BIOZONE

VCE | BIOLOGY UNITS 3&4

SAMPLE PACKET
FOR CLASSROOM TRIAL

CHAPTER 1

Nucleic Acids and Proteins

Key terms

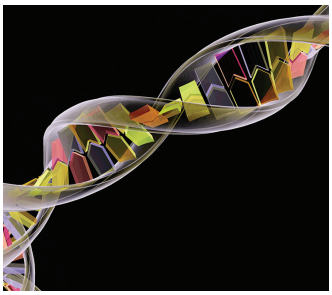
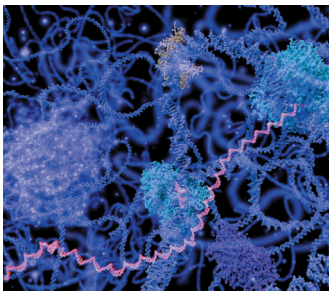
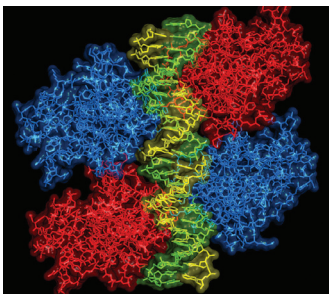
adenine
anticodon
base-pairing rule
coding strand
cytosine
denaturation
DNA
double-helix
exon
fibrous protein
gene
gene expression
genetic code
genome
globular protein
guanine
hydrogen bonding
intron
nucleic acids
nucleotides
operator
operon
peptide bond
polypeptide
primary structure
promoter
protein
proteome
purine
pyrimidine
quaternary structure
regulatory gene
repressor
ribosome
RNA (mRNA, rRNA, tRNA)
secondary structure
semi-conservative replication
structural gene
template strand
terminator sequence
tertiary structure
thymine
transcription
translation
uracil

Nucleic acids are information molecules

Key knowledge

Activity number

- ☐ 1 Describe the structure of DNA and explain how its structure provides a mechanism for self-replication. Include reference to the base-pairing rule, the anti-parallel strands, and the role of hydrogen bonding between purines and pyrimidines. — 1 3 5
- ☐ 2 PRAC Investigate the nature of DNA by making a DNA extraction. — 2
- ☐ 3 PRAC Create a model of DNA to demonstrate the base pairing rule. — 3
- ☐ 4 Describe the structure of the three types of RNA (mRNA, tRNA, and rRNA) and their functional roles in cellular activities. Compare and contrast RNA and DNA. — 3
- ☐ 5 Describe how nucleic acids encode the instructions for the synthesis of proteins in cells, including reference to the relationship between the base sequence in a nucleic acid and the order of the amino acids in a polypeptide chain. — 6
- ☐ 6 Describe the features of the genetic code, including: — 7
  - 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.
- ☐ 7 Explain what is meant by a gene. Describe the steps involved in gene expression including transcription, RNA processing (eukaryotic cells), and translation. Identify where in the cell each of these steps occurs. — 8-10
- ☐ 8 Outline what is involved in RNA processing, 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? — 9

Gene structure and regulation

Key skills and knowledge

- ☐ 9 Describe the structure of a gene, distinguishing between structural and regulatory genes. Where are regulatory genes located in relation to the genes they control? How is this different for prokaryotes and eukaryotes? — 11
- ☐ 10 Describe the operon model of gene expression in prokaryotes, recognising that both gene induction and gene repression are involved in the regulation of gene expression in bacteria. Explain gene repression in prokaryotes (e.g. the *trp* operon) in which the transcription of genes that are normally transcribed all the time are switched off. Contrast gene repression with a gene induction model (*lac* operon). — 12

The structure and function of proteins

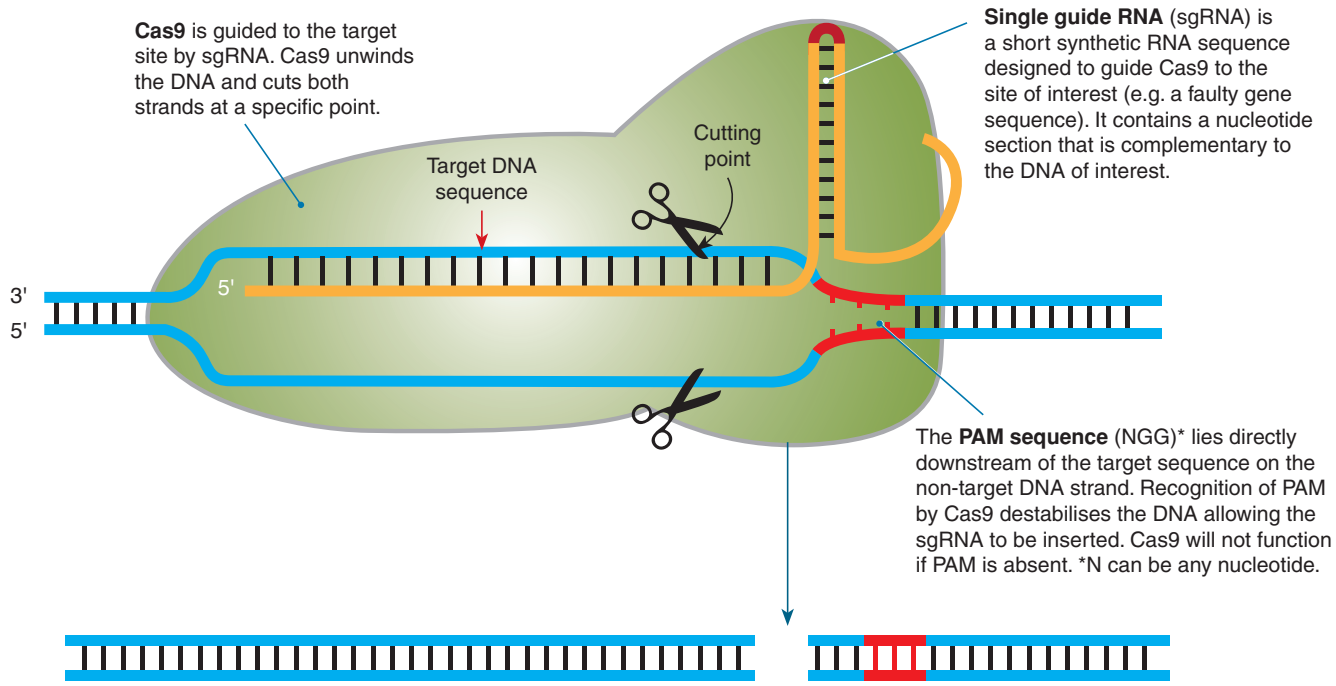
Key skills and knowledge

- ☐ 11 Explain how a polypeptide is synthesised from amino acid monomers. Explain how the properties of amino acids determine how they interact and how these interactions create the hierarchical levels of structure that produce a functional protein. — 13 14
- ☐ 12 PRAC Create a model to investigate the hierarchical nature of protein structure.
- ☐ 13 Explain how protein shape is related to function and compare the functional roles of globular and fibrous proteins. Identify and describe the diverse roles of proteins making up an organisms's proteome. — 15-17
- ☐ 14 Describe how proteins are modified after translation for different roles. Interpret diagrams to explain how the rough endoplasmic reticulum, Golgi apparatus, and associated vesicles are involved in the packaging and export of proteins from the cell via the protein secretory pathway. — 18 19

24 New Tools: Gene Editing with CRISPR

Key Idea: CRISPR is a complex comprising Cas9 endonuclease and sgRNA. The CRISPR complex cuts DNA at very specific sequences and can be used to edit genes.

CRISPR-Cas9 (shortened to CRISPR and pronounced crisper) is an endonuclease complex occurring naturally in bacteria, which use it to edit the DNA of invading viruses. CRISPR is able to target specific stretches of DNA and edit it at very precise locations. Two key components are required for CRISPR to work: an RNA guide that locates and binds to the target piece of DNA and the Cas9 endonuclease that unwinds and cuts the DNA. The technology has potential applications in correcting mutations responsible for disease, switching faulty genes off, adding new genes to an organism, or studying the effect of specific genes. It represents a major advance because it allows more precise and efficient gene editing at much lower cost than ever before.



The cut DNA can be repaired using one of the following methods:

Gene knock in "gene editing"

A new DNA sequence is inserted into the DNA break. For example allows a faulty gene sequence can be replaced with the correct sequence to restore normal gene function.

Gene knock out "gene silencing"

Errors occur as the cell's normal repair mechanisms mend the broken DNA, causing the insertion or deletion of bases. The resulting frame-shift mutation changes the way the nucleotide sequence is read, either disabling gene function or producing a STOP signal. This technique can be used to silence a faulty gene.

1. What are the roles of the following in CRISPR gene editing:

   (a) Cas9: _____

   (b) sgRNA: _____

2. Outline two ways CRISPR can be used to edit genes: _____

   _____

   _____

   _____

3. What benefits are offered by CRISPR technology? _____

   _____

   _____

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26 Applications of Profiling

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

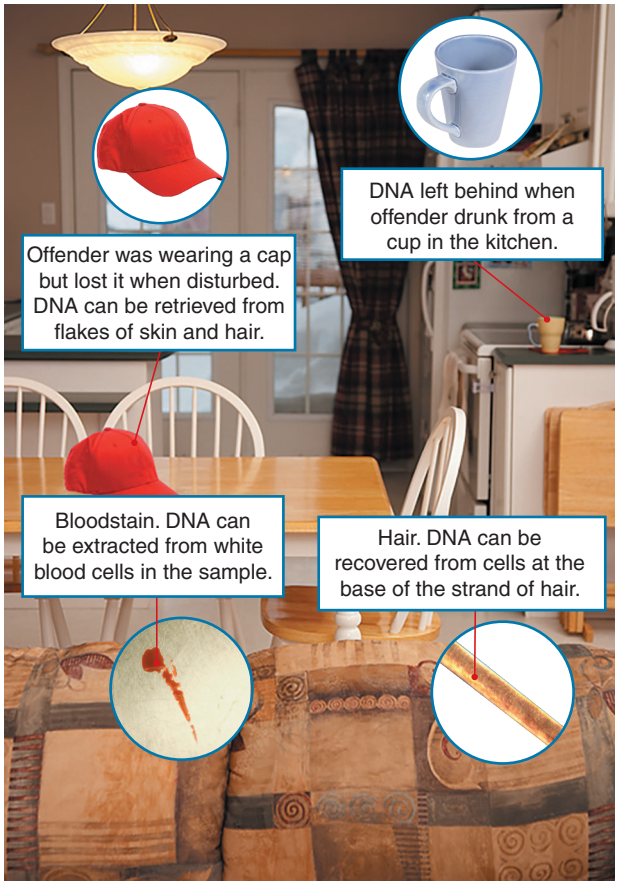
The use of DNA as a tool for solving crimes such as homicide is well known, but it can also has several other applications. DNA evidence has been used to identify body parts, solve cases of industrial sabotage and contamination, for paternity testing, and even in identifying animal products illegally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

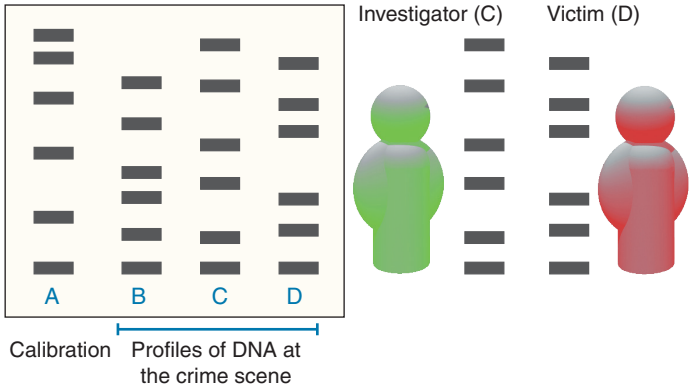
Using DNA to solve crimes

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.

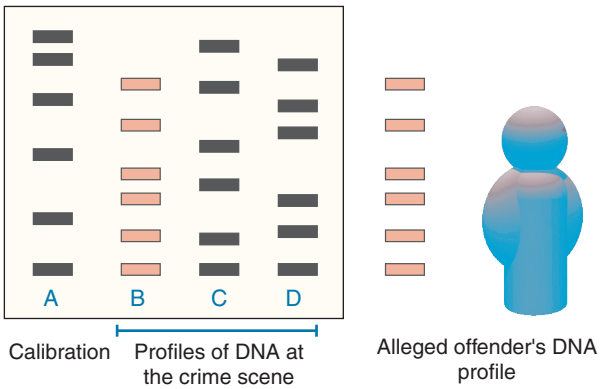




There are two different ways an offender can be identified through DNA profiling.

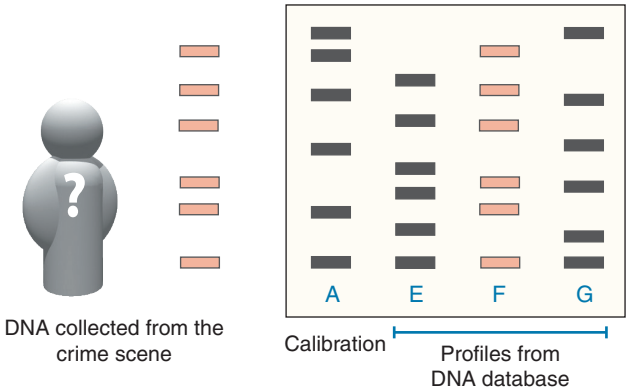
1. If a person is suspected of a crime, a sample of their DNA can be taken (e.g. blood sample) and compared to DNA evidence collected at the crime scene. A match indicates they are the offender. If there is no match, the person can be cleared as a suspect.
2. In cases where the suspect is unknown, biological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

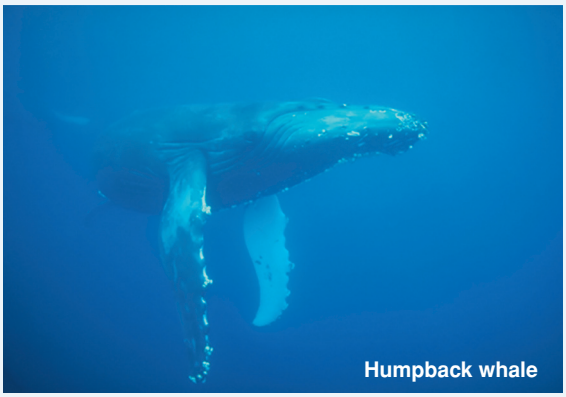
DNA profiling can be used to determine paternity (and maternity) by looking for matches in alleles between parents and children. It is used in cases such as child support or inheritance. DNA profiling can establish the certainty of paternity (and maternity) to a 99.99% probability of parentage.

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.

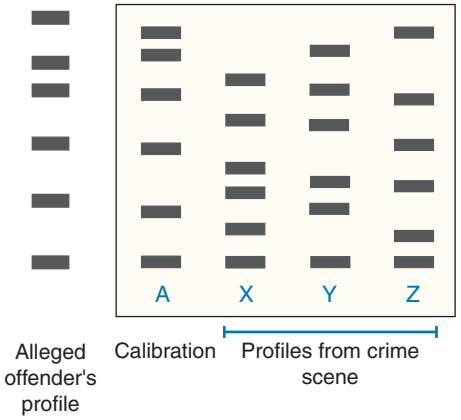
Between 1999 and 2003, researchers used DNA profiling to investigate whale meat sold in markets in Japan and South Korea. They found 10% of the samples tested were from fully protected whales including western grey whales and humpbacks. They also found that many more whales were being killed than were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

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

   (a) Could the man be the biological father? _____

   (b) Explain your answer: _____

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46 Investigating Photosynthetic Rate

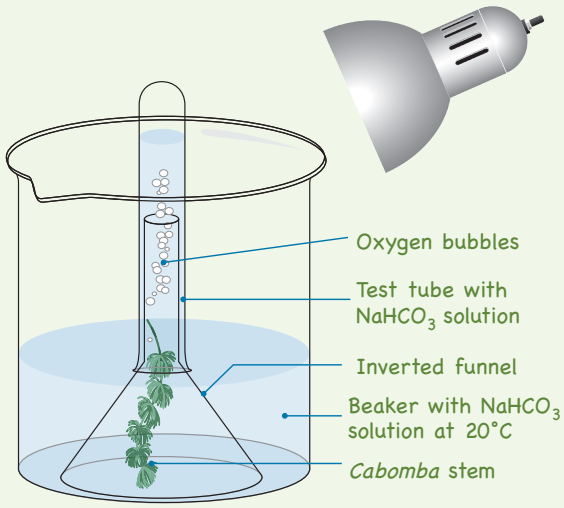
Key Idea: Measuring the production of oxygen provides a simple way to measure the rate of photosynthesis.

The rate of photosynthesis can be investigated by tracking the substances involved in photosynthesis. These include measuring the uptake of carbon dioxide, the production of oxygen, or the change in biomass over time. Measuring the rate of oxygen production provides a good approximation of the photosynthetic rate and is relatively easy to carry out.

Investigation 4.1 Investigating photosynthetic rate

See appendix for equipment list.

1. Weigh 0.8–1.0 grams of *Cabomba aquatica* stem on a balance. Cut the stem underwater and invert to ensure a free flow of oxygen bubbles.
2. Place into a beaker filled (at approximately 20°C) with a solution containing 0.2 mol/L sodium hydrogen carbonate (to supply carbon dioxide).
3. Invert a funnel over the *Cabomba* and then invert a test tube filled with the sodium hydrogen carbonate solution on top to collect any gas produced.
4. Place the beaker at distances 20, 25, 30, 35, 40, 45, and 50 cm from a 60W light source. Measure the light intensity with a lux meter at each interval.
5. Leave the *Cabomba* stem to acclimatise to the new light level for 5 minutes before recording data. Count the bubbles for a period of three minutes at each distance and record.



6. Alternatively the volume of gas captured in the test tube can be measured and recorded.

Distance (cm)	Light intensity (lx)	Bubbles counted in three minutes	Bubbles per minute	Volume (mL)
50 cm				
45 cm				
40 cm				
35 cm				
30 cm				
25 cm				
20 cm				

1. Use the data to draw a graph of the bubble produced per minute vs light intensity:

2. Why is measuring light intensity directly in lux better than inferring light intensity from the measured distance?

_____

_____

_____

4. The sample of gas collected during the experiment was tested with a glowing splint. The splint reignited when placed in the gas. What does this confirm about the gas produced?

_____

5. Why is measuring gas collected rather than bubbles produced a more accurate why of recording data?

_____

_____

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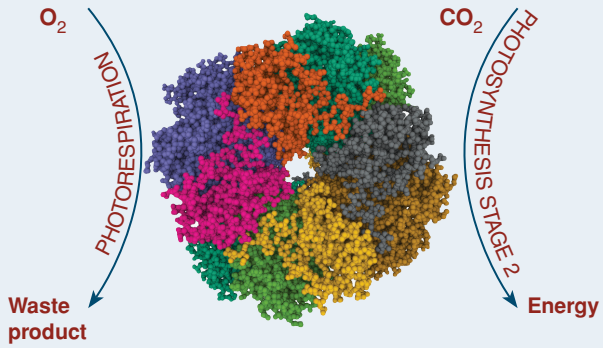
45 Adaptations for Maximising Photosynthesis

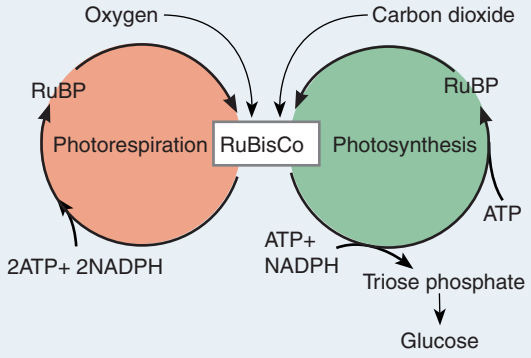
Key Idea: RuBisCo is an inefficient enzyme and some plant groups have evolved ways to reduce the mistakes it makes and so increase the efficiency of photosynthesis.

RuBisCo is an enzyme involved in the fixation of carbon in photosynthesis. It is very inefficient at this process. Not only does it carry out a very low number of reactions per second, but 20% of the those reactions involve oxygen instead of carbon dioxide (a process called photorespiration). This produces molecules the plant can't use and so costs the plant energy. Some groups of plants have evolved processes that separate oxygen from the air from carbon dioxide and so improve the efficiency of RuBisCo.

RuBisCo is not specific



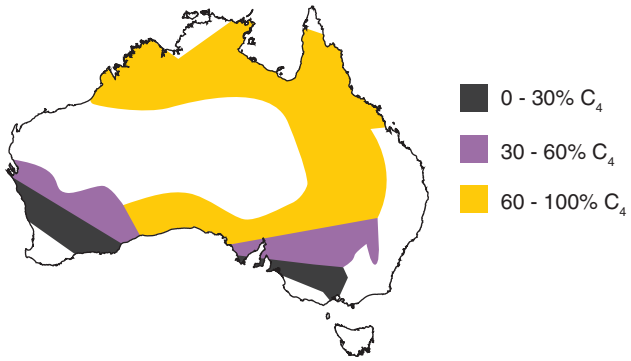
RuBisCo catalyses the carboxylation (adding of carbon) of the molecule ribulose-1,5-bisphosphate (RuBP) in the first step of the light independent reactions in photosynthesis. Unfortunately it does not always discriminate between carbon dioxide and oxygen and can add oxygen to RuBP instead. The plant then wastes energy in breaking down the resulting molecule in a process called photorespiration.



Photosynthetic strategies

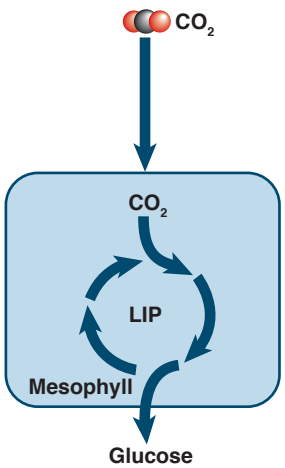
- In about 85% of plants on Earth, the first detectable compound made in photosynthesis is a 3-carbon compound called glycerate 3-phosphate (GP). These plants are called C_3 plants.
- However, in some plants a 4-carbon molecule is made first and a unique leaf anatomy allows CO_2 to concentrate around Rubisco, reducing photorepsiration and increasing photosynthetic efficiency. These plants, which include cereals and tropical grasses, are called C_4 plants. They have high rates of photosynthesis, thriving in environments with high light levels and warm temperatures. The high productivity of C_3 plants at high temperatures gives them a competitive advantage in tropical climates. CAM plants also produce oxaloacetate as their first photosynthetic compound but produce it at night, storing carbon dioxide until light is available.

% C_4 plants across Australia



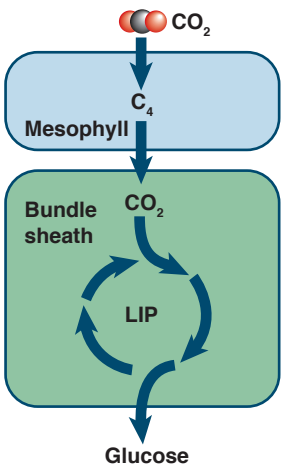
The photosynthetic strategy that a plant possesses is an important factor in determining its distribution. Many of the enzymes of C_4 plants have optimum temperatures well above 25°C, so they thrive in hot tropical and sub-tropical climates. Under these conditions, they out-compete most C_3 plants because they achieve higher photosynthetic rates. The proportion of C_4 plants in Australia is greatest near the tropics and arid interior.

C_3 plant



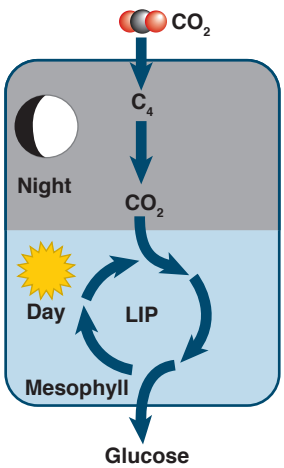
In C_3 plants carbon dioxide is fixed directly from the air. Stomata must be open (which lets air in, but also water out). The light independent phase (LIP) occurs in the leaf mesophyll of the leaf. This leaves RuBisCo exposed to oxygen, reducing photosynthetic efficiency.

C_4 plant



In C_4 plants, carbon dioxide is fixed in a two step process. Carbon dioxide is used to produce oxaloacetate in the leaf mesophyll. This diffuses deeper into the leaf. CO_2 is released to RuBisCo deeper in the leaf away from oxygen, increasing efficiency.

CAM plant



In CAM plants stomata are opened at night to take in CO_2 (stored as oxaloacetate). This reduces water loss on hot days. During the day stomata are closed, reducing RuBisCo exposure to oxygen and again increasing photosynthetic efficiency.

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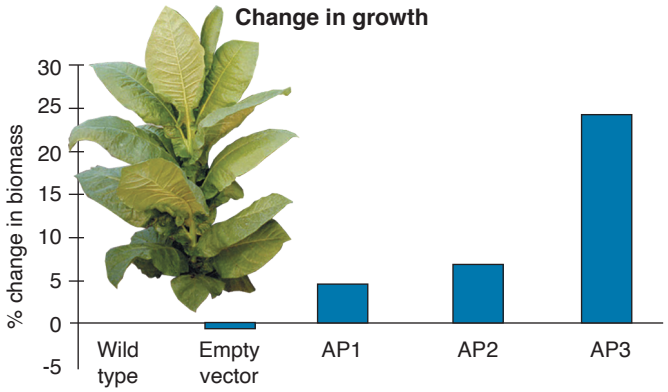
Increasing photosynthesis efficiency

- About 20% of the time RuBisCo uses oxygen instead of CO_2, producing a plant toxic molecule. The plant wastes energy passing the molecule along a biochemical pathway in order to break it down and recover the original useful molecule. As the temperature increases this problem becomes worse.
- Recently scientists genetically engineered cells of a tobacco plant (a C_3 plant) to shortcut the photorespiration pathway. They used *Agrobacterium tumefaciens* to insert genes from various organisms, including *E. coli*, *Chlamydomonas reinhardtii,* and *Arabidopsis thaliana*, into tobacco plant cells. Three strains of engineered tobacco plant were produced, each with an alternative photorespiration pathway.



Synthetic glycolate metabolism pathways stimulate crop growth and productivity in the field. Paul F. South *et al*, Science 04 Jan 2019

- By short-cutting the photorespiration pathway, photosynthetic efficiency would increase and the pant could divert more energy to growth. This could lead to larger, more efficiently grown crops, producing more food for a growing world population.
- The plants, AP1, AP2, and AP3 were grown and tested. The strain AP3 produced the best result. First generation plants had a biomass increase of 20%. Second generation AP3 plants had a biomass average increase of about 24% and up to 37%.

1. Explain why C_4 plants have a competitive advantage over C_3 plants in the tropics: _____

2. Explain why CAM plants have a competitive advantage over C_4 and C_3 plants in arid situations: _____

3. Explain what C_4 plants achieve by carrying out the light independent reactions inside the bundle sheath:

4. Study the map of Australia showing the distribution of C_4 plants. Explain the distribution pattern in terms of their competitive advantage and the environmental conditions required for this advantage:

5. Suggest why increasing the ambient CO_2 concentration increases the rate of photosynthesis in C_3 plants:

6. Why would genetically engineering a crop plant to short circuit the photorespiration pathway potentially increase crop yields?

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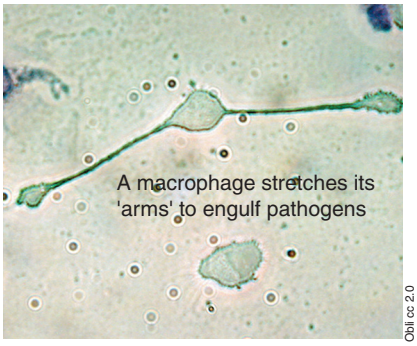
68 The Innate Immune Response

Key Idea: The innate immune response provides a rapid response to contain and destroy pathogens. Inflammation is an important part of the response.

The innate immune system provides protection against a pathogen, even if it has never encountered it before. The innate response is very fast and provides general protection (it is not antigen specific), but does not provide long lasting immunity. Many different cells and processes are involved. The primary outcome is to destroy and remove the cause of infection. This is achieved through containing the infection through inflammation and then recruitment of immune cells to destroy the pathogen. During this process a series of biochemical reactions (the complement system) are activated to destroy the pathogen and recruit immune cells to the site.

Phagocytic cells of the innate immune system



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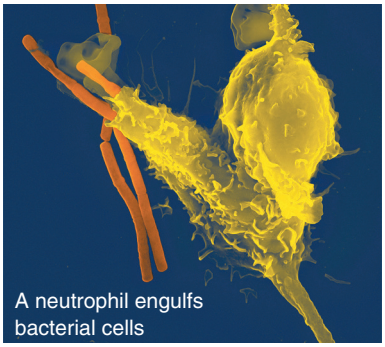
Macrophage

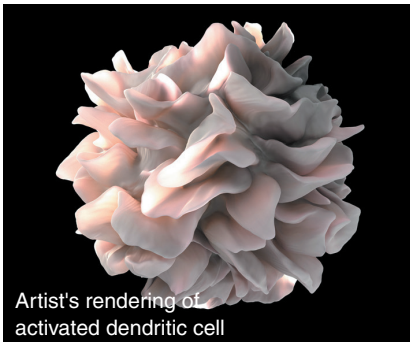
Macrophages are very large and are highly efficient phagocytes. They are found throughout the body and move using an amoeboid movement (above) to hunt down and destroy pathogens. Macrophages also have a role in recruiting other immune cells to an infection site.



Volker Brinkmann PLOS cc 2.5

Neutrophil

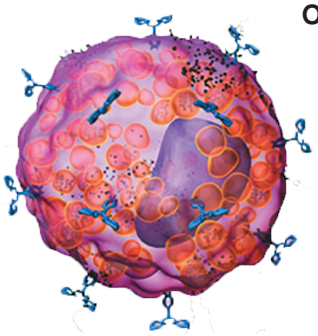
Neutrophils are the most abundant type of phagocyte and are usually the first cells to arrive at the site of an infection. They contain toxic substances that kill or inhibit the growth of bacteria and fungal pathogens. Neutrophils release cytokines which amplify the immune response and recruit other cells to the infection site.



Dendritic cell

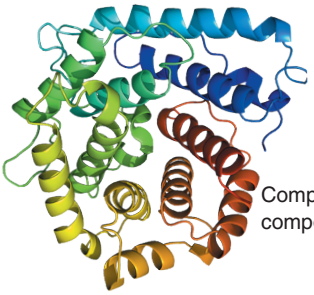
Dendritic cells are present in tissue that are in contact with the external environment (e.g. skin, and linings of the nose, lungs, and digestive tract). They act as messengers between the innate and adaptive immune system by presenting antigen materials to the T cells of the immune system.

Other cells and processes of the innate immune response



Mast cells

Mast cells contain a lot of histamine, a chemical involved in both inflammation and allergic responses. When activated, histamine is released from the mast cell causing the blood vessels to dilate and become leaky. The increased permeability allows phagocytes to reach the site of infection.



Complement proteins

The complement system comprises a number of different proteins. The proteins circulate as inactive precursors until they are activated. Complement proteins have three main roles: phagocytosis, attracting macrophages and neutrophils to the infection site, and rupturing the membranes of foreign cells.

The process of inflammation

The inflammatory process is a protective response to pathogen invasion. It has several functions: (1) to destroy the cause of the infection and remove it and its products from the body; (2) if this fails, to limit the effects on the body by confining the infection to a small area; (3) replacing or repairing tissue damaged by the infection.

1. Outline the role of the following phagocytes in the innate immune response:

(a) Macrophages: _____

_____

(b) Neutrophils: _____

_____

(c) Dendritic cells: _____

_____

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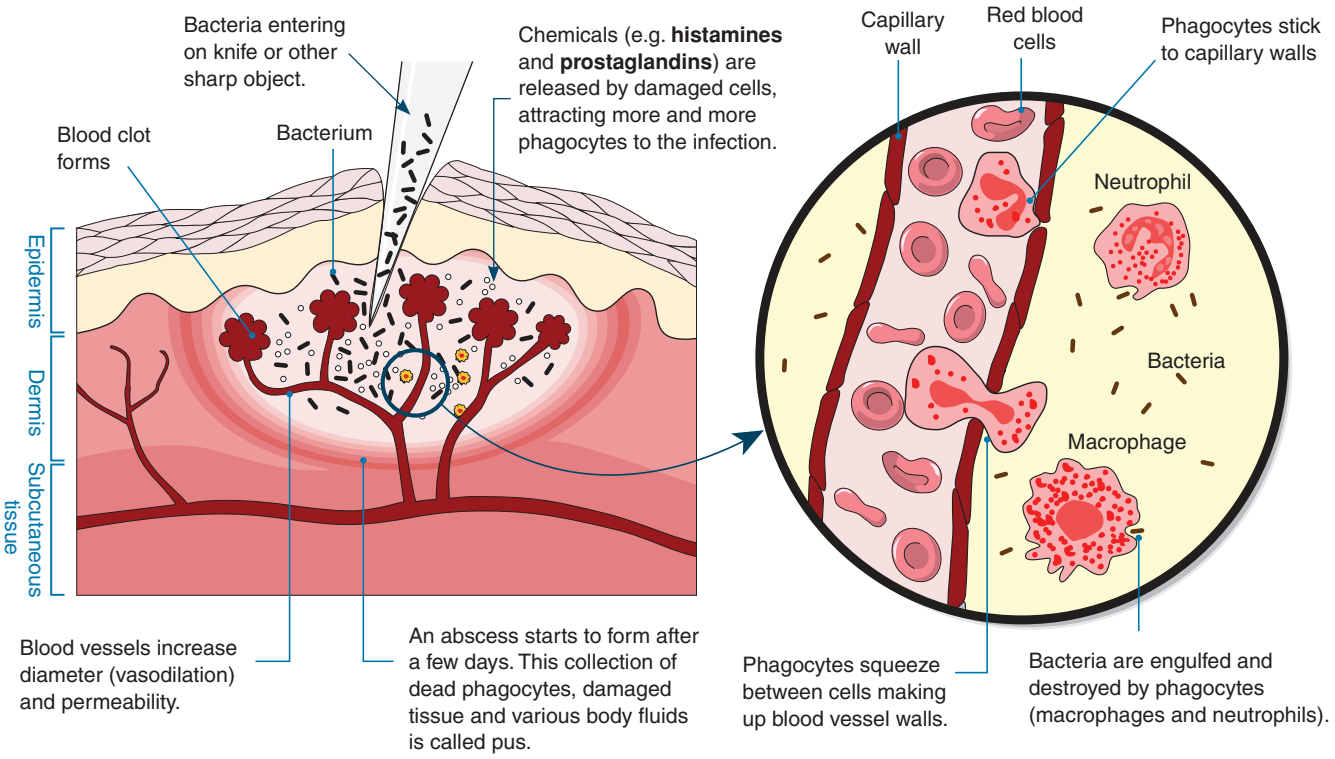
The inflammatory response



Stages in the inflammatory response

Increased diameter and permeability of blood vessels
Blood vessels increase their diameter and permeability in the area of damage. This increases blood flow to the area and allows defensive substances to leak into tissue spaces.

Phagocyte migration and phagocytosis
Within one hour of injury, phagocytes appear on the scene. They squeeze between cells of blood vessel walls to reach the damaged area where they destroy invading microbes.

Tissue repair
Functioning cells or supporting connective cells create new tissue to replace dead or damaged cells. Some tissue regenerates easily (skin) while others do not at all (cardiac muscle).

2. What role does the complement system play in immunity? _____

_____

_____

3. Outline the three stages of inflammation and identify the beneficial role of each stage:

(a) _____

_____

(b) _____

_____

(c) _____

_____

4. What role do mast cells play in inflammation? _____

_____

_____

5. Why does pus form at the site of infection? _____

_____

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69 Phagocytes and Phagocytosis

Key Idea: Phagocytes are mobile white blood cells that ingest microbes and digest them by phagocytosis.

Phagocytosis is the process by which a cell engulfs another cell or particle. Cells which do this are called phagocytes. All types of phagocytes (e.g. neutrophils, dendritic cells, and macrophages) are white blood cells. These specialised cells have receptors on their surfaces that can detect antigenic material, such as microbes. They then ingest the microbes and digest them by phagocytosis. As well as destroying microbes, phagocytes also release substances called cytokines that help to coordinate the overall response to an infection. Macrophages and dendritic cells also play a role in antigen presentation in processing and presenting antigens from ingested microbes to other cells of the immune system.

1 Detection and interaction
Microbe coated in chemical markers is detected by the phagocyte, which attaches to it. Chemical markers coating the foreign material (e.g. a bacterial cell), mark it as a target for phagocytosis.

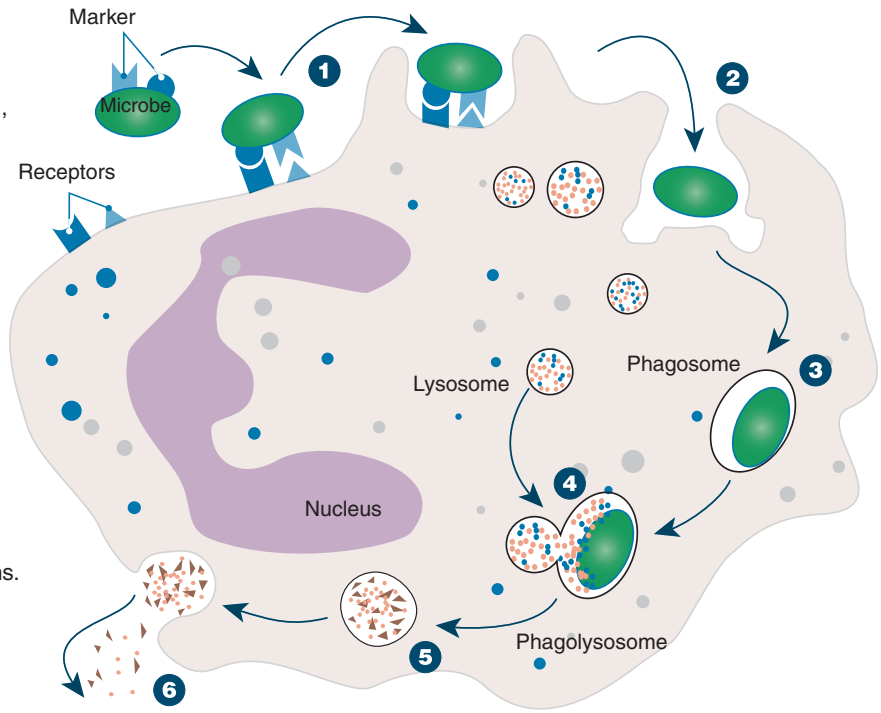
2 Engulfment
The markers trigger engulfment of the microbe by the phagocyte. The microbe is taken in by endocytosis.

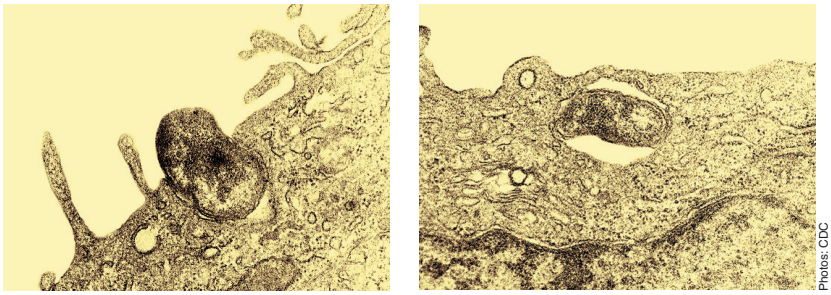
3 Phagosome forms
A phagosome forms, enclosing the microbe in a membrane.

4 Fusion with lysosome
Phagosome fuses with a lysosome containing powerful antimicrobial proteins. The fusion forms a phagolysosome.

5 Digestion
The microbe is broken down into its chemical constituents.

6 Discharge
Indigestible material is discharged from the phagocyte.





Photos right: A cell ingests and engulfs a bacterium by phagocytosis.

Photos: CDC

1. Identify the white blood cells capable of phagocytosis: _____

2. Explain the role of chemical markers and phagocyte receptors in enhancing phagocytosis: _____

3. What is the purpose of phagocytosis and how is involved in internal defence? _____

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135 Genomic Comparisons and Relatedness

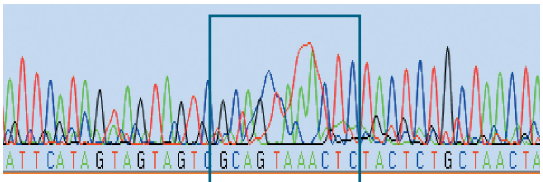
Key Idea: Comparing nucleotide sequences in DNA provides detailed information about relatedness between organisms.

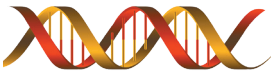
DNA sequencing provides the precise order of nucleotides in a DNA molecule. This information, which can now be analysed using sophisticated computing, allows researchers to compare sequences between species in much more detail than is possible with DNA hybridisation. Not only can areas of difference 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

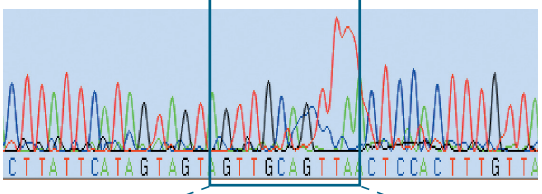
Improved DNA sequencing techniques and powerful computing software have allowed researchers to accurately and quickly sequence and compare entire genomes (all an organism's genetic material) within and between species.

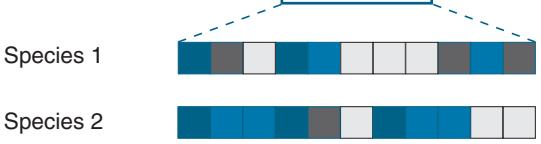
Once DNA sequences have been determined, they are aligned and compared to see where the differences occur (right). DNA sequencing generates large volumes of data and the rise in computing power has been central to modern sequence analyses. The technological advances have been behind the new field of bioinformatics, which uses computer science, statistics, mathematics, and engineering to analyse and interpret biological data.





DNA: Species 2





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".

1. (a) What advantages does DNA sequence comparison have over DNA hybridisation? _____

_____

_____

(b) How is this an advantage in determining evolutionary relationships? _____

_____

_____

2. 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 most closely related: _____

(b) Identify the two species that are least closely related: _____

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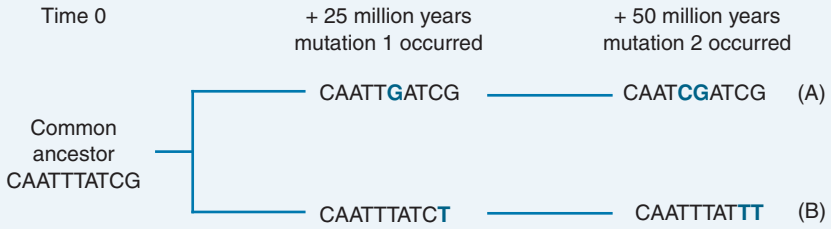
136 Molecular Clock Theory

Key Idea: The molecular clock hypothesis proposes that mutations occur at a steady rate and that changes in DNA sequences between species can determine phylogeny.

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 a theoretical example, the DNA sequence for a gene in two species (A & B, right) 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 mya.

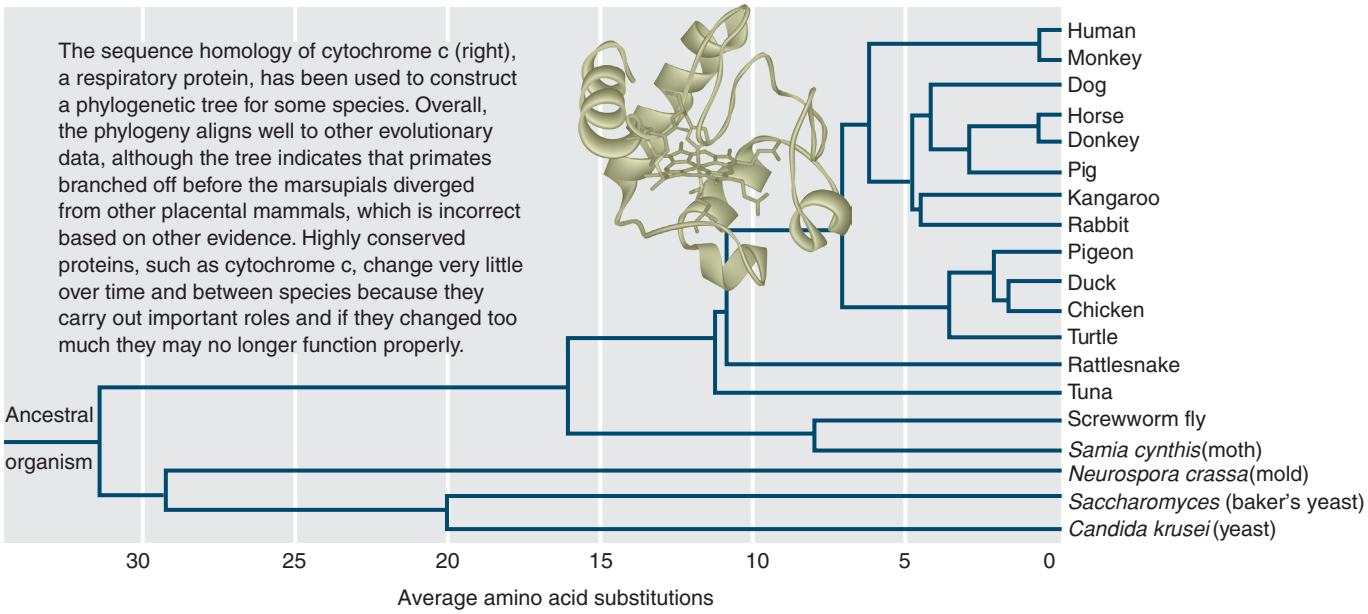


Cytochrome *c* and the molecular clock theory

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
Human		Gly	Asp	Val	Glu	Lys	Gly	Lys	Lys	Ile	Phe	Ile	Met	Lys	Cys	Ser	Gln	Cys	His	Thr	Val	Glu	Lys
Pig												Val	Gln			Ala							
Chicken				Ile						Val		Val	Gln			Ala							
Dogfish										Val		Val	Gln			Ala							Asn
Drosophila	<<									Leu		Val	Gln	Arg		Ala							Ala
Wheat	<<		Asn	Pro	Asp	Ala		Ala				Lys	Thr	Arg		Ala						Asp	Ala
Yeast	<<		Ser	Ala	Lys			Ala	Thr	Leu		Lys	Thr	Arg		Glu	Leu						

This table 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 sequence homology of cytochrome c (right), a respiratory protein, has been used to construct a phylogenetic tree for some species. Overall, the phylogeny aligns well to other evolutionary data, although the tree indicates that primates branched off before the marsupials diverged from other placental mammals, which is incorrect based on other evidence. 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.



1. Describe a limitation of using molecular clocks to establish phylogeny: _____

_____

_____

2. For cytochrome *c*, suggest why amino acids 14 and 17 are unchanged in all the organisms shown in the table: _____

_____

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Identifying Key Science Skills and Online Support

The tab system is a useful way to identify important parts of the **VCE Biology study design (2022 - 2026)**. The colour coded page tabs show where "**Key Science Skills**" are addressed. The tabs also allow you to see at a glance if online support is provided and if there are content or concept links with other activities.

KEY SCIENCE SKILLS

Develop aims and questions, formulate hypotheses and make predictions

- Identify, research, and construct aims and questions
- Identify variables in controlled experiments
- Formulate hypotheses to focus investigation
- Predict possible outcomes

Plan and conduct investigations

- Determine methodology, classification and identification, controlled experiments, correlational studies, fieldwork, literature review, modelling, simulations
- Design and conduct investigations, considering procedures, error, amount of data
- Work independently and collaboratively adapt methodology

Construct evidence-based arguments and draw conclusions

- Distinguish scientific and non-scientific ideas
- Evaluate data for evidence-based support of aims, prediction, or hypothesis
- Use reasoning to construct scientific arguments and to draw and justify conclusions
- Identify and describe limitations of conclusions
- Discuss implications of findings

Comply with safety and ethical guidelines

- Demonstrate safe lab practices using risk assessments
- Apply relevant health and safety guidelines
- Demonstrate ethical conduct when undertaking and reporting investigations

Analyse, evaluate and communicate scientific ideas

- Use appropriate terminology
- Discuss relevant biological information, ideas, concepts, theories, and models
- Analyse and explain how models and theories are used
- Critically evaluate and interpret scientific and media texts
- Analyse and evaluate bioethical issues
- Use clear and concise expression
- Acknowledge sources of information

Generate, collate, and record data

- Systematically generate and record primary data, collate secondary data
- Record and summarise data, including use of a logbook
- Organise and present data
- Plot graphs showing liner and non-linear relationships

Analyse and evaluate data and investigation methods

- Process quantitative data using mathematics
- Identify and analyse experimental data qualitatively
- Identify outliers and contradictory data
- Repeat experiments and evaluate methods

ONLINE SUPPORT

Resource Hub

This tab indicates the activity is supported with online content, through the Resource Hub.

Easy navigation to video clips, animations, 3D models, databases, and spreadsheets to support the activities in the book.