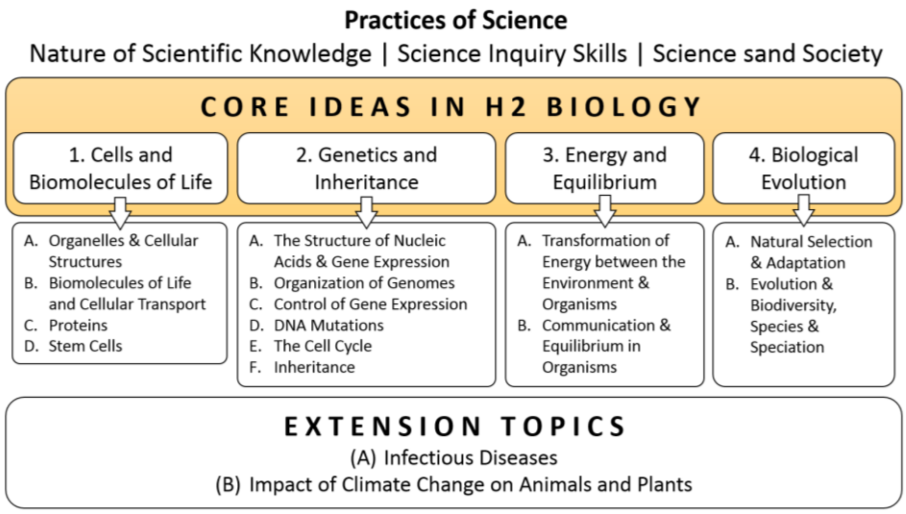
Tampines Meridian Junior College

JC2 H2/9744 Biology 2024

Core Idea 4A | 4B

13. Biological Evolution



SYLLABUS OVERVIEW

No.	Overarching Idea	Topics
1	**Core Idea 1** The Cell and Biomolecules of Life	Cell – The Basic Unit of Life
2		Biomolecules of Life and Cellular Transport
3	**Core Idea 2** Genetics and Inheritance	Genetics and Inheritance (I) – The Cell Cycle
4		Genetics and Inheritance (II) – DNA Replication and Gene Expression
5		Genetics and Inheritance (III) – DNA Mutations and their Consequences
6		Genetics and Inheritance (IV) – Organisation of Genome & Control of Gene Expression in Eukaryotes *[Includes Core Idea 1D: Stem Cells]*
7		Genetics and Inheritance (V) – Molecular Techniques in DNA Analysis
8		Genetics and Inheritance (VI) – Organisation and Inheritance of Viral Genomes
9		Genetics and Inheritance (VII) – Organisation of Genome & Control of Gene Expression in Prokaryotes
10	**Core Idea 3** Energy and Equilibrium	Transformation of Energy – Photosynthesis and Cellular Respiration
11	**Core Idea 2** Genetics and Inheritance	Genetics and Inheritance (VIII) - Inheritance
12	**Core Idea 3** Energy and Equilibrium	Communication and Equilibrium in Multicellular Organisms
13	**Core Idea 4** Biological Evolution	Biological Evolution
14	**Extension Topic A** Infectious Diseases	Immunity and Infectious Diseases
15	**Extension Topic B** Impact of Climate Change on Animals & Plants	Climate Change – Causes and Impacts on Animals and Plants

NARRATIVES

Core Idea 4 – Biological Evolution – helps students make sense of biology and the biodiversity of life on earth. Three important concepts within evolutionary biology are the:
1. definition of evolution and descent with modification;
2. processes of evolutionary change, natural selection and genetic drift; and
3. patterns of evolutionary relationships (depicted as phylogenetic trees or cladograms).

The following questions should help students frame their learning:

- Why are there so many similarities among organisms yet so many different plants, animals and microorganisms?
- Why does biodiversity matter?

Natural selection is the major driving mechanism of evolution

The essential features of natural selection contribute to the change in the genetic makeup of a population over time. Darwin's theory of natural selection (and, in parallel, Wallace's similar observations and conclusions) states that inheritable variation occurs in individuals in a population.

Due to competition for resources that are often limited, individuals with more favourable variations or phenotypes are more likely to survive and produce more offspring, thus passing on the alleles that code for those traits to subsequent generations. Fitness is a measure of evolutionary success as indicated by the number of surviving offspring left to produce the next generation. It is worth noting that individual organisms do not evolve; rather, it is populations that evolve.

As the environment is always changing, a diverse gene pool is important for the long-term survival of a species. Genetic variation within a population contributes to the diversity of the gene pool. Changes in genetic information may be silent (with no observable phenotypic effects) or result in a new phenotype, which can be favourable, detrimental or neutral to the organism. The interaction of the environment and the phenotype determines the fitness of the phenotype; thus, the environment does not direct the changes in DNA, but acts upon phenotypes that occur through random changes in DNA. These changes can involve alterations in DNA sequences, changes in gene combinations and/or the formation of new gene combinations. Note that there is no perfect genome for organisms.

Although natural selection is usually the major mechanism for evolution, genetic change in populations can occur through other processes, including mutation, genetic drift, sexual selection and artificial selection. Inbreeding, small population size, non-random mating, absence of migration and a net lack of mutations can lead to a loss of genetic diversity.

Evidence of evolution by natural selection is derived from a wide range of studies, e.g. in biochemistry, morphology, genetic information from existing and extinct organisms, geology and physical science. Phylogenetic trees serve as dynamic models that show common ancestry while geographical distribution and the fossil record provide the evolutionary link between ancestral and present-day organisms.

The process of evolution explains the diversity of life

Changes in the gene pools of populations can occur as a result of environmental changes (including those caused by human activities) or major natural catastrophes. A diverse gene pool is vital for the survival of species when such changes occur. Small populations are especially sensitive to these forces. Mutations in DNA and recombination during meiosis are sources of variation; new genes and combinations of alleles may confer new phenotypes.

Speciation and extinction have occurred throughout Earth's history and life continues to evolve within a changing environment, thus explaining the diversity of life. New species arise when two populations diverge from a common ancestor and become reproductively isolated. Common core biological processes e.g. metabolic pathways like photosynthesis and respiration and the universal genetic code support the idea of common ancestry. Phylogenetic trees are used to model evolutionary relationships and 'descent with modification'.

LEARNING OUTCOMES

Core Idea 4A: Natural Selection and Adaptation

Natural selection occurs only if there is both variation in the genetic information between organisms in a population and variation in the expression of that genetic information, i.e. trait variation leads to differences in performance among individuals. The traits that positively affect survival are more likely to be reproduced and thus are more common in the population.

The interaction of four factors is considered in evolution:
1. The potential for a species to increase in number;
2. The genetic variation of individuals in a species due to mutation and sexual reproduction;
3. The competition for an environment's limited supply of the resources that individuals need in order to survive and reproduce; and
4. The ensuing proliferation of the organisms able to survive and reproduce better in that environment.

Adaptation results from the accumulation of favourable genetic changes through natural selection, since organisms that are anatomically, behaviourally and physiologically well-suited to a specific environment are more likely to survive and reproduce. This differential survival and reproduction of organisms in a population that have an advantageous, heritable trait leads to an increase in the proportion of individuals in future generations that have the favourable trait and to a decrease in the proportion of individuals that do not.

Adaptation also means that the distribution of traits in a population can change when conditions change. Changes in the physical environment, whether naturally occurring or human induced, have thus contributed to the expansion of some species, the emergence of new distinct species as populations diverge under different conditions, and the decline (and sometimes the extinction) of some species.

Species become extinct because they can no longer survive and reproduce in their altered environment. If members cannot adjust to change that is too fast or drastic, the opportunity for the evolution of the species is lost.

Candidates should be able to:

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.

Core Idea 4B: Evolution and Biodiversity, Species and Speciation

Genetic information provides evidence of evolution. DNA sequences vary among species, but there are many overlaps; in fact, the ongoing branching that produces multiple lines of descent can be inferred by comparing the DNA sequences of different organisms. Such information is also derivable from the similarities and differences in amino acid sequences and anatomical structures.

Candidates should be able to:

a) Define biological evolution as descent with modification and explain the link between micro-evolution and macro-evolution
b) 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.
c) Explain the various concepts of the species (biological, ecological, morphological, genetic and phylogenetic concepts).
d) Define biological classification as the organization of species according to shared characteristics and describe how evolutionary relationship is established.
e) 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).
f) Define phylogeny as the organization of species to show their evolutionary relationships.
g) 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.

LECTURE OUTLINE

1. Introduction to diversity and biological evolution

2. Darwin's theory of natural selection and evolution

[Campbell Biology 9th edition, Chapter 22, 23.1, 23.4]

- 2.1 Lamarck's theory of evolution proven wrong by Darwin's theory
- 2.2 Darwinism: Darwin's theory of evolution
- 2.3 Neo-Darwinism – Darwinism explained with Mendelian genetics
- 2.4 Evolution as a result of natural selection – The British peppered moth
- 2.5 Selection pressure and the three modes of natural selection
- 2.6 Why population is the smallest unit that can evolve
- 2.7 Why variation is important for natural selection to operate
- 2.8 How variation is created in a population
- 2.9 How genetic variation is preserved in a population
  - 2.9.1 Diploidy
  - 2.9.2 Neutral mutation
  - 2.9.3 Heterozygote advantage

3. Factors that alter allele frequency and hence drive evolution in a population

[Campbell Biology 9th edition, Chapter 23.3]

- 3.1 Natural selection
- 3.2 Sexual selection
- 3.3 Genetic drift: the founder effect and bottleneck effect
- 3.4 Gene flow
- 3.5 Mutation

4. Speciation: the evolutionary process by which new species arise

[Campbell Biology 9th edition, Chapter 24.1, 24.2]

- 4.1 The concepts of species
  - 4.1.1 Biological species concept
  - 4.1.2 Morphological species concept
  - 4.1.3 Phylogenetic species concept
  - 4.1.4 Genetic species concept
  - 4.1.5 Ecological species concept
- 4.2 Speciation as a result of reduced gene flow
  - 4.2.1 Geographical isolation (Allopatric speciation)
  - 4.2.2 Physiological isolation (Sympatric speciation)
  - 4.2.3 Behavioral isolation (Sympatric speciation)

5. Evidence that support the theory of natural selection and evolution

[Campbell Biology 9th edition, Chapter 26.2, 26.3]

- 5.1 Homology
  - 5.1.1 Anatomical homology
    - 5.1.1.1 Fossil records
  - 5.1.2 Molecular homology
    - 5.1.2.1 DNA homology
    - 5.1.2.2 Protein homology
  - 5.1.3 Biogeography
  - 5.1.4 Comparison between anatomical and molecular evidence

6. Divergent and convergent evolution

- 6.1 Divergent evolution
- 6.2 Convergent evolution

7. Classification and phylogeny *[Campbell Biology 9th edition, Chapter 26.1]*

- 7.1 Classification
  - 7.1.1 Hierarchical classification / Linnaean taxonomy
  - 7.1.2 Binomial nomenclature
- 7.2 Phylogeny

1. Introduction to diversity and biological evolution

Learning outcome:
Core Idea 4B
(a) Define biological evolution as descent with modification and explain the link between micro-evolution and macro-evolution

- **Biodiversity** can be defined as the **totality of genes, species and ecosystems** in a region at a given time.

- **Evolution** is also known as **descent with modification**. It is the **change in allele frequency** of a **population over time**. In another words, current living species are descendants of ancestral species that were different from the present-day ones.

- **Microevolution** is the **change** in the **allele frequencies within a population for a given species** over generations. It refers to evolutionary changes on a **small scale,** i.e. **within a species** (Fig. 1.1a)

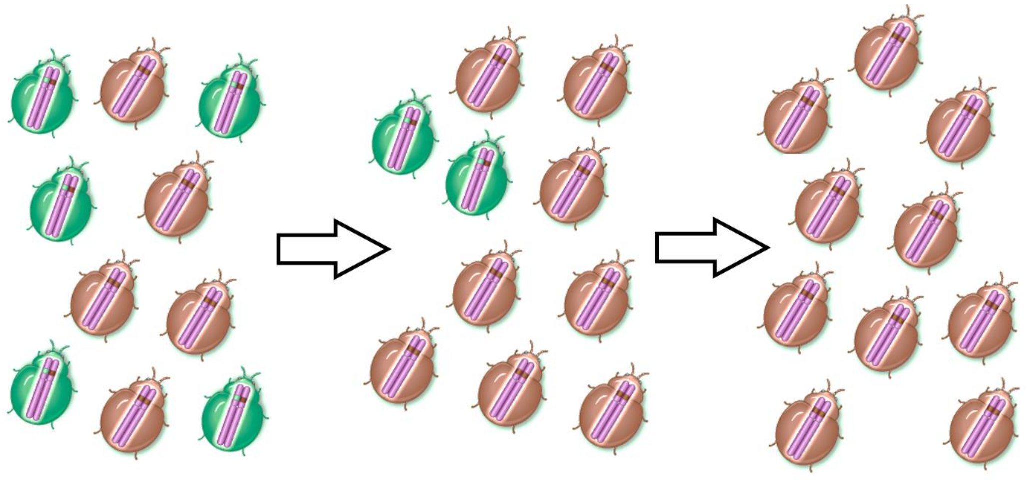
- **Macroevolution** refers to evolutionary changes on a **larger scale**, **beyond a single species** (e.g. origin of mammals) (Fig. 1.1b)

    - Macroevolutionary studies tend to draw heavily from the fossil record (Section 5.1.1.1).
    - Fossils document the emergence of new life forms (section 4), how their geographic distribution changed over time (Section 5.1.3), and ultimately when they went extinct.

- Over long periods of time (billions of years), as microevolution occurs again and again within species, new species that differ greatly from their ancestors may form. *(Refer to section 4.2 on Speciation)*

- The **formation of new species**, together with many **extinction events** occurring to other species, results in **macroevolution**.

- Thus, microevolution can be said to lead to macroevolution.



Total allele = 20
No. of 'green' allele (B) = **5**
No. of 'brown allele (b) = **15**
Allele frequency of B = **25%**
Allele frequency of b = **75%**

Total allele = 20
No. of 'green' allele (B) = **2**
No. of 'brown allele (b) = **18**
Allele frequency of B = **10%**
Allele frequency of b = **90%**

Total allele = 20
No. of 'green' allele (B) = **0**
No. of 'brown allele (b) = **20**
Allele frequency of B = **0%**
Allele frequency of b = **100%**

Fig. 1.1a: Microevolution happens on a small scale (within a single population)

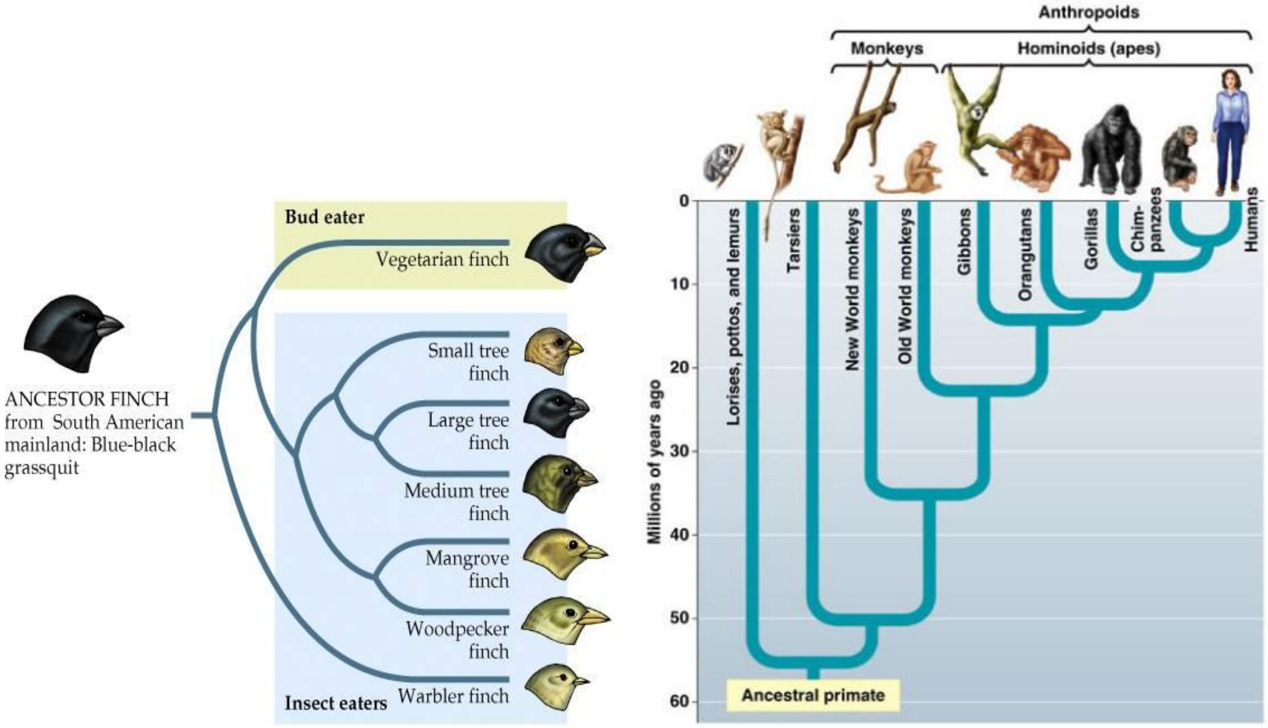


Fig. 1.1b: Macroevolution happens on a larger scale, often resulting in the formation of new species (e.g. Finches) and even new taxonomic groups (e.g. primates)

- **Adaptation** refers to the inheritance of characteristics of organisms that enhance their survival and reproduction in specific environments.

- **Traits** (i.e. phenotypes) can be inherited or acquired.

- **Evolution involves only inherited traits**.

Inherited Traits	Acquired Traits
Individual inherited genes from parents, hence phenotype is determined by the genetic component of each parent.	Individual is driven by necessity and gain of phenotype is a result of exercising a particular body part.
Can be inherited. i.e. passed down to the next generation.	Cannot be inherited. i.e. cannot be passed down to the next generation.
Example: A child is likely to be tall if both parents are tall and vice versa.	Example: A fair-skinned individual can become tanned under exposure to the sun.

2. Darwin's theory of natural selection and evolution

2.1 Lamarck's theory of evolution proven wrong by Darwin's theory

Jean-Baptiste de Lamarck (1744 – 1829)

- There were several earlier theories explaining how organisms changed over time.
- French biologist Jean-Baptiste de Lamarck published his theory of evolution in 1809, the year Charles Darwin was born.
- After studying various fossil records, Lamarck put forward the first comprehensive model that attempted to explain how life evolves.

Lamarck's theory of evolution (Fig. 1.2a)

- One key part of Lamarckian evolution is the theory of *use and disuse*.
- Lamarck proposed that organisms are driven by necessity and would gain physical attributes as a result of exercising that particular body part. E.g. the giraffe stretches it neck to eat leaves from trees and as a result, it will have a longer neck.
- Parts of the organisms that are not used will deteriorate.
- Organisms will then pass on the traits/modifications acquired during their lifetime to their offspring. E.g. the giraffes will then have offspring with long necks.
- The cycle repeats itself and the species develops specific and unique adaptations. E.g. the offspring also stretch their necks and continue to produce giraffes with longer necks.
- As a result, organisms change over time. E.g. over time, the giraffe's neck grew longer.
- Lamarck also proposed that organisms have an innate drive to become more complex.

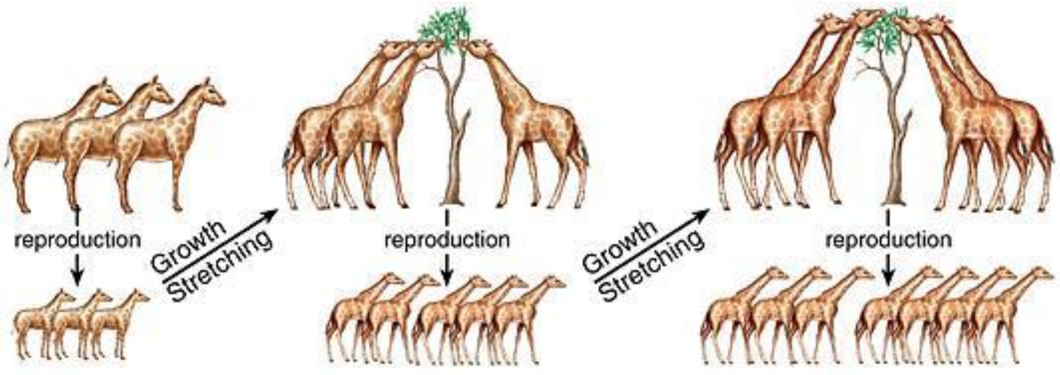
Charles Darwin (1809 – 1882)

- In 1831, Darwin embarked on a five-year survey voyage around the world on the HMS *Beagle*.
- His studies of specimens around the globe led him to formulate his theory of evolution and his views on the process of natural selection.
- In 1859, he published a detailed explanation of his theory in his best-known work, *On the Origin of Species by Means of Natural Selection*

Darwin's theory of evolution (Fig. 1.2b)

- Darwin's Theory of Evolution states that the environment would select individuals that are most adapted for it to survive and reproduce.
- Individuals are only considered 'successful' or 'fit' if they live long enough to reproduce to give rise to viable and fertile offspring with the adaptations (i.e. 'fitness' – the ability to survive and reproduce).
- Individuals that are unfit for survival in the current environment will be eliminated.
- The appearance and characteristics of a species will change over time as a result of the natural selection. These organisms are said to have evolved and may be classified as new species.
- Darwin called the process 'descent with modification'.

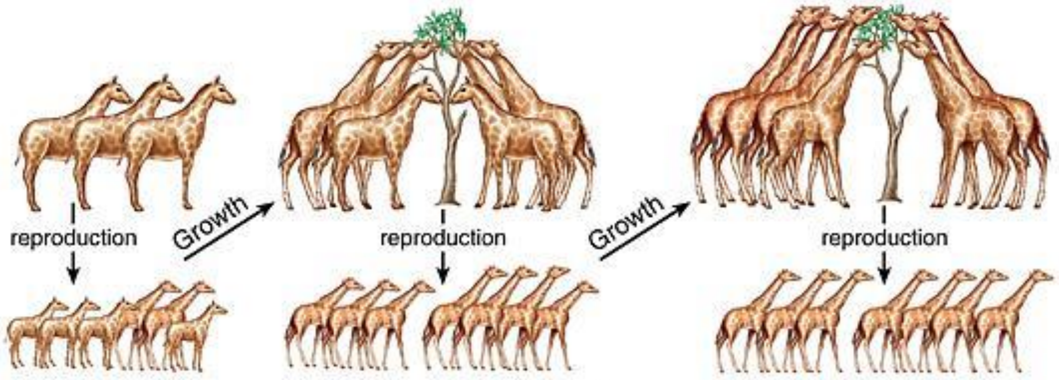
Learning point:
You have studied the mechanisms of inheritance in earlier chapters. Comment on Lamarck's theory. Can organisms pass on the traits acquired during their lifetime to their offspring? Give an example to illustrate.



Proposed ancestor of giraffes has characteristics of modern-day okapi.

The giraffe ancestor lengthened its neck by stretching to reach tree leaves, then passed the change on to offspring.

(a) **Lamarck's theory: variation is acquired.**



Some individuals born happen to have longer necks.

Over many generations, longer-necked individuals are more successful, perhaps because they can feed on taller trees. These successful individuals have more offspring and pass the long-neck trait on to them.

(b) **Darwin's theory: variation is inherited.**

Fig. 1.2: (a) Lamarck's theory of evolution. **(b)** Darwin's theory of evolution

Lamarckism	Darwinism
• Lamarck proposed that parts of the body that were used extensively to cope with the environment become larger and stronger while the parts that are not used deteriorate. • Lamarck also proposed that the modifications acquired during an organism's lifetime can be passed along to its offspring. • E.g. A population of giraffes (or the ancestors of the modern giraffe) feeds on leaves on trees. • The giraffes will stretch their necks constantly and hence they will develop longer necks. • The giraffes then reproduce and their offspring will have longer necks than the previous generation.	• Darwin proposed that some organisms are better already adapted to survive than others in a particular environment due to variation. • Darwin theorised that the organisms that are better adapted to survive will pass on their adaptations to their offspring. • E.g. A population of giraffes (or the ancestors of the modern giraffe) competes for food. • Some giraffes have longer necks than others and can reach leaves that are higher on the trees. • The giraffes with longer necks will outcompete the ones with shorter necks and are more likely to reproduce, thus the next generation will have longer necks.

2.2 Darwinism: Darwin’s theory of evolution

Evolution by means of natural selection – descent with modification (Year 1859)

- Darwin’s theory of evolution states that the environment would select individuals that are most **adapted** for it to survive and reproduce.
- Individuals are only considered ‘successful’ or ‘fit’ if they **live long enough to reproduce** and give rise to viable and fertile offspring with the adaptations (i.e. ‘fitness’ – the ability to survive and reproduce).
- Individuals that are unfit for survival in the current environment will be eliminated.
- The appearance and characteristics of a species will change over time as a result of such **natural selection**. These organisms are said to have **evolved** and may be classified as new species.
- Darwin called the process ‘**descent with modification**’.

Take Note!

Darwin did not know about **DNA**, **genetics** and the **mechanisms of inheritance**. He theorised that characteristics were passed down from parent to offspring via “factors”.

The main features of Darwinian evolution

1) *Populations possess great reproductive capabilities*

   - All individuals of a population are capable of producing **large numbers of offspring**. Individuals within a population produce more offspring than are needed to replace themselves.
   - e.g. A fern can produce 50 million spores each year. If all these spores developed, they would cover an area just slightly less than the size of North America within a year’s time.

2) *Constancy of population size*

   - However, the size of most populations remains relatively constant. This is because most offspring **die before they reach reproductive age** or fail to mate to produce offspring.
   - e.g. Not all the spores produced by a fern will grow into new ferns. Ferns that do grow from the spores may not survive long enough to produce more spores.

3) *There is a struggle for survival*

   - From the two previous observations, Darwin summarised that members of a species are **constantly competing** with each other for resources like food, shelter, mates, territory, etc.
   - Therefore only a few individuals would **survive long enough to reproduce**.
   - Many will **die** in the **struggle for survival**.
   - Hence population numbers would remain **constant** over time.

4) *There is variation within a population*

- Individuals in a population are *different* from one another, hence there is **variation within a species**. (Fig. 2.1)

Fig. 2.1: Variation in color patterns in single species of ladybird *Harmonia axyridis*.

5) *The survival of the fittest individuals by natural selection*

- The environment exerts **selection pressure** (weather, predation, food supply, etc) on individual of a population.
- The individuals with the **features/characteristics** best suited for the prevailing environment are more likely to survive.
- They will be better adapted to **survive to reproductive age** to produce **fertile**, **viable offspring**. These individuals are at a **selective advantage**.
- Conversely, those unable to withstand the environmental pressures, **die before reaching reproductive age**. These individuals are at a **selective disadvantage**.

6) *Fit individuals produce similar offspring*

- Successful individuals produce offspring with characteristics or traits **similar** to themselves.
- These offspring are more likely to be **successful if the selection pressure remains the same**.

7) *There will be an accumulation of favourable traits in the population over generations*

- Individuals with advantageous traits have a higher chance of survival, hence they will produce more offspring.
- This unequal ability of individuals to survive and reproduce will lead to **certain advantageous traits becoming fixed in the population** over time

2.3 Neo-Darwinism: Darwinism explained with Mendelian genetics

- In the 20th century, Darwin's theory was modified in the light of evidence from genetics, molecular biology, palaeontology, ecology and ethology (study of behaviour) to explain the inheritance of certain traits.
- Genes are expressed into phenotypic traits.
- The evolution of an organism may be defined as the **change in allele frequency in a population over time**.

The main features of Neo-Darwinian evolution

1) *Populations possess great reproductive capabilities*

   - All individuals of a population are capable of producing **large numbers of offspring**. Individuals within a population produce more offspring than are needed to replace themselves.
   - E.g. A fern can produce 50 million spores each year. If all these spores developed, they would cover an area just slightly less than the size of North America within a year's time.

2) *Constancy of population size*

   - However, the size of most populations remains relatively constant. This is because most offspring **die before they reach reproductive age** or fail to mate to produce offspring.
   - E.g.: Not all the spores produced by a fern will grow into new ferns. Ferns that do grow from the spores may not survive long enough to produce more spores.

3) *There is a struggle for survival*

   - From the two previous observations, Darwin summarised that members of a species are **constantly competing** with each other for resources like food, shelter, mates, territory, etc.
   - Therefore only a few individuals would **survive long enough to reproduce**.
   - Many will **die** in the **struggle for survival**.
   - Hence population numbers would remain **constant** over time.

Note the differences in phrasing and terms used from point (4) onwards.

4) *There is variation within a population:*

   - Individuals in a population are ***genetically different*** from one another, hence there is **variation** within a species.

5) *The survival of the fittest individuals by natural selection:*

   - The environment exerts **selection pressure** (weather, predation, food supply, etc) on individual of a population.
   - The individuals with the ***alleles*** **coding for traits** best suited for the prevailing environment are more likely to survive.
   - They will be better adapted to survive to reproductive age to produce **fertile, viable offspring**. These individuals are at a **selective advantage**.
   - Conversely, those with ***alleles*** coding for traits unable to withstand the environmental pressures, **die before reaching reproductive age**. These individuals are at a **selective disadvantage**.

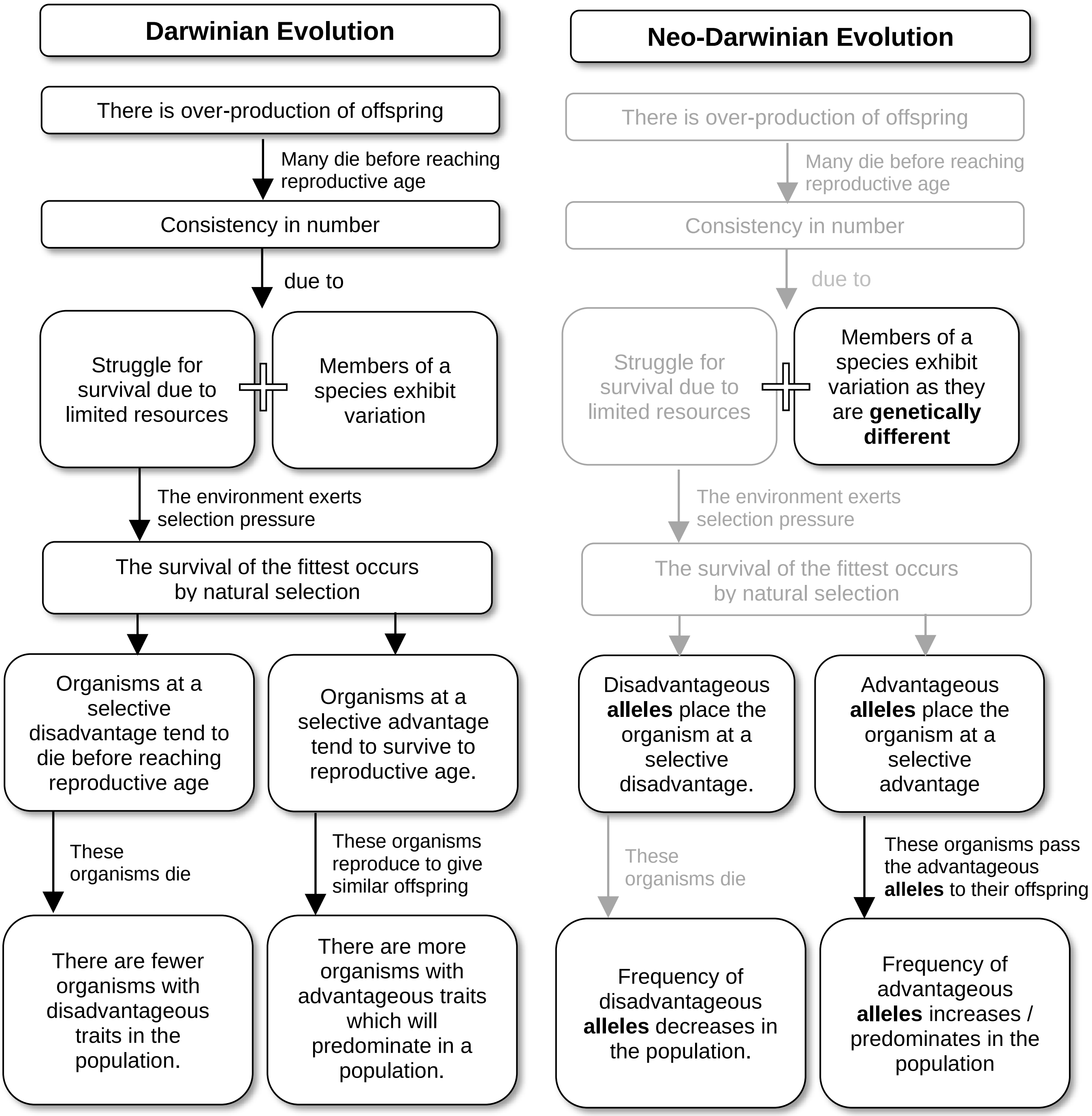
6) *Fit individuals produce similar offspring:*

- Successful individuals produce offspring with characteristics or features **similar** to themselves. These offspring have inherited the ***alleles*** from both their parents.
- These offspring are more likely to be **successful if the selection pressure remains the same**.

7) *There will be an accumulation of favourable alleles in the population over generations:*

- Individuals with ***advantageous alleles*** have a higher chance of survival, hence they will produce **more offspring**.
- This unequal ability of individuals to survive and reproduce will lead to **certain *advantageous alleles* becoming fixed in the population** over time.
- **Over time**, there would be ***changes in allele frequency in a population***. The frequency of **advantageous alleles increases** and that of **disadvantageous alleles decreases**.

Concept Map 1 – Darwinism and Neo-Darwinism



Darwinian Evolution

There is over-production of offspring

Many die before reaching reproductive age

Consistency in number

due to

Struggle for survival due to limited resources + Members of a species exhibit variation

The environment exerts selection pressure

The survival of the fittest occurs by natural selection

Organisms at a selective disadvantage tend to die before reaching reproductive age

These organisms die

There are fewer organisms with disadvantageous traits in the population.

Organisms at a selective advantage tend to survive to reproductive age.

These organisms reproduce to give similar offspring

There are more organisms with advantageous traits which will predominate in a population.

Neo-Darwinian Evolution

There is over-production of offspring

Many die before reaching reproductive age

Consistency in number

due to

Struggle for survival due to limited resources + Members of a species exhibit variation as they are **genetically different**

The environment exerts selection pressure

The survival of the fittest occurs by natural selection

Disadvantageous **alleles** place the organism at a selective disadvantage.

These organisms die

Frequency of disadvantageous **alleles** decreases in the population.

Advantageous **alleles** place the organism at a selective advantage

These organisms pass the advantageous **alleles** to their offspring

Frequency of advantageous **alleles** increases / predominates in the population

Think about it…

1. What happens to the appearance of the population after the frequency of certain alleles changes?
2. Does the environment stop exerting selection pressure on the organisms?
3. Does the process of natural selection cease?

2.4 Evolution as a result of natural selection – The British peppered moth

Pre-Industrial Revolution

- In the 1700s, the trees in the British countryside forest were mostly covered in light grey lichens.
- The light grey moths were well camouflaged in this environment.
- Thus the light grey moths were at a selective advantage while the dark coloured moths were at selective disadvantage at that particular time.
- The dark-coloured moths existed as the result of mutation *(**NOTE:** variation already exists in the population)*
- Their numbers were still relatively low as compared to the light grey form because they were easily seen and preyed upon by birds and eliminated from the population.

During Industrial Revolution

- From the 1850s, when the Industrial Revolution reached the town of Manchester, the pollution from the factories stained the bark of the trees in the nearby forests black.
- In this changed environment, the dark-coloured form of the moth was at a selective advantage as it now has the advantageous colouration that camouflages it from predators.
- Selection pressure (predation by bird) was exerted on the populations of moths and the numbers of the light grey form of the moth decreased while the dark-coloured forms predominated.
- More dark-coloured individuals survived long enough to reproduce as compared to light-coloured individuals.
- Hence populations of the peppered moth (*B. betularia*) today comprise mainly of the dark-coloured individuals with a small percentage of light grey forms.

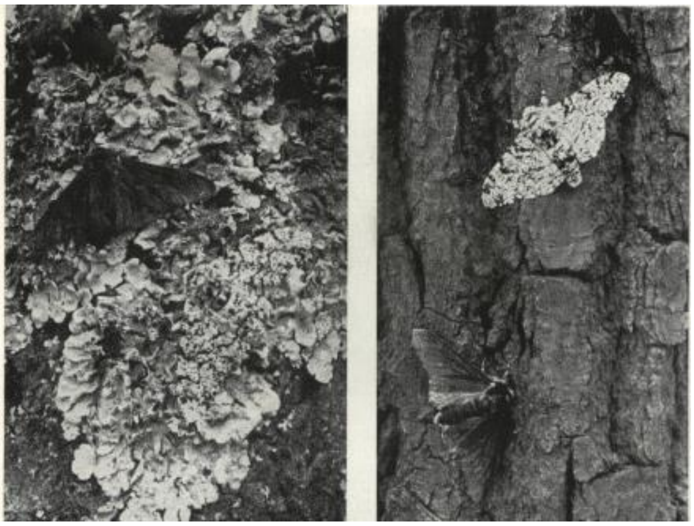


Fig. 2.2: A pair of peppered moths (light & dark) on a tree trunk during pre-industrial (left) and industrial revolution period (right).

Exercise: Darwinism and Neo-Darwinian

Refer to the passage in Section 2.4 on The British peppered moth and answer the questions below.

	Darwinism	**Neo-Darwinism**
Identify the environment.		
Identify the relationship between organism of interest and the environment.		
Identify the selection pressure in the organism's / population's environment.		
Identify the (genetic) variation that is important for natural selection to operate.	*Variation:*	*Genetic variation:*
Darwinism: Identify characteristics of the organism that the selection pressure favours or does not favour and how the identified features confer selective advantage or selective disadvantage on the organism. **Neo-Darwinism:** Identify the alleles possessed by the organism that the selection pressure favours / does not favour and how the identified allele confers selective advantage or selective disadvantage on the organism:	*Pre-Industrial Revolution, in the early 1700s:* *After the Industrial Revolution, 1750-1850:*	Pre-Industrial Revolution, in the early 1700s: After the Industrial Revolution, 1750-1850:
Explain the result after industrial revolution.		

2.5 Selection pressure and the three modes of natural selection

- Selection is the process by which organisms which appear physically, physiologically and behaviourally better adapted to the environment will survive to reproduce fertile and viable offspring. Organisms that are not so well adapted will either fail to reproduce or die.

- Selection depends on the **existence of phenotypic variation** within the **population**

- Selection pressure acts on the **phenotype** to allow organisms with existing characteristics to survive in a particular environment.

- When a **population increases in size, environmental factors e.g. food availability become limiting**.

- This produces **competition** for resources within the population, organism exhibiting characteristic of competitive advantage will obtain the resources, survive and reproduce.

- Individuals in a population exhibit a range of phenotypes that are **normally distributed** (Fig. 2.3, top).

- However, the shape of the curve changes with the types of selection (Fig. 2.3)

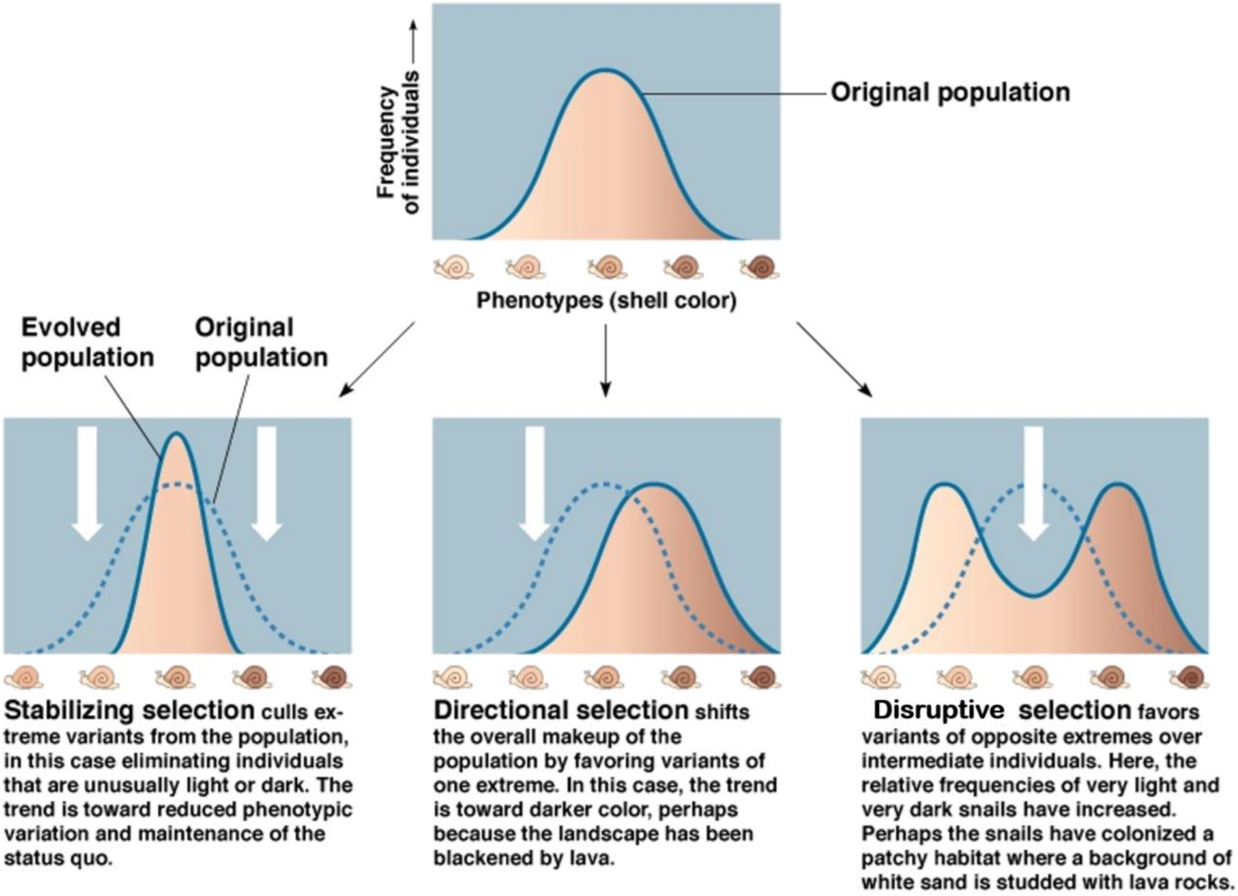


Fig. 2.3: Three types of selection outcomes using shell colour of snail as an example.

(1) Stabilizing selection

- This selection favours the **intermediate phenotype** out of a range of phenotypes.
- It operates when phenotypic features coincide with optimal environmental conditions and competition is not severe.
- It usually occurs when the environment remains constant.
- The **extremes** in variation are **selected against**, resulting in a narrower range of phenotypes in the population.
- The **mean phenotype does not change**.
- E.g. fur length in the snowshoe hare:
  - Hares with extremely short fur and extremely long fur will be at a **disadvantage** at 25°C. **Selection pressure** operates to **eliminate individuals with the alleles** for extremely long and short fur lengths. (Fig.2.4)

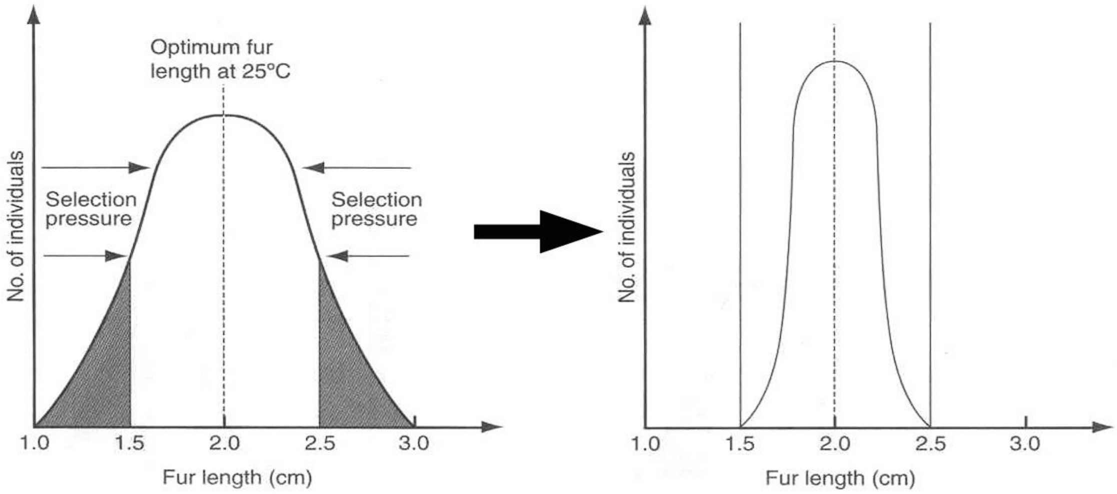
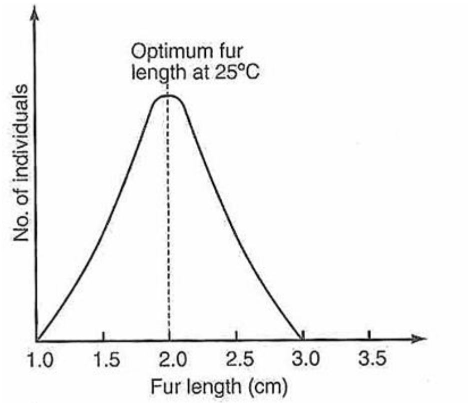


Fig. 2.4: Stabilizing selection.

(2) Directional Selection

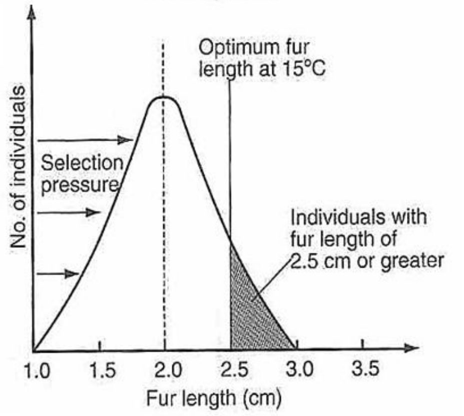
- This form of selection operates in response to **gradual changes in environmental conditions**. It operates on the range of phenotypes existing within the population
- The selection pressure tends to select phenotypes at **one extreme** of the range of phenotypes.
- The **mean phenotype changes**.

a)



At 25°C, individuals with allele for fur length of 2cm are at a **selective advantage**. This allele is present at a **higher frequency** in the population. The alleles for shorter and longer fur lengths are present in the population, but at **lower frequencies**. (Fig. 2.5a)

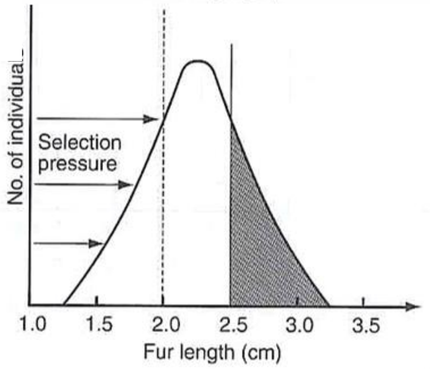
b)



If the climate changes and the temperature of the habitat changes to 15°C, **selection pressure is exerted** on the population of snowshoe hares.

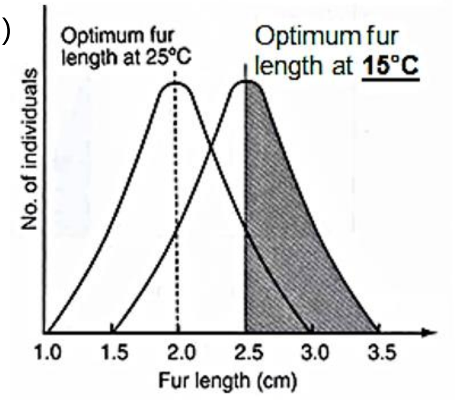
Hares with fur length >2cm would be at a **selective advantage**. Individuals with longer fur would **survive to produce fertile and viable offspring.** (Fig. 2.5b)

c)



More individuals with the **alleles for longer fur** will survive as they **inherited the alleles** from their parents. (Fig. 2.5c)

d)



Eventually, the **allele for longer fur length (2.5cm)** would predominate and exist at **higher frequency** while the **alleles for shorter fur length** would be present at **lower frequency** (Fig. 2.5d).

(3) Disruptive Selection

- This selection **favours** individuals at **both extreme** phenotypes out of a range of phenotypes. This is a **rare** form of selection.

- The **mean phenotype does not change**.

- It occurs when selection pressure is exerted on the middle range of variation for a particular trait. Fluctuating environmental conditions within an environment may favour this kind of selection resulting in the population being split into two distinct sub-populations.

- E.g. (Fig. 2.6): The mice have colonised a patchy habitat made up of light and dark rocks. **Mice with dark-coloured coat** will be **at a selective advantage in environment with dark rocks** as they are well camouflaged and not eaten by predators.

- **Mice with light-coloured coat** will be **at a selective advantage in environment with light rocks** as they are less likely to be preyed upon by predators.

- However, **mice with intermediate colour** are **at a selective disadvantage in both light and dark rocks environment** as they are easily seen by the predators and will be eliminated from the population.

- After many generations, two sub-populations of mice will be produced – one population with dark-coloured coat and another population with light-coloured coat. The allele for for dark-coloured coat would be fixed in one population and the allele for light-coloured coat would be fixed in another population. The mice with the allele for intermediate coat colour would be at a selective disadvantage, so the allele for intermediate coat colour would be found at lower frequencies.

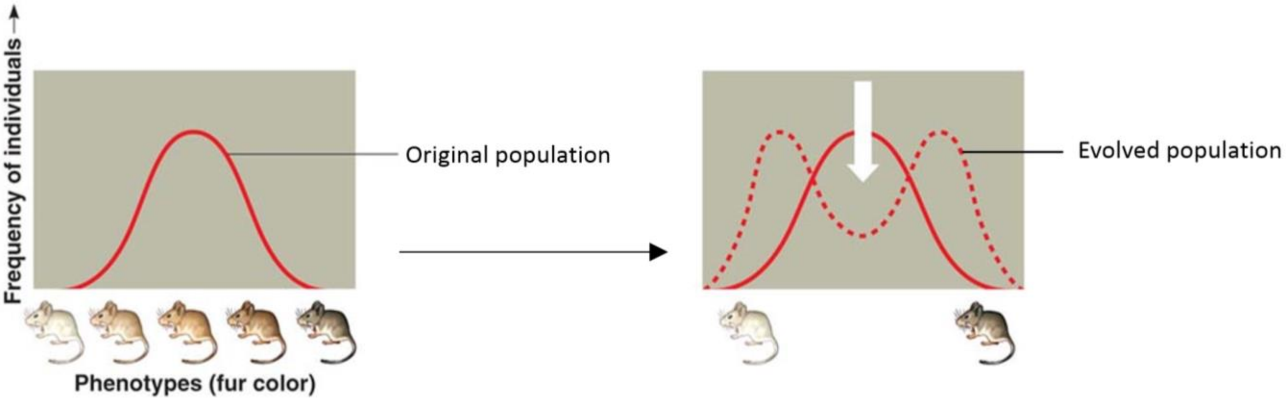


Fig. 2.6: Disruptive selection

2.6 Why a population is the smallest unit that can evolve

- One common misconception about evolution is that individual organisms evolve. It is true that natural selection acts on individuals: Each organism's traits affect its survival and reproductive success compared with other individuals. But the evolutionary impact of natural selection is only apparent in the **changes in a population of organisms over time**.

- A population comprises a group of individuals of the **same species** that live in the same area and interbreed, producing fertile offspring.

- Evolution involves <u>**changes in allelic frequencies within a population**</u> over generations, and such changes do not occur in an individual.

- Only a <u>**population**</u> **of interbreeding individuals can evolve** but not individual by itself. This is because evolution requires the individual to pass on its alleles to its offspring.

2.7 Why variation is important for natural selection to operate

- Variation within a population must exist before natural selection can take place.
- Members of a population are **genetically different** thus **exhibit variation** within the population.
- Environmental change acts as selection pressure to select those individuals with advantageous trait or allele.
- Variation is important as it **decreases the chances of extinction**.
- The more variation a species has, the higher the chances of the species surviving different types of environmental change.

2.8 How genetic variation <u>arises</u> in a population

1. **New genes/alleles** arise from **gene and chromosomal mutations** (*Refer to Gene Expression*). However, organisms very rarely pass mutations gained in their lifetime to their offspring unless the mutation arose during gamete formation.

2. **Meiosis** can contribute to **genetic variation** due to recombination of alleles via
    - Crossing over between non-sister chromatids of a pair of homologous chromosomes during prophase I.
    - Random assortment and segregation of homologous chromosomes at metaphase I and anaphase I respectively.
    - Random assortment and segregation of non-identical sister chromatids at metaphase II and anaphase II respectively.

3. **Random fusion of gametes** results in genetic variation during **fertilisation.**

4. Phenotypic variation can also arise as a result of **environmental influence**. Genes can **interact with the environment** to give rise to variation. (*Refer to Interitence*)
5. **Migration** into a population from another population, together with **random mating**, promote **gene flow**. For example, human gene flow is promoted with global travelling. Gene flow **increases variation within a population** by introducing **new alleles** to another population.

2.9 How genetic variation is preserved in a population

- Natural selection tends to produce genetic uniformity in a population by eliminating unfavorable alleles. This tendency is opposed by a few mechanisms that preserve variation.

2.9.1 Diplody

- As most eukaryotes are diploid organisms (two alleles present at each gene locus), a considerable amount of genetic variation is **hidden from selection pressure in the form of recessive alleles**.

- This variation is only exposed to selection when two heterozygotes mate and produce offspring homozygous for the recessive allele.

- Dominant alleles will appear more frequently in phenotypes and be selected for or selected against more rapidly.

- Recessive alleles on the other hand, exhibit no effect in the heterozygous state.

- Such **recessive allele may be harmful** but can **persist without being eliminated** from the population when heterozygote individuals reproduce.

- Example of lethal alleles which are recessive: mutated CFTR allele that causes cystic fibrosis.

2.9.2 Neutral mutation

- While many new mutations that are harmful are removed quickly by natural selection, some mutations are **neutral** and are **not selected for or against**, and thus being preserved in the population.

- Examples include: (1) mutation that produces alleles that code for traits which are selectively neutral, (2) mutation in non-coding regions, (3) mutation that changes the last base of a triplet, resulting in the same amino acid being coded for.

- The only mechanism that can alter the frequencies of neutral alleles is genetic drift (*Section 3.3*).

2.9.3 Heterozygote advantage

- Disease-causing mutations and lethal alleles which confer selective disadvantage, would usually be eliminated from the population by natural selection.

- However, in certain environments, **heterozygote individuals are at a selective advantage** and are more likely to **survive and reproduce** to pass on the deleterious (lethal) allele to the offspring compared to homozygous individuals. An example of this is **sickle cell anaemia**. Heterozygote individuals with sickle cell trait have a higher chance of survival in regions where **malaria** is prevalent.

- **Case study:** High Hb^S allele frequency in African regions where malaria is prevalent (Fig. 2.7)

    - Hb^AHb^A individuals – susceptible to malaria infection and subsequent death

    - Hb^SHb^S individuals – suffer from sickle-cell anemia. Die before reaching reproductive age

    - Hb^AHb^S individuals – phenotypically normal and are protected from malaria

- Malaria parasites (*Plasmodium*) infect and kill red blood cells.

- In heterozygotes (Hb^AHb^S), RBC which are infected with *Plasmodium* turns sickle-shape and are destroyed by white blood cells in the spleen, killing the *Plasmodium* that they habour (Fig. 2.8). This prevents that *Plasmodium* from further reproduction.

- The heterozygote individuals (Hb^AHb^S) are at a selective advantage in West Africa as they are more likely to survive a malarial infection and reproduce, passing on the otherwise disadvantageous Hb^S allele to their offspring.

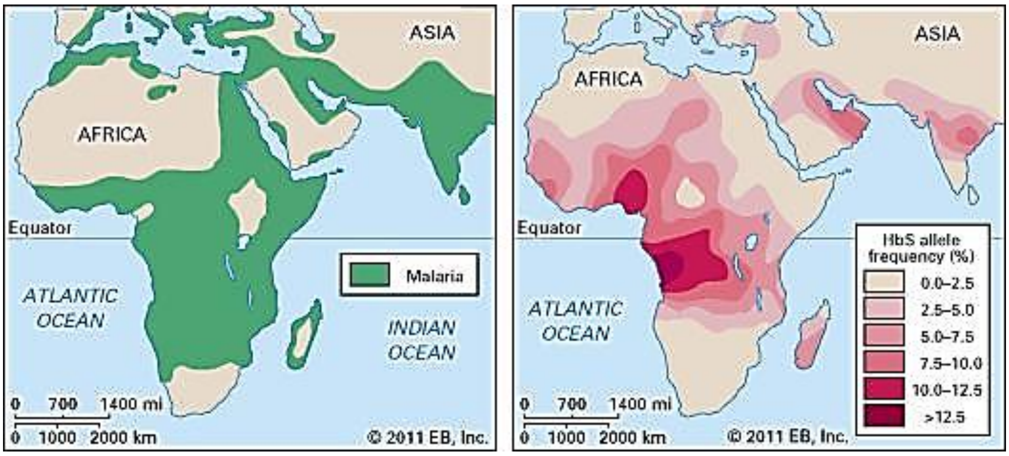


Fig. 2.7: Correlation between malaria occurrence and HbS allele frequency in Africa.

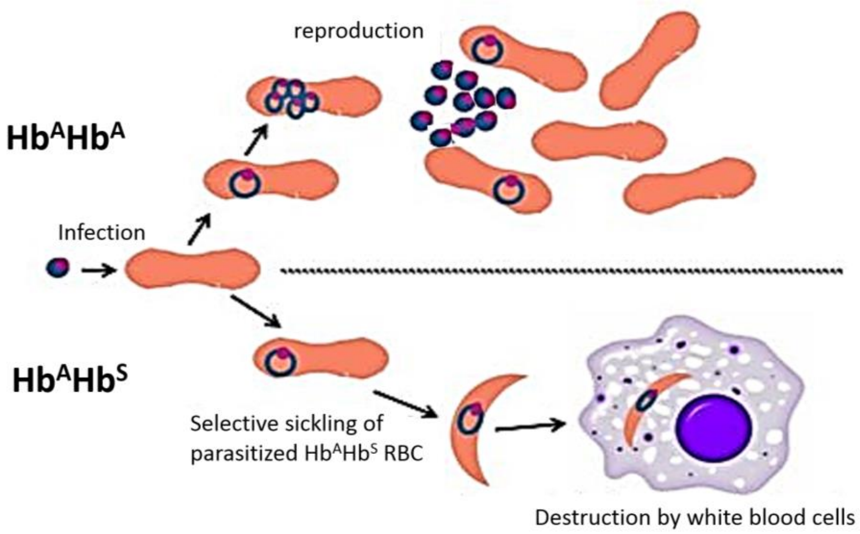


Fig. 2.8: The schematic diagram shows what happens in red blood cells in a normal (Hb^AHb^A) person with malaria after invasion of a red blood cell by a Plasmodium parasite. When the parasite is mature, the infected red blood cell essentially bursts and releases new parasites, each one of which can invade a new red blood cell.
The red blood cells in an Hb^AHb^S heterozygote with malaria: the red blood cell, which appears normal at the time of invasion, once infected undergoes sickling (probably as a result of deoxygenation and lowering pH caused by the parasite), and thus it falls easy prey to white blood cells in the spleen, in other organs and even in the peripheral blood.

3. Factors that alter allele frequency and hence drive evolution in a population

- The evolution of living organisms is the consequence of two processes. First, evolution depends on the **genetic variability generated by mutations**, which continuously arise within populations. Second, it also relies on **changes in the frequency of alleles within populations over time**.

3.1 Natural selection

- As discussed in *Section 2*, natural selection is a process of determining which alleles are passed on to the next generation by virtue of the relative selective advantages when expressed as phenotypes.

- Hence **selection pressure** can be seen as a means of **increasing or decreasing the frequency of an allele** within the gene pool and these changes in allele frequency lead to evolutionary change.

  Note: *gene pool refers to all copies of every type of allele at every locus in all members of the population*

- The extent of selection and time taken depend upon the nature of the mutant allele and the effect of it on the phenotype under the prevailing environment conditions.

- Example – Resistance of fruit fly to the insecticide DDT
  - The fruit fly (*Drosophila melanogaster*) has an allele that confers resistance to several insecticide, including DDT.
  - This allele has a frequency of 0% from flies collected from the wild in the early 1930s, prior to DDT use.
  - However, in flies collected after 1960 (following >20 years of DDT usage), the allele frequency is 37%.
  - This allele either arose by mutation between 1930 and 1960 or that it was present in 1930s, but very rare. The rise in frequency of this allele occurred because DDT selects for flies with the advantageous allele, and against those without.

3.2 Sexual selection

- Sexual selection occurs when some members of a population mate more often than other members.

- Individuals with certain inherited characteristics are more likely than other individuals to obtain mates.

- This is **mating based on phenotype**, which is any observable trait in an organism, including differences in appearance and behaviour.

- It is easy to see that if one male mates four times as much as the average male of his generation, his alleles stand to increase proportionately in the next generation.

- Differential mating success among members of one sex in a species often is based on **choices made by members of the opposite sex in that species**.

3.3 Genetic drift: the founder effect and bottleneck effect

- If you flip a coin 1,000 times, a result of 700 heads and 300 tails might make you suspicious about that coin. But if you flip a coin 10 times, an outcome of 7 heads and 3 tails would not be surprising. The smaller the number of coin flips, the more likely it is that chance alone will cause a deviation from the predicted results.

- **Chance events** alone (rather than natural selection) can also cause allele frequencies to fluctuate unpredictably from one generation to the next, especially in small populations – a process known as **genetic drift** (Fig. 3.1).

- Certain circumstances can result in genetic drift having a significant impact on a population. Two examples are the **founder effect** and the **bottleneck effect**.

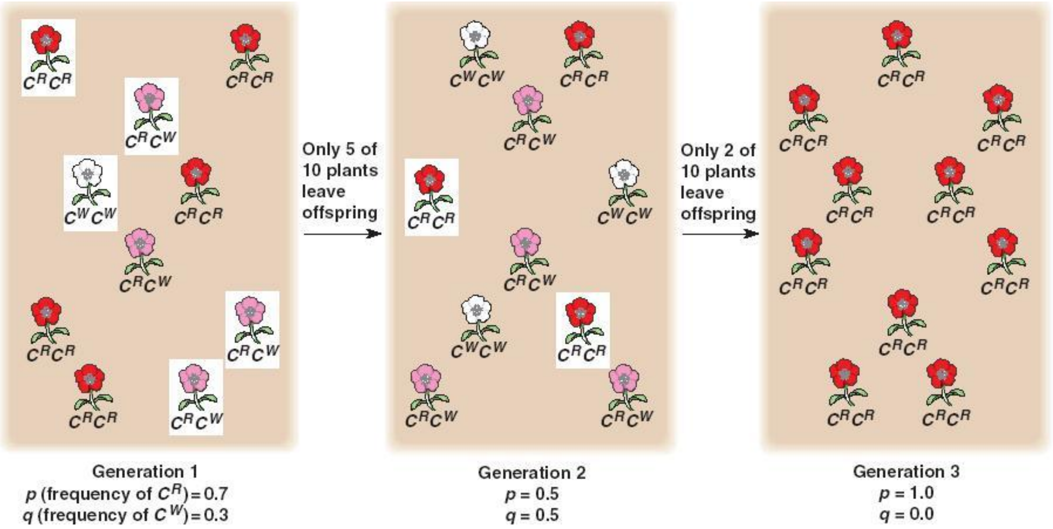


Fig. 3.1: Genetic drift. The small wildflower population has a stable size of 10 plants. Suppose that by chance, only 5 plants of generation 1 (those in white boxes) produce fertile offspring (this could occur, for example, if only those plants happened to grow in a location that provided enough nutrients to support the production of offspring). Again by chance, only 2 plants of generation 2 leave fertile offspring. As a result, by chance the frequency of the C^W allele first increases in generation 2, then falls to zero in generation 3.

(1) The founder effect

- When a few individuals become **isolated** from a larger population this smaller group may **establish a new population** whose gene pool differs from the source population. This is called the **founder effect** (Fig. 3.2).

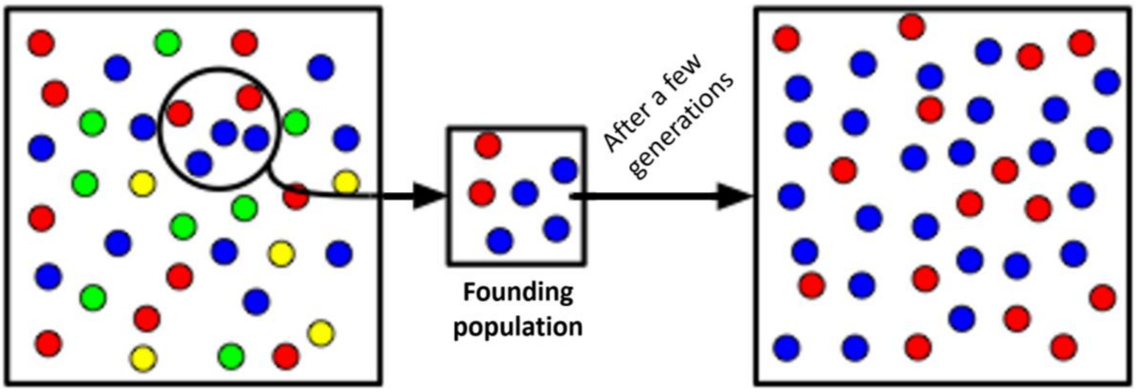


Fig. 3.2: The founder effect. When the environment operates on the colonizing/founding population, the diversity of descendants would be low as there was already a limited range of alleles available in the population

- ***Example*****:** Darwin's finches were hypothesised to have descended from mainland birds which had colonised the formerly unoccupied ecological niches of the Galàpagos Islands after being blown out to sea by freak weather conditions. The finches on the islands today are of different species but are all closely related to each other.

- ***Example*****:** In the 1680s, Ariaantje and Gerrit Jansz emigrated from Holland to South Africa, one of them bringing an allele for the mild metabolic disease called **porphyria**. Today, more than 30,000 South Africans carry this allele and in every case examined, it was traceable back to this couple.

(2) The bottleneck effect

- The **bottleneck effect** is the situation where there is a **drastic reduction in population size**.
- Drastic change in environmental conditions or disasters (e.g. fire, flood) may reduce the size of a population significantly.
- The small surviving population may not be representative of the original population's gene pool (Fig. 3.3).
- By chance alone, certain alleles will be overrepresented among the survivors, while others underrepresented or even eliminated altogether from the gene pool.
- Bottleneck effect usually reduces the overall genetic variability in a population because at least some alleles are likely to be lost from the gene pool.

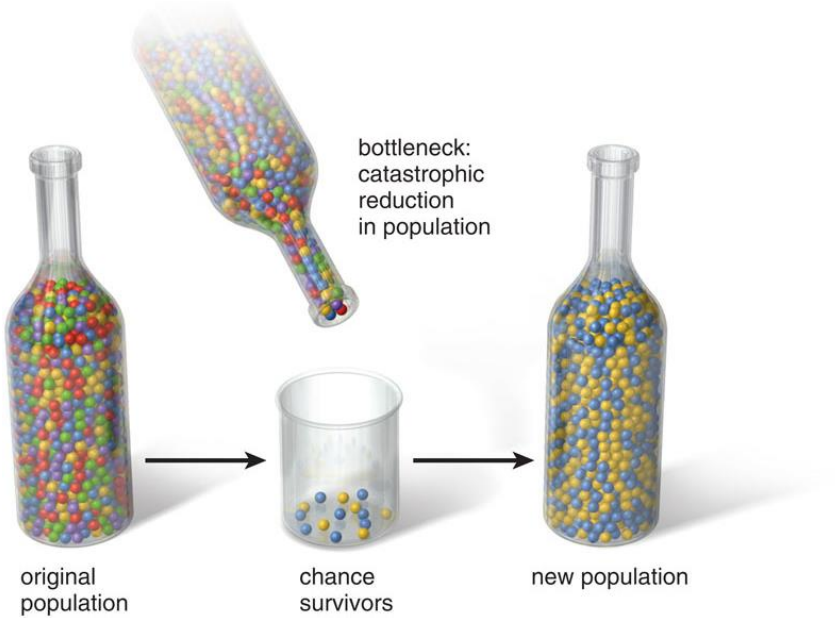


Fig. 3.3: The bottleneck effect. Shaking just a few marbles through the narrow neck of a bottle is analogous to a drastic reduction in the size of a population. By chance, the blue and yellow marbles are over-represented in the surviving population. The red and green marbles are totally eliminated.

- ***Example*****:** Northern elephant seals have reduced genetic variation probably because of a population bottleneck that humans inflicted on them in the 1890s. Hunting reduced their population size to as few as 20 individuals at the end of the 19th century. Their population has since rebounded to over 30,000, but their genes still carry the marks of this bottleneck: they have much less genetic variation than a population of southern elephant seals that was not so intensely hunted.

Effects of genetic drift: a summary

1. **Genetic drift is significant in small populations.** Chance events can cause allele to be disproportionately over- or under-represented in the next generation. Although chance events occur in populations of all sizes, they tend to alter allele frequencies substantially only in small populations.

2. **Genetic drift can cause allele frequencies to change at random.** Because of genetic drift, an allele may increase in frequency one year, then decrease the next; the change from year to year is not predictable. Thus, unlike natural selection, which in a given environment consistently favors some alleles over others, genetic drift causes allele frequencies to change at random over time.

3. **Genetic drift can lead to a loss of genetic variation within populations.** By causing allele frequencies to fluctuate randomly over time, genetic drift can eliminate alleles from a population. Because evolution depends on genetic variation, such losses can influence how effectively a population can adapt to a change in the environment.

4. **Genetic drift can cause harmful alleles to become fixed.** Alleles that are neither harmful nor beneficial can be lost or become fixed entirely by chance through genetic drift. In very small populations, genetic drift can also cause alleles that are slightly harmful to become fixed. When this occurs, the population's survival can be threatened.

3.4 Gene flow

- **Gene flow** is the movement of alleles into or out of a population due to movement of fertile individuals or their gametes. Gene flow increases variation within a population by introducing new alleles to another population (Fig. 3.4).

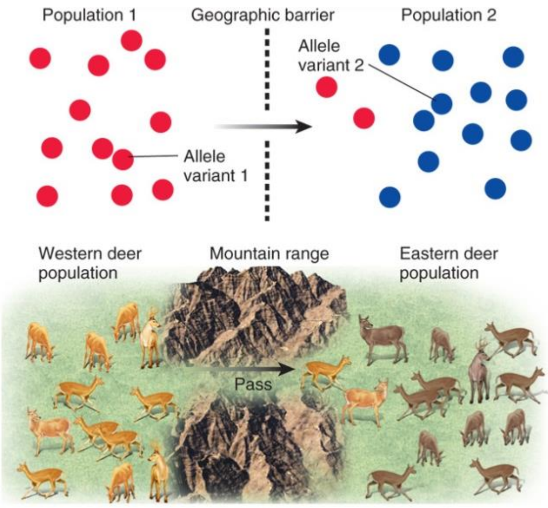


Fig. 3.4: Gene flow permits the introduction of allele 1 from population 1 to population 2, thus changing the allele frequency of allele 1 in population 2.

- Gene flow can transfer alleles that improve the ability of populations to adapt to local conditions.

- ***Example:*** Gene flow has resulted in the worldwide spread of several insecticide resistant alleles in the mosquito *Culex pipiens* (a vector of the West Nile virus). In their population of origin, these alleles increased because they provide insecticide resistance. These alleles were then transferred to new populations, where again, their frequencies increased as a result of natural selection.

- Gene flow has become an increasingly important agent of evolutionary change in human populations. Humans today move much more freely about the world than in the past. As a result, mating is more common between members of populations that previously had very little contact, leading to an exchange of alleles (through random mating) and fewer genetic differences between those populations.

- Interestingly, **reduced gene flow** between two populations of the same species, as a result of **isolations (e.g. geographical, behavioural)** can drive the evolution of the two populations into **two distinct species** over time.

3.5 Mutation

- A primary mechanism for microevolution is the formation of new alleles by *mutation*.

- New mutations can alter allele frequencies, but because mutations are rare, the change from one generation to the next is likely to be very small.

- Nevertheless, mutation ultimately **can have a large effect** on allele frequencies when it produces new alleles that confer **strong selective advantage** to the organism.

- **Mutations in gametes** will be **inherited** by the next generation whereas **mutations in somatic** cells **will not be inherited**. Hence mutations in gametes are more significant.

4. Speciation: the evolutionary process by which new species arise

- **Speciation** is an evolutionary process by which one species **diverges** into **two or more species** as a result of **accumulated genetic differences** due to **changes in allele frequencies** (*Section 3*).

- Speciation explains not only differences between species, but also similarities between them. When one species splits into two, the species that result share many **structural similarities** because they are **descended from a common ancestral species** ('*descend with modification*'). *(Fig. 4.1)*

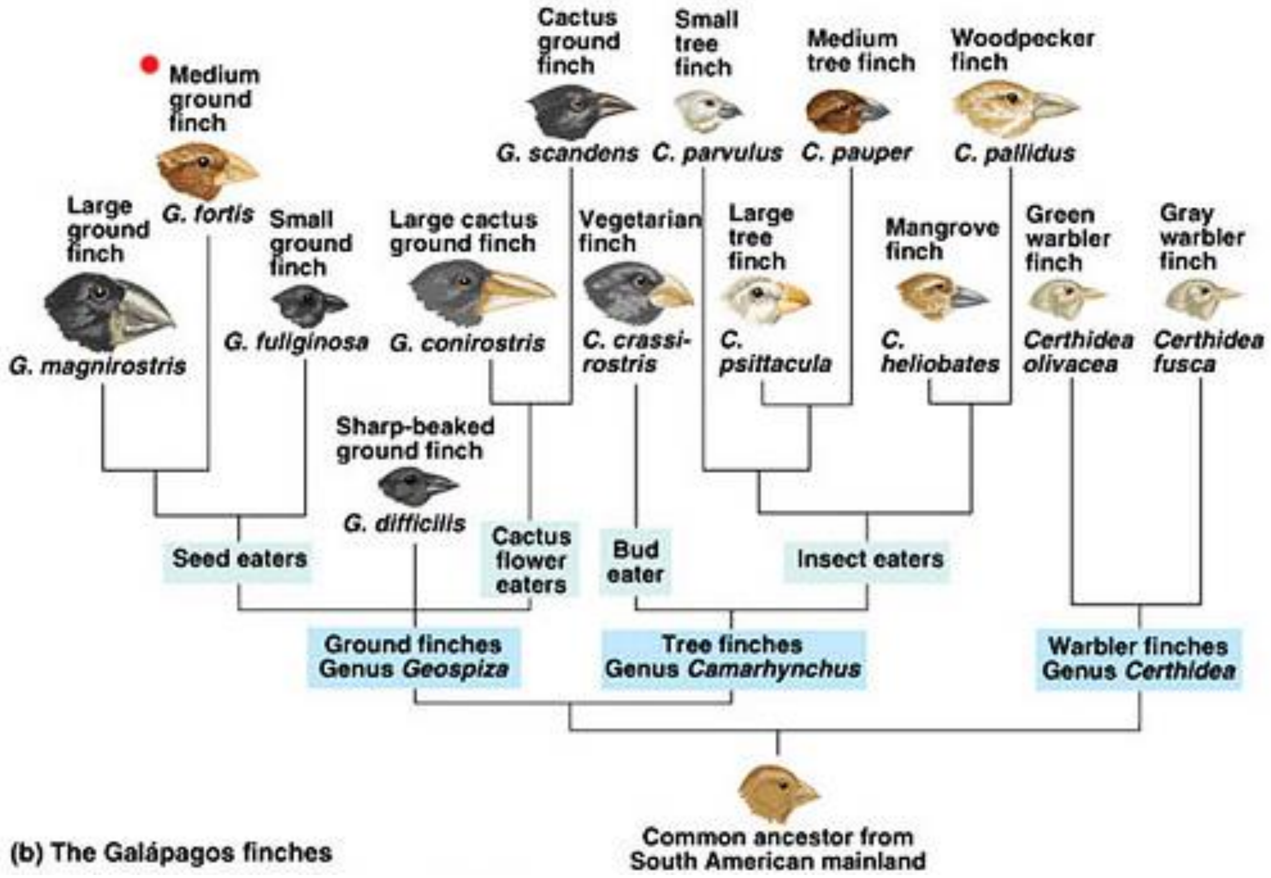


Fig. 4.1: Many species of the finches residing on the Galapagos Islands are thought to originate from one common ancestor through process of speciation. Though they look different from one another, they share many structural similarities for the fact that they descended from a common ancestral species.

4.1 The concepts of species

- *Species* is Latin for “kind”.
- *Species* is the basic unit of biological classification and a taxonomic rank (*Section 7*).
- Each species possess its own distinct structural, behavioural and ecological characteristics.
- A species may be defined in several ways – morphologically, biologically, phylogenetically, genetically and ecologically.
- There are advantages and disadvantages to each definition.

4.1.1 Biological species concept

- According to this concept, a species is a group of populations whose members have the potential to **interbreed in nature** and **produce viable and fertile offspring**.

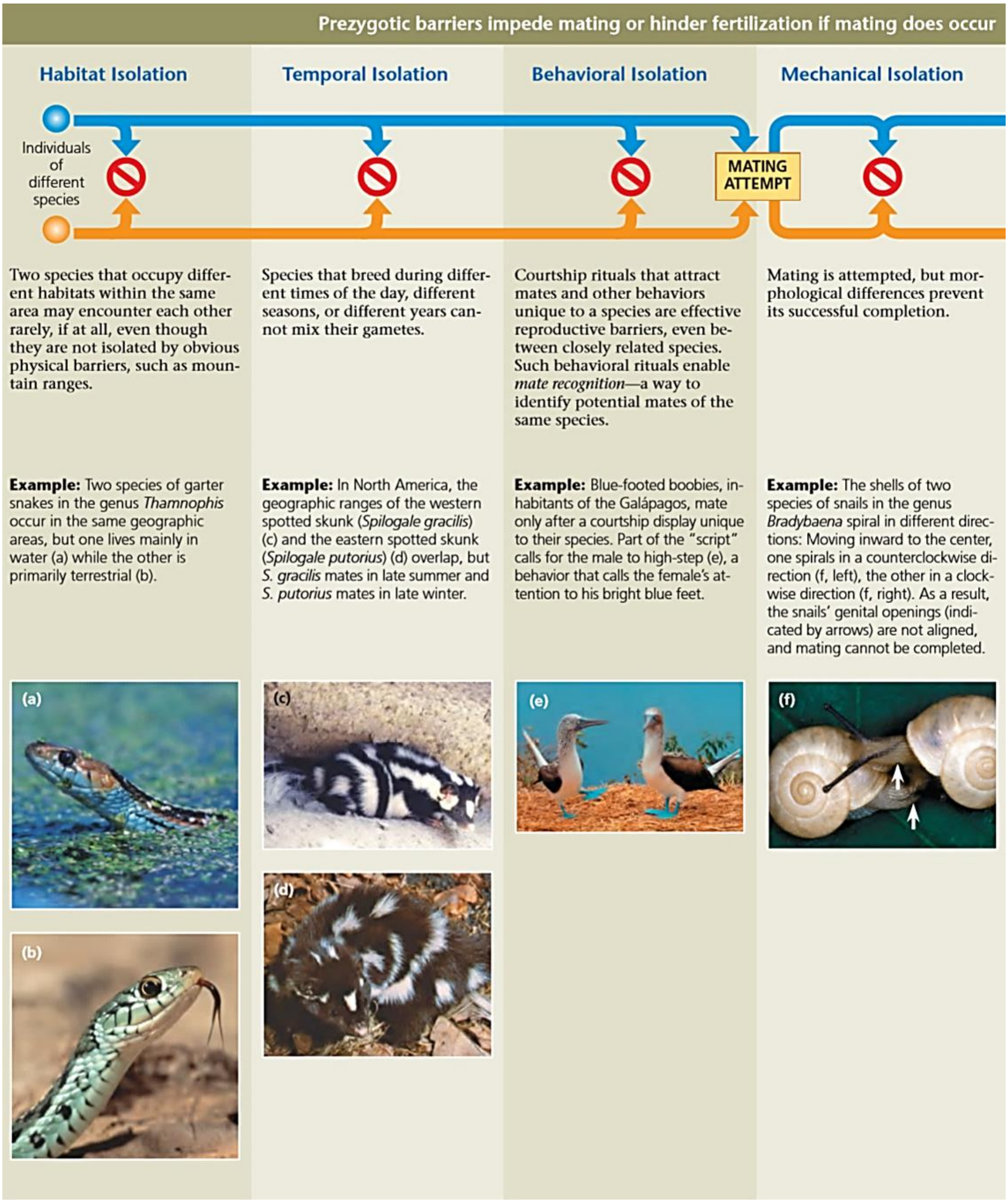
- The biological species concept emphasizes on **reproductive isolation** – the existence of biological barriers (Fig. 4.3) that impede members of two species from interbreeding and producing viable, fertile offspring.

- Thus, the members of a biological species are united by being reproductively compatible.

- This concept has the following **limitations**:

  - It cannot be applied to organisms that reproduce **asexually** e.g. bacteria.
  - It does not apply to **extinct species** known to us by fossil records as mating can no longer be observed.
  - There is significant difficulty involved in **observing mating in the wild**, especially for microscopic organisms, plants that reproduce via pollination and marine organisms that release their gametes into water. It would be impossible to determine which organism was mating with which.
  - There are many pairs of species (especially in plants) that are morphologically and ecologically distinct, and yet gene flow occurs between them. An example is the grizzly bear and polar bear, whose hybrid offspring has been dubbed ‘grolar bears’ (Fig. 4.2).

Fig. 4.2: Hybridization between two species of bears in the genus *Ursus*.



Prezygotic barriers impede mating or hinder fertilization if mating does occur

Habitat Isolation

Two species that occupy different habitats within the same area may encounter each other rarely, if at all, even though they are not isolated by obvious physical barriers, such as mountain ranges.

Example: Two species of garter snakes in the genus *Thamnophis* occur in the same geographic areas, but one lives mainly in water (a) while the other is primarily terrestrial (b).

Temporal Isolation

Species that breed during different times of the day, different seasons, or different years cannot mix their gametes.

Example: In North America, the geographic ranges of the western spotted skunk (*Spilogale gracilis*) (c) and the eastern spotted skunk (*Spilogale putorius*) (d) overlap, but *S. gracilis* mates in late summer and *S. putorius* mates in late winter.

Behavioral Isolation

Courtship rituals that attract mates and other behaviors unique to a species are effective reproductive barriers, even between closely related species. Such behavioral rituals enable *mate recognition*—a way to identify potential mates of the same species.

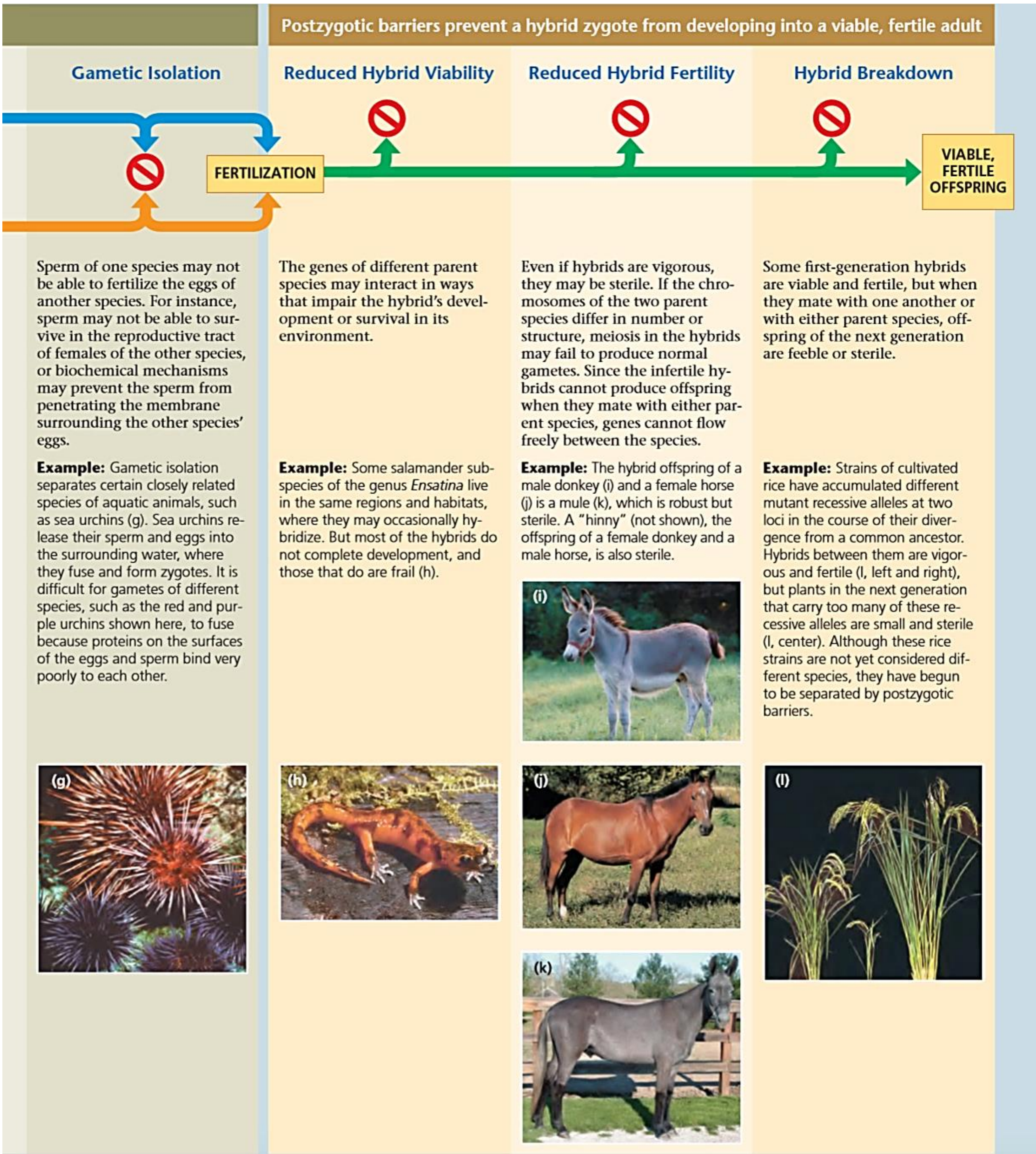
Example: Blue-footed boobies, inhabitants of the Galápagos, mate only after a courtship display unique to their species. Part of the "script" calls for the male to high-step (e), a behavior that calls the female's attention to his bright blue feet.

Mechanical Isolation

Mating is attempted, but morphological differences prevent its successful completion.

Example: The shells of two species of snails in the genus *Bradybaena* spiral in different directions: Moving inward to the center, one spirals in a counterclockwise direction (f, left), the other in a clockwise direction (f, right). As a result, the snails' genital openings (indicated by arrows) are not aligned, and mating cannot be completed.

Fig. 4.3: Various reproductive barriers that prevent two species from producing viable and fertile offspring.



Gametic Isolation

Sperm of one species may not be able to fertilize the eggs of another species. For instance, sperm may not be able to survive in the reproductive tract of females of the other species, or biochemical mechanisms may prevent the sperm from penetrating the membrane surrounding the other species' eggs.

Example: Gametic isolation separates certain closely related species of aquatic animals, such as sea urchins (g). Sea urchins release their sperm and eggs into the surrounding water, where they fuse and form zygotes. It is difficult for gametes of different species, such as the red and purple urchins shown here, to fuse because proteins on the surfaces of the eggs and sperm bind very poorly to each other.

Reduced Hybrid Viability

The genes of different parent species may interact in ways that impair the hybrid's development or survival in its environment.

Example: Some salamander subspecies of the genus *Ensatina* live in the same regions and habitats, where they may occasionally hybridize. But most of the hybrids do not complete development, and those that do are frail (h).

Reduced Hybrid Fertility

Even if hybrids are vigorous, they may be sterile. If the chromosomes of the two parent species differ in number or structure, meiosis in the hybrids may fail to produce normal gametes. Since the infertile hybrids cannot produce offspring when they mate with either parent species, genes cannot flow freely between the species.

Example: The hybrid offspring of a male donkey (i) and a female horse (j) is a mule (k), which is robust but sterile. A "hinny" (not shown), the offspring of a female donkey and a male horse, is also sterile.

Hybrid Breakdown

Some first-generation hybrids are viable and fertile, but when they mate with one another or with either parent species, offspring of the next generation are feeble or sterile.

Example: Strains of cultivated rice have accumulated different mutant recessive alleles at two loci in the course of their divergence from a common ancestor. Hybrids between them are vigorous and fertile (l, left and right), but plants in the next generation that carry too many of these recessive alleles are small and sterile (l, center). Although these rice strains are not yet considered different species, they have begun to be separated by postzygotic barriers.

Fig. 4.3 (cont'd): Various reproductive barriers that prevent two species from producing viable and fertile offspring.

4.1.2 Morphological species concept

- This concept defines a species in terms of a **unique set of structural/physical features.**

- Most of the species recognised by taxonomists are based on physical resemblance and differences (e.g. number of petals, type of leaves).

- Historically used since the time of Carolus Linnaeus in the 16th century (the "Father of Taxonomy") to classify organisms.

- Advantage: it can be applied to both asexual and sexual organisms.

- Limitations:

    - Similarity in structure does not equate an evolutionary relationship. E.g. Koalas of Australasia have evolved fingerprints that are very similar to those of humans, but humans (mammals) and koalas (marsupials) are not closely related.

    - This concept relies on subjective criteria; researchers may disagree on which structural features distinguish a species.

4.1.3 Phylogenetic species concept

- This concept defines a species as the **smallest set of organisms that share a common ancestor**, **forming one branch on the tree of life**.

- Biologists trace the phylogenetic history of a species by comparing its characteristics, such as morphology and/or molecular sequences, with those of other organisms.

- Such analyses can distinguish groups of individuals that are sufficiently different to be considered separate species.

- Advantage: it can be applied to both asexual and sexual organisms.

- Limitation: the difficulty with this species concept is determining the degree of difference required to indicate separate species.

4.1.4 Genetic species concept

- This concept defines species as a group of **genetically compatible, interbreeding** natural populations that is **genetically isolated from other such groups**.

- This concept focuses on **genetic isolation** rather than reproductive isolation which distinguishes the Genetic Species Concept from the Biological Species Concept.

- Genetic data from mitochondrial and nuclear genomes is used to study genetic differences in the genome of different species e.g. nucleotide differences in the mitochondrial cytochrome b gene of different species. (Refer to Section 5.1.2.1 on the use of multiple sequence alignment method to classify organisms)

- Limitation: Need to determine the magnitude of genetic difference required to indicate separate species.

4.1.5 Ecological species concept

- This ecological concept defines a species as a set of organisms adapted to the same **ecological niche**.

- An ecological niche is the sum total of how members of a species interact with the biotic (living) and abiotic (non-living) part in its environment.

- This concept defines a population of organisms which are **adapted to the same set of resources in their habitat**. The forms and behaviour of organisms are adapted to the resources they exploit and habitats they occupy. Each species will evolve to exploit resources that it is better adapted to.

- E.g. two species of salamanders might be similar in appearance but differ in the foods they eat or in their ability to tolerate dry conditions.

- Limitation**:** may be difficult to apply definition to species that are extinct as cannot be certain about its role in the biological community

- Advantage: accommodates **asexual species**, whereas the biological species concept does not.

4.2 Speciation as a result of reduced gene flow

- Speciation is the process of formation of a new species by which one species diverges from another at some point along the evolutionary timeline. Distinct species usually derive from one ancestral group.

- The definition of speciation would also depend on which concept is being used to define a species.

- By the most commonly used **biological species concept**, a new species is said to be formed when a population can **no longer interbreed** with another closely-related population to form **fertile and viable offspring**.

- As mentioned in *Section 3*, factors such as **natural selection**, **genetic drift**, **gene flow** and **mutations** can act on the population to drive evolution and eventually speciation.

- In this section, the focus is on how various **isolation factors** such as **geographical isolation**, **physiological isolation** and **behavioural isolation** reduce gene flow and hence promote evolution and eventually speciation.

4.2.1 Geographical isolation

- Geographical isolation **reduces gene flow between the two groups within the population**.

- **Different mutations** arise, **natural selection** (due to different selection pressures in the two environments) and **genetic drift** may **alter allele frequencies in different ways** in the separated populations.

- Over time, as the isolated populations **accumulate different types of advantageous alleles**, the **gene pool from the two populations becomes so distinct** that members of the populations will **no longer be able to interbreed**, resulting in two populations becoming **reproductively isolated from one and other**.

- When this happens, by the biological species concept, the two populations become two new species.

- When new species are formed as a result of such geographical isolation, it is known as **allopatric speciation** as opposed to **sympatric speciation**, where no geographical isolation is involved. (*Section 4.2.2 and 4.2.3*)

- Geographical isolation may occur in two ways (Fig. 4.4):
    - A group colonizes a new habitat (the founder effect)
    - New physical barrier divides a population

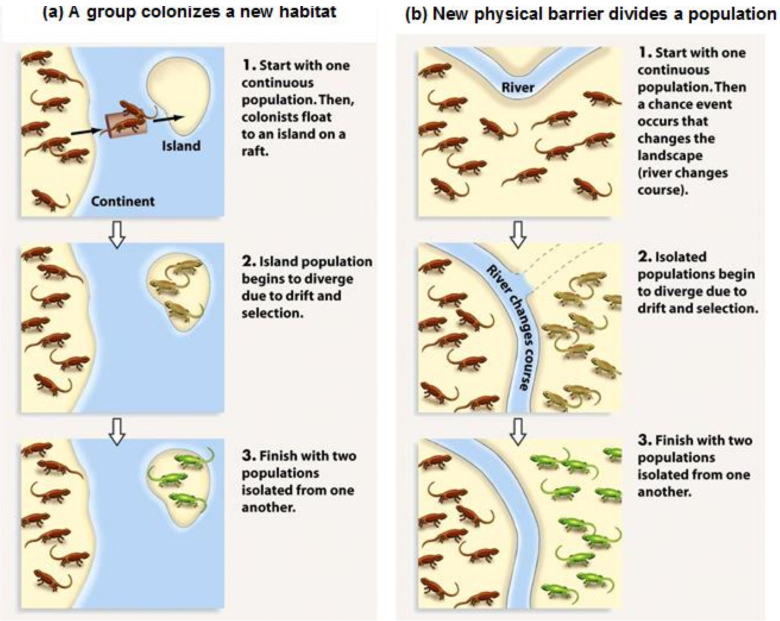


Fig. 4.4: Allopatric speciation involves geographical barrier that prevents gene flow between the two populations.

- *Example 1* – The two species of antelope squirrels inhabiting opposite rims of the Grand Canyon (Fig. 4.5)

Fig. 4.5: Two species of antelope squirrels inhabit opposite rims of the Grand Canyon.
On south rim is Harris's antelope squirrel (*Ammospermophilus harrisi*) and on the north rim is the closely related white-tailed antelope squirrel (*Ammospermophilus leucurus*).

- *Example 2* – Salamanders from the Central Valley in California (Fig. 4.6)

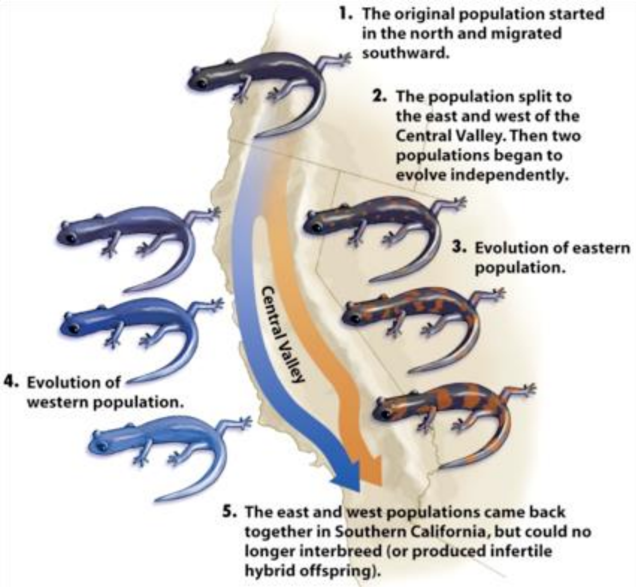


Fig. 4.6: Allopatric speciation in Salamanders. When the western and eastern salamanders finally meet again at the south of Central Valley, they have accumulated enough genetic differences (due to mutations, changes in allele frequency etc.) that they are no longer able to interbreed.

4.2.2 Physiological isolation

- The formation of a new species hinges on **reproductive isolation** as define by Biological Species Concept. The existence of biological factors (barriers) can impede members of two species from interbreeding and producing viable, fertile offspring. Such new species are formed **without geographical isolation**. This is known as **sympatric speciation**.

Examples of physiological isolation:

(1) Mechanical isolation

- The incompatibility of the anatomical structure of the reproductive organs prevents the transfer of gametes between species (Fig. 4.7).

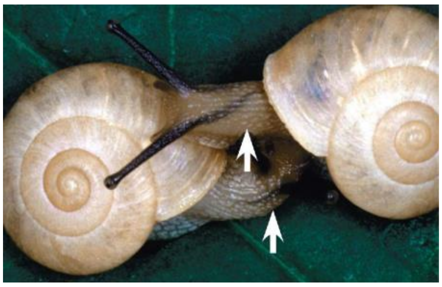


Fig. 4.7: Mechanical isolation – The shells of two species of snails in the genus *Bradybaena* spiral in different directions: Moving inward to the center, one spirals in a counterclockwise direction (left), the other in a clockwise direction (right). As a result, the snails' genital openings (indicated by arrows) are not aligned, and mating cannot be completed.

(2) Gametic isolation

- Sperm of one species may not be able to fertilize the eggs of another species. For instance, sperm may not be able to survive in the reproductive tract of females of the other species, or biochemical mechanisms may prevent the sperm from penetrating the membrane surrounding the other species' eggs.

- Gametic recognition may be based on the presence of specific molecules on the coat around the egg which may adhere only to complementary molecules on the sperm cells of the same species.

- For example, gametic isolation separates certain closely related species of aquatic animals, such as sea urchins. Sea urchins release their sperm and eggs into the surrounding water, where they fuse and form zygotes. It is difficult for gametes of different species, such as the red and purple urchins, to fuse because proteins on the surfaces of the eggs and sperm bind very poorly to each other.

(3) Reduced Hybrid Viability

- Genetic incompatibility between the two species may abort development of the hybrid zygote at some embryonic stage.

- For example, some salamander subspecies of the genus *Ensatina* live in the same regions and habitats, where they may occasionally hybridize. But most of the hybrids do not complete development, and those that do are frail. Thus they cannot become one single species.

(4) Reduced Hybrid Fertility

- Even if hybrid is vigorous, they may be sterile. If the chromosomes of the two parent species differ in number or structure, meiosis in the hybrids may fail to produce normal gametes. Since the infertile hybrids cannot produce offspring when they mate with either parent species, genes cannot flow freely between the species.

- For example, the hybrid offspring of a male donkey and a female horse is a mule, which is robust but sterile. A “hinny”, the offspring of a female donkey and a male horse, is also sterile.

(5) Temporal isolation

- Different species have different mating seasons or flowering seasons. Different species may also become **sexually mature at different times** of the year, hence decreasing the possibility of reproduction.

4.2.3 Behavioral isolation

- Behavioral isolation, a type of isolating mechanism, occurs when two populations are capable of interbreeding but have **differences in courtship rituals** or other behavourial strategies that prevents mating.

- Many insects and animals like birds have **species-specific mating displays** which include visual, olfactory, auditory and tactile stimuli.

- For example, the eastern and western meadowlarks (Fig. 4.8) have similar body shapes and colorations. However, because their **courtship songs and other behaviors are different enough, they do not interbreed should they meet in the wild**. Gene flow between them is prevented.

Fig. 4.8: The eastern meadowlark (*Sturnella magna*, left) and the western meadowlark (*Sturnella neglecta*, right).

5. Evidence that support the theory of natural selection and evolution

- In *The Origin of Species*, Darwin lamented the lack of fossils showing how earlier groups of organisms gave rise to new groups.

- In the last 150 years, new discoveries have filled many of the gaps that Darwin identified. In this section, three types of data that document the pattern of evolution and illuminate the processes by which it occurs will be explained – **homology**, the **fossil record**, and **biogeography**.

5.1 Homology

- A first type of evidence for evolution comes from analysing similarities among different organisms. **Evolution** is a process of **descent with modification**: Characteristics present in an ancestral organism are altered in the population of descendants over time as they face different environmental conditions.

- As a result, related species can have characteristics that have an underlying similarity yet function differently. **Similarity resulting from common ancestry** is known as **homology**. ***The more recently two species have shared a common ancestor, the more homologies they share, and the more similar these homologies are.***

5.1.1 Anatomical homology

- Anatomy involves the study of the **physical structures of living organisms**.

- Similarities in structure or the **presence of <u>homologous structures</u> in different species** is known as **homology**. Homology amongst species is hypothesized to have arisen via evolution. Certain species exhibit similar structures because they have a **common ancestor**.

- Example 1: Homologous Structure: pentadactyl limbs of mammals
  - The **pentadactyl forelimbs** of all **mammals**, including humans, cats, whales, and bats, showed a **common basic plan** with the **same arrangement of bones** from the shoulder to the tips of the digits, even though these appendages have very **different functions**: lifting, walking, swimming, and flying (Fig. 5.1).

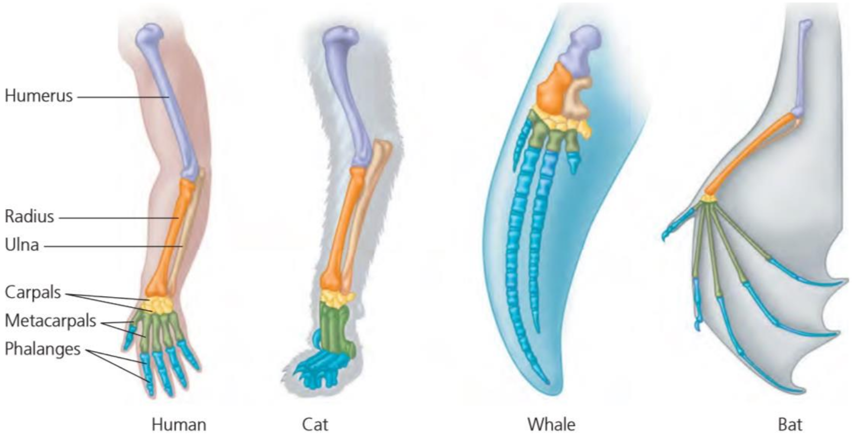


Fig. 5.1: Mammalian pentadactyl limbs: homologous structures. Even though they have become adapted for different functions, the forelimbs of all mammals are constructed from the same basic skeletal elements: one large bone (purple), attached to two smaller bones (orange and tan), attached to several small bones (gold), attached to several metacarpals (green), attached to approximately five digits, each of which is composed of phalanges (blue).

- Example 2: Homologous Structure: Beaks of the Galapagos finches (Fig. 5.2)
    - Previously, the finches occupied the South American mainland, but somehow managed to arrive at the Galapagos Islands, over 600 miles away. They occupied an ecological niche with little competition.
    - As the population began to flourish in these advantageous conditions, there is **intra-specific** (within species) **competition** for food on the islands.
    - There is **variation** (already exists) in the size of beak in the finches due to **genetic differences** as a result of **mutations**.
    - The different environments of the different islands each exerts a **different selection pressure** (e.g. type of food) on the birds with different size of beak.
    - Those with the **advantageous allele** will be **selected for** and survive to **pass on the advantageous allele** to reproduce viable and fertile offspring.
    - Over many generations, the **accumulation of genetic differences** eventually leads to the formation of distinct species from a single ancestral one where the different species **can no longer interbreed** to reproduce **fertile and viable offspring** (biological species concept).
    - The different species of Darwin's finches share a **homologous structure** (beak) that is **modified from that of a common ancestor** and specialised to perform a variety of **different functions**, e.g. to feed on different types of food

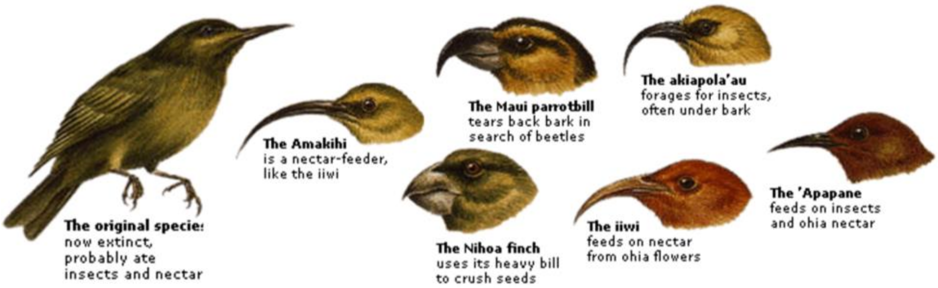


Fig. 5.2: The Galapagos finches show variation in their beaks, each adapted for a particular type of food.

5.1.1.1 Fossil records

- The fossil record documents the pattern of evolution, showing that past organisms differed from present-day organisms and that many species have become extinct. Fossils also show the evolutionary changes that have occurred in various groups of organisms.

- Fossil records are the **preserved remains** of the **ancestral species** of plants and animals. They include bones, shells, imprints of organisms preserved in stone and preserved footprints.

- Fossil record shows that over time, **descent with modification** produced increasingly large differences among related groups of organisms, ultimately resulting in the diversity of life we see today.

- Fossil records are important in helping scientists establish evolutionary relatedness based on homology because they:

  1. allow geologists to **estimate the time of existence** of the organism through carbon-dating (Fig. 5.3) or determining the geological strata (Fig. 5.4) in which fossil was found.

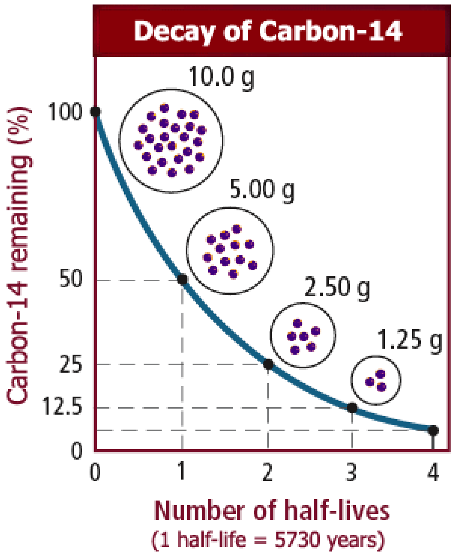


Fig. 5.3: Through photosynthesis, plants absorb both forms of Carbon, 12 and 14, from carbon dioxide in the atmosphere. Animals eat plants, other animals eat animals and thus every living organism has carbon 12 and 14 in same ratio as it is in atmosphere. As soon as a living organism dies, it stops taking in new carbon. Carbon-12 being stable remains same but the carbon-14 decays and is not replaced. By looking at the ratio of carbon-12 to carbon-14 in the fossil and comparing it to the ratio in a living organism, it is possible to determine the age of a formerly living thing fairly precisely. If Carbon-14 content is 50% of usual ratio that means fossil is 5700 years old, if it is 25% then fossil is about 11000 years old.

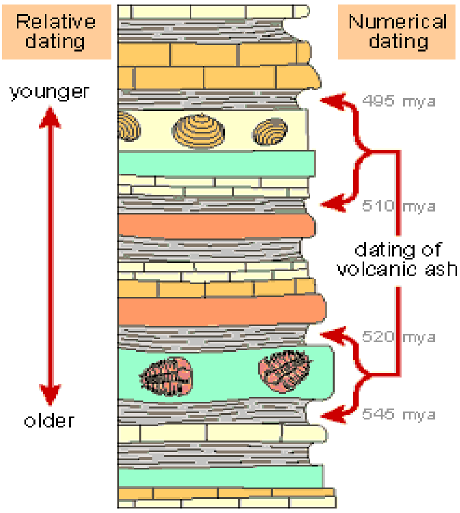


Fig. 5.4: Fossils are generally found in sedimentary rock. Sedimentary rocks can be dated using radioactive carbon, but because carbon decays relatively quickly, this only works for rocks younger than about 50-60 thousand years. So in order to date older fossils, scientists look for layers of igneous rock or volcanic ash above and below the fossil. Scientists date igneous rock using elements that are slow to decay, such as uranium and potassium. By dating these surrounding layers, they can figure out the youngest and oldest that the fossil might be.

2. allow scientists to hypothesize how the **organism looked like in the past**.
3. allow evolutionary biologists to study the **structure of extinct species** in order to discover possible evolutionary relationships between past and present species (Fig. 5.5).

Fig. 5.5: A fossil of the megacheiran (an extinct class of arthropod that possessed enlarged appendages) *Leanchoilia illecebrosa*, showing its characteristic forceps-like great appendages. This species is a close relative of the more rare *Alalcomenaeus* and is likewise a distant relative of scorpions and spiders.

4. provide evidence of **transitional forms** along the evolutionary history – the intermediate species that link ancestral species with modern species (Fig. 5.6).

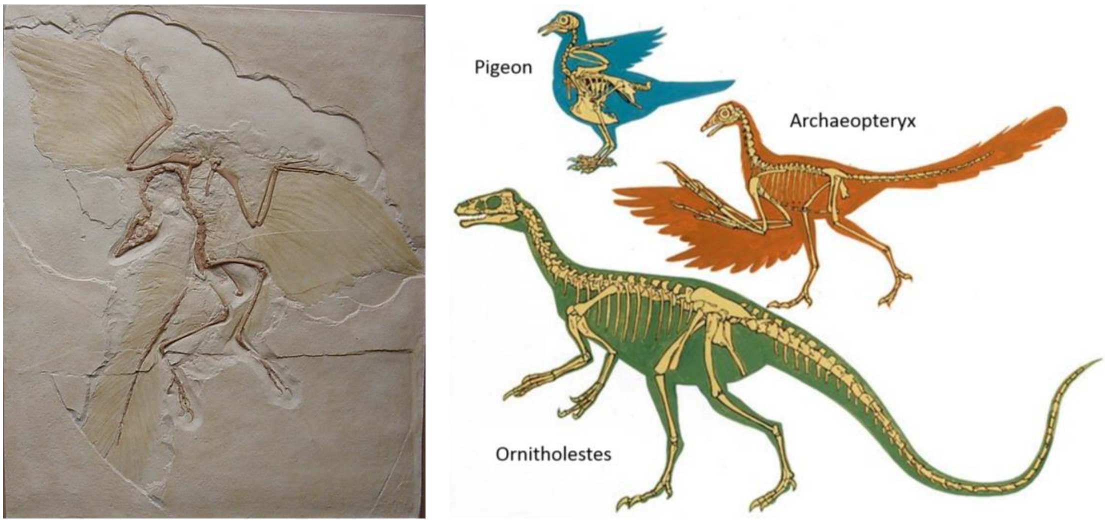


Fig. 5.6: A particularly important and still contentious discovery is *Archaeopteryx lithographica* found in the Jurassic Solnhofen Limestone of southern Germany, which is marked by rare but exceptionally well preserved fossils. Archaeopteryx is considered by many to be the first bird, being of about 150 million years of age. It is hypothesized to be an intermediate between the birds that we see flying around in our backyards and the predatory dinosaurs like Ornitholestes.

5.1.2 Molecular Homology

- Molecular homologies can be used to determine evolutionary relatedness.

- Every organism has DNA or RNA as its genetic material. This genetic material is inherited by offspring.

- When an ancestral species gives rise to two or more descendants, those descendants will initially exhibit fairly high overall similarity in their DNA. However, as the descendants evolve independently, they will **accumulate more and more differences in their DNA**.

- Hence, organisms that are **more distantly related will accumulate a greater number of differences in DNA sequence**, whereas **two species that are more closely related should share a greater similarity in their DNA sequence**.

- The molecular differences between homologous molecules of related species are due to different **selection pressures** in different environments acting on existing variation. Over many generations, **changes in allele frequencies** occur. In addition, **mutations** lead to **changes in nucleotide sequences** or **changes in amino acid sequences** in proteins, which is evidence that evolution occurred (Fig. 5.7, *haemoglobin polypeptide as an example*).

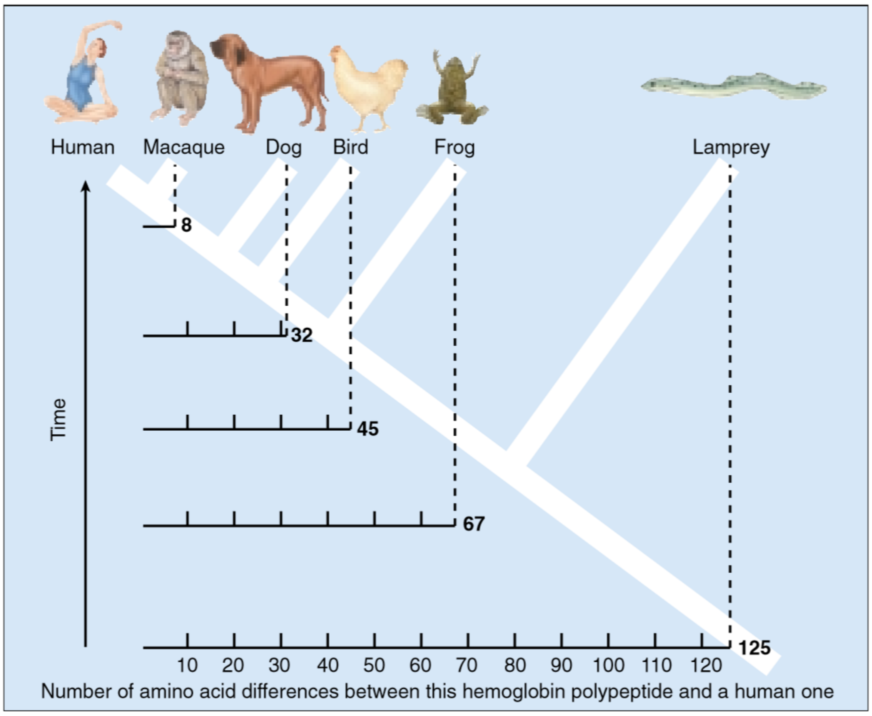


Fig. 5.7: Molecules reflect evolutionary divergence. You can see that the greater the evolutionary distance from humans, the greater the number of amino acid differences in the vertebrate hemoglobin polypeptide.

5.1.2.1 DNA homology

- All organisms utilize the **same kind of nucleotides** to synthesize their genetic material (DNA).
- The **more closely related two species are**, the **fewer nucleotide base pair differences** they have.
- Similarities in **homologous DNA sequences** imply a **common ancestry**.

(A) Comparison of nucleotide sequences through multiple sequence alignment

- **Homologous DNA sequences** from two species are **aligned** and **compared**. (Fig. 5.8)

- With the aid of computer programs, the exact **number of nucleotide differences** between two species can be accurately **determined**.

- The **more identical the DNA nucleotide sequences** of the two species, the **more recently** they would have **evolved from a common ancestor**. Thus, the **more closely related** they would be.

- **Mitochondrial DNA** (mtDNA) is commonly used to determine the phylogenetic relationship between species. Phylogenetic relationship shows how species are related to a common ancestor.

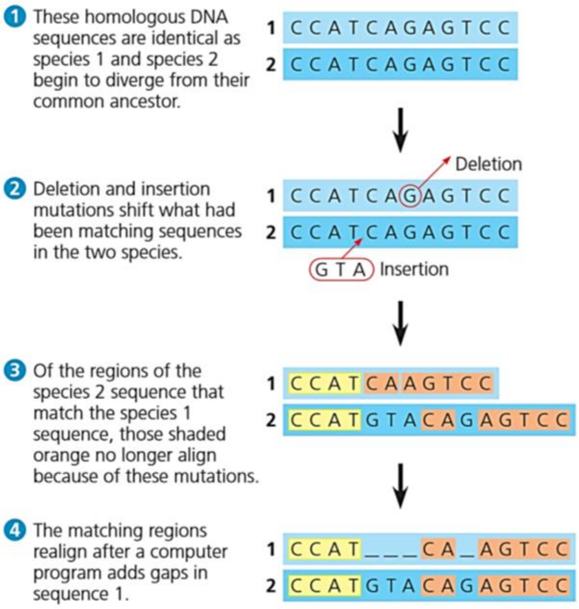


Fig. 5.8: Aligning segments of DNA. Systematists search for similar sequences along DNA segments from two species (only one DNA strand is shown for each species). In this example, 11 of the original 12 bases have not changed since the species diverged. Hence, those portions of the sequences still align once the length is adjusted.

Properties of mtDNA (Fig. 5.9)

- Animal mtDNA is a small (15-20 kb) circular molecule, composed of 37 genes coding for 22 tRNAs, 2 rRNAs and 13 mRNAs.

- The mRNAs code for proteins involved in electron transport and oxidative phosphorylation.

- mtDNA **lacks introns**

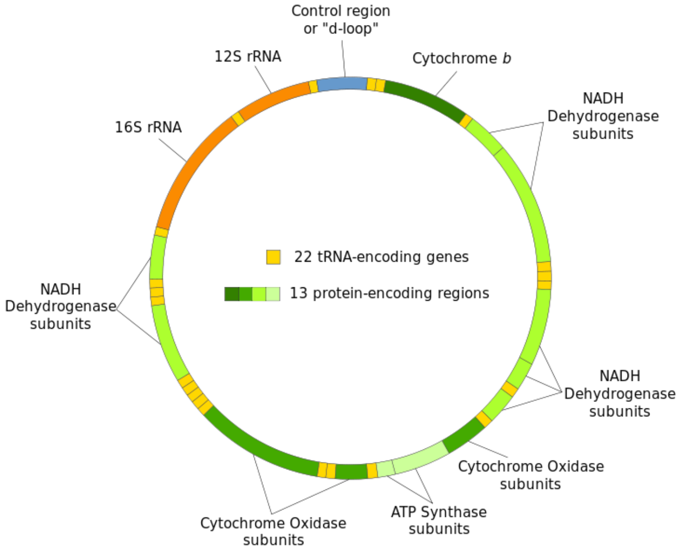


Fig. 5.9: Mitochondrial DNA and the genes it carries.

Why mtDNA is commonly used for phylogenetic studies

1. mtDNA is present in all eukaryotes.

2. mtDNA has a **high level of genetic variation** due to high rate of mutation in the **non-coding sequences** (control region) which can be used to determine phylogenetic relationships among **recently diverged species**. This high rate of mutation of mtDNA is due to the absence of DNA repair mechanism in mitochondria.

3. Mitochondrial **genes** encode many proteins involved in **respiration** (e.g. cytochrome oxidase) and **genes** that code for the **ribosomal RNA** (e.g. 16S rRNA gene). Hence, **mutations** to these genes are likely to be **lethal in an individual**, and therefore are less likely to be passed on to offspring. Hence, over time in a **population**, these **genes evolve at a much slower rate** (highly conserved) and are useful in determining phylogenetic relationships among species that **diverged hundreds of millions of years ago**.

4. mtDNA **lacks germline recombination** i.e. there is no crossing over, independent assortment of mtDNA. Thus, variation in the mtDNA sequence is largely by mutation.

5. mtDNA is **inherited through the maternal line**. This enables genealogical researchers to trace maternal lineage far back in time.

6. The probability of recovery of mtDNA from very small or degraded biological samples is higher than the one of nuclear DNA, because the mitochondrial DNA molecules exist in **thousands of copies per cell**, while nuclear DNA has only two copies per cell

(B) Total genome comparison through DNA-DNA hybridization

- DNA-DNA hybridisation provides a way of comparing the **total genome** of two or more species.

- This method operates on the basic principle of complementary base-pairing and the denaturation of the DNA molecule.

- Fig. 5.10 illustrates the process of DNA-DNA hybridisation. This is an example of how DNA can be studied to look for evidence of evolution.

- In this technique, DNA obtained from different species are allowed to form DNA-DNA hybrids. DNA-DNA hybrids with **more complementary regions** will **denature at higher temperatures** (due to higher number of hydrogen bonds) while DNA-DNA hybrids with fewer complementary regions will denature at lower temperatures.

- **Species with more complementary regions** between them are considered to be **more closely related** than species that exhibit fewer complementary regions.

- When this technique was applied to primate relationships, it suggested that humans and chimpanzees carry DNA more similar to each other than to the DNA of orang-utans or gorillas.

DNA-DNA Hybridisation

1) First, DNA samples are obtained and cut into fragments using enzymes.

2) These DNA fragments can be denatured by heating to give single-stranded DNA.

3) The single-stranded DNA from two or more species is then mixed together and allowed to hybridise back into the double-stranded form.

4) Complementary regions of DNA from different species can form complementary base pairing between them, forming hybrid double-stranded DNA.

5) As they are different species, the match between the two strands will not be perfect since there are genetic differences between the species.

6) The more imperfect the match (or the fewer the complementary regions present), the weaker the attraction between the two strands.

7) The hybrid double-stranded DNA is then heated again and the temperature at which 50% of the DNA hybrid double-stranded DNA have been denatured is determined.

8) Hybrids with more complementary regions will denature a higher temperatures while hybrids with fewer complementary regions will denature at lower temperatures.

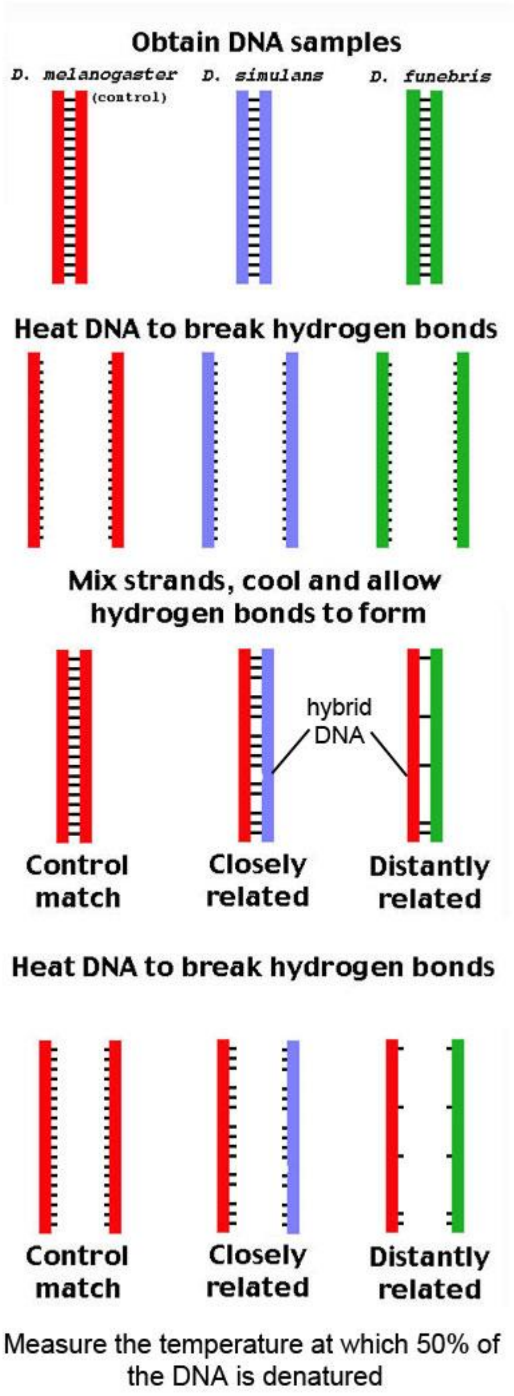


Fig. 5.10: How DNA-DNA hybridization is carried out.

5.1.2.2 Protein homology

- All organisms utilize the same set of amino acids to synthesize proteins.

- Phylogenetic relationships can be studied using the analysis of molecular structure of proteins of the organism.

  - Haemoglobin is a **protein molecule** responsible for the transport of oxygen in the blood of certain animals.

  - It comprises **two alpha** and **two beta chains**.

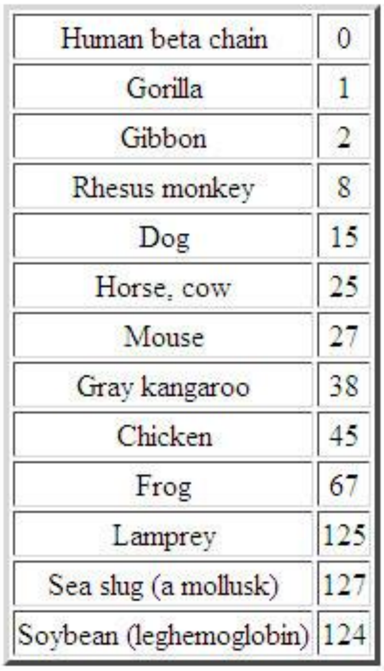
  - The **primary structure** (i.e. **amino acid sequence**) of haemoglobin chains can be analysed through multiple sequence alignment to determine the relatedness of different species.

  - The numbers in Fig. 5.11 represent the number of **amino acid differences** between the **beta chain** (146 amino acids) of human haemoglobins and the haemoglobins of other species.

  - For example, a gibbon's haemoglobin differs from human haemoglobin by two amino acids

  - In general, the number is **inversely proportional** to **the closeness of relationship**.

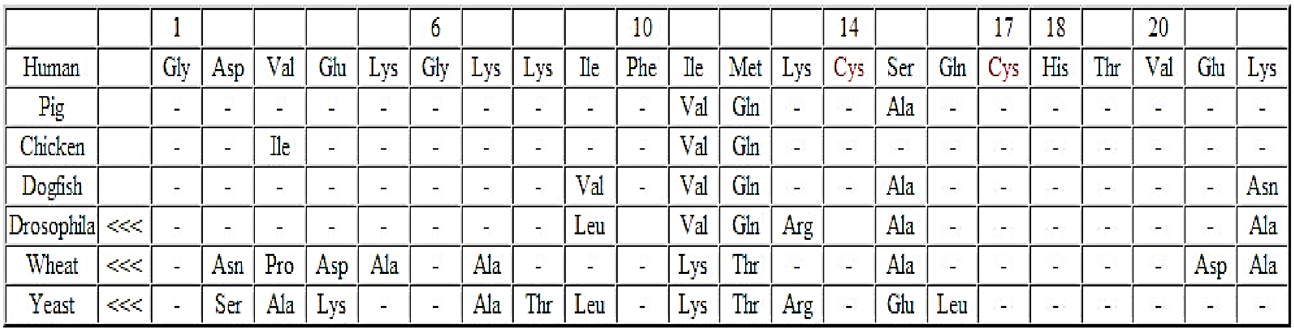
  - As seen from Fig. 5.11, humans and gorillas differ by one amino acid while humans and soybean plants differ by 124 amino acids.



Human beta chain	0
Gorilla	1
Gibbon	2
Rhesus monkey	8
Dog	15
Horse, cow	25
Mouse	27
Gray kangaroo	38
Chicken	45
Frog	67
Lamprey	125
Sea slug (a mollusk)	127
Soybean (leghemoglobin)	124

Fig. 5.11: Amino acid differences in haemoglobin (the beta chain) of different species.

- Another popular protein commonly used for phylogenetic studies in **cytochrome c** (Fig. 5.12), an electron carrier found in the inner mitochondrial membrane for respiration.



		1					6				10				14			17	18		20		
Human		Gly	Asp	Val	Glu	Lys	Gly	Lys	Lys	Ile	Phe	Ile	Met	Lys	Cys	Ser	Gln	Cys	His	Thr	Val	Glu	Lys
Pig		-	-	-	-	-	-	-	-	-	-	Val	Gln	-	-	Ala	-	-	-	-	-	-	-
Chicken		-	-	Ile	-	-	-	-	-	-	-	Val	Gln	-	-	-	-	-	-	-	-	-	-
Dogfish		-	-	-	-	-	-	-	-	Val	-	Val	Gln	-	-	Ala	-	-	-	-	-	-	Asn
Drosophila	<<<	-	-	-	-	-	-	-	-	Leu		Val	Gln	Arg		Ala	-	-	-	-	-	-	Ala
Wheat	<<<	-	Asn	Pro	Asp	Ala	-	Ala	-	-	-	Lys	Thr	-	-	Ala	-	-	-	-	-	Asp	Ala
Yeast	<<<	-	Ser	Ala	Lys	-	-	Ala	Thr	Leu	-	Lys	Thr	Arg	-	Glu	Leu	-	-	-	-	-	-

Fig. 5.12: The amino acid sequence of part of cytochrome c protein from various species were aligned and compared. Dash (-) indicates that the amino acid is the same one found at that position in the human cytochrome c.
From this data, with just 3 amino acid difference, pig is most closely related to human. Yeasts, with 11 amino acid difference, is the most distantly related to human.

  - Cytochrome *c* is found in the **mitochondria** of **every aerobic eukaryote including plants and animals**. The amino acid sequences of many of these cytochrome c molecules have been determined and comparisons have shown that they are related.

  - Human cytochrome *c* contains 104 amino acids and 37 of these have been found at **equivalent positions** in every cytochrome *c* that has been sequenced. It was assumed that each of these molecules has descended from a precursor cytochrome in a primitive microbe that existed over 2 billion years ago. In other words, these **molecules are homologous across species and originated from the common ancestor of the eukaryotes**.

  - The first step in comparing cytochrome *c* sequences is to **align them to find the maximum number of positions that have the same amino acid**. As in the previous example, the primary structure of the protein is compared across species.

  - **The more identical amino acid positions** there are between two molecules of different organisms, **the more recently they have evolved from a common ancestral molecule** and thus the more closely related.

5.1.3 Biogeography

- Biogeography is the **study of the geographical distributions of animals and plants**, including fossils.

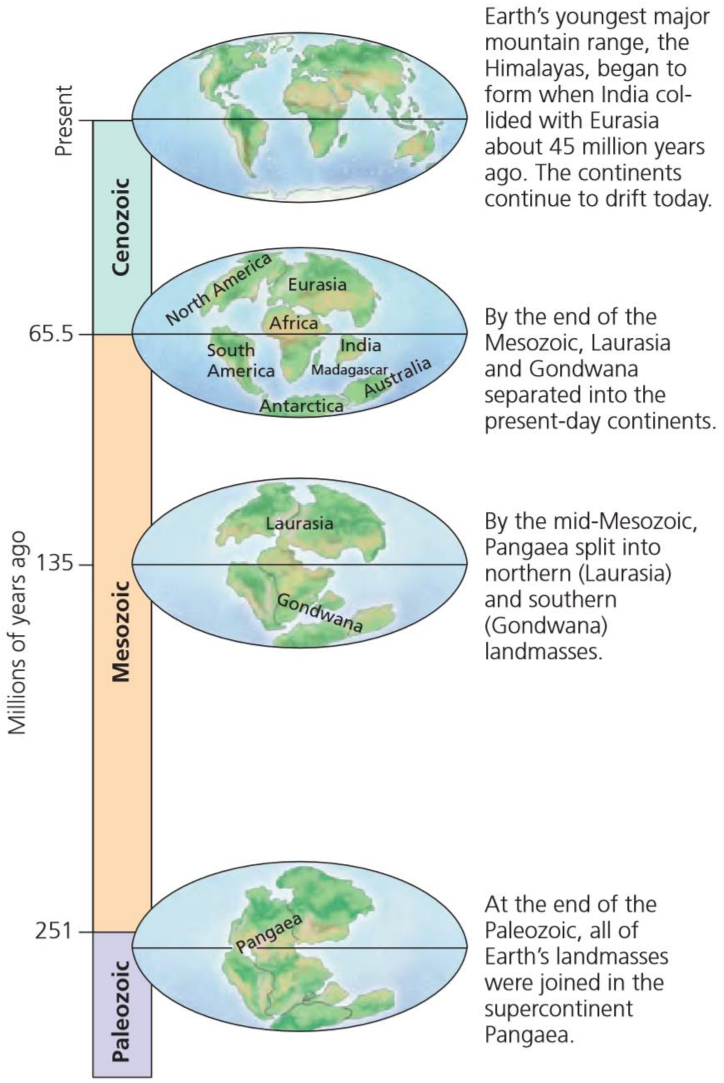
- The geographical distribution of organisms allows scientists to hypothesise how certain species can evolve into different species via divergent evolution when subjected to **different environments**. The **distribution of fossils** also provides evidence for evolution in the past.

- Species tend to be **more closely related to other species from the same area** than to other species with the same way of life but living in different areas.

Example 1: The Continent of Pangaea and continental drift

- The geographic distribution of organisms is influenced by many factors, including continental drift, the slow movement of Earth's continents over time.

- About 250 million years ago, these movements united all of Earth's landmasses into a single large continent called Pangaea. Roughly 200 million years ago, Pangaea began to break apart; by 20 million years ago, the continents we know today were within a few hundred kilometres of their present locations (Fig. 5.13).



Earth's youngest major mountain range, the Himalayas, began to form when India collided with Eurasia about 45 million years ago. The continents continue to drift today.

By the end of the Mesozoic, Laurasia and Gondwana separated into the present-day continents.

By the mid-Mesozoic, Pangaea split into northern (Laurasia) and southern (Gondwana) landmasses.

At the end of the Paleozoic, all of Earth's landmasses were joined in the supercontinent Pangaea.

Fig. 5.13: The history of continental drift during the Phanerozoic eon.

- The separation of the continents would explain why **some species on different continents share common phylogenetic lineages**.

- Continental drift also promotes **allopatric speciation** on a grand scale. When supercontinents break apart, regions that once were connected become **geographically isolated**. As the continents drifted apart over the last 200 million years, each became a separate evolutionary arena, with lineages of plants and animals that diverged from those on other continents

- Evidence for this include:

  1. Fossils of reptiles found in South Africa were also found in Brazil and Argentina in South America (Fig. 5.14).

  2. Fossils of amphibians and reptiles found in Antarctica were also found in South Africa, India, and China (Fig. 5.14).

  3. Most of the marsupial mammals alive today are confined to South America and Australia. But if these two continents were connected by Antarctica in the Mesozoic (Fig. 5.15), one might expect to find fossils of marsupials there. In March 1982, this prediction was fulfilled with the discovery of the remains of Polydolops, a 9-ft marsupial, in Antarctica.

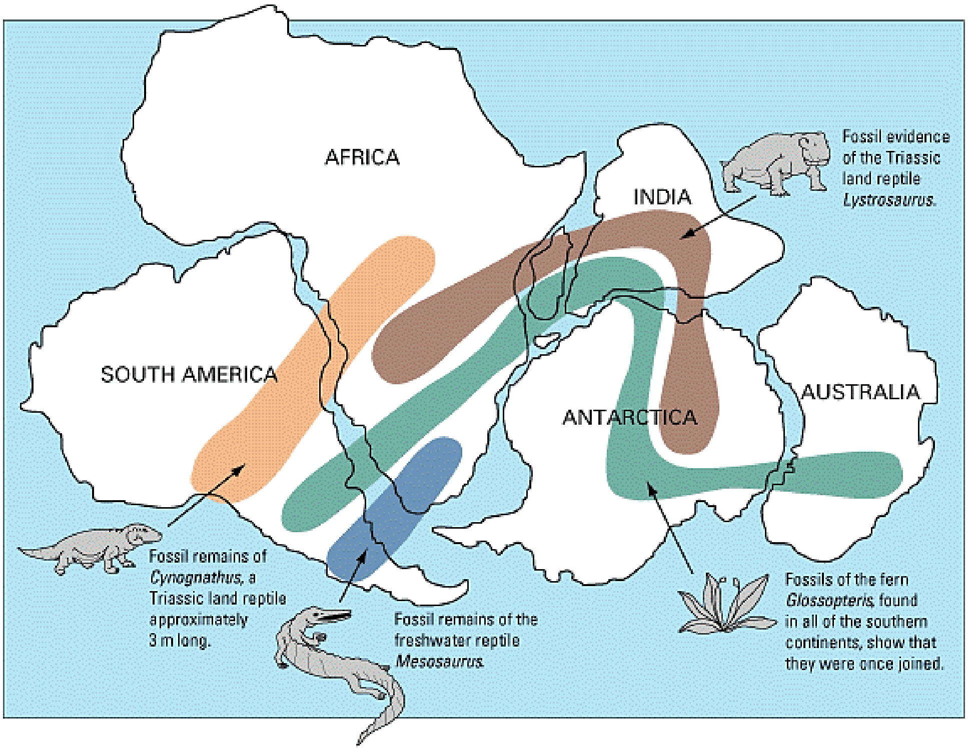


Fig. 5.14: The distribution of fossil remains across the continents.

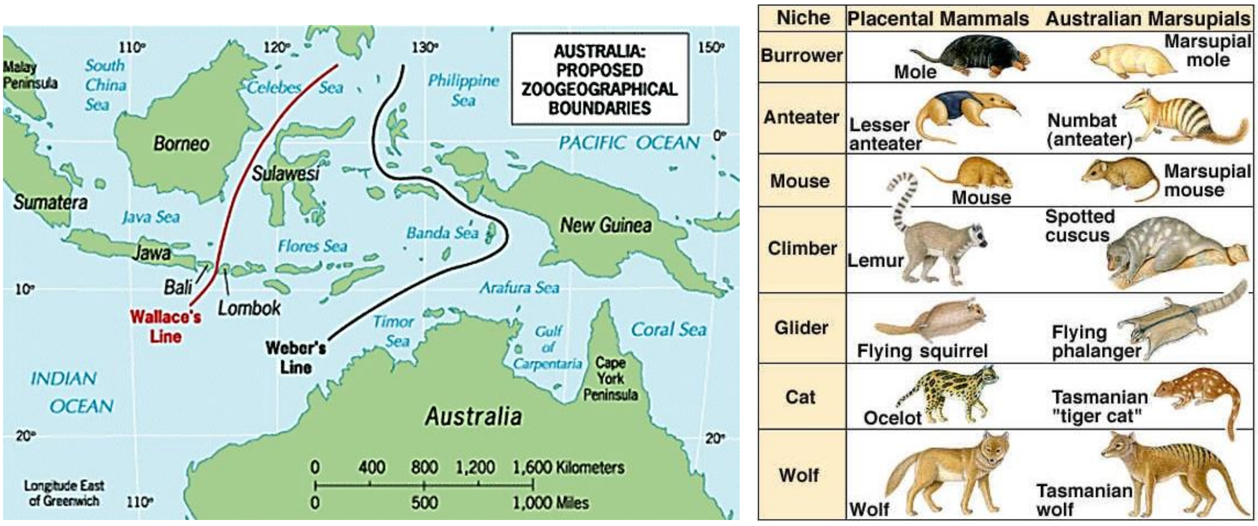
- Another observation evident of the effect of continental drift came from the well-known work of Alfred Russel Wallace, a contemporary of Charles Darwin, was a naturalist who came to South-East Asia to classify novel species.

- The best known of all Wallace's work is his proposal of **Wallace's Line**, a boundary separating the faunal regions of Asia (to the west of it) and Australasia (to the east).

- **Wallace’s line** (Fig. 5.15, *left*) demarcates these two faunal provinces, most distinctly noticed between the islands of Bali (western) and Lombok (eastern) that are separated by only a narrow strait of 20 km.

- Wallace studied the distribution of species and noticed distinct differences in species found in different regions of Asia – to the west of Wallace's Line (Borneo and the Malayan Peninsula) were birds (and other plants and animals) with Asian features and to the east (New Guinea and Australia) were those with distinctly Australian features.

- The Australian marsupial mammals like the Tasmanian "tiger cat" resembles the ocelots of Asia, but they are more closely related to the other marsupials in Australia than any other carnivores from the Asian continent (Fig. 5.15, *right*).



Niche	Placental Mammals	Australian Marsupials
Burrower	Mole	Marsupial mole
Anteater	Lesser anteater	Numbat (anteater)
Mouse	Mouse	Marsupial mouse
Climber	Lemur	Spotted cuscus
Glider	Flying squirrel	Flying phalanger
Cat	Ocelot	Tasmanian "tiger cat"
Wolf	Wolf	Tasmanian wolf

Fig. 5.15: Wallace's line and the convergent evolution of placental mammals (Asia) and marsupial mammals (Australia).

Example 2: The Hawaiian archipelago islands (Fig. 5.16)

- The Hawaiian archipelago is one of the world's great showcases of adaptive radiation.

- Located about 3,500 km from the nearest continent (North America), the volcanic islands are progressively older as one follows the chain toward the northwest; the youngest island, Hawaii, is less than a million years old and still has active volcanoes.

- Each island was born "naked" and was gradually populated by stray organisms that rode the ocean currents and winds either from far-distant land areas or from older islands of the archipelago itself.

- The physical diversity of each island, including immense variation in elevation and rainfall, provides many opportunities for **evolutionary divergence by natural selection**.

- Multiple invasions followed by speciation events have ignited an explosion of adaptive radiation in Hawaii.

- Most of the thousands of species that inhabit the islands are found nowhere else on Earth.

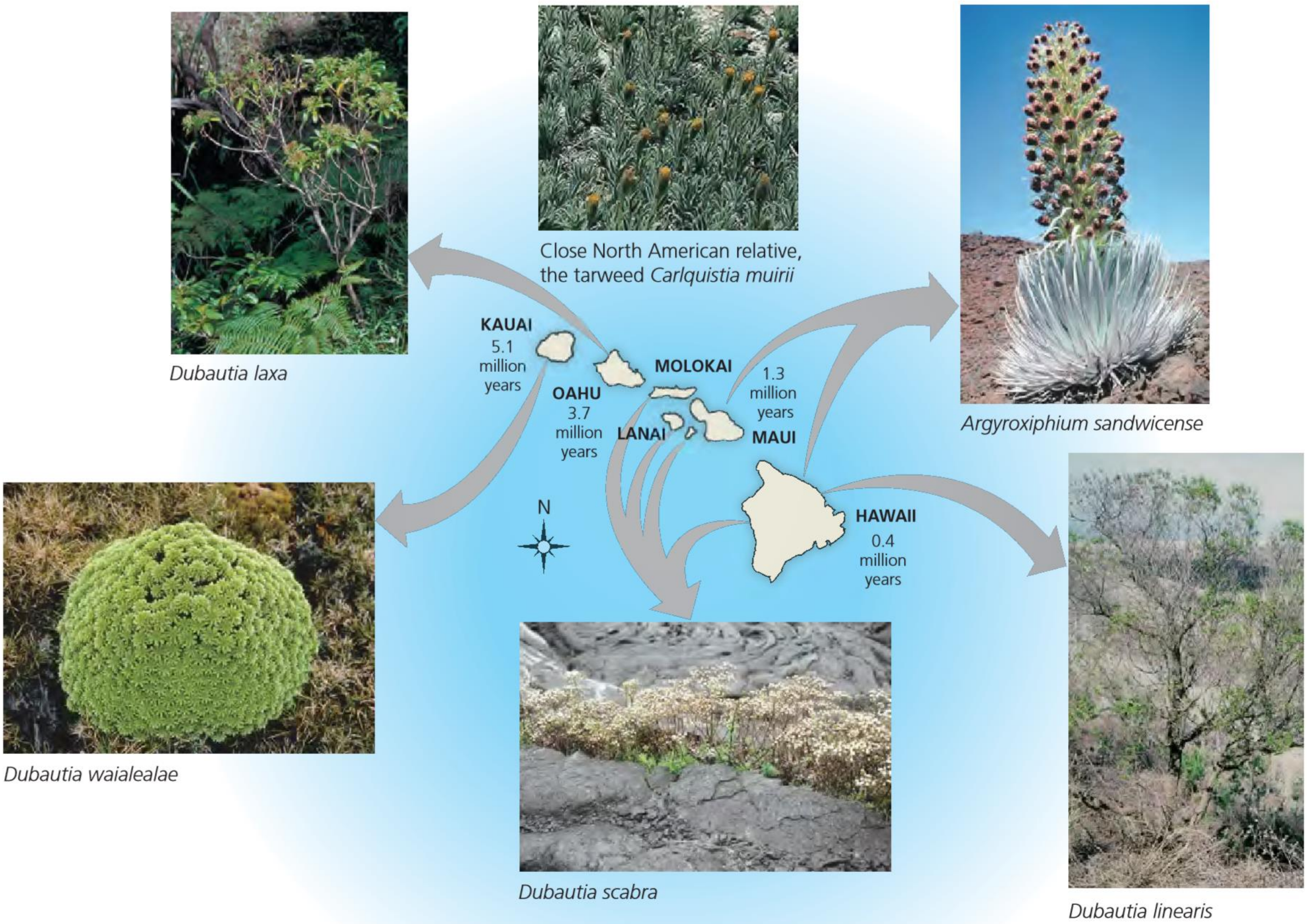


Fig. 5.16: Adaptive radiation on the Hawaiian Islands. Molecular analysis indicates that these remarkably varied Hawaiian plants, known collectively as the "silversword alliance", are all descended from an ancestral tarweed that arrived on the islands about 5 million years ago from North America. Members of the silversword alliance have since spread into different habitats and formed new species with strikingly different adaptations.

5.1.4 Comparison between anatomical and molecular evidence

	Molecular Evidence	Anatomical Evidence
1.	All organisms on earth share the **same kind of genetic information** – DNA and RNA.	There is **no single universal physical structure** that can be used to compare the relationships between all organisms.
2.	It is **objective**. Homologous nucleotide sequence / sequence of amino acid of homologous protein are compared It is **quantitative** / quantifiable and can be subjected to statistical analysis	Can be **subjective** (features to be compared and their relative importance determined by scientists), It is **qualitative**.
3.	Similarity in DNA sequences reflect common ancestry as DNA is inherited / passed down from previous generations of organism / ancestral organism.	Organisms with similar morphology tend to be more closely related. However, there could be exceptions - similar organisms may be distantly related but display similar morphology due to convergent evolution (e.g. dolphins and fish).
4.	As DNA is being compared, it takes into consideration changes in non-coding sequences (which are not expressed in phenotype). Hence more complete comparison	Unable to account for changes in non-coding sequences as they are not expressed in the phenotype. Takes into account only features which are expressed, less complete in comparison
5.	As DNA is being compared, it takes into account silent mutation.	Does not take into account of silent mutation as silent mutation does not result in a change in phenotype.
6.	Can be used to compare species that are anatomically indistinguishable.	Anatomically indistinguishable species cannot be compared (e.g. mushroom and human).
7.	Can be used to assess relationship between species that share few morphological similarities	Species that share only a few morphological similarities may pose difficulties.

6. Divergent and convergent evolution

6.1 Divergent evolution

- In *Section 5.1.1*, we discussed how **descent with modification** can result in **homologous structures**, such as the limbs of mammals and the beaks of Galapagos finches.

- These are two examples of **divergent evolution** (also called **adaptive radiation**), whereby a group of organisms from a **common ancestry** share a **homologous structure** that is modified and specialised to perform a variety of **different functions**.

- Such homologous structures is due to the **different selection pressures** in different environment, those individuals with selective advantageous traits or alleles were selected for and reproduce to pass on their advantageous alleles to reproduce fertile and viable offspring.

- For example, the need to adapt to sea condition results in the evolution of the flippers in dolphins. The need to adapt to flight condition results in the evolution of wings in bats.

- Over many generations, the **allele frequency changes differently** within the **different populations**.

- When **sufficient accumulation** of these **genetic changes** occurs within these different populations, the two populations can diverge into different species when they **can no longer interbreed** to produce **fertile and viable offspring** (biological species concept).

6.2 Convergent evolution

- **Different geographical areas** sometimes exhibit groups of plants and animals of **strikingly similar appearance**, even though the organisms may be distantly related.

- It is difficult to explain so many **similarities** as the result of coincidence. Instead, natural selection appears to have favoured **evolutionary adaptations in similar environments**.

- Because selection in these instances has tended to favour changes that made the two groups more alike, their phenotypes have converged. This form of evolutionary change is referred to as **convergent evolution**.

- Convergent evolution is the **independent development** of **similar structures** in groups of organisms with **different common ancestors.** This is often observed in organisms living in **similar environments**.

- Such similar structures are known as **analogous structures**.

Example 1: The Marsupial-Placental Convergence (Fig. 6.1)

- In the best-known case of convergent evolution, two major groups of mammals, marsupials and placentals, have evolved in a very similar way, even though the two lineages have been living independently on separate continents.

- Australia separated from the other continents more than 50 million years ago, after marsupials had evolved but before the appearance of placental mammals.

- As a result, the only mammals in Australia have been marsupials, members of a group in which the young are born in a very immature condition and held in a pouch until they are ready to emerge into the outside world.

- Thus, even though placental mammals are the dominant mammalian group throughout most of the world, marsupials retained supremacy in Australia.

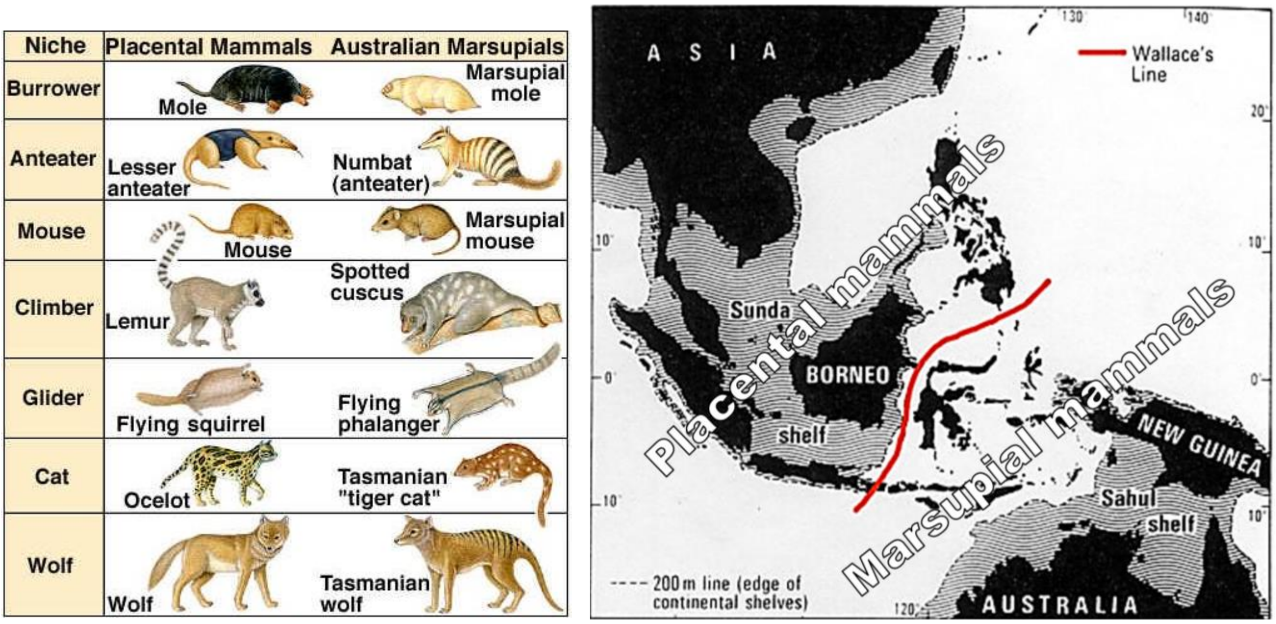


Fig. 6.1: Convergent evolution. In Asia, placental mammals like ocelots and wolves are carnivorous animals. West of Wallace's Line (*Section 5.3*), in the Australasian region, the Tasmanian "tiger cat" and Tasmanian wolf have evolved to fill in the ecological niche occupied by carnivores. However, the Asian wolf (placental mammals) and the Tasmanian wolf (marsupial mammals) are not related. There are also burrowing forms, grazing forms, gliding forms, and even long-snouted ant-eating forms which have evolved independently in the two groups. They are distantly related (on the molecular level) due to their evolutionary history, yet have many physical features in common that allow them to survive in similar environmental conditions.

Example 2: Wing structure of various flying organisms (Fig. 6.2)

- The structure of wings in bats (stretched skin), butterflies (membranes and scales supported by veins) and birds (feathers) have evolved differently in structure, but serve the same purpose.

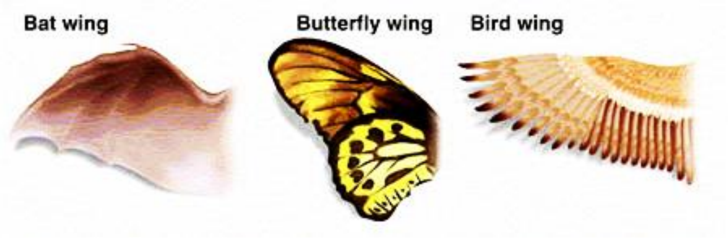


Fig. 6.2: Convergent evolution. Bats, birds and insects come from different ancestry but due to the need to adapt to similar environment (similar selection pressure), they evolve wings independently.

In summary...

- **Convergent evolution** results in **analogous structures** which are used for **a similar function**, in organisms of **different evolutionary lineages**.

- **Divergent evolution** results in **homologous structures** in organisms that share **common ancestry**, but homologous structures **may not necessarily have similar functions**.

7. Classification and Phylogeny

- Species were initially organized purely according to particular characteristics. This **organization of species according to shared characteristics** is known as **classification**. (Fig. 7.1a).

- Subsequently, species were also organized **to show their evolutionary relationships**. This is organization is known as **phylogeny**. (Fig. 7.1b)

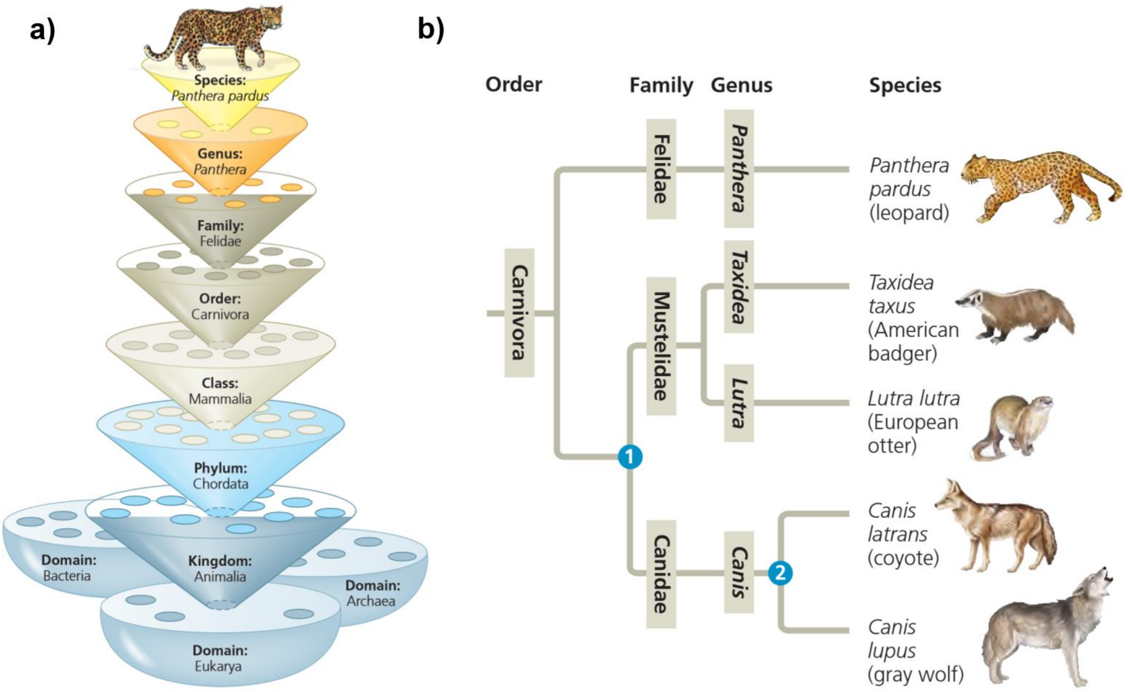


Fig. 7.1: (a) Classification – organization of species purely according to particular characteristics. **(b)** Phylogeny – the organization of species according to particular characteristics which takes into consideration the evolutionary relationship between the species.

7.1 Classification

- **Biological classification** is the organization of species **based on shared characteristics**. Classification **may not take into consideration evolutionary relationships** between species due to the lack of information about genetics.

- The hierarchical classification system was first established in the 16th century by Carolus Linnaeus in an attempt to name and classify the diversity of organisms.

- The early system used easily **identifiable physical features** to classify organisms. With the development of new disciplines in biology (e.g. genetics, biochemistry, developmental biology, etc.), more elaborate features could be used.

- The Linnaean system has two main characteristics:
  - Binomial naming system (a two-part name for each species).
  - Hierarchical classification into broader taxonomic categories.

7.1.1 Binomial nomenclature

- Common names for organisms – such as monkey, finch, and lilac – convey meaning in casual usage, but they can also cause confusion. Each of these names, for example, refers to more than one species. Moreover, some common names do not accurately reflect the kind of organism they signify. Consider these three “fishes”: jellyfish (a cnidarian), crayfish (a small lobsterlike crustacean), and silverfish (an insect).

- To avoid ambiguity when communicating about their research, biologists refer to organisms by **Latin scientific names**.

- The two-part format of the scientific name, commonly called a **binomial**, was instituted in the 18th century by Carolus Linnaeus.

- The first part of a binomial is the name of the genus (plural, genera) to which the species belongs.

- The second part, called the specific epithet, is unique for each species within the genus.

- An example of a binomial is *Panthera pardus*, the scientific name for the large cat commonly called the leopard. Notice that the first letter of the genus is capitalized and the entire binomial is italicized (underlined when handwritten).

- Many of the more than 11,000 binomials assigned by Linnaeus are still used today, including the optimistic name he gave our own species – *Homo sapiens*, meaning “wise man”.

7.1.2 Hierarchical classification / Linnaean taxonomy

- In addition to naming species, Linnaeus also grouped them into a hierarchy of increasingly inclusive categories.

- The first grouping is built into the binomial: Species that appear to be closely related are grouped into the same genus. For example, the leopard (*Panthera pardus*) belongs to a genus that also includes the African lion (*Panthera leo*), the tiger (*Panthera tigris*), and the jaguar (*Panthera onca*). Beyond genera, taxonomists employ progressively more comprehensive categories of classification called the **Linnaean taxonomy**. (Fig. 7.2)

- **Linnaean taxonomy** places related genera in the same **family**, families into **orders**, orders into **classes**, classes into **phyla** (singular, phylum), phyla into **kingdoms**, and, more recently, kingdoms into **domains**.
  (*Mnemonics*: **K**ing **P**hilip **C**ame **O**ver **F**or **G**ood **S**oup)

- The named taxonomic unit at any level of the hierarchy is called a **taxon** (plural, taxa). In the leopard example, *Panthera* is a taxon at the genus level, and *Mammalia* is a taxon at the class level that includes all the many orders of mammals.

- Each taxon possesses features which are diagnostic / distinguishing.

- As we move from kingdom to species,
  - The **number of similarities** between the members of each taxon **increases**.
  - The **number of members** in each taxon **decreases**.

- Therefore, a hierarchy is the grouping of organisms in ranks of increasingly smaller and more specific categories.

Taxa	Human	Distinguishing characteristics of each group		Leopard
Kingdom	Animalia	Multicellular heterotrophic eukaryotic organisms.		Animalia
Phylum	Chordata	Presence of a notochord, a dorsal nerve cord, pharyngeal silts and a post-anal-tail at some stage of life.		Chordata
Class	Mammalia	Have mammary glands, fur, three middle ear bones and sweat glands.		Mammalia
Order	Primates	Well-developed cerebellum, five digits on fore and hind limbs and opposable thumbs	Meat-eating mammal.	Carnivora
Family	Hominidae	Tailless primates sharing >97% of their DNA with the modern human genome	Carnivorous cats, sensitive whiskers, large eyes, large ears.	Felidae
Genus	*Homo*	Bipedal, larger cranial capacity.	Physical adaptations for roaring.	*Panthera*
Species	*sapiens*	Bipedal, developed brain, ability to reason, language, tool usage	Massive skull, powerful jaws. Fur markings: rosettes without internal spots	*pardus*

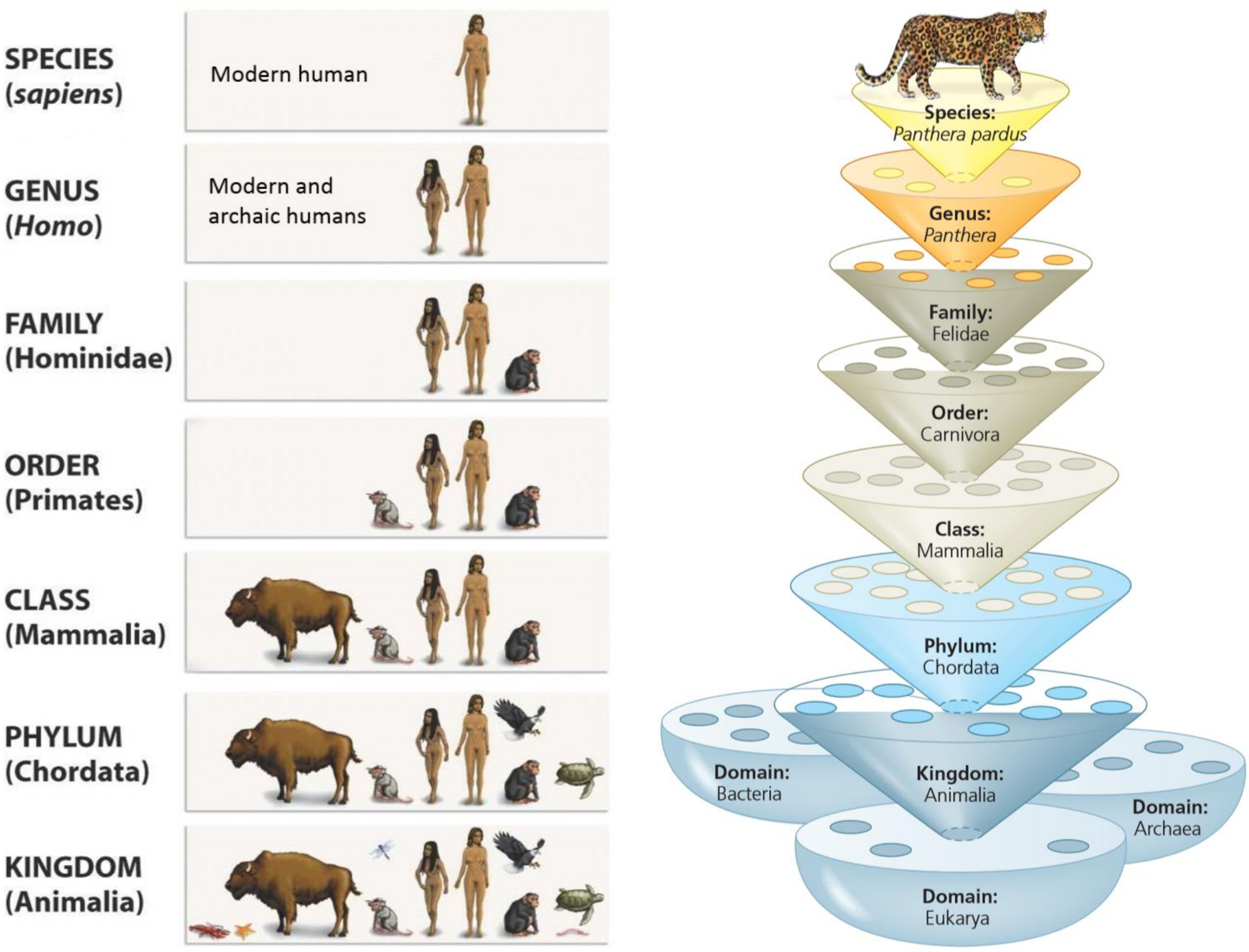


Fig. 7.3: Biological classification of the human being (*Homo sapiens*) and the leopard (*Panthera pardus*). The distinguishing features of each group is briefly described.

7.2 Phylogeny

- **Phylogeny** is the **organisation of species to show the evolutionary relationship between the species**. It is not the same as Linnaean classification as not all species have been classified according to their evolutionary relationships yet.

- The major role of phylogeny is to determine the **ancestral relationships** among known species (both living and extinct).

- The evolutionary history of a group of organisms can be represented in a branching diagram called a **phylogenetic tree** (sometimes called a phylogram or cladogram).

- As shown in Fig. 7.3, the branching pattern often matches how taxonomists have classified groups of organisms nested within more inclusive groups.

- Sometimes, however, taxonomists have placed a species within a genus (or other group) to which it is not most closely related. One reason for misclassification might be that over the course of evolution, a species has lost a key feature shared by its close relatives. If DNA or other new evidence indicates that such a mistake has occurred, the organism may be reclassified to accurately reflect its evolutionary.

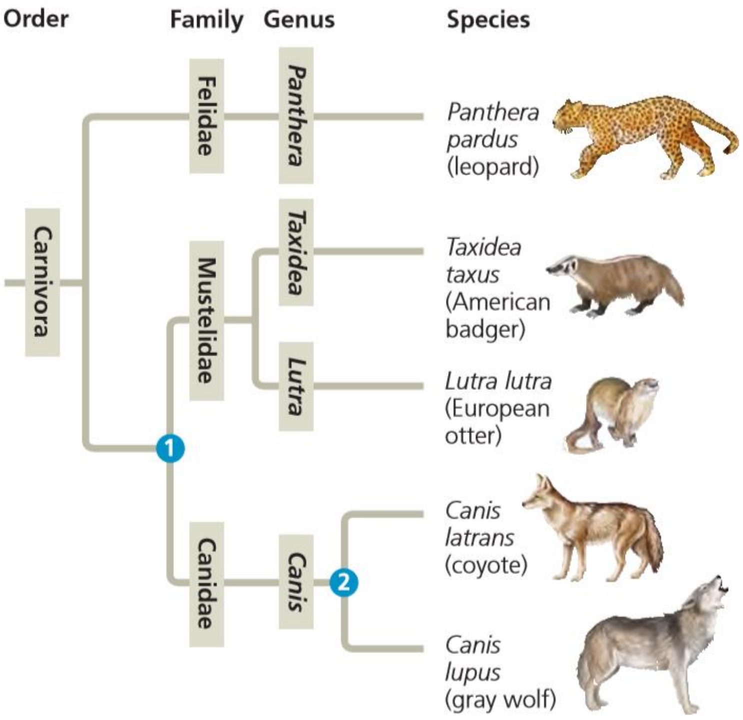


Fig. 7.3: The connection between classification and phylogeny. Hierarchical classification can reflect the branching patterns of phylogenetic trees. This tree traces possible evolutionary relationships between some of the taxa within order Carnivora, itself a branch of class Mammalia. The branch point 1 represents the most recent common ancestor of all members of the weasel (Mustelidae) and dog (Canidae) families. The branch point 2 represents the most recent common ancestor of coyotes and gray wolves.

- Biologists attempt to place species into groups called **clades**, each of which includes an **ancestral species** and **all of its descendants** (Fig. 7.4). Clades are nested within larger clades.

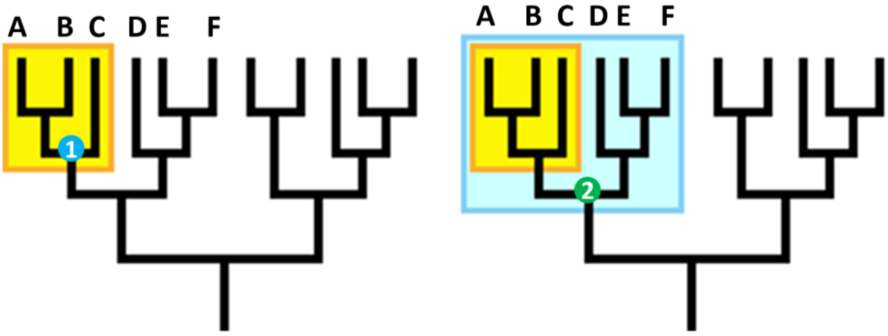
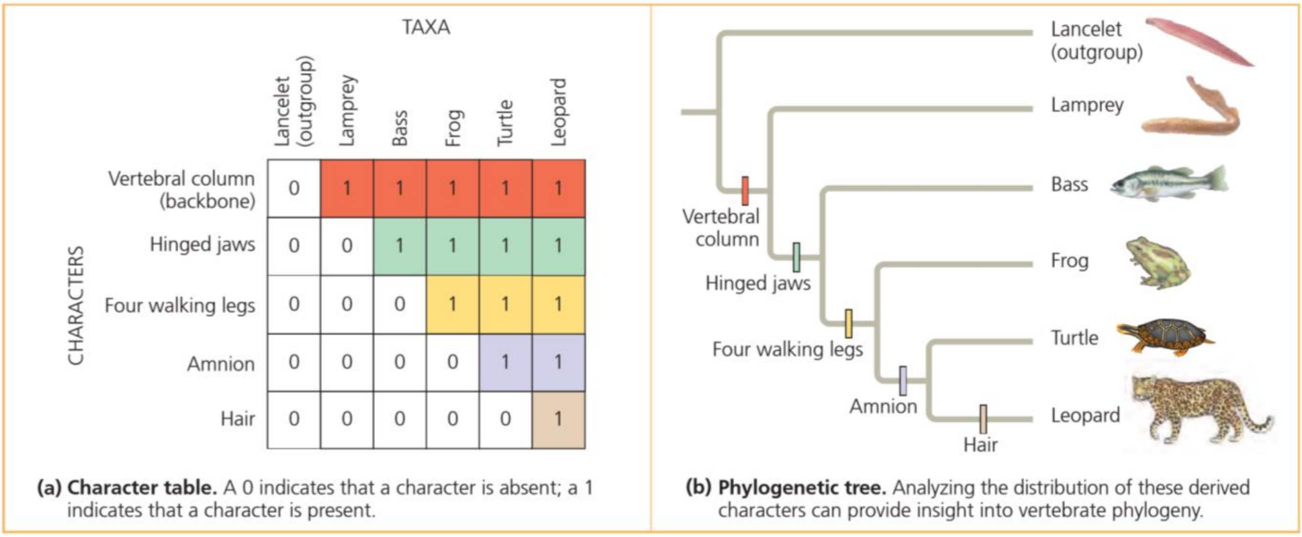


Fig. 7.4: The clade on the left includes common ancestor 1 and species A – C. This clade can be nested within a larger clade (shown on the right), which includes ancestor 2 and species A – F.

- How to read a phylogenetic tree (Fig. 7.4):
  - Species A is more closely related to species B than to species C.
  - The common ancestor of species A–C (1) diverged at a later stage along the evolutionary timeline than the ancestor of species A–F (2).
  - Species D evolved before species E and F.

- As a result of descent with modification, organisms both share characteristics with their ancestors and differ from them. On this basis, a phylogenetic tree can be constructed based on such similarities and differences (Fig. 7.5).



TAXA

CHARACTERS	Lancelet (outgroup)	Lamprey	Bass	Frog	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amnion	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table. A 0 indicates that a character is absent; a 1 indicates that a character is present.

(b) Phylogenetic tree. Analyzing the distribution of these derived characters can provide insight into vertebrate phylogeny.

Fig. 7.5: Constructing a phylogenetic tree. The characters used here include the amnion, a membrane that encloses the embryo inside a fluid-filled sac.

- In the phylogenetic trees we have presented so far, the lengths of the tree's branches do not indicate the degree of evolutionary change in each lineage.

- Furthermore, the chronology represented by the branching pattern of the tree is **relative** (earlier versus later) **rather than absolute** (how many millions of years ago).

- With data from **molecular homology** and **fossil records**, a tree that **places branch points in the context of geologic time** can be constructed to provide more information about the evolutionary relationship.

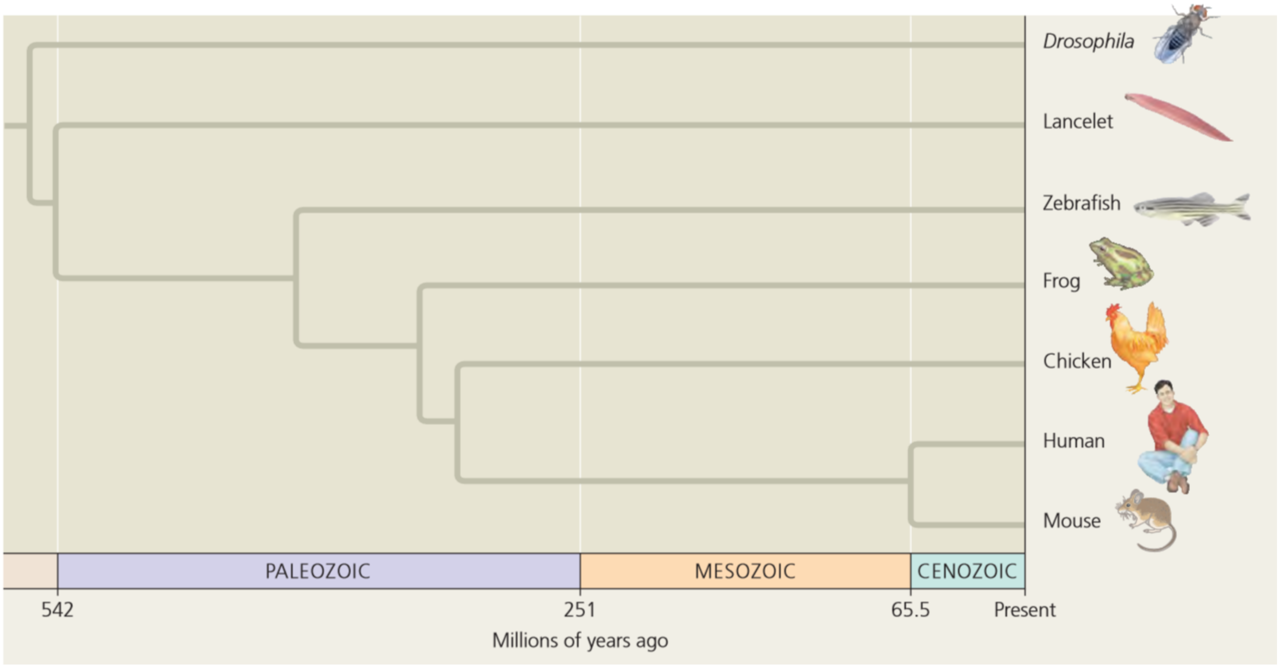


Fig. 8.6: Branch lengths can indicate time. This tree is based on molecular data and the branch points are mapped to dates based on fossil evidence. Thus, the branch lengths are proportional to time.

Exercise:
Estimate the time in which the common ancestor of the following species existed:
(i) Human and mouse:
(ii) Zebrafish and chicken:

NATIONAL GEOGRAPHIC

DNA Reveals How Darwin's Finches Evolved

A study finds that a gene that helps form human faces also shapes the beaks of the famously varied Galápagos finches **– 11 February 2015**

Scientists have identified a genetic mechanism that explains how birds develop different beak shapes in response to changes in their environment, a vivid illustration of evolution working at the most rudimentary level.

Ground finches (left) tend to have large beaks for cracking seeds. Warbler finches spear insects.

The research involves the finches of the Galápagos Islands. The birds are iconic because they prompted Charles Darwin to puzzle over why their beaks are so diverse, one of the questions that set him along the path to formulating his theory of evolution by natural selection.

In the study published Wednesday in the journal Nature, scientists identify a gene that plays a role in influencing the shape of birds' beaks, by making them more pointed or more blunt.

Different beak shapes and sizes allow finches to exploit different food resources. For example, a bird with a bigger, blunter beak is better able to eat large, tough seeds.

“By analyzing modern technology, we can pinpoint the individual genes that contributed to adaptive evolution,” said Leif Andersson, a geneticist at Sweden’s Uppsala University and Texas A&M University and lead author of the study.

About 1.5 million years ago, the pointed-beaked ancestor of the finches arrived on the Galápagos from the South American mainland. The birds have since evolved into 15 closely-related species, with different beak shapes, body size, feeding behavior and songs.

The Nature study sheds light on how aspects of their evolution occurred at the level of genes. It is based on the genetic sequencing of 120 birds across all of Darwin’s finch species.

The researchers compared the genomes of two finch species with blunt beaks with the genomes of two species with pointed beaks. In 15 regions of their genetic makeup, the “blunts” were especially different from the “pointeds.” And in those 15 regions, a particular gene stood out: ALX1.

ALX1 is a piece of genetic machinery crucial for cranial development in humans and other vertebrates. A child born with the ALX1 gene switched off can suffer craniofacial deformities, such as a cleft palate.

Now the scientists had stumbled across the same gene in birds. Given the gene’s role in the cranial development of humans, it made sense that ALX1 was associated with beak formation.

In further support of the idea, the researchers found that all the finches with blunt beaks shared a similar form of the gene, while those with pointed beaks shared another form.

In a series of studies done several decades ago, Peter and Rosemary Grant of Princeton University famously demonstrated that a particular species, the medium ground finch, could undergo rapid and repeated evolutionary changes. Specifically, the birds’ beak size and shape adapted over a few generations in response to severe changes in their environment.

The genome study sheds light on how that might have occurred. The data shows that the medium ground finches with blunt beaks had variants of the ALX1 gene that were different from the variants of the gene of those with pointed beaks.

“The discovery of ALX1 [gene] was very exciting because it is the first discovery of a gene controlling beak shape that varies not only across species but also among individuals” of the medium ground finch population, said the Grants, in a emailed response to questions. The Grants, who are married, are co-authors of the Nature study.

A lot of evolution is driven by random mutations. The process of natural selection favors mutations that provide some advantage, and organisms evolve in particular directions. But in the Galápagos, another mechanism was at play as well.

In their fieldwork, the Grants noticed that individuals of two different finch species would sometimes pair off, a process known as hybridization. In theory, that should transfer genes from one population to another. But the evolutionary consequences of this were unknown.

The Nature study shows that the process of hybridization had indeed mixed the different variants of ALX1 and has thus played an important role in the evolution of Darwin’s finches.

“The surprise is that the gene has moved between species,” said Steve Jones, professor of genetics at University College London, who wasn’t involved in the study. “It is a classic case of Darwinian evolution, but with a twist.”

Glossary of Terms

abiotic components: non-living chemical and physical factors in the environment.

analogous structures: structures in different species that are different in basic structures because of different ancestry. Analogous structures perform similar functions.

biotic components: all the organisms that are part of the environment.

clade: group of organisms consisting of a single common ancestor and all the descendants of that ancestor.

cladogram: family tree showing the ancestral relationships among known species (both living and extinct).

ecological niche: **sum total of an organism's use of biotic and abiotic resources in its environment, how it "fits into" an ecosystem.**

ecology: the study of how organisms interact with their environments.

frameshift mutation: mutation occurring when the number of nucleotides inserted or deleted is not a multiple of three, resulting in the improper grouping of the following nucleotides into codons.

genetic mutation: any event that changes genetic structure or; any alteration in the inherited nucleic acid sequence of the genotype of an organism.

genetics: The study of heredity and hereditary variation.

homologous structures: Structures in different species that are similar in basic structures because of similar ancestry. Homologous structures may perform different functions.

hybrid: An individual that is the offspring of two different species.

hybridisation: The process of crossing or mating two species.

natural selection: The process in nature by which, according to Darwin's theory of evolution, only the organisms best adapted to their environment tend to survive and transmit their genetic characteristics in increasing numbers to succeeding generations while those less adapted tend to be eliminated.

phylogenetic relationship: evolutionary relationship.

phylogenetics: study of evolutionary relatedness among the various groups of organisms (e.g. species).

phylogeny: evolutionary history of a set of organisms consisting of a set of species.

population: group of individuals of the one species that live in a particular geographical area.

recombinant chromosomes: chromosomes created when crossing over combines the DNA from different sources.

selective advantage: genetic advantage of one organism over its competitors that causes it to be favored in survival and reproduction rates over time.

selective pressure: Any phenomena which alters the behavior and fitness of living organisms within a given environment. It is the driving force of evolution and natural selection.

species: A group of organisms which have numerous features in common and are normally capable of interbreeding and producing viable offspring.

systematics: the study of biological diversity in an evolutionary context.

taxon: A group of organisms within the taxonomic hierarchy. Plural: taxa

taxonomy: the study of the principles, rules and methods of classification. It is a branch of systematics.

variation: The difference between members of the same sp