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12 Diversity Indices

Key Idea: Diversity indices quantify the biodiversity in an area and can be used to measure ecosystem health.

The health of an ecosystem can be assessed by measuring both the number and relative abundance of organisms present. A change in species composition over time can therefore indicate changes in that ecosystem's status. Certain **indicator species** are also useful in this respect as they are associated with habitats of a particular status, e.g. unpolluted water. Scientists quantify biodiversity using a diversity index. Diversity indices take account of both the species evenness and species richness and can be used to assess environmental stress (or recovery).

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 following simple formula. Communities with a wide range of species produce a higher score than communities dominated by larger numbers of only a few species.

$$D = 1-(\sum(n/N)^2)$$

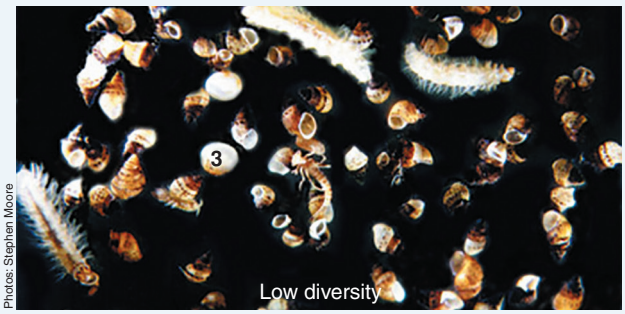
D = Diversity index
N = Total number of individuals (of all species) in the sample
n = Number of individuals of each species in the sample

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 $D = 1 - (\sum(n/N)^2)$ is:

	Species	n	n/N	$(n/N)^2$
A	(backswimmer)	12	0.300	0.090
B	(stonefly larva)	7	0.175	0.031
C	(silver water beetle)	2	0.050	0.003
D	(caddisfly larva)	6	0.150	0.023
E	(water spider)	5	0.125	0.016
F	(mayfly larva	8	0.20	0.040
		$\Sigma n=40$	$\Sigma(n/N)^2=0.201$	

D = 1-0.201 = 0.799



Photos: Stephen Moore

Using diversity indices and the role of indicator species

To be properly interpreted, indices are usually evaluated with reference to earlier measurement or a standard ecosystem measure. The photographs above show samples from two stream communities, 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 photographs also show indicator species. The left hand image shows a stonefly (1) and an alderfly larva (2). These species (together with mayfly larvae) are typical of clean, well oxygenated water. The right hand image is dominated by snails (3), which are tolerant of a wide range of conditions, included degraded environments.

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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Studying biodiversity

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	$(n/N)^2$
Species 1	35		
Species 2	14		
Species 3	13		
Species 4	12		
Species 5	8		
Species 6	6		
Species 7	6		
Species 8	4		
	$\Sigma n = 98$		$\Sigma(n/N)^2 =$

Species	Number of animals (n)	n/N	$(n/N)^2$
Species 1	74		
Species 2	20		
Species 3	3		
Species 4	3		
Species 5	1		
Species 6	0		
Species 7	0		
Species 8	0		
	$\Sigma n = 101$		$\Sigma(n/N)^2 =$

Species 1
Mite

Species 2
Ant

Species 3
Earwig

Species 4
Woodlice

Species 5
Centipede

Species 6
Longhorn beetle

Species 7
Small beetle

Species 8
Pseudoscorpion

3. Write a hypothesis for this investigation: _____

_____

_____

4. (a) Complete the two tables above by calculating the values for n/N and $(n/N)^2$ for the student's two sampling sites:

   (b) Calculate the Simpson's Index of Diversity for site 1: _____

   (c) Calculate the Simpson's Index of Diversity 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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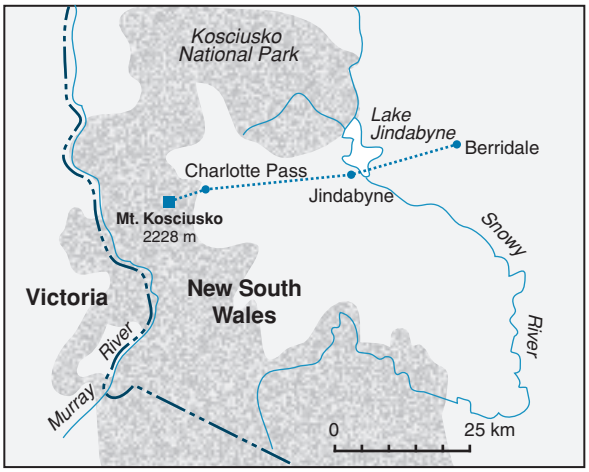
22 Community Change With Altitude

Key Idea: Changes in physical factors associated with increasing altitude produce marked bands of vegetation (zonation).

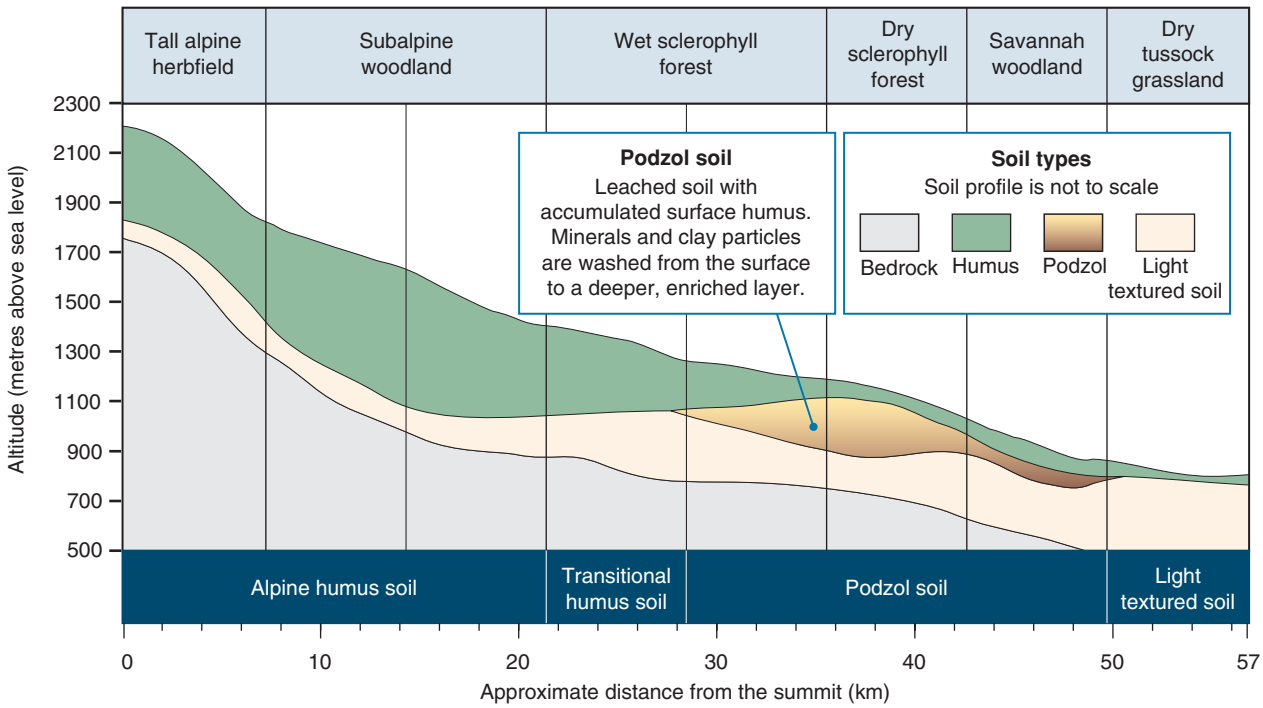
The Kosciusko National Park lies on the border between Victoria and New South Wales. In 1959, a transect between Berridale and the summit of Mt. Kosciusko was sampled. The map on the right shows the transect as a dotted line representing a distance of some 50-60 km.

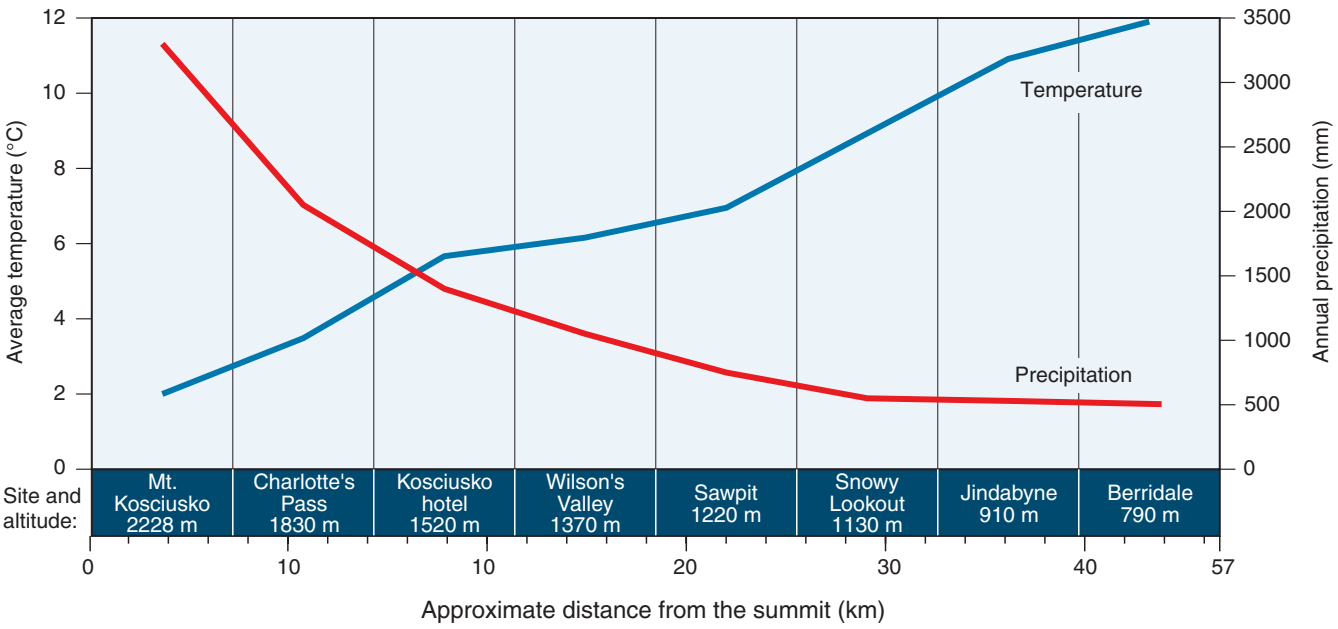


The distribution of plant species on Mount Kosciusko is affected by changes in the physical conditions with increasing altitude. The two graphs below show (1) the profile of the transect showing changes in vegetation and soil types with increasing altitude and (2) the changes in temperature and rainfall (precipitation) with altitude.

The low altitude soil around Berridale has low levels of organic matter supporting dry tussock grassland vegetation. The high altitude alpine soils are rich in organic matter, largely because of slow decay rates.

Profile of Mount Kosciusko





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1. Calculate the vertical distance (change in altitude) in metres, between Berridale and Mount Kosciusko: _____

2. Name the three physical factors illustrated on the previous page: _____

_____

3. Using the diagrams and graphs on the previous page, describe the following physical measurements for the three sample sites listed below:

	Altitude (m)	Temperature (°C)	Precipitation (mm)	Soil type
Berridale:				
Wilson's Valley:				
Mt Kosciusko:				

4. Study the graph of temperature vs altitude. How does the temperature change with increasing altitude?

_____

5. Study the graph of precipitation vs altitude. How does the precipitation change with increasing altitude?

_____

6. Why is the leaf litter slow to decay in alpine soil? _____

_____

7. What is the name given to the banded distribution pattern of the vegetation on the slopes of Mt. Kosciusko?

_____

8. Wet sclerophyll forest is found part way up the slope of Mt. Kosciusko.

   (a) Study the profile on the previous page and determine the altitude range for wet sclerophyll forest (in metres):

   _____

   (b) What physical factor probably prevents the wet sclerophyll forest growing at a lower altitude?

   _____

   (c) What physical factor probably prevents the wet sclerophyll forest growing at a higher altitude?

   _____

9. Name a physical factor other than temperature or precipitation that changes with altitude: _____

_____

10. Describe another example of a banded pattern of species distribution in response to an environmental gradient:

_____

_____

11. Discuss the contribution of environmental gradients to community diversity: _____

_____

_____

_____

_____

_____

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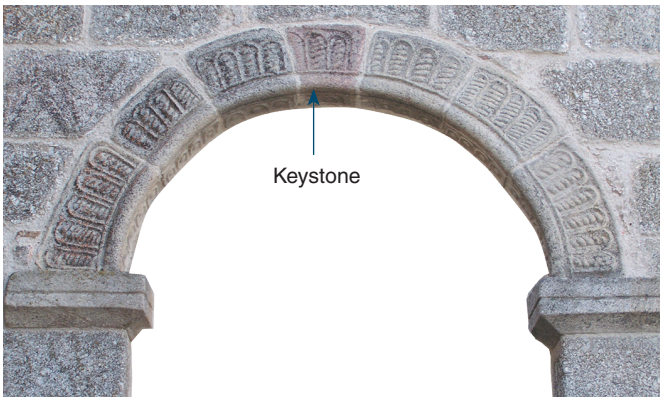
58 The Role of Keystone Species

Key Idea: All organisms within an ecosystem contribute to its structure and functioning, but keystone species have a disproportionate effect on ecosystem processes.

Although every species has a role in ecosystem function, some have a disproportionate effect on ecosystem processes and stability (how unchanging the ecosystem is over time). These species are called **keystone species** and they are important because they play a pivotal role in the way the ecosystem works, e.g. as top predators or by recycling nutrients. The loss of a keystone species can have a large and rapid impact on the structure and function of an ecosystem, changing the balance of relationships and leading to instability. This has important implications for ecosystem management because many keystone species are endangered.

Why are keystone species important?

A keystone species is one that plays a unique and crucial role in the way an ecosystem functions. Often, but not always, keystone species are top predators. The role of the keystone species varies from ecosystem to ecosystem, but the loss of a keystone species from any ecosystem has a domino effect, and a large number of species can be affected. This can lead to can rapid ecosystem change or the collapse of the ecosystem completely.



The term keystone species comes from the analogy of the keystone in a true arch (above). An archway is supported by a series of stones, the central one being the **keystone**. If the keystone is removed the arch collapses.

Ochre starfish: Paine removed these in his study to see what the effect would have on the rocky shore community.

Keystone species in action

The idea of the keystone species was first hypothesised in 1969 by Robert Paine. He studied an area of rocky seashore, noting that diversity seemed to be correlated with the number of predators (ochre starfish) present (i.e. diversity declined as the number of predators declined).

To test this he removed the starfish from an 8 m by 2 m area of seashore. Initially, the barnacle population increased rapidly before collapsing and being replaced by mussels and gooseneck barnacles. Eventually the mussels crowded out the gooseneck barnacles and the algae that covered the rocks. Limpets that fed on the algae were lost and the number of species present in the study area dropped from 15 to 8.


Keystone: predator

Top predators, such as Australia's dingo, are often keystone species. Many conservationists regard dingoes as a functional replacement for native predators that are now extinct, such as the Tasmanian tiger. Dingoes have a varied diet and are a major constraint on introduced species, such as a foxes and pigs, thereby helping to maintain native mammal diversity.


Keystone: seed dispersal

istockphotos.com

The endangered southern cassowary is a key species in Australia's wet tropics. They are obligate frugivores (fruit eaters), and their gut passes seeds, unharmed, into a pile of manure. More than 200 plant species depend on the cassowary to disperse their seeds, yet their populations are all declining. Their loss would also mean the loss of an ecological role.


Keystone: critical food source

Gnangarra cc 2.5

All species of banksias produce large amounts of nectar, and are a vital component of food chains in the Australian bush. In the Avon Wheatbelt region of Western Australia, the acorn banksia is the sole source of nectar for honeyeaters at certain times of the year. The loss of this plant species would also result in the loss of honeyeaters from the region.

1. Why are keystone species so important to ecosystem function? _____

_____

_____

_____

_____

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Australian keystone species

Albert kok cc3.0

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.

Marjorie Lundgren cc3.0

Cockatoo grass (*Alloteropsis semialata*) is found through tropical savannas in northern and north eastern Australia. Cockatoo grass is an early developer in the wet season, providing a food source to many animal species before other plant species are available. Cockatoo grass is considered to be a keystone species because at certain times of the year it is the only food source available for two endangered species, the golden-shouldered parrot and the Northern bettong, a small marsupial. Young cockatoo grass is a preferred food source cattle and pigs, so it is easily overgrazed, leaving little for the wild species that rely on it. Conservation efforts are made to protect stands of cockatoo grass in some areas.

Andrew Mercer cc 4.0

The grey-headed flying fox (*Pteropus poliocephalus*) is found in a variety of habitats along the east coast of Australia, including Victoria. The grey-headed flying fox feeds on the fruit and nectar of over 180 species of trees, including Australian natives *Eucalyptus*, *Banksia*, palms, and myrtles. It will fly up to 50 km each night looking for food and this allows it to fulfill an important ecological role by dispersing the pollen and seeds of a wide range of plants. Its role is especially important in the subtropical rainforests as it is the only mammalian species to consume nectar and fruit in these regions. The species is under threat from the loss of foraging and roosting habitat and control measures by horticulturists to prevent crop losses.

2. For each species below, summarise the features of its ecology that contribute to its position as a keystone species:

(a) Acorn banksia: _____

_____

_____

(b) Southern cassowary: _____

_____

_____

(c) Dingo: _____

_____

_____

(d) Tiger shark: _____

_____

_____

(e) Cockatoo grass: _____

_____

_____

(f) Grey-headed flying fox: _____

_____

_____

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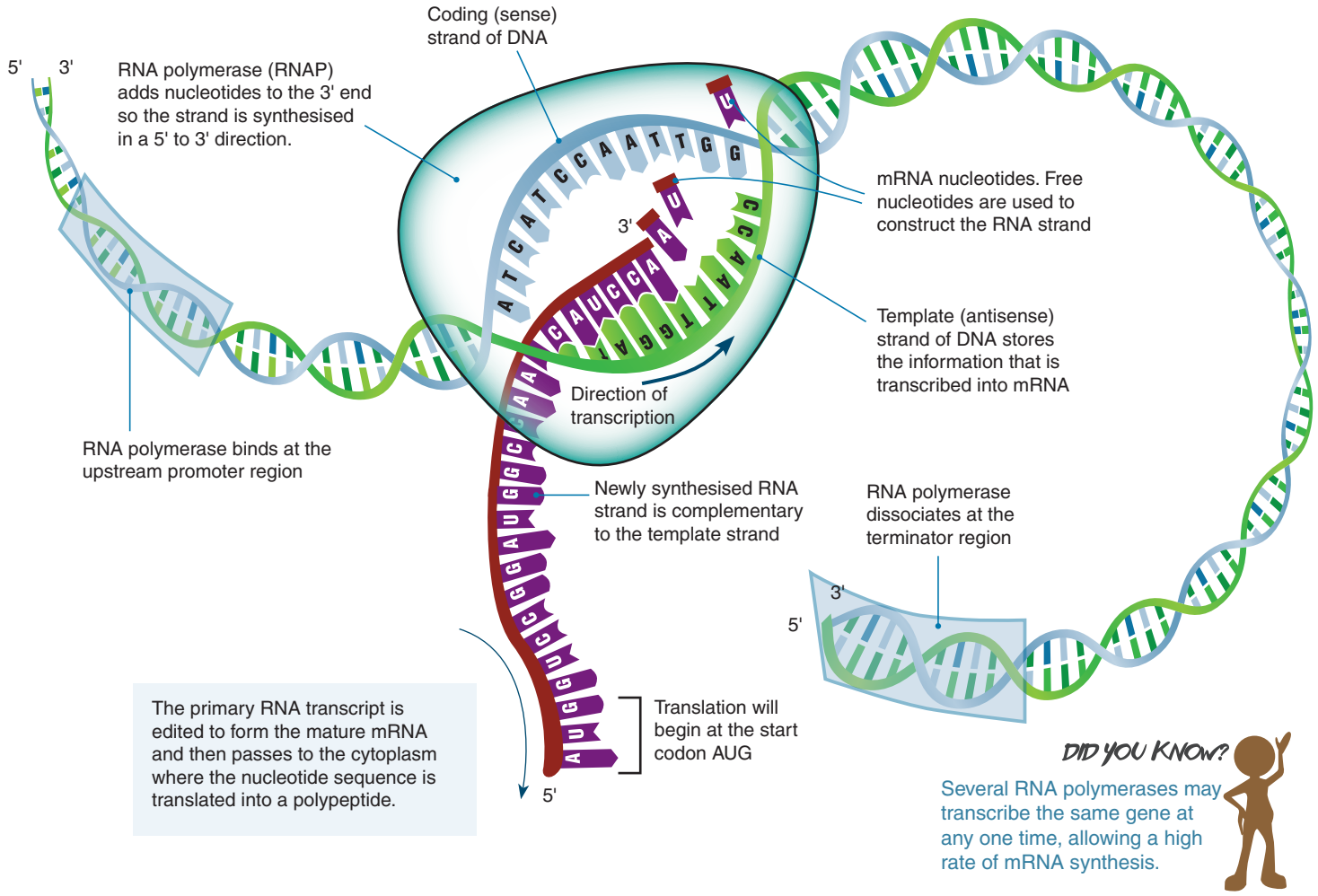
120 Transcription in Eukaryotes

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)



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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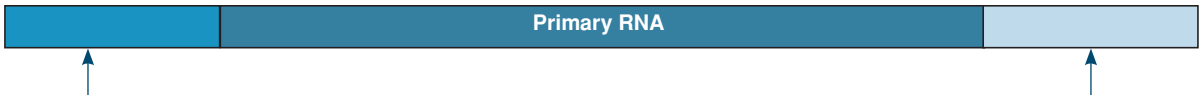
123 mRNA Processing in Eukaryotes

Key Idea: Primary mRNA molecules are modified after transcription so that the mRNA can exit the nucleus. Post transcriptional modification also enables the cell 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. Modifications to the 5' and 3' ends of the transcript enable the mRNA to exit the nucleus and remain stable long enough to be translated. Other post transcriptional modifications remove non-protein coding intronic DNA and splice exons in different combinations to produce different protein end products.

Primary RNA is modified by the addition of caps and tails

- After transcription, both ends of the primary RNA are modified by enzymes to create 'caps' and 'tails' (below). These modifications protect the RNA from degradation and help its transport through the nuclear pore.

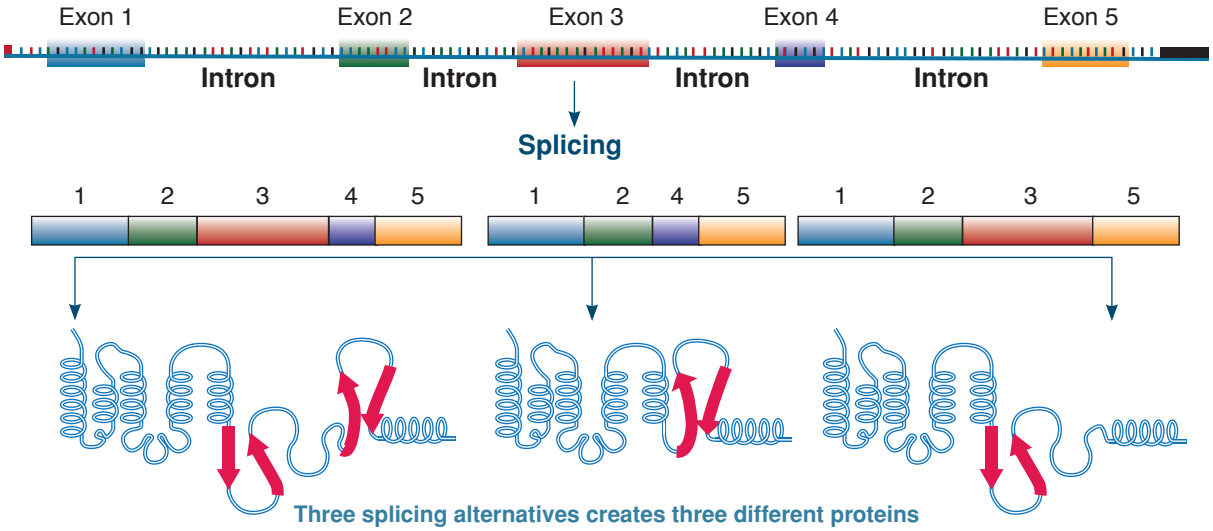


5' modification (capping)
A guanine nucleotide cap is added to the 5' end of the primary transcript to protect it from degradation during transport from the nucleus to the cytoplasm.

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

Post transcriptional modification

- Human DNA contains 25,000 genes, but produces up to one million different proteins. Each gene must therefore produce more than one protein. This is achieved through both post-transcriptional modification of the mRNA as well as post translational modifications, such as glycosylation and addition of phosphates.
- Primary RNA contains both protein coding exons and non-protein coding introns. Introns are usually removed after transcription and may be processed to create regulatory elements such as microRNAs. The exons are then spliced together ready to be translated. However, there are many alternative ways to splice the exons and these alternatives create variations in the translated proteins. The most common method of alternative splicing involves exon skipping, in which not all exons are spliced into the final mRNA (below). Other splicing options create further variants.



Three splicing alternatives creates three different proteins

1. What is the purpose of the caps and tail on mRNA? _____

_____

2. (a) What happens to the intronic sequences in DNA after transcription? _____

   (b) What is one possible fate for these introns? _____

3. How can so many proteins be produced from so few genes? _____

_____

_____

4. If a human produces 1 million proteins, but human DNA codes for only 25,000 genes, on average how many proteins are produced per gene?

_____

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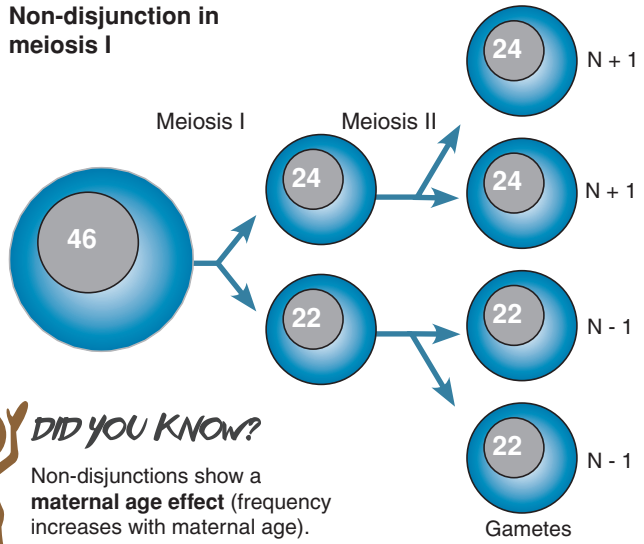
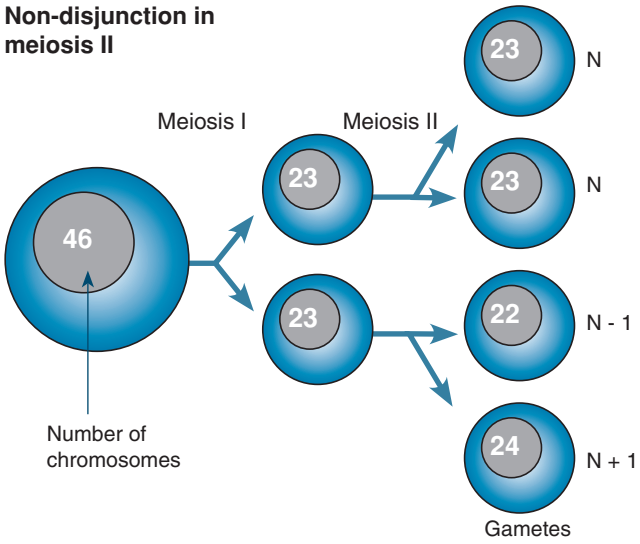
135 Non-Disjunction Can Produce Aneuploidies

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.





DID YOU KNOW?

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

Down Syndrome (Trisomy 21)

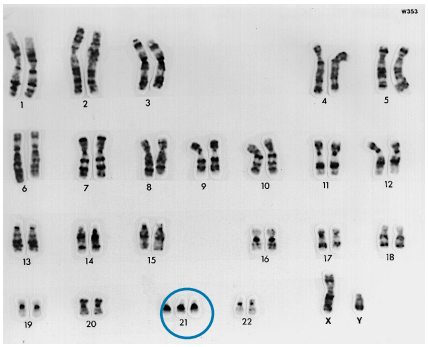


Photo: Waikato Hospital

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 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.

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. What is the maternal age effect and what are its consequences? _____

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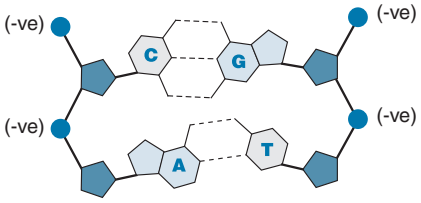
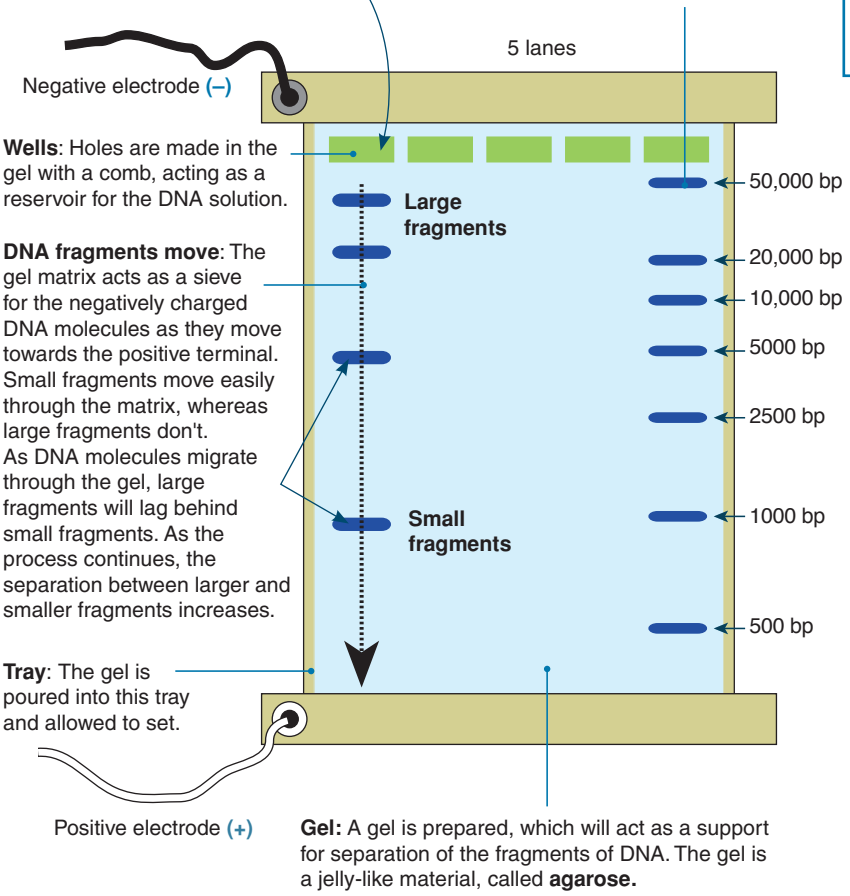
150 Gel Electrophoresis

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.



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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Recognition sites for selected restriction enzymes

Enzyme	Source	Recognition sites
***Eco*RI**	*Escherichia coli* RY13	G A A T T C
***Hae*III**	*Haemophilus aegyptius*	G G C C
***Hind*III**	*Haemophilus influenzae* Rd	A A G C T T
***Hpa*I**	*Haemophilus parainfluenzae*	G T T A A C
***Hpa*II**	*Haemophilus parainfluenzae*	C C G G
***Mbo*I**	*Moraxella bovis*	G A T C
***Taq*I**	*Thermus aquaticus*	T C G A

DNA fragments for gel electrophoresis are produced by restriction digestion of DNA using restriction enzymes. Restriction enzymes are produced by bacteria as a method of eliminating foreign DNA. About 3000 different restriction enzymes have been isolated. Around 600 are commonly used in laboratories.

Restriction enzymes are named according to the species they were first isolated from, followed by a number to distinguish different enzymes isolated from the same organism.

4. (a) A scientist uses *Hpa*II to cut a length of DNA. State the recognition site for *Hpa*II: _____

   (b) Circle where on the DNA sequence below *Hpa*II would cut the following DNA sequence:

   GTTAGGCCCGGCTAGCTTGACCAGTCCCGGGTCACAGTCTCTGACCCGGCTTTAGACACACTCCGGTTACTACCG

5. In 1988, the disease BLAD (Bovine Leukocyte Adhesion Deficiency) specific to Holstein cattle, was affecting the U.S. dairy industry. The disease was traced to the bull Osborndale Ivanhoe. The disease is recessive and two alleles are needed for its expression. The disease is caused by two mutations of the CD18 gene. One of the affected regions is shown below. The DNA of three individuals is shown: an unaffected individual, a carrier, and an affected individual.

Unaffected	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGGCCTGTACTACCTGATGGACCTCT	Allele 1
	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGGCCTGTACTACCTGATGGACCTCT	Allele 2
Carrier	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGACCTGTACTACCTGATGGACCTCT	Allele 1
	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGGCCTGTACTACCTGATGGACCTCT	Allele 2
Affected	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGACCTGTACTACCTGATGGACCTCT	Allele 1
	GTGACCTTCCGGAGGGCCAAGGGCTACCCCATCGACCTGTACTACCTGATGGACCTCT	Allele 2

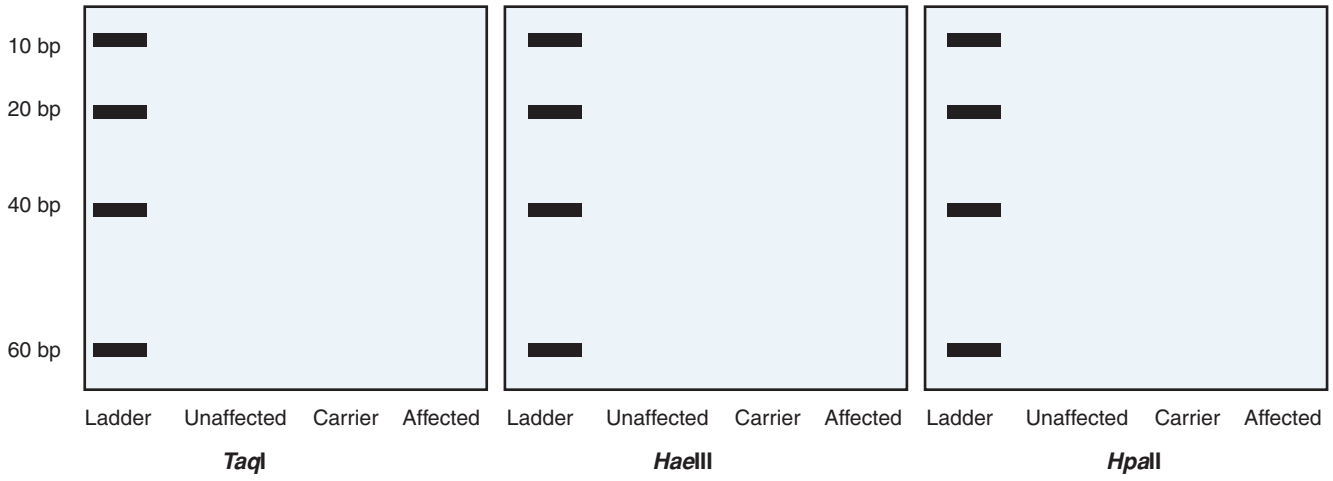
   (a) Use the restriction enzymes *Taq*I, *Hae*III, and *Hpa*II to "cut" the sequences. Write the length of the segments produced in the spaces below.
   [NOTE: *Taq*I cuts between T and C. *Hae*III cuts between G and C. *Hpa*II cuts between C and C]

   *Taq*1: Unaffected: _____ Carrier: _____ Affected: _____

   *Hae*III: Unaffected: _____ Carrier: _____ Affected: _____

   *Hpa*II: Unaffected: _____ Carrier: _____ Affected: _____

   (b) On the gels below draw in the bands that would be seen for each individual for each restriction enzyme:



   (c) Decide which restriction enzyme(s) would be useful for identifying carriers of BLAD: _____

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168 Disruptive Selection in Darwin's Finches

Key Idea: Disruptive selection in the finch *Geospiza fortis* produces a bimodal distribution for beak size.

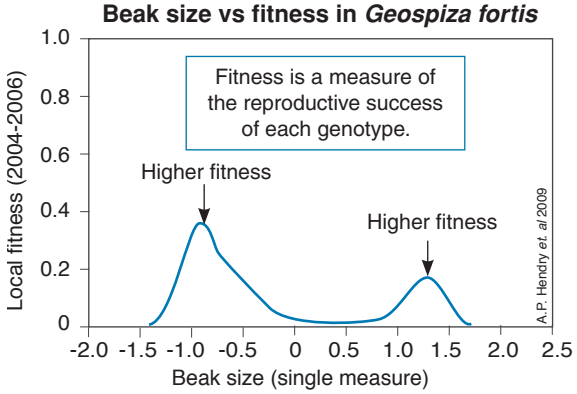
The Galápagos Islands, 970 km west of Ecuador, are home to the finch species *Geospiza fortis*. A study during a prolonged drought on Santa Cruz Island showed how **disruptive selection** can change the distribution of genotypes in a population. During the drought, large and small seeds were more abundant than the preferred intermediate seed size.

Beak sizes of *G. fortis* were measured over a three year period (2004-2006), at the start and end of each year. At the start of the year, individuals were captured, banded, and their beaks were measured.

The presence or absence of banded individuals was recorded at the end of the year when the birds were recaptured. Recaptured individuals had their beaks measured. The proportion of banded birds in the population at the end of the year gave a measure of fitness. Absent individuals were presumed dead (fitness = 0).

Fitness related to beak size showed a bimodal distribution (left) typical of disruptive selection.

Beak size vs fitness in *Geospiza fortis*

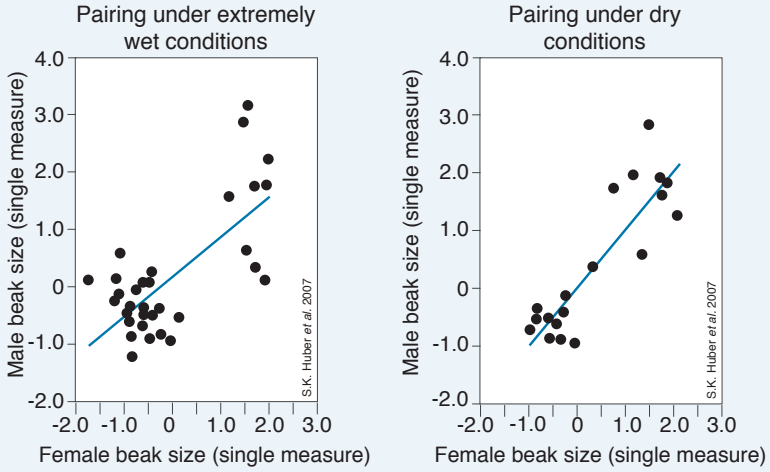


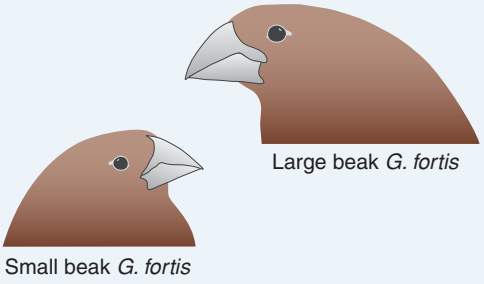
Fitness showed a bimodal distribution (arrowed) being highest for smaller and larger beak sizes.

Measurements of the beak length, width, and depth were combined into one **single measure**.

Jeff Podos

Beak size pairing in *Geospiza fortis*





A 2007 study found that breeding pairs of birds had similar beak sizes. Male and females with small beaks tended to breed together, and males and females with large beaks tended to breed together. Mate selection maintained the bimodal distribution in the population during extremely wet conditions. If beak size wasn't a factor in mate selection, the beak size would even out.

1. (a) How did the drought affect seed size on Santa Cruz Island? _____

_____

(b) How did the change in seed size during the drought create a selection pressure for changes in beak size?

_____

_____

_____

_____

2. How does beak size relate to fitness (differential reproductive success) in *G. fortis*? _____

_____

_____

_____

3. (a) Is mate selection in *G. fortis* random / non-random? (delete one)

(b) Give reasons for your answer: _____

_____

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