- Has acidic properties

Molecules consisting of N and H atoms:

AMINO GROUP ($-NH_2$)

- Ionisable (pH dependant)
- Has basic properties

Molecules consisting of P and O atoms:

PHOSPHATE GROUP ($-OPO^{2-}_3$ of $-PO^{2-}_4$)

- Central P atom with 4 bonds to oxygen atoms
- Ionisable (pH dependant)
- Has acidic properties

Molecules consisting of S and H atoms:

SULFHYDRYL GROUP (-SH)

- 2 -SF groups can react (redox reaction) to form a disulfide
- Disulfide bonds help maintain tertiary and quaternary structures of proteins

<u>Isomers</u>

- It is 2/more molecules with the same chemical formula but different molecular structures

Stereoisomers

- Biological structures (amino acids) can exist as 2 stereoisomers
  - Only 1 isomer occurs naturally
- Importance of stereoisomers:
  - Drug = Ibuprofen. Condition = pain and inflammation. Effective stereoisomer = S-Ibuprofen. Ineffective stereoisomer = R-Ibuprofen
  - Drug = Albuterol. Condition = asthma. Effective stereoisomer = R-Albuterol. Ineffective stereoisomer = S-Albuterol

Structural isomers

- Formed by the positional exchange of function groups (glucose and fructose)
  - Glucose – aldehyde
  - Fructose – ketone

<u>Reactions involving function groups</u>

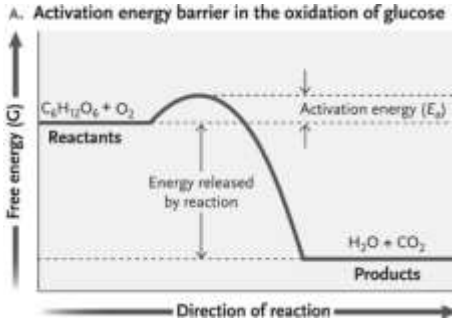
- Components of a water molecule (-H or -OH) are removed from/added to a function group during chemical reactions
  - During the assemble/degradation of macromolecules

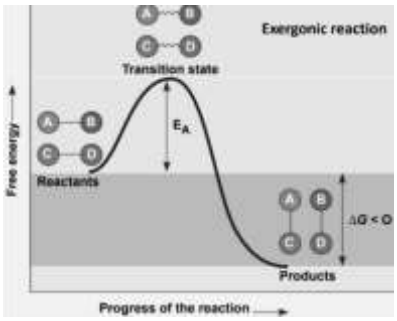
ENERGY AND ENZYMES

Activation energy (E_a), catalysts, active sites, factors influencing activity, regulation of activity and feedback inhibition

Activation energy (E_a)

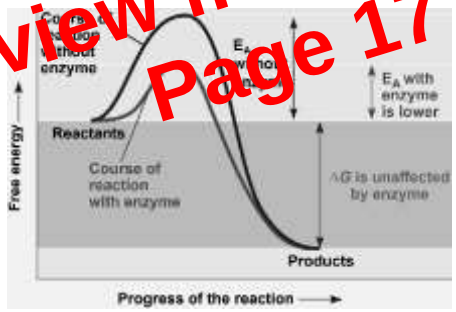
- Chemical reaction between molecules entails breaking/forming chemical bonds
- E_a is the initial energy needed to destabilise existing chemical bonds and the minimum energy required to initiate a chemical reaction
- Activation energy is from the reactants to the activation complex (G not change)
    - Activation complex: unstable transition state from reactants to products

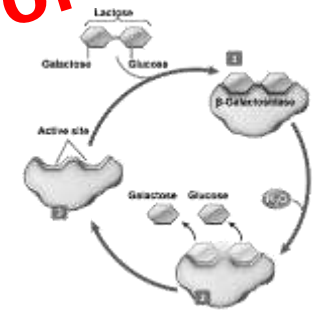




- E_a serves as a barrier for exergonic (spontaneous) reactions
- E_a is overcome by adding heat or using a catalyst (lower than E_a barrier)
- Catalyst: chemical agent which increases the rate of the reaction by lowering the activation energy and without being used/changed by the reaction (enzymes)

Effect of an enzyme of E_a





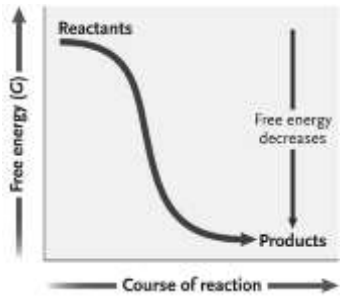
Enzymes

- They are substrate specific (proteins) – specificity is coupled to the enzymes structure and binds the substrate via the active site on the enzyme
    - An enzyme has an active site that the substrate attaches to, and it is an induced fit between the enzyme and substrate

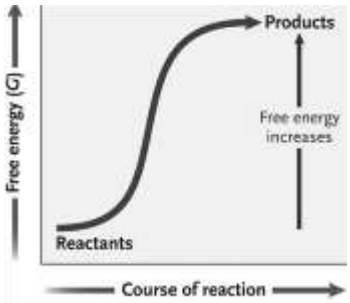
Product less free energy (G) than reactant (reactant gave up energy when = product)
Reaction is spontaneous

2. **Endergonic reaction – energy added**
   $\Delta G \geq 0$ (positive – adding)
   Product more free energy (G) than reactant
   Reaction not spontaneous (energy required for froward direction)

Free energy change (ΔG) in exergonic



Free energy change in endergonic



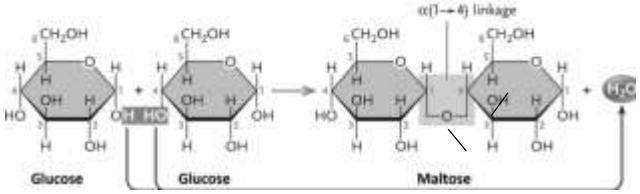
<u>Exergonic and Endergonic reactions</u>

Individual reactions form part of a metabolic pathway with 2 types:

1. **Catabolic pathway**
   Breakdown of complex molecules to simpler compounds
   Energy released (exergonic)
   Glycolysis – glucose
2. **Anabolic pathway** (biosynthetic)
   Build-up of complex molecules from simpler compounds
   Energy is used (endergonic)
   Photosynthesis

Disaccharide formation

- Formation of maltose involves:
  - Breaking and making bonds (change in enthalpy ΔH is small)
  - Turning 2 monosaccharides into 1 large disaccharide and 1 small water (change in entropy ΔS is negative - ordered)
  - Change in free energy ΔG is positive – require energy to proceed



<u>ATP: energy currency of the cell</u>

- Cells supply energy to drive endergonic reactions in form of ATP (adenosine triphosphate)

- **Prokaryote**: **DNA** is suspended **inside** the **cell** (**nucleoid**) **without** being **separated** from other cellular components therefore **no nuclear envelope**
- **Eukaryote**: **DNA** is **enclosed** in a **nucleus** by the **nuclear envelope** therefore the **nucleus** is a **separate** structure inside the cell

Phylogenetic tree (tree of life) has 3 domains: bacteria, archaea and eukarya

- Each domain represents a major trunk and includes a group of organisms with unique characteristics

Bacteria (prokaryotic)

- **Unicellular** (one celled) organisms
- Only visible under **microscope**
- Live as **producers**, **consumers**, or **decomposers**
- **Simple** cellular organisms (internal structure and DNA)
- Metabolically the most **diverse group**
- Some groups have **unique structural molecules** and mechanisms of **photosynthesis**

Archaea (prokaryotic)

- **Unicellular** and live as **producers/decomposers**
- Achaeans inhabit **extreme environments** (hot springs, extreme salty ponds, or habitats with little/no oxygen)
- Some with **distinctive structural molecules** and **primitive form** of **photosynthesis**
- Some molecular and biochemical traits of a eukaryote (**DNA**, **RNA/protein synthesis**)

Eukarya (eukaryotic)

PROTISTS (algae and protozoans)

- Not a kingdom as the organisms do **not share a common ancestor**
- **Diverse group** of **single** celled and **multi**-cellular eukaryotes
- Protozoans (common) are primarily unicellular, and algae can be unicellular/large multicellular seaweeds
- Protozoans are **consumers/decomposers** and algae are **photosynthetic producers**

KINGDOM PLANTAE (flowering plants, conifers, and mosses)

- **Multi**-cellular
- Carry out **photosynthesis** and are **producers**
- **Stationary** organisms (except pollen and seeds)

KINGDOM FUNGI (yeast, mould, and fungi)

- Highly **varied** group of **unicellular**/**multi**-cellular species

- *Biosignature*: specific **organic molecules** that were **formed** by **cellular activity** (steroid-like molecule only formed by cyanobacteria) dated to 2.5 bya
- *Microfossils*: **remains** of a **cell** that has **decayed** and **filled** with **Ca carbonate** or **silica** (filamentous and single celled prokaryotes) dating back to 2 bya

Origins of eukaryotic cells (distinguish from prokaryotic cells)

1. *Nuclear envelope* (membrane): **separates DNA** from **cytoplasm** and other **organelles** evolved through **endocytosis** (**folding** in of **plasma membrane**) then **closed genetic** material and formed **Golgi** and **endoplasmic reticulum**
2. *Endo-membrane system* in cytoplasm: creates **compartments** with specialised **metabolic/synthetic functions** – mitochondria, endoplasmic reticulum, Golgi body
    - **Mitochondria** and **chloroplasts** are different as they contain their **own DNA** replicated **in** the **organelle** – **genes** are **transcribed** and **translated** to **synthesise proteins** then divide through **binary fission** (like bacteria)

THEORIES FOR ORIGINS OF MITOCHONDRIA AND CHLOROPLASTS IN EUKARYOTIC CELLS

Endosymbiotic theory (Lynn Margulis):

- **Mitochondria** and **chloroplasts** originated from **mutualistic** associations between 2 **prokaryotic cells** therefore both **organelles evolved** from **bacteria** that had been **engulfed** by **another prokaryotic cell**
- **Symbiosis**: **engulfed bacteria** developed an **interdependent** relationship with new **host**. **Engulfed bacteria** are **endosymbionts** as they live **inside host** and **relationship** between the cells = **endosymbiosis**
- **Endosymbionts** benefit by living in a **protected** environment and received **nutrients** from host, **host** benefits as the **endosymbionts** provide **products** from metabolic processes
- Overtime some **genes** were **lost** from the **genomes** of the mitochondria and chloroplasts therefore **no longer exist on own**
- Some **genes** were **deleted** from **endosymbiont genome** because there were **copies** in **hosts genome**
- Other genes were **transferred** from **chromosome** of **endosymbiont** to **nuclear genome** of **host** and become **dependent** on host

Discoveries

- 1674: Royal Society of London received a package at a gentleman scientists lab from Holland and it came from a man who built the world's most powerful microscope (hidden kingdom). There was a long letter in Dutch about tiny animals that swam like eels and were extremely small. Royal society had a microscope but never saw the organisms, so they thought the Dutchman was crazy
- Antony Van Laden Hoek was not a scientist (linen-merchant) he inspected cloth with magnifying glass and was obsessed with lenses (microscope). He used a tiny

    - **Plant fixing nitrogen**: microbes fix nitrogen in nodules on roots of pulse crop by taking **nitrogen** from the **air** and converting it to **carbohydrates**
    - Cells use **NH_4^+** to produce **amino acids** and **nucleotides**
    - **N-fixation**: **prokaryotic** process and way to **replenish** N sources needed by plants/animals (all organisms use N fixed by prokaryotes)
- **Reproduction**:
    - **Binary** fission: **parent cell divides** to form **2 daughter cells** (**exact** copies)
    - **Conjugating** (some): 2 parent cells **mate** and **exchange plasmids** therefore **genes** carried **on plasmid** is transferred (**sex pilus** – strand attaching the 2)
    - **Endospores** (not many): **dormant** cell that can **survive adverse environmental** conditions and carry **bacterial genome** and some **cytoplasm**

Domain Bacteria

GRAM POSITIVE BACTERIA (purple)

- Live as **chemo heterotrophs**
- **Human pathogens** – *Bacillus anthracis* (anthrax), *Staphylococcus aureus* (pimples, pneumonia, meningitis), *Streptococcus pyogenes* (strep throat, scarlet fever)
- Many beneficial spp. – *Lactobacillus* (**yoghurt** and **fermented foods**) and many mammalian gut inhabitants (**help** with **digestion**)

CYANOBACTERIA (photosynthesis, oxygen and nitrogen)

- **Gram negative photoautotrophs** with blue green colour performing **photosynthesis** using chlorophyll
- **Contributed** to **O_2 atmosphere** as they produced the first O_2
- **Eukaryotic chloroplasts** evolved from them
- Some species **fix atmospheric N_2** into **organic** compounds

SPIROCHETES (termite guts)

- **Gram negative helically spiralled** bacteria with **flagella**
- *Treponema pallidum* (syphilis) and *Borrelia burgdorferi* (Lyme disease)
- Beneficial spirochetes in **termite guts** help **digest cellulose**

CHLAMYDIAS (parasites)

- **Gram negative** bacteria **lacking peptidoglycan**
- Obligate intra-cellular **parasites**
- *Chlamydia trachomatis* (chlamydia STD)

PROTEOBACTERIA (medical and agriculture)

- **Relative fitness** = **variants** contribute different members of **offspring** to the **next generation** which leads to a **variation** in **phenotypes** and **genotypes** (change) and acts on the phenotypes and through selection on phenotypes alters allele frequencies (genotype)
    - Allowing **reproductive success** (reproduce **high number** of **offspring**)
    - Those with **favourable traits** (**advantageous** in competing for **resources**) therefore have a high **relative fitness**
    - Variation must be **heritable** to **influence future generations**
- When **individuals reproduce**, all (**favourable/unfavourable**) alleles are **transferred** to **next generation** so natural selection acts on **all traits** at **all stages** and has **minimal effect** on **traits** that appear **after reproductive life** (Huntington disease) so it cannot cure i.e. cancer that happens later in life so it must **occur** in **germ life**
    - Can be slow as have extra/negative alleles (unfavourable) are also inherited

<u>Natural selection = change in phenotypes (average trait between generations):</u>

Directional selection (one direction)

- *Moegistorhynchus longirostris* and *Lapeirousia anceps* – moving towards creating a long tongue to get the nectar in the long tubes therefore higher success
- **One side** of the bell curve so **one extreme** has the **highest fitness**, **mean shifts** from left to right
- Select the most **extreme phenotype** have **highest relative fitness** (smallest dog/fastest horse) and through **time** the trait value **increases towards 1 extreme**
    - Force alleles to one side = **lower the alleles**
- Artificial selection – hotter and hotter chilis

Stabilising selection (optimal)

- In the **middle** (higher and narrow) of the bell curve have **highest relative fitness**, **even** on both sides, **variation decreases**, mean doesn't change so frequency of **alleles frequencies decreases**
- **Intermediate** phenotypes have **highest selection** therefore have **middle value** between **both extremes**
- **Selection against both extremes**: eggs too small not have offspring and too big cannot be laid – stabilise
- Wasp's parasite more flies in small galls so selecting for bigger and bigger galls and birds consume more flies in large galls so selecting for smaller and smaller galls

   a. **Heterozygous advantage**: **heterozygotes** have a **higher relative fitness** than homozygotes therefore **both alleles retained** still allowing variation and no elimination of alleles – Malaria and sickle cell disease which is heterozygous therefore preventing blood cells from Malaria (HbSHbS individuals die, HbAHbA have a high mortality during infections and HbAHbS likely to survive)
   b. **Differential selection** in single populations: therefore is **balanced polymorphism** and **phenotype** is based on the **environment** they live in (snails in fields = yellow and wooded habitats = brown as birds eat those less camouflaged)
   c. **Frequency dependant** selection: **common** forms **eliminated** at **disproportionately high** rate and **uncommon** forms at **disproportionately low** rate. **Proportional** line shows **elimination** in **proportion** to **availability**
3. *Selectively neutral alleles*: **different forms** of a protein (coded by different alleles) **function equally well**. **Neutral mutations** = **genetic variation** with **no phenotype** change

<u>Adaptation and evolutionary constraint</u>

- **Adaptive trait**: any **product** of **natural selection** that **increases relative fitness** in the environment (**reproduce** successfully and favourable/**advantageous** traits)
   - Reflect a compromise between selective pressures – under selection by many agents on certain variants of traits
- **Adaptation**: **accumulation** of **adaptive traits** over time
- **Current traits** had **different functions** in the **past** therefore **cannot test hypothesis** about **influence** of traits of **extinct** species on relative **current** fitness (serves advantage): humans walking upright is an adaptive trait but only served a purpose in the beginning as they needed to look for predators (no longer useful)
- Animals' adaptive exoskeleton helps with gravity but in fossils the exoskeleton evolved millions of years ago in the sea before the moved to land where gravity was not needed therefore was developed for protection (selection by predators)
   - But challenged evolution as needs to shed to grow and limits size therefore now it is a constraint
- **Not all** traits are **adaptive**, some are the **products** of **chance events** and **genetic drift**
- **Environments change** but **selection** favours **variants** that are **successful** under conditions experienced by **parents**
- **Mutations** are **rare** (slow) so **selection** acts on **existing variation** therefore **adaptive changes** involve **small modifications** of **existing structures** – therefore constrained to only acting on variations that exist not redesigning

<u>Summary</u>

- Differential **reproductive success** of **phenotypic variants** leads to **evolutionary change** across generations
- **Mechanism** = **natural selection** and **process** = **evolution**
- **Agents** of evolution cause **microevolution** change in **gene pools** (allele frequencies) of populations

HISTORY OF BIODIVERSITY

- **Adaptive radiation**: **rapid speciation** in response to **strong natural selection** produces a group of **related species** which occupy **different habitats** and use **different food** sources (niches)
    - One central main species **diverges** and produces different types of that specific species (radiates outwards)
    - **Ancestral species** enters a **new adaptive zone** that are open (radiate) which is a morphological key innovation (nectar spurs and wings of birds)/**extinction** of a successful **group**
    - Galapagos finches and Hawaiian honeycreepers
- Evolutionary processes and speciation are counteracted by extinction

<u>Extinction</u>

Natural extinction

- **Death** of **all individuals** of a **species/evolutionary lineage decreasing biodiversity**
- Occurs are a **low rate** where the **extinct** species are **replaced** by new species as **environments change** and **poorly adapted** species will **not survive/reproduce**

Mass extinction

- Species **vanish** faster than they can be **replaced** and the **biodiversity** of a specific species **crashes** where more than **50%** of the **population** becomes **extinct** over a **short geological timescale**
- ORDOVICIAN mass extinction (444 mya) occurred after **Gondwana** moved to **South Pole** because of **cooled climate**, **glaciation**, and **lowered sea levels** – eliminated shallow **marine environments** and extinction of **organisms** in habitat
- PERMIAN (290-245 mya) mass extinction caused by **climate warming** as **volcanic eruptions** that **released carbon dioxide** in the atmosphere **increasing** the **temperature** by 6 degrees therefore **warming oceans** released **methane** which further **increased temperatures**. More than **85%** of living species disappeared – **trees**, **trilobite/marine species**, **reptiles**, and **insects** at the end of the Permian-Triassic-Jurassic period (sharp decrease)
- CRETACEOUS (145-65 mya) mass extinction caused by **asteroid impact** where **dust clouds blocked** the **sunlight** for **photosynthesis**. **50%** if all living species **disappeared** – **dinosaurs** at the end of the Cretaceous-Tertiary period (65 mya)

brains (process more information) indicates they hunted and ate more meat
    - From 1 mya – *H. naledi* which is a mixture of primitive traits shared with australopithecines and modern *Homo*

Tempo of morphological change

- **Phyletic gradualism** hypothesis: most **morphological change occurs gradually** over **long periods** of **time** (transition fossils such as trilobites/intermediate forms)
- **Punctuated equilibrium** hypothesis: lineages have **long periods** of **morphological equilibrium** (no change) then **brief periods** (**short period** (microevolution) of time) of **sudden/burst** branched **speciation/morphological change**
- Change happens readily in isolate populations, so transition fossils are rare

Evolution of morphological novelty

- **Allometric growth**: **different parts** develop at **different rates** and alternating them can provide different outcomes such as modern humans have a less slanted face, not prognathous, larger brains, smaller teeth and developed chin (rate of jaw growing of chimps is faster than skull and human skull develop at same rate as chin)
- **Changes in the timing** of developmental events in **reproduction** (**heterochrony**): Paedomorphosis is Salamanders (gills are present and then lost)
    - Paedomorphosis in *Delphinium* – petals developing faster in different species
- **Modification of existing structures**: **selection recruits existing structures** for new **functions** resulting in **rapid changes**
    - Feathers in non-flying ancestors evolved from reptile scales as insulting so feathers recruited for gliding and then flying
    - Exoskeleton of animals moving onto land is recruited for function of gravity
- **Evolutionary developmental biology**: **changes** in **genes regulating embryonic development** leading to morphological novelty
    - Body parts of organisms develop in a controlled sequence – genetic instructions from the single zygote cell
    - **Homeotic genes** – **code** for **transcription factors** which **bind** to **regulatory** sites in DNA **controlling expression** of other genes = **morphology**
    - **Genetic toolkit**: many animals **share** a **set** of several **homeotic genes** determining the **basic body plan** – they switch other **genes on/off**
    - **Morphological** novelty can arise through **evolutionary changes** in **regulatory genes** which **changes expression** of **existing gene networks**
    - **Modern synthesis**: **accumulation** of **mutations** results in **new genes** which **codes** for **new structures/protein** is a contradiction to

Mesozoic era in Triassic period – Pangea broke up (>201.6 mya) Jurassic period (201.6 mya) – gymnosperms, terrestrial habitats and dinosaurs and then Cretaceous period – angiosperms (145.5 mya)

Phanerozoic eon (same as ape-like ancestors) Cenozoic era (same as ape-like ancestors) Quaternary period Holocene epoch – humans (0.01 mya) [Oligocene period – ape-like]

Earth history

- **Continental drift**: Late Cambrian (514 mya) which is one land – Late Permian (255 mya) where Pangaea identified super continent – Late Jurassic (152 mya) where Gondwana (South America, India, and Africa) and Laurasia (North America/Asia) identified – Late Cretaceous (66 mya) where oceans and continents were identified
- **Plate tectonics** (crossed plates floating on semi-solid mantel with currents = slow movement across globe, built at oceanic ridges and absorbed into mantel at oceanic trenches) and **climate change** (continental drift): circulation in oceans and earths orbit has changed – dry spells where water is locked up with ice and connectivity of land masses. Life affects climate such as angiosperms

- **Cataclysmic change**: unpleasant catastrophic damage that can eject dust/affect sunlight causing climate change
    - Massive volcanic eruptions
    - Meteorites/asteroid impact

Historical biogeography

- **Distributions** of **organisms** through **evolutionary time** (Darwin)
    - **Continuous** distribution (**vicariance**) – **habitats broken** up (geographical barrier or some part becoming moist and other part rainfall)
    - **Disjunct** distribution (**dispersal**) – desserts – results from **organisms moving between habitats**
    - *Nothofagus* is everywhere on all land masses therefore evolved on Pangea before the break-up of the super continent or it was present in Antarctica therefore disjunct of Australia, Antarctica, and South America

4. When river **change course** again allowing the species to come into **contact**, they do **not produce** and therefore **not** allowing **fertile** offspring as there could have before (secondary contact). If they do interbreed **offspring** must be **infertile**

LONG DISTANCE DISPERSAL (islands – Galapagos finches)

1. A few individuals of a **species** from the **mainland** arrive on **isolated islands** A and B – geographically isolated populations on edge of range
2. Over time they **differentiate** into **new species** (populations diverge) on the islands due to **different environment** conditions and then the species on i.e. island B colonize islands C and D therefore no gene flow
3. **Founder** effects: **populations diverge** from the **range centre** and from **one another**
4. **Later** on C species **colonises** island A and the D species colonise island B (secondary contact) – **isolated** populations **diverge** forming **distinct** species prevent interbreeding

Parapatric speciation – beside

- Individuals **colonize** a **neighbouring** habitat (were the same phenotypes)
- There is **gene flow** across the boundary – **ecological** (habitat) **barrier**
- There are **different genetic variants** favoured in each habitat (different phenotypes)
    - Reduce gene flow as those with wrong genotype in wrong habitat will have a low fitness level
- Can't differentiate between Parapatric and secondary contact

Sympatric speciation – together

- **Divergence** and **reductive isolation** between **subgroups** in a single population (mixture of different phenotypes)
- No physical or ecological barrier – in the **same population**
- Host races: walking stick species eat different plant species, and these organisms could evolve into different species/gain certain traits based on the plant, apple maggot fly complete lifecycle on different hosts – thorns, apple, cherry (fruit) creating temporal isolation of fruit and revolves to isolation of fly species, polyploidy (double of chromosome numbers) and evolved from diploid parents as offspring will be triploid – sterile therefore reproductively isolated from other species (angiosperms and agriculture – crops to produce larger fruit/sterile seedless variants)

<u>Genetic basis of speciation</u>

Genetic divergence in allopatry

- **Postzygotic isolation** – accidental by-product of **selection**, **genetic drift**, **mutations**
    - Hybrid inviability: 2 genes (fish) – genetic change needed to = speciation
    - Hybrid sterility: 4 genes (fly) and 55 genes (frog)

    - Anopheles consist of 6 different species with different ecology and systemics allowed **targeting** of the species with Malaria and **control** larvae
- **Carl Linnaeus** is the father of **binomial nomenclature**
    - **Latin** name for each species – **genus** (genera) and **species** name which is based on the **morphological species concept** to classify organisms
    - Grouped similar traits based on morphology to form clusters = hierarchy
- **Binomial system**: **first** part of the name identifies the **genus** (group of organisms that **share** many **traits**), and the **second** part is the **specific epithet** which is **species** name
- **Taxonomy**: science that **identifies**, **names**, and **classifies organisms**
    - Order of specific to not specific: species (distinct traits), genus (share traits), family, order, class, phylum, kingdom – move up similarities decrease
    - Advantage: **no uncertainty** in **taxonomy** of organisms
- **Taxonomy hierarchy**: each **species** belongs to a **taxon** (taxa) at each **level** of organisation (birds' taxon = Aves – Class)
- **Common names** used – different countries have different common names for same organisms (1 organism can have different common names) therefore difficult to know which species talking about so binomial important

<u>Phylogenetic trees</u>

- Darwin: all **organisms share** a **distant common ancestor** and **evolution** produces **branching patterns** of evolutionary **relationships** which **fits** with **Linnaeus hierarchy**
    - **Species** in a **genus share** more **recent common ancestor** than species in class
- **Phylogenetic** tress are **hypotheses** of **evolutionary relationships** between **taxa** and phylogenetic classification reflects evolutionary history (hierarchy)

Interpreting a phylogenetic tree

- **Read** from **tips** (letters) to **root** (base/node) – read up to down **move back in time**
- Sequence of **nodes** indicates the sequence of **evolution** of **clades** (**node** is a common **ancestor**) – A and B are joined by a common ancestor recently (closely related)
- **Horizontal** distance across tree indicates **nothing** about relationship – B and C not related (**distantly related** as related at root)
- **Nodes** with **more** than **1 branch** indicate **unresolved** relationships
- Any **clade** can be **rotated** around a node **without changing relationships**
- **Clade** consisting of **multiple species** that share a **common ancestor** (more than 1)
    - **Sister clades**: **2 clades** share **recent common ancestor**. There are nested hierarchy clades (clades within clades): node (ancestor) – straight

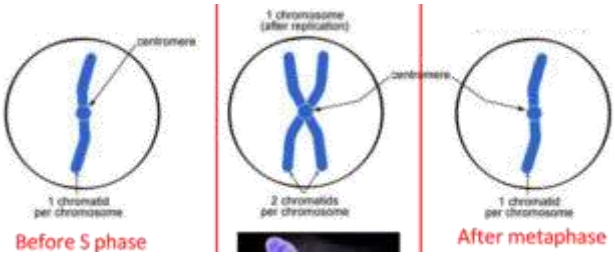
- **Homologous characters** = **phenotypic** characters with **heritable genetics** which arose in **common ancestors** – similar due to presence in ancestors (human, cat, whale, and bat)
    - **Similar** in **anatomical** details/**surrounding** structures but slightly **different** due to **differences** in **selection pressure** therefore suited for different **functions**: phalanges, ulna and radius, humerus, ball & socket movement
    - Developed from the **same embryonic tissue** is similar ways
- **Homoplastic characters** = **phenotypic similarities** that evolved **independently** in different lineages, they are **not similar** because they were **present in a common ancestor** but rather as result of **convergent evolution** (skin and feathers)
    - **Similar selective pressures** not common ancestors
    - Forelimbs in flying vertebrates: wing surface have large surface area for flight
- **Morphology** = these **differences** are **genetic** and can be used to **compare extinct** and **living** organisms but is **not** enough on its own to **reveal evolutionary relationships**
  Behaviour = when **morphology** is **similar** you can use behavioural traits – **prezygotic characters** is what **animals** use to **recognise** each other (calls/pollen)
- **Molecular DNA** data = **similar DNA sequences** with **chromosomes**, **histones**, DNA **double helix** and **base pairs** therefore creating **similar proteins** (only variable characters used for relationships): extraction of DNA and sequences of DNA
    - Fewer changes of base pairs between species = more recently related species
    - **Advantages** = produces **lots** of **data** as each **base** pair is an **independent** character, useful in **distantly related** groups/**closely related** organism and **not influenced** by **environment** (no **plasticity**)
    - **Disadvantage** = only **4-character states** (A, C, T, G) – **homoplasy** by change (same base at locus) is a problem as **bases** may be the **same** but **not** because of their presence in a **shared ancestor**

<u>Cladistics analyses</u>

- **Cladistic methods** are based on **shared derived characters** because in **direct common ancestors** and not ancestors deeper in time = **synapomorphies**
    - Morphological similarity is not good enough unless similarities reflect descent with modification – needs characters with **2/more character states** (which evolved first – distance ancestors and which was derived – direct ancestors)
- **Characters** and **character states**:
    - Character – eye colour and character states – blue, brown, or green
    - Molecular characters – nucleotide bases and states – A, C, T, G

Result of mitosis

- **2 daughter cells** with **genetic duplicates** of **each other** and to the **parent cell** (G1)
- Chromosomes different through cycle: count chromosome by centromere
    - **1 chromosome** (single – gamete) with **1 chromatid** = **double** (2 chromatids)
    - **Homologous pairs** (double stranded)
    - Homologous pairs **separate** to **ends** (**double** stranded)
    - **Anaphase 2**: back to **single** stranded – **gamete**



Defects of regulation of cell cycle

- **Cancer**: normal cells = **abnormal cells** = multiply = malignant cancer
    - Grows **own blood vessels** (angiogenesis) and **invade** surrounding tissue
    - **Overactive cell cycle** forms abnormal growth (cancer)
- **Wounds** that **do not heal** have a defective cell cycle

3 checkpoints for the regulation of the cell cycle:

1. *G1/S transition*: parent cell **DNA correct**, enough **resources** to replicate **DNA** and **build** extra **protein**, **environment** (size, volume, and nutrients) – will not increase in size
2. *G2/M transition*: **DNA replication** and **commits** cell to **mitosis** (cell will not enter point in DNA replication incomplete/defective)
3. *Checkpoint M/mitotic*: before metaphase did **spindle assemble**, and did **chromosomes attach** to spindle to **align** on **metaphase plate** (crucial for 2 genetically identical cells produced)

Questions:

1. Describe **cell cycle**: G1 for growth of cell, S phase for DNA replication, G2 for growth and preparation for mitosis which is all interphase and then it is Mitosis for cell division
2. **Stages of mitosis** and what happens: Prophase – chromatin into chromosomes, nuclear envelope breaks down, chromosomes attach to spindle fibres by centromere; Prometaphase – microtubules rapidly assemble and disassemble as they grow out of the centrosomes, seeking out attachment sites at chromosome kinetochores (complex platelike structures that assemble on one

face of each sister chromatid at its centromere); Metaphase – chromosomes align along metaphase plate; Anaphase – sister chromatids are pulled to the opposite poles; Telophase – nuclear membrane reforms, chromosomes decondense into their interphase conformations; Cytokinesis – division of cytoplasm into two daughter cells.

3. Describe **formation and action of mitotic spindle**: long protein fibres called microtubules extend from the centrioles in all directions forming a spindle. Spindle fibres are made up of microtubules which form a protein structure that divides the genetic material in a cell and is necessary to equally divide the chromosomes
4. Name and describe what happens at **each cell cycle control point**: G1 for nutrients for growth needed and no damage of DNA (cell destroyed), G2 needs to have DNA replicated completely and no damage of DNA (repaired/replaced), Mitosis needs chromosomes attached to spindle fibres in metaphase and all chromosomes to be moved to poles in anaphase (repaired/replaced)

	Before Interphase	After Interphase	After Mitosis
Chromosomes	2n = 46 (single)	2n = 46 (double) Count centromere	46
Chromatids	46 (not double yet)	92	46

MEIOSIS

Division of sexual cells enabling sexual reproduction and generates genetic variability

- Embryo transfer:
  - Stimulating eggs develop and egg retrieval – egg fertilised by sperm cells
  - Embryo development and embryo transfer to uterus for implantation

<u>Sexual life cycle</u>

1. **Diploid multicellular** organism (46 chromosomes) undergoes **meiosis** (ovary/testes)
2. **Gametes** are formed being **haploid** (n) – egg cell or sperm cell with 23 chromosomes (22 autosomes and 1 sex chromosome/gonosome X/Y)
3. **Fertilisation** occurs when **2 haploid gametes fuse** (1 maternal and 1 paternal)
4. **Zygote** that is **diploid** is formed (2n) and **mitosis** occurs = **multicellular** organism

<u>Sexual reproduction</u>

- **Haploid** sperm – **spermatozoa** (n) and **haploid** egg – **oocyte** (n) undergo **fertilisation** where there is the **fusion** of haploid cells to produce a **diploid zygote** (2n) – homologous chromosomes (same gene, same locus but different form of same gene)
- Diploid zygote **carries chromosomes from two parents** – maternal homologue and paternal homologue

- Homozygous: it is an individual that is homozygote – homozygous for a particular allele of the gene (homozygous recessive or homozygous dominant)
- **Heterozygotes**: **alleles** of the gene are **different** (**hybrid**) – produces **2** types of **gametes** (Pp = P and p)
- Heterozygous: it is an individual that is heterozygote – heterozygous for the pair of different alleles of a gene
- **Hybrid**: **offspring** of parents with **different traits**
- **Dominant** allele (uppercase): **determine trait expressed** when paired with recessive allele (Pp/PP)
- **Recessive allele** (lowercase): **expresses trait** only when **2 copies** of allele is present (pp)

<u>Mendel's monohybrid crossings</u>

- He studied a variety of characteristics one at a time (seed form/cotyledon, flower colour, pod form/colour, stem place/size)
- He focussed on **alternative forms** (**alleles**) which is the trait of **phenotypes** (flower colour – white/purple)
    1. **Phenotypes**: **observable characteristics** – height, biomass, lead shape and describes the **collective expression** of a **genotype** in conjunction with the **environment** on observable characteristics
- **Cross fertilisation** of the **parent generation** (P) is followed by **self-fertilisation** of the **offspring** (F1 × F1)
- **F1** generation will be **hybrid** when **2 homologous parents** with **different alleles** breed (**100**%). **F2** generation will always be in ratio of **3:1** when **self-fertilisation** happens (**75:25**%)

3rd conclusion – Principle of segregation: Mendel's first law of heredity

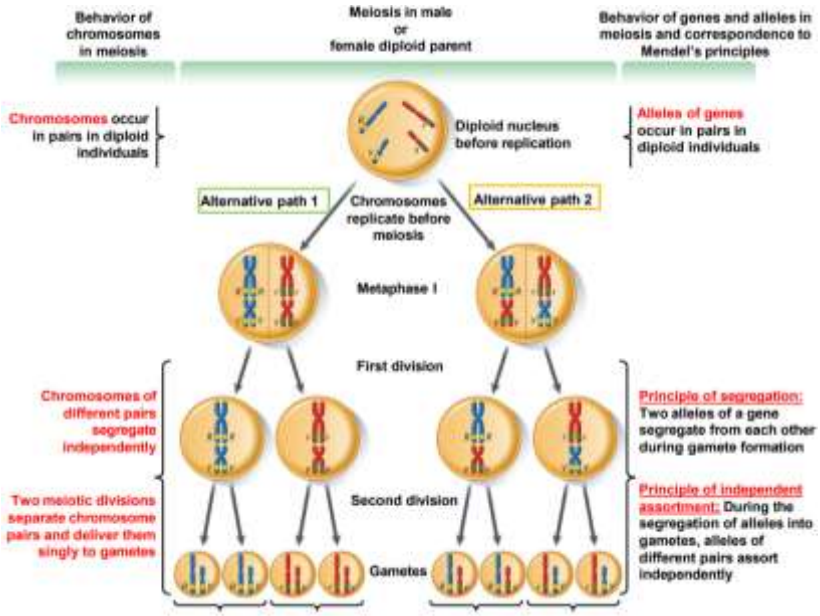
- The **pairs** of **alleles** separate/**segregate** in meiosis during **gamete formation** so that half the gametes carry one allele and the other half carry the other allele and that **each gamete** only consists of **1 allele** for **each gene**

Testcrosses

- It is a **test** to **determine**/**predict** the **genotype** (homozygous/heterozygous) of an organism with a **dominant phenotype** for a trait by looking at offspring
    1. Organism expressing the **dominant phenotype** (**unknown** genotype) for a trait is crossed with a **known homozygous recessive** individual (pp) – testcross
    2. If **half offspring** shows **recessive** trait and **half** shows **dominant** trait (50:50), then the **unknown** genotype is **heterozygous** (**Pp**)
    3. **All offspring** show **dominant** trait (hybrid) then **unknown** is **homozygous** (**PP**)

<u>Dihybrid crosses</u>

- There is **independent assortment** of genes leading to **random fusion** of **4 different male gamete** with **4 different female gametes** for F_2 generation
- **F1** (**cross** fertilisation) generation is **hybrid** for the 2 different genes. **F2** generation (**self**-fertilisation) is **9:3:3:1**



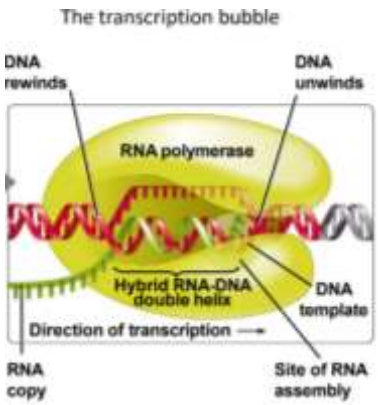
4th conclusion – Principle of independent assortment:

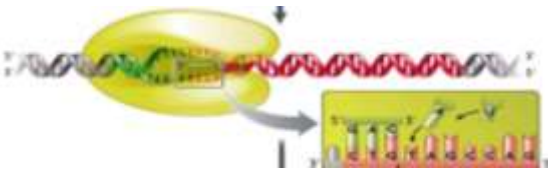
- **Segregation** of different **genes** carrying **different traits** occurs **independently** during gamete formation – **alignment** of **homologous** pairs in **metaphase** can occupy **different positions** and in **anaphase** they **separate independently**

Later modification and additions to Mendel's hypothesis

1. **Incomplete** dominance: **heterozygotes** have **intermediate phenotypes** (mixture of each allele) – RR with WW = RW (**pink**)
   A **different letter** represents a **different allele** for a gene (**no dominant/recessive**)
   RW with RW = 1 RR, 2RW, 1WW = 1:3 ratio
2. **Co-dominance**: alleles have approximately the **same effect in individual** (both combined and equal) – RR with WW = RW (**red and white spots**)
3. **Multiple alleles** – **more** than **2** different **alleles** for a **gene**
   Blood types (I) = I^A, I^B and i where I^A I^B are co-dominant and i is recessive
   I^A I^B = AB phenotype, ii = O phenotype, I^A i or I^A I^A = A phenotype, I^B i or I^B I^B = B phenotype. + or – on blood group = presence or not of antigen (- mother with + child = body produce antibodies and attack foetus)

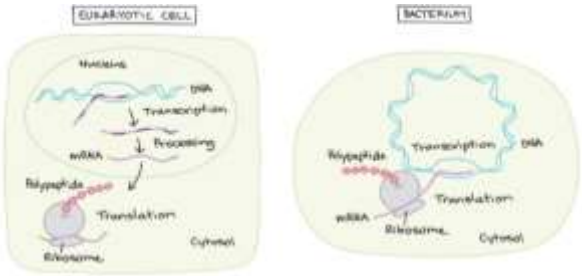
Blood Type	Antigens	Antibodies	Blood Types Accepted in a Transfusion
A	A	Anti-B	A or O
B	B	Anti-A	B or O
AB	A and B	None	A, B, AB, or O
O	None	Anti-A, anti-B	O

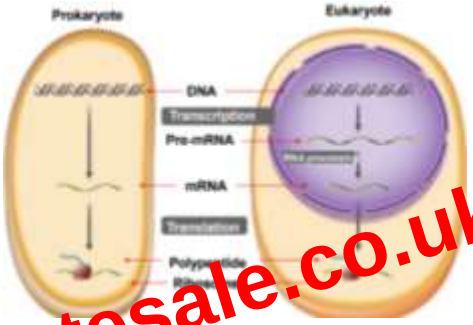




Differences in transcription and translation in prokaryotes and eukaryotes

- Eukaryotes: transcription in nucleus, processing (each end of RNA molecule is modified), mRNA molecule leaves nucleus, in cytoplasm where translation occurs, and ribosomes are involved

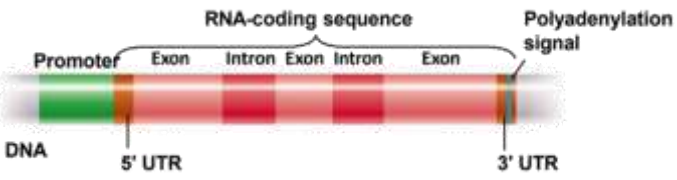




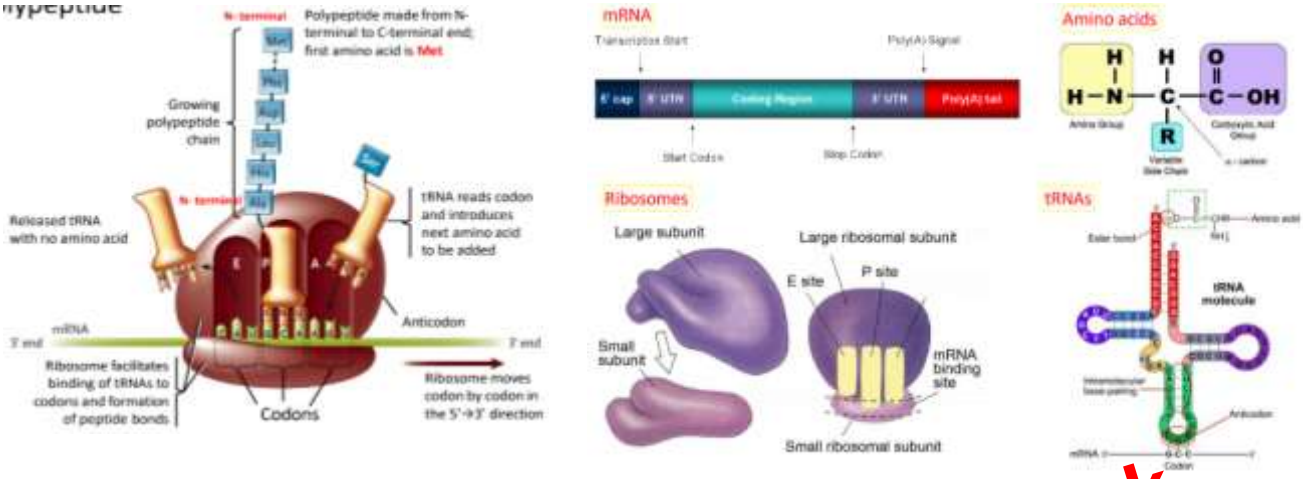
Eukaryotic protein coding genes and contain non-coding elements

- Transcribed in **eukaryotic pre-mRNA**:
  - **Exons** (protein coding – involved in protein synthesise) and **introns** (non-protein coding and absent in prokaryotes)
  - **5' UTR** (untranslated region) and **3' UTR** (untranslated region)
  - **Polyadenylation signal**/tail at 3' (proteins bind) (absent in prokaryotes) as prokaryotes have terminating end

- Modifications of pre-mRNA in protein coding genes (**pre-mRNA transcription**):
  - **RNA polymerase transcribes** the gene
  - **5' cap (GTP) added** on pre-mRNA after **transcription begins** by a capping enzyme and it **protects 5'** from RNA digesting enzymes and **site** where **ribosome** attach to mRNA (at the cap there is a G: 3 phosphate molecules)
  - **Transcription continues past** the **end** of the gene and **stops** at **cleavage site**



  - Enzyme responsible to **aminoacyl-tRNA synthetases**
- **E** – exit, **A** – aminoacyl and **P** – peptidyl **site** on **large subunit** of a ribosome and the **small subunit** of a ribosome situated on the **mRNA**: **aminoacyl-tRNA** carrying the **next aa** to be **added** to **polypeptide** binds at **A site** on mRNA, **tRNA** caring **growing polypeptide chain** bound at **P site** and **tRNA without aa** binds to **E site** before **exiting** ribosome (RIBOSOME MOVES ON MRNA and reads codon as moved from 5' to 3' and join amino acid)



Stage 1: initiation

- Methionine (**AUG**) **amino acid** attaches to the **initiator tRNA** at **3'** (GTP) and has an **anticodon** attached to **start** the **codon** at the **bottom** the **anti-codon attaches** the **mRNA** codon on the **small subunit** of the ribosome
- **Initiation complex components** assemble on the **start codon** of the **mRNA** which is situated on the **P site** of the **large subunit** of the ribosome after **scanning** has taken place **from** the **5' cap** on the **smaller subunit**
- **GTP** is **released** as **GDP** and a **phosphate** molecule
- **Base-pairing**: **binding** of **tRNA** & **mRNA** through **scanning**