Evolution

Binomial Nomenclature of a Species

- Common names can cause confusion as they may refer to more than one species or may not accurately reflect the kind of organism they signify
- Scientific name avoids ambiguity when referring to a specific species
- Binomial nomenclature consists of 2 parts: First part is the name of the genus the species belongs to and is capitalised; Second part is the specific epithet
- Entire scientific name is italicised

Hierarchical Classification

- Species are grouped into a hierarchy of increasingly inclusive categories based on homologies
- Closely related organisms are grouped into the same taxon which is a named taxonomic unit at any level of hierarchy
- In decreasing order of inclusivity: Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species

Concepts of Species
General definition:

1. **Capable of interbreeding and producing fertile, viable offspring
2. **Reproductively isolated from other species
3. Common gene pool and same chromosome number
4. Similar morphological, physiological and behavioural features

Concept	Definition	Advantages	Limitations
Biological	A group of organisms capable of <u>interbreeding</u> and producing <u>fertile, viable offspring</u>	<u>Can be interbred</u> to see if they produce fertile, viable offspring if being studied	Cannot be applied to <u>asexually reproducing organisms</u> and <u>extinct species</u> whose breeding behaviour cannot be observed
Ecological	A group of organisms sharing the <u>same ecological niche*</u>	Applies to both organisms that reproduce <u>sexually and asexually</u>	Cannot be applied to <u>unrelated species that occupy similar niche</u>

Morphological	A group of organisms that share <u>similar body shape</u> and other structural features	Applies to both organisms that reproduce <u>sexually and asexually</u>	Difficult to determine the <u>degree of difference</u> to separate species and what structural features should be used to distinguish them Some organisms may be <u>superficially similar</u> due to convergent evolution but have different evolutionary origins
Phylogenetic	Smallest group of organisms that share a <u>most recent common ancestor</u> and can be distinguished from other such groups Obtained by comparing homologous morphological structures and molecular sequences with those of other organisms	<u>Avoids mistakenly classifying</u> organisms based on superficial morphological similarities as the characteristics compared are based on common ancestry/homology	<u>Difficult to determine</u> the most recent common ancestor of a species

*Niche = The place where an organism lives + its interactions with the environment

Natural Selection

1. Overproduction of offspring
2. Constancy of numbers
3. Struggle for existence
4. **Variation within a population
5. Survival of the fittest by natural selection
6. Like produces like
7. Formation of new species

How to explain:

- Natural populations <u>overproduce offspring</u>
- However, population <u>numbers remain fairly constant</u> as
- Many <u>fail to reach reproductive age</u> due to competition for scarce resources, predators, diseases and environmental factors
- Individuals within a population have genetic ==**variation**== (due to genetic mutations) and hence show phenotypic differences for <u>natural selection</u> to act on
  - (For bacteria/viruses) Some bacteria/viruses mutate to develop antibiotic/antiviral resistance
- Variants with favourable characteristics have a selective advantage and are hence, <u>selected for</u> and <u>more likely to survive and reproduce</u>
- Produce fertile viable offspring, <u>passing on their alleles</u> coding for favourable traits to their offspring
- Proportion of individuals with favourable traits increases over time leading to an <u>increase in favourable allele frequencies</u>
- (Only if speciation) Over hundreds and thousands of generations, evolutionary changes occur and may form new species if each population becomes reproductively isolated

Disruption of Gene Flow (Geographical/Physiological/Behavioural isolation ⇒ Speciation)

- Describe Geographical/Behavioural/Physiological isolation
  - Geographical → Physical barrier between 2 sub-populations → Allopatric isolation
    - e.g. Darwin finches on Galapagos Islands
  - Behavioural → Unique mating rituals/Preferences of individuals → Sympatric isolation
    - e.g. Eastern and Western Meadowlarks developed different calls
  - Physiological → Unique physiology of individuals → Sympatric isolation
    - e.g. *Howea forsteriana* and *Howea belmoreana* palm trees on Lord Howe Island → difference in soil types: calcareous soil vs volcanic soil ⇒ difference in flowering times
- Prevents interbreeding → <u>Disruption of gene flow</u>
- Exposed to different environments and hence different **selection pressures**
  - Even for physiological and behavioural isolation e.g. Different soil types ⇒ Different selection pressures, Preferential mating ⇒ Different selection pressures
- Since there is ==**variation**== in phenotypes in the population, those with <u>favourable characteristics selected for</u> and are more likely to survive, reproduce and pass on their alleles to the next generation, those with unfavourable characteristics selected against
- <u>Evolutionary changes occur independently</u> and different <u>genetic mutations are accumulated over time</u> in each sub-population ⇒ <u>Allele frequencies change</u> due to natural selection and genetic drift
- (Only if speciation) Over hundreds and thousands of generations, evolutionary changes occur and each sub-population may become reproductively isolated, forming new species and can no longer interbreed to produce fertile viable offspring
  - Reproductive isolation can be pre or post zygotic
  - Pre-zygotic prevents mating/fertilisation e.g. geographical/physiological/behavioural isolation
  - Post-zygotic prevents hybrids from developing into fertile adults (hybrid sterility)/zygote mortality

Gene Flow = Transfer of alleles from one population to another due to the movement of fertile

individuals/gametes

Why is the population the smallest unit that can evolve? (possible essay)

- Define population: A **population** is a group of <u>interbreeding</u> individuals of the <u>same species</u> and sharing a <u>common geographic area</u>
- Define evolution: **Evolution** is a measure of changes in allele frequencies in a population over time
- **Variation** must exist in a population for natural selection to take place
- **Natural selection** acts on individuals in a population and results in individuals being selected for or against
- Individuals cannot evolve/don't change in their lifetimes
- Individuals can only **pass on their favourable alleles** to the next generation
- And introduce new alleles through **mutation** during the formation of gametes
- Over many generations, allele frequencies of favourable characteristics increase over time, leading to evolution

Variation = Phenotypic differences between individuals in a population due to genotypic differences

- Importance
  - Raw material for natural selection to act on
  - When environmental changes occur → Some individuals have a selective advantage → Selected for through natural selection
  - Without variation, either all organisms will be selected for or against → Sudden change in environmental conditions may lead to extinction of the species

How variation in populations arises

- Mutations
  - <u>Random gene mutations</u> such as substitution, deletion or insertion of a nucleotide resulting in change in sequence of nucleotide bases → change in amino acid sequence → change in unique 3D conformation of the protein → change in function of the protein → change in phenotype
    - e.g. base substitutions/deletions/insertions
  - <u>Chromosomal mutations</u> resulting in change in chromosomal structure and number
- Meiosis
  - <u>Independent assortment of homologous chromosomes</u> during metaphase I and subsequent segregation during anaphase I
    - Results in 2^n <u>different combinations of maternal and paternal chromosomes</u> in daughter cells where n is the number of chromosome pairs
  - <u>Random orientation of sister chromatids</u> during metaphase II and subsequent separation during anaphase II

- Crossing over between non-sister chromatids of homologous chromosomes
    - Results in new combinations of alleles on chromosomes
- Sexual reproduction
    - Random fusion of gametes during fertilisation
        - Results in greater number of genotypic combinations of a zygote

Preservation of recessive alleles (possible essay)

- **Heterozygote protection**
    - Occurs in diploid organisms with 2 copies of each gene
    - Heterozygous = 2 different alleles at 1 gene locus where dominant alleles can mask the effect of recessive alleles
    - Homozygous recessive genotype has disadvantageous phenotype which is selected against but does not manifest in heterozygotes ⇒ Heterozygotes survive
    - Heterozygotes able to pass on recessive allele to their offspring when they interbreed, maintaining recessive allele in the population
- Balancing selection = Natural selection maintains 2 or more alleles at a gene locus
    - **Heterozygote advantage**
        - Heterozygotes may have greater fitness than both types of homozygotes
        - e.g. Heterozygote individuals selected for
            - HbAHbA ⇒ Individuals have normal haemoglobin ⇒ Susceptible to malaria
            - HbSHbS ⇒ Individuals have sickle cell anaemia ⇒ Early death
            - HbAHbS ⇒ Individuals do not develop sickle cell anaemia + Less chance of contracting malaria
                - Maintains both HbA and HbS alleles in the population
                - Sickle shape of RBC ⇒ Lower oxygen carrying capacity ⇒ Malaria parasite cannot survive
                - Heterozygotes have selective advantage in regions of endemic malaria over both homozygotes
        - Heterozygotes able to pass on recessive allele to their offspring when they interbreed, maintaining recessive allele in the population
    - **Frequency dependent selection**
        - Selective advantage of the phenotype depends on the relative frequency of the particular phenotype
        - Frequency of each phenotype oscillates over time but is kept close to 50%, maintaining both alleles
        - e.g. Left-mouthed and Right-mouthed scale eating fish in Lake Taganyika
            - Prey guards against attack from the more common phenotype of the scale-eating fish in the lake
        - Selection favours whichever phenotype is least common
- Neutral mutations = mutations that are selectively neutral
    - Silent mutations = Mutated sequence still codes for the same amino acid
    - Conservative mutations = Mutated sequence codes for chemically similar amino

acid
- Mutations in <u>non-regulatory</u>, <u>non-coding regions</u>
- Thus, no change in protein structure and function + no change in quantity of protein produced

Homology = Similar <u>anatomical</u>, <u>molecular</u> and <u>embryological</u> characteristics found in different species due to <u>common ancestry</u>. Developed into different forms due to natural selection as they faced different environmental conditions (**descent with modification**).

<u>How do anatomical, embryological and molecular homology support Darwin's theory of evolution by natural selection (with examples)</u>

- Basis
    - Organisms that look very different may share an underlying similarity called **homology** because of <u>shared common ancestry</u>
    - Characteristics present developed into different forms due to natural selection as they faced different environmental conditions (**Descent with modification**)
- Anatomical homology
    - Similarity in <u>morphological structures</u>
    - *e.g. Pentadactyl forelimb structure of all tetrapods
        - Forelimbs of humans, whales, bats have <u>same arrangement of bones</u> but <u>different functions</u>: lifting, swimming and flying and <u>look superficially different</u>
        - <u>Modification of the five-digit pentadactyl forelimb</u> structure of the common ancestor due to natural selection resulted in the different forms of the pentadactyl limb to <u>suit their specialised functions/environments</u> (Descent with modification)
- Embryological homology
    - Similarity in <u>structures during embryonic development</u>
    - e.g. All vertebrates have <u>gill slits</u> during the <u>early stages in their embryonic development</u>
        - Gill slits develop into structures with very different functions such as gills in fishes and parts of the ears and throat in humans
        - <u>Basic embryological body plan</u> in ancestral species was modified in different descendant species as the selection pressures changed due to differences in environments (Descent with modification)
    - Degree of relatedness: The longer the embryological development remains similar, the more closely related the organisms
- Molecular homology
    - Similarity in <u>DNA, RNA and amino acid sequences</u>
    - e.g. <u>Cytochrome C</u> and <u>p53</u> genes
        - <u>Nucleotide sequences</u> are <u>significantly similar/conserved</u> ⇒ Produce <u>proteins</u> with the <u>same function</u> in all organisms ⇒ Shared common ancestry
        - Important enough that every organism possesses them and produce proteins that carry out the same function in different organisms

- Ancestral gene nucleotide sequence modified over many generations due to <u>accumulation of genetic mutations</u> ⇒ Selection pressures favoured some mutations over others
    - The greater the similarity in the sequence of the gene, the more closely related the 2 species are

Biogeography = The study of the past and present geographic distribution of organisms
<u>How does biogeography support evolutionary deductions based on homologies?</u>

- Biogeographical realms
    - All modern species descended from a common ancestor
    - Closely related organisms and common ancestor usually located in the same biogeographical regions (State where if given)
    - Explain how descent with modification from ancestral species takes place
        - e.g. Apes (Gorillas, Orang utans, Bonobos and Chimpanzees) are only found in the forests of Africa and Asia
- Continental drift
    - All modern species descended from a **common ancestor**
        - Ancestors originally able to move around freely throughout ancient supercontinent as continents originally in close proximity
        - Continental drift ⇒ Populations distributed/isolated in different continents
    - Descent with modification
        - Disruption of gene flow
        - Different selection pressures ⇒ Natural selection ⇒ Phenotypic differences ⇒ Over time, speciation
        - e.g. Lungfish (Continental drift) found in Australia but fossils of related species also found in South America and Africa
- Island biogeography (e.g. Darwin's Finches)
    - Finches on the Galapagos islands similar to those found on the South American mainland ⇒ Likely to <u>share a common ancestry</u>
    - However, there are now 13 different island species
    - Different islands had many different environments which presented <u>many different ecological niches</u>
    - Ancestral finches exposed to <u>different selection pressures</u> ⇒ Those best adapted were selected for, able to survive and reproduce ⇒ Pass on their alleles to the next generation
    - <u>Evolutionary changes occurred independently</u> in each sub-population ⇒ <u>Allele frequencies change</u> due to natural selection, genetic drift and genetic mutation ⇒ Over hundreds and thousands of generations, each sub-population becomes <u>reproductively isolated</u> ⇒ New species
    - Biogeographic distribution of finches supports the deduction of **descent with modification** from a common ancestor as ancestral species from the mainland evolved into many different species through **adaptive radiation**

- **Adaptive Radiation** = Rapid increase in number of species produced from a common ancestor upon introduction into new environments

Fossils = Relics/Impressions of organisms that lived in the past that are preserved in rock

- Carbon dating → Find out how old a fossil is
- Show how homologous structures have modified through time
- Show <u>ordered sequence of progression</u> of modification of homologous structures from ancestral species to modern descendent species through a series of <u>transitional</u> forms
  - Each species preceded by a logical and related ancestor through descent with modification
- e.g. Horse fossils
  - Ordered sequence of progression in terms of lengthening of limbs, toe reduction and increase in tooth size over time as the environment changed from dense forests to open grasslands
  - Most favourable characteristics were selected for through natural selection
- e.g. Transitional fossils such as Tiktaalik
  - Tiktaalik is a transitional fossil animal which illustrates an evolutionary transition between fishes and tetrapods providing strong evidence that fish are ancestors to modern tetrapods
  - Had fish gills and scales like its fish ancestors and had tetrapod leg bones, lungs , upward positioned eyes and a mobile neck like its tetrapod descendants

Molecular Methods to Determine Phylogeny
Importance of using molecular methods:

- All living organisms contain nucleic acids which captures evolutionary changes
- More closely related species ⇒ Greater number of similar nucleotide sequences in nucleic acids + Greater number of similar amino acid sequences in proteins
- Better understanding of evolutionary relationships and has led to extensive revisions of the classification of all life-forms

Advantages (possible essay)

1. <u>Objective</u> as molecular character states are <u>unambiguous</u> (A, C, G, T)
2. <u>Quantitative</u> as it can easily be <u>converted to a numerical form</u> for statistical analysis
   - <u>Degree of relatedness</u> can be <u>inferred and quantified</u> by calculating nucleotide differences between species
3. Can compare <u>all</u> organisms which <u>share homologous genes</u> as they are all based on nucleic acids
4. Can compare <u>morphologically indistinguishable</u> organisms due to convergent evolution or are very closely related
5. Changes in nucleotide sequences accumulate over time with <u>clockwork regularity</u>, <u>molecular clock</u> allows us to <u>estimate the time of speciation</u> of a particular species
6. <u>Does not underestimate/exaggerate differences</u> unlike morphological analysis
   - Some molecular differences may not be reflected as differences in morphological character, some small genetic differences may result in major phenotypic differences

7. <u>Remotely related organisms</u> such as bacteria, humans and sunflowers can also be compared since they <u>share some proteins</u> such as cytochrome c
8. Both living and dead tissue can be used + Not necessary to have an entire specimen
9. Large set of characters can be studied relatively <u>quickly</u>
10. Sequences can be accessed electronically for easy comparisons and classification

Benefits of using mitochondrial DNA (e.g. cytochrome b)

- <u>Does not undergo recombination</u>, thus any changes in DNA is **solely** <u>due to accumulation of mutations over time</u> → Ideal candidate for <u>molecular clock</u> as mutations occur at <u>constant rate</u>
- <u>High rate of mutation</u> allows differences in mtDNA to sufficiently distinguish between closely related species or even individuals from the same species
  - Due to <u>lack of proof-reading mechanism</u> during mitochondrial DNA replication
  - Due to DNA being damaged by <u>reactive oxygen radicals</u> generated in the mitochondrion
- Contains many homologous genes e.g. cytochrome b gene ⇒ Good basis of comparison

Neutral theory of molecular evolution

- Most mutations that exist at molecular level are neutral mutations = mutations that are <u>selectively neutral</u> ⇒ No selective advantage or disadvantage on its phenotype
  - Silent mutations → mutated sequence still codes for the <u>same amino acid</u>
  - Conservative mutations → mutated sequence codes for <u>chemically similar amino acid</u>
  - Mutations in <u>non-regulatory</u>, <u>non-coding regions</u>
- Disadvantageous mutations quickly removed by natural selection
- Advantageous mutations quickly brought to fixation (i.e. no longer mutates), hence remaining in the population
- Neutral mutations accumulate at a <u>constant rate</u> ⇒ Forms the basis for the molecular clock
- Since most mutations are selectively neutral, most evolutionary changes in populations are due to <u>genetic drift</u> rather than natural selection

Explain the relationship between classification and phylogeny.

1. Classification is the organisation of species according to particular characteristics and may not take into consideration the evolutionary relationship between species
2. Phylogeny is the organisation of species according to particular characteristics which takes into consideration the evolutionary relationship between the species
3. Phylogenetic classification where species are categorised into hierarchical classification based on the evolutionary relationships derived from phylogeny

	Classification	**Phylogeny**
Basis of grouping organisms	Based on <u>morphological similarities</u> NOT evolutionary history of organisms	Traces <u>evolutionary history</u> based on <u>ancestor-descendant relationships</u>
System of organising organisms	<u>Naming system</u> where each organism is grouped into a domain, kingdom, phylum, class, order, family, genus and species using a <u>hierarchical classification system</u>	Assigned a <u>position on a phylogenetic tree</u> relative to their evolutionary relationship with other organisms where more closely related organisms are grouped closer together on the phylogenetic tree
How species are presented	Binomial nomenclature	Phylogenetic tree
Nature of characteristics	Based on <u>morphological characters</u> only	Makes use of <u>homologous characteristics</u> derived from a common ancestor - morphological, anatomical, embryological, molecular characteristics and fossil records
Ease of placing an organism into a group	Easily placed into well defined group	Cannot immediately place an organism into phylogram as evolutionary history needs to be established from multiple sources
Accuracy of classification	May wrongly classify organisms that are not related but look similar due to convergent evolution	Rarely classifies wrongly as convergent evolution will be placed in separate branches
Inference of speciation events	Does not allow inference of historical speciation events	Indicates speciation events as the node of the phylogenetic tree
Inference of relationships	Cannot infer how closely related 2 species are	Allows accurate inference of how closely related 2 species are by looking at how recently they diverged from their common ancestor

Inference of common ancestors	Does not allow inference of common ancestors	Allows inference of common ancestors. Descendants of a common ancestor are represented in the same branch
Application of molecular clock	Not possible to apply molecular clock to date speciation events	Can apply molecular clock to infer time of speciation