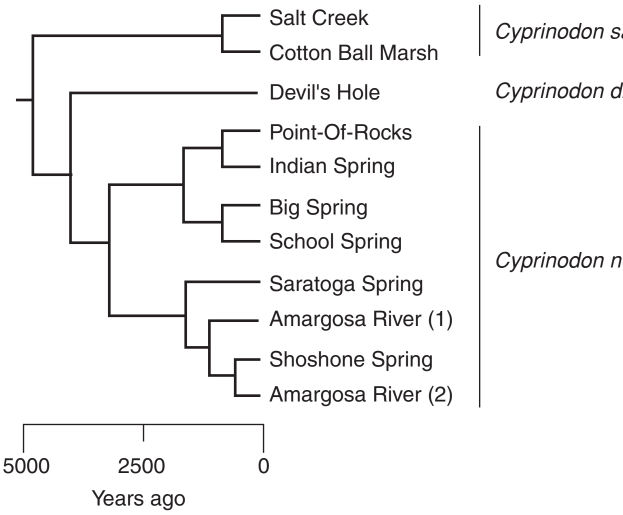
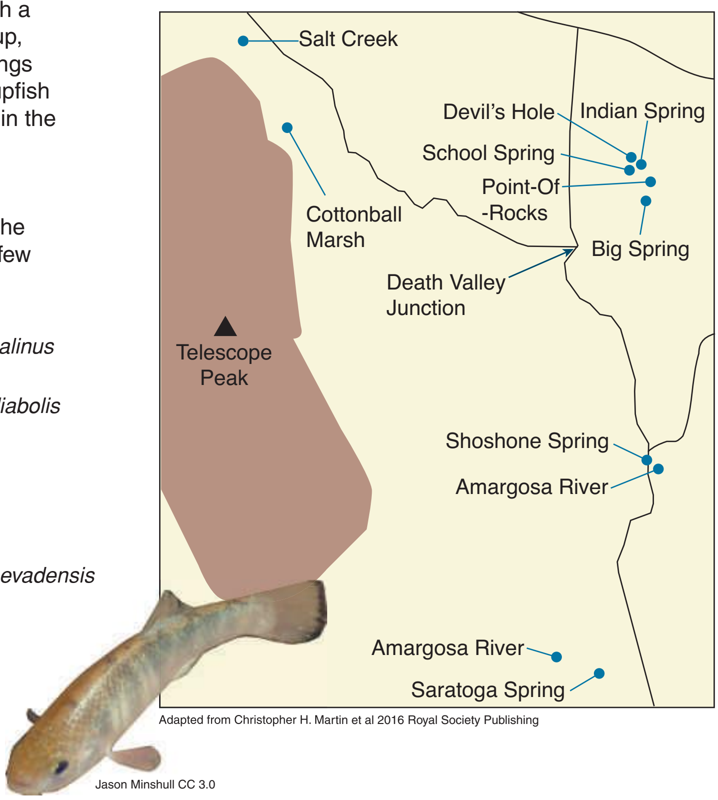
## Allopatric speciation in Death Valley pupfish

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? __________

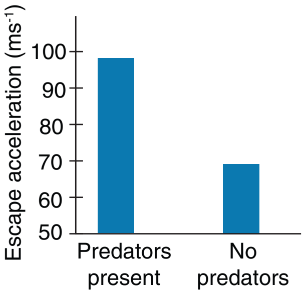
10. How many subspecies of *Cyprinodon nevadensis* are there? __________

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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# 171 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.

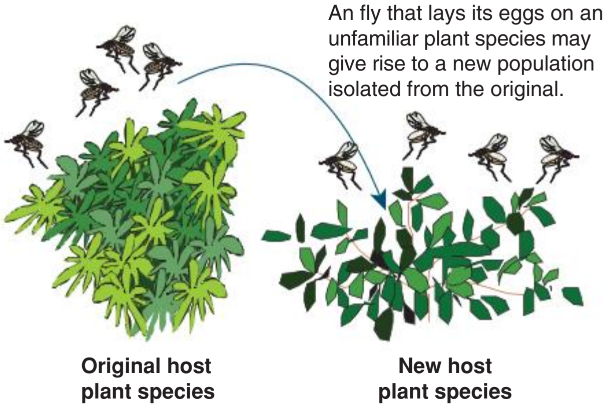
## Speciation through niche differentiation

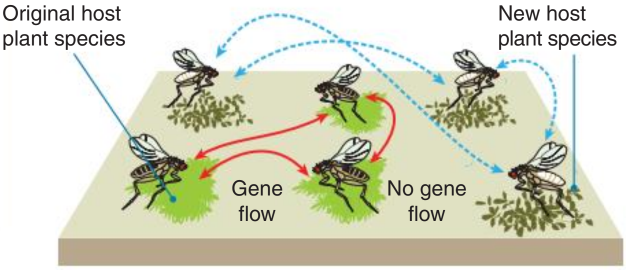
### Niche isolation

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.



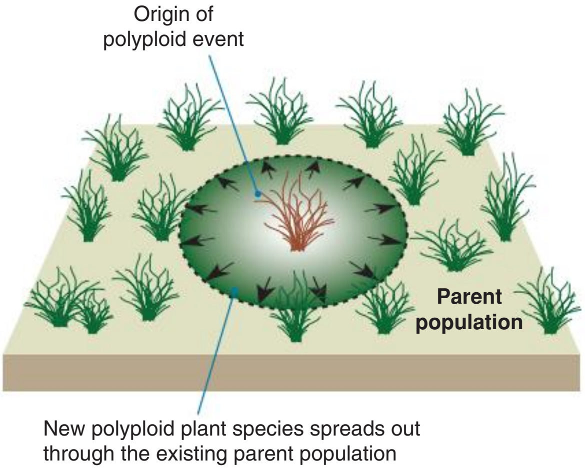


## Instant speciation by polyploidy

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 apple maggot flies

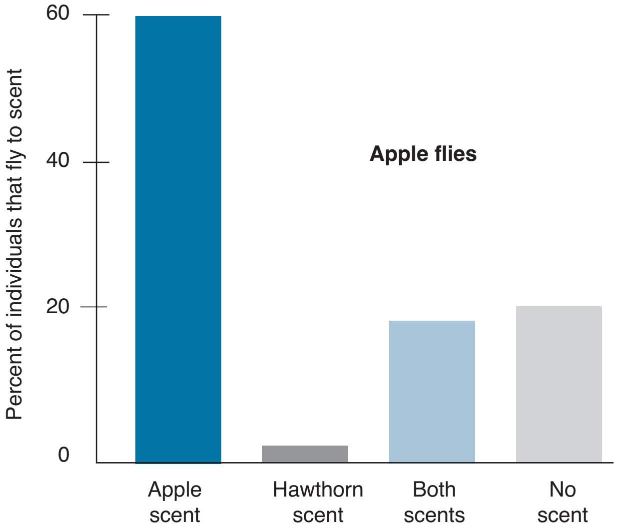
Apple maggot flies are native to North America. They infest the fruit of apple trees, laying eggs in the fruit, which develop into maggots that burrow into and eat the fruit. However, apple trees are not native to North America and were introduced less than 300 years ago.

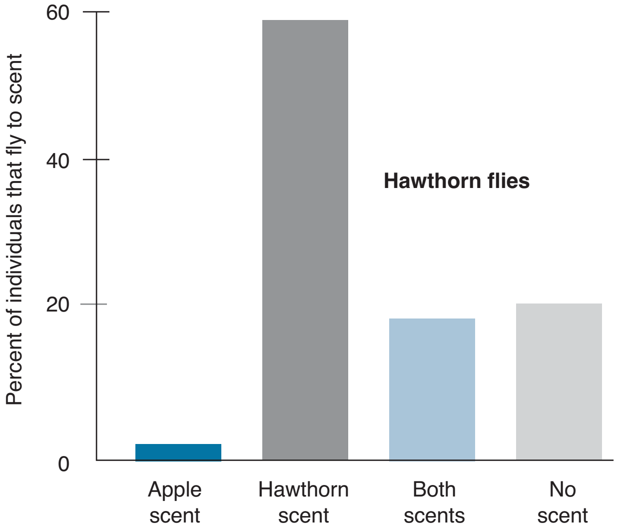

Joseph Berger, Bugwood.org

Research found that apple maggot flies also infest the fruit of native hawthorns. More importantly, flies that develop from maggots infesting hawthorns mated and laid eggs on hawthorns (hawthorn flies). Flies that develop from maggots that infested apples preferred to mate and lay eggs on apples (apple flies). Only 6% of matings took place between flies from different fruits.

Other experiments show the flies discriminate between scents on a genetic basis and have alleles associated with attraction to hawthorn or apple scent.

This separation of individuals by preference of apples or hawthorns has been a consequence of the introduction of apple trees. Although the flies are morphologically and genetically the same, their behavior has separated them into different populations on the pathway to speciation.





4. What plant did the apple maggot fly infest before apple trees were introduced to North America?

5. What kind of natural selection is occurring in the apple maggot fly?

6. (a) Explain the mechanisms that are causing this selection to occur:

(b) How might these mechanisms affect the future evolution of the apple maggot fly?

7. Apple fruits tend to drop earlier in the season that hawthorn fruits. How might this enhance the separation of apple flies and hawthorn flies?

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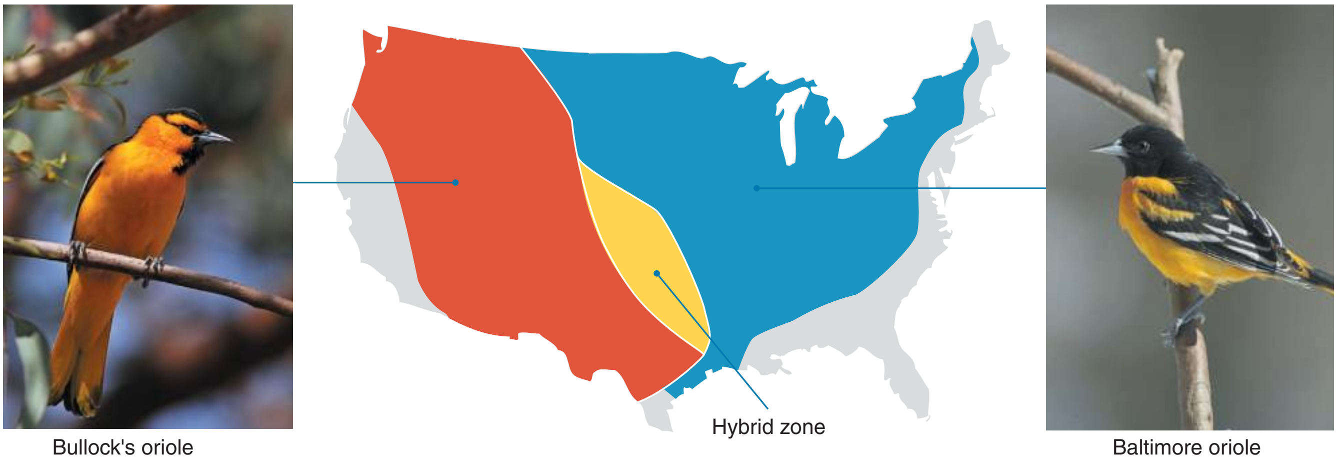
# 172 Parapatric Speciation

**Key Idea**: Speciation can occur when a part of a population expands it niche before establishing a separate population.

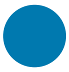
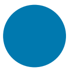
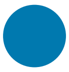
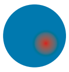
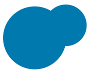
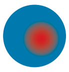
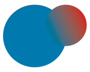
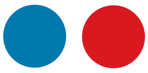
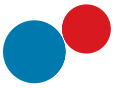
In parapatric speciation, a population enters a new niche and gene flow is reduced between the population in the new niche and parent population. Eventually gene flow ceases, isolating a new species. For this to happen, mating must be non-random, i.e. mates select each other based on niche preference, 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



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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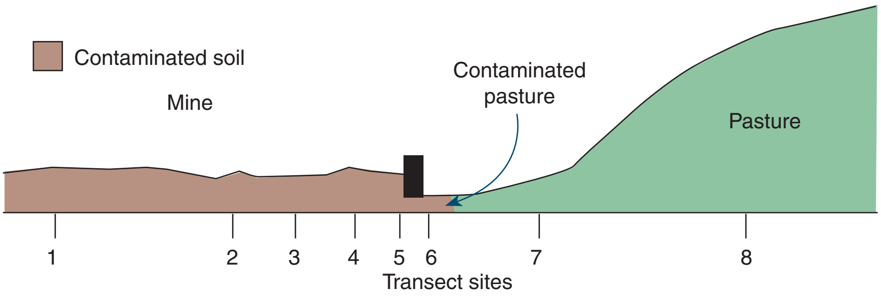
## Parapatric speciation in pasture grasses

A well documented example of parapatric speciation is that of the grasses *Agrostis capillaris (tenius*) (browntop) and *Anthoxanthum odoration* (sweet vernal) growing on pasture and contaminated soil around mine sites.

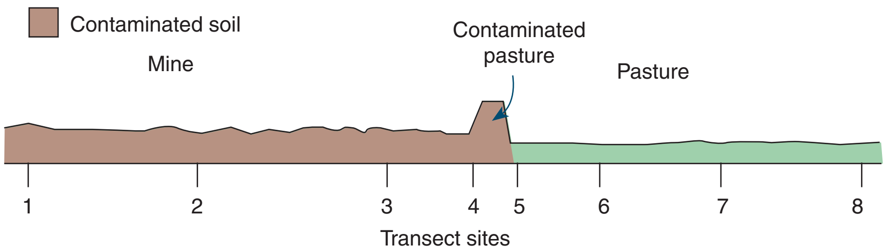
**Drws-y-Coed mine (Wales)** *Agrostis capillaris*




John M CC 2.0

Dam below Drws-y-Coed copper mine

**Trelogan mine (Wales)** *Anthoxanthum odoration*



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 that 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***

| | | 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 |


Henri0800 cc 3.0

**Flowering isolation in *Anthoxanthum odoration***

| | | 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


James Lindsey cc 3.0

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 odoration* is parapatric:

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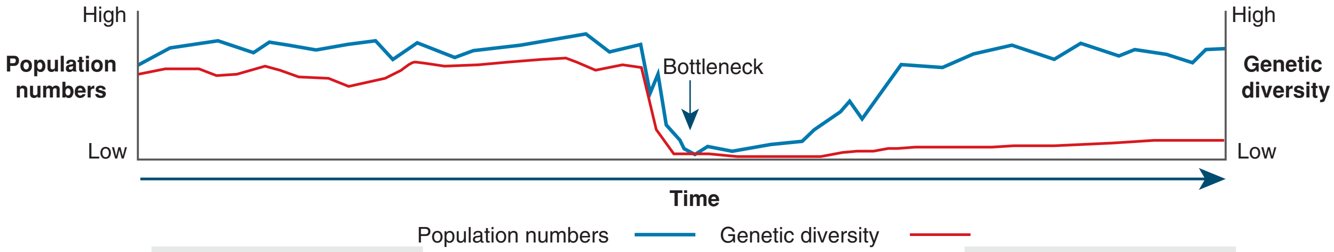
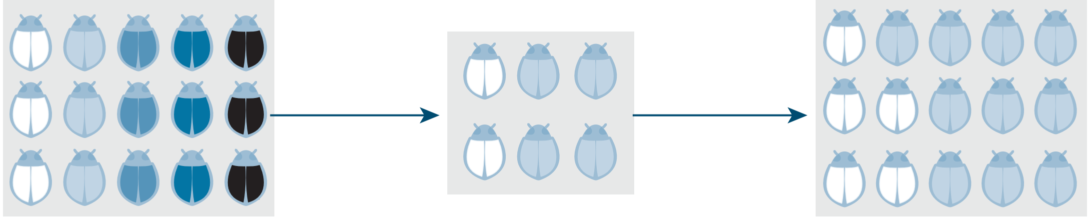
# 173 Population Bottlenecks: The Role of Diversity

**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**





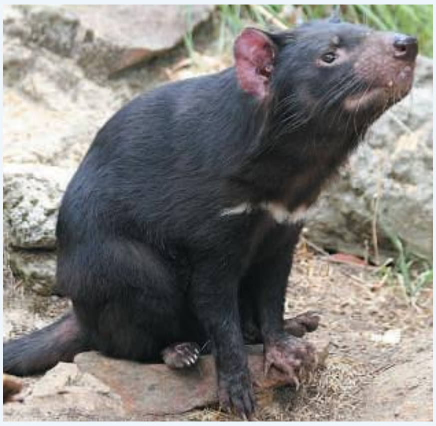
Large, genetically diverse population.

Population numbers are drastically reduced. Much of the genetic diversity is lost.

Population numbers increase again, but the larger population has low genetic 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: ______________________

______________________

______________________

______________________

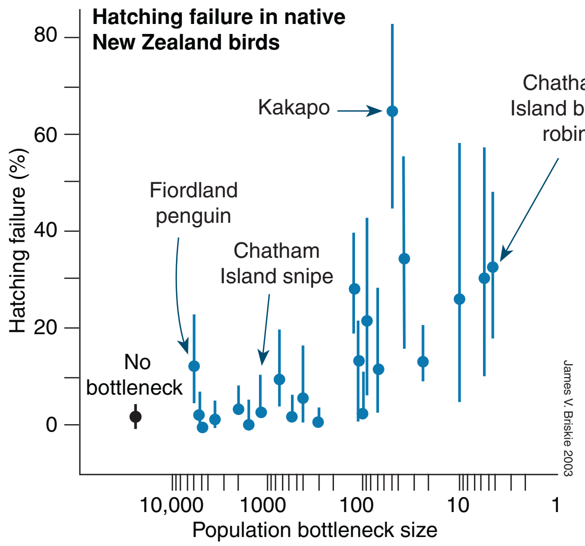
______________________

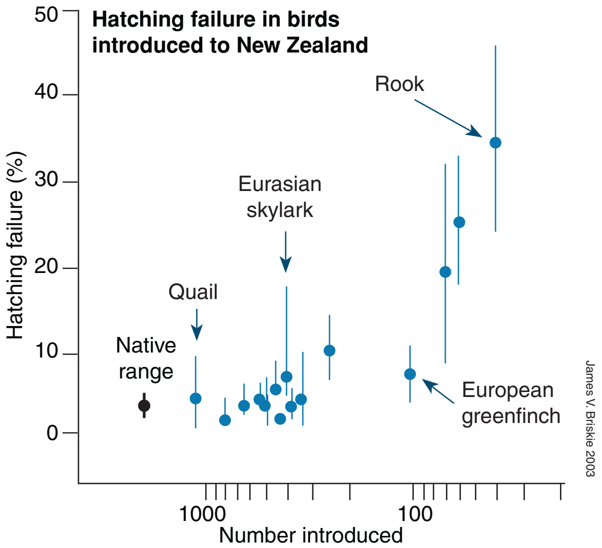
______________________

**ISBN: 978-1-927309-86-5**

## Population bottlenecks affect hating rates in birds

- Severe bottlenecks reduce genetic diversity 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 150.


The Chatham Island black robin population was just 5 in 1980, but has risen to 200. 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? ____________________

**ISBN: 978-1-927309-86-5**

# 174 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 *Drosophilia* flies and *Tetragnatha* spiders.

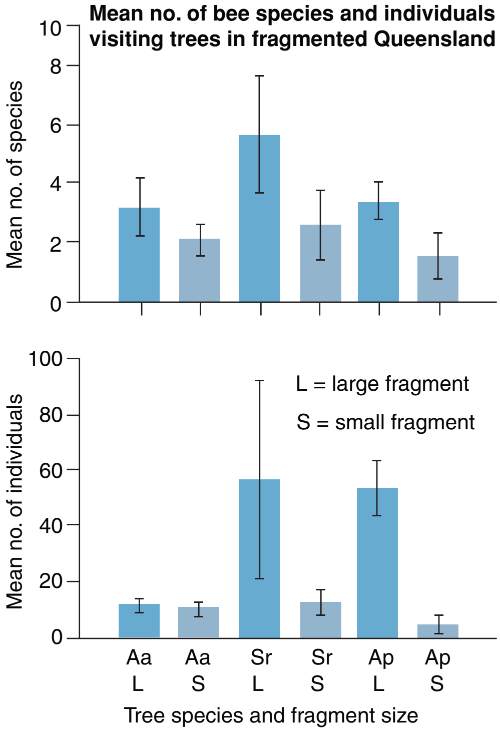
- There are at least 12 species of *Tetragnatha* spiders on Hawai'i. Studies of three from forest fragmented by a 160 year old lava flow show genetic differences between isolated populations in two of the species. The third species showed little genetic difference between population isolates. This may 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 caused by a lava flow from Kilauea volcano.

USGS

## 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.



**Mean no. of bee species and individuals visiting trees in fragmented Queensland forest**

Tobias J. Smith et al Ecol Evol. 2018 Aug; 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?

10 70 166

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# 175 Species Conservation

**Key Idea**: Species conservation requires there to be a minimum population size and a minimum area for the population to live in.

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. This could be because the food they eat is scarce (e.g. a particular berry from a particular plant) or they need a large population of prey to support them. What's more, each species needs a minimum population size to remain viable. Viability relies on minimising inbreeding and the effects of genetic drift. In some animal species, breeding is dominated by a few males, which reduces genetic variability in small populations. For these species, the number of males to females is also important when determining population viability.

## Minimum viable population:

The minimum viable population (MVP) is the smallest number of individuals needed to have a certain probability of maintaining a population or species over a predetermined length of time. A common benchmark is a 95% probability of survival over 100 years. However, given that many species have long generation spans it is often more useful to use generations. Forty generations is often used.

## Minimum area requirements

The minimum area requirement (MAR) can be calculated from the area required by an individual and the MVP. Given that individuals often pair up when mating the MAR can be calculated as:

MAR = 0.5 x home range size x MVP

The MAR can also be calculated from the density of individuals in an area. This is generally accepted as being more reliable (as home ranges tend to vary in size):

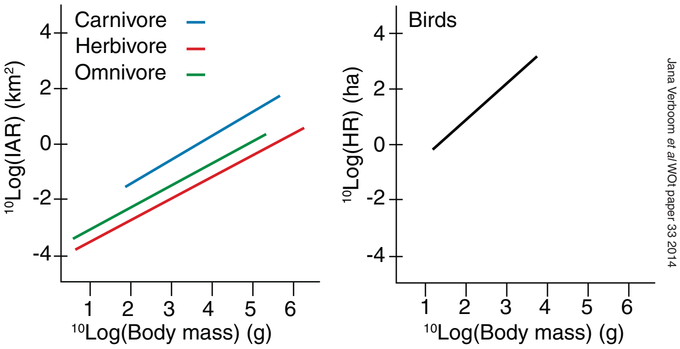
MAR = MVP x population density

However there is also a relationship between a individual's area requirement (IAR) and body size in mammals and IAR and home range (HR) in birds. These relationships can also be used to calculate MAR.
In these cases MAR can be calculated by:

$$\text{MAR}_{\text{mammals}} = \text{MVP} \times \text{IAR}$$

$$\text{MAR}_{\text{birds}} = \text{MVP} \times \text{HR} / 200$$

**Area requirment and body mass**



Jana Verboom *et al* WOt paper 33 2014

| 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 |
| Capricorn silvereye | | 1911 | 11 | 0.51 (HR) |
| Lord Howe Island woodhen | | 604 | 496 | 67.8 (HR) |

## 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.

Green corridors linking regions of forest in Queensland.

1. Explain the different uses of time when calculating MVPs: ______________________________

______________________________

______________________________

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 Lord Howe Island woodhen: ______________________________

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# 176 Technology and Human Evolution

**Key Idea**: Technology has driven and continues to drive recent human evolution.

There is a tendency to think our technology has freed us from evolution. We now use technology to help us survive in many different ways, so it is easy to think that natural selection no longer plays a part in human evolution (or at least its role is reduced). However evidence shows that humans may actually be evolving faster than many other animals. Some of this is due to our technology, which produces new selection pressures, but also due to genetic drift. Cultural changes also have an effect on evolution, especially changes that alter behaviour or the age of reproduction.

## Blame it on farming

**The overbite**: Try making the sound an f or a v makes. In both cases you will find you place your top incisor teeth on top of your bottom lip to produce the sound. This kind of sound is called a labiodental fricative because it is produced by friction from air moving between your top teeth and your bottom lip.

Before around 10,000 years BCE, people's top and bottom front teeth generally aligned, but modern humans, especially in Western cultures, have a slight over bite where the bottom teeth close behind the top teeth. This makes it easier to pronounce "f"s and "v"s. The change in dental formation can be seen to occur at the time humans became proficient at farming. Farming produces softer food to eat (e.g. breads and fruits) and results in less force on the lower jaw when chewing, which reduces its growth.

Research shows that an overbite reduces the effort needed to pronounce "f"s and "v"s by about a third. The ability to pronounce "f"s and "v"s meant new sounds and words developed and resulted in the development of new languages. About 76% on Indo-European languages contain labiodental fricatives. However, negatives of this is diet (and smaller jaw) are crowding of the teeth, cavities, and impaction of wisdom teeth.

**Lactose tolerance**: Domestication of livestock, especially cattle, was also responsible for the evolution of lactose tolerance in Western cultures at about the same time. People who could digest milk as adults suddenly had a greater fitness than others. People of European and African descent are generally lactose tolerant.

**Measles**: Measles may have evolved because of farming. Research shows that the virus evolved from Rinderpest (cattle plague). With humans in close proximity, the virus jumped to humans as measles around 900-1200 CE, about the same time as cities large enough to maintain the virus became more common. The resulting epidemics undoubtedly affected the human gene pool, killing many non-resistant people. Notably, this occurred when measles reached the Americas in the 1500s, killing up to two thirds of the native population.

## Modern culture affects evolution

Modern Western culture affects human evolution in subtle ways. Increasingly, people in Western cultures are choosing to have children when they are older (late 20s-40s). However, mutations during gamete formation increase significantly with age, increasing the rate of heritable mutations relative to people reproducing when they are younger.

Technology assisted sex selection in some cultures can skew sex ratios and reduce genetic choice for mates.

Modern medicine has increased life expectancy, mostly by increasing the number of children surviving to reproductive age. This increases total genetic variation, as without modern medicine only the few strongest or luckiest survived. At the same time, technologies can now test for fetal abnormalities in pregnancy, and these pregnancies may be terminated.

Modern humans have a slight overbite.

Lactose tolerance developed around 10,000 years ago, providing a new and nutritious food source.

CDC

Measles has killed hundreds of millions of people eliminating many genetic combinations from the global gene pool.

1. Explain why, even with technology to "shield" us from the environment, human evolution will continue:

2. How do disease epidemics affect human evolution?

SHE

# 177 KEY TERMS AND IDEAS: Did You Get It?

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

adaptive radiation ..........

allopatric speciation ..........

common ancestor ..........

convergent evolution ..........

divergent evolution ..........

phyletic gradualism ..........

punctuated equilibrium ..........

reproductive isolation ..........

speciation ..........

species ..........

sympatric speciation ..........

**A** The most recent individual from which all organisms in the group are directly descended.

**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** A form of divergent evolution in which there is rapid speciation of a lineage to fill many different ecological niches.

**E** A model for the evolution of different forms over a long period of time but with only slight changes occurring between successive generations.

**F** The formation of new species in the course of evolution.

**G** The situation in which members of a group of organisms breed with each other but not with members of other such groups.

**H** Speciation in which the populations are physically separated.

**I** Population of individuals that can interbreed to produce viable offspring.

**J** The division of one species into two or more separate species.

**K** Speciation as a result of reproductive isolation without any physical separation of the populations, i.e. populations remain within the same range.

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 (delete one) Mechanism of isolation: ______________________________

(b) Many plants have unique arrangements of their floral parts that stops transfer of pollen between plants:

Prezygotic / postzygotic (delete one) 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 (delete one) 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 (delete one) Mechanism of isolation:______________________________

3. 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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# 178 Synoptic Questions: Unit 4, Topic 2

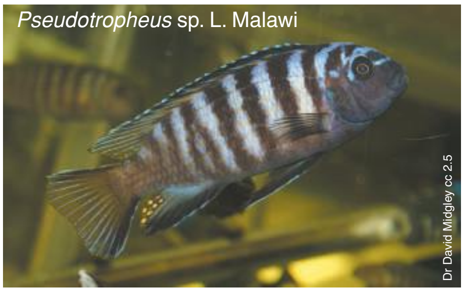
1. Compare and contrast the role of genetic drift and natural selection in changing the genetic makeup of a population:

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.

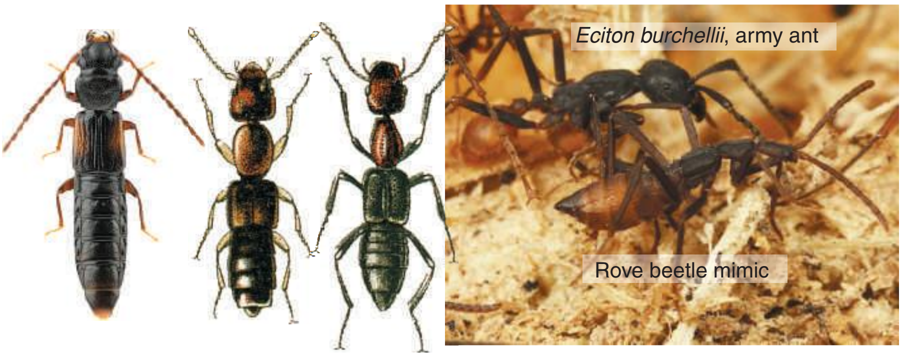
Similarly, in the diverse family of rove beetles, the phenomenon of social parasitism has evolved independently in at least 12 geographically isolated lineages. These beetles mimic different species of army ants in body shape, behaviour, and pheromone chemistry, tricking the ants into accepting the beetles into the colony, where they then consume the ant young.


*Tropheus* sp. L. Tanganyika

Bobby 111 cc 3.0


*Pseudotropheus* sp. L. Malawi

Dr David Midgley cc 2.5



©Taku Shimada (permission with credit)

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 coniferous tree *Wollemia* was only known from fossils until 1994 when living specimens were discovered in remote rainforest in New South Wales. The wild population is fewer than a hundred trees and their locations are still kept secret in an effort to protect them. Genetic testing shows little genetic difference between individual trees showing that the species has gone through a severe (and ongoing) genetic bottleneck. The tree has been propagated and is now planted in botanical gardens around the world.


Akerbeltz CC 3.0

(a) Define the term population bottleneck:

(b) Explain the effect of the bottleneck on the genetic diversity of the *Wollemia* population and discuss the likely implications for the persistence of this critically endangered species:

4. 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:


Haleakala silversword

5. 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*

SE Thorpe

**ISBN: 978-1-927309-86-5**

# Internal Assessment 3: Research Investigation

Activity number

**Key terms**

- anecdote
- bias
- data
- evidence
- opinion
- reliability
- validity

## Choosing a claim to evaluate

*Key skills and knowledge*

☐ 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.

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.

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.

☐ Your response could be written report should be 1500-2000 words. A multimodal presentation should be 9-11 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.

## Effective science communication

*Key skills and knowledge*

☐ 1 Understand the characteristics of effective science communication. The biological information you present must be accurate, the biological concepts and models must be clearly explained, it must be clear why the findings are important, and the information presented must be appropriate for purpose and audience.

☐ 2 When explaining biological concepts specific to the investigation be sure to define key terms and use appropriate biological terminology.

☐ 3 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.

## The nature of evidence

*Key skills and knowledge*

☐ 4 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.

☐ 5 In your research evaluate the validity, reliability, and authority of data, including acknowledging any possible errors or bias.

# 179 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.

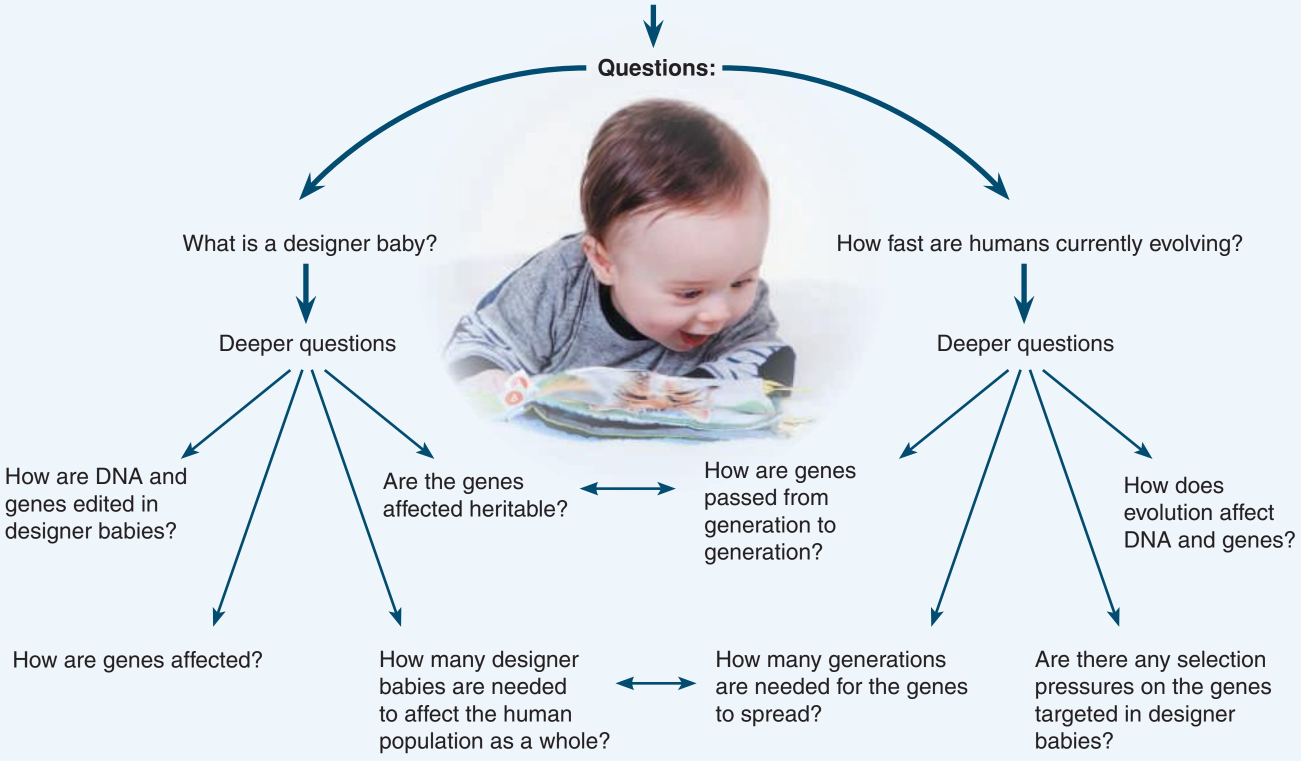
Research of any kind starts with a claim, hypothesis, or idea. This may be seemingly trivial: e.g. "fans make you feel cooler". Such a claim may seem obvious, but unless you test it you'll never know for sure. Sometimes evidence goes against what people claim or "know" to be true. "The Great wall of 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.

Consider the claim:

**"Designer babies will accelerate the pace of human evolution"**



**Questions:**

What is a designer baby?

Deeper questions

- How are DNA and genes edited in designer babies?
- How are genes affected?
- Are the genes affected heritable?
- How many designer babies are needed to affect the human population as a whole?

How fast are humans currently evolving?

Deeper questions

- How are genes passed from generation to generation?
- How many generations are needed for the genes to spread?
- Are there any selection pressures on the genes targeted in designer babies?
- How does evolution affect DNA and genes?

## 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.

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 your 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 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 Popular Mechanics, 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.

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

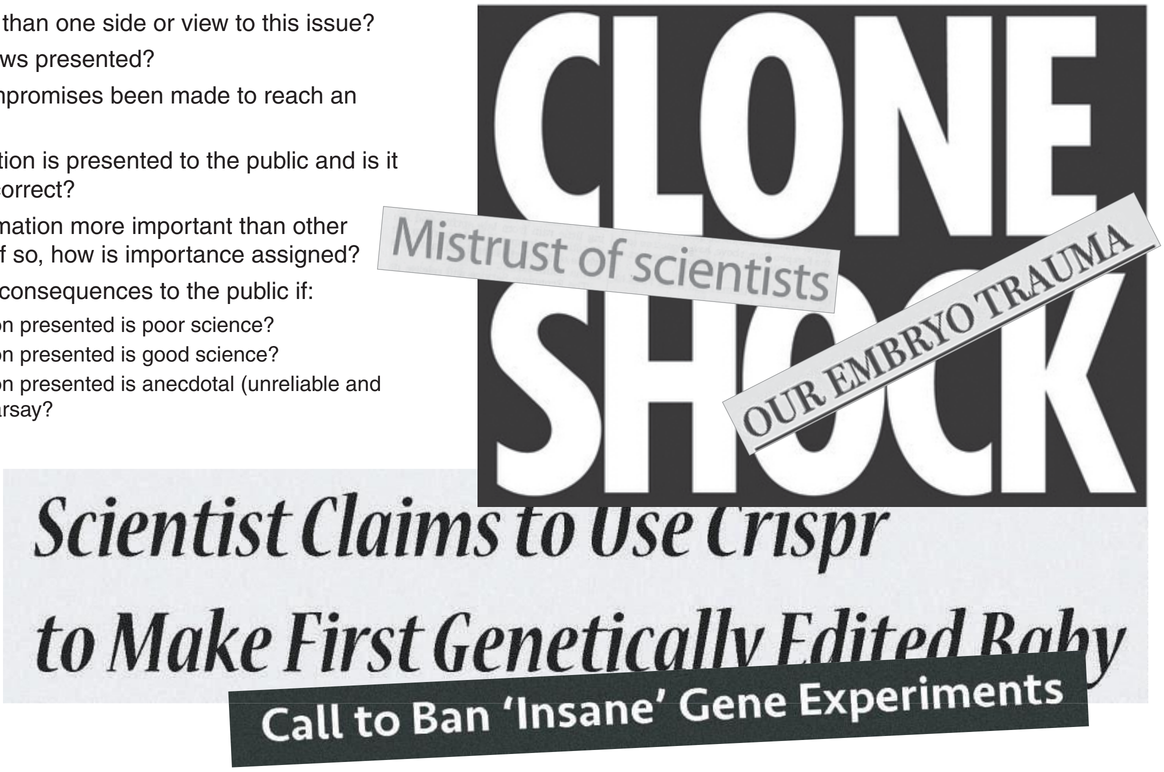
Balanced reporting provides unbiased information where both the positive and negative aspects are presented without a particular emphasis on either. The reporting of scientific information should always be unbiased and a statement of fact backed by evidence. Unfortunately, a lot of information reported 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?



CLONE SHOCK

Mistrust of scientists

OUR EMBRYO TRAUMA

Scientist Claims to Use Crispr to Make First Genetically Edited Baby

Call to Ban 'Insane' Gene Experiments

## 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

## Birth weight data for activity 154

The birth weights for 100 babies are displayed below.

---

3.740
3.830
3.530
3.095
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4.180
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3.400
3.380
2.660
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3.955
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3.780
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4.510
3.800
4.170
4.400
3.770
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3.825
3.130
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3.220
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