

CORE IDEA 4: BIOLOGICAL EVOLUTION
TOPIC: BIOLOGICAL EVOLUTION

Learning Outcomes:

- (a) Explain why variation (as a result of mutation, meiosis and sexual reproduction) is important in natural selection.
- (b) Explain, with examples, how environmental factors act as forces of natural selection.
- (c) Explain the role of natural selection in evolution.
- (d) Explain why the population is the smallest unit that can evolve.
- (e) Explain how genetic variation (including harmful recessive alleles) may be preserved in a natural population.
- (f) define biological evolution as descent with modification and explain the link between micro-evolution and macro-evolution
- (g) explain how evidence based on homologies identified in biochemical data (molecular homologies) and the fossil record (anatomical homologies), together with biogeography, supports Darwin's theory of evolution
- (h) explain the various concepts of the species (biological, ecological, morphological, genetic and phylogenetic concepts)
- (i) define biological classification as the organisation of species according to shared characteristics and describe how evolutionary relationship is established
- (j) explain how new species are formed with respect to geographical isolation (allopatric speciation) and behavioural or physiological isolation within the same geographical location (sympatric speciation)
- (k) define phylogeny as the organisation of species to show their evolutionary relationships
- (l) explain the importance of the use of genome sequences in reconstructing phylogenetic relationships and state the advantages of molecular methods, including multiple sequence alignment (nucleotide and amino acid), in classifying organisms.

References:

Campbell and Reece. *Biology*. (11th edition). Chapter 23: Microevolution, P. 540 – 559, Chapter 21: How Evolution Works, P. 504 – 521, Chapter 22: Phylogenetic Reconstruction, P. 523 – 542, Chapter 24: Species and Speciation, P. 564 – 580, Chapter 25: Macroevolution, P. 583 – 607 (or any corresponding chapters in other editions)

A Bridge to O Level Biology
(6093 syllabus)

You should have learnt to:

- (j) describe the difference between continuous and discontinuous variation and give examples of each
- (k) state that variation and competition lead to differential survival of, and reproduction by, those organisms best fitted to the environment
- (l) give examples of environmental factors that act as forces of natural selection
- (m) explain the role of natural selection as a possible mechanism for evolution
- (n) give examples of artificial selection such as in the production of economically important plants and animals

1 INTRODUCTION

- Evolution refers to a process of **descent with modification** from a **common ancestor**. It involves a **change in allele frequencies** within a population over generations.
- **Allele frequency** refers to the relative proportion of the alleles of a gene present in a population. For example, in China, 85% of the adult population are lactose intolerant, carrying the recessive allele for β -galactosidase.
- Evolution is a scientific theory that explains the great biodiversity present on Earth. **Biodiversity** refers to **number and variety of organisms** (flora and fauna) found within a specified geographical region. It can also refer to the **variability within and between species** and **within and between ecosystems**.

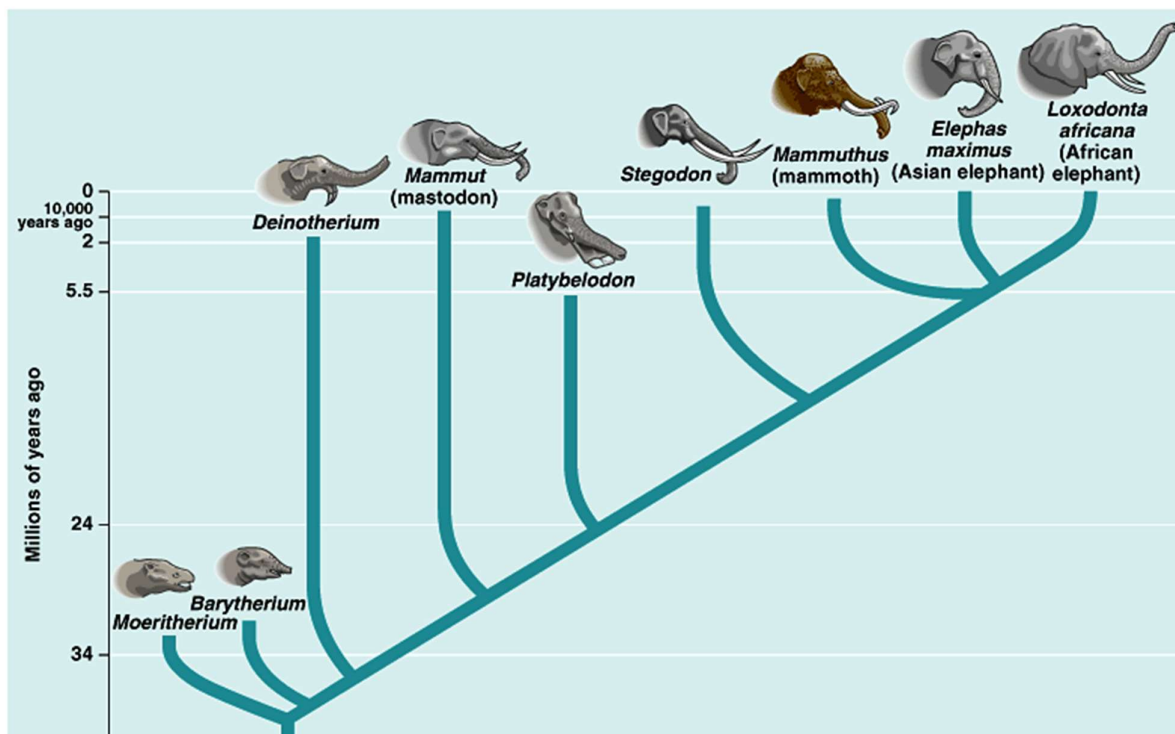


Fig. 1.1: Descent with modification.

PRACTICES OF SCIENCE
(POS 1.1 and 1.3, pg. 4 syllabus)

The Evolution of the Theory of Evolution

Jean-Baptiste Lamarck was one of the bigger proponents for evolution before Darwin's time. He suggested that species change through time and proposed a progressive change along a scale of improving characteristics (exemplified in Fig. 1.2). However, his suggested mechanism for evolution was inaccurate and was not well accepted by the scientific community of that time.

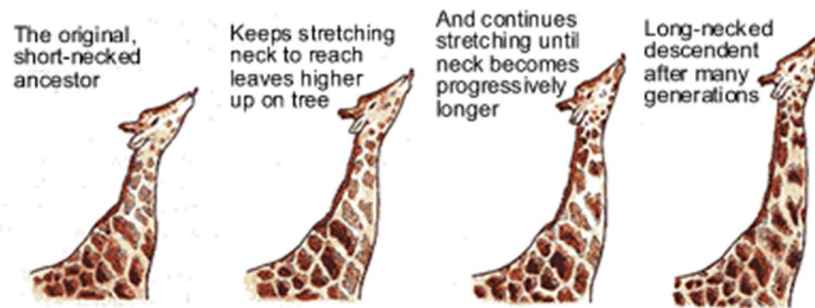


Fig. 1.2: Lamarck's proposed theory of evolution.

In the 1980s, **Charles Darwin**, a naturalist, toured a large part of the world on a famous voyage on *HMS Beagle* collecting data on geology, as well as biology. He travelled for five years and his keen observations on both geology and biology led him to formulate the theory of natural selection. He recorded his ideas in numerous journals and for almost twenty years gathered enough evidence and wrote out his theory carefully before he published the famous book of *On the Origin of Species by Means of Natural Selection*. Before Darwin published his book, **Alfred Wallace**, another naturalist (also known as the father of modern biogeography), came up with the same idea of evolution by natural selection. The two co-founders of the theory of evolution corresponded during this time, providing Darwin greater assurance of his proposed mechanism.

Darwin's theories were also influenced by economist **Thomas Malthus**, who argued that human population is kept constant despite overproduction of offspring, due to limited resources.

Darwin proposed his mechanism for evolution without any knowledge in DNA and genetics. Six years after Darwin's proposal, **Gregor Mendel** published his paper in 1865 on the discrete particles of inheritance we now define as genes. Modern evolution now incorporates the principles of Mendelian genetics and knowledge of molecular biology (e.g. DNA, mutations and allele frequency), synthesising Darwin's theory of evolution into **Neo-Darwinian theory of evolution**.

2 VARIATION

- **Variation** in a population refers to genotypic and / or phenotypic differences between individuals in a population.
- Variations in populations are due to **mutation** and **sexual reproduction**.

(a) Mutation

- Mutation results in the **production of new alleles**, increasing the **gene pool** of a population. A **gene pool** refers to the **sum of all the alleles present at all gene loci of all individuals in a population** at any one time.
- Somatic mutations are lost with the death of the individual while germline mutations in gametes can be passed on to the next generation.
- Types of mutation include: (i) **gene mutation**: a change in the sequence of nucleotide bases of DNA in a gene, and (ii) **chromosomal aberration**: a change in chromosome number or chromosome structure. (*Reference to CI 2.6 DNA Mutations and CI 2.7 Chromosomal Aberrations*)

(b) Sexual reproduction

- Sexual reproduction generates **new combinations of alleles** (but does not create new alleles).
- Variation in sexual reproduction is due to: (i) **crossing over and exchange of segments between non-sister chromatids** of homologous chromosomes, (ii) **independent assortment**, (iii) **random segregation**, and (iv) **random fertilisation of gametes**. (*Reference to CI 2.3 Cell and Nuclear Division: Meiosis*)

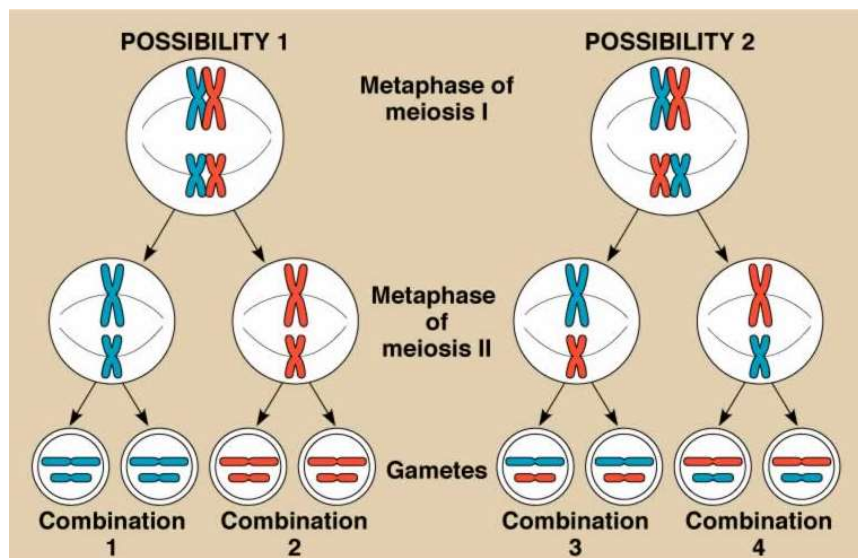


Fig. 2.1.1: Independent assortment in meiosis.

3 MICROEVOLUTION

- **Microevolution** involves a change in **allele frequencies** within the **gene pool** of a population over generations.
- Microevolution can occur through the following mechanisms: (i) **natural selection**, (ii) **sexual selection**, (iii) **artificial selection**, (iv) **genetic drift**, and (v) **gene flow**.

Learning Outcome (a):

Explain why variation is important in natural selection.

Learning Outcome (c):

Explain the role of natural selection in evolution.

3.1 NATURAL SELECTION

- **Natural selection** refers to the process by which biotic and abiotic factors in the **environment** act as **selection pressures** and **select for** individuals with **inherited traits** that are **best suited to the given environment**.
- Individuals in a population exhibit variation in their heritable traits, and those with traits that are better suited to the environment are more likely to experience higher **survival rate** and **reproductive success** (i.e. fitness). Therefore, they are more likely to survive till reproductive age and pass down favourable **alleles** to their offspring.

3.1.1 Features of Natural Selection

(a) Overproduction of offspring

- All organisms can produce large number of offspring. If all offspring reproduce successfully, there would be an exponential increase in population size.

(b) Constancy of numbers

- Despite an overproduction of offspring, most populations remain relatively constant in size as many of the offspring do not reproduce successfully (e.g. die before reaching reproductive age).

(c) Struggle for existence

- Overproduction of offspring leads to constant competition between individual organisms for limited resources, such as food, shelter, and mates. As such, only some individuals (with advantageous traits) reproduce successfully.

(d) Variation among individuals within a population

- Individuals in a population differ in characteristics from each other. These variations, which **arise spontaneously**, are a pre-requisite for evolution by natural selection. Many of these traits are heritable (i.e. can be passed down from parent to offspring).

(e) Survival of the 'fittest' by natural selection

- Among the variety of individuals, some are better adapted to their respective environment and hence can survive to reproductive age and produce viable, fertile offspring. These individuals are **selected for** by their environment while those that are less well adapted will be eliminated.

(f) Like produces like

- Individuals who survive and reproduce successfully are likely to produce offspring like them. Thus, advantageous traits determined by **favourable alleles** are passed on to the offspring.

(g) Formation of a new species

- Individuals with **advantageous traits** are more likely to survive and reproduce. Thus, the **proportion of individuals** having the advantageous traits will increase (while those without them will decrease) with each successive generation. Over a long period of time, with **genetic isolation** (i.e. no gene flow), a new species can form.

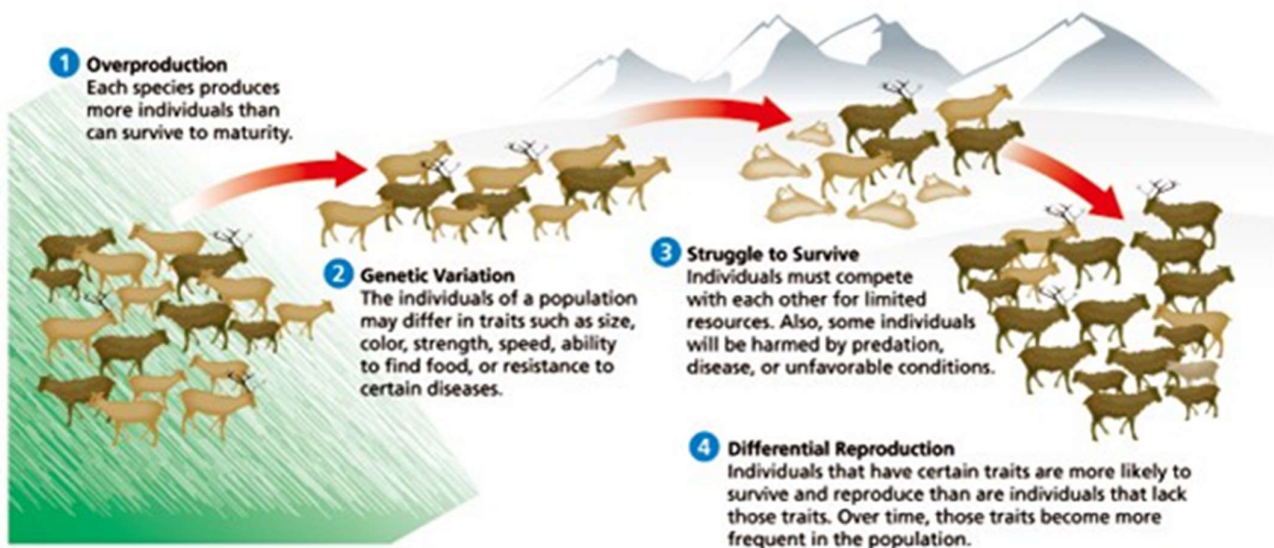


Fig. 3.1.1.1: Features of natural selection.

3.1.2 Process of Natural Selection

Example: Galapagos finches

- The Galapagos Islands are islands formed from volcanic activity from underground hotspots. These islands are 'sterile' (devoid of life forms) when first formed. Thus, Darwin hypothesized that any lifeform e.g. finches he observed on the island must have migrated from the nearest mainland e.g. South America.

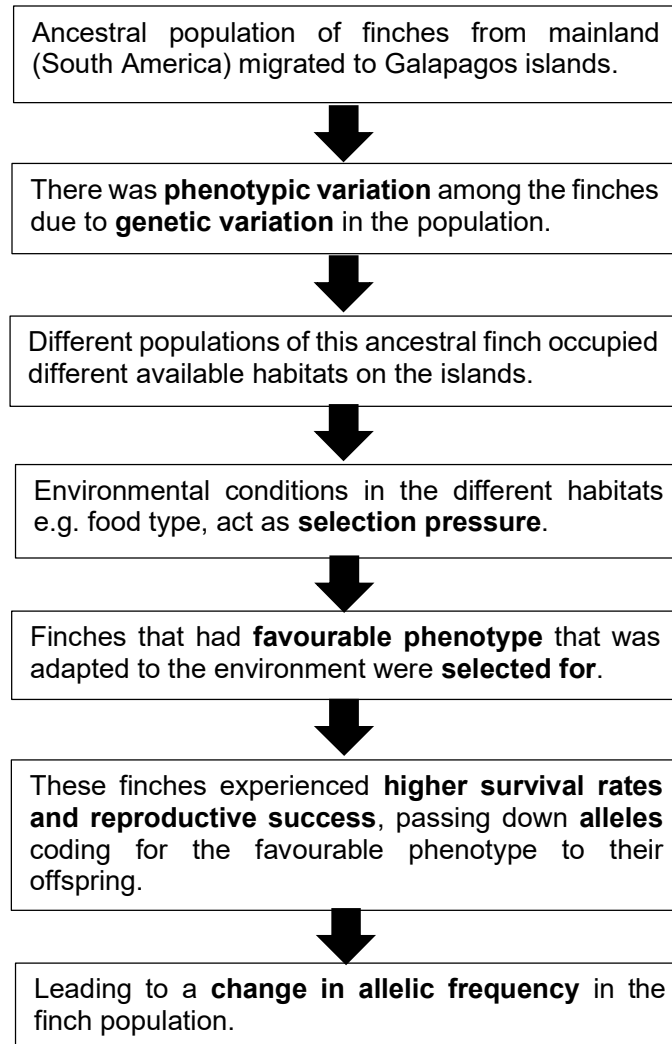


Fig. 3.1.2.1: Process of Natural Selection.

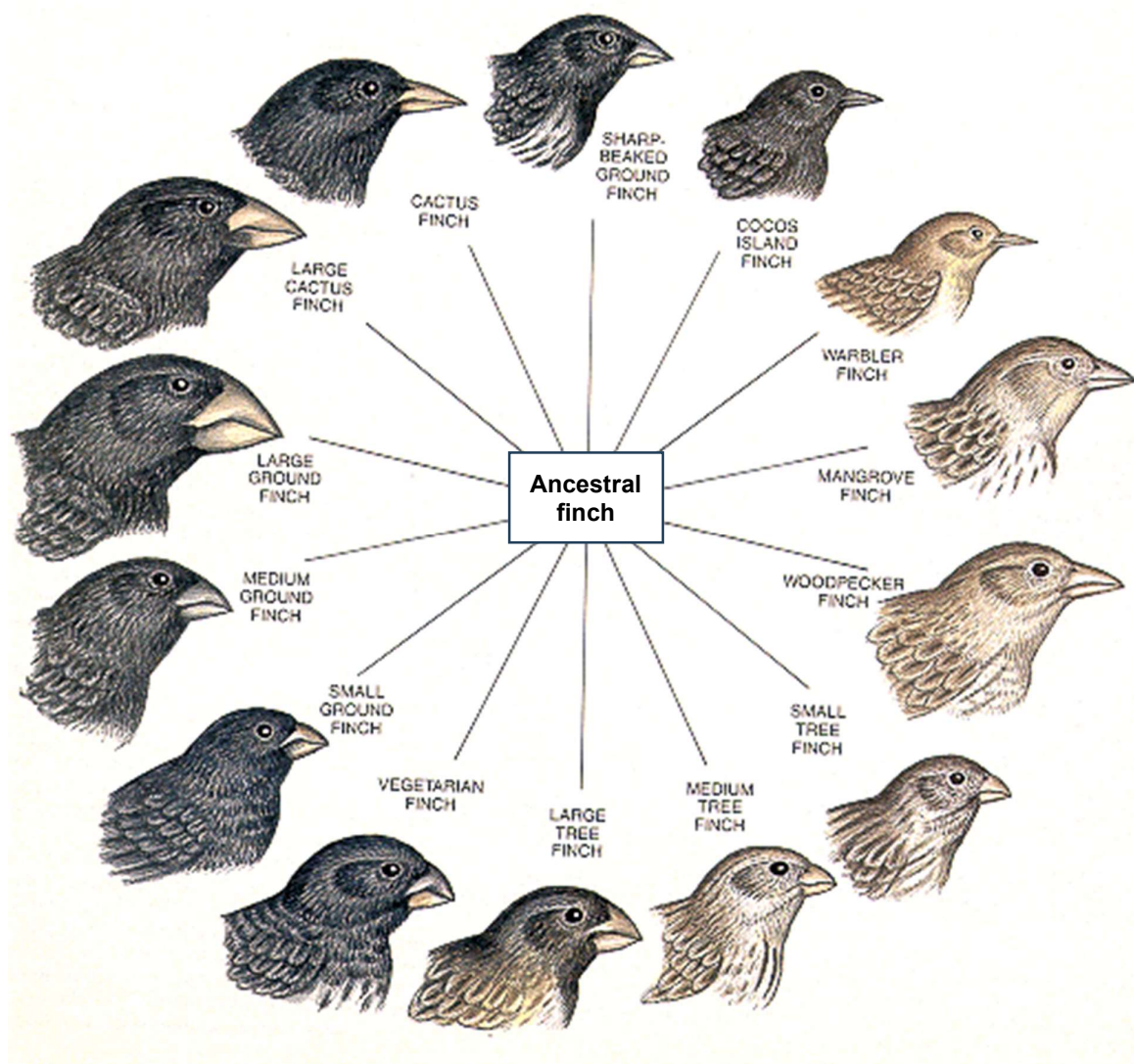


Fig. 3.1.2.2: Galapagos finches.

3.1.3 Modes of Natural Selection

- Natural selection can alter the frequency distribution of heritable traits, depending on which phenotypes in a population are favoured. Selection pressure acts to select for and against phenotypes in the population, leading to a change in frequency of phenotypes (and thus alleles) in the offspring.
- Selection can either change the frequency of certain phenotypes and the alleles responsible for them within a population (i.e. **directional** and **disruptive** selection) or be an agent for stability (i.e. **stabilising** selection).

(a) Stabilising selection

- Stabilising selection occurs when selection favours the **intermediate phenotypes** over the extreme phenotypes. This results in **reduced** variation for the selected characteristic.
- Example: The birth weight of human babies ranges from ~ 3 to 4 kg. Babies who are either much smaller or larger have higher rates of mortality.

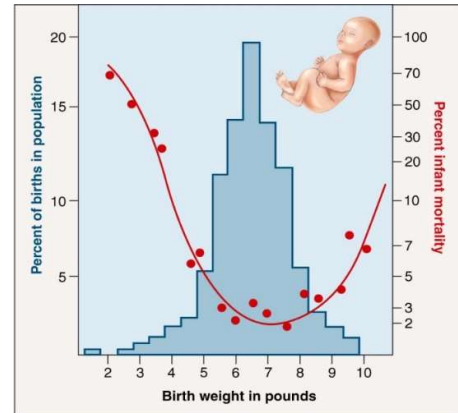


Fig. 3.1.3.1: Stabilising selection of human baby weight.

(b) Directional selection

- Directional selection occurs when selection favours individuals exhibiting **one extreme** of a phenotypic range. This leads to a shift of frequency curve for phenotypic character in **one direction**.
- Example: Industrial melanism of peppered moths, where the favoured colour of the moth shifted to a darker shade due to the effects of human industrialisation. (*Case study is presented on page 14.*)

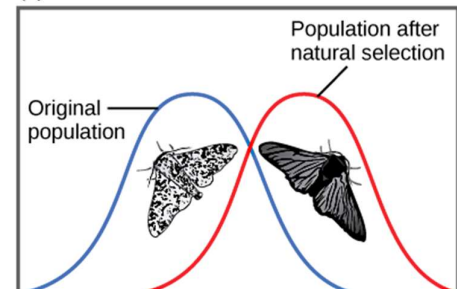


Fig. 3.1.3.2: Directional selection of peppered moth colour.

(c) Disruptive selection

- Disruptive selection occurs when selection favours **both extreme** phenotypes over the intermediate phenotypes. This leads to a shift in the frequency curve for phenotypic character in **two opposing directions**, resulting in the formation of two sub-populations.
- Example: The black-bellied seed cracker finches in Cameroon display two distinctly different beak sizes, as small-billed birds feed mainly on soft seeds and large-billed birds feed mainly on hard seeds. Birds with intermediate-sized beaks are inefficient at cracking both types of seeds.

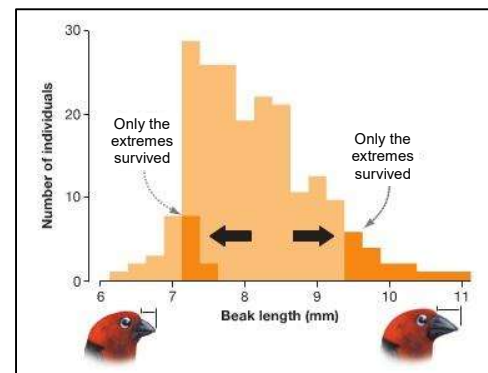


Fig. 3.1.3.3: Disruptive selection of finch beak size.

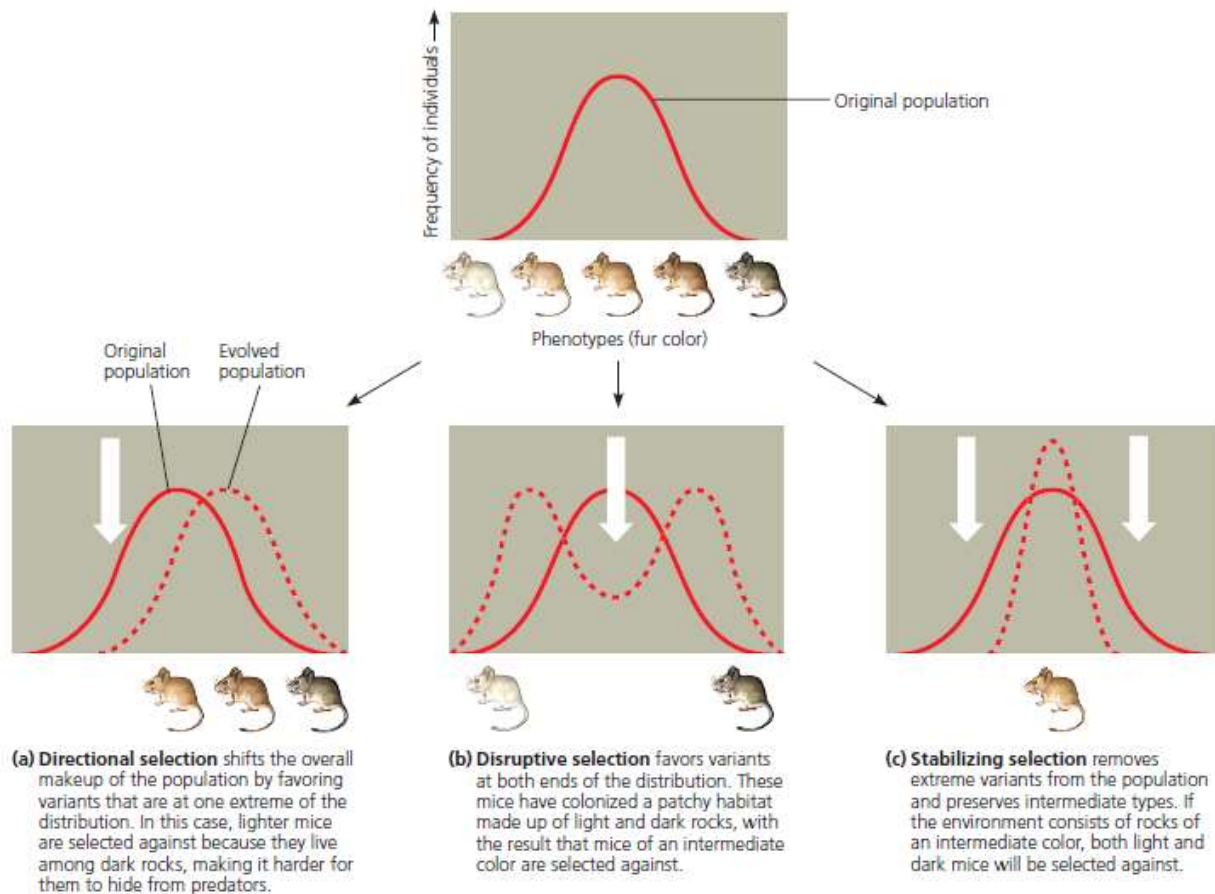
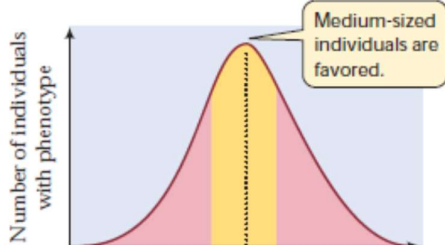
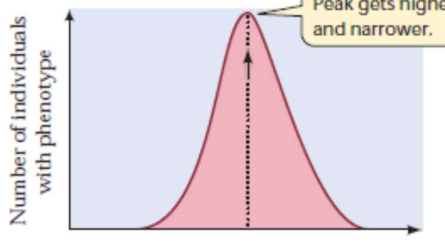
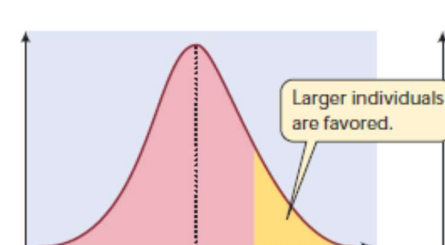
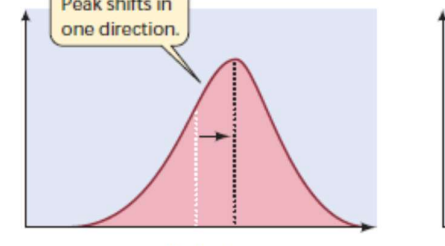
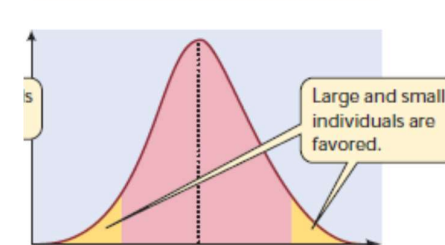
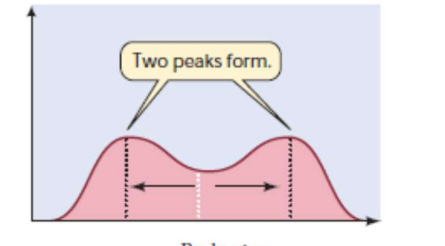


Fig. 3.1.3.4: Modes of natural selection.

Summary of the types of selection

Feature Graph	Stabilising selection	Directional selection	Disruptive selection
	(a) Stabilizing selection reduces variation but does not change the mean.  Medium-sized individuals are favored. Selection  Peak gets higher and narrower. Body size	(b) Directional selection changes the mean value of the character (in this case, toward larger size).  Larger individuals are favored. Selection  Peak shifts in one direction. Body size	(c) Disruptive selection favors both extremes and produces two peaks in the distribution of a character.  Large and small individuals are favored. Selection  Two peaks form. Body size
Effect on population	Favours the intermediate in a range of phenotypes; Operates against extreme phenotypes in the range; Increase in the allele frequency at the mean and a decrease in those at the extremities of the phenotype; Successful individuals are the average phenotypes; Similar distribution curve is retained in subsequent generations as the same characteristics are passed on;	Favours one extreme in a range of phenotypes: Shifts the phenotype of the population towards one extreme; Selection continues until a new mean represents the optimal phenotype for a new set of environmental conditions; Stabilising selection then takes over to maintain the new mean;	Favours phenotypes at both extremes: Operates against intermediate phenotypes in the range; Leads to more than 1 modal class, results in binomial distribution, splitting into 2 sub-populations; If gene flow between the 2 sub-populations is disrupted, each may give rise to a new species (speciation);
Environmental conditions	Constant	Gradual change	Fluctuating
Effect on evolution	Does not promote evolutionary change	Brings about evolutionary change	Rare but can cause evolutionary change
Example	Birth weight in humans	Antibiotic resistance	Different beak sizes in finches

3.1.4 PRESERVATION OF GENETIC VARIATION

Learning Outcome (e):

Explain how genetic variation (including harmful recessive alleles) may be preserved in a natural population.

- Natural selection results in individuals with favourable trait being selected for and those without being selected against. Alleles possessed by individuals who are selected against are removed from the gene pool when the individual dies before reproducing. This results in loss of genetic variation in the population.
- However, alleles which do not code for the favourable trait under present environmental conditions may give individuals a selective advantage when selection pressure changes with the environment.
- Genetic variation may be preserved by **heterozygote protection** and **heterozygote advantage**.

(a) Heterozygote Protection

- **Heterozygote protection** refers to the **phenomenon** where individuals carrying one copy of a recessive allele (heterozygotes) do not express the associated trait or disorder due to the presence of a dominant allele.
- In diploid organisms, recessive alleles that are less favourable than their dominant counterparts can persist as they are passed down to the next generation by **heterozygous** individuals.
- Deleterious effects of such recessive alleles are masked by dominant alleles. Hence, recessive alleles are only exposed to the effects of natural selection in **homozygous recessive** individuals.
- **Heterozygote protection** maintains a large pool of alleles that might not be favoured under present conditions, but some of which could bring new benefits when the environment changes.

(b) Heterozygote Advantage

- **Heterozygote advantage** is another **phenomenon** whereby individuals who are heterozygous for a specific gene (carrying one dominant and one recessive allele) have a **higher relative fitness** compared to either homozygous dominant or homozygous recessive individuals.
- As such, heterozygotes have **greater selective advantage** over homozygous dominant and homozygous recessive individuals.

Example: Gene locus for β -globin subunit in haemoglobin

- **Homozygotes** with the Hb^A allele ($Hb^A Hb^A$) produce normal haemoglobin and thus normal red blood cells.
- **Homozygotes** with the Hb^S allele ($Hb^S Hb^S$) produce abnormal haemoglobin that distort the shape of red blood cells, resulting in sickle-shaped red blood cells, leading to **sickle cell anaemia**. Homozygotes suffer high mortalities even before the age of 5 and are naturally selected against.
- **Heterozygotes** ($Hb^A Hb^S$) produce a mixture of normal and abnormal haemoglobin, but may suffer symptoms of sickle cell anaemia in low oxygen concentrations (e.g. at a high altitude above sea level) They produce both sickle-shaped and normal red blood cells, leading to the **sickle cell trait**.
- In malaria-prone regions e.g. Africa, **heterozygotes** are protected from the effects of malaria due to the shorter life span of the sickle-shaped red blood cells. Thus, they have a **selective advantage** compared to the homozygotes.
- Homozygotes with normal red blood cells ($Hb^A Hb^A$) are selected against due to the high infection rate with malaria. Homozygotes with sickle-shaped red blood cells ($Hb^S Hb^S$) are selected against due to high mortality from anaemia.

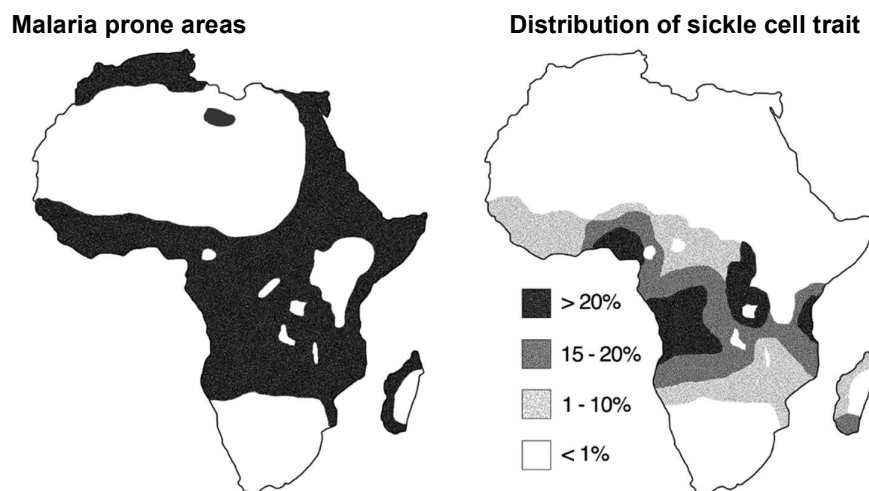


Fig. 3.1.4.1: Map showing malaria prone areas and distribution of sickle cell trait.

3.1.5 ENVIRONMENTAL FACTORS AS FORCES OF NATURAL SELECTION

Learning Outcome (b):

Explain, with examples, how environmental factors act as forces of natural selection.

- Different biotic and abiotic factors in the **environment** act as **selection pressures**, **selecting for** individuals within the population with favourable traits, and **selecting against** individuals without these traits.

Example 1: Industrial Melanism of Peppered Moths (*Biston betularia*)

- During pre-industrial revolution in the 1700s:
 - Most of the trees in the British countryside were covered in **light grey lichen**. Hence, the **light-coloured moths** were well camouflaged in this environment, and were at a **selective advantage**.
 - In 1848, **spontaneous mutation** led to the presence of **black peppered moths**. However, their numbers were low compared to the light-coloured forms (allele frequency of about 0.01%), as they were easily seen by predators and were eliminated from the population. Hence, the **dark-coloured moths** were at a **selective disadvantage**.
- During the industrial revolution in the 1900s:
 - As a result of pollution, lichens on the bark of trees were killed and barks were covered with **soot**. **Light-coloured moths** were not camouflaged and were **selected against** (i.e. at a **selective disadvantage**), while **dark-coloured moths** were well-camouflaged against the soot-covered tree trunks and were **selected for** (i.e. at a **selective advantage**). As such, the **frequency of the allele coding for the melanic form in the population increased**.
- At present:
 - Improvement in air standards result in trees returning to normal (covered with lichen). Hence, the frequency of allele for the melanic form in the population has decreased.



Fig. 3.1.5.1: Industrial melanism in peppered moths.

Example 2: Antibiotic Resistance in Bacteria

- Variation in resistance to antibiotics (i.e. antibiotic-resistant strains and non-resistant strains) exists naturally in bacterial strains. **Spontaneous mutations** can give rise to **antibiotic resistant strains**, through (i) producing enzymes that digest antibiotics, (ii) using alternative metabolic pathways or (iii) preventing antibiotics from binding to bacterial cell surface.
- When antibiotics were used, non-resistant strains were killed. **Antibiotic resistant strains** had a **selective advantage**; hence they were able to survive and reproduce by binary fission, passing on the allele for antibiotic resistance to their offspring. As such, **the frequency of the allele for antibiotic resistance in the population increases**.

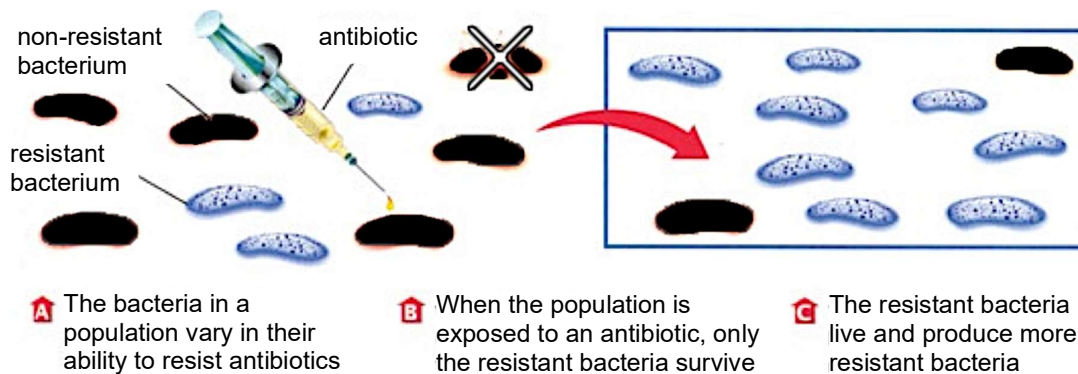


Fig. 3.1.5.2: Antibiotic resistance in bacteria.

DID YOU KNOW?

Methicillin-resistant *Staphylococcus aureus* (MRSA)

Staphylococcus aureus is a bacterium found on the skin or in nasal passages of humans with no negative effect. However, certain strains of this species, known as **methicillin-resistant *S. aureus* (MRSA)**, are of clinical significance, causing fatal infections.

In 1943, penicillin became the first widely used antibiotic. However, by 1945, more than 20% of *S. aureus* strains in hospitals were resistant to penicillin, producing an enzyme, penicillinase, which could destroy penicillin. Researchers began developing antibiotics that were not destroyed by penicillinase, but some *S. aureus* populations developed resistance to each new drug within a few years.

In 1959, doctors began using the antibiotic methicillin, which deactivates a protein that bacteria use to synthesise cell walls. However, some bacterial populations were able to synthesise cell walls using a different protein that was not affected by methicillin, surviving the methicillin treatments. Over time, these resistant individuals became increasingly common, leading to the spread of MRSA. The present-day MRSA strains are resistant to multiple antibiotics, posing much difficulty in the treatment of MRSA infections.

CHECKPOINT 1

With reference to the two examples (industrial melanism and antibiotic resistance), identify the features of natural selection.

Features	Industrial Melanism		Antibiotic Resistance
	Pre-Industrialisation	Post-Industrialisation	
environment			
selection pressure			
advantageous trait			
how the trait is advantageous			

3.2 GENETIC DRIFT

- **Genetic drift** refers to the **random change in allele frequencies** from one generation to the next, **due to chance** alone.
- Genetic drift is usually observed in small populations (or small gene pools) as the effect is greater in proportion as compared to large populations.
- Genetic drift often leads to a **decrease in genetic variation**. Certain alleles may be represented in only a few individuals. If these individuals fail to reproduce, these alleles may be lost from the population.
- Genetic drift can occur by **founder effect** and **bottleneck effect**.

Founder Effect

- **Founder effect** refers to the change in allelic frequency in a population due to a small group of individuals (with a non-representative gene pool) being **isolated** from the larger population and establishing a new population in a new location.
- These founders represent a portion of the original gene pool, resulting in **reduced genetic variation**.

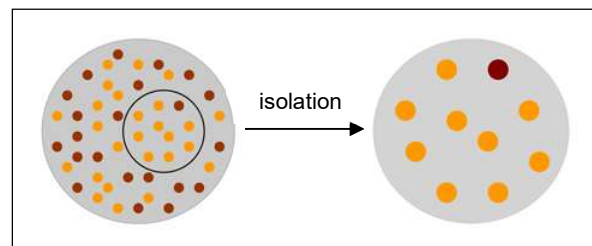


Fig. 3.2.1: Illustration showing founder effect.

Bottleneck Effect

- **Bottleneck effect** refers to the change in allelic frequency in a population due to a **sudden change in environment** (e.g. catastrophic events, natural disasters, disease, etc), resulting in a drastic **reduction** in population size.
- The resulting survivors represent a portion of the original gene pool, resulting in **reduced** genetic variation. Even when the population increases to its original size, a portion of its original genetic diversity remains lost.

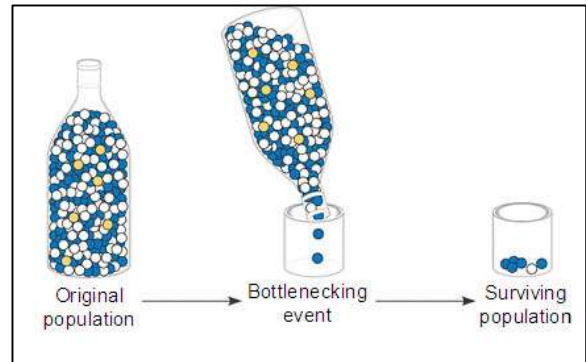


Fig. 3.2.2: Illustration showing bottleneck effect.

3.3 GENE FLOW

- **Gene flow** refers to the transfer of alleles from one population to another. This may be achieved by migration of fertile individuals and subsequent interbreeding (transfer of gametes between populations).
- Gene flow may result in **increase or decrease** in genetic variation **within populations**, but results in an overall **decrease** in variation **between populations**.

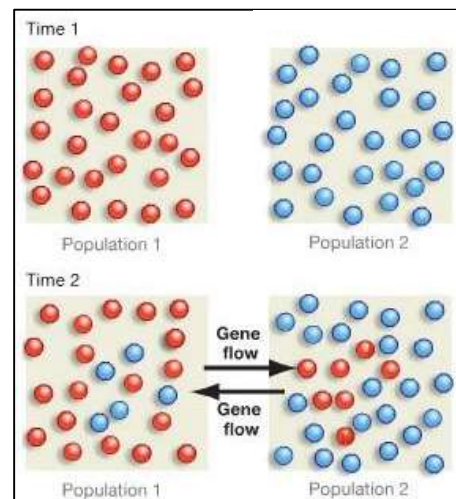
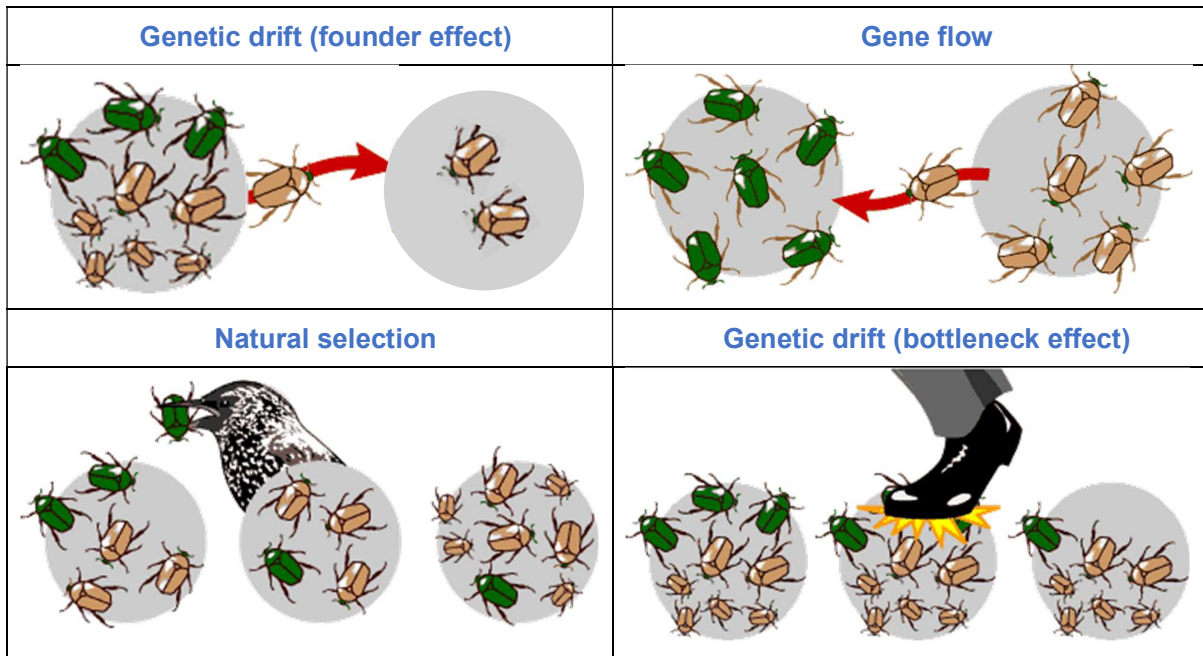


Fig. 3.3.1: Illustration showing gene flow.

CHECKPOINT 2

Identify the mechanisms of microevolution for each of the diagrams.



DID YOU KNOW

Relevance of Microevolution to Human Populations

Bottleneck Effect

Human actions can create severe bottlenecks for other species. For example, in the 1890s, hunters reduced the population of northern elephant seals in California to about 20 individuals. Since then, this mammal has been protected, and the population has increased to over 30 000 in number. However, researchers found no variation upon examining 24 gene loci in a sample of seals. In contrast, populations of a closely related species, the southern elephant seal, exhibited considerable genetic variation at these loci.

Founder Effect

The Afrikaner population of Dutch settlers in South Africa has a high frequency of the allele that causes Huntington's disease. This is because the original small population of Dutch colonists carried the allele with disproportionately high frequency.

Gene Flow

Humans today move much more freely about the world than in the past. As a result, gene flow has become an important agent of evolutionary change in human populations that were previously quite isolated. Gene flow represents an important factor preventing speciation in modern man.

3.4 POPULATION AS THE SMALLEST UNIT THAT CAN EVOLVE

- A **population** is defined as a localised group of individuals that are **capable of interbreeding and producing viable, fertile offspring**.
- Although mechanisms of microevolution, such as natural selection, occur through interactions between individual organisms and their environment, **individuals do not evolve**.
 - An individual organism has the same genetic makeup all its life (except for mutations acquired during its lifetime) and represents only one generation.
 - For example, the presence of hard seeds does not cause the beak depth of the individual black-bellied seed cracker finch to deepen. The finches, whether selected for or against by the selection pressure, remain the same in their lifetime.
- The selection process results in a change in the allele frequency of the characteristic in the population, not the individuals. Thus, **the population is the smallest unit that can evolve**.

4 BIOLOGICAL CLASSIFICATION

- To make sense of the **diversity of organisms**, it is necessary to **group similar organisms** together and organize these groups in a non-overlapping **hierarchical arrangement**.
- At the lowest level of the hierarchy, the organisms in each group form a species. There are **various concepts of the species** that have been adopted to classify organisms with highly similar characteristics as a single species.

Learning Outcome (i):

Define biological classification as the organisation of species according to shared characteristics and describe how evolutionary relationship is established

4.1 Biological Classification

- Classification is the **organisation of species according to characteristics**. Classification **may not** take into consideration **evolutionary relationship** between the species.
- A common type of classification is **phenotypic classification**. It is concerned with grouping individual species into **phenotypic classes** based on the **morphology** of organisms.
- Carolus Linnaeus (1748) developed a system of classifying every known organism in his time. The system is based on creating and differentiating organisms in terms of **structural similarities and differences**. With improvements in science and technology, many other similarities, and differences, such as embryological and molecular relationships, are also taken into consideration.
- There are several variations to the classification of life. Among them are:
 - The two-empire system, with top-level groupings of Prokaryota (or Monera) and Eukaryota empires.
 - The five-kingdom system with top-level groupings of Protista, Monera, Fungi, Plantae, and Animalia.

- The most recent three-domain system, introduced by Carl Woese in 1990, with top-level groupings of Archaea, Eubacteria, and Eukarya domains.

Linnaeus 1735	Haeckel 1866 ^[1]	Chatton 1937 ^[3]	Copeland 1956 ^[5]	Whittaker 1969 ^[7]	Woese et al. 1977 ^[8]	Woese et al. 1990 ^[9]
2 kingdoms	3 kingdoms	2 empires	4 kingdoms	5 kingdoms	6 kingdoms	3 domains
(not treated)	Protista	Prokaryota	Monera	Monera	Eubacteria	Bacteria
					Archaeobacteria	Archaea
			Protoctista	Protista	Protista	
Vegetabilia	Plantae	Eukaryota	Plantae	Fungi	Fungi	
			Plantae	Plantae	Plantae	
Animalia	Animalia		Animalia	Animalia	Animalia	
						Eukarya

Fig. 4.1: Table of the different classification systems

4.2 Taxonomy

- Taxonomy is the **science of naming and classifying organisms** into groups, based on **shared features** (especially morphological features).
- Organisms are **grouped into taxa** (singular: taxon), where members of a particular taxon share a **common set of key diagnostic features** that distinguishes it from the other taxa.
- Taxonomy follows a system of **hierarchical classification**, where **each lower taxonomic rank** is contained within a more inclusive higher taxonomic rank. Hierarchical classification refers to the grouping of organisms into **levels of increasingly inclusive categories**. A category in any rank unites groups in the level below it, based on **shared characteristics**.
- Examples of hierarchical classification:

Taxon Group	<i>Humans</i>	<i>Cabbage</i>
Domain	Eukarya	Eukarya
Kingdom	Animalia	Plantae
Phylum	Chordata	Tracheophyta
Class	Mammalia	Angiospermae
Order	Primates	Dicotylodoneae
Family	Hominidae	Brassicaceae
Genus	<i>Homo</i>	<i>Brassica</i>
Species	<i>sapiens</i>	<i>oleracea</i>

- Organisms are classified into the following **taxonomic groups** based on **shared features**: **Kingdom, Phylum, Class, Order, Family, Genus, and Species**.
 - Species** that appear similar (i.e. most shared features) are grouped into the same **genus**. Similar genera are grouped into the same **family**, similar families are grouped into the same **order**, similar orders are grouped into the same **class**, similar classes are grouped into the same **phylum**, similar phyla are grouped into the same **kingdom**.
- Down the taxonomic ranks, there is **decreased number** of organisms, and **increased shared features** amongst organisms.

Domain
Kingdom
Phylum
Class
Order
Family
Genus
Species

Fun mnemonics to help you remember the hierarchy!
Dear King Philip Can Overthrow Five Giant Stones

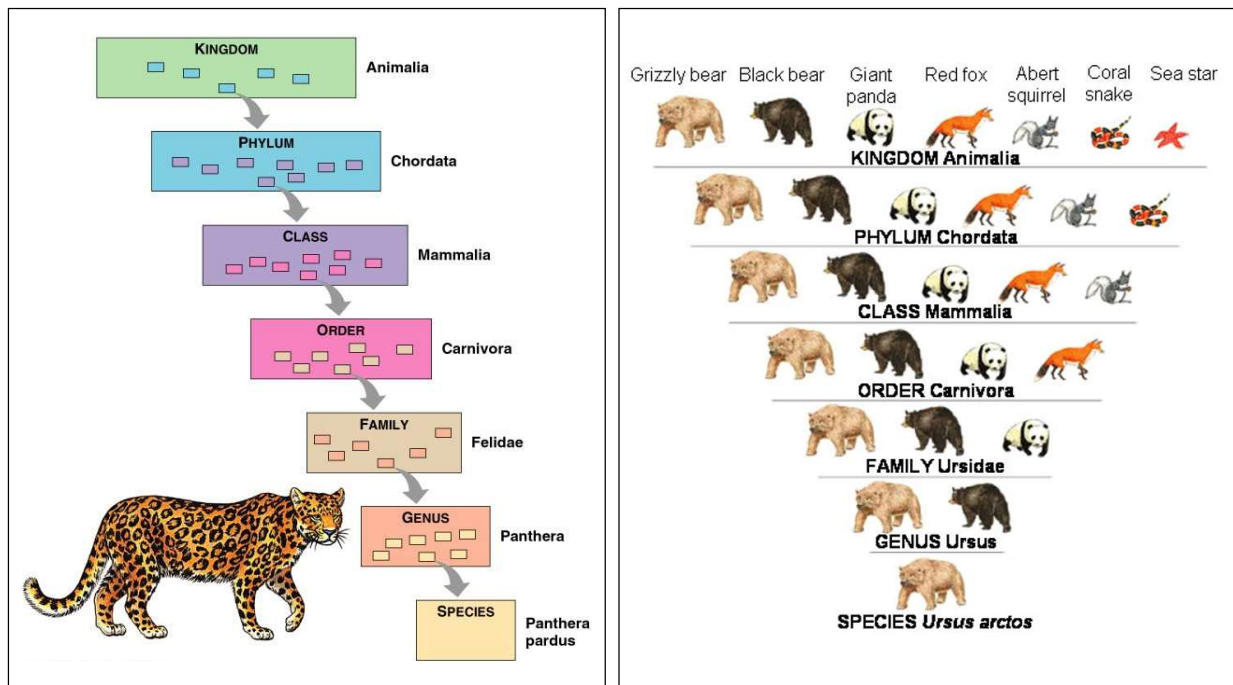


Fig. 4.2: Examples showing hierarchical classification of *Panthera pardus* (left) and *Ursus arctos* (right).

4.3 Binomial nomenclature

- The binomial system of nomenclature was first developed by Carolus Linnaeus, a Swedish botanist, in the mid-18th century.
- Binomial nomenclature refers to a **system of giving a scientific name** to each organism.
- Organisms are identified by their Latin scientific names consisting of a **genus name** and a **species name** (specific epithet).
- Binomial nomenclature follows certain rules:
 - (i) The **genus name** begins with **upper case**, and the **specific epithet** in **lower case**.
 - (ii) The genus can be **abbreviated** to one letter.
 - (iii) The scientific name is in *italics* in print and underlined when handwritten.
 - (iv) No two species can have the same name.
- For example, *Homo sapiens* (*H. sapiens*)
- **Advantages** of using binomial nomenclature in naming organisms include:
 - (i) Each species can be **easily identified** with only **two words**.
 - (ii) A **universal name** can be used to describe each organism.
 - (iii) It **avoids confusion** result from the use of common names which may differ or which may be used to describe more than one species.

4.4 Phylogeny

- Unlike classification which may not take into consideration evolutionary relationship between the species, phylogeny is the **organisation of species** according to **characteristics** which takes into consideration the **evolutionary relationship** between the organisms.

Learning Outcome (k):

Define phylogeny as the organisation of species to show their evolutionary relationships.

- Phylogeny is the study of **evolutionary history** of a group of organisms based on **common ancestor-descendant relationships**.
- Phylogeny involves grouping of individual species into evolutionary categories that reflect **divergence from an ancestral form**, through the use of **homology** (such as anatomical or molecular homology).
- **Homology** refers to similar characteristics in different species due to common ancestry.

- **Phylogenetic relationships** between organisms are usually represented in the form of a **phylogenetic tree** (cladogram).
- The relationships are represented by two-way branch points. **Each branch point (node)** represents a **common ancestor**, and the branches represent the divergence of two or more species (evolutionary lineages) from the common ancestor.
- The length of the **horizontal line** is indicative of the **time**.

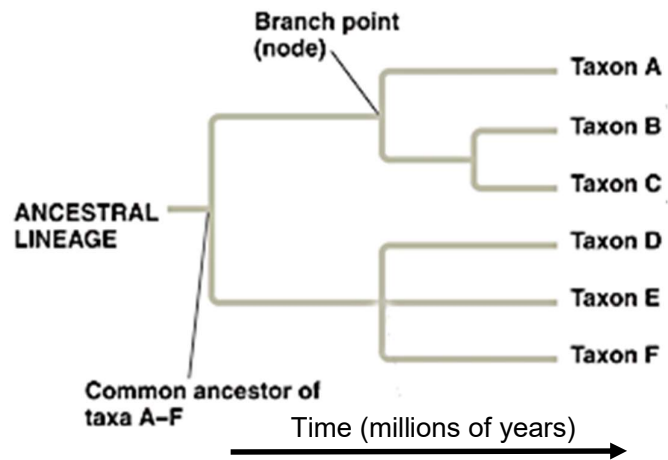


Fig. 4.4.1: Phylogenetic tree.

- Phylogenetic trees can be constructed by determining the **degree of evolutionary relatedness** using **evidence** from anatomical and molecular **homologies**.

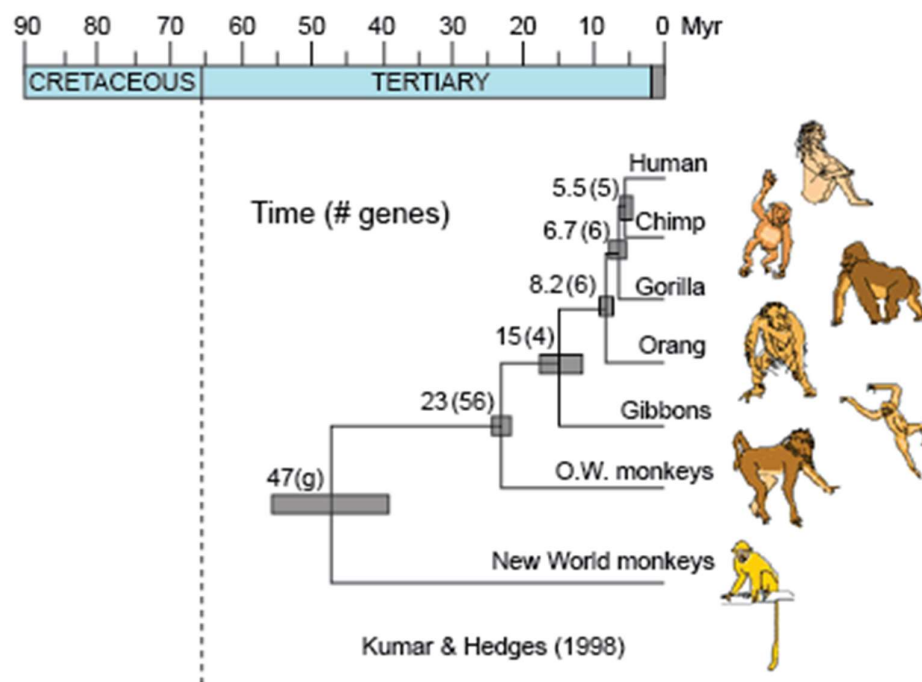


Fig. 4.4.2: Phylogenetic tree of primates

- The taxon groups (group of organisms determined to be a unit) in a phylogenetic tree can be **monophyletic**, **polyphyletic** or **paraphyletic**.
 - Monophyletic groups** include all the descendants of a common ancestor.
 - Polyphyletic groups** consist of several evolutionary lines that do not share the same most recent common ancestor (i.e. contains taxa with more than one recent ancestor).
 - Paraphyletic groups** include some but not all of the descendants of a common ancestor.
- Within a tree, a **clade** is defined as a group of species that **includes an ancestral species and all its descendants**. Hence, a valid clade is **monophyletic**, while polyphyletic and paraphyletic groups lack information about some members of a clade.

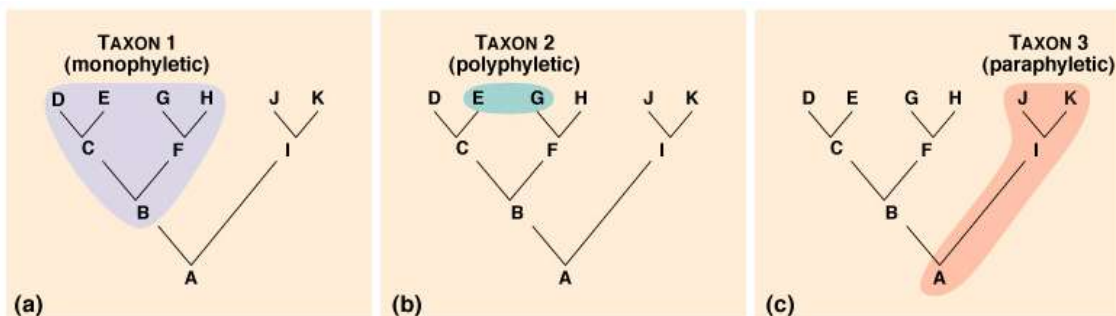


Fig. 4.4.3: (a) Monophyletic, (b) polyphyletic, and (c) paraphyletic groups.

- Combining hierarchical classification and phylogeny **allows the tracing** of possible evolutionary relationships between and within taxa. The **branching** of phylogenetic trees reflects the **hierarchical classification** of groups nested within the **more inclusive groups**.

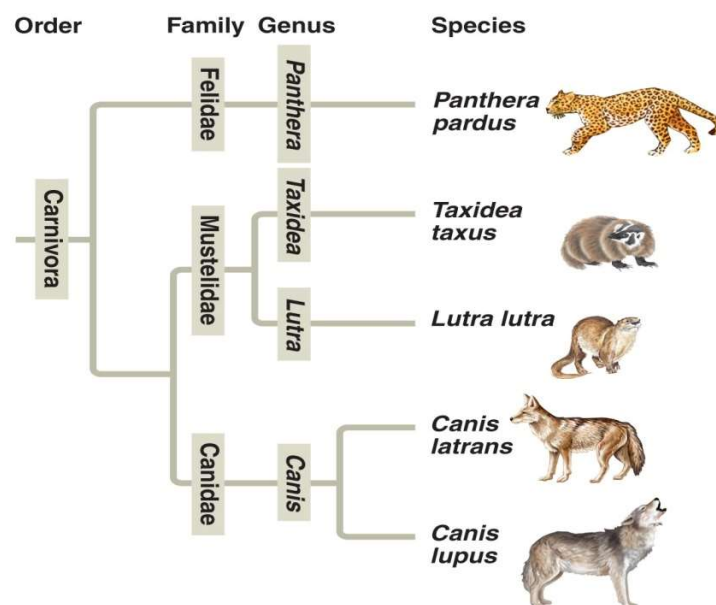


Fig. 4.4.4: Connection between classification and phylogeny.

CHECKPOINT 3

Fill in the table below to identify the differences between taxonomy and phylogeny.

Features	Taxonomy	Phylogeny
Basis of classification		
Method used		
Ranking of groups		
Reflection of evolutionary history		
Purpose		

5 MACROEVOLUTION

Learning Outcome (f):

Define biological evolution as descent with modification and explain the link between micro-evolution and macro-evolution

5.1 Biological Evolution

- Biological Evolution involves:

- **Micro-evolution**

Refers to **changes in allelic frequencies** within the gene pool of a population from one generation to the next (short term). Micro-evolution can occur through mechanisms like natural selection, genetic drift, and gene flow.

- **Macro-evolution**

Refers to the **descent of different species** from a **common ancestor** over many generations (long term) leading to the **diversification, rise and extinction** of different groups of organisms through **geologic times**.

It involves the evolution of taxa higher than the species level (for example, genera, families, orders, classes), commonly entailing **major morphological changes**.

- **Disruption of gene flow** and **accumulation of allelic changes** in populations' gene pools (micro-evolution) can eventually, **over long periods of time**, lead to macro-evolution, where populations of organisms **evolve to become different species** i.e. speciation.

Learning Outcome (h):

Explain the various concepts of the species (biological, ecological, morphological, genetic and phylogenetic concepts).

5.2 Species Concept

- Species represent the **lowest and smallest taxonomic** group in the classification of organism that **share certain similarities**.
- Various concepts have been used to define and identify what constitutes a species, such as the **biological, morphological, ecological, genetic, and phylogenetic species concepts**.

Table 5.1: Table of species concepts

Species Concept and Definition of Species	Advantages	Limitations
Biological species concept (BSC) A group of organisms that have the potential to interbreed in nature to produce fertile, viable offspring	1) BSC is most widely used by scientists 2) Categorisation is objective	1) Cannot be used for classification of extinct organisms and asexually reproducing organisms 2) Does not consider potential for geographically isolated populations to interbreed
Morphological species concept (MSC) A group of organisms which show similarities in measurable anatomical features and physical appearance	1) Can be applied to extinct organisms through observation of fossils 2) Can be applied to both sexual and asexual organisms	1) Categorisation can be subjective 2) Does not consider organisms displaying sexual dimorphism and life stage polymorphism
Ecological species concept (ESC) A group of organisms adapted to the same ecological niche (<i>A niche is the function or position of a species within an ecological community, i.e. how members of the species interact with the non-living and living parts of their environment.</i>)	1) Can be applied to sexual and asexual organisms 2) Reflects adaptation of organisms to different environmental conditions	1) Cannot be used for classification of extinct organisms as niche cannot be observed 2) Difficulty in determining extent of overlap between ecological niches of two or more organisms

Species Concept and Definition of Species	Advantages	Limitations
Genetic species concept (GSC) A group of genetically compatible interbreeding natural populations that is genetically isolated from other such groups	1) Advances in DNA molecular techniques allowed robust analysis of DNA sequences between organisms 2) Categorisation is quantifiable by calculating degree of genetic divergence from different aspects of the genome (mitochondrial and nuclear genes)	1) Difficulty in determining degree of difference between gene pools to be considered 'isolated'.
Phylogenetic species concept (PSC) The smallest group of organisms that share a common ancestor, forming a branch on the phylogenetic tree.	1) Considers various forms of homologies (anatomical, embryological and molecular) 2) Reflects evolutionary history 3) Can be applied to sexual and asexual organisms	1) Difficulty in determining degree of difference required to consider two or more organisms a separate species

CHECKPOINT 4

The statements each describe different concepts of the species.

1. The smallest distinct group of organisms that share a recent common ancestor that is not shared with any other groups.
2. A group of organisms able to interbreed with each other regardless of appearance, which is unable to breed with any other group.
3. A group of organisms that are consistently distinct, defined by anatomical or physical similarities, regardless of other considerations.
4. A group of organisms that occupy a single niche that is slightly different from that of any other group of organisms in the same area.

Which row matches the different concepts of a species to the correct statements?

	ecological	morphological	phylogenetic
A	1	4	2
B	2	1	3
C	3	2	4
D	4	3	1

()

5.3 Speciation

Learning Outcome (j):

Explain how new species are formed with respect to geographical isolation (allopatric speciation) and behavioural or physiological isolation within the same geographical location (sympatric speciation).

- Speciation refers to the **divergence of one species from another** at some point along the evolutionary timeline.
- Mechanisms of micro-evolution result in **changes** in the **inherited characteristics** and **allelic frequencies** in the **gene pool** of a population over time.
- These changes may lead to **reproductive barriers**, preventing interbreeding of individuals from different populations and the production of fertile offspring.
- According to the Biological Species Concept (BSC), a new species is said to be formed when a population can **no longer interbreed** with another population.

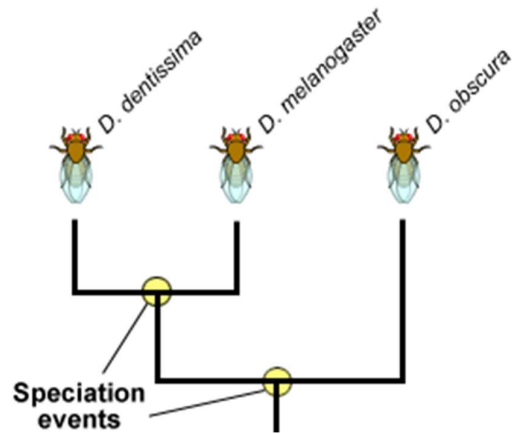


Fig. 5.2: Speciation events as shown in a phylogenetic tree.

5.3.1 Reproductive Barriers

- Reproductive barriers are mechanism that **prevents organisms of different populations from interbreeding successfully**. These barriers **isolate gene pools** of different species and can be categorized into either prezygotic or postzygotic barriers.

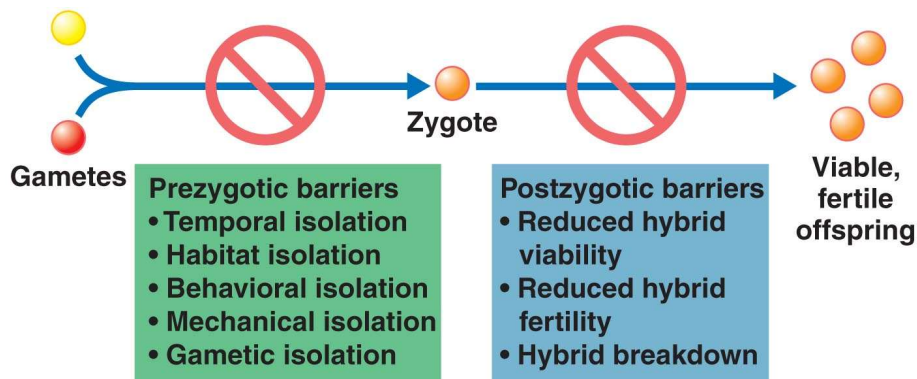


Fig. 5.3.1: Prezygotic and postzygotic barriers to reproduction. (Refer to Annex B & C)

(i) Prezygotic barriers

- Prezygotic barriers, which **prevent mating between individuals or fertilization of gametes** include:
 - a) Temporal isolation: Reproduction (i.e. mating or flowering) at different seasons or timing
 - b) Habitat isolation: Populations living in different habitats because of geographical or ecological isolation
 - c) Behavioural isolation: Differences in mating rituals, which are only recognized by individuals of the same species
 - d) Mechanical isolation: Structural incompatibility in female and male sex organs
 - e) Gametic isolation: Male and / or female gametes unable to survive before fusion or unable to fuse due to incompatibility

(ii) Postzygotic barriers

Postzygotic barriers **prevent the development of viable, fertile offspring after the formation of a zygote.**

- a) Reduced hybrid viability: Hybrids fail to develop or to reach structural maturity
- b) Reduced hybrid fertility: Hybrids reach sexual maturity but are sterile and unable to produce functional gametes
- c) Hybrid breakdown: Offspring of hybrids unable to survive or are infertile.

5.3.2 Modes of Speciation

- Speciation occurs through either allopatric speciation or sympatric speciation.

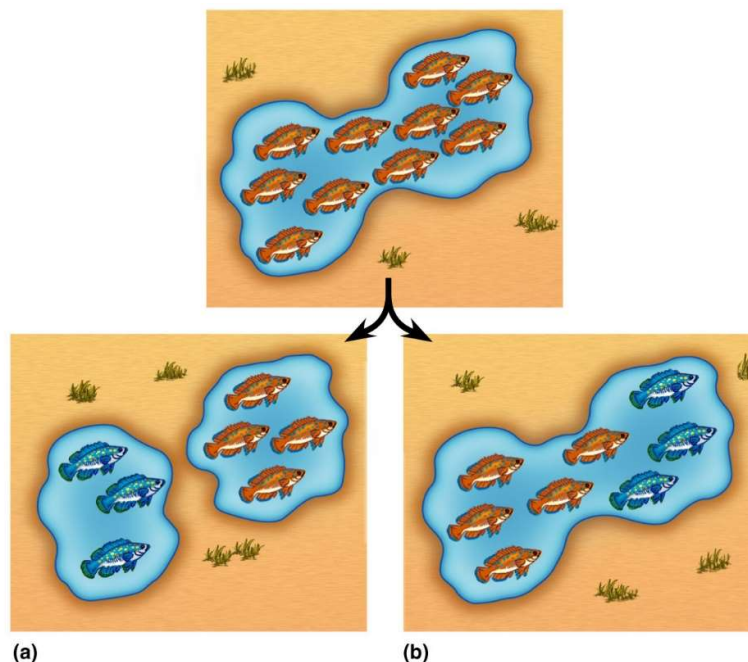


Fig. 5.3.2: Modes of speciation; (a) allopatric speciation, and (b) sympatric speciation.

(i) Allopatric Speciation

- Allopatric speciation occurs when two species are formed due to **geographical isolation**. When a **geographical barrier** occurs between two populations, gene flow is disrupted.
- The gene pools of the separated populations **accumulate different alleles** due to presence of **different selection pressures**. New alleles also arise independently from **mutations** in the separated populations.
- These events lead to **genetic divergence** where the gene pools of the two populations become different from each other. As the populations become more or more genetically different, reproductive barriers (prezygotic and/or postzygotic barriers) may appear preventing the two populations from interbreeding. **Reproductive isolation** has thus occurred leading to speciation.
- E.g. Adaptive radiation of Galapagos finches
 - **Adaptive radiation** describes the **rapid speciation** of a **single or a few species** to fill **many ecological niches** forming many new species from the ancestral population.
 - Phenotypically different but related species of finches were observed on the different islands of the Galapagos chain.
 - The ancestral finch was a ground-dwelling, seed-eating finch. Upon inhabiting different islands in the Galapagos chain, finches **occupied niches with different food sources**. The different food sources acted as **selection pressure** selecting for finches with **different beaks**. Those with beaks allowing access to the available food source have **selective advantage** and thus experience **greater survival** and **reproductive success**, passing down the allele for the beak type to its offspring.
 - Over time, generations of finches on different islands exhibit different beak phenotype and evolve to become different species.

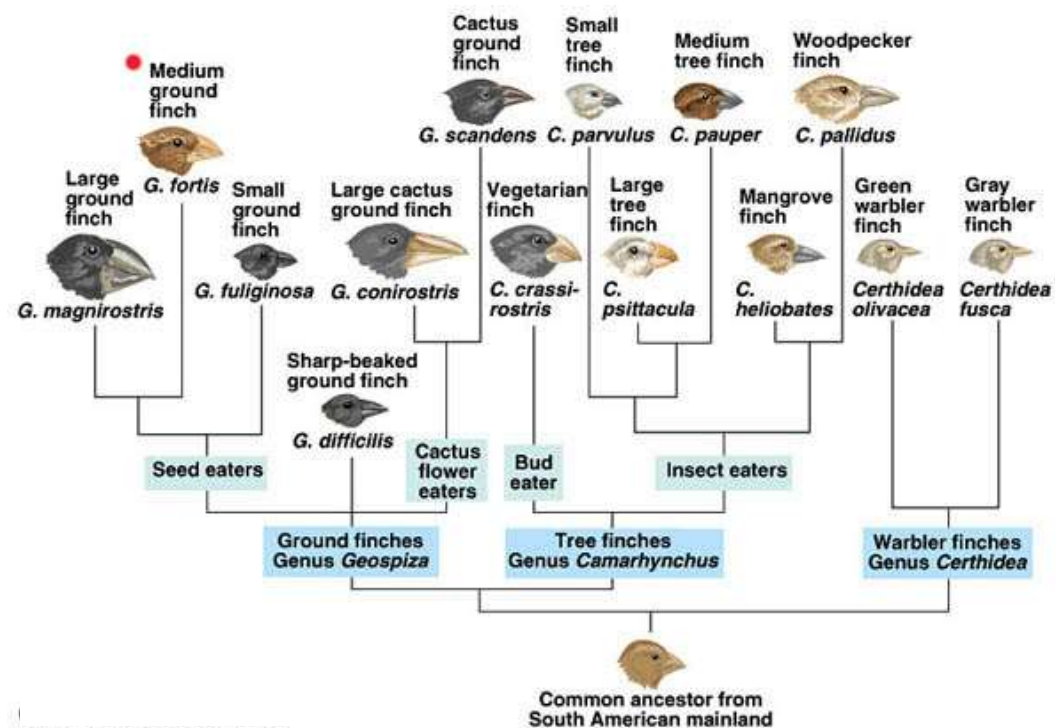


Fig. 5.3.3: Adaptive radiation of finches (Allopatric Speciation)

(ii) Sympatric speciation

- Sympatric speciation occurs when two species are formed due to **behavioural or physiological isolation within the same geographical location**.
- A **speciation event** occurs resulting in **genetic differences** that leads to **reproductive barriers** causing the two populations to be now **reproductively isolated**.
- E.g. Evolution of bread wheat (*Triticum aestivum*)
 - Two closely related species in the same geographical location may interbreed to produce a hybrid offspring. The hybrid may be sterile as pairing of chromosomes in meiosis is not possible due to absence of homologous chromosomes.
 - However, a **chromosomal mutation** due to **non-disjunction**, may occur to result in the formation of a **polyploid**. These polyploids are then able to **self-fertilize** to produce **viable, fertile offspring**. But they are **not able to interbreed** with either parent species due to difference in chromosome number. This physiological isolation leads to reproductive isolation, resulting in speciation.

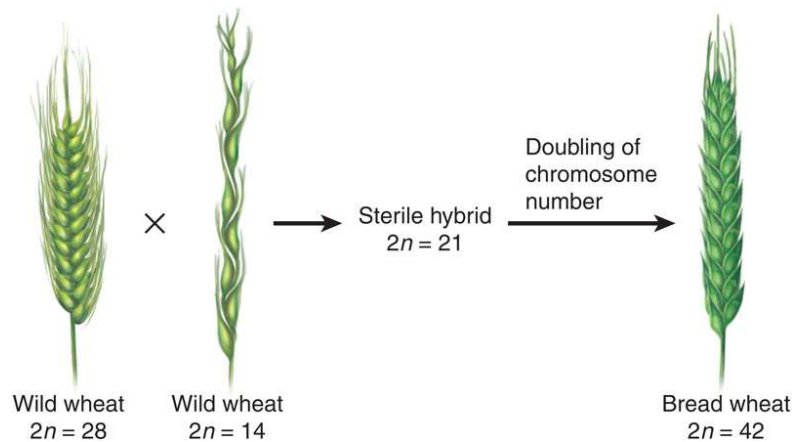


Fig. 5.3.4: Polypoidy in plants (Sympatric Speciation)

6 EVIDENCE FOR EVOLUTION

- As natural selection and evolution occur over long periods of time, it may not be possible for direct observation of its occurrence. Hence, observations in **homology**, **fossil record** and **biogeography** serve as evidence for evolution.

Learning Outcome (g):

Explain how evidence based on homologies identified in biochemical data (molecular homologies) and the fossil record (anatomical homologies), together with biogeography, supports Darwin's theory of evolution.

- Homology** refers to **similarities** in characteristics in anatomy or biochemistry, found in different species due to **common ancestry**.
- Darwin's theory of evolution of **descent with modification** (where new species descend from ancestral species through the **accumulation of modifications** as the population **adapts to a different environment**) serves to explain how **related species** have **characteristics** with underlying **similarities** even though they serve very **different functions**.

6.1 Anatomical Homology

- Organisms with anatomical homology have **similar morphological structures** such as bone, organs etc. **derived from a common ancestor**. Examples of anatomical homology include **homologous structures** and **vestigial structures**.

6.1.1 Homologous Structures

- Homologous structures have **similar basic structures** in different species but play **different functions**. Homologous structures are derived from a **common ancestor** but may play different functions in different species due to **divergent evolution**.
- E.g. Pentadactyl limb in vertebrates
 - The pentadactyl limb in all tetrapods consists of the same basic structure (five sets of bones) but play different functions depending on the environment in which the organism is found.

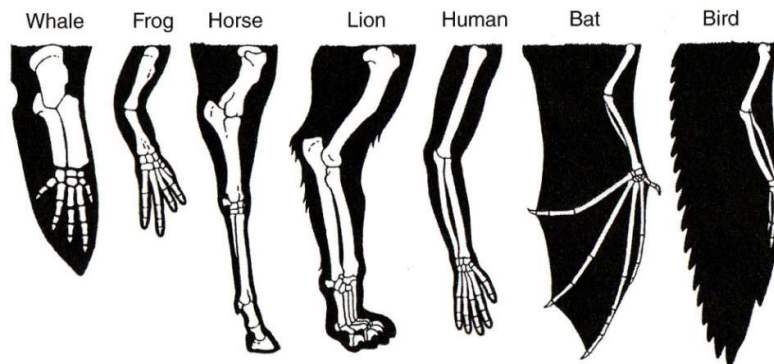


Fig. 6.1.1: Homologous structures

6.1.2 Analogous Structures

- Analogous structures have **different basic structures** but play **similar functions**. Analogous structures are **not** derived from a **common ancestor** but may play similar functions in **different species** due to **convergent evolution**.

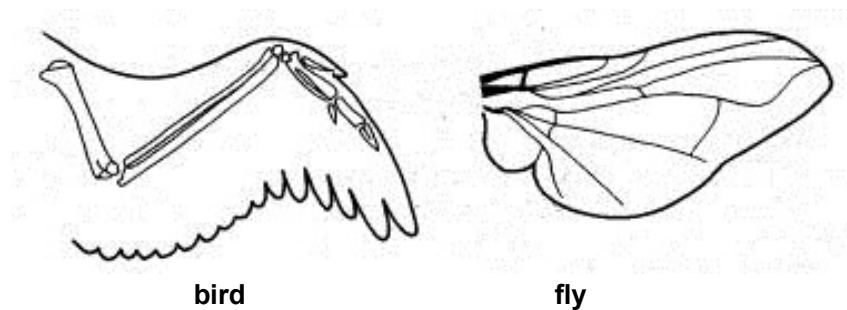


Fig. 4.1.2: Analogous structures

Anatomical homology can be revealed in fossil records to provide evidence for the theory of evolution. Fossils are remains (usually bones) or imprints of organisms which are preserved due to deposition of sediment over long periods of time.

6.1.3 Vestigial structures

- Vestigial structures are anatomical structures with **reduced or no functions**. They are **remnants** of structures that had **important functions in ancestors** but are **no longer important or less important** for survival.
- Example: Vestigial pelvis of whales and snakes which are structural remnants of a common ancestor, as the pelvis is no longer required for articulation of hind limbs.

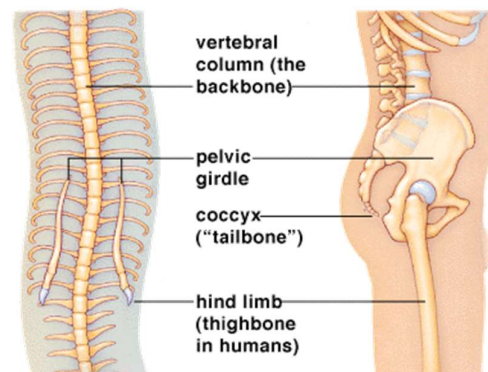


Fig. 6.1.3: Vestigial structures in snake (left) and humans (right).

CHECKPOINT 5

Fill in the blanks in the table of differences between divergent and convergent evolution.

Features	Divergent Evolution	Convergent Evolution
Population source		
Geographical region		
Selection pressure		
Morphology		
Characteristics		

6.2 Molecular Homology

Learning Outcome (I):

Explain the importance of the use of genome sequences in reconstructing phylogenetic relationships and state the advantages of molecular methods, including multiple sequence alignment (nucleotide and amino acid), in classifying organisms.

- Molecular homology refers to **similarities in nucleotide and amino acid sequences** of an organism, indicating inheritance (derived) from a common ancestor.
- All organisms contain the same genetic material (DNA and RNA), and the genetic code is universal.
- Molecular homology studies can be used to establish evolutionary relationship between different species.
 - **Closely related species** (diverged from a recent ancestor) **accumulate fewer mutations** due to recent divergence. Hence, they have **greater similarity** in DNA and amino acid sequence, exhibiting **greater evolutionary similarities** in both base sequence in a similar gene and amino acid sequence in a similar protein.
 - **Distantly related species** (diverged earlier from an ancestor) **accumulate more mutations** due to earlier divergence. Hence, they have **less similarity** in DNA and amino acid sequence, exhibiting **less evolutionary similarities** in both base sequence in a similar gene and amino acid sequence in a similar protein.

- E.g. Comparison of amino acid differences in cytochrome c in different organisms allow us to calculate the number of substitutions that have occurred per amino acid site.

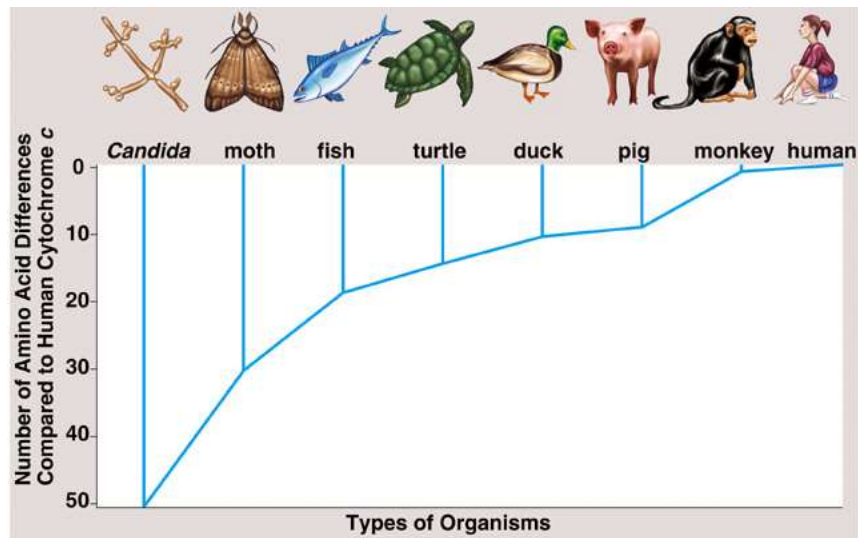


Fig. 6.2.1: Molecular comparison of cytochrome c in various organisms.

Comparing DNA From Different Species via DNA Hybridization

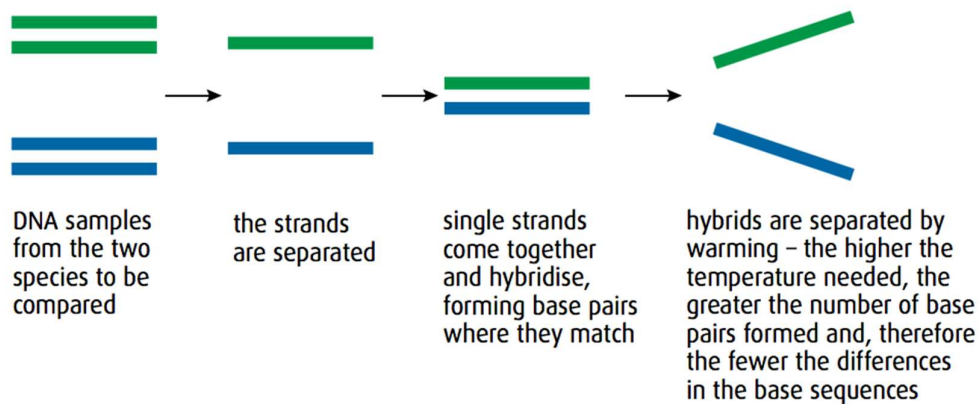


Fig. 6.2.2: How DNA sequences between different species can be analysed

CHECKPOINT 6

Table 4 shows the amino acid composition of cytochrome c in Organism **Q** to **T**.

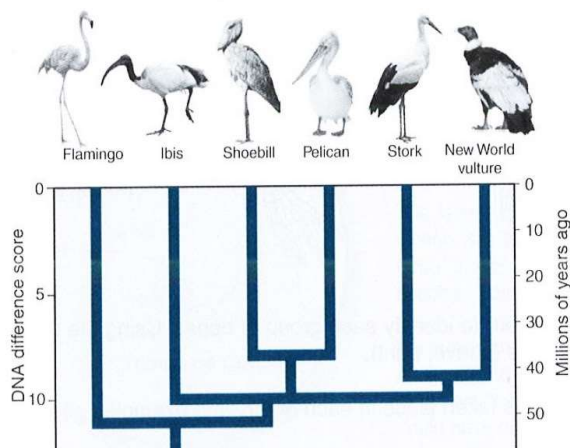
Table 4

Amino Acid	Organism Q	Organism R	Organism S	Organism T
Alanine	10%	10%	10%	10%
Arginine	4%	4%	4%	4%
Aspartic acid	6%	6%	6%	6%
Cysteine	6%	6%	6%	4%
Glutamic acid	12%	12%	8%	8%
Glycine	4%	2%	4%	4%
Valine	2%	1%	4%	6%

With reference to Table 4, state the two most closely related organisms.

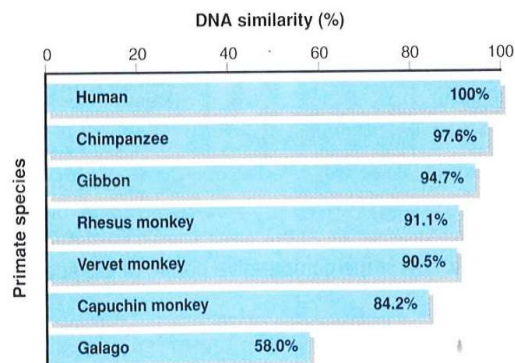
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CHECKPOINT 7



The relationships among the New World vultures and storks have been determined using DNA hybridisation. It has been possible to estimate how long ago various members of the group shared a common ancestor.

Similarity of human DNA to that of other primates



The genetic relationships among the primates has been investigated using DNA hybridisation. Human DNA was compared with that of the other primates. It largely confirmed what was suspected from anatomical evidence.

Fig. 7 The use of DNA hybridisation to establish the evolutionary relationships between different organisms.

- Study the graph showing the results of DNA hybridisation between human DNA and that of other primates in Fig. 5.
 - Which is the most closely related primate to humans? _____
 - Which is the most distantly related primate to humans? _____
- Estimate the DNA difference score for:
 - Shoebills and pelicans: _____
 - Storks and flamingos: _____
- On the basis of DNA hybridisation, estimate how long ago did the ibises and New World vultures shared a common ancestor.

.....

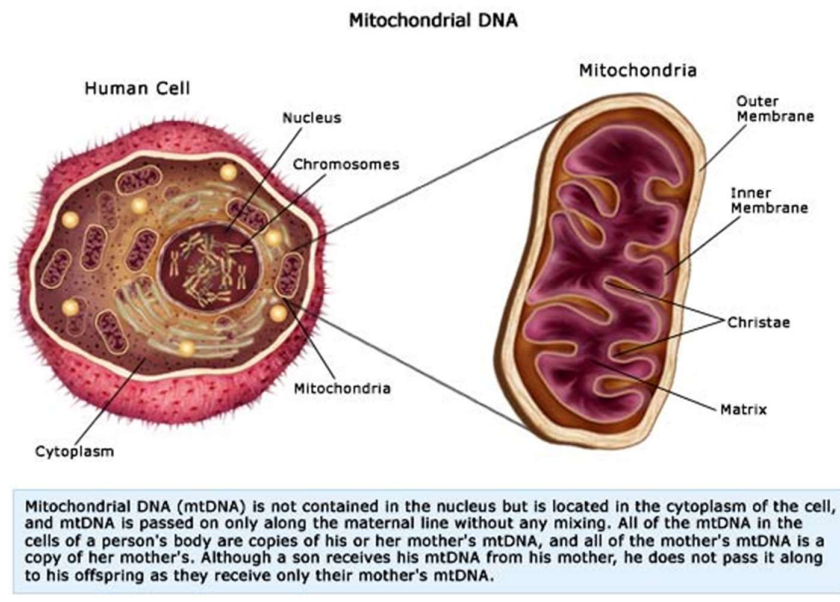
Advantages of Molecular Methods

- Molecular methods are **objective** and **unambiguous** as it compares DNA bases (A, C, G, T) or amino acid sequences which are **universal** to all organisms. The use of morphology e.g. shape of skull or colour of fur, can be subjective.
- Molecular data is **precise** and **accurate**.
- It is **quantifiable** thus allows for inference of the degree of relatedness between organisms that are morphologically very different e.g. bacteria and mammals.
- It allows for the **comparison of genetic divergence of two populations** within the same species **which are morphologically similar**.
- It offers a **limitless set of characters to be studied** as each nucleotide or amino acid position can be considered a character to distinguish between species.
- Advances in DNA molecular techniques like DNA sequencing, PCR and availability of electronic databases and software for analysis allow **easy comparison of large amount molecular data**.

Mitochondrion DNA (mtDNA) are often compared when doing molecular studies. WHY?

Inheriting mtDNA

- Whenever an egg cell is fertilised, nuclear chromosomes from a sperm cell enter the egg and combine with the egg's nuclear DNA, producing a mixture of both parents' genetic code.
- The **mtDNA from the sperm cell**, however, is left outside the egg cell. The fertilised egg thus contains a mixture of the father and mother's nuclear DNA and **an exact copy of the mother's mtDNA**, but **none of the father's mtDNA**. The result is that mtDNA is passed on only along the **maternal line**.



*This means that all of the mtDNA in the cells of a person's body are copies of his or her mother's mtDNA, and all of the mother's mtDNA is a copy of her mother's, and so on. mtDNA is always inherited **only** from the mother.*

Reasons why mtDNA are used:

1. They are **present in large numbers** in each cell, so fewer samples is required.
2. They have a **higher rate of substitution** (mutations where one nucleotide is replaced with another) than nuclear DNA making it easier to resolve differences between closely related individuals.
3. They are **inherited only along the maternal line** which allows tracing of a direct genetic line.
4. **No recombination occurs for mtDNA**. The process of recombination in nuclear DNA (except the Y chromosome) mixes sections of DNA from the mother and the father creating a garbled genetic history.

6.3 Fossil Record

- Fossils are **preserved remains** of organisms, providing evidence of past life forms which have since become extinct.
 - Parts of organisms that are rich in minerals (bones, teeth and shells) harden as fossils.
 - Deposition of layers of sediment result in the formation of layers of rocks called strata.
- Fossils provide evidence of evolutionary changes.
 - Fossils can be dated by determining the position of the fossil in the layers (strata) of sedimentary rock. The deeper the stratum the organism is found in, the earlier it existed. Its formation can also be dated by calculating the natural radioactive decay of certain elements such as potassium and carbon (carbon dating using ^{13}C).
 - When fossils are compared in chronological order, similarities and differences in structural features show evolutionary succession of organisms and how homologous structures have been modified over time.

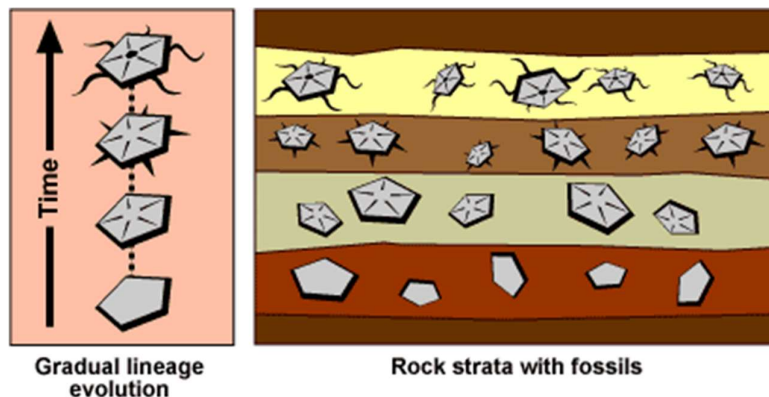


Fig. 6.3.1: Evolutionary succession of organisms as seen from fossils.

- Fossils of transitional (intermediate) species **link ancestral species to its descendants**.
 - **Transitional fossils** share characteristics of modern descendants and prehistoric ancestors, providing evidence to support the deduction that evolution occurred between the two forms.
 - E.g. *Archaeopteryx*, the earliest known bird from 150 million years ago, is a transitional species of birds and reptiles. It possesses characteristics of modern birds (wings, feathers and reduced digits) and small bipedal dinosaurs (teeth in a heavy jaw and a long bony tail).
 - Based on phylogenetic studies, birds and reptiles were thought to have evolved from a common ancestor. However, evidence of the existence of such an ancestral species was not known for a long time until the fossil of the *Archaeopteryx* was unearthed.



Fig. 6.3.2: Fossil of *Archaeopteryx*.

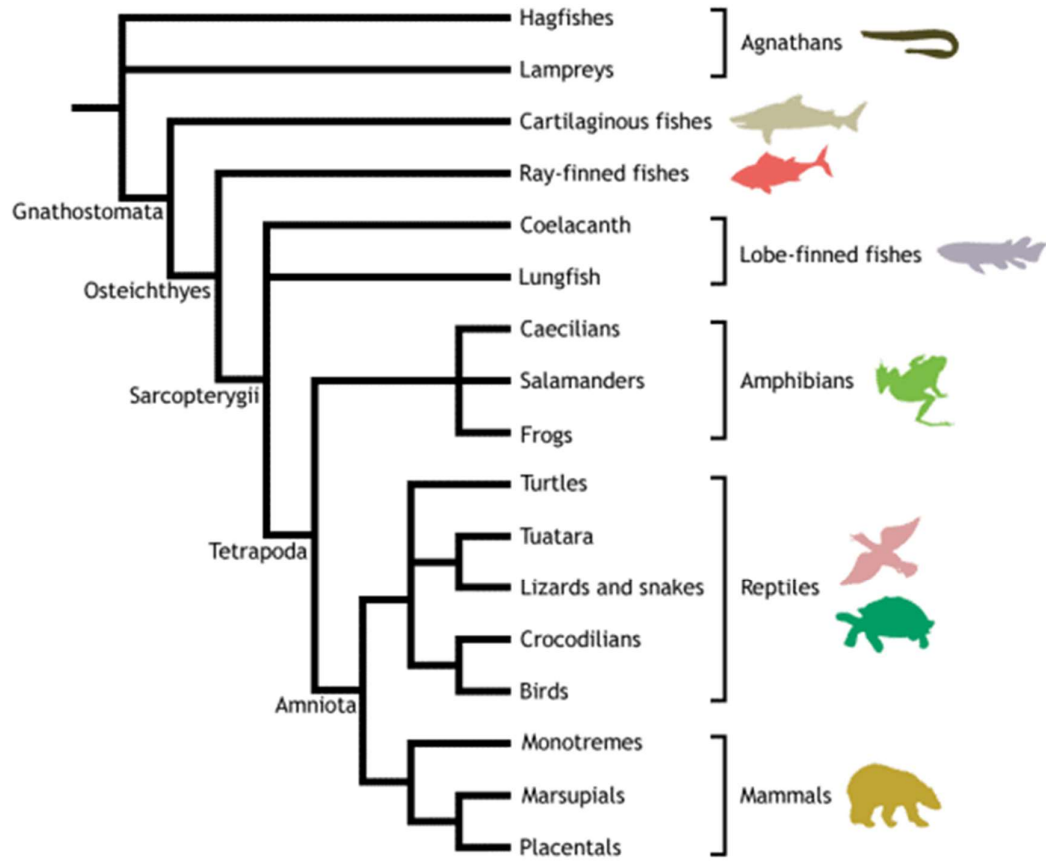


Fig. 6.3.3 Phylogenetic tree of reptiles and birds

6.4 BIOGEOGRAPHY

- Biogeography refers to the study of **geographical distribution** of extinct and modern species. The geographical distribution of organisms reflects their **evolutionary history**, and the interactions they have with the environment.
- **Closely related species** tend to be found in the **same geographic region**, and most island species are closely related to species from the nearest mainland or neighbouring island.
- E.g. Finches on Galapagos Islands
 - The finches found on Galapagos Islands (which emerged from the ocean floor) are more like South American finches than to those of more distant regions. This is because the islands were first colonized by finches from the neighbouring mainland rather than those from distant regions as they are less likely to be separated by geographical barriers. These populations then evolve over time as they adapt to the new environment, leading to the formation of a new species.

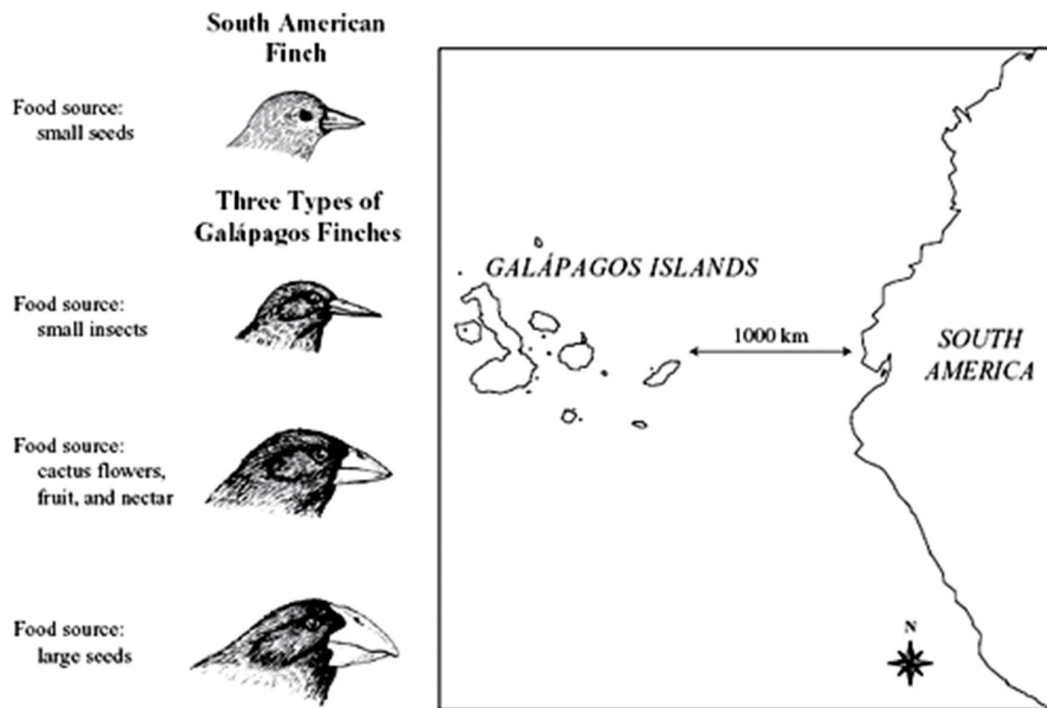


Fig. 6.4.1: Closely related finches species from neighbouring islands.

- **Different species** (that may look similar) are found in **distant geographic regions** despite similar ecological niches.
- E.g. Australian sugar gliders and North American flying squirrel

The Australian sugar glider (a marsupial, i.e. mammal that completes embryonic development in external pouch) and North American flying squirrel (a eutherian, i.e. mammal that completes embryonic development in uterus) share analogous structures. Both have gliding mechanisms that are adapted to similar environments in similar ways.

However, biogeography shows that they are found in distant habitats in different continents and evolved independently from different ancestors. They share analogous structures that play the same function of gliding. Thus, this provides evidence that structures for gliding evolved independently from different ancestors through convergent evolution.

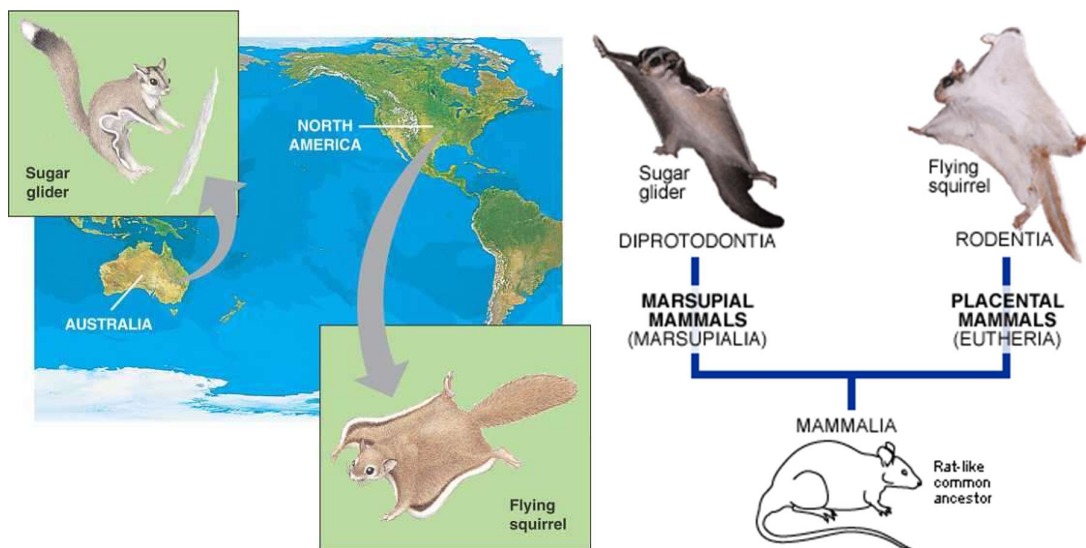


Fig. 6.4.2: Different species with superficial similarities found in distant regions.

DID YOU KNOW

Supercontinent Pangaea

“Why are some closely related species found in distant geographical regions?”

The geographical distribution of species can be influenced by **continental drift**. About 250 million years ago, land masses were united into a single supercontinent **Pangaea** (meaning ‘all land’). The formation of Pangaea had a tremendous environmental impact that reshaped biological diversity by causing extinctions and providing new opportunities for taxonomic groups that survived the crisis.

50 million years later, Pangaea began to separate, forming continents of the present day. **The separation of the continents explains why some species on different continents share common phylogenetic lineages.**

For example, marsupials are mostly only found in Australia, with some found in South America, New Guinea, and Madagascar. Fossils of marsupials were eventually found in Antarctica, which linked South America to Australia as Gondwana.

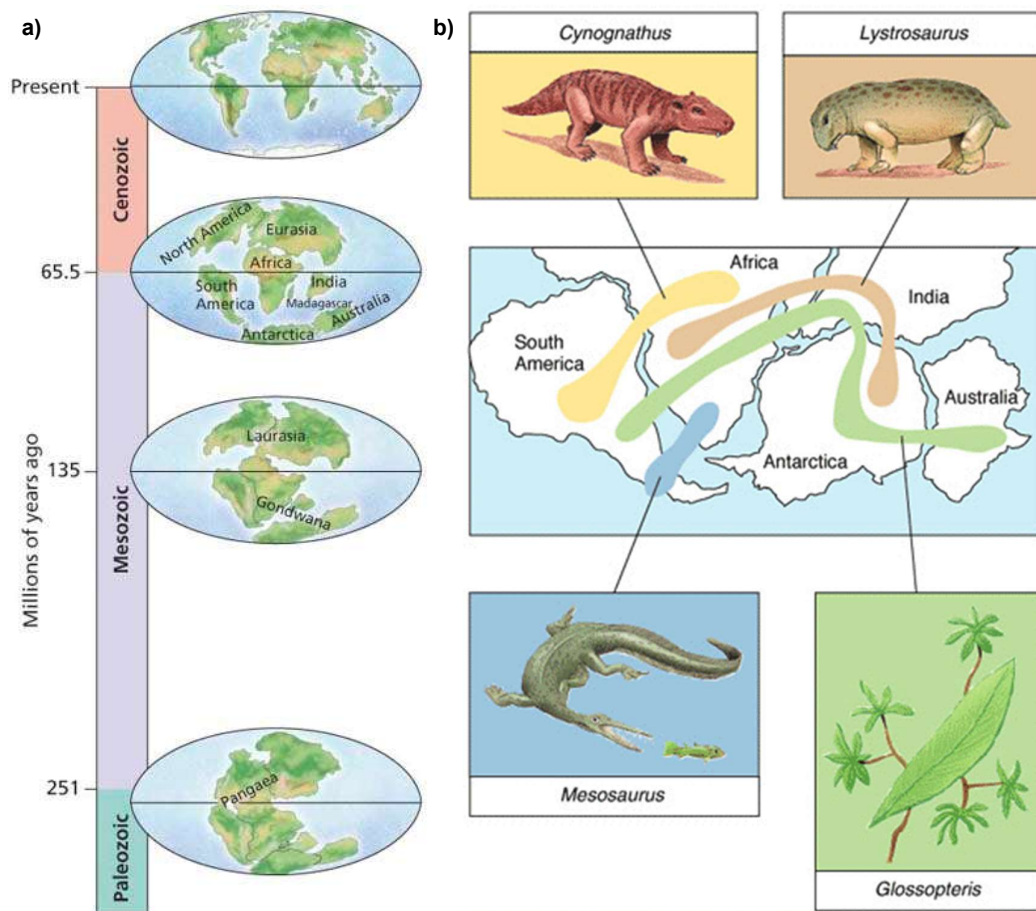


Fig. 6.4.3: (a) History of continental drift, and (b) observation of similar fossils across present-day continents.

CHECKPOINT 8

Circle T or F for each of the following statements.

- 1 In the taxonomic hierarchical classification system, there is decreased number of organisms and similarities between these organisms as we move down the taxonomic rank: kingdom, phylum, class, order, family, genus, and species. T / F
- 2 Phylogeny traces ancestor-descendant relationships between organisms based on molecular and anatomical homologies. T / F
- 3 Due to mutation, sexual recombination and sexual reproduction, variation is present in natural populations and this allows for the possibility of speciation when changes in selection pressures occur. T / F
- 4 Heterozygote protection helps to maintain stable frequencies of two or more phenotypic forms in a population. T / F
- 5 Natural selection is an interaction between individual organisms and their environment, and this result in the evolution of the individuals. T / F
- 6 Somatic mutations that confer an evolutionary advantage can be passed down to offspring. T / F
- 7 Disruptive selection is the only mode of natural selection that brings about evolutionary adaptation. T / F
- 8 Natural selection always results in increased genetic variation. T / F
- 9 Natural selection is an evolutionary mechanism which creates new traits that are best suited for the existing environment for individuals in the population. T / F
- 10 Natural selection is the primary mechanism of adaptive evolution. T / F
- 11 Antibiotics have created drug resistance to antibiotic-resistant drugs. T / F
- 12 Genetic drift results in decrease in genetic variation. T / F
- 13 Transfer of alleles between populations result in speciation. T / F
- 14 Allopatric speciation occurs in populations living in the same geographic location. T / F
- 15 According to the biological species concept, individuals in a species are able to interbreed, producing viable, fertile offspring. T / F
- 16 Homologous structures are similar structures with similar functions in different species, and these structures were derived from different ancestors due to convergent evolution. T / F
- 17 According to molecular homology, the more closely related two species, the more similar its gene sequences. T / F