



Edith Cowan University

2021 ATAR Revision Seminar

ATAR Biology

Curriculum Dot points

Examination and study tips

Revision notes Examination questions

Examination marker comments

Prepared and presented by

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The Exam!

The first 2 pages of the biology exam will look like this. **READ** the information carefully. It tells you what is and is not allowed.

Read the Extended Response questions first. Use this time to start planning your answer.

Time allowed for this paper

Reading time before commencing work: ten minutes
 Working time: three hours

Number of additional answer booklets used (if applicable):

Materials required/recommended for this paper

To be provided by the supervisor

This Question/Answer booklet
 Multiple-choice answer sheet

To be provided by the candidate

Standard items: pens (blue/black preferred), pencils (including coloured), sharpener, correction fluid/tape, eraser, ruler, highlighters

Special items: non-programmable calculators approved for use in this examination

If you do not hand in any unauthorised material you will be in breach and risk being awarded a zero score.

Important note to candidates

No other items may be taken into the examination room. It is **your** responsibility to ensure that you do not have any unauthorised material. If you have any unauthorised material with you, hand it to the supervisor **before** reading any further.

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Unauthorised materials includes any drawing or pen marks on your hands, watches, phones, notes left in your pockets, and erasable pens.

Structure of this paper

Section	Number of questions available	Number of questions to be answered	Suggested working time (minutes)	Marks available	Percentage of examination
Section One Multiple-choice	30	30	40	30	30
Section Two Short answer	5	5	90	100	50
Section Three Extended answer Unit 3	2	1	50	40	20
Unit 4	2	1			
Total					100

1.3mins per question!

18mins per question

25mins per question

Answer 1 question for each unit.

Instructions to candidates

1. The rules for the conduct of the Western Australian external examinations are detailed in the *Year 12 Information Handbook 2018*. Sitting this examination implies that you agree to abide by these rules.
2. Write your answers in this Question/Answer booklet preferably using a blue/black pen. Do not use erasable or gel pens.
3. Answer the questions according to the following instructions.

Do NOT be caught out bringing the incorrect equipment to the exam. You must write your answers in PEN!

Section One: Answer all questions on the separate Multiple-choice answer sheet provided. For each question, shade the box to indicate your answer. Use only a blue or black pen to shade the boxes. Do not use erasable or gel pens. If you make a mistake, place a cross through that square, then shade your new answer. Do not erase or use correction fluid/tape. Marks will not be deducted for incorrect answers. No marks will be given if more than one answer is completed for any question.

- Shade the box
- Mistake? Cross the box

Section Two: Write your answers in this Question/Answer booklet. Wherever possible, confine your answers to the line spaces provided.

Section Three: Consists of two parts each with two questions. You must answer one question from each part. Tick the box next to the question you are answering. Write your answers in this Question/Answer booklet.

- Clearly indicate the question you are answering

4. You must be careful to confine your answers to the specific questions asked and to follow any instructions that are specific to a particular question.
5. Supplementary pages for planning/continuing your answers to questions are provided at the end of this Question/Answer booklet. If you use these pages to continue an answer, indicate at the original answer where the answer is continued, i.e. give the page number.

Science Inquiry Skills

Variables

Writing a hypothesis: **The independent variable changed the dependent variable by...**

- A hypothesis states a relationship between variables.
- A prediction is what you expect to happen if your hypothesis is supported.
- An ***independent variable*** is the factor chosen and manipulated by the experimenter.
- A ***dependent variable*** is the factor responding to the independent variable. (It is dependent upon the independent variable) The experimenter collects results about this variable.
- A ***Controlled variable*** is the factor which is the same for all the subjects being tested. It stays the same for the whole experiment.

Example:

A student wanted to test whether the amount of fertilizer would affect the height of bean plants.

The **independent variable** was the amount of fertilizer because the experimenter chooses how much they would put on the plants.

The height the beans grew is the **dependent variable**, because it depended upon how much fertilizer was put on the plant. The student had no control over how high the beans would grow. He collected results about the height of the plants.

The **controlled variables** were everything that stayed the same; like the amount of water and soil, the type of plant, the size of the pot, the position of the pots.

Drawing Scientific Tables

Scientists collect results when completing experiments. These results need to be recorded in an organised way or else they may become mixed up. There are some rules for drawing tables:

- It must have a TITLE that reflects the experiment.
- Each column or row needs a label.
- All units of measurement should be written in the label square NOT the result squares.
- The DEPENDENT variable goes along the top (columns).
- The INDEPENDENT variable on the left-hand side (rows).
- Use a RULER and PENCIL.

**DEPENDENT VARIABLE
(TIME)**

Table 1: Volume of a marble and speed.

INDEPENDENT VARIABLE (MARBLE VOLUME)	Time taken to roll 2 metres (secs)					Speed (ms ⁻¹)
	Marble volume (cm ³)	trial 1	trial 2	trial 3	average	
	20	30	32	31	31	0.06
40	23	20	24	22.3	0.08	

Calculating averages

When scientists experiment, they will repeat an experiment many times. Measuring more than once is called having "trials". The trial measurements need to be averaged. To find the average you need to add all the trials together than divide by the number of trials.

E.g. the average time taken to roll 2 metres for the 20cm³ marble was:

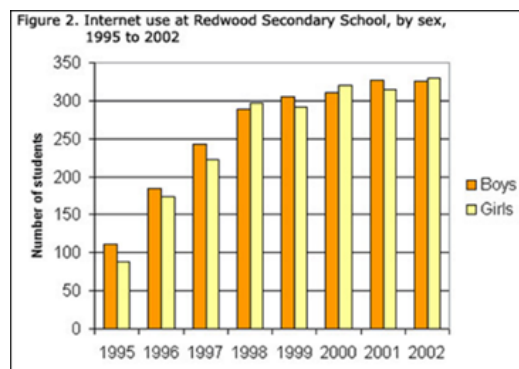
- $30 + 32 + 31 = 93$;
- $93 \text{ divided by } 3 = 31$
- The average time is 31secs.

The average is the number used for any further calculations. For example; the table above shows the speed of the marble. The average time was used to calculate the speed of the marble.

Bar Graphs

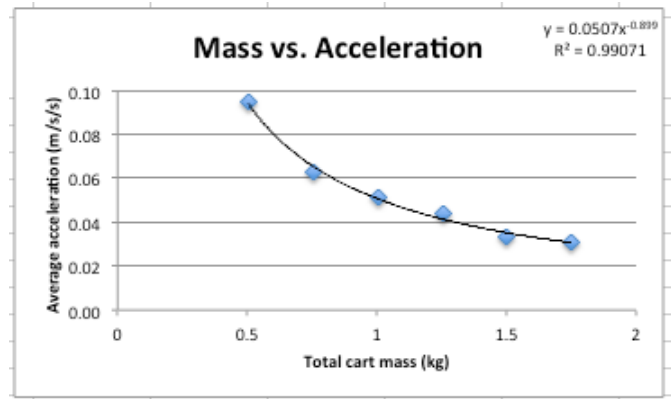
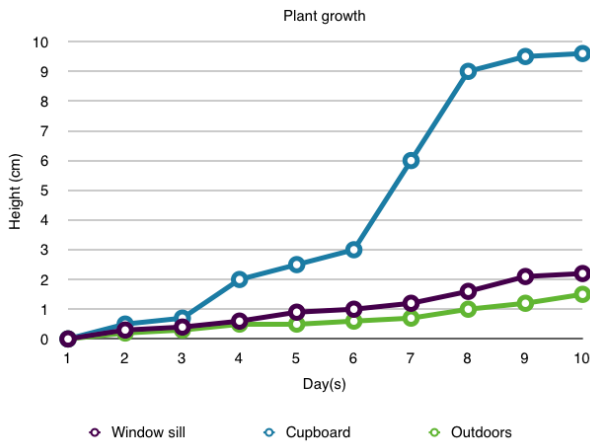
Bar Graphs are used when one set of data is **non-numerical and discontinuous** (or discrete); for example, when measuring the rainfall for every month. The months are discontinuous data.

Bar graphs are useful for comparing data.



Line Graphs

Line graphs are used when both sets of **data are numerical or continuous**, for example mass versus acceleration or growth over several days.



"Doubt kills more dreams than failure ever will."

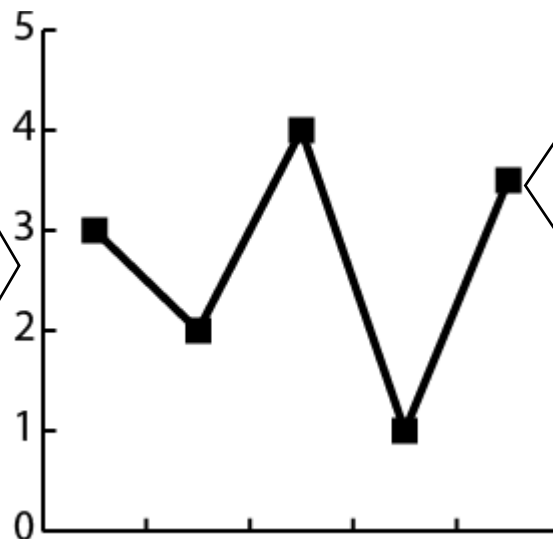
Karim Seddiki

The **title** tells people what the graph is about. It needs to have the **independent AND dependent variable** in it.

The effect of water volume on seedling growth

The vertical axis has the **DEPENDENT VARIABLE** on it. The axis label should have the **variable name** and the **units of measurement in brackets**. eg

Height of seedling (cm)



The line is **drawn in with a ruler**- joining the dots together.

If there is **more than one line** there must be a **key** to say which line is which.

The horizontal axis has the **INDEPENDENT VARIABLE** on it.

The axis label should have the **variable name** and the **units of measurement in brackets**. eg

Amount of water (mL)

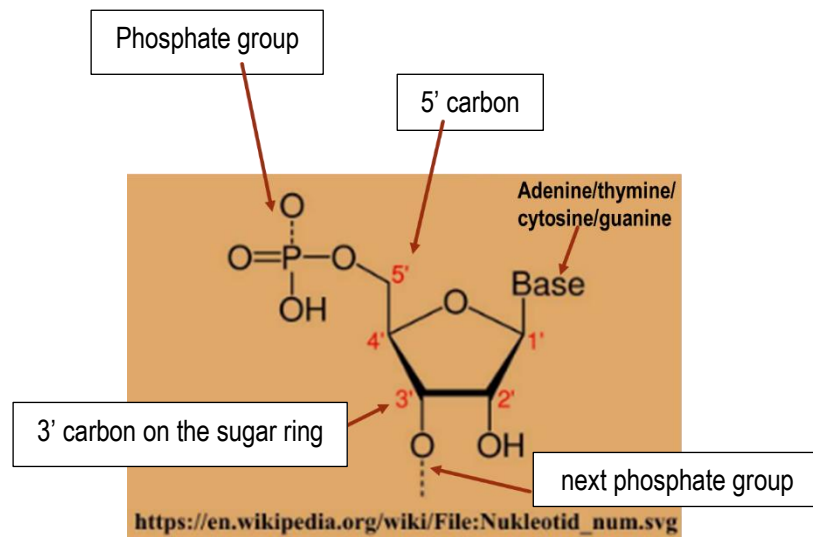
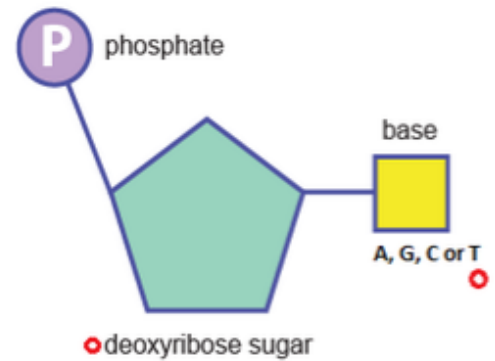


iream

Unit 3: Continuity of the Species

DNA

- 5- carbon deoxyribose sugar
- Negatively charged phosphate group
- Organic *nitrogen-containing* (nitrogenous) compound [BASE]
 - Adenine
 - Thymine
 - Guanine
 - Cytosine
- Sugar-phosphate backbone.
- Nitrogenous bases form hydrogen bonds holding the 2 backbones together like a twisted ladder.
- The nitrogenous bases form pairs: adenine-thymine (2 hydrogen bonds)
guanine-cytosine (3 hydrogen bonds)
- A nucleotide is made up of 1 sugar, 1 phosphate and 1 nitrogenous base.
- DNA has 'directionality'.
 - Described as 5' to 3' (5-prime to 3 prime)
 - The 5 and 3 relates to the C on the 5 carbon atoms of the sugar ring. (numbered 1-5)
 - The 5' end starts with a phosphate group
 - The 3' end finishes with a sugar



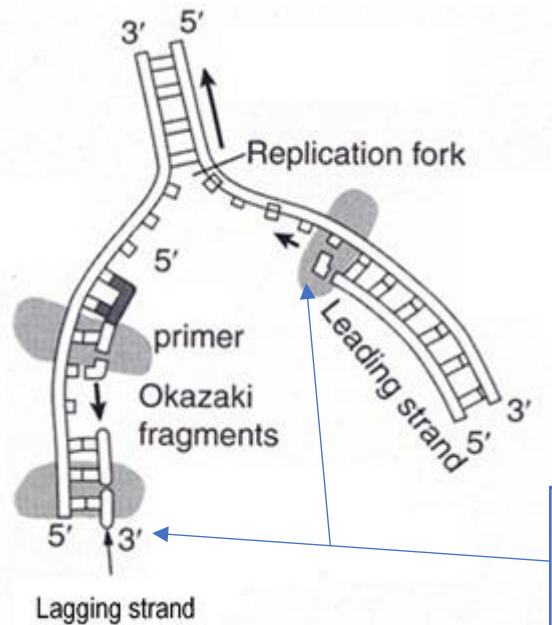
DNA v's RNA

DNA	RNA
2 long strands of nucleotides, double helix	1 strand of nucleotides
Encodes inheritable material	Functional- ie protein synthesis
Deoxyribose sugar (one less oxygen atom)	Ribose sugar
thymine	uracil

DNA Replication

- The **purpose of DNA replication** is to produce two identical copies of a **DNA** molecule. This is essential for cell division during growth or repair of damaged tissues. **DNA replication** ensures that each new cell receives its own copy of the **DNA**.

DNA ligase joins Okazaki fragments by bonding free ends.

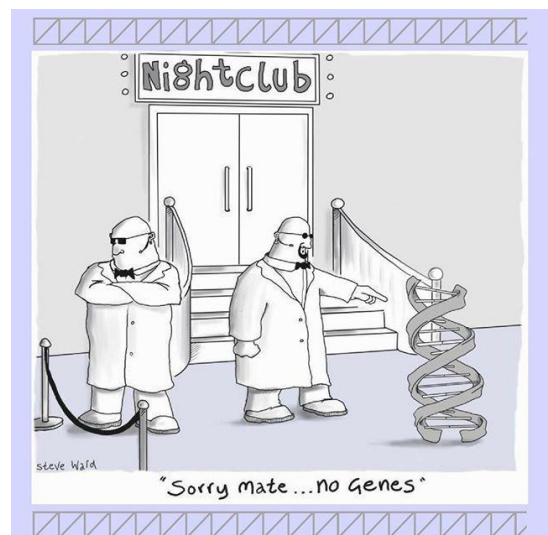


DNA polymerase adds nucleotides to the primer- at the 3' end of the new strand.

(Diagram adapted from: Surfing National Biology Unit 3 Heredity and Continuity of Life Science Press 2016)

The Process

1. DNA helicase unzips the double helix (parental strands) by breaking the hydrogen bonds.
 - This exposes the nucleotide bases
 - Separation of parental DNA strands occurs a small section at a time.
 - The junction between the unwound single strands of DNA and the double helix is called the replication fork. The replication fork moves along the double helix as it unwinds.
2. Each of the single strands are now a template.
 - Primers (RNA primase) locate the origin point. A primer is a short sequence of RNA.
 - DNA Polymerase attaches free nucleotides to the single strands (matching the bases A-T G-C).
 - Nucleotides always join onto the 3' end of the new strand.
 - The single strands are antiparallel- meaning they run opposite directions.
- The Leading strand runs continuously.
- The Lagging strand runs away from the replication fork; therefore, it is discontinuous. It is slower and more fragmented because the nucleotides can only be joined to the 3' end, creating gaps.
 - These fragments are called Okazaki fragments.
3. DNA ligase joins the okazaki fragments together.
 - DNA Ligase removes and replaces primers, making the strand continuous.
 - DNA ligase joins fragments by catalysing phosphodiester bonds.
 - Two new strands (helix's) are formed however, it is a semi-conservative process, meaning for each of the DNA strands- one is new while the other is from the parental molecules (old strand).



The Genetic Code

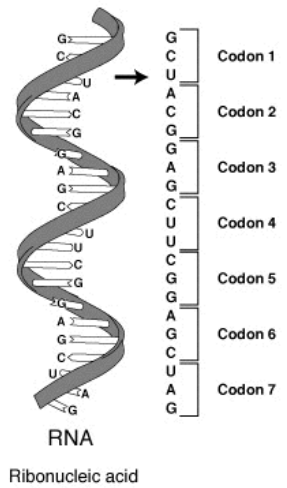
- A set of rules by which the genetic information in DNA or mRNA is translated into proteins.
- Stored as a 3-base sequence on mRNA called **codons** (triplet)
- Each codon represents an amino acid. [there are 20 amino acids all together]

All cells:

- hold ALL the known DNA
- not ALL types of protein are made in all the cells.
- This depends upon the function/location of the cell [called gene regulation].
 - Eg stomach cells make hydrochloric acid but salivary glands do not.
- DNA stays in the Nucleus.

There are 2 steps to protein synthesis

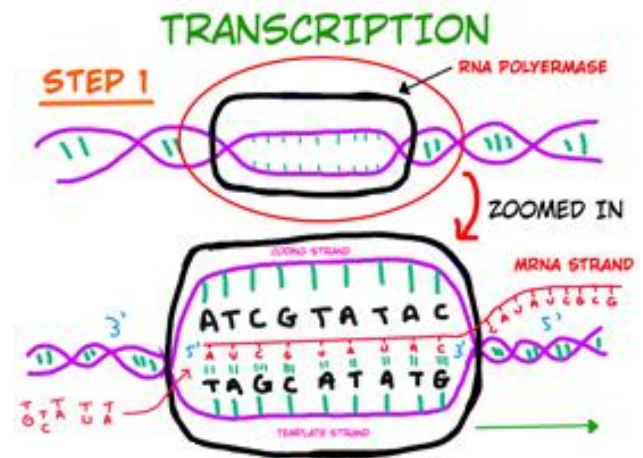
1. Transcription [nucleus]
2. Translation [cytoplasm- in the ribosome]



https://en.wikipedia.org/wiki/Genetic_code#References

TRANSCRIPTION: (*transcribing/copying the DNA sequence*) Messenger RNA synthesis

- A region of the DNA unwinds and unzips, exposing the nucleotide bases of both strands.
- Only 1 strand is used to synthesis the mRNA → **template strand**.
- The **non-template strand** has the same sequence as the generated mRNA (with the exception of U for T).
- Initiation: The **promotor** sequence (AUG/methionine) marks the beginning of a gene.
- Elongation: **RNA polymerase** binds with the promotor, signalling to the DNA to unwind, and begins to make the mRNA, by adding complementary free nucleotides to the 3' end.
- Termination: A **base** sequence (UAA, UAG, UGA) signals the stopping point.
- The Pre-mRNA is released and the DNA zips up and twists itself into a double helix.
- Introns are spliced out, and the exons joined together.
- A poly-A tail is added for stability to one end and a methylated cap to the other.
- The mRNA is now mature and ready to leave the nucleus.

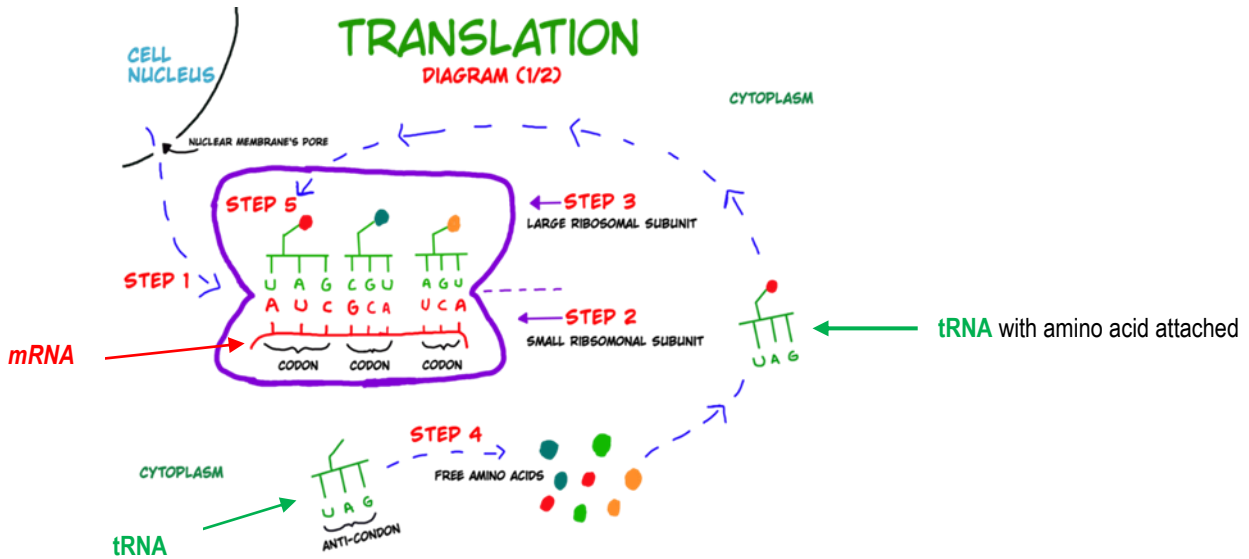


TRANSLATION (*interpreting/reading the mRNA*): Protein synthesis

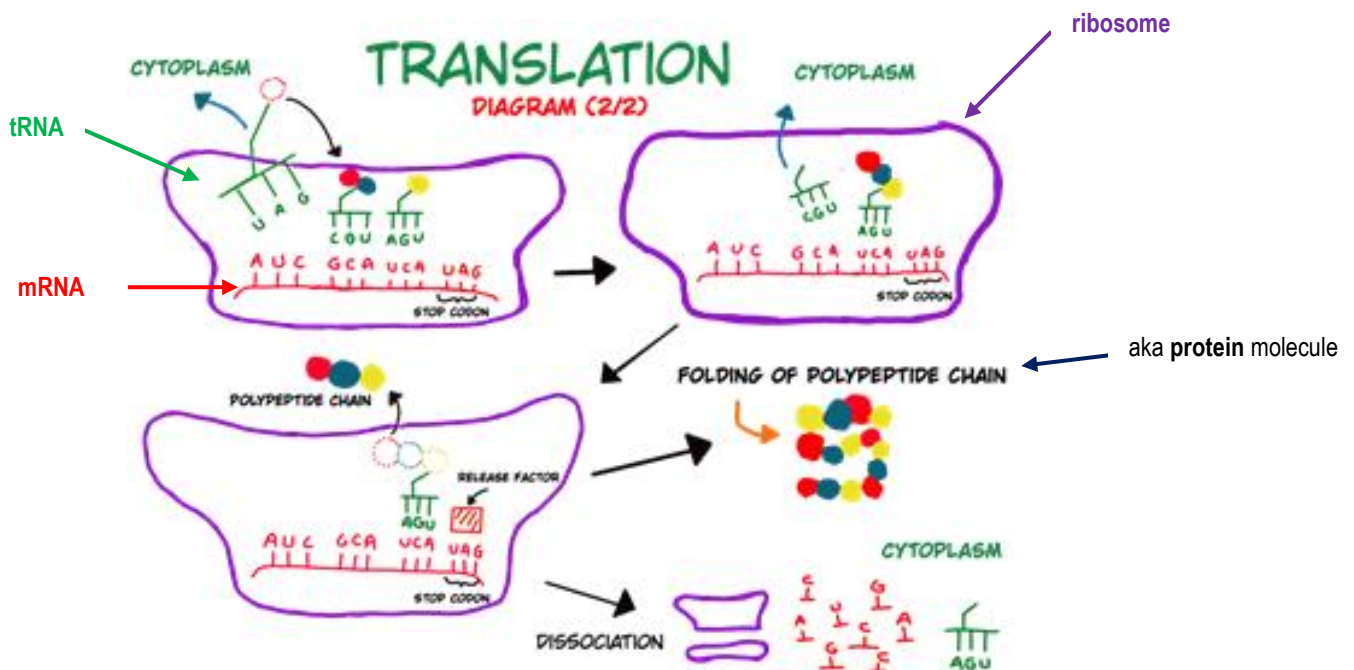
- Occurs in the cytoplasm.
- mRNA attaches to ribosome.
- Ribosomes are formed in the nucleus using ribosomal RNA and proteins.
 - 2 sub-units- 40 S and 60 S
 - These are the functional units of translation
 - Unbound ribosomes- float freely
 - Bound ribosomes are attached to endoplasmic reticulum.
 - Chains of ribosomes are called polyribosomes.
- **tRNA** or transfer RNA
 - Transfer amino acids to ribosomes
 - Free floating molecules in the cytoplasm.
 - The base of the tRNA is the anti- codon- complementary to the codon on the mRNA.
 - The amino acid attaches to the top of the tRNA.
 - The codon AUG is a start codon and begins all sequences.

Stages of Translation

1. Initiator tRNA [in small 40 S ribosome subunit] recognises an mRNA strand [cytoplasm]
2. Ribosome subunit binds to the methylated cap on the mRNA,
3. Scans to locate the AUG (methionine) start codon.
4. Large 60 S ribosome subunit joins to the 40 S.
5. Ribosome then moves along the mRNA.
6. Elongation: The tRNA anticodon [complementary bases] bonds to the mRNA codon binding site.



8. This continues until a stop codon (UAA, UAG, UGA) is reached.
9. Therefore the amino acids are linked according to the sequence of nucleotide base codons [in mRNA].
10. The ribosome catalyses **peptide bonds** between the amino acids, forming a **polypeptide** [or protein].
11. Termination: The polypeptide releases from the tRNA when complete. It will then either fold to become a protein or join another polypeptide and then fold into a protein.
12. tRNA returns to the cytoplasm to be reused. mRNA is released from the ribosome and is broken down, the nucleotides are re-used in transcription.



Biotechnology:

The use of living things to make new products or systems.

Traditional	Modern (Genetic Engineering)
The manipulation of crops/animals through “selective breeding”.	Also known as Genetic Engineering, changing the genetic sequence of an organism through human use of biotechnology techniques. The products are Genetically Modified Organisms – OR <i>Transgenic</i> organisms.
Examples <ul style="list-style-type: none"> Breeding animals that display particular traits. Double muscled cattle. Belgian Blue Use of micro-organisms to create beer, bread, wine 	Examples <ul style="list-style-type: none"> Tomatoes resistant to mildew Corn resistant to insect attacks Golden Rice (beta-carotene enriched rice to help combat malnutrition in developing countries)

Biotechnology requires the use of biological “tools”. These are mostly derived from organisms. They are used to:

- Synthesising, cutting and pasting DNA
- Viewing and analysing DNA

TOOL	What do they do	Further detail
Cutting	<ul style="list-style-type: none"> Enzymes called “Restriction endonucleases” or <u>Restriction enzymes</u> are used for this. They cut DNA at specific <u>restriction sites</u>. They are naturally occurring in bacteria. 	<ul style="list-style-type: none"> Sticky ends cut leaves 2 ends with <u>exposed nucleotide bases</u>. Joins are <u>specific</u> to recognition sites. Blunt ends Cut leaves 2 ends with NO exposed nucleotide bases. Joins to any blunt end, non-specific (no nucleotides to match to)
Recombining (Ligation)	<ul style="list-style-type: none"> The combining of 2 samples of DNA using <u>recombinant DNA technology</u>. DNA ligase is used to “glue” the two restriction fragments together. The ligase creates phosphodiester bonds between the 3’ and 5’ ends. 	<ul style="list-style-type: none"> <u>Sticky ends</u> join more effectively and efficiently than <u>blunt ends</u>.
Amplification	<ul style="list-style-type: none"> <i>Polymerase Chain Reaction</i> (PCR) is used to make more DNA. 	Process: <ol style="list-style-type: none"> <u>Denaturation</u> heated to separate & denature DNA strands. 95°C <u>Annealing</u> mixture cooled, single strand DNA primers form H-bonds with target sequence. 60°C <u>Extension</u> heat stable DNA polymerase adds nucleotides to the 3’ end-DNA strands copied. [5’→3’] 72°C
Visualisation	<ul style="list-style-type: none"> <i>Gel Electrophoresis</i> Separates macromolecules or fragments of macromolecules by size. Eg DNA, RNA, proteins 	<ol style="list-style-type: none"> Agarose gel as medium: cloned DNA fragments added to wells at one end, along with known DNA for comparison <u>Sieving</u>: electric current applied, fragments move through gel. Smaller fragments move further than larger fragments. [-ve to +ve end, PO₄ group has -ve charge] <u>Visualisation</u>: post electrophoresis stain applied. Fragments appear as bands. Size & molecular weight of each fragment is determined
	DNA Profiling can be used to compare samples. <ul style="list-style-type: none"> All individuals have a unique DNA profile except for twins. 	Process <ol style="list-style-type: none"> DNA sample- hair, skin, blood. Restriction enzymes used to cut DNA at specific sites- gel electrophoresis separates fragments. DNA fragments transferred to nylon sheets and dye is added. <ul style="list-style-type: none"> This pattern is the DNA finger print Can now be used to compare against other samples. <u>STRs</u>: simple tandem repeats- found on specific locations, vary from person to person. Used as markers. The more markers that are present more assuredly with identification.

Gene Probes

- Searches for genes
- A gene probe binds to target sequences in DNA
- The probe is a specific single length of single stranded DNA; complementary to the targeted gene sequence.
- The DNA being investigated is heated to separate the strands. The single stranded probe will bind to any complementary sequences.
- To trace the gene probes, they may have
 - a radioactive tag- shows up in photographs
 - a fluorescent dye tag- exposed under UV light
- Uses
 - Finding a certain fragment of gene after the sample has been separated by gel electrophoresis
 - Identifying the position of a gene on a chromosome
 - Identifying the allele of a specific gene associated with a genetic disease.

Microarray

- Allows thousands of genes to be tested at the same time.
- Thousands of DNA probes arrayed on a single microscope slide of glass or a silicon chip.
- Each probe is complementary to a target gene in the cell.
- mRNA of cell is extracted & reverse transcribed into DNA.
- The copied DNA [cDNA] is labelled with a fluorescent marker.
- The labelled cDNA is hybridised (allowed to bind) with the probes.
- A scanner measures the amount of fluorescence – the stronger the fluorescence the more active the gene.

Microarray can be used to detect a genetic disease

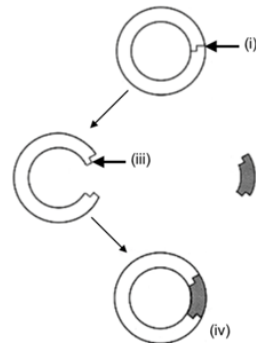
- Switched on genes are more active, for example uncontrolled cell division which causes cancer.
- Switched off genes are less active, for example the genes that suppress tumour growth.

DNA Sequencing

- Determination of the exact nucleotide sequence of a gene.
- Used to identify individuals with deletion mutations, or substitution mutations.
- Completed by gel electrophoresis or an automated DNA sequencer.
- Fluorescent dyes are used to track the nucleotides.
- A computer analyses the gel to read the sequence.

Gene Cloning

(iii) COMPLEMENTARY STICKY ENDS ALLOW FOREIGN GENE FRAGMENT TO BIND TO PLASMID.



(i) RESTRICTION SITE- PLASMID IS SPLICED BY RESTRICTION ENZYME.

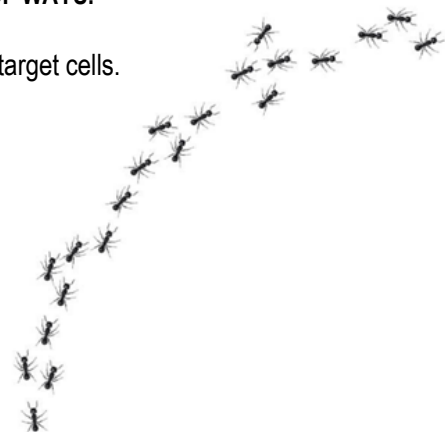
(ii) THE SAME RESTRICTION ENZYME CLEAVES/SPLICES/CUTS THE FOREIGN GENE SEQUENCE

(v) THE RECOMBINANT DNA IS ADDED TO A BACTERIAL CULTURAL WHERE SOME BACTERIAL CELLS ABSORB IT. BACTERIA IS CULTURED AND GROWN, MAKING MULTIPLE COPIES OF THE RECOMBINANT DNA.

(iv) DNA LIGASE GLUES/BINDS DNA FRAGMENT TO PLASMID TO FORM RECOMBINANT DNA

(vi) THESE GENES (RECOMBINANT DNA) CAN BE TRANSFERRED IN ANUMBER OF WAYS:

- via plasmids inserted directly into the organism.
- genes can be spliced into a virus and them introduced into the target cells.
- via liposomes.
- via agrobacterium



The Continuity of Life: Cellular Reproduction

“The unbroken and consistent existence or operation of something over time.”

- ☞ All cells originate from existing cells
- ☞ For life to continue genetic information must be passed on to the next generation.

∴ the continuity of living things is the transference of DNA from existing cells to new cells, this process is recurring and ongoing.

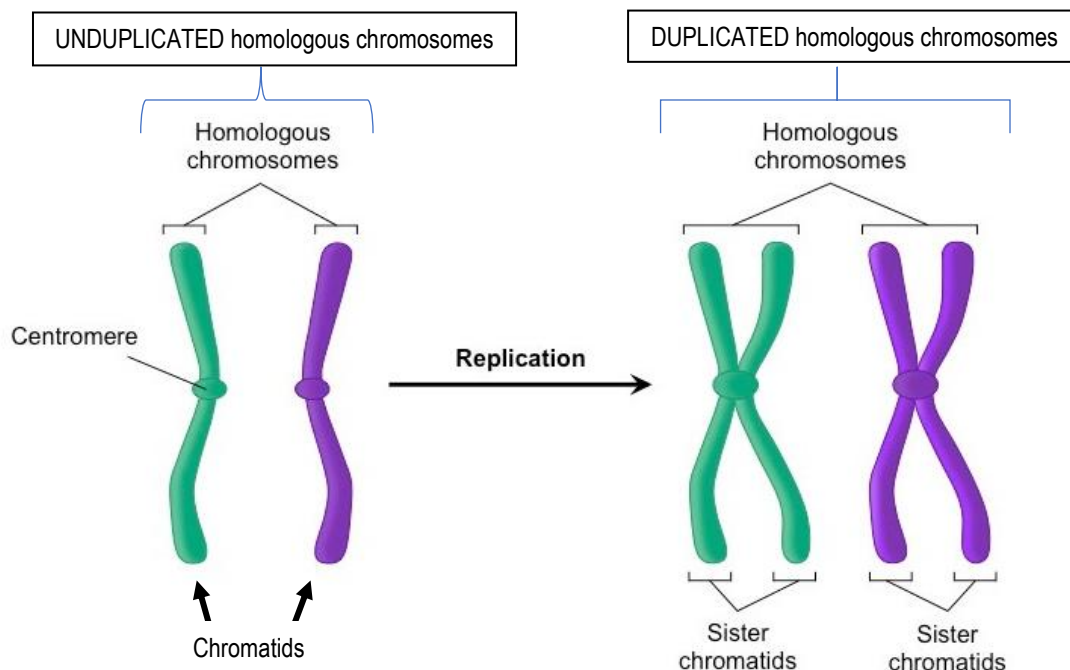
The transfer of DNA is facilitated by:

- ☞ Binary fission
- ☞ Mitosis
- ☞ Meiosis
- ☞ Fertilisation

Chromosomes

Eukaryotes	Prokaryotes
<ul style="list-style-type: none"> • DNA found in nucleus, chloroplasts and mitochondria. • DNA not visible in nucleus unless cell is dividing. • Histones aid in coiling the DNA. • 1 DNA + associated proteins = chromosome. • Chromosomes occur in pairs. • Each somatic (body) cell is diploid, ($2n$), contains the full complement of chromosomes eg in humans = 46. • 22 homologous (matched) pairs called autosomes. • 23rd pair is xx (homologous) in females but xy (heterosome) in males. These are the sex chromosomes. • Sex chromosomes are haploid (n). 	<p>In general</p> <ul style="list-style-type: none"> • Single circular chromosomes found in cytoplasm. • Often joined to the cell membrane. • Can make up a distinct area known as the nucleoid. • Haploid (one copy of gene). • Additional DNA can be found in plasmids. <ul style="list-style-type: none"> ○ Maybe none or more than one. ○ Non-essential genes commonly found here. ○ Replicate independently.

Anatomy of a chromosome



<https://ib.bioninja.com.au/standard-level/topic-3-genetics/33-meiosis/sister-chromatids.html>

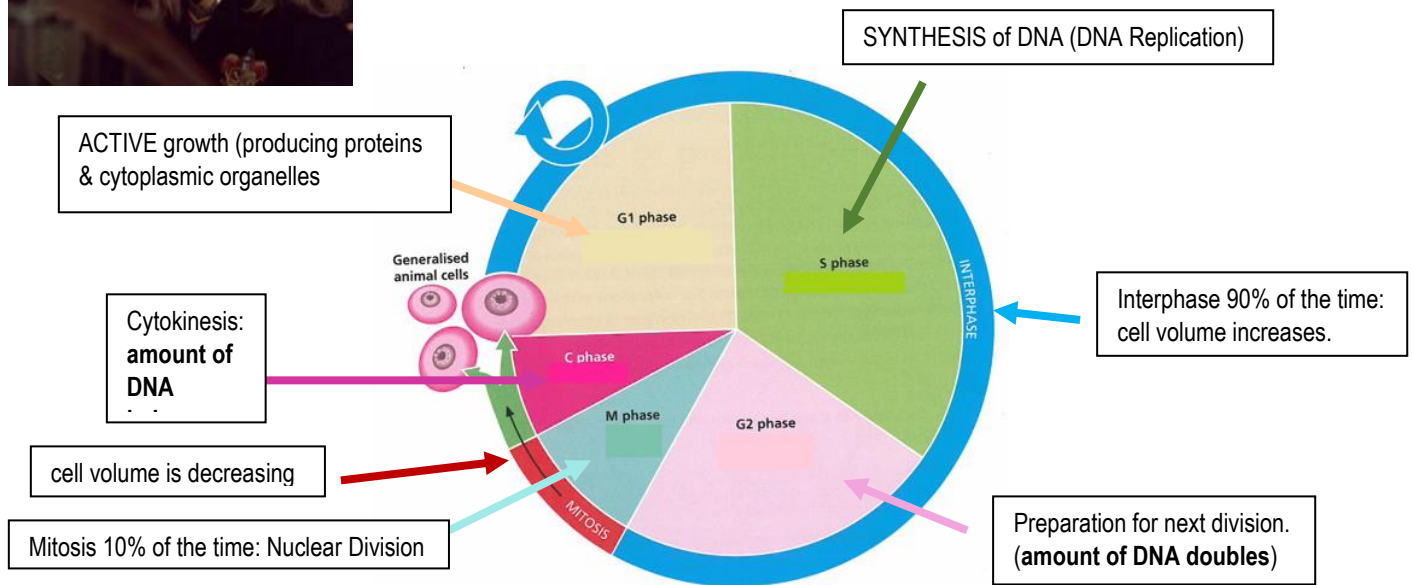


Cell Reproduction

Cell cycle: sequence of events from one cell division to another. It is a continuous cycle, running through the various phases.

Length of cycle varies.

Phases can be identified by the amount of DNA present.



Mitosis

- creates new cells for growth and repair.
- the 2 new daughter cells produced are identical to the parent cell.
- increases the number of cells.
- 5 phases: [IPMAT]
 - Interphase: normal cellular activities. Nucleus appears “stained”, chromosomes NOT visible.
 - Prophase: chromosomes visible, nuclear membrane disappears, chromosomes appear as 2 chromatids joined together.
 - Metaphase: chromatids line up at the centre of the cell, spindle forms.
 - Anaphase: centromere divides and chromatids separate, moving to opposite ends of the cell.
 - Telophase: spindle disappears, chromosome condense, nuclear membrane reforms, cytokinesis begins.

Meiosis

- creates gametes (sperm, pollen, ova)
- 4 daughter cells- genetically unique.
- 2 divisions: Reduction Division and Meiosis II
 - Reduction Division (Meiosis I)
 - Prophase I: chromosomes visible, nuclear membrane disappears, chromosomes appear as 2 chromatids joined together. CROSSING OVER occurs.
 - Metaphase I: chromatids line up (RANDOM ASSORTMENT) at the centre of the cell, spindle forms.
 - Anaphase I: sister chromatids remain attached, homologous chromosomes separate.
 - Telophase I & cytokinesis
 - Meiosis II
 - Prophase II: second spindle forms
 - Metaphase II: sister chromatids line up at equator and attach to spindle
 - Anaphase II: centromeres separate, and sister chromatids pull apart to opposite poles.
 - Telophase II and cytokinesis: spindle disappears, nuclear membrane reappears, cytokinesis begins.

A word on variation.

Variation is important because during times of environmental change there is a greater likelihood of some individuals will hold favourable genes that allow them to survive. Environmental changes may include:

- disease outbreaks,
- climate change,
- ecosystem changes ie introduction of a predator, or competitor.

Variation is increased by:

- the process of **meiosis**
 - **Crossing Over**- (during prophase 1) allows for genetic exchange of material, again random.
 - **Law of Segregation**- when alleles separate into the gametes this is done independently from other genes (random/in no particular order)
- **fertilisation**: ova are fertilised by a random sperm/gamete. It is pure chance as to which gametes meet.

Mutations

- changes to the DNA genetic make-up of a cell.
- a mutation may have NO deleterious effect or may be harmful.
- may be spontaneous, occurring during DNA replication.
- can be caused by biological agents such as viruses & bacteria.
- can be caused by mutagens: chemical (alcohol, agent orange...), various affects [see page 68 Nelson Biology Units 3&4] or physical (radiation), often affect N-bases causing distortion to double helix [see page 67 Nelson Biology Units 3&4].



Types of Mutations		
Point	Single nucleotide affected	
Substitution	One nucleotide replaced by another	
Insertion	Additional (1 or more) nucleotides added	Both these mutations may lead to a "Frameshift". When this occurs the DNA sequence is read incorrectly, the sequence makes no sense so the protein cannot be made.
Deletion	Loss of 1 or more nucleotides	

eg Frameshift mutation

Normal	mRNA	AUG	GGG	GCC	AAA	AGU	UAG	UUUG...
	polypeptide	Met	Gly	Ala	Lys	Ser	Stop	
Insertion						+U		
	mRNA	AUG	GGC	GCC	AAA	UAG	UUAGUUUG...	
	polypeptide	Met	Gly	Ala	Lys	Stop		
Deletion						-G		
	mRNA	AUG	GGC	CCA	AAA	GUU	AGU	UUG
	polypeptide	Met	Gly	Pro	Lys	Val	Ser	Leu
				Random				

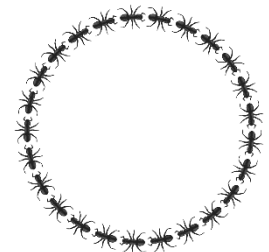


image from ScienceDirect.com

Effects of Mutations on survival	
Neutral	Protein product unchanged, survival unaffected
Deleterious	Harms overall operation/processes of organism, affects survival
Beneficial	Generation of beneficial allele, survival increases

- somatic mutations occur in the body cells eg cancer
- germ-line mutations occur in the gametes; therefore, they are inheritable. eg developmental abnormalities which may lead to spontaneous abortion or congenital defects (present at birth) such as Trisomy21 (Downs Syndrome).



Brain Break!!



Patterns of Inheritance

A monohybrid cross determines the possible outcomes for one particular gene. eg;

A heterozygous yellow pea plant is crossed with another heterozygous yellow pea plant. What are the possible genotypes and phenotypes of the offspring. Show all working out.

Y = yellow y = green ← **1 mark for the allele key**

P: Yellow x Yellow

Yy x Yy

	Y	y	
Y	YY	Yy	<p>75% (or $\frac{3}{4}$) Yellow</p> <ul style="list-style-type: none"> • 25% (or $\frac{1}{4}$) homozygous yellow • 50% (or $\frac{2}{4}$) heterozygous yellow <p>25% (or $\frac{1}{4}$) homozygous green</p> <p>1 mark for correct phenotype & ratios</p>
y	Yy	yy	

Some Tips!

- In heterozygous gene always put the dominant allele first. eg Tt **NOT** tT
- Choose 1 letter to represent the gene- capital for dominant, lower case for recessive. eg Tt **NOT** Td
- Choose letters that clearly distinguish between a capital and lower case. eg Tt, Gg, Hh, Nn, **NOT** Ww, Ss, Cc, Pp, Yy etc...

Incomplete Dominance and Codominance

- With *incomplete dominant* traits neither allele is dominant. In a heterozygous individual the trait's phenotype is a mix of both alleles. For example, pink snap dragon flowers have one red allele and one white allele.
- *Codominant traits* have both alleles expressed. For example, Roan cattle have red hair and white hair.
- The alleles are dominant, so they are written as capital letters. EG pink snapdragon = RW. This is one of the few times different letters are used.

Example: A red snapdragon is crossed with a white snapdragon

	RR x WW	
	R	R
W	RW	RW
W	RW	RW

100% RW heterozygous pink snapdragons

Multiple alleles

Some traits have more than 2 possible alleles, for example rabbit hair colour has 4 possible alleles. Not many genes have more than two alleles. Around 30% of human genes are di-allelic (2 alleles), almost 70% are mono-allelic (have NO variation). Humans have 3 possible alleles for the ABO blood type system.



Example: In dogs the 'agouti locus' is multiple alleles. The alleles are:

a colour locus which has

- A = black
- a^w = agouti
- a^t = bicolour

Phenotype	Possible genotypes
Black	AA, Aa^w , Aa^t
Agouti	$a^w a^w$, $a^w a^t$
Bicolour	$a^t a^t$



A homozygous black dog is mated with a homozygous agouti dog.

Parents black coat x agouti coat
 AA x $a^w a^w$

	A	A
a^w	Aa^w	Aa^w
a^w	Aa^w	Aa^w

F₁ generation: 100% Aa^w heterozygous black coat.

Sex-linkage

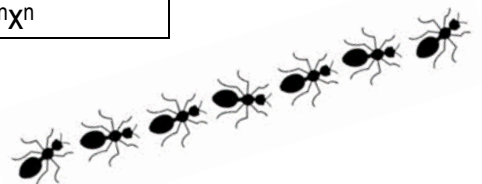
Some genes are linked to the x or y chromosome. To understand the inheritance of these traits you first need to understand how gender (sex) is inherited. All females have xx chromosomes, while men have xy chromosomes. The following punnet square shows how gender is inherited.

		Father	
		x	y
Mother	x	xx	xy
	x	xx	xy

50% xy chance male, 50% xx female

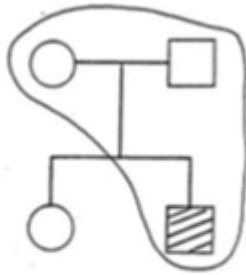
Sex-linked traits are shown as superscript on the relative chromosome. eg haemophilia (a recessive gene) would be represented as:

Phenotype	Genotype
male- normal blood	$x^N y$
male- haemophilia	$x^n y$
female- normal blood	$x^N x^N$
female- haemophilia carrier	$x^N x^n$
female- haemophilia	$x^n x^n$



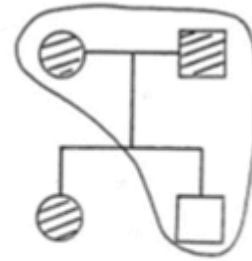
Pedigree patterns to look for!

Recessive Trait:



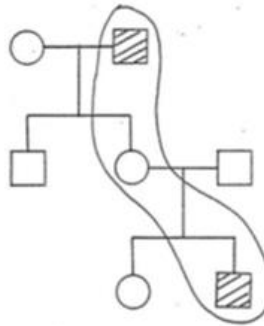
CAN'T BE D (AD OR XD)
MUST BE R

Dominant Trait:



CAN'T BE R (AR OR XR)
MUST BE D

Sex-linked Recessive Trait:



LIKELY TO BE XR

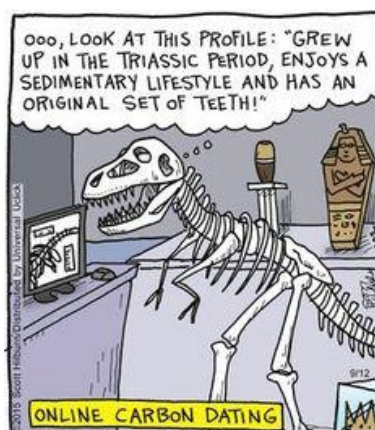
The Fossil Record

- Fossils are preserved remains and traces of organisms.
- Fossils only form under particular circumstances; therefore, *they are limited* in what they can tell us.
- Fossils do give us insight into past life forms.
- Many intermediary forms of organisms have been found in the fossil record, eg *Archaeopteryx*, a reptile with wings/feathers.
- Two theories for the fossil record:

Gradualism	Punctuated Equilibrium
Evolution occurs as a steady, slow divergence lineage at an even pace. This theory says that sudden bursts of evolution are an illusion- due to a lack of evidence or gaps in the fossil record.	States that a species will remain stable for long periods of time but may then quickly change into a new species. This may be in response to a rapid change in the environment.

Dating Fossils

Absolute	Relative
Assigns a numerical age in years to a fossil or rock. <ul style="list-style-type: none"> ◦ Radio-dating ◦ Electron spin resonance ◦ Luminescence ◦ Based on physical or chemical properties of materials in rock. 	Used to determine the age of a rock/fossil relative (in comparison) to the other rocks/fossils around it. Does not give an age in years, can only say that a given fossil in a set location is older or younger than the other fossils in that location.



Evidence for Evolution

Comparative Anatomy

- Homologous Structures: common physiological structures shared by different organisms, that stem from a *common* ancestor. Only organisms with a common ancestor can have structures with the same basic arrangement. Examples include
 - pentadactyl limb:
 - ; 5 digits at the end of a limb. seen in all mammals. same basic structure but modified (evolved) for different purposes eg bat wing, seal fin, human hand.
 - lizard skin; scales have changed (evolved) to suit environment lizard lives in. eg hard scales for defence or protection from water loss.
 - leaves; all leaves have same basic function but vary according to environment. eg hard dry leaves v's fleshy water holding leaves.
- Vestigial homologous structures: no longer provide a purpose or function. Examples include:
 - appendix in humans- correlates to caecum found in other herbivores such as gorillas.
 - pelvis in whales- shrunken but corelates to pelvises in other mammals.
- Analogous Structures: organs or anatomy with the same function BUT are different structurally therefore are evidence that organisms are NOT related. Examples include:
 - shark fin v's dolphin fins: developed due to common environment not a common ancestor.
 - octopus eye v's human eye: octopus eye has nerve fibres behind sensory (no blind spot), human eye nerves are in front of sensory cells (blind spot).
- Comparative Embryology: structural similarities at the embryonic stage. eg all chordates, at some stage, have a dorsal notochord, pharyngeal slits, dorsal nerve chord, tail past the anus.

Biogeography

The study of the distribution of organisms and ecosystems across the world and through geologic time. Examples include:

- Australian Flora and Fauna: unique due to isolation of land mass, however similarities between other southern hemisphere islands/land masses. This is evidence for the existence of Gondwanaland.
- Wallace's Line (see Nelson Biology Units 3&4 Fig 6.8 page 167)

Divergent Evolution	Convergent Evolution
A single species disperses (spreads) over a variety of new environments, difference between the groups increases until speciation occurs. ADAPTIVE RADIATION.	Unrelated organisms evolve similar adaptations in response to their environment. Often seen as analogous structures.
Eg marsupial common ancestor for koalas, Tasmanian devils, marsupial moles. each of these species evolved according to their diet.	Eg ant-eaters: echidnas, pangolins, aardvarks and numbats. Many analogous structures such as a long snout, but no common ancestor.

Molecular

Protein Conservation	Genetic Composition
<ul style="list-style-type: none"> A protein that is well suited to its function will be <u>conserved</u>. proteins are coded for by alleles (DNA sequence) Protein sequences across species can be compared. conserved proteins can be identified and used to show evolutionary relationships. the greater the number of shared genes the more closely related the species are. 	<ul style="list-style-type: none"> "mutation rate" is the frequency of neutral mutations (fairly constant rate), used as a baseline rate of mutation that occurs naturally in DNA. This mutation rate is specific for each species. Changes in mutation rate can show an estimate of evolutionary divergence.

Phylogenetic Trees

A diagram representing the evolutionary relationship between species. The same information can be drawn up in numerous ways. see below.

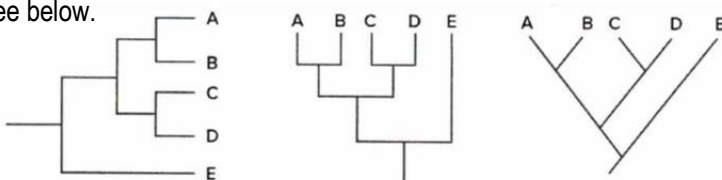
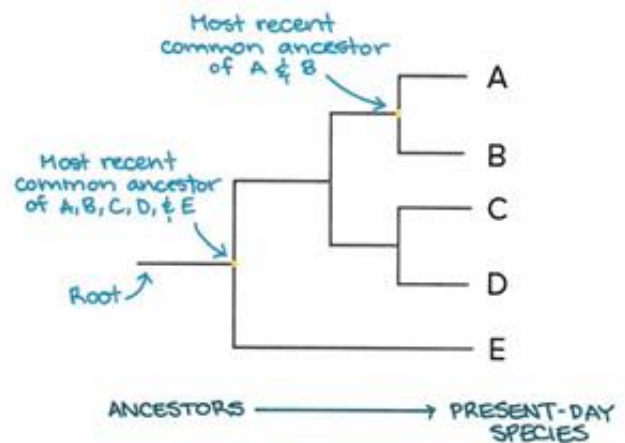


Image modified from *Taxonomy and phylogeny: Figure 2* by Robert Bear et al.. CC BY 4.0



Macroevolution	Microevolution
<p>“Macro” or large changes in allele frequency Occurs over a long period of time (generations) Is a result of the accumulation of microevolutionary changes over time. Eg appearance of feathers on theropod dinosaurs, leading to the evolution of birds.</p>	<p>“Micro” or small changes- this type of evolution relates to any change in allele frequency in a population. These allele frequency changes may or may not lead to macroevolution. Caused by mutation, genetic drift, natural selection and/or gene flow. Eg insect resistance to pesticide, Peppered moth- increased frequency of dark coloured moth during the Industrial Revolution.</p>

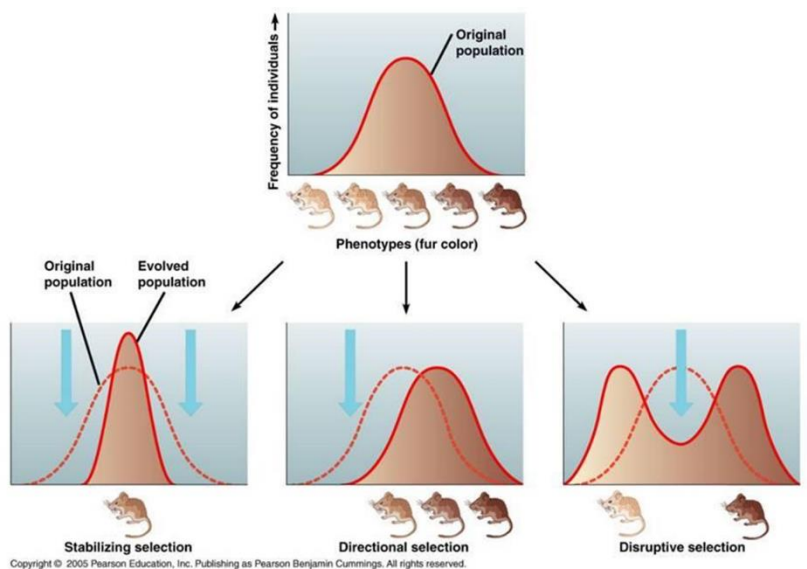
Natural Selection... “the selection of those alleles (genes) in a population that give an organism greater survival advantage.”
Organisms with favourable genes will survive and reproduce, passing on those favoured genes- increasing the proportion of those alleles in the gene pool.

The process

1. Populations have **genetic diversity**- some characteristics are more favourable for survival than others.
2. The **struggle for survival**. In the natural environment there are limiting factors and selection pressures eg competition (eg food, space, breeding sites), predators, disease.
3. **Survival of the Fittest**. Individuals with characteristics that help them to survive to (therefore are more ‘fit’) *live to reproductive age- passing on their genes to the next generation*.
4. These genes (alleles) become more frequent in the gene pool. This *may* lead to speciation.
5. **Speciation**. If a population is isolated from the original population, these allele frequency changes may become permanent and a new species forms (unable to breed fertile offspring with the original population)

Natural selection is the only process that leads to **adaptive evolution** or speciation which results in the formation of a new species.

- **Stabilising selection:** when the environment is unchanging [stable], natural selection favours gene held by parents.
- **Directional selection:** natural selection selects one extreme variation, leading to change over time.
- **Disruptive selection:** natural selection selects in favour of the two extremes of variation. Often occurs after an event such as a drought that may have wiped out a food source or habitat.



Speciation occurs when a single population becomes two separate populations become **reproductively isolated**, causing physical, biological or behavioural barriers.

Pre-reproductive isolating mechanisms	Post-reproductive isolating mechanisms
<ul style="list-style-type: none"> Prevent organisms from being able to interact. Geographic barriers: seas, rivers, mountains, distance, habitat. Temporal (time): breed at different times of the year or day. Behaviour: differing courtship rituals. Morphology: different reproductive structures. 	<ul style="list-style-type: none"> These mechanisms do not prevent mating but will not produce fertile offspring. Gamete mortality Zygote mortality Hybrid sterility (is not effective in plants)

Allopatric speciation v's sympatric speciation

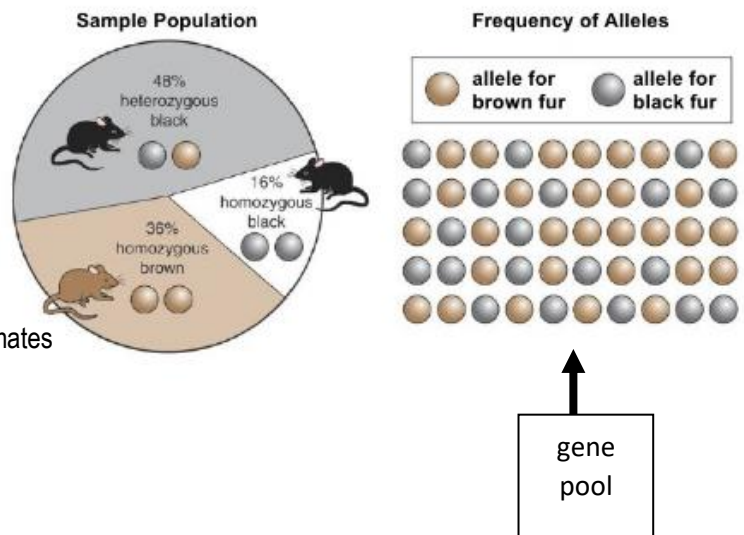
Allopatric speciation.	Sympatric speciation.
<ul style="list-style-type: none"> Most common Populations become physically separated by geographical barriers. 	<ul style="list-style-type: none"> The evolution of two or more new species from a single population within the same place. Due to choosing different food sources, or mates. Changing behaviours.

Allele Frequency

Gene Pool: total range of alleles in a population.

Frequency of alleles is NOT constant, it is affected by:

- Mutation of an allele
- Immigration (movement into a population)
- Emigration (movement out of a population)
- Reproduction rate (number of offspring per year)
- Selection pressures such as sexual selection of mates
- Selective breeding (artificial selection)



Allele frequency is also affected by:

- Genetic drift
- The Bottleneck effect
- The Founder effect

Genetic flow refers to the movement of genes into and out of the gene pool.

- Immigration brings new genes into a population
- Emigration removes genes from a population
- E.g. The Indigenous Australian population did not contain the B allele for blood until after Europeans came to Australia.

Genetic drift: random changes in **small** populations.

- Fertilisation is a random event involving chance.
- In large populations this randomness in inheritance is not noticeable.
- In small populations some alleles may not be passed on, leading to their loss from the gene pool.

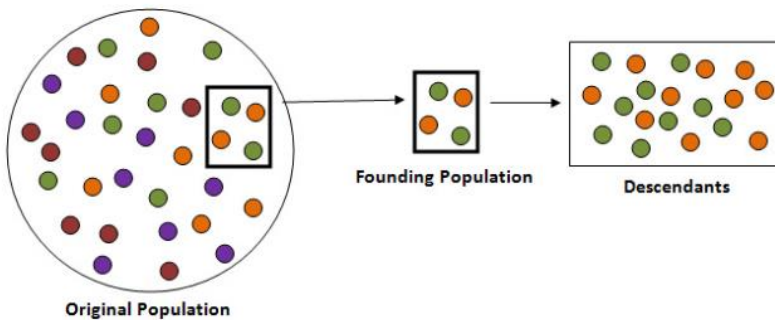
The Bottleneck effect- an example of genetic drift

- Alleles are lost (by chance) through an event such as hunting, natural disaster. Population dramatically decreases.
- Creates a 'bottleneck'- only some alleles are passed on.
- Population recovers; however, the gene pool has changed- less variation.

The Founder effect- an example of genetic drift

- occurs when a few individuals emigrate away from the main population to a new area, founding a new population [new gene pool] isolated from the original group. This new gene pool may not fully represent the original gene pool.
- Genetic diversity is reduced.
- Deleterious recessive alleles may become more frequent.
- Often seen in human populations which have particular cultural or religious beliefs.

eg Amish population in USA: founding group had 200 individuals, at least 1 settler had Ellis-van Creveld syndrome. This syndrome is more prevalent in the Amish population than in the wider mainstream gene pool. [Populations like the Amish have very little to no gene flow.]



<http://www.liberaldictionary.com/founder-effect/>



Extinction and Conservation

POPULATIONS WITH REDUCED DIVERSITY FACE INCREASED RISK OF EXTINCTION.

- Large populations can be more resilient than small populations- probably because they have a larger, more DIVERSE gene pool than a small population.
- The greater the pool of alleles there are to draw from the greater the chance of some individuals surviving environmental changes.
- Therefore, many CONSERVATION efforts focus on maintaining GENETIC DIVERSITY.

Conservation planning to maintain viable gene pools includes consideration of:

Biogeography

- the study of the **distributions of animals and plant species** and **how those distributions relate to the environment**, to the origin of the species and to the changes that have occurred over time.
- Spatial organisations of biological diversity:
 - Nature reserves/conservation areas need to be large enough/ have suitable conditions to maintain viable populations of (target) species.
- Characteristics (abiotic & biotic):
 - temperature, elevations, soil types, typical species (plants & animals)
- Studies of biogeography help Conservationists make decisions about whether or a species needs monitoring, or active protection.

Reproductive behaviour

- Behaviour associated with mating or rearing young, this includes:
 - mating systems,
 - courtship,
 - sexual behaviour
 - fertilisation.
- Reproductive behaviour may change in captivity or outside of natural environment or if directed by humans (e.g. in zoos) or in small area.

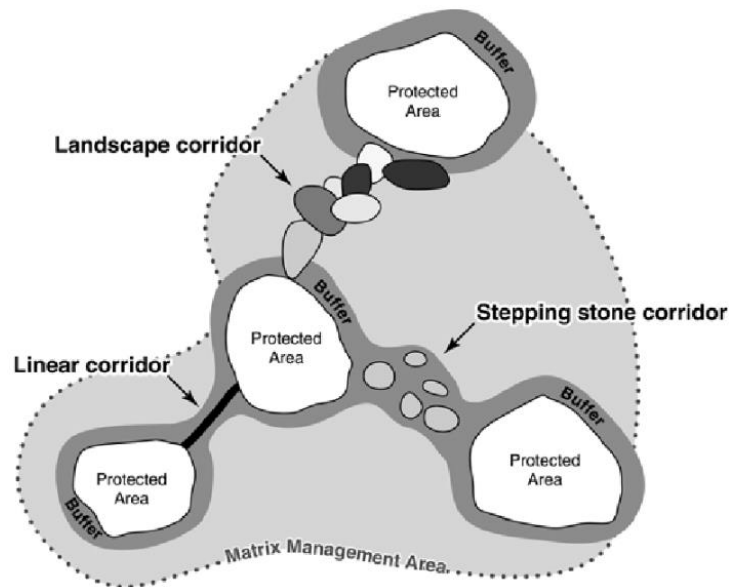
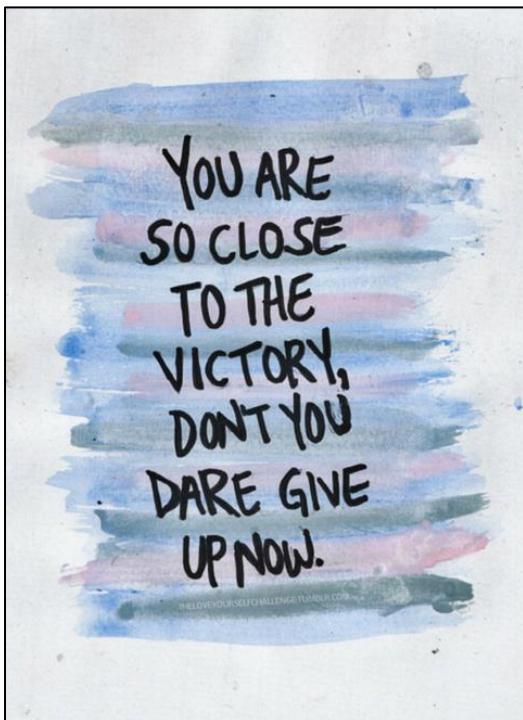
Population Dynamics

- the study of number, gender, age, relatedness of individuals.
- About how and why populations change size.
- Conservation planning should be based around smallest viable population size.

Conservation methods include:

- monitoring using biotechnology
 - eDNA (environmental DNA- non-invasive) from water, scat.
 - identification
 - relatedness to prevent inbreeding in captive populations
 - bioremediation to remove pollution from environment
- Reserves
- Translocation of animals from densely populated areas to areas of reduced population.
- Captive breeding programs
- Seed banks
- Wildlife corridors
- Artificial nesting sites
- Habitat preservation through National Parks.
- Sustainable and managed logging

*you are
capable
of amazing
things*



Congratulations! You have now completed your revision booklet!

Edith Cowan University would like to wish all students the best of luck with their future exams!