TOPIC 7: INHERITANCE AND EVOLUTION

Competency: The learner appreciates the transmission of traits from one generation to the next, and the mechanisms that drive change in a gene pool, by analyzing the concepts of inheritance and evolution, so as to make informed decisions regarding inheritable conditions, for genetic engineering, conservation biology, and health.

Learning Outcomes:

The learner should be able to:

a) Analyze the structural and functional significance of nucleic acids in meiosis and mitosis, their role in cellular functions, and how mutations in nucleotide sequences can contribute to disease (cancer). (u, s, gs, v/a)

b) Assess gene technology techniques, their applications in various fields, and the associated ethical Implications.(u, s, gs, v/a)

c) Apply Mendelian principles to predict inheritance patterns and utilize mathematical models to analyze allele frequencies and genotype distributions within populations.(u, s)

d) Examine different forms of allele interactions (autosomal linkage, multiple alleles, codominance and incomplete dominance), including their examples and influence on phenotypic expression. (u, s, gs)

Unpacking of learning outcomes

Learning outcomes	Content breakdown
a) Analyze the structural and functional significance of nucleic acids in meiosis and mitosis, their role in cellular functions, and how mutations in nucleotide sequences can contribute to disease (cancer).(u, s, gs, v/a)	**1. Concept of nucleic acids** focusing on; ▪ Structures of nucleic acids based on their 3D models for; Deoxyribonucleic acid (DNA), Ribonucleic acid (RNA) and Chromosome. ▪ Base-pairing rules. ▪ Properties of the genetic code. ▪ DNA replication ▪ Theories/model of DNA replication (semi-conservative, conservative & Dispersive) **2. Concept of Protein synthesis.** **3. Concept of cell division:** focusing on the events of cell division during: **(a)** Mitosis **(b)** Meiosis. **4. Concept of cancer focusing on;** ▪ Causes and risk factors. ▪ Prevention, and management strategies. ▪ Relationship between cell division and cancer.
b) Assess gene technology techniques, their applications in various fields, and the	**(i) Concept of gene technology** focusing on; ▪ Types of gene technology such as Recombinant DNA technology, Gene cloning and PCR.

associated ethical Implications.(u, s, gs, v/a)	▪ Steps involved during the different techniques of gene technology. ▪ Applications of the different types of gene technology in various fields. ▪ Implications of gene technology ▪ Ethical, social and environmental implications of gene technology, in line with GMOs.
c) Apply Mendelian principles to predict inheritance patterns and utilize mathematical models to analyze allele frequencies and genotype distributions within populations.(u, s)	**1.** Concept of Mendelian inheritance, focusing on the patterns of inheritance as well as predicting ratios **(i)** Relating Mendel's laws (1st and 2nd) **(ii)** Using genetic crosses to demonstrate Mendel's first law of inheritance. **(iii)** Using genetic crosses to demonstrate Mendel's second law of inheritance. **2. Concept of population genetics:** **(i)** Terminologies used **(ii)** Demonstration of Hardy Weinberg principle. **(iii)** Using calculations to predict allele frequencies. **(iv)** Factors that upset genetic equilibrium.
d) Examine different forms of allele interactions (autosomal linkage, multiple alleles, codominance and incomplete dominance), including their examples and influence on phenotypic expression. (u, s, gs)	**3.** Concept of non-mendelian inheritance, focusing on their examples and influence on the phenotypic expressions **(i)** Autosomal linkage **(ii)** Multiple alleles **(iii)** Incomplete dominance **(iv)** Codominance etc.
e) Analyze evolutionary advancements in key life processes (circulation, reproduction, gaseous exchange, coordination, movement, and excretion), as well as their suitability for survival across different species. (u, s, gs, v/a)	**1.** Introduction to the concept of evolution; **2.** Evolutionary advancement in life process i.e. circulation, reproduction, Gaseous exchange, coordination, movement and excretion across different species. **3.** Significance of these advancements for the survival of living organisms in their environments.
f) Assess speciation and resistance, mechanisms driving them, and factors contributing to extinction events, through comparison of historical and	**4. Concept of isolation mechanisms** **(i)** Types/categories of isolating mechanism **(ii)** How isolating mechanisms contribute to evolution and speciation. **5. Concept of speciation**

contemporary examples. (u, s, gs, v/a)	**(i)** Types of speciation. **(ii)** Factors that contribute to speciation. **(iii)** Mechanisms of speciation **6. Concept of mass extinctions:** **(i)** Causes of /factors that contribute to mas extinctions **(ii)** Major extinctions, their timelines, ke events involved and their causes. **(iii)** Effects of mass extinctions. **(iv)** Contribution/role of mass extinction t evolution. **7. Concept of natural selection in action:** **(i)** Case studies of antimicrobial and pesticid resistance. **(ii)** How resistance arises (antimicrobial an pesticide resistance). **(iii)** Solutions for antimicrobial and pesticide resistance.

INTRODUCTION:

NUCLIEC ACIDS

These are biological macromolecules (very large molecules) that store and transmit genetic information in all living things. They are called so because of where they were first discovered and their chemical properties i.e., They are called **"nucleic"** because they were first extracted from the nucleus of a white blood cell and also termed as **"acids"** because chemically, they have acid properties since the phosphate group in their backbone releases hydrogen ions (H^+) in solution, which makes the molecule acidic in nature.

Types of nucleic acids

There are two main types of nucleic acids found in all living organisms;

- Deoxyribonucleic acid (DNA)
- Ribonucleic acids (RNA)

Location and function of nucleic acids:

Nucleic acid	Location	Function
DNA	• Nucleus (eukaryotic cells) • Mitochondria • Chloroplasts (in plants) • Nucleoid region (in prokaryotes)	▪ Stores genetic information of an organism. ▪ Directs protein synthesis ▪ It is passed to the offsprings during reproduction.

RNA: occur in three types: **mRNA,** **rRNA &** **tRNA**	• Nucleus • Nucleolus • Cytoplasm • Ribosomes	▪ Carries genetic code from DNA to ribosomes for protein synthesis. ▪ Transfers amino acids to the ribosomes during translation ▪ Forms structural and functional part of ribosomes. ▪ Catalyzes protein synthesis.

Structural composition of nucleic acids

All the nucleic acids being very large complex molecules (polymers), they are made up of many smaller repeating units called **nucleotides**. Each nucleotide consists of three main components:

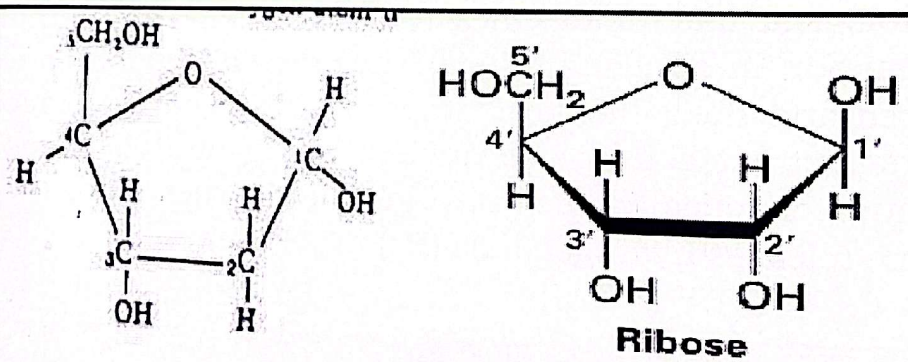
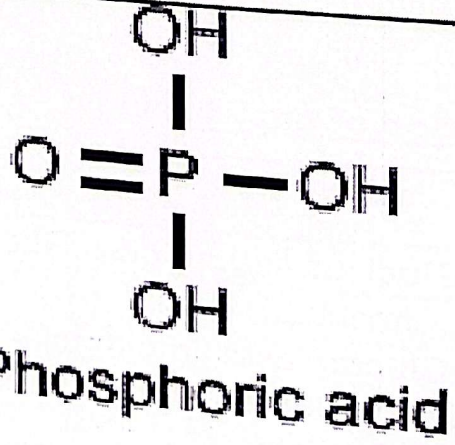
(a) Phosphate group:

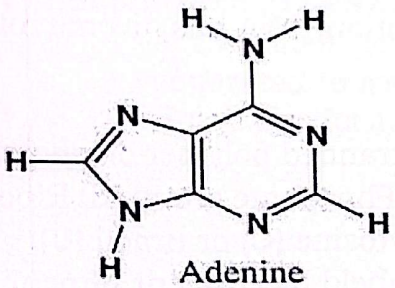
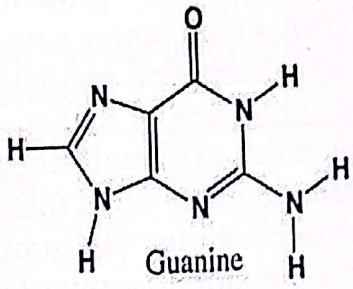
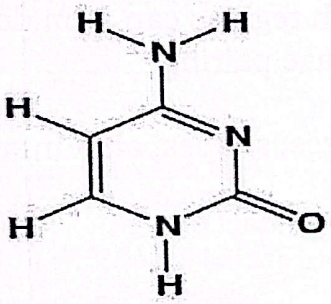
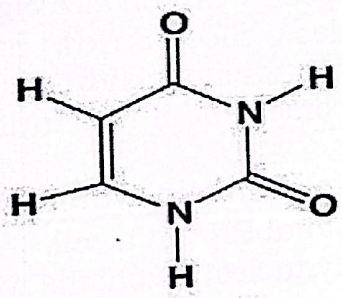
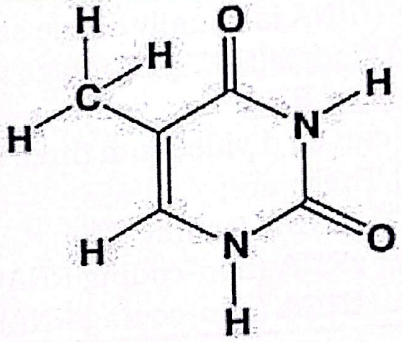
(b) Pentose sugar: This is a five carbon sugar. These can either be a Deoxyribose (in DNA) or Ribose (in RNA). The ribose sugar differs from the Deoxyribose sugar from only having an additional oxygen atom at carbon atom 2.

(c) Nitrogen base: These are organic molecules containing nitrogen. They are five different bases which are divided into two groups;

(i) Purines: These are double ringed structures comprising of a six-sided and a five -sided ring. Two examples are **Adenine (A)** and **Guanine (G).**

(ii) Pyrimidine: These are single ringed structures, each with six sides. Examples **cytosine (C), Thymine (T)** and **uracil (U).** Note that Thymine is found only in DNA while Uracil is found only in RNA.

Component	Structural illustration
Pentose sugar	 **Deoxyribose** **Ribose** **(In RNA)**
Phosphate group	 **Phosphoric acid**

Purines	 Adenine	 Guanine
Pyrimidine	 Cytosine  Uracil **(Occurs only in RNA)**	 Thymine **(Occurs only in DNA)**

Note:

The three components of the nucleotides combine in a condensation reaction (a water molecule is lost) which involves formation of;

- Nucleoside when pentose sugar joins to an organic base (pentose sugar + organic base).
- Nucleotide, when nucleoside joins to a phosphate group.
- By similar condensation reaction between the sugar and phosphate groups of two nucleotides, a dinucleotide is formed by phosphodiester bonds.
- Continued condensation reaction leads to formation of polynucleotide.

The **sugar-phosphate-sugar backbone** is formed when the 3' carbon on one sugar joins to the 5' carbon on the next sugar by **phosphodiester bonds** repeatedly to form a **polynucleotide** (long chain of nucleotides) with organic bases protruding outwardly.

A. RIBONUCLEIC ACIDS (RNA)

This is a single stranded nucleic acid found in all living cells. It plays a central role in the flow of genetic information, as explained in the central dogma of molecular biology.

DNA ⟶ RNA ⟶ protein.

Unlike DNA which stores genetic information, RNA has diverse roles in gene expression, protein synthesis and regulation.

General structure of RNA

RNA molecules are small/short, single stranded polymer of **ribonucleotides**. Each RNA **nucleotide** is made up of three parts: **(i)** Phosphate group **(ii)** Ribose sugar **(iii)** Nitrogen base - either adenine **(A)**, guanine **(G)**, cytosine **(C)** or uracil **(U)**.

The sugar-phosphate-sugar backbone is held by covalent **phosphodiester bonds.**

Note:

- RNA is usually single stranded, though regions can form double stranded hairpin loops (tRNA) due to complementary base pairing.

Types of RNA

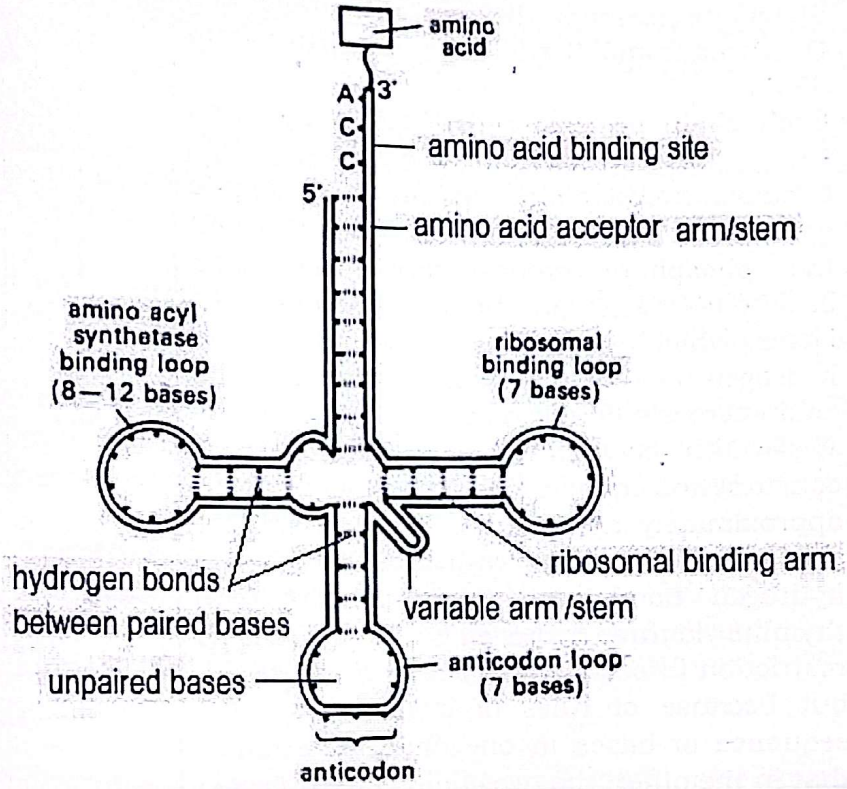
RNA can be divided into three types whose sizes, shapes, amounts/abundance and roles vary. These are;

1. **mRNA** (coding RNA)
2. **rRNA** (non-coding RNA)
3. **tRNA** (non-coding RNA)

Type of RNA	Features
1. Ribosomal RNA (rRNA)	Forms 80% of the total RNA in a cell. rRNA in different species vary in size e.g. in humans 18S rRNA has 1868 nucleotides while 28S rRNA has 5025 nucleotides. It is permanently combined with protein to form catalytic component of ribosomes and it is manufactured in nucleolus. **Function:** ▪ rRNA is a site of protein synthesis in cells.
2. Messenger RNA (mRNA)	Forms 3-5% of the total RNA in a cell. Single stranded polynucleotide chains with 5' to 3' polarity Average size of eukaryotic mRNAs is 1500 to 2000 nucleotides It is manufactured in the nucleus. **Function:** ▪ mRNA carries coded information from DNA to ribosomes in the cytoplasm
3.Transfer RNA (tRNA)	Forms about 15% of the total cell RNA. Primary structure in all tRNA has sequences of about 73 to 93 nucleotides. The 3' end of the chain always terminates with the sequence CCA, where amino acid attaches while the 5' end terminates in base **G**. The secondary structure forms a cloverleaf shape with 4 hydrogen bonded base-paired stems. The cloverleaf contains three non-base-paired loops: (i) Amino acyl synthatase binding loop (ii) Anticodon (iii) Ribosomal binding loop. The tertiary structure is a compact "L" shape whereby the anticodon stem and acceptor stem form a double helix. The anticodon is a single stranded loop at the bottom. **Function:** tRNA carries amino acids in the cytoplasm to ribosomes.

Adaptations of tRNA:

- Active sites (anticodon and amino acid) are maximally separated to avoid interference
- Small size for mobility readily.



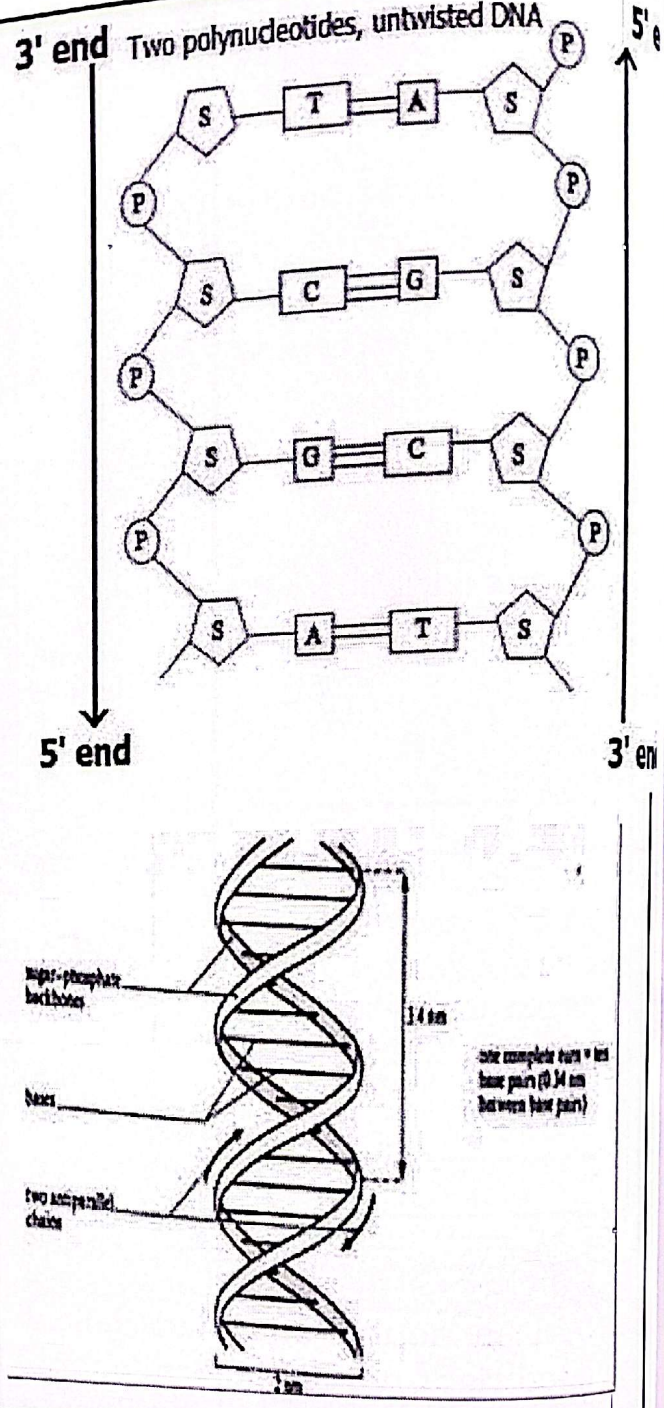
B. DEOXYRIBONUCLEIC ACIDS (DNA)

DNA is a double-stranded helical structure consisting of two polynucleotide chains twisted right handed helical shape. Each of the polynucleotide chains is extremely long and may contain many million nucleotide units, with a pentose sugar is always deoxyribose and organic bases are adenine, guanine, cytosine and thymine but never uracil.

Structure of DNA according Crick and Watson in 1953

Description	illustration

- It consists of two long polynucleotide chains/strands coiled around each other to form a right handed double helix.
- The chains/strands run in opposite directions, meaning they are antiparallel i.e., One runs from5'-3' while the other runs from 3'-5'.
- Each chain is composed of repeating units called nucleotides, and each nucleotide contains a deoxyribose sugar, a phosphate group and a nitrogenous base. The sugar and the phosphate groups form the outer backbone, sugar phosphate backbone with bases which project at right angles and hydrogen bond with the bases of the opposite chain across a double helix.
- The width between the two backbones is constant and equal to the width of a base pair, approximately about 2nm. The pairings are always cytosine pairs with guanine via two hydrogen bonds and adenine pairs with thymine via three hydrogen bonds. There is no restriction in sequence of bases in one chain, but because of rules of base pairing, the sequence of bases in one chain determines that in the other, the two chains are thus said to be complementary.
- The helix makes one complete turn approximately every 10 base pairs, spanning the length of about 3.4nm per turn.



Adaptations of DNA to its functions

- Has sugar-phosphate backbone held together by strong covalent phosphodiester bonds to provide greater stability.
- The two sugar-phosphate backbones are antiparallel which enables purine and pyrimidine nitrogen bases to project towards each other for complimentary pairing.
- Sugar-phosphate backbones are two / it is double stranded to provide maximum stability.
- The two sugar-phosphate backbones form a double helix to protect bases/hydrogen bonds.
- It is a Long/large molecule to ensure storage of much information.
- The double helical structure of DNA allows it to be compact so as to easily fit in the nucleus.
- Has numerous base sequence which allows a lot of information to be stored.

- It is double stranded for replication to occur semi-conservatively/ strands can act as templates.
- There is complementary base pairing between A-T and G-C for accurate replication/identical copies can be made.
- Weak hydrogen bonds enable unzipping/separation of strands to occur readily.
- It contains many hydrogen bonds which increase stability of the entire DNA molecule.

Theories of DNA replication

DNA replication is the process by which the parent DNA molecule makes another copy of itself. Three theories/ models were put forward to help explain how DNA replication occurs, namely;

1. **Fragmentation hypothesis (Dispersive hypothesis)**: This theory proposes that the parent DNA molecule breaks into segments and new nucleotides fill in the gaps precisely so as to form the new daughter DNA.
2. **Conservative hypothesis:** This theory proposes that the complete parent DNA molecule acts as a template for the synthesis of the new daughter molecule, which is assembled from new nucleotides but the parental DNA molecule remains unchanged.
3. **Semi-conservative hypothesis:** This theory proposes that the parent DNA molecule separates into its two separate strands and each of which acts as a template for the formation of a new complementary daughter DNA strand. The two daughter molecules formed therefore contain half the parent DNA and half new DNA.

Note:

- The semi conservative hypothesis was shown to be the most correct mechanism by which DNA replicates based on the work of Meselsohn and Stahl (1958) in their experiment on bacterium E.coli using radioactive ^{15}N. Their experiment showed that DNA replication preserves one old strand in each new double helix.

DNA replication by semi-conservative model

DNA replication is the process by which parent DNA molecule makes another copy of itself, semi conservatively (1 new, 1 old strand together).It occurs during the synthesis phase **(S-phase)** of interphase during the cell cycle. It is described as **semi-conservative** because each newly formed DNA molecule consists of:

- One parental (old) strand
- One newly synthesized (daughter) strand.

Enzymes and Proteins Involved

1. **Helicase**: This enzyme unwinds and separates the two DNA strands by breaking hydrogen bonds.
2. **Topoisomerase:** This enzyme relieves supercoiling ahead of the replication fork.
3. **Single-strand binding proteins (SSBPs)**: These proteins stabilize unwound strands, preventing them from re-annealing/rebinding.
4. **RNA-Primase**: This enzyme synthesizes short RNA primers to provide free 3' OH ends for DNA polymerase.

5. **DNA polymerase III:** This add free nucleotides to the growing strand in 5' → 3' direction.
6. **DNA polymerase I:** This enzyme remove RNA primers and replaces them with DNA nucleotides.
7. **DNA ligase:** This enzyme seals gaps/nicks between fragments, forming a continuous DNA strand.
8. **Sliding clamp proteins:** These proteins hold DNA polymerase onto the template strand for efficient replication.

Steps/mechanisms of DNA replication (semi-conservative model)

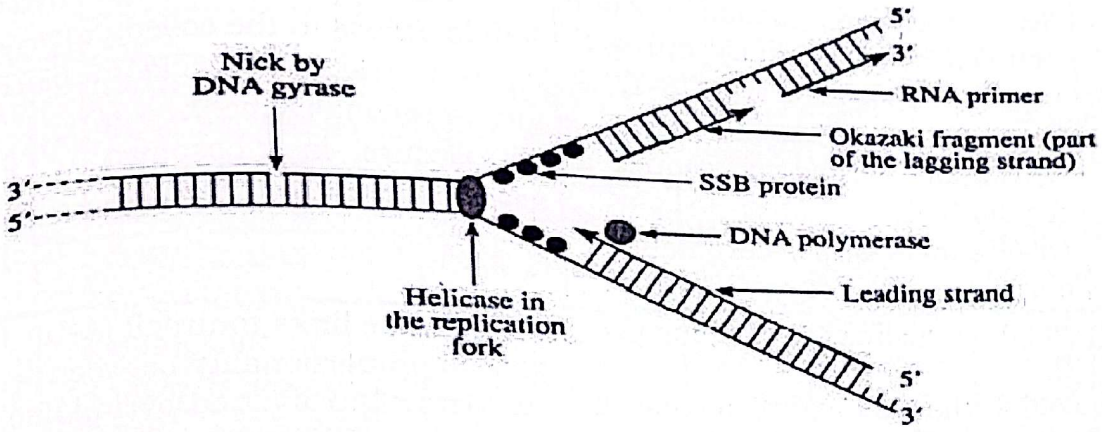
The events of DNA replication can be divided into three stages;

1. **Initiation:**
   - The enzyme DNA Helicase untwists and unzips DNA by breaking the hydrogen bonds to expose the bases, forming a replication bubble with two replication forks (Y-shaped) moving in opposite directions. (DNA is replicated a bit at a time and the whole molecule is never completely uncoiled at once).
   - SSBPs bind to the exposed single strands, preventing them from rejoining.
   - Topoisomerase relieves torsional strain caused by unwinding/removes supercoiling.
   - The enzyme RNA Primase lays down short RNA primer (~10 nucleotides long in eukaryotes) at the 3' end of the old DNA strand to guide the action of DNA polymerase. DNA polymerase cannot initiate synthesis on its own; it needs a free 3'-OH group.
2. **Elongation:**

Elongation occurs in two different manners due to the antiparallel structure of DNA strands; that's the leading and lagging strand.

   - DNA polymerase enzyme removes the RNA primer from the new strand and then moves along the exposed base sequences of the leading strand (read in 3' → 5' direction), attaching free DNA nucleotides of complementary bases to create a new DNA strand as it goes synthesizing the new strand continuously in the 5' → 3' direction.
   - The lagging strand replicated discontinuously leaving short fragments called **Okazaki fragments.** Each fragment requires its own primer and the DNA polymerase synthesizes these fragments in the 5' → 3' direction
   - Another enzyme, called DNA ligase joins adjacent Okazaki fragments on the lagging strand by forming phosphodiester bonds thus producing complete continuous strand.
   - RNA primers are removed by DNA polymerase I and the gaps are filled with DNA nucleotides complementary to the template.
3. **Termination:**
   - In prokaryotes, replication ends when replication forks meet or at specific termination sequences while in eukaryotes, replication ends when replication bubbles fuse.
   - The two new daughter molecules then coil up again to reform the double helix structure.

Illustration of DNA replication



Note:

- *The replication of the leading strand requires only one RNA primer while the lagging strand requires that each fragment has its own primer.*
- *Several molecules of DNA polymerase act simultaneously at multiple sites, each assembling a separate section of the new strand of DNA and these new DNA segments are then joined together by the enzyme DNA ligase.*
- ***Proofreading and Error Correction:*** *DNA polymerases have* **3' → 5' exonuclease activity,** *allowing them to remove mismatched bases. This proofreading ensures high fidelity (error rate ~1 in 10^9 nucleotides).*

Evidence for semi-conservative model by Meselson-Stahl experiment (1958)

- *E. coli* bacteria was grown in heavy nitrogen (^{15}N) which was then incorporated into their DNA.
- The bacteria whose DNA was having the heavy isotope of N was then transferred to medium with light nitrogen (^{14}N) isotope.
- After one replication, DNA of intermediate density (^{15}N–^{14}N hybrid) was formed.
- After two successive replications, half intermediate density DNA and half-light DNA was formed.
- **Conclusion:** DNA replication is **semi-conservative.**

COMPARISON OF DNA AND RNA

Similarities

Both: **(1)** are polymers of nucleotides **(2)** carry genetic information **(3)** have same purine bases adenine and guanine plus pyrimidine bases cytosine **(4)** originate from the nucleus **(5)** occur in the cytoplasm

Differences:

Aspect	Deoxyribonucleic Acid (DNA)	Ribonucleic Acid (RNA)
Function	(i) It's the blueprint of biological guidelines in organisms (ii) Stores genetic information for a long time and transmits it.	(i) Helps carry out DNA's blueprint guidelines. (ii) Transfers genetic code needed for the creation of proteins from the nucleus to the ribosome.

Structure	(iii) Double-stranded. (iv) Hydrogen bonds occur between complementary nitrogen bases of opposite strands (A-T, C-G) (v) Spirally twisted to produce a regular helix (vi) Occurs in form of chromatin or chromosomes	(iii) Single-stranded. (iv) Base pairing through hydrogen bonds occurs in the coiled parts (v) The strand may fold at places to form a secondary helix (vi) Occurs in ribosomes or forms association with ribosomes
Base Pairing	(vii) Adenine links to thymine (A-T) (viii) Purine and pyrimidine bases are in equal number	(vii) Adenine links to uracil (A-U) (viii) No proportionality between numbers of purine and pyrimidine bases.
Location	(ix) Much of DNA is in the nucleus of a cell, little in mitochondria and chloroplasts.	(ix) Much of RNA is in the cytoplasm, little in the nucleus.
Stability	(x) Deoxyribose sugar in DNA is less reactive because of C-H bonds. (xi) Stable in alkaline conditions. (xii) Long lived	(x) Ribose sugar is more reactive because of C-OH (hydroxyl) bonds. (xi) Not stable in alkaline conditions. (xii) Some RNA are very short lived while others have somewhat longer life.
Propagation	(xiii) DNA is self-replicating.	(xiii) RNA is synthesized from DNA when needed.
Unique Features	(xiv) DNA is protected in the nucleus, as it is tightly packed.	(xiv) RNA strands are continually made, broken down and reused.
Size	(xv) Very large/long (has over a million nucleotides) (xvi) Quantity is fixed in a cell	(xv) Much shorter (Depending on the type, RNA contains 70 – 12,000 nucleotides). (xvi) Quantity is variable
Types	(xvii) Only two types: intra nuclear and extra nuclear DNA	(xviii) Three different types: mRNA, tRNA and rRNA.

GENETIC CODE

The genetic code is the set of rules by which information encoded in genetic material DNA or mRNA sequences is translated into proteins (amino acid sequences) by living cells. It specifies how sequences of nucleotide bases (A, U, G, & C) correspond to amino acids, which are the building blocks of proteins.

Structure of the genetic code:

A codon is a sequence of three consecutive nucleotides in mRNA. Each codon corresponds to a specific amino acid or a signal (start or stop) during protein synthesis.

The total number of codons:

- Since there are **4** nucleotide, the possible codons are $4^3 = 64$ codons.
- Out of the **64** codons; **61** codons code for amino acids.
- **3** codons are stop codons (**UAA, UAG** and **UGA**)

The genetic code chart / table

BASE		SECOND BASE U	C	A	G		
FIRST BASE	U	UUU: Phenylalanine UUC: Phenylalanine UUA: Leucine UUG: Leucine	UCU: Serine UCC: Serine UCA: Serine UCG: Serine	UAU: Tyrosine UAC: Tyrosine UAA: Stop UAG: Stop	UGU: Cysteine UGC: Cysteine UGA: Stop UGG: Tryptophan	U C A G	THIRD BASE
	C	CUU Leucine CUC: Leucine CUA: Leucine CUG: Leucine	CCU: Proline CCC: Proline CCA: Proline CCG: Proline	CAU: Histidine CAC: Histidine CAA: Glutamine CAG: Glutamine	CGU: Arginine CGC: Arginine CGA: Arginine CGG: Arginine	U C A G	
	A	AUU: Isoleucine AUC: Isoleucine AUA: soleucine AUG: Methionine	ACU: Threonine ACC: Threonine ACA: Threonine ACG: Threonine	AAU: Asparagine AAC: Asparagine AAA: Lysine AAG: Lysine	AGU: Serine AGC: Serine AGA: Arginine AGG: Arginine	U C A G	
	G	GUU: Valine GUC: Valine GUA: Valine GUG: Valine	GCU: Alanine GCC: Alanine GCA: Alanine GCG: Alanine	GAU: Aspartic acid GAC: Aspartic acid GAA: Glutamic acid GAG: Glutamic acid	GGU: Glycine GGC: Glycine GGA: Glycine GGG: Glycine	U C A G	

Properties of genetic code:

Property	Explanation
1. Triplet nature	Each codon consists of three nitrogenous bases. Therefore, the nucleotides of mRNA are arranged as a linear sequence of codons.
2. Non-overlapping	In translating mRNA molecules, the codons do not overlap but they are "read" sequentially/read in a continuous sequence of three bases at a time without overlapping
3. Commaless/Continuous	This means that no codon is reserved for punctuations. The code is read continuously, without punctuation marks or gaps between codons. Only stop codons terminate translation.
4.Non-ambiguous (unambiguous)	A particular codon will always code for the same amino acid (Each codon codes for only one specific amino acids). The same codon shall never code for two different amino acids.
5. The code has polarity	The code is always read in a fixed direction, i.e., in the 5'→3' direction. Translation always proceeds in this orientation to maintain correct protein synthesis.
6. Degeneracy/redundancy	More than one codon can specify the same amino acid; For example, except for tryptophan and methionine, which have a single codon each, all other 18 amino acids have more than one codon. **Biological advantages of degeneracy**

	▪ It permits essentially the same complement of enzymes and other proteins to be specified by microorganisms varying widely in their DNA base composition. ▪ It provides a mechanism of minimizing mutational lethality. E.g. Substitution of the third base-**U** in **GUU** (for Valine) with **C/A/G** does not change the amino acid coded for.
7. Some codes are start codons	In most organisms, **AUG** codon is the start or initiation codon, i.e., the polypeptide chain starts either with methionine (eukaryotes) or N-formylmethionine (prokaryotes).
8. Some codes are stop codons	Three codons **UAG, UAA** and **UGA** are the chain stop or termination codons. They do not code for any of the amino acids. These codons are also called **nonsense codons**, since they do not specify any amino acid.
9. The code is universal	Same genetic code is found valid for all organisms ranging from bacteria to man.

PROTEIN SYNTHESIS

This is refers to a cellular process of producing proteins from the genetic code in DNA. It occurs in two main stages;

1. **Transcription:** This making of mRNA from DNA, that's to say a length of DNA (gene) is copied into mRNA (DNA → RNA).
2. **Translation:** This involves translating the base sequence in mRNA into an amino acid sequence in a protein (RNA → Protein).

Note:

- In eukaryotes, there is also RNA processing between these two stages, known as post-transcriptional modifications.

Key Enzymes (proteins) and molecules involved:

- **Helicase & Topoisomerase**: These unwind and relieve DNA supercoiling.
- **RNA polymerase**: This synthesizes RNA using a DNA template.
- **Spliceosome**: This removes introns during RNA processing.
- **Aminoacyl-tRNA synthatase**: This charges tRNA with the correct amino acid.
- **Ribosome (rRNA + proteins)**: This serves as a site for protein synthesis.
- **Peptidyl transferase (rRNA function)**: This facilitates the formation of a peptide bonds between adjacent amino acids.

(a) **Transcription (DNA → mRNA):** This is a process/mechanism by which the base sequence of a section of DNA representing a gene is converted into the complementary base sequence of mRNA. It is basically a process of synthesizing mRNA strand which is complementary to the DNA template strand. It is catalyzed by **RNA polymerase** with the help of other enzymes and factors.

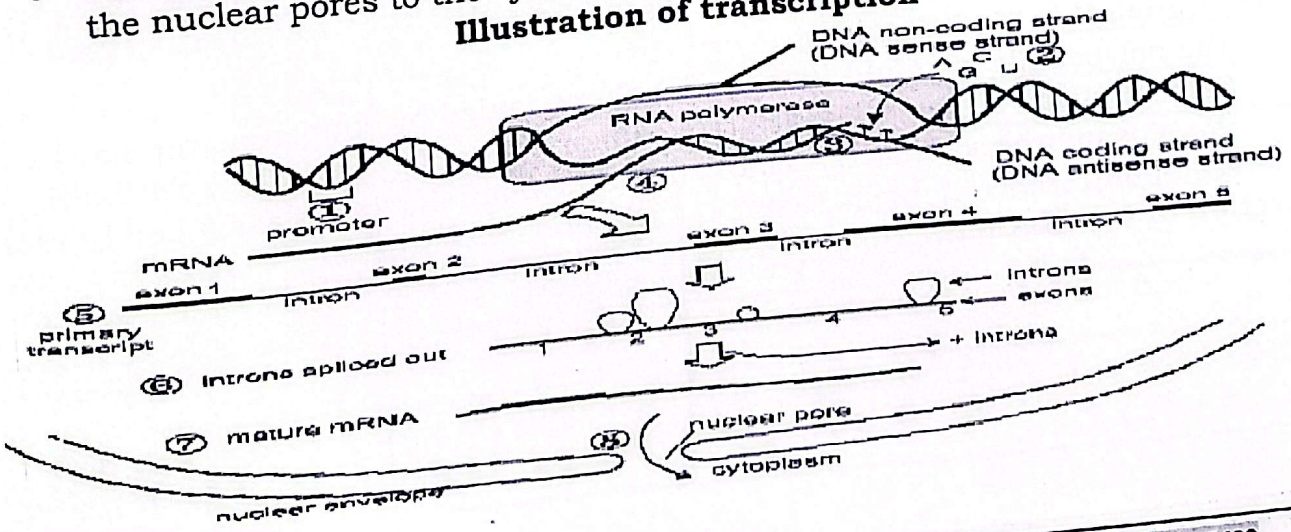
Step-by-step process of transcription:

1. **Unwinding and strand separation**

- The enzyme **helicase** (and in eukaryotes, with the help of **topoisomerase**) unwinds the double-stranded DNA at the site of a gene by breaking/melting the weak hydrogen bonds between the bases of the two strands. This creates a **transcription bubble**, where the two strands are separated.
- One strand serves as the **template strand (antisense strand)** for mRNA synthesis, while the other is the **coding strand (sense strand)** which has the same sequence as mRNA (except T → U).

2. **Initiation:**
   - The enzyme, **RNA polymerase** binds to a specific DNA sequence called the **promoter region** (e.g., the TATA box in eukaryotes). *Transcription factors* help RNA polymerase locate and bind to the promoter region.
   - DNA unwinds further at the start site, allowing RNA polymerase to begin RNA synthesis.
3. **Elongation**
   - RNA polymerase moves along the DNA template strand in the **3' → 5'** direction, adding ribonucleotides that are complementary to DNA bases, following the rules of base pairing between DNA and RNA hence forming mRNA transcript in the **5' → 3'** direction.
   - Behind the RNA polymerase, the DNA double helix reforms, leaving only the RNA transcript.
4. **Termination**
   - In prokaryotes, termination occurs when RNA polymerase encounters a **terminator sequence** (could form a hairpin loop structure).
   - In eukaryotes, a polyadenylation signal (AAUAAA) marks the termination.
   - The pre-mRNA (in eukaryotes) or mRNA (in prokaryotes) is released.
5. **mRNA processing (Eukaryotes only)/post-transcriptional modifications:**
   - **Capping**: A 5' cap (modified guanine) is added to protect RNA and aid ribosome recognition.
   - **Polyadenylation**: A poly-A tail (~200 adenines) is added at the 3' end for stability and export.
   - **Splicing**: Non-coding regions (**introns**) are cut out by the **spliceosome**, and coding regions (**exons**) are joined together.
   - The final product (mature mRNA) which is fully processed exits the nucleus via the nuclear pores to the cytoplasm.

Illustration of transcription

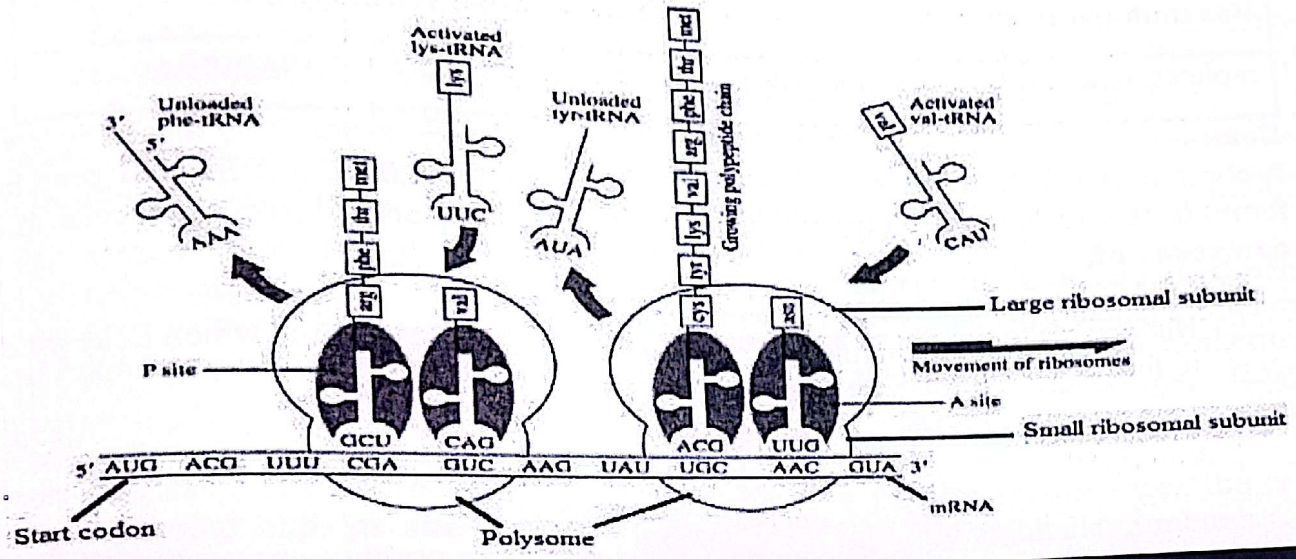


(b) Translation (mRNA → Protein): This is a process/mechanism by which the sequence of bases in mRNA molecule is converted into a sequence of amino acids in a polypeptide chain. It is basically the decoding of mRNA by ribosomes to assemble a specific sequence of amino acids into a polypeptide. It occurs on ribosomes and several ribosomes may be attached on the mRNA strand like beads on a string to form a ***polysome/polyribosome***. The advantage this is that it allows several polypeptides to be synthesized at the same time. Each ribosome is composed of a small and large subunit but these are always separate but only combine during translation.

Step-by-step process/mechanism of translation

1. **Initiation**
   - The small ribosomal subunit binds to the **5'** end of mRNA (the ribosome-binding site in prokaryotes or 5' cap in eukaryotes).
   - The ribosome scans for the **start codon** (AUG) on the mRNA strand.
   - A specific initiator, **aminoacyl-tRNA** having complementary anticodon (UAC) and carrying the first amino acid, methionine pairs with the start codon.
   - The large ribosomal subunit then joins to form a complete ribosome.
   - The initiator, aminoacyl-tRNA sits at the **P site** of the ribosome.
2. **Elongation**
   - The next/second codon on the mRNA is exposed at the **A site**.
   - A complementary aminoacyl-tRNA carrying the correct amino acid binds to the second codon on mRNA via its anticodon.
   - The enzyme called **Peptidyl transferase** forms **peptide bond** between the amino acid in the P site and the new amino acid in the A site forming a dipeptide.
   - The ribosome then shifts (translocates) to the next codon such that the empty tRNA exits from the **E site,** moves back to the cytoplasm to be reconverted into a new aminoacyl-tRNA while the tRNA still holding the growing chain moves to the **P site**. The A site becomes open for the next incoming tRNA.
   - This cycle repeats, lengthening the polypeptide chain.
3. **Termination**
   - When the ribosome reaches on of the **stop codons,** (UAA, UAG, UGA), no tRNA matches it. Instead, a release factor protein binds to the ribosome.
   - The completed polypeptide, with its primary structure as determined by the DNA is released, and the ribosome disassembles.
4. **Post-translation Modifications**
   - The polypeptide may **fold into its 3D shape** (aided by chaperone proteins).
   - Some proteins are **modified** (e.g., phosphorylation, glycosylation, cleavage).
   - Proteins may be sorted to specific cellular destinations (cytoplasm, membranes, secretion).

Illustration of translation



Comparison between transcription and translation

Similarities

- Both occur in 5' to 3' direction.
- Both require ATP

Differences

- DNA is transcribed while mRNA is translated
- Transcription produces mRNA while translation produces polypeptides/ protein
- RNA polymerase for transcription while ribosomes for translation/ ribosomes in translation only
- Transcription occurs in the nucleus (of eukaryotes) while translation occurs in the cytoplasm at endoplasmic reticulum.
- tRNA is needed for translation but not transcription

Compare the processes of DNA replication and transcription

Similarities

Both: **(1)** involve unwinding the helix **(2)** involve separating the two strands **(3)** involve breaking hydrogen bonds between bases **(4)** involve complementary base pairing **(5)** involve **C** pairing with **G** **(6)** work in a 5` to 3` direction **(7)** involve linking/ polymerization of nucleotides **(8)** DNA or RNA polymerase require a start signal.

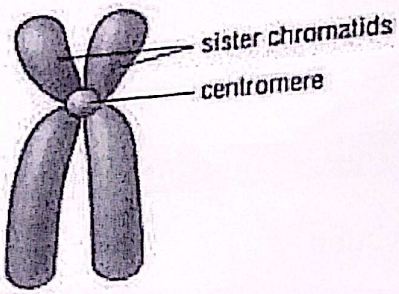
Differences

DNA replication	Transcription
Involves DNA nucleotides, where the pentose sugar is deoxyribose, and the base adenine pairs with thymine	Involves RNA nucleotides where the pentose sugar is ribose, and the base adenine pairs with uracil
Both strands are copied	Only one strand copied not both
Ligase enzyme / no Okazaki fragments are involved	No ligase enzyme / no Okazaki fragments

Has multiple starting points	Has only one starting point
replication gives two DNA molecules	whilst transcription gives mRNA

Note:
A chromosome is a highly organized threadlike structure made of DNA and proteins found in the nucleus of eukaryotic cells and in the cytoplasm of prokaryotic cells. It is **composed of;**

(i) DNA
(ii) Histone proteins: These are positively charged proteins around which DNA winds to form structural units.

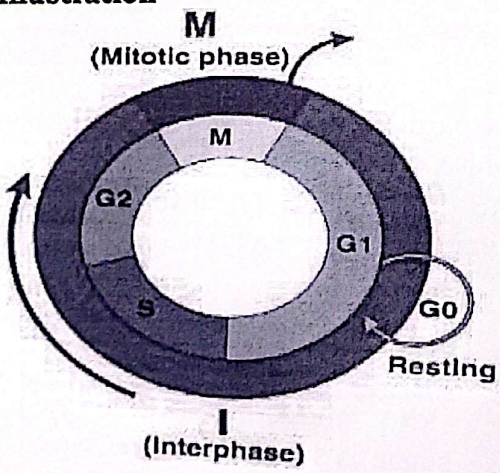


THE CELL CYCLE

This refers to a sequence of events that occur between one cell division and the next. It represents a sequence of events by which a cell duplicates its genome, synthesizes the other cellular constituents and eventually divides into two daughter cells. It may also mean the life of a cell from the time it is first formed from a dividing parent cell until its own division into two cells. Cell division is one phase of the cycle. The cell cycle is divided into two basic phases:

1. **Interphase.**
2. **M Phase (Mitotic or Meiotic phase)/Actual cell division.**

Illustration



1. Interphase:

This is a portion of the cell cycle between cell divisions/the time between cell divisions. It represents that time when a cell is preparing for the next phase, the M phase. This phase accounts for 90% of the cell cycle and all the events that occur during Interphase are very important for the successful completion of mitosis or meiosis. Interphase is divided into three phases namely;

- **G_1 phase.**
- **S phase.**
- **G_2 phase.**

Note:

Some cells often pause in **G_1** before DNA replication and enter a resting state called **G_0** phase (quiescent phase).They may remain in this phase for days to years before resuming cell division. Cells which have exited the cell cycle and now at **G_0** remain metabolically active but no longer proliferate unless called on depending on the requirement of the organism. Therefore, no DNA synthesis and preparation for cell division occurs.

Most of the cells in an animal's body are in **G_0** phase. In non-dividing cells like most neurons, mature muscle cells and brain cells, they remain there permanently while others such as liver cells can resume **G_1** phase in response to factors released during injury.

Phase	Events
G_1 phase (first gap): It represents the time gap following cell division and the preceding DNA replication (*interval between mitosis and initiation of DNA replication*). **Note:** *Soon after cell division, the daughter cells are about half the size of the original parent cell.* *G_1 represents the primary growth phase of the cell.*	• The cell becomes metabolically active/metabolic rate increases. • Intensive cellular synthesis occurs in which many new cell organelles are made, it makes enough mitochondria, cytoskeletal elements, endoplasmic reticulum, ribosomes, Golgi apparatus. Centriole replication also starts but it is completed in **G_2**. • The cell grows up to a mature size/ the cell increases in mass and organelle number. ***Note:*** All chromosomes exist in single-chromatid form as they are uncoiled.
S phase (synthesis Phase): This is the phase in which the cell synthesizes a replica of its genome. DNA synthesis or replication occurs. **Note:** *If the initial quantity of DNA in the cell is denoted as 2n, then after replication it becomes 4n. However, the number of chromosomes does not vary, that's to say, if the number of chromosomes during G_1 phase was 2n, it will remain 2n at the end of S phase.*	• ***DNA replication* takes place.** Each chromosome now consists of two sister chromatids, attached to each other at the centromere. Chromosomes after replication remain fully extended and uncoiled; hence appear invisible under light microscope. • Histone proteins are also synthesized. **Note:** A centromere is a point of constriction on the chromosome, containing specific DNA sequence to which is bound a disk of protein called a ***kinetochore***. This disk functions as an attachment site for fibers that assist in cell division.
G_2 phase (second gap): This represents the time gap following DNA synthesis and the preceding cell division. It is therefore the time when the cell prepares for cell division. **Note:** **G_2** represents the second growth phase in which preparations are made for genomic separation.	• Synthesis of proteins like tubulin occurs in preparation for nuclear divisions. • Cell growth continues to occur. • Replication of mitochondria and synthesis of microtubules occurs. • In plants, chloroplasts also replicate during this phase and other organelles replicate. • Centrioles replicate. • Chromosomes condensation begins and microtubules begin to assemble at a spindle.

Note:

- Originally, Interphase used to be called a **resting stage** because under ligh microscope, the chromosomes were invisible and thus little was seen to b happening. But now, it's worth noting that Interphase is an active time when a ce is either growing and preparing to divide or fulfilling its specialized function in multicellular individual. Cells actually spend most of their time in Interphase. Th cell grows throughout Interphase and thus the G_1 and G_2 segments of Interphase ar periods of active growth, when proteins are synthesized and cell organelles produced

1. M phase (Mitotic or Meiotic phase)

M phase refers to a phase/a stage of the cell cycle where the actual cell division take place. It comes after interphase (G1, S, and G2 phases) and is much shorter in duratio compared to interphase. M-phase includes two tightly linked processes:

(i) Nuclear division (karyokinesis); either ***mitosis or meiosis***

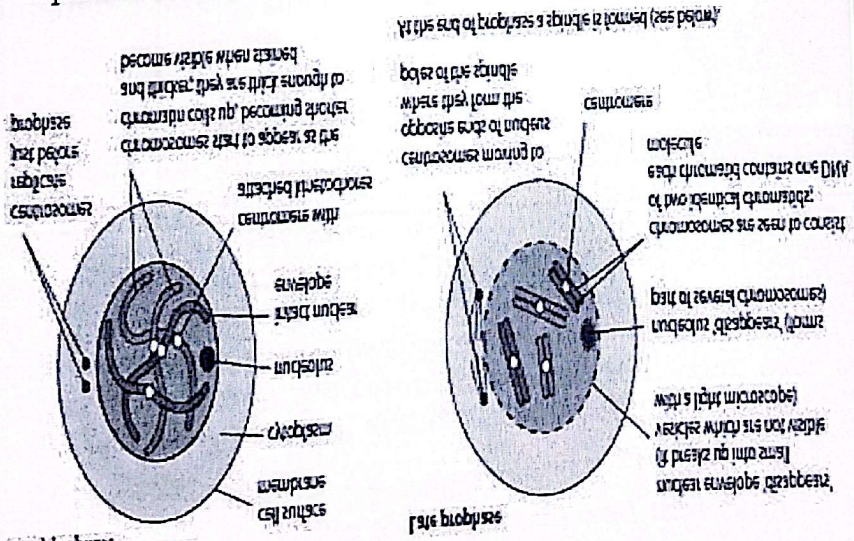
(ii) Cytokinesis (cytoplasm division).

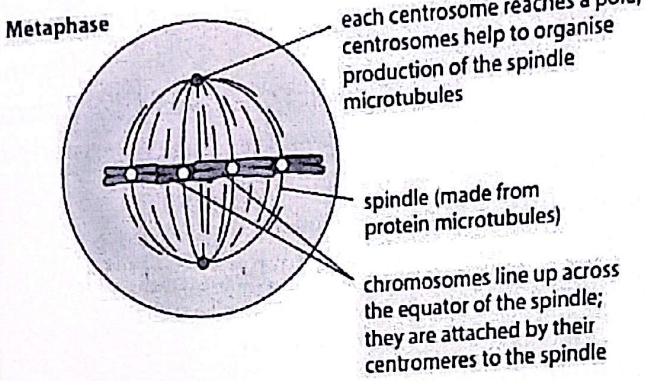
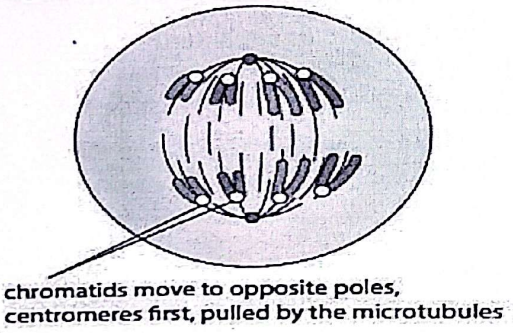
Note: *In nuclear division, depending on the cell type for example somatic cells undergo mitotic cell division while gamete cells undergo Meiotic division.*

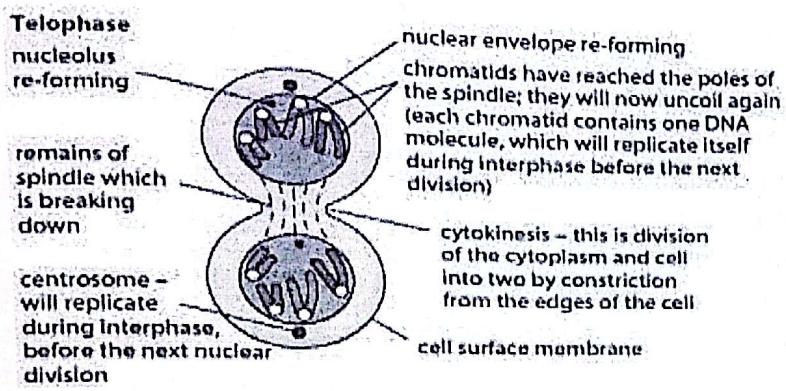
Mitosis

This is a type of nuclear division (karyokinesis), in which a parent cell divides into two daughter cells each containing the same number of chromosomes as the parent cell. It therefore divides the replicated chromosomes to form two daughter nuclei with identical chromosomes and genes except when mutation occurred. Mitosis is usually accompanied by Cytokinesis (cytoplasm division) that results in two daughter cells. Mitosis is a continuous process although it's often subdivided into four main stages, namely;

(i) Prophase.
(ii) Metaphase
(iii) Anaphase
(iv) Telophase

Stages	Events	Significance
Prophase	• Chromatin condense into a tightly coiled, folded, shorter and thicker visible structures called chromosomes (each with 2 sister chromatids joined at the centromere). • Nucleolus disintegrates and disappears. • Two pairs of centrioles/centrosomes (only in animal cells) migrate to the opposite poles of the cell. However, centrioles are absent in plant cells but are capable of forming spindle fibres. • Centrioles extend a radial array of microtubules called **asters** (star shaped structures) toward the plasma membrane when they reach the poles of the cell. Asters firmly support the centrioles against the membrane and stiffens the point of micro-tubular attachment during the retraction of the spindle. Plant cells, which have rigid cell walls, do not form asters. • Mitotic spindle begins to form from centrosomes. • The nuclear envelope breaks down and the endoplasmic reticulum reabsorbs its components. The breakdown leaves the chromosomes un-enveloped in the cell's cytoplasm. • Spindle fibers attach to the chromosomes at specialized structures called kinetochores (small disc-shaped structures at the surface of the centromere of each sister chromatid which serve as the sites of attachment of spindle fibres to the chromosomes). 	• Ensures chromosomes are compact and easier to move. • Establishes spindle apparatus for accurate chromosome alignment and separation.

Metaphase	• Chromosomes align singly at the equatorial plane (metaphase plate) of the cell. During the alignment, each sister chromatid face the opposite poles. • The spindle fibers attach firmly to kinetochores of each sister chromatid. • A "metaphase checkpoint" ensures all chromosomes are properly attached to spindle fibers before separation begins.  	• Guarantees that sister chromatids are lined up for equal distribution. • Prevents chromosome mis-segregation, reducing the risk of genetic imbalance in daughter cells.
Anaphase	• Centromeres split, separating the sister chromatids. • Spindle fibers shorten, pulling chromatids (now called daughter chromosomes) towards the opposite poles. • Cell elongates as non-kinetochore microtubules push against each other.  	• Ensures each pole receives an identical set of chromosomes. • Equal separation is critical for maintaining genetic stability in daughter cells.

Telophase	• Chromosomes arrive at opposite poles and begin to de-condense back into chromatin. • Nuclear envelope reforms around each set of chromosomes, forming two daughter nuclei. • Nucleolus reappears. • Spindle apparatus disassembles.  	• Restores normal nuclear structures in daughter cells. • Prepares the cell for completion of division (cytokinesis).

Cytokinesis

This is a phase in the cell cycle when a cell actually divides. It refers to a process by which the cytoplasm of the parental cell is divides to form two daughter cells. The cytoplasm is separated into two nearly equal parts with each part enclosing one of the newly formed daughter nuclei. This may happen during or soon after Telophase. Cytokinesis occurs differently in both animal and plant cells as discussed below.

Cytokinesis in animal that lack cell walls; Cytokinesis begins with the formation of a **cleavage furrow** *(shallow groove in the cell surface near the old metaphase plate)* midway between the two poles of the dividing cell which pinches the cell into two parts. The cleavage furrow occurs by the action of microfilaments. A ring of contractile actin filaments forms just inside the plasma membrane, in the middle. Myosin motor proteins associate with these actin filaments and use ATP to contract hence causing actin filaments to slide. As myosin moves the ring of actin filaments on the inside of the plasma membrane, the ring shrinks in size and tightens. Since the ring is attached to the plasma membrane, the shrinking ring pulls the membrane with it causing the plasma membrane to pinch inward. The actin and myosin filaments continue to slide past each other, tightening the ring further, until the original membrane pinches in two and cell division is complete. The cleavage furrow deepens until the parent cell is pinched in two, producing two completely separated cells, each with its own nucleus and share of cytosol, organelles, and other sub cellular structures.

Cytokinesis In plant cells:
There is no cleavage furrow due to a rigid cell wall that can't be squeezed into two by actin filaments. Instead, vesicles from Golgi apparatus containing cell wall materials move by microtubules to the middle of the cell, where they join to form a **cell plate**. The cell plate continues to grow outwards as new vesicles fuse with it, until its surrounding membrane fuses with the interior surface of the existing plasma membrane along the

perimeter of the cell. As a result, it divides the cell into two new daughter cells. Cellulose is then laid down on the new membranes, creating two new cell walls. The space between the daughter cells becomes impregnated with pectins and is called a **middle lamella.**

Comparison of mitosis in plants and animals

Similarities:

In both;

- Spindle fibres form
- During Prophase, chromosomes condense
- Before metaphase, the nuclear envelope breaks down.
- Spindle attaches to chromosomes at centromeres
- At metaphase, the chromosomes align at the equator
- At anaphase, chromosomes move towards opposite poles
- At Telophase, the nuclear envelope appears again, chromosomes de-condense, and the spindle breaks down.

Differences

Mitosis in animal cells	Mitosis in plant cells
Occurs almost all over the body	Occurs at apical, lateral and intercalary meristems only.
Centrioles present	Centrioles absent
Cytokinesis occurs by cleavage	Cytokinesis occurs by formation of cell plate.
Cell becomes round before division	Cell shape does not change before division
A furrow is formed between two daughter cells	A solid middle lamella forms between two daughter cells
Mitotic apparatus contains asters	Mitotic apparatus lacks asters
Spindle degenerates at cytokinesis	Spindle (phragmoplast) persists at cytokinesis.
Several hormones induce cell division, not one specifically	It is induced by a specific hormone called cytokinin

Significances of mitosis

1. **Facilitates growth of organisms**: It provides new cells required for an increase in body size of multicellular organisms.
2. **Facilitates tissue repair and replacement**: It replaces worn-out, old, or damaged cells (e.g., skin cells, red blood cells) which enables healing of wounds through regeneration of identical cells.
3. **Serves as a basis for asexual reproduction**: In unicellular organisms (e.g., *Amoeba, Paramecium*), mitosis forms the basis of asexual reproduction. In plants and some animals, mitosis produces structures for vegetative propagation (e.g., runners, tubers, bulbs).
4. **Allows maintenance of genetic stability**: Daughter cells formed by mitosis are genetically identical (clones) to the parent cell due to precise duplication and equal

distribution of chromosomes. Therefore, mitosis maintains the chromosome number constant across cell generations ($2n \rightarrow 2n$).

5. **Facilitates regeneration of some body parts in some animals:** In some organisms (e.g., starfish, planaria), lost parts can be regenerated by mitotic divisions.

Meiosis (reduction division)

This is a type of nuclear division that occurs in sexually reproducing organisms, in which a single diploid (2n) cell undergoes **two** successive nuclear divisions (meiosis I and meiosis II) but only one round of DNA replication, producing four haploid (n) daughter cells, each genetically different from the parent cell and from one another. It ensures reduction of chromosome number by half and introduces genetic variation through crossing over and independent assortment.

Significance s/ Importance of Meiosis

1. **Ensures maintenance of diploid chromosome number**: Meiosis reduces chromosome number from diploid to haploid in gametes which prevents doubling of chromosome number after fertilization, thereby maintaining species stability.
2. **Introduces genetic variation:** Events which occur during meiosis such as *crossing over* (exchange of genetic material between homologous chromosomes) during **prophase I** introduces new gene combinations. *Independent assortment* of homologous chromosomes during **metaphase I** results in diverse gametes. This variation serves as the raw material for evolution and natural selection.
3. **Formation of haploid gametes and spores:** Meiosis serves a key process in the formation of reproductive cells which serves as a basis for sexual reproduction.
4. **Ensures genetic stability across generations**: By halving the chromosome number in gametes, meiosis ensures that after fertilization, the zygote has the correct diploid chromosome number hence me
5. **May lead to elimination of harmful mutations**: Through recombination and random assortment, deleterious alleles may be lost or masked, contributing to genetic health of populations.
6. **Evolutionary significance**: Meiosis increases adaptability of populations to changing environments by generating genetic diversity which serves as the raw material for evolution and natural selection.

How meiosis causes almost infinite genetic variation / diversity

- Meiosis produces haploid male and female gametes which randomly fuse during fertilization thus creating new combinations of parental genes.
- **Crossing over** during **prophase I** of meiosis can separate and rearrange genes located on the same chromosome to form genetically non-identical gametes.
- **Independent assortment** of homologous chromosomes on metaphase plate during **metaphase I** with respect to which paternal and maternal homologue is on either side forms different combinations of parental chromosomes in gametes. The number of possible combinations of maternal and paternal homologues is **2n**, where **n** = the haploid number of chromosomes.

- During **Segregation / separation** of homologues in **anaphase - I** and sister chromatids at **anaphase II**, alleles for dominant / recessive traits go to **opposite poles** whereby only one of a pair of alleles goes into a single gamete.

Illustration to show crossing over

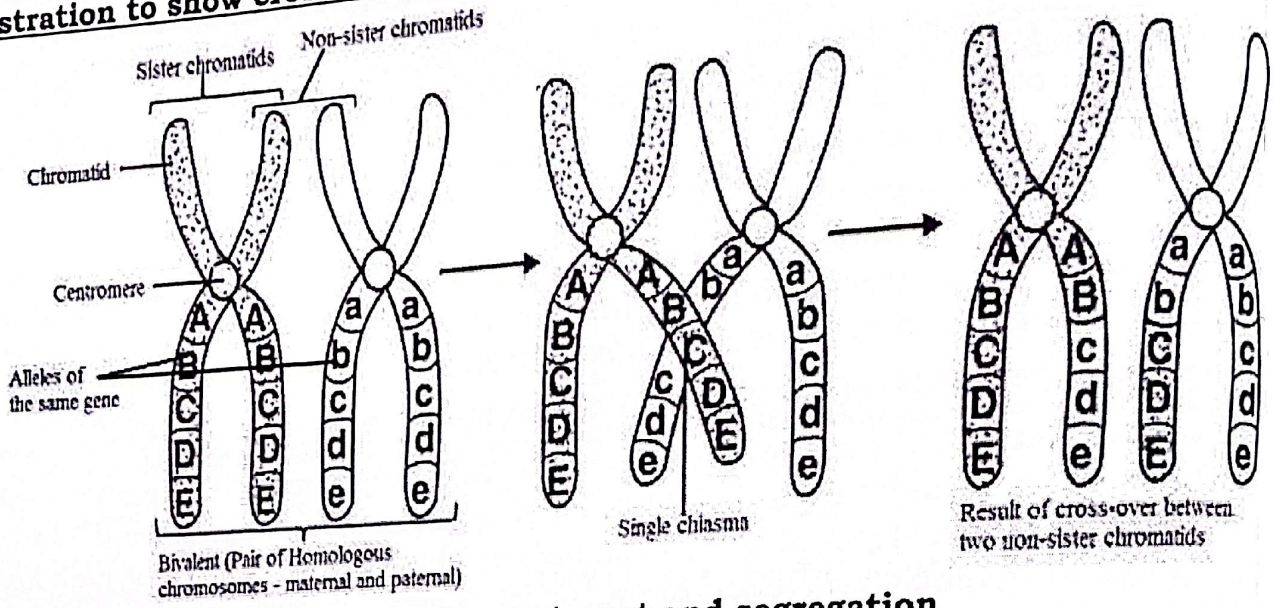
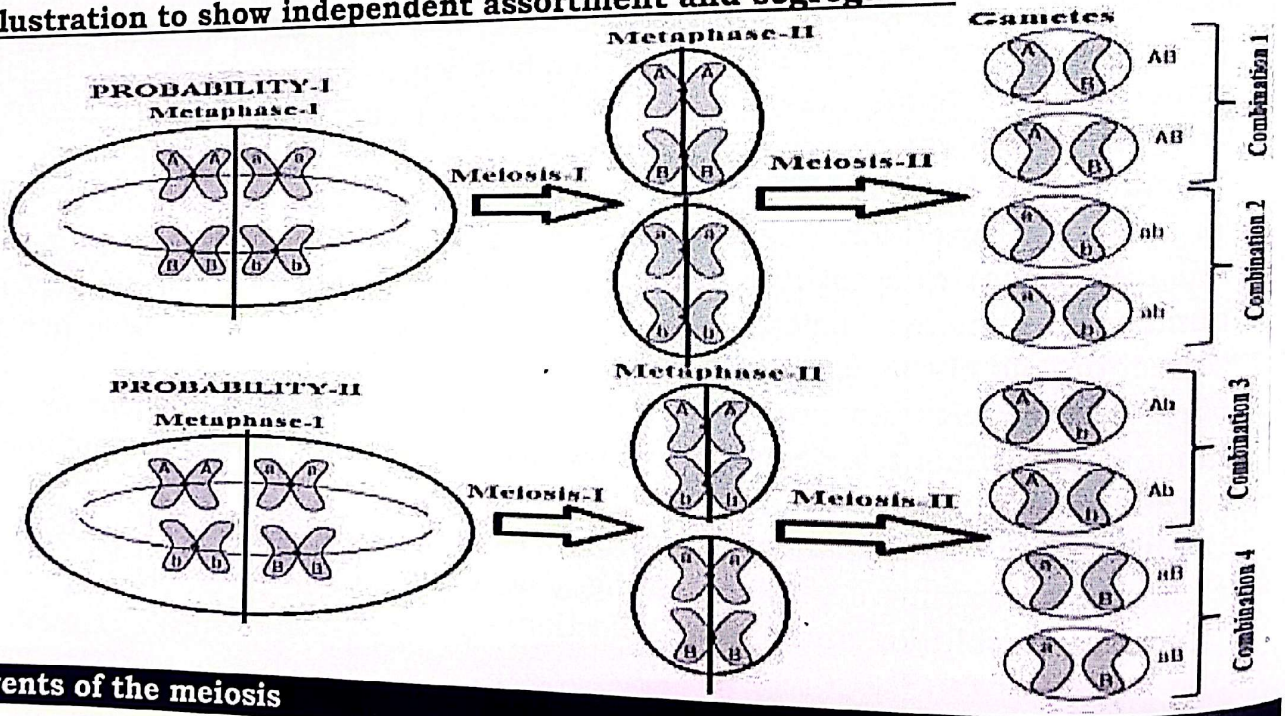
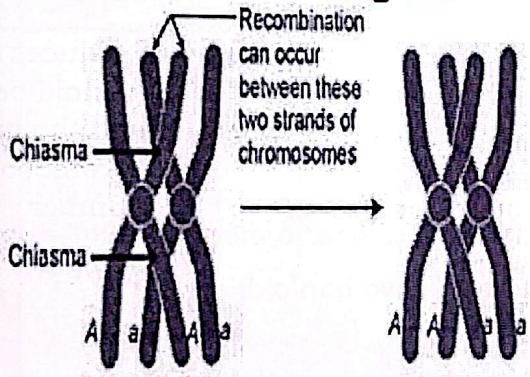
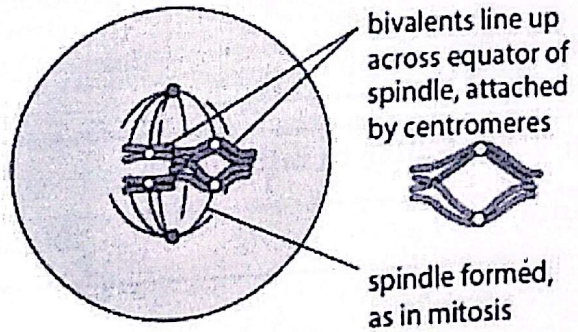


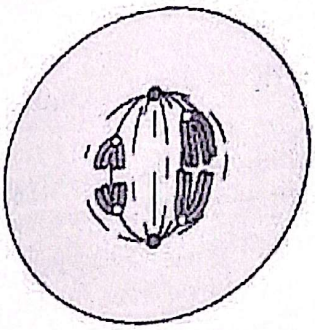
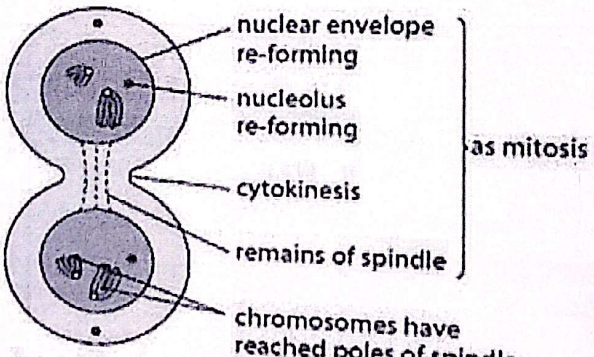
Illustration to show independent assortment and segregation



Events of the meiosis

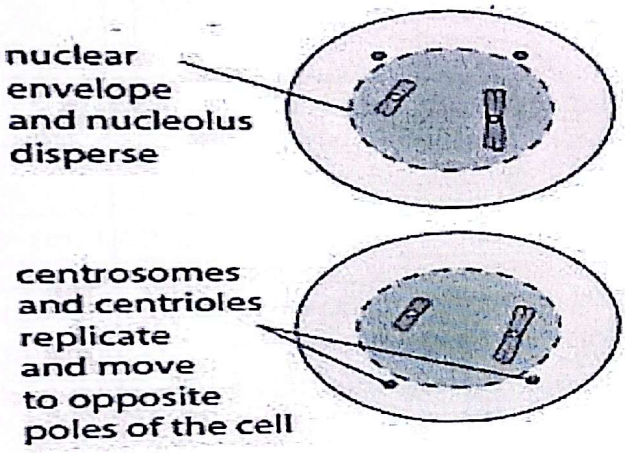
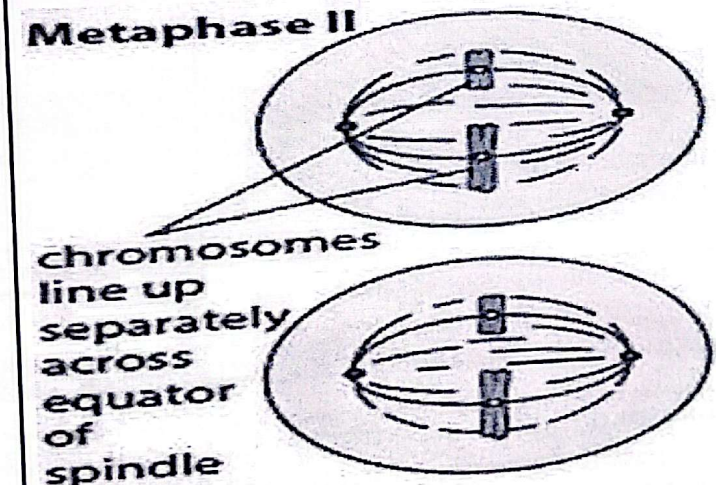
Stage	Events	Significance

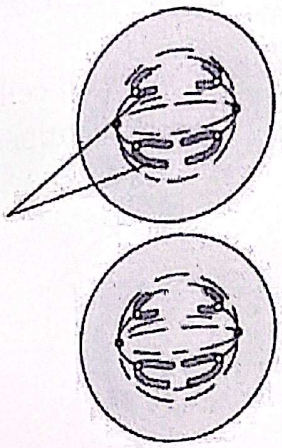
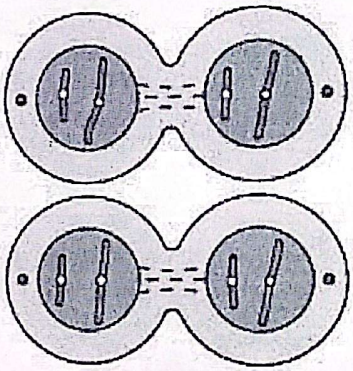
Prophase I	This is the longest and most complex stage, divided into 5 sub-stages: **(i) *Leptotene:*** Chromosomes condense and become visible. Spindle start to form. **(ii) *Zygotene:*** Homologous chromosomes pair up (synapsis) forming bivalents (tetrads). Nucleolus has disappears. **(iii) *Pachytene:*** Crossing over occurs between non-sister chromatids at chiasmata. **(iv) *Diplotene:*** Homologous chromosomes start to separate but remain attached at chiasmata. **(v) *Diakinesis:*** Chromosomes become fully condensed; nuclear envelope breaks down; spindle forms. **Illustration of crossing over**  	▪ Crossing over produces new genetic combinations that create genetic variations among organisms of the same parents. It is very important in evolution of species ▪ Pairing ensures proper segregation of homologous chromosomes.
Metaphase I	• Bivalents (homologous chromosome pairs) align at the equatorial plate. • Spindle fibers attach to kinetochores of homologous chromosomes. **Metaphase I** (showing crossing over of long chromatids)  	• Ensures random assortment of maternal and paternal chromosomes → genetic variation.

Anaphase I	• Homologous chromosomes (not sister chromatids) separate and move to opposite poles. • Sister chromatids remain attached at centromeres. **Anaphase I** Centromeres do not divide, unlike in mitosis. Whole chromosomes move towards opposite ends of spindle, centromeres first, pulled by microtubules.  **Note:** A key difference between meiosis and mitosis is that in meiosis during anaphase I, the sister chromatids are still together whereas in mitosis, they separate	• Reduces chromosome number from diploid (2n) to haploid (n).
Telophase I	• Chromosomes arrive at poles. • Chromosomes become long, thin hence not easily seen. • Nucleolus reappears and nuclear membrane/envelope reforms around each set of chromosomes. • Cytokinesis usually follows, producing two haploid cells. **Telophase I**  Animal cells usually divide before entering meiosis II.	• Produces two haploid cells with half the original chromosome number.

Meiosis II (second meiotic division): Very similar to mitosis

Stage	Events	Significance

Prophase II	• Chromosomes shorten and thicken (condense) again (if they had decondensed). • Chromatids are still attached at the centromeres. • Centrioles migrate to opposite poles. • New spindle fibers form in each haploid cell. • Nuclear envelope breaks down and disappears. • Nucleolus degenerates and disappears. 	• Prepares chromosomes for separation of sister chromatids.
Metaphase II	• Chromosomes align singly along the equatorial plate. • Spindle fibers attach to kinetochores of each chromatid. 	• Ensures proper orientation for chromatid separation.

Anaphase II	• Centromeres split. • Sister chromatids separate and move to opposite poles.  centromeres divide and spindle microtubules pull the chromatids to opposite poles	• Guarantees each daughter cell receives one copy of each chromosome.
Telophase II	• Chromatids (now called chromosomes) reach poles. • Nuclear envelopes reform around each set. • Cytokinesis follows, producing four haploid daughter cells.  This is like telophase of mitosis, but in meiosis telophase II four haploid daughter cells are formed	•Produces 4 genetically distinct haploid cells (gametes/spores).

COMPARISON OF MEIOSIS AND MITOSIS

Similarities

- Both involve cytokinesis to form daughter cells from a parent cell.
- Both follow the same fundamental sequence of events i.e. Interphase, prophase, metaphase, anaphase, and Telophase.
- Both involve the breakdown of the nuclear membrane during prophase.
- Both involve the separation of genetic material into two groups, followed by cell division.
- Both involve the reformation of the nuclear membrane in each cell during Telophase.
- Both involve alignment of chromosomes at the metaphase plate.
- Both are energy consuming processes, that is require

Differences

Mitosis	Meiosis
It results into formation of two daughter cells	It results into formation of four daughter cells
Daughter cells formed are identical to the mother cell/genetically identical	Daughter cells are different from the mother cell/genetically different
It occurs in somatic cells during growth and development and in asexual reproduction	It occurs during the formation of gamete cells in germ cells
No crossing over occurs	Crossing over occurs
It occur in haploid, diploid and polyploidy cells	It occurs in diploid cells only
Chiasmata are not formed	Chiasmata are formed
Homologous chromosomes do not associate	Homologous chromosomes associate
There is no formation of bivalents	Bivalents are formed in prophase I.
It involves only one nuclear division	It involves two successful nuclear divisions

CANCER

Cancer is a group of diseases characterized by uncontrolled, abnormal cell division that may invade nearby tissues and spread (metastasize) to other parts of the body. Unlike normal cells, cancer cells escape growth regulation mechanisms and continue dividing indefinitely.

Causes of Cancer

The causes of cancer can be categorized as follows;

Causes	Description
Genetic mutations	▪ Changes in DNA sequences of proto-oncogenes, tumor suppressor genes, or DNA repair genes can trigger cancer. For example: Mutation in the p53 tumor suppressor gene leads to loss of cell cycle control.
Carcinogens (Environmental agents/factors)	▪ Substances that can cause cancer by damaging DNA. For Examples: Tobacco smoke, asbestos, benzene, aflatoxins, radiation (UV & X-rays).
Viruses and Microorganisms	▪ Certain viruses integrate their genetic material into host DNA, leading to uncontrolled cell proliferation. For examples: Human papillomavirus (HPV → cervical cancer), Hepatitis B and C viruses (liver cancer), and Epstein-Barr virus (Burkitt 's lymphoma).

Hormonal factors	▪ Prolonged exposure to certain hormones can stimulate excessive cell division. For example: Estrogen linked to breast and endometrial cancers.
Chronic Inflammation and Immune Suppression	▪ Persistent inflammation damages tissues and increases mutation rates. ▪ Immunocompromised individuals have reduced ability to destroy abnormal cells.

Cancer risk factors

The chances of developing cancer are influenced by certain risk factors, which are conditions, behaviors or exposures that increase the likelihood of cancer development. They can be categorized into two categories;

Category	Explanation
Modifiable risk factors (controllable): These factors can be changed/ be avoided or controlled such as smoking, diet, alcohol use, physical inactivity, infections, and exposure to harmful substances.	(a) **Lifestyle factors:** lifestyle habits such as tobacco smoking, excessive alcohol consumption, unhealthy/poor diet (high-fat, low-fiber), obesity and physical inactivity all put a person at a higher risk of getting certain types of cancer. (b) **Environmental exposure:** Exposure to radiations, industrial chemicals like asbestos, benzene, heavy metals, or certain industrial pollutants like pesticides all do increase the risk of cancer. (c) **Biological factors:** Biological factors such as viral diseases and hormonal factors can increase a person's risk of getting certain types of cancer, For example, viral infections like HPV can cause cervical cancer, and Hepatitis B & C can cause liver cancer while HIV can cause Kaposi sarcoma. Long term use of hormone replacement therapy (HRT) or birth control pills can increase breast and endometrial cancer risk.
Non-modifiable (uncontrollable) risk factors: These factors can't be changed such as age, genetics and family history.	(a) **Age:** The risk of cancer increases with age due to accumulation of genetic mutations over time. (b) **Family history/genetics:** Inherited mutations can increase certain cancer risks (e.g., BRCA1 & BRCA2 increase breast/ovarian cancer risk). (c) **Sex:** some cancers are sex-specific (eg. prostate cancer in men, cervical cancer in women) while others are more common in one sex due to hormonal differences. (d) **Ethnicity/Race:** Certain cancers are more common in particular ethnic groups, partly due to genetic differences and lifestyle patterns.

Preventive measures for cancer

Cancer prevention aims to minimize risk factors and also detect the disease early for early management. The measures applied can be categorized into three;

Category of prevention	Explanation
Primary Preventive measures: These aim at reducing risk factors	▪ Avoid tobacco and limit alcohol intake. ▪ Eat healthy diet (fruits, vegetables, fiber-rich foods; reduced processed/red meat). ▪ Do regular physical activity and maintain a healthy body weight. ▪ Get Vaccinated (e.g., HPV vaccine, Hepatitis B vaccine). ▪ Limit exposure to radiation and carcinogenic chemicals. ▪ Practice safe sex to reduce cancer-linked viral infections.
Secondary Preventive measures: These include Early detection and screening	▪ Regular medical screening tests. For example pap smears (for cervical cancer), mammograms (for breast cancer), colonoscopy (for colorectal cancer) etc. ▪ Genetic testing for hereditary cancer risk.
Tertiary Preventive measures: These aim at reducing complications/aim at managing the disease and preventing recurrence.	▪ Post-treatment surveillance: Regular/Timely treatment and follow up to prevent recurrence or progression. ▪ Rehabilitation: Offering of physical, psychological, and social support. ▪ Lifestyle adjustments: observing healthy practices to reduce relapse of the risk.

Cancer treatment and management strategies

The treatment and management of cancer depends on cancer type, stage and patient health. The approaches maybe curative, palliative or supportive. These strategies include;

1. **Surgery:** This strategy involves removal of tumor mass (cancerous tissue) and nearby affected tissues. It is most effective when cancer is localized.
2. **Radiotherapy:** This involves use of ionizing radiations/high energy rays to destroy cancer cells or shrink tumors.
3. **Chemotherapy:** This involves use of cytotoxic drugs to kill rapidly dividing cells. The chemicals used may impose aggressive side effects like hair loss, nausea, and immune suppression.
4. **Targeted therapy**: This involves use of drugs designed to attack specific molecular targets or block cancer cell growth pathways (e.g., HER2 inhibitors in breast cancer).
5. **Immunotherapy:** This involves boosting the immune system so as to fight or attack the cancer cells (e.g., checkpoint inhibitors, CAR-T cell therapy).
6. **Hormone therapy**: This involves blocking hormones that promote cancer growth (e.g., tamoxifen in breast cancer, androgen deprivation in prostate cancer).
7. **Palliative and supportive care**: Supportive treatment to relieve symptoms and improve quality of life in advanced cancer stages.
8. **Stem cell and bone marrow transplantation**: For blood cancers like leukemia.

Relationship between cell division and Cancer

1) **Normal cell division (Mitosis):** In healthy cells, division is tightly regulated by cell cycle checkpoints (G1, G2, and M phases). Tumor suppressor genes stop uncontrolled division, while proto-oncogenes promote growth when needed.
2) **Cancer and uncontrolled cell division:** Mutations in proto-oncogenes (growth promoting genes that code for proteins that regulate normal cell growth and division) causes them to become oncogenes (mutated or abnormally activated forms of proto-oncogenes that drive uncontrolled cell proliferation), thus promoting continuous division. Mutations in tumor suppressor genes can lead to loss of control over division. Therefore, DNA repair mechanisms fail leading to accumulation of mutations that cause malignant transformation.
3) **Apoptosis avoidance:** Normal cells undergo programmed cell death (apoptosis) if damaged while Cancer cells evade apoptosis and continue dividing.
4) **Hallmarks of cancer linked to cell division:**
   - Sustained proliferative signaling.
   - Evading growth suppressors.
   - Enabling replicative immortality (via telomerase activation).
   - Genome instability and mutation accumulation.
5) **Metastasis and Uncontrolled Growth:** Due to uncontrolled mitosis, cancer cells form tumors. Some cells break away, enter blood/lymph, and establish secondary tumors (metastases).

Gene Technology and Its key techniques

Gene technology refers to a collection of methods used to manipulate, modify, and study genetic material for various purposes in medicine, agriculture, industry, and research. The central aim of gene technology is to understand gene function, control gene expression, and apply this knowledge to solve biological and practical problems.

Key techniques of gene technology:

The key techniques include;

(a) Recombinant DNA Technology.
(b) Gene Cloning.
(c) Polymerase Chain Reaction (PCR)

Recombinant DNA Technology

This refers to a set of techniques used to artificially combine DNA molecules from different sources (species or individuals) to form a new set of genetic instructions and then inserted into a host organism to express desired traits or produce useful products. It forms the basis of modern genetic engineering and biotechnology.

Major Key steps involved:

1. **Identification and isolation of the gene of interest**: The specific gene responsible for a desired trait is identified and then is extracted from the donor organism. The desired gene is isolated using methods such as; restriction enzymes (like restriction endonucleases which cut DNA at precise sequences, producing sticky or blunt ends), use of chemical methods to synthesize the gene or making cDNA from mRNA using reverse transcriptase.

2. **Selection & insertion of desired DNA into a suitable vector**: Here, suitable vectors such as; plasmids, bacteriophages, or cosmids are used to carry/transfer foreign DNA into a host.
3. **Cutting and ligation of DNA**: Here, both the vector DNA and donor DNA are cut using the same restriction endonucleases; creating complementary sticky ends or blunt ends. The DNA ligase enzyme then joins the donor DNA fragment with the vector DNA to form recombinant DNA.
4. **Introduction of recombinant DNA into host organism:** The recombinant DNA is introduced into a host cell such; as bacteria (commonly E. coli), yeast, or other host cells like animal cell. The methods used include; Transformation, Transduction, electroporation, microinjection or biolistics.
5. **Cloning and selection of recombinants**: Here, the host cells multiply, and colonies containing the recombinant DNA are identified using marker genes (e.g., antibiotic resistance) and then selected.
6. **Expression and harvesting**: The foreign gene is expressed, producing proteins (e.g., insulin, growth hormones) or desired traits. The desired protein is finally extracted and purified for commercial use.

Applications of recombinant DNA technology

Sector	Use(s)
Medicine	• Production of human insulin, growth hormone, clotting factors, Interferons etc. • Development of vaccines like Hepatitis B recombinant vaccine. • Gene therapy for correcting genetic disorders like cystic fibrosis. • Diagnosis of diseases using recombinant DNA probes.
Agriculture	• Development of genetically modified (GM) crops resistant to pests, or herbicides (e.g, Bt cotton, Golden rice)
Industry	• Production of enzymes like amylases, proteases, cellulases used in food, detergents and textiles. • Synthesis of biofuels and biodegradable plastics.
Research	• Studying gene functions by introducing or knocking out genes. • Creating transgenic animals for biomedical research. • DNA fingerprinting and forensic applications.

Gene Cloning

This is a process of making multiple identical copies of a particular/specific gene or DNA fragment by inserting it into a suitable host organism through recombinant DNA technology. Therefore, it is essentially an outcome of recombinant DNA technology, but with a focus on producing multiple identical copies of a gene for analysis, manipulation, or practical use.

Types of cloning:

1. **Molecular (gene) cloning:** This involves insertion of a specific DNA fragment into a vector to produce multiple copies.

2. **Cell cloning:** This involves production of genetically identical cells.
3. **Organism cloning (reproductive cloning):** This is where an entire organisms are cloned (e.g., Dolly the sheep, cloned using somatic cell nuclear transfer).

Steps in Molecular Gene Cloning:

1. Isolation of target gene from donor organism.
2. Insertion into a cloning vector (like plasmids).
3. Introduction into host cells (via transformation).
4. Replication of host cells, leading to amplification of the target gene.
5. Selection and screening for cells carrying the desired gene.
6. Gene expression analysis or large-scale production.

Applications of gene cloning

Sector	Use(s)
Medicine	• Production of therapeutic proteins such as; human insulin, growth hormone, clotting factors, Interferons etc. • Development of vaccines like Hepatitis B recombinant vaccine. • Gene therapy (insertion of normal genes to treat/correct genetic disorders like cystic fibrosis.
Agriculture	• Creation of transgenic plants with resistance to pests, herbicides or harsh climates. • Development of nutritionally enhanced crops e.g., golden rich in vitamin A.
Industry	• Large scale production of enzymes for detergents, food and textiles. • Microbial fermentation to produce biofuels and biodegradable plastics.
Research	• Studying gene structure, function and regulation. • Production of transgenic animals for biomedical studies. • DNA fingerprinting, forensic analysis and evolutionary studies.

Polymerase Chain Reaction (PCR)

This is a molecular biology technique used to amplify (make many copies of) a specific DNA segment, generating millions of copies from a very small initial sample within a short time in vitro (outside a living organism).

Key Components required for PCR:

i) **Template DNA:** This contains the target sequence to be amplified.

ii) **Primers:** These are short synthetic oligonucleotides that are complementary to the target regions, that's to say they are short DNA sequences that define the region to be amplified.

iii) **DNA polymerase:** Usually **Taq Polymerase**, a heat-stable DNA polymerase from *Thermus aquaticus* is required.
iv) **dNTPs (nucleotides):** These serve as building blocks for new DNA strands.
v) **Buffer solution:** This provides the optimal pH and ionic environment
vi) **Thermocycler:** This is the machine that controls temperature changes.

Major Steps in PCR:

1. **Denaturation (94–98°C):** Here, the double-stranded DNA melts and separates into single strands as the hydrogen bonds break.
2. **Annealing (50–65°C):** The synthetic primers bind (anneal) to the complementary target sequences on the single stranded DNA template.
3. **Extension/Elongation (72°C):** Here, the DNA polymerase extends the primers, synthesizing new DNA strands using dNTPs (Taq polymerase synthesizes new DNA strands by adding nucleotides).
4. **Repetition**: The cycle is repeated 25–40 times, exponentially increasing DNA copies.

Applications of PCR

Sector	Use(s)
Medical and clinical applications	• Disease diagnosis, that is to say detection of pathogens like HIV, TB, SARS-CoV-2 etc. • Genetic testing, that's to say identification of mutations causing diseases. • Cancer research, that's to say identification of oncogenes and tumor markers.
Forensic science	• DNA fingerprinting for criminal investigations. • Identification of individuals from biological samples (blood, hair, saliva) etc
Molecular biology research	• Cloning of genes for recombinant DNA technology. • Sequencing DNA and studying gene expression. • Mutagenesis studies.
Agriculture and environment	• Detection of GMOs (genetically modified organisms) • Studying plant pathogens. • Environmental monitoring of microbial populations.
Evolutionary and anthropological studies	• Analysis of ancient DNA from fossils. • Tracing human ancestry/evolutionary relationships and migration patterns.

Implications of gene Technology

These refer to the consequences, effects and impacts (positive or negative) that result from using gene technology.

Positive Implications	Negative implications/concerns
1. Medicine: • Production of human insulin, interferons, and vaccines. • Gene therapy to correct defective genes. • Development of personalized medicine. • Early disease diagnosis through PCR and genetic markers. **2. Agriculture:** • Development of genetically modified (GM) crops resistant to pests, diseases, and drought. • Enhanced nutritional value of foods (e.g., Golden Rice with vitamin A). • Increased crop yields, contributing to food security. **3. Industry:** • Production of biofuels and biodegradable plastics. • Large-scale production of enzymes for detergents, food, and beverages. **4. Research and Conservation:** • Study of evolutionary relationships through genetic analysis. • Conservation of endangered species through cloning and genetic banks. • Detection of biodiversity and monitoring ecosystems.	**1. Ethical Issues:** • Cloning of organisms raises moral and religious concerns. • Genetic modification of humans (designer babies) is controversial. • Privacy concerns in genetic testing. **2. Health and Environmental Risks:** • GM crops may lead to development of resistant pests ("super-pests"). • Possible allergenic effects of genetically modified foods. • Escape of genetically modified organisms into the wild may disrupt ecosystems. **3. Socioeconomic Concerns:** • Dependence of farmers on biotech companies for seeds. • Unequal access to gene therapy and advanced medicine, widening the healthcare gap.

Ethical, social and environmental implications of gene technology on GMOs

Genetically modified organisms (GMO) is any living organisms (plant, animal or microorganism) whose genetic material (DNA) has been altered using genetic engineering techniques. It involves inserting, deleting or modifying specific genes to give the organisms new traits that do not occur naturally through mating or natural recombination. Gene technology, particularly the creation and use of genetically modified organisms (GMOs), has transformed agriculture, medicine, and industry.

However, it raises a number of concerns which can be categorized as; ethical, social and environmental implications;

Category	Explanations
1. Ethical implications	**a) Human health and safety** • Concerns that GMO foods may have unintended health effects such as allergies or long-term impacts on human health. • Ethical debate arises over the adequacy of safety testing before GMO products reach consumers. **b) Genetic manipulation of humans:** • Gene therapy and genetic engineering raise questions about the possibility of "designer babies", where genetic traits like intelligence, physical appearance, or athletic ability could be selected. • Some religious and cultural groups consider altering genetic material as interfering with natural or divine order. **c) Animal welfare:** • GM animals are often used for research or food production (e.g., fast-growing salmon, cows producing therapeutic proteins). Therefore, the ethical issues include animal suffering, unnatural traits, and whether humans have the moral right to alter other species. **d) Equity and Justice** • Access to advanced gene technologies and therapies is often limited to wealthy countries or individuals, raising ethical concerns of global inequality. • Farmers may face patent restrictions that limit their rights to save and reuse seeds.
2. Social implications	**a) Food security:** • GM crops can improve yields and resistance to pests, helping to address hunger. • However, there is public skepticism and mistrust toward GMO foods, leading to consumer resistance in some regions. **b) Cultural and religious beliefs:** • Some communities reject GMO foods because they are considered unnatural or against religious dietary laws (e.g., if genes from animals are inserted into plants). **c) Corporate control** • Large biotechnology companies often control GMO seeds and may enforce intellectual property rights. This creates farmer dependency on multinational corporations, potentially reducing local autonomy in agriculture.

	d) Public perception and trust: • Lack of transparency in labeling GMO foods can erode public trust. • Calls for mandatory labeling reflect the right of consumers to make informed choices. **e) Socioeconomic Inequality:** • Wealthy nations and companies benefit more from gene technology than poorer communities. • Small-scale farmers may be disadvantaged if unable to afford GMO seeds, fertilizers, or licensing fees.
3. Environmental implications	**a) Biodiversity loss:** • GMO crops often lead to monocultures, reducing genetic diversity in agriculture. • Cross-pollination between GM and non-GM plants may contaminate wild species, potentially threatening natural biodiversity. **b) Pest and weed resistance:** • Overuse of pest-resistant GM crops (e.g., Bt cotton) can cause insects to evolve into "super-pests." • Similarly, herbicide-tolerant crops may encourage the emergence of "super-weeds." **c) Impact on non-target species:** • GM crops engineered to produce toxins (e.g., Bt toxin) may inadvertently harm beneficial insects, soil organisms, or other non-target species. **d) Soil and ecosystem health:** • Changes in farming practices due to GM crops (such as increased herbicide use) can affect soil fertility, microbial communities, and water quality. **e) Gene escape and ecological imbalance:** • Modified genes may escape into the wild, causing uncontrolled ecological changes. For example: Herbicide-resistant genes spreading to wild relatives, creating invasive species.

GENETICS

Genetics refers to the branch of science which deals with the scientific study of heredity and variation amongst organisms of the same species. It accounts for the occurrence of similarities and differences among organisms of the same species; as well as explaining how traits are transmitted to offsprings from their parents. The transmission or the process by which characters/traits are passed from the parents to the offsprings is what

is known as ***heredity***; while the differences among organisms of the same species is known as ***variation***.

It's important to understand that the characteristics of an individual organisms are influenced by both the genetic factors inherited from their parents and the environmental factors where the organisms lives.

Terms used in genetics

1) **Chromosome:** This is thread-like structure located in the nucleus of eukaryotic cells and bears genes that determine characteristics.
2) **Chromatid:** This is one half of the duplicated chromosome split longitudinally.
3) **Ploidy:** This refers to the number of complete sets of chromosomes present in the nucleus of a cell of an organism. Diploid organisms like humans have two sets, represented by **2n** while haploid cells have one set being represented by **n**.
4) **Gene:** This is a basic unit of the hereditable material found on the chromosome and responsible for controlling a particular trait/character Or It is a section/segment of DNA that codes for a particular protein which determines a given characteristic.
5) **Allele:** This is the alternative form of the same gene which control contrasting character. Each gene has two or more alleles. For study purpose, each allele is represented by a letter like T, H etc.
6) **Locus:** This is the point on a chromosome where a gene or allele is located.
7) **Genotype:** This refers to the genetic composition/make up of an organism. It states which alleles of the genes are present.
8) **Phenotype:** This refers to observable/physical appearance or the outward expression of an organism. It's determined by the interaction between the genotype and the environment.
9) **Dominant gene/allele**: This refers to a gene /allele whose effect is seen in the phenotype/expresses itself in both heterozygous and homozygous forms. It is represented by capital (upper case letters) like T, N etc
10) **Recessive gene/ allele**: This refers to a gene/allele whose effect is not phenotypically expressed in the heterozygous state or it is an allele that can only express itself phenotypically in the homozygous form as it is suppressed by the dominant allele in the heterozygous form. It is represented by small (lower case letters) like t, n etc
11) **Homozygous**: This is a genotype consisting of two identical alleles of the same gene like TT, GG, tt. It can be homozygous dominant if both alleles are dominant (TT, GG) or homozygous recessive if both alleles are recessive (tt, gg)
12) **Heterozygous:** This is a genotype consisting of two dissimilar alleles of the same gene like Tt, Hh, Bb.
13) **Fertilization:** This is the fusion of the male and female gametes to form a zygote.
14) **Pure breeding line:** This is a breed of organism that consistently show the same phenotype from generation to generation when bred within its self.
15) **Hybrid**: This is an offspring produced by two parents of different pure lines.

16) **F1 generation:** This is a generation of offspring that has descended directly from crossing two pure breeding lines.

17) **F2 generation:** This is a generation of offspring obtained by crossing two F1 generation individuals

18) **Test cross:** This is a type of back cross which involves crossing an offspring having a dominant character with its recessive parent in order to determine the genotype of that offspring.

19) **Back cross:** This is the mating of an offspring with one of its parents.

Mendel's genetic experiments and principles of inheritance

This mechanism of inheritance was discovered by an Austrian monk and biologist known as *Gregor Johann Mendel (father of inheritance)* who carried out a number of genetic experiments using the garden pea plants *(Pisum sativum);* which he grew in the vegetable garden in his monastery. He later observed many sexually reproducing organisms and found out that they had variations among themselves despite being of the same species. The experiments conducted were a basis for his laying down of his principles.

Why Mendel used garden peas

- They occurred in many varieties with distinct characters
- The plants were easy to cultivate
- All their offsprings were fertile
- They have a short life cycle that they reproduced so quickly
- The plants also had many contrasting characters with no intermediates
- Their reproductive structure were enclosed in petals which allowed for production of pure breeding plants due to self-pollination over many generations

Monohybrid inheritance & Mendel's genetic experiments

Monohybrid inheritance refers to the inheritance of a single pair of contrasting characteristics. Examples include, inheritance of height, blood groups, albinism, sickle cell anaemia, and sex linked characteristics etc.

In one of Mendel's genetic experiments with the garden peas, he crossed tall garden pea plants with short garden pea plants. In order to properly manage the cross, Mendel covered the stigma of all flowers of one group, and removed all the anthers from the flowers of another group of the garden pea plants in order to prevent self-pollination, and transferred pollen using a brush. The resultant seeds were planted and he observed that all the $\mathbf{F_1}$ offsprings were tall. He then selfed the $\mathbf{F_1}$ pea plants to get **F_2 generation.** This generation comprised of a mixture of tall and short pea plants in a ratio of ***3 tall: 1 short plants.*** This **3:1** ratio became known as Mendel's monohybrid ratio of the dominant and recessive characters respectively in the F_2 generation.

Observation;

- Mendel was able to observe that neither of the F_1 nor F_2 had intermediate phenotypes.

Conclusions from Mendel's genetic experiments about the mechanism of inheritance:

- The phenotypic characteristics of an organism are under the control of internal factors (these factors were later named genes)

- It is these factors that are transmitted from the parents to the offsprings i.e. (from one generation to the next).
- For each character, an organism inherits from the parents two alleles (internal factors), one from each parent and it is these factors which account for variations in inherited characters.
- The factor which phenotypically appears in $\mathbf{F_1}$ generation is dominant to the one which fails to phenotypically show up in $\mathbf{F_1}$ but instead appears in the $\mathbf{F_2}$ generation.
- During sexual reproduction, the egg cell and the sperm cell makes an equal contribution to each of the characteristics of the offspring such that the offspring has both male and female parental characteristics. This is because the two alleles for each heritable character separates or segregate during formation of gametes in meiosis and end up in different gametes.
- He then concluded that inheritance is **not** by the mixing/blending of features to produce intermediates but rather the process by which **internal factors** of the body **may or may not** express themselves in the phenotype. From his conclusions, Mendel was able to formulate his first law of inheritance which is well known as the law of monohybrid inheritance/law of segregation/law of particulate inheritance

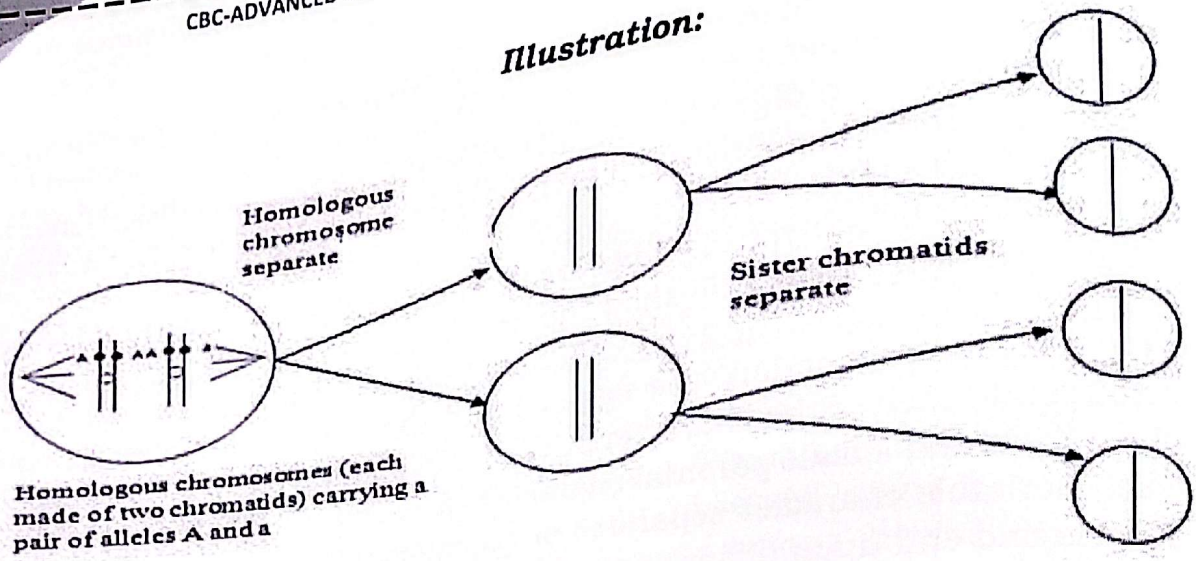
Fist Mendel's law of inheritance states that ***"The characteristics of an organism are controlled by internal factors which occur in pairs but only one can be carried in a single gamete".***

Later with advancements in technology and microscopy, internal factors later came to be known as **genes** and Mendel's first law was modified. It can **modernly** be stated as follows. "*The characteristics of a diploid organism are controlled by alleles which occur in pairs but singly in gametes*".

Explanation of Mendel's first law of segregation by meiosis

Mendel's first law can currently be explained/accounted for in terms of meiosis. The genes which determine organisms' characters usually occur in two alternative forms called alleles located on homologous chromosome. During anaphase 1 of meiosis, these homologous chromosomes separate (segregate) and move to opposite daughter nuclei. Subsequent cell division results into two gamete cells each containing one of the two alleles; therefore the alleles occur as pairs in body cells but singly in gamete cells.

Illustration:



A full genetic explanation of Mendel's first law and the 3:1 ratio

Let;

T represent the allele for tallness, t represents the allele for shortness

Parents	:	male	x	female
Phenotypes	:	Tall	x	short
Genotypes	:	TT	x	tt
Meiosis				
Gametes		T T		t t
Random fertilization	:			
F_1 genotypes	:	Tt Tt Tt Tt		

Offspring phenotypes: **All tall**

Genotypic ratio : **All Tt,**

To obtain F_2 generation, F_1 hybrids were selfed as shown below

Let;

T represent the allele for tallness, t represents the allele for shortness

Parents : male x female

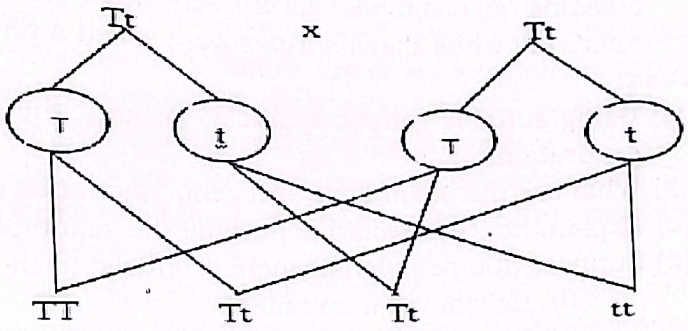
Phenotypes : Tall x tall

Genotypes : Tt x Tt

Meiosis

Gametes

Random fertilization :



F_2 genotypes :

F2 phenotypes : Tall : Tall : Tall : short

Genotypic ratios: 1TT: 2Tt: 1tt;

Phenotypic ratios: 3 Tall: 1 Short

Mendel carried out many other experiments on peas and other organisms and all gave consistent results as shown below:

Character	Parental phenotypes	F_1 generation	F_2 generation	Ratio
Stem length	Tall X Short	All tall	787tall, 277short	2.84:1
Seed colour	Green X Yellow	All yellow	6022yellow, 2001green	3.01:1
Seed shape	Round X Wrinkled	All round	5474 round, 1850wrinkled	2.96:1
Seed coat	Coloured X White	All coloured	705 coloured, 224 white	3.15:1
Pod colour	Green X Yellow	All green	428 green, 152 yellow	2.82:1
Pod shape	Inflated X Constricted	All inflated	882 inflated, 299 constricted	3:1
Flower position	Terminal X Axial	All axial	651 axial, 207 terminal	3.14:1
Flower colour	Purple X white	All purple	705 purple, 224 white	3:1

Note:

- It became so obvious to predict which trait of a given pair is dominant over the other. In a cross starting with pure breeding parental stocks, all the F_1 hybrids show the dominant trait. In addition, a larger proportion of the F_2 hybrids show the dominant trait while those showing the recessive one are always fewer in number.
- In case of individuals showing the dominant trait (as phenotype), the genotype may either be Homozygous dominant or heterozygous. Such genotypes can be distinguished by performing a test cross; that is, crossing the unknown with a homozygous recessive individual.
- Appropriate letters are always 'let' or used to represent respective alleles involved.

- Across (X) must be indicated to symbolize mating between the parents.
- Directive words must be indicated to define each step of the cross.
- In case of identical gametes, only one can be indicated.

TRIAL ITEMS

1. In a garden pea plant there are two forms of heights i.e. tall and short. When a pure breeding tall pea plant was crossed with a short pea plant all the offsprings obtained where tall when the offsprings were selfed a phenotype ration was obtained in F_2.

Task:

(a) Using suitable genetic symbols, workout the genotypes and phenotypes of the F_2 generation.
(b) What are the phenotypic and genotypic ratios of the F_2 generation?
(c) Explain how you would determine the genotype of F_1 tall pea plants formed.
(d) Suppose 300 pea plants where produced in the F_2 generation
  (i) How many were tall?
  (ii) How many were short?

2. Suppose a man who is a tongue roller marries a woman who is a non-tongue roller and all the children obtained in F_1 are tongue rollers.

Task:

(a) Work out the phenotypic and genotypic ratio as obtained in F2 generation.
(b) What is the probability that the 4th born is a non-tongue roller?

Dihybrid inheritance and Mendel's second law of inheritance

Dihybrid inheritance refers to the inheritance of two pairs of contrasting characteristics simultaneously/ is the inheritance of two different traits controlled by two different genes located on different loci (different chromosomes) in the same organism. It involves simultaneous transmission of two pairs of alleles from parents to the offsprings. It was also studied extensively by Gregor Mendel using the garden pea plants.

For instance, in one of his experiments; Mendel crossed pure breeding **tall** pea plants with **red** flowers with pure breeding **dwarf** plants having **white** flowers. All in the F_1 progeny were **tall with red flowers**. This showed just like Mendel had discovered before that the alleles for tallness and red flowers were dominant to those for dwarfness and white flowers respectively.

Mendel went ahead to self-pollinate the F_1 plants and obtained an F_2 progeny, this comprised of a variety of phenotypes as summarised as follows.

- **315 Tall with red flowers**
- **101 Tall with white flowers**
- **108 Dwarf with red flowers**
- **32 Dwarf with white flowers**

These give the respective phenotypic ratios as **9:3:3:1**, being known as **Mendel's Dihybrid ratio**, which is the ratio of phenotypes in the F_2 generation for a Dihybrid cross. From that cross and many other similar crosses, Mendel was able to make the following observations:

- Both phenotypes/characters (height and flow... separated and behaved indepe... but

- Two of the F2 phenotypes resembled one or the other of the parental phenotypes while two new combinations of phenotypes appeared in the F_2; (Tall/white and Dwarf/red). These are known as recombinants.
- The allomorphic pairs of characteristics (controlled by different alleles of the same gene) occurred in a phenotypic ratio of 3 dominant: 1 recessive. e.g. 3 tall: 1 dwarf and 3 red: 1 white.

Therefore, when Mendel considered the inheritance of two characteristics simultaneously, he concluded that these characteristics are inherited independently and each pair of alleles separates during meiosis such that each of the alleles combines randomly with either alleles of another pair. Basing on the above observations, Mendel formulated his second law known as the ***law of independent assortment.*** The Mendel's second law states that; **"Any one of a single pair of characters may combine randomly with either one from another pair"**

Since the two genes controlling the two traits (height and colour) in the garden peas Mendel used above were located on different chromosomes, this allowed independent assortment of their alleles during gamete formation such that the gametes formed could combine in all possible combinations, producing the **9:3:3:1**, phenotypic ratio in **F_2**. Below is a full genetic explanation of the **9:3:3:1** dihybrid ratio of phenotypes in the **F_2** generation for the above dihybrid cross.

Let; *T represent allele for tallness, t for dwarfness*

R represent allele for red flowers, r for white flowers

Parents	:	Male	X	Female
Phenotypes	:	Tall, red flowered	X	Dwarf, white flowered
Genotypes	:	TTRR	X	ttrr
Meiosis	:	↓		↓
Gametes	:	all (TR)		all (tr)
Random fertilization	:	All TtRr		
F_1 genotypes	:			

Phenotypic ratios : All Tall with red flowers.

By selfing F_1 plants;

	Male	×	Female
Parents	Tall, red flowered	×	Tall, red flowered
Phenotypes	TtRr	×	TtRr
Genotypes			
Meiosis			
Gametes	TR Tr tR tr		TR Tr tR tr

Random fertilization

♂ \ ♀	TR	Tr	tR	tr
TR	TTRR	TTRr	TtRR	TtRr
Tr	TTRr	TTrr	TtRr	Ttrr
tR	TtRR	TtRr	ttRR	ttRr
tr	TtRr	Ttrr	ttRr	ttrr

Therefore, the F_2 phenotypic ratio is: **9** Tall with red flowers: **3** tall with white flowers: 3 short with red flowers: **1** short with white flowers.

Note:

When performing a dihybrid cross;

- Alleles of the same gene cannot pass into the same gamete (they segregate during meiosis). For example, allele **T** can only be present in the same gamete with **R** or **r** but not with **t or** another **T** while allele **t** can only be present in the same gamete with **R** or **r** but not **T** or **t** just like in the example above.
- The possible combination of gametes during fertilization can be shown using a Punnet square (after the Cambridge geneticist R. C. Punnet). This minimizes errors when listing the combinations.

In summary; the following can be noted from Mendel's hypotheses:

- Each characteristic of an organism is controlled by a pair of alleles.
- During meiosis, each pair of alleles segregate (separates) and each gamete receives one of each pair. This is known as the law of segregation.
- During gamete formation, either one of a pair of alleles can pass into the same gamete with either one from another pair. This is known as the law of independent assortment.
- Each allele is transmitted one generation to the next as a discrete unit
- Each diploid organism inherits one allele for each character from each of the two parents.
- If an organism has two unlike alleles for a given gene, one may be expressed (dominant) at total exclusion of the other (recessive).

Explanation of Mendel's second law of inheritance by meiosis

Mendel's second law can be explained/accounted for on the chromosomal basis by meiosis. During formation of gametes by meiosis, the distribution of each allele from a single pair is entirely independent of alleles from other pairs. This in turn depends on the random orientation of the homologous chromosomes onto the equatorial spindle in metaphase **I.** Subsequent separation during anaphase I leads to a variety of allele

	Male	×	Female
Parents	Tall, red flowered	×	Tall, red flowered
Phenotypes	TtRr	×	TtRr
Genotypes			
Meiosis			
Gametes	TR Tr tR tr		TR Tr tR tr

Random fertilization

	TR	Tr	tR	tr
TR	TTRR	TTRr	TtRR	TtRr
Tr	TTRr	TTrr	TtRr	Ttrr
tR	TtRR	TtRr	ttRR	ttRr
tr	TtRr	Ttrr	ttRr	ttrr

Therefore, the F_2 phenotypic ratio is: **9** Tall with red flowers: **3** tall with white flowers: 3 short with red flowers: **1** short with white flowers.

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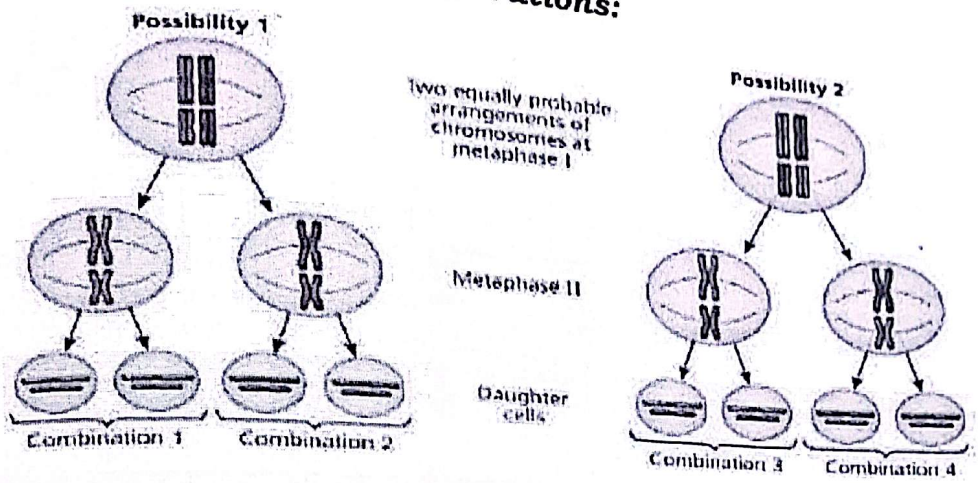
combinations in gametes. In this process; any one of a single pair of alleles can combine randomly with either one form another pair.

Illustrations:



Therefore, for the haploid number of chromosomes = n, the total number of possible combinations in gametes is given by 2^n.

Worked examples

1. When a pure breeding broad and long winged female fly was crossed with a narrow and vestigial winged male fly all the F_1 offsprings obtained had a broad abdomen and long wings.

Task:

(a) Using suitable genetic symbols work out the phenotypes and genotypes that were obtained in F_2 generation.

(b) Suppose 480 flies were obtained in F_2, work out the numbers of the flies for each phenotype class.

(c) How many of these flies were recombinants.

Responses for part (a)

Let; B represent allele for broad abdomen, b for narrow abdomen

L represent allele for long wings, l for vestigial wings

Parents : Male X Female

Phenotypes : Broad abdomen, Long wings X Narrow abdomen, vestigial wings

Genotypes : BBLL X bbll

Meiosis :

Gametes : all BL all bl

Random fertilization :

Fgenotypes : All BbLl

Selfing F1 offsprings to obtain F2 generation

		Male	×	Female
Parents	:	Broad abdomen	×	Broad abdomen
Phenotypes	:	Long winged	×	vestigial winged
		BbLl	×	BbLl
Genotypes	:			
Meiosis	:			
Gametes	:	BL Bl bL bl		BL Bl bL bl

Random fertilization

	BL	Bl	bL	bl
BL	BBLL	BBLl	BbLL	BbLl
Bl	BBLl	BBll	BbLl	Bbll
bL	BbLL	BbLl	bbLL	bbLl
bl	BbLl	Bbll	bbLl	bbll

F_2 phenotypes: **9** broad abdomen and long wings: **3** broad abdomen and vestigial wings: **3** narrow abdomen and long wings: **1** narrow abdomen and vestigial wings.

Responses for part (b)

Phenotypic ratios = 9:3:3:1, Total ratio = (9+3+3+1) = 16

- Number of flies = $\left(\frac{Ratio}{Total}\right) x480$ Flies
- Broad abdomen, long winged = $\frac{9}{16}$ X 480 = **270 flies**
- Broad abdomen, vestigial winged = $\frac{3}{16}$ X 480 = **90 flies**
- Narrow abdomen, long winged = $\frac{3}{16}$ X 480 = **90 flies**
- Narrow abdomen, vestigial winged = $\frac{1}{16}$ X **90 flies**

Responses for part(c)

- Number of recombinants = (90 + 90) flies = **180 flies**

TRIAL ITEMS

1) In guinea pigs, there are two alleles for hair colour and two for hair length. In a breeding experiment, all the **F_1** phenotypes produced from a cross between pure breeding short black-haired and long white-haired parents had short black hair.
Task: Explain;
(a) Which alleles are dominant
(b) The expected **F_2** phenotypes.

2) In the garden pea plant, the gene controlling flower colour is located on the different chromosome with that controlling height. Suppose a pure bleeding tall red flowered plant is crossed with a white short flowered plant, the F1 offsprings obtained are tall red flowered plants. If the F1 offsprings are selfed,
(a) What would be the phenotypic ratio in the **F_2** generation?
(b) If 700 pea plants are formed in **F_2** generation, what would be number of pea plants in each phenotypic category?
(c) How would you experimentally determine the genotypes of the **F_1** plants?

EXCEPTIONS OF MENDEL'S LAWS/NON-MENDALIAN INHERITANCE

The following forms of inheritance do not conform to the process of inheritance as illustrated by Mendel.

1. Linkage.
2. Incomplete dominance.
3. Co-dominance.
4. Multiple alleles.
5. Lethal genes
6. Epistasis
7. Pleiotropic inheritance.
8. Polygenic inheritance

} Gene interactions.

Gene linkage

Linked genes are more than two genes located on the same chromosome but controlling different characteristics and are inherited together as a single unit.

Linkage refers to the occurrence of more than one gene on the same chromosome which are inherited together along with the chromosome as a single block **or** the existence of genes determining different characteristics on the same chromosomes such that the two are inherited together. Therefore, linked genes are genes located on the same chromosome and hence they are inherited together as a single unit.

Note:

- *If genes are linked, they do not separate and thus in such a cross, the dihybrid ratio of 9:3:3:1 is never obtained.*

Types of gene linkage

- Autosomal gene linkage
- Sex linkage

(a) **Autosomal gene linkage:** This refers to genes linked on autosomes (non-sex chromosomes. There two types of autosomal gene linkages;

(i) **Complete linkage:** This is a condition where two or more genes are located so close to each other on the same chromosome such no crossing over occurs between them together. No genetic recombination occurs between them.

(ii) **Incomplete linkage:** This is a condition where two or more genes are located relatively further apart on the same chromosome such that crossing over occurs between them. There is formation of new genetic recombination. These genes may not be inherited together.

However, linked genes do not show independent assortment during gamete formation and therefore the phenotypic ratio obtained in $\mathbf{F_2}$ is **3:1** instead of the expected **9:3:3:1** for the two linked characteristics. Sometimes crossing over occurs, thereby separating the linked genes on the chromosomes leading to the formation of recombinant gametes during meiosis and this gives an $\mathbf{F_2}$ phenotypic ratio of **9:3:3:1** for the linked characteristics where crossing over occurred.

Example on linkage

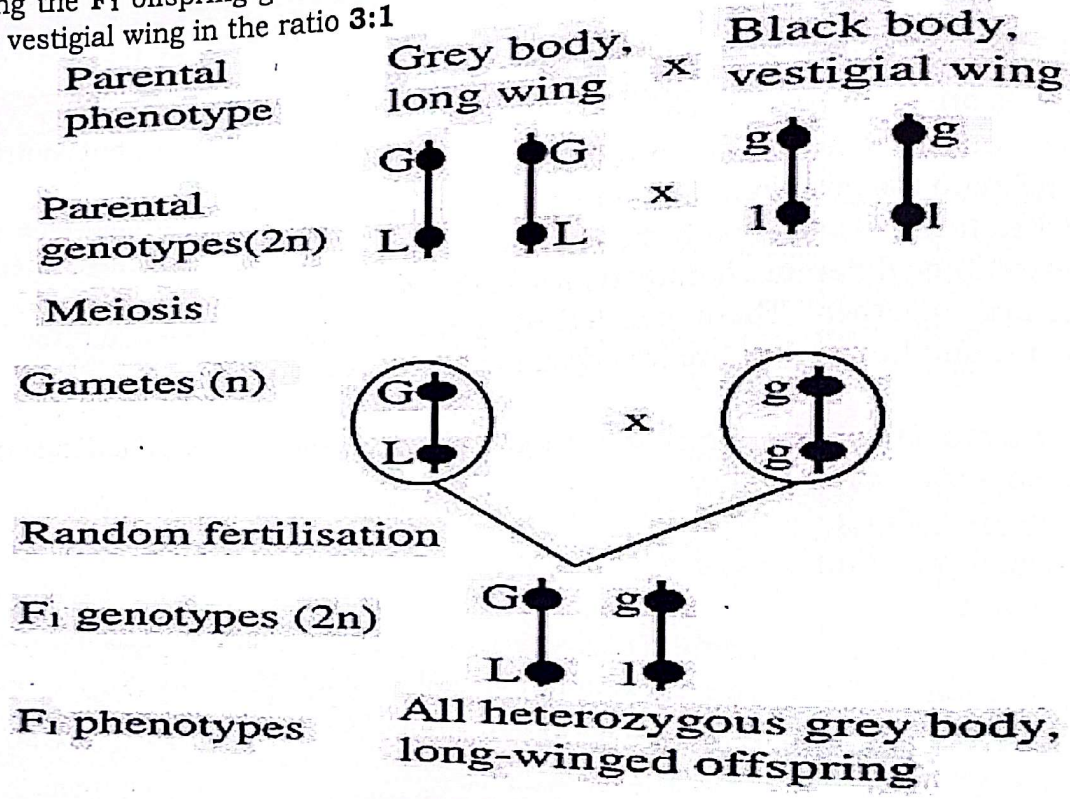
In drosophila flies the genes controlling body color and the length of wings occur on the same chromosomes and are linked together. Consider a cross between a pure breeding grey bodied long winged fly with a black bodied vestigial winged fly whereby the grey bodied is female while the black bodied is male. If all the $\mathbf{F_1}$ flies obtained here are grey

bodied and long winged. What are the phenotypic and genotypic ratios of the F_2 flies if the genes;

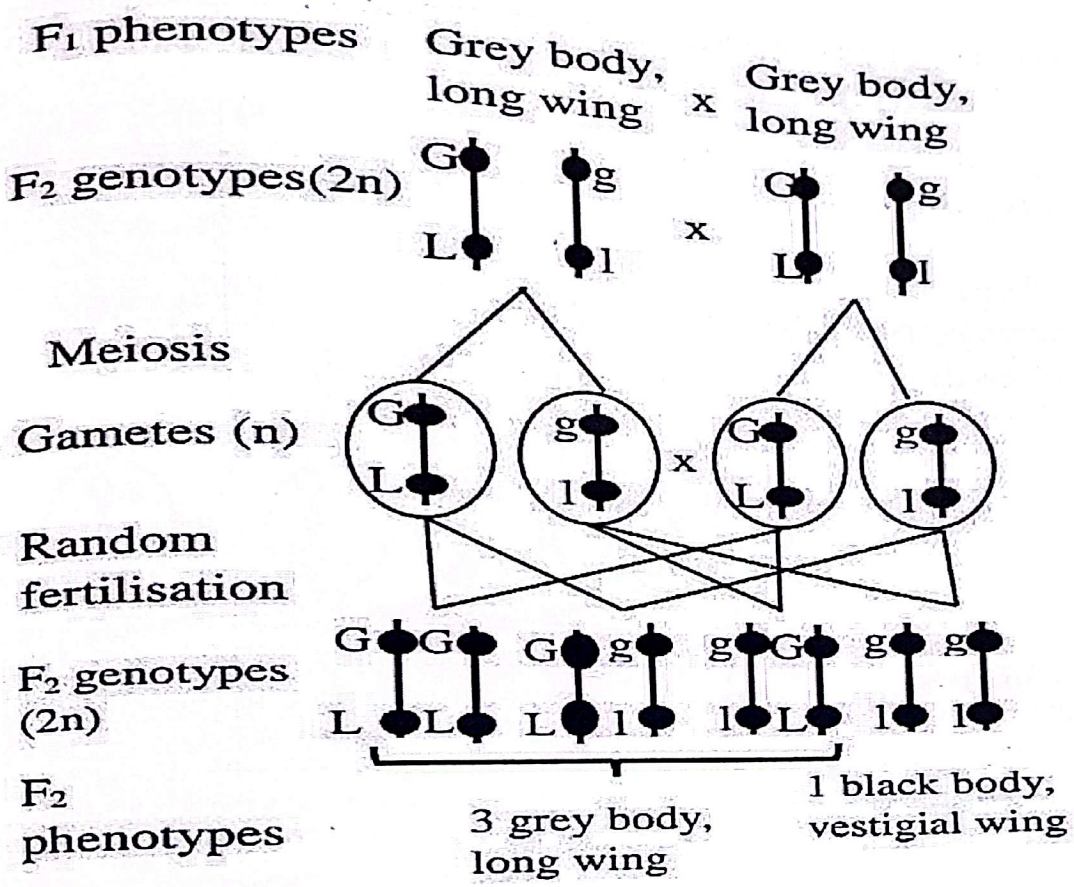
- **Let G represent the allele for grey body**
- **Let g represent the allele for black body**
- **Let L represent the allele for long wings**
- **Let l represent the allele for vestigial wings.**

Note:

When true breeding grey bodied long winged flies are crossed with true breeding black bodied vestigial winged flies, all the F_1 offsprings have grey bodies and long wings. Selfing the F_1 offspring gives rise to F_2 offspring with grey body long wing and black body vestigial wing in the ratio **3:1**



Selfing F1 offspring,



The F_2 phenotypic ratio is **3:1** similar to that of monohybrid inheritance instead of the **9:3:3:1** dihybrid ratio.

Note:

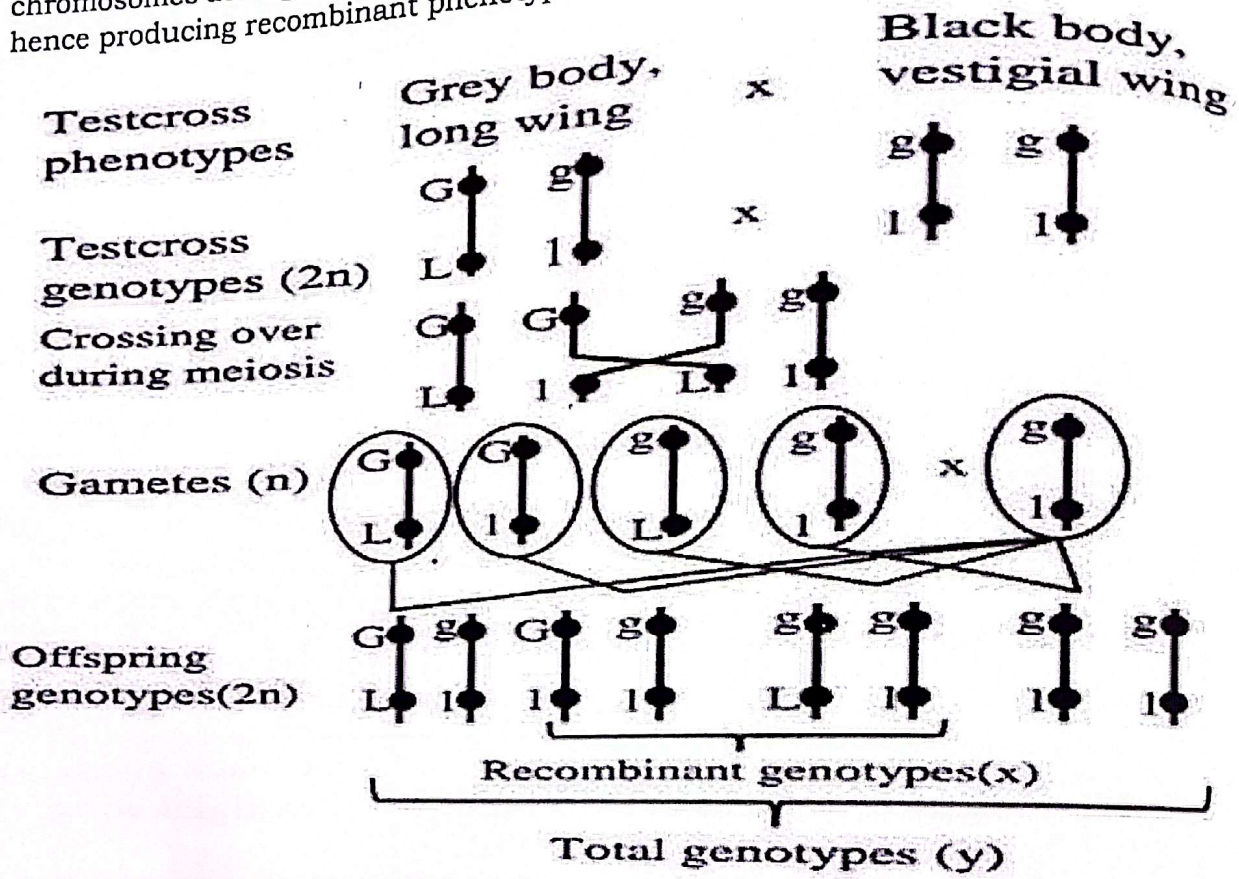
Surprisingly, the above 3:1 ratio of parental phenotypes is never obtained in practice. This is because total linkage is rare. Instead approximately equal numbers of parental phenotypes are obtained with significantly few recombinant phenotypes also in approximately equal numbers.

This was confirmed and explained by an ***American scientist Thomas H. Morgan.*** In a cross between a grey, long winged drosophila heterozygous for both traits with a black, vestigial winged drosophila (This is a test cross). Morgan predicted that in the normal Mendelian inheritance; parental phenotypes and recombinants would be obtained in a ratio of **1:1:1:1**. If genes were completely linked, parental phenotypes would be obtained in a ratio of **1:1**. To his disappointment; even after performing the test cross several times, Morgan never obtained the predicted outcomes. He instead obtained approximately equal numbers of the parental phenotypes with significantly few recombinant phenotypes also in approximately equal numbers as summarised below.

- **41.5% grey, long winged**
- **41.5% black, vestigial winged**
- **8.5% grey, vestigial winged**
- **8.5% black, long winged**

Morgan explained his results in terms of **crossing over** such that the responsive genes are located on the same chromosomes (linked) with the alleles of each gene on homologous chromosomes. As a result, alleles were exchanged between homologous

chromosomes during meiosis, leading to formation of new gene combinations in gametes hence producing recombinant phenotypes; as shown below.



Trial item

1. A homozygous purple-flowered short stemmed plant was crossed with a homozygous red-flowered long stemmed plant and all the **F_1** plants had purple flowers and short stems. When the F_1generation was taken through a test cross, the following progeny was produced
   - 53 purple flowered short stemmed
   - 47 purple flowered long stemmed
   - 49 Red flowered short stemmed
   - 45 red flowered long stems.

Task:

(a) Explain the results fully. (Note that once a test cross is carried out and all the phenotypes obtained are almost in equal proportions, then this implies that the genes are located on different chromosomes (not-linked).

Crossing over and cross over values

During crossing over, the frequency of crossovers which take place was found to be dependent on the distribution and arrangement of chromosomes. This is given by the cross over value/frequency aka recombination frequency. This is calculated as a percentage ration of recombinants to the total number of offsprings.

$$CoV = \frac{Number\ of\ recombinants}{Total\ number\ of\ offsprings} x100$$

Example

In a test cross carried out on a grey long winged drosophila, the following results were obtained

Phenotype	Number of offsprings
Grey, long winged	965
Black, vestigial	944
Black, long winged	206
Grey, vestigial winged	185

Solution:

$$CoV = \frac{Number\ of\ recombinants}{Total\ number\ of\ offsprings} x100$$

$$CoV = \frac{206 + 185}{(965 + 944) + (206 + 185)} x100$$

$$= 17\%$$

Trial item

In maize, the genes for coloured seed and full seed are dominant to the genes for colourless and shrunken seed. Pure breeding strains of double dominant variety were crossed with a double recessive variety and a test cross of the f_1 generation produced the following results

Coloured full	380
Colourless shrunken	396
Coloured shrunken	14
Colourless full	10

Task:

(a) Calculate the distance between the genes for coloured seed and seed shape

Note:

- The COV also indicates the **relative distance between** linked genes and the possibility of successful crossing over during meiosis, in the above case the distance between adjacent genes is 17 units. These values can also be used to position genes along the chromosome a process called **gene mapping**.

Sample item on construction of gene maps:

Consider the cross over values involving for different genes P, Q, R and S.

The distance separating these four genes is shown below;

P-Q = 24%

R-P = 14%

R-S = 8%

S-P = 6%

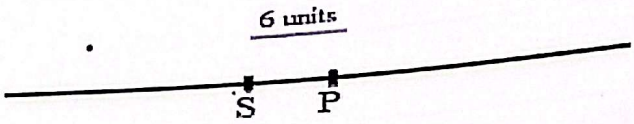
Task:

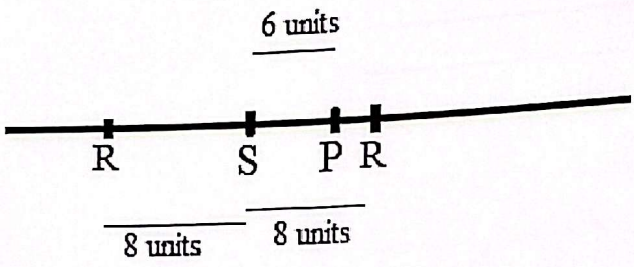
(b) Draw the chromosome map to show the position of these chromosomes.

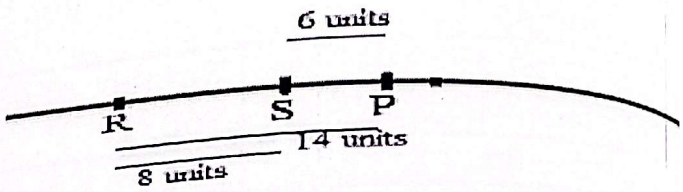
Approach to construction of gene maps:

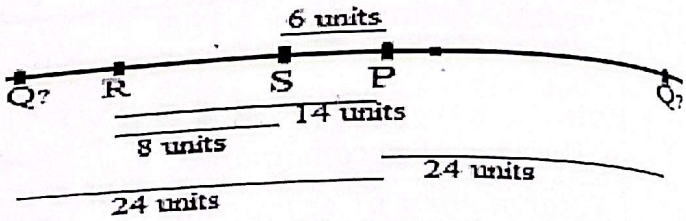
- Draw the chromosome map for these genes
- Insert the positions of the genes with the smallest cross over value first in the middle of the chromosome map
- Examine the next largest cross over value and insert both possible positions of its genes on the chromosomes relative to either S or P.

- Repeat the procedure for the entire remaining cross over values until you reach the largest cross over values.









Incomplete dominance

This is a condition or a form of inheritance where neither of the two alleles of the same gene controlling a particular trait is completely dominant over the other such that the heterozygous offsprings show a phenotype which is a blend or intermediate between that of the parents. Therefore the F1 individuals do not resemble any of the parents but rather are a blend of the parental phenotypes eg. A cross between a black and a white parent gives an offspring with grey colour. It occurs **mainly in plants**. For example, Petal colour in snapdragon plants:

Since in incomplete dominance no allele dominates the other in the phenotype but instead forms intermediate phenotypes, therefore the parental phenotypes are represented using ***different capital letters.***

Example

In a snap dragon plant, when a red flowered is crossed with a white flowered plant, all the F1 plants obtained are pink flowered. When the F1 are selfed, the F2 phenotypic ratio is **1:2:1** instead of **3:1** monohybrid ration. Using suitable genetic diagrams, explain the above results.

Genetic illustration of incomplete dominance

Let R represent the allele for red flower colour

Let W represent the allele for white flower colour.

Parental phenotype (2n): red flowered x white flowered

Parental genotype (2n): RR x WW

Meiosis

Gametes (n) all R, all W

Fertilization

F1 genotype (2n): RW

F1 genotypic ratio: all RW

F1 phenotypic ratio: all pink flowered plants

When selfed F1 x F1

Parental phenotype: pink flowered plant x pink flowered plant

Parental genotype (2n): RW X RW

Meiosis

Gametes (n) R, W, R, W

Fertilization

Offspring genotype (2n): RR, RW, WR

F2 genotypic ratio: 1RR: 2RW : 1WW

F2 phenotypic ratio: 1Red: 2pink : 1White

Co-dominance

This is a condition or a form of inheritance where both alleles of a gene determining a particular character all show up/express themselves equally such that the heterozygous offsprings show a mixture of both the parental phenotypes. Therefore, the alleles controlling the phenotypes of both parents co-exist in heterozygous state or equally express themselves to produce a phenotype which is a mixture of the two parents. e.g. black parent crossed with a white parent gives offspring with both white and black spots. It mainly occurs mostly **in animals.** In co-dominance, the alleles for each of the parental trait are represented with different capital letters.

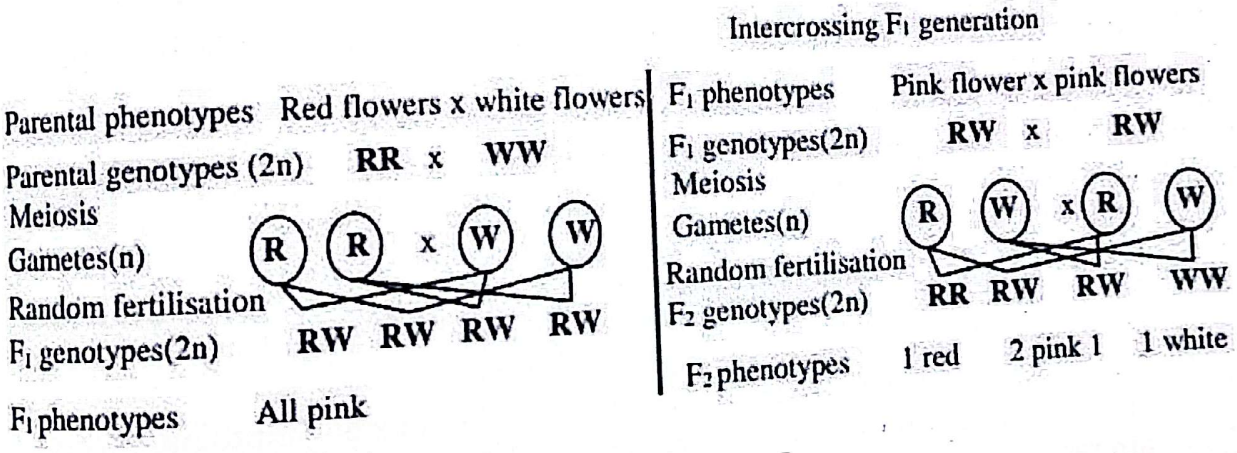
Examples of co-dominance include the following;

- The gene that determines coat color in cattle.
- Inheritance of blood group AB in man
- Inheritance of sickle cell trait

Inheritance of coat colour in cattle.

Consider a cross between a red bull and a white cow whose F_1 offsprings are selfed. Workout the genotypes and phenotypes in F_1 **and** F_2 generation stating in each case the ratios. When the F1 roan offspring are selfed, the F_2 offspring will be red, roan and white in the ratio **1 red: 2 roan: 1 white** as shown below.

- **Let R represent the allele for red bull**
- **Let W represent the allele for white cow**



Inheritance of sickle cell anaemia

This is an abnormal condition in which the red blood cells collapse into a sickle shape under low oxygen concentration due to the presence of abnormal haemoglobin (Hbs) in the red blood cells. The normal haemoglobin is found in red blood cells with a bi concave disc shape

Explanation of sickle cell anaemia arise?

Sickle cell anaemia is caused by a substitution mutation, in which an amino acid known as ***glutamic acid,*** responsible for the formation of normal haemoglobin is replaced by another amino acid called ***Valine*** which leads to the formation of **HbS** in the red blood cells. Haemoglobin is made of four polypeptide chains, two α-chains which are 141 amino acids long and two β-chains which 146 amino acids long. The substitution mutation occurs at the sixth amino acid in the β-chain, this results in wrong amino acid, Valine, being incorporated into two of the β-polypeptide chains. **Valine** is non-polar and hydrophobic which makes its presence in the haemoglobin (**HbS**) less soluble

when deoxygenated. Therefore when HbS loses its oxygen, the molecules come out of solution and crystallize (solidify) into rigid rod-like fibres. These change the shape of the red blood into a sickle shape.

Effects of sickling red blood cells:

a) Anaemia: This is occurs because the sickle cells are destroyed which lowers the amount of oxygen to be carried leading to acute anemia. This leads to;
- Fatigue (weakness).
- Poor physical development.
- Dilation of the heart which may lead to heart failure.
- Infections which lead to frequent illness

b) Interference with circulation of blood because the cells get jammed in capillaries and small arteries. This leads to;
- Heart damage which leads to heart failure
- Lung damage which leads to pneumonia
- Muscle and joint damage which leads to rheumatism and pain
- Gut damage which leads to abdominal pain
- Kidney damage which leads to kidney failure
- Liver damage

c) Enlargement of the spleen because the sickle shaped red cells collect in the spleen for destruction.

Note:
- The effects above make the homozygous sufferers to often die before reproductive age.
- The allele that causes the erythrocytes to have a distorted form in sickle-cell anaemia also causes these blood cells to rupture easily, thereby inducing anaemia. This gene can also be described as ***pleiotropic*** since it has more than one effect in an organism.
- In heterozygous individuals, half of the haemoglobin molecules made are abnormal form Hb^S and half are normal form Hb^A i.e. the alleles Hb^A and Hb^S are co-dominant and the faulty gene is not recessive.
- The heterozygous people are not affected by the above symptoms/effects except at unusually low oxygen concentrations, such as when flying in an unpressurised aircraft or when climbing at high altitude, that's then when some of the cells become sickled.
- The heterozygous condition is known as **sickle cell trait**. These individuals have a selective advantage over non carriers (both homozygous normal and sufferers) because they are far less susceptible to malaria (the malaria parasite multiplies inside normal red blood cells) so are more likely to survive in malaria infested areas, and pass on their genes to the next generation. A single copy of the sickle-cell allele increases resistance to malaria. The increased resistance to the plasmodium parasite in heterozygotes, as a result of two reasons:

  (i) The consistent change in oxygen levels between normal and sickle cells makes it difficult for the parasite to adapt. In such cases, the immune system of the body easily eliminates the parasites before the disease is established rendering resistance to the heterozygotes.

(ii) Plasmodium parasite feeds on haemoglobin and in heterozygotes of sickle cell, the crystallization of the abnormal haemoglobin makes it harder for the parasite to digest (less digestible) and survive on. This also renders resistance to carriers of sickle cell.

Genetic crosses illustrating inheritance of sickle cell anaemia.

(a) Consider a normal man marrying a sickle cell anaemia woman.

(b) Also consider another man who is a carrier of sickle cell anaemia marries a woman who is also a carrier of the same disease.

Task: Work out the phenotypic and genotypic ratios arising from these two marriages.

Note:

If a normal man marries a woman with sickle cell anemia, the $\mathbf{F_1}$ offsprings will be phenotypically normal but carriers and if two carriers of sickle cell anaemia mate, the F_1 offspring phenotypic ratio will be **1 normal :2 carriers: 1 Sickler.**

Solution

Let Hb^A represent the allele for normal red blood cells

Let Hb^S represent the allele for sickle celled red blood cells.

Parental phenotypes: normal man x sickler woman

Parental genotypes (2n): Hb^A Hb^A x Hb^S Hb^S

Meiosis

Gametes (n): all Hb^A all Hb^S

Fertilization:

F_1 genotype (2n): Hb^AHb^S

F_1 phenotype: All are carriers

Parental phenotype: sickler man x sickler woman

Parental genotype (2n): Hb^AHb^S x Hb^AHb^S

Meiosis

Gametes (n): Hb^A Hb^S Hb^A Hb^S

Fertilization

Hb^AHb^S Hb^AHb^S Hb^AHb^S Hb^AHb^S

F_1 genotypic ratio: 1 Hb^AHb^S: 2 Hb^AHb^S: 1 Hb^S Hb^S

F_1 Phenotypic ratio: 1 Normal: 2 carriers: 1 Sickler.

Note:

- Carriers (heterozygotes) of sickle cell anemia show the sickle cell trait, a co-dominant condition, in which most of the red blood cells have normal hemoglobin and only about 40% of the red blood cells have abnormal haemoglobin S. This produces mild anemia and prevents carriers of the sickle cell trait from contracting malaria. This is because when the plasmodium that causes malaria enters a red blood cell with abnormal haemoglobin S, it causes extremely low oxygen tension in the cell which leads to the cell sickling in heterozygotes. These sickled cells are quickly filtered out of the blood stream by the spleen, thus eliminating the parasites.

Multiple alleles

Multiple alleles is where a single character is determined by a gene which has more than two alleles (has 3 or more alleles). Although it is possible that a given character can be

controlled by a gene which has more than two alleles, it is only any two alleles that can occur at a single locus at any one time.

Examples of Characteristics tics controlled by multiple alleles include;

- **Blood groups in humans**
- **Coat color in rabbits**
- **Eye color in rabbits and mice**

Inheritance of ABO blood system:

The ABO blood group system is controlled by three alleles of a gene I (isohaemogglutinogen) occur at a single locus any time. These alleles are;

- **I^A for antigen A.**
- **I^B for antigen B.**
- **I^O for no antigen.**

It should be noted that the alleles I^A and I^B are co-dominant and are both dominant to I^O **(recessive)**. The transmission of the three alleles occurs in a normal Mendelian fashion. The table below summarizes the possible phenotype and blood group.

BLOOD GROUP/PHENOTYPE	GENOTYPE
A	I^AI^A **(AA)** –homozygous for blood group A
	I^AI^O **(AO)** – heterozygous for blood group A
B	I^BI^B **(BB)** – homozygous for blood group B)
	I^BI^O **(BO)** –heterozygous for blood group B
AB	I^AI^B **(AB)** – heterozygous for blood group AB
O	I^OI^O **(OO)** – homozygous for blood group O

Examples:

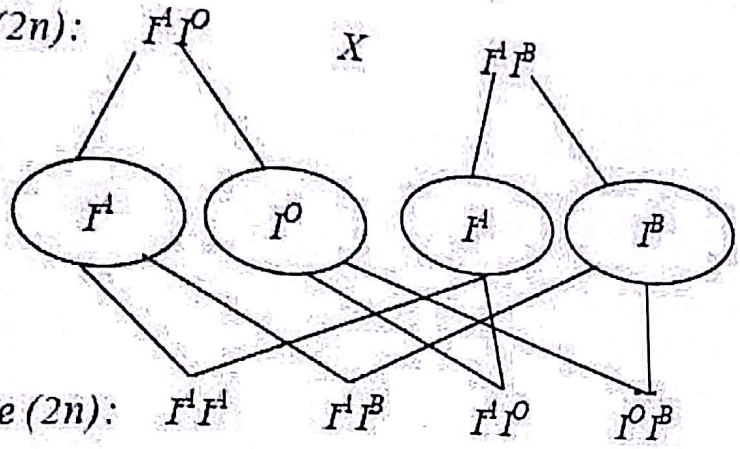
1. A man having blood **A** marries a woman having blood group **AB**. What are the possible genotypes and phenotypes of their offsprings if the man is heterozygous for blood group **A**?
   - Let I^A represent the allele for formation of antigen **A**
   - Let I^B represent the allele for formation of antigen **B**
   - Let I^O represent the allele for no formation of antigen **A** or **B**

Parental phenotype: blood group A x blood group AB

Parental genotype (2n): I^AI^O X I^AI^B

Meiosis

Gametes (n)



Offspring genotype (2n): I^AI^A I^AI^B I^AI^O I^OI^B

F2 genotypic ratio: $1I^AI^A$: $1I^AI^B$: $1I^AI^O$: $1I^OI^B$

F_2 phenotypic ratio: 2 blood group A: 1blood group AB: 1blood group B

Trial items.

1. A boy has blood group **A** and his sister has blood group **O**. which combination of genotypes and phenotypes do you think their parents have. Show your working.

Gene interactions

This occurs when two or more different gens influence the expression of a single trait. Therefore, certain phenotypes of organisms are produced/ affected by an interaction of two or more genes located at different loci on a chromosome.

The common gene interactions are;

(a) Epistasis.
(b) Polygenic interactions.

(a) EPISTASIS:

This is where a gene at one locus suppresses or masks the action/effect of another gene at a different locus. The gene which suppresses or masks is called the **epistatic gene** while the one being suppressed (masked) is called the **hypostatic gene.** Unlike in complete dominance which involves interactions of alleles at the same locus, epistasis involves interaction between genes at different loci. Therefore, the classical dihybrid ratio (9:3:3:1) is altered into modified rations depending on the type of epistasis.

Types of epistasis:

There are many different types of epistasis. Some of which include the following;

(i) **Recessive epistasis (9:3:4)**
(ii) **Dominant epistasis (12:3:1)**
(iii) **Duplicate recessive epistasis/complementary genes (9:7)**

Recessive epistasis: This is the type of epistasis where the epistatic allele is recessive, such that its presence in homozygous condition, suppresses the phenotypic expression of the dominant allele located on another locus. Therefore, both alleles must be recessive

to block the effect of the second gene. This type of epist... phenotypic ratio from 9:3:3:1 to 9:3:4.

Example

- **Inheritance of coat colour in mice**

In mice, the gene for coat colour has 2 alleles, that's one for black and another one for brown. Black coat colour (**B**) is dominant to brown coat colour (**b**). However, another gene determines whether a pigment will be deposited in the hair. If a dominant allele of this gene (**C**) is present, the colour (black or brown) is deposited. If only the recessive alleles are present (**cc**), no pigment is deposited and the mouse is white (albino). Therefore, the recessive gene at one locus (cc) masks the phenotypic expression of other gene locus (**BB, Bb or bb**). The alleles of '**B**' locus express themselves only when epistatic locus has dominant alleles like **CC** or **Cc**.

Activity:

- Determine the results of crossing two mice that are heterozygous for both genes (black colored, CcBb x CcBb)

Dominant epistasis (12:3:1) : This is where a dominant allele at one locus masks the expression of alleles at another locus. Only one copy of a dominant allele is enough to suppress the other gene, e.g. Fruit colour in squash, where Gene W= inhibits pigment (W=white fruit, ww=allows fruit colour to form) and Gene Y= pigment type (Y=yellow and yy=green). Therefore if W is present, the fruit is white, regardless of Y alleles.

Activity:

- Determine the results of crossing two squash plant that are heterozygous for both genes, (Yellow fruit, WwYy x WwYy)

Duplicate recessive epistasis (complementary genes): Here both genes need to atleast one dominant allele to produce the phenotype. If either locus is homozygous recessive, the phenotype is altered. For example; Flower colour in sweet pea, where Gene C and gene P both are needed for purple colour. Gene cc or pp result into white flowers (no pigment). The crosses give 9purple:7 white

Activity:

- Determine the results of crossing two sweet pea plants that are heterozygous for both genes, purple colour, CcPp x CcPp)

(b) POLYGENIC INHERITENCE

This is where a given single character (trait) is determined by more than two genes located on different loci, each having a small and additive effect on the phenotype. Such genes have a cumulative effect on the phenotype, with an organism having only dominant alleles lying at one extreme and an organism with only recessive characteristics lying at the other extreme. Intermediates are usually very many and form a continuum (gradual difference in appearance).

Polygenic inheritance gives rise to continuous variation with organisms showing a gradual difference in characteristics from one extreme to another.

Examples of characteristics in humans inherited in this way include;

- Skin color in humans.
- Pattern of finger prints

- Intelligence
- Human height.
- Eye colour in humans
- Milk yield in cattle.

Lethal genes

These are mutant genes which cause death of an individual possessing them. They interfere with the vital functions that are necessary for survival such as metabolism, development or organ formation. Lethality (death of the bearer) can occur before (early development/embryonic stage) or after birth/later in life. In addition to causing death, many lethal genes also control or influence other observable characters before they kill/cause death to the organism

Example of lethal gene conditions:

- Yellow coat colour in mice.
- Huntington's disease in humans, death occurs later in life.
- Sickle cell anaemia (in humans), death occurs if no medical care is given.
- Creeper legs in chickens.
- Manx Cats (no tails)

Characteristics of lethal genes:

- They cause death either at embryonic, juvenile or adult stages depending on the type.
- They often result from mutations in essential genes.
- They can be dominant or recessive in expression.
- Lethal alleles often maintain themselves in populations through heterozygotes that survive.
- Their effect is often masked in heterozygous condition but expressed in homozygous condition.

Types of lethal genes

1) **Recessive lethal genes:** These cause death only when present in homozygous condition/the organism inherits two copies of the allele. The heterozygotes survive but may sometimes show mild effects. For example:

(b) **Yellow coat colour in mice.** The gene for yellow coat (Y) is dominant for colour but recessive lethal.

(c) Sickle cell anaemia (humans): Homozygous recessive condition is often lethal without medical care.

Dominant lethal genes: These alleles cause death of the organism even if the organism only inherits a single copy. They are very rare in a population because they typically cause the organism's death before they can reproduce and pass on the gene. For example, Achondroplasia (dwarfism) and Huntington's disease (is an example of dominant lethal allele but because of its late onset, it can be passed on to offsprings).

Genetic illustrations for inheritance of yellow coat colour in mice

The gene that determines coat color in mice is a lethal gene. In mice, there are two colours determined by two alleles of the same gene i.e. yellow and grey (agouti). If two

yellow mice are crossed, they produce both yellow and grey offspring however these offsprings appear in a phenotypic ration of **2 yellow: 1 grey** instead of **3:1**. This is because the homozygous dominant yellow mice die in the uterus which reduces the phenotypic ratio. The yellow mice produced are always heterozygous and this changes the monohybrid genotypic ratio from **1:2:1 to 2:1.** Therefore, the phenotypic ratio of **2:1** is indicative of lethal alleles or genes.

Let Y represent the allele for yellow coat color

Let y represent the allele for grey coat color.

Parental phenotype (2n): yellow mouse x yellow mouse

Parental genotype (2n): Yy X Yy

Meiosis

Gametes (n) Y y Y y

Fertilization

Offspring genotype (2n): YY Yy Yy yy

YY dies before birth and therefore the offspring phenotype will be 2 yellow: 1 grey

Lethal genes in Manx cats:

Cats possess a gene for producing a tail. The tailless Manx phenotype in cats is produced by an allele that is lethal in its homozygous state. The allele interferes with normal spinal development, in heterozygous cats this results in lack of a tail. When two Manx cats are mated, the ratio of the offsprings produced is **2 Manx cats to 1 long tailed cat.**

Task:

(b) Show the cross between a Manx cat and a normal cat.

Lethal genes in creeper's chicken:

Another example is the "creeper" allele in chickens, which causes the legs to be short and stunted. This phenotype in chickens called the creeper condition is caused by an autosomal mutation and displays itself as a chicken that has short and stunted legs. Chicken embryos that are homozygous for the creeper condition have severe developmental problems and never hatch from their eggs.

What are the different phenotypes and the associated phenotypic and genotypic ratios that may result from a cross of two chickens with the creeper condition? Show your working with a punnet square.

Note:

- Creeper is a dominant gene, heterozygous chickens display the creeper phenotype.
- If two creeper chickens are crossed, one would expect to have (from Mendelian genetics) 3/4 of the offspring to be creeper and 1/4 to be normal.
- Instead the ratio obtained is 2/3 creeper and 1/3 normal.
- This occurs because homozygous creeper chickens die.

- **Let P represent the allele for short and stunted legs**
- **Let p represent the allele for normal long legs**

	P	p
P	PP lethal	Pp creeper
p	Pp creeper	pp normal

Pleiotropy

This is a condition in which a single gene influences two or more seemingly unrelated traits in an organisms. The gene involved is called a pleiotropic gene. This happens because the product of one gene (protein, enzyme or hormone) can take part in multiple biochemical or developmental pathways.

Examples of pleiotropy

- Sickle cell anaemia (humans): The defective gene causes multiple effects such as sickled RBCs, organ failure, anemia etc.
- Albinism: The defective gene causes multiple effects such as very light skin, while or light hair, pink or light colored eyes etc.
- Phenylketonuria (in humans).
- Yellow coat colour in mice: The Y gene in mice controls multiple effects such as lethality and coat colour.

POPULATION GENETICS

Population genetics is the branch of biology that studies the genetic composition of populations and how it changes over time due to evolutionary processes. In simple terms, it is the study of how genes (alleles) are distributed in a population and how their frequencies are influenced by factors such as: Mutations, natural selection, genetic drift, gene flow or non-random mating. The study provides the mathematical structure for the study of micro evolutionary process.

Microevolution refers to the change in one gene pool or the allele frequencies that occur within a population over time. Mainly due to mutations, genetic drift, gene flow, selection (natural and artificial), gene flow for example industrial melanism, microevolution of resistance to antibiotics, pesticides etc.

Macroevolution refers to speciation or evolutionary changes at a level higher than the species level, resulting into formation of a higher taxonomic group such as class or genus.

Some biologists believe that macroevolution results from a build-up of small changes due to microevolution. One common **misconception** about evolution is that individual organisms evolve. It is true that natural selection *acts* on phenotypic characteristics of individuals to determine the fate of genotype. Each organism's combination of traits affects its survival and reproductive success compared to other individuals. So, it's only those individuals that can reproduce successfully before death that contribute to the

future species but the evolutionary impact of natural selection is only apparent in the changes in a *population* of organisms over time, for this reason; *though individual organisms are acted upon by natural selection, its populations that evolve but not individuals. The population is the smallest unit of evolution.*

Terms used in population genetics:

1. **A population** is a group of organisms of the same species living together in a given habitat at a given time.
2. **A species** refers to a group of organisms with similar features which can interbreed successfully to produce fertile offsprings.
3. **Gene pool** refers to the total collection of alleles present in a sexually reproducing population. A population whose gene pool shows consistent change from generation to generation is said to be undergoing evolutionary change while a **static gene pool** is one where genetic variation is inadequate to bring about evolutionary change.
4. **Allele frequency** refers to the total number of copies of a given allele expressed as a percentage of the total number of alleles for that gene in a population. For example, in human beings, production of body pigments is determined by a dominant allele while the recessive allele results into no pigment production (albinism). The frequencies of the dominant and recessive alleles are 99% and 01% respectively. Since the total percentage is 100%; so 99 + 01 = 100. However, frequencies in population genetics are usually represented as decimals rather than percentages or fractions, → 0.99 + 0.01 = 1.00.

Mathematically; if we let **p** and **q** to represent the dominant and recessive allele frequencies respectively, **Then p + q = 1**..... **(I)**

From equation **(i)** above; if the allele frequency of either allele is known, the allele frequency of the other can be determined. E.g. If the allele frequency of the recessive allele is 25%, Then q = 0.25. Using p + q = 1, p = 0.75.

5. **Genotype frequency** refers to the total number of individuals carrying a particular genotype expressed as a percentage of the total population. In most populations, it's only possible to estimate the frequency of two alleles in a homozygous recessive state as this is the only genotype which can be directly observed phenotypically. E.g. 1 person in 10000 is albino. Albinism is known to be a recessive character, for the person to be an albino, they must be possessing two copies of the defective allele (homozygous recessive). The mathematical relationship between the frequencies of alleles and genotypes in populations was developed by Hardy and Weinberg. The relationship is therefore known as the '***Hardy-Weinberg principle***'.

Hardy-Weinberg's principle/Hardy-Weinberg equilibrium

This is a fundamental concept in population genetics which states that ***"The allele and genotype frequency of a large sexually reproducing population remains constant from generation to generation provided that certain disruptive factors like mutation, gene flow, genetic drift and selection do not act"***. The gene pool of such a population remains static and the population is said to be in Hardy-Weinberg equilibrium, it cannot undergo evolutionary change.

Assumptions of hardy-Weinberg principle:

For equilibrium/principle to hold or to be maintained, the following conditions/ factors must be met/fulfilled;

(i) Provided the population size is sufficiently large so as to minimize the effects of random genetic drift.
(ii) Mating should be random such that no sex selection occurs.
(iii) All genotypes should be equally fertile such that there is no selection or genetic load.
(iv) No mutations should occur as these tend to increase genetic diversity.
(v) Provided generations do not overlap.
(vi) There should be no emigration or immigration, that is to say, there is no gene flow between populations.
(vii) Natural selection should not act, as this would favour some genotypes over others.

Note:

- In prevalence of the above factors, the frequencies of all alleles and genotypes will remain constant over generations. In case all or at least one of the above factors is reversed, the frequencies are prone to change and the stability of the population is upset. This initiates evolutionary change.

Hardy-Weinberg equation

This is a mathematical relationship between the frequencies of alleles and genotypes in a population. This can be used to calculate genetic changes in populations.
Considering a population with a certain gene occurring in two allelic forms, one homozygous for a dominant allele **A** and the other for a recessive allele **a**; all the F1 off-springs will be heterozygous (**Aa**).

- Let **p**= frequency of allele **A**
- Let **q**= frequency of allele **a**

Since there are only two alleles; then **P+q= 1**

Genotype frequencies:

	A(p)	**a(q)**
A (p)	AA (pxp)	Aa (pxq)
a(q)	Aa (pxq)	aa (qxq)

- Homozygous dominant (AA)=$\mathbf{p^2}$
- Heterozygous (Aa)= **2pq**
- Homozygous recessive (aa)=$\mathbf{q^2}$

Thus; $\mathbf{p^2 + 2pq + q^2 = 1}$

Worked example

One person in 10,000 is an albino, calculate the genotype frequencies for the individuals who are homozygous dominant, homozygous recessive and those who are heterozygous.
Note: The albino genotype frequency is 1 in 10000. Since albino is recessive;

$q^2 = 10,000 = 0.0001$
$q^2 = 0.0001$
$q = \sqrt{0.0001} = \mathbf{0.01}$. Therefore, the frequency of the albino allele is 0.01 or 1%
Since p+q = 1

$p = 1 - q$; then $p = 1 - 0.01 = 0.99$

- Therefore, the frequency of the dominant allele in the population is 0.99 or 99%

Since $p = 0.99$

$p^2 = 0.99 = 0.9801$

- Therefore, the frequency of the homozygous dominant genotype is 0.9801 or 98%

$2pq = 2x0.99x0.01 = 0.0198$

- The frequency of heterozygous genotype is 0.0198.

Trial items

1. In a population of 200 plants, 128 are homozygous tall, 64 are heterozygous tall and 8 are dwarf. Using suitable symbols, state the genotype of all the plants
   (i) Calculate the allele frequency of t and T.
   (ii) Calculate the genotype frequency.

2. In a Caucasian population, the frequency of individuals affected by cystic fibrosis is approximately 1 in 2500. This is a recessive disorder and affected individuals are homozygotes. If q represents allele frequency of the disease, find the frequency of the carrier genotype.

3. In a human population the gene responsible for tongue rolling is dominant over the gene for non-tongue rollers. The population of tongue roller is 84% and non-tongue roller is 16%. Find the percentage of individuals, who are,
   (i) Homozygous for tongue rolling.
   (ii) Heterozygous for tongue rolling.

4. In a school, students were asked to roll their tongues. The results obtained showed that out of 450 students, 378 were rollers and the rest non-rollers. The ability to roll one's tongue is determined by a dominant gene ***R*** and the lack of this ability is due to a recessive gene ***r***.

Task: Determine the total number of the **R** and ***r*** alleles in the school.

Factors responsible for changes in allele frequencies of the population

The four major sources of genetic variation within a gene pool are;

- Crossing over during meiosis
- Independent segregation during meiosis
- Random fertilization
- Mutation

Other factors that can contribute to changes in allele frequency are include;

1. Natural selection:

This tends to favour alleles and genotypes that produce environmentally adapted phenotypes, leading to increase in their frequencies while those that are less adapted to the environment are eliminated hence their frequencies decline.

2. Gene flow:

This refers to the movement/continual interchange of alleles from one population to another as a result of interbreeding among the members of the two populations. This results into introduction of new alleles hence from other populations leading to change in the allele frequencies of the population. However, gene flow is said to be conservative

to evolutionary change in the long run. It tends to ensure uniform distribution of alleles in all populations which reduces genetic variation and increases uniformity among organisms as all populations share a common gene pool, this limits the action of natural selection. For this reason, interrupting gene flow is a prerequisite to evolutionary change and speciation.

3. Mutations:

These are random occurrences which change the genetic constitution of organisms. They greatly increase genetic diversity, where advantageous mutations are favored by natural selection and disadvantageous ones are phased out.

4. Non-Random mating:

This occurs when there is sexual selection (a mechanism on non-random mating). It occurs when the presence of one or more inherited characteristics increases the likelihood of successful fertilization. In such cases, only organisms having certain characteristics will have high chances of reproducing hence passing on their traits to next generations, while those without such features will have reduced reproductive potentials. Only some alleles will be passed to next generation leading to change in their frequencies. Examples include eye colour in drosophila (females prefer red-eyed males), colour patterns in insects and birds, petal size and colour in flowers etc.

5. Genetic drift:

This refers to the change in the gene frequencies within a population as a result of chance rather than by natural selection. Although chance events occur in populations of all sizes, they alter allele frequencies substantially only in small populations. A phenomenon associated with genetic drift is the ***founder effect.*** A small population may become isolated from a large population and it may not be truly representative of the original population in terms of allele and genotype frequencies. Some alleles may be absent while others may be disproportionally represented. Continuous breeding within the pioneer population will produce a gene pool with allele frequencies different from that of the original parent population; this is known as the founder effect (as it occurs in the founder population). In the same way, a sudden change in the environment, (such as a fire or flood) may drastically reduce the size of a population, just by chance, certain alleles may be overrepresented among the survivors, others may be underrepresented, and some may be absent altogether. Ongoing genetic drift is likely to bring about changes in the allele frequencies of the population and may result into a gene pool that is different from the original population. This is referred to as the ***bottleneck effect,*** (named so because the population passed through a restricted path

Random genetic drift may lead to the following;

- Total loss of some alleles from the population, due to death of the few individuals carrying such alleles
- Total extinction of the population
- The population becoming much better adapted to the environment.
- Wide divergence of the population from the parent population, and all these occur just by chance rather than natural selection.

Note:

Whereas genetic drift may lead to a reduction in variation within a population it can increase variation within the species as a whole. Small isolated populations may develop

characteristics unusual of the main population which may have a selective advantage if the environment changes. In this way genetic drift can contribute to the process of speciation.

6. Genetic load:
This is the existence within the population of disadvantageous alleles in heterozygous genotypes. Very many disadvantageous alleles are able to exist in populations in heterozygous forms as in this form they are rarely expressed phenotypically for possible elimination by environmental selection, for example albinism, colour blindness, sickle-cell anemia, etc. The maintenance of fairly high frequencies of a recessive allele which may be potentially hazardous in a homozygous recessive state is referred to as the **heterozygous advantage**. The most obvious example is illustrated by the sickle-cell trait. **Sickle-cell trait** is a condition when an individual has one copy of the normal allele for hemoglobin production and a recessive allele for abnormal hemoglobin. Such heterozygotes/carriers have both normal and sickle-shaped red blood cells and this is referred to as sickle-cell trait. Sickle-cell carriers have consistently shown a high resistance to malaria much more than both the normal and the sick. This therefore confers a selective advantage to the heterozygotes leading to consistently high frequencies of the sickle cell allele especially in such areas as the tropics where malaria is prevalent.

Explanation:
The carriers have both normal and sickle-shaped red blood cells, the former contain very low levels of oxygen due to abnormal hemoglobin while the latter contain high oxygen levels. This makes it difficult for the plasmodia parasites to survive in the low oxygen environments in sickle cells and to adapt to constantly changing oxygen contents. Some of them die while others are effectively eliminated by the body defense system before establishment of the disease leading to resistance.

Evolution

Evolution is the gradual change in the heritable characteristics of populations of organisms over successive generations, leading to the diversity of life on Earth. It explains how modern species have descended from ancient ancestors through modification. Evolution is a unifying concept in biology because it provides a framework to understand the origin, diversity, adaptation, and relationships among organisms.

Evidence for Evolution

1. Fossil record – shows transitional forms and chronological order of organisms.
2. Comparative anatomy – homologous structures (e.g., forelimbs of vertebrates) suggest common ancestry.
3. Comparative embryology – similarities in early development across species.
4. Molecular biology – similarities in DNA and proteins (e.g., cytochrome c).

Major Theories of Evolution

Lamarck's Theory (Theory of Inheritance of Acquired Characteristics). This was proposed by Jean-Baptiste Lamarck (1744–1829).

Key ideas:

1. Use and disuse – organs become stronger or weaker depending on use (e.g., giraffes stretching necks).
2. Inheritance of acquired traits – traits developed during an organism's lifetime are passed on to offspring.

Example: Giraffes originally had short necks, but by stretching to reach leaves, their necks elongated and this was inherited by their offspring.

Criticism: Modern genetics shows that acquired traits (like a muscular body) are not inherited; only genetic traits are passed on.

Contribution: First to propose that organisms change over time due to environmental influence.

2. **Darwin's Theory (Theory of Natural Selection): This was** proposed by Charles Darwin (1809–1882) in his book On the Origin of Species (1859).
Based on observations from his voyage on the HMS Beagle, especially in the Galápagos Islands.

Main principles:

1. Overproduction – organisms produce more offspring than can survive.
2. Variation – individuals within a population show variations (some favorable, some not).
3. Struggle for existence – organisms compete for limited resources (food, mates, space).
4. Survival of the fittest – individuals with favorable variations (adaptations) survive and reproduce.
5. Descent with modification – favorable traits accumulate over generations, leading to new species.

Example: Darwin's finches in the Galápagos – different beak shapes evolved depending on available food sources.

3. **Modern Theory of Evolution (Neo-Darwinism / Synthetic Theory):** This combines Darwin's natural selection with genetics and other biological disciplines. **It was** developed in the 20th century through the works of scientists like Fisher, Haldane, Dobzhansky, and Mayr.

Key aspects:

1. Genetic variation arises from mutations, genetic recombination, and gene flow.
2. Natural selection acts on this variation, favoring beneficial traits.
3. Population genetics explains how allele frequencies change in populations over time.
4. Speciation occurs when populations become reproductively isolated and diverge.
5. Other evolutionary forces: Mutation – introduces new genetic traits; Genetic drift – random changes in allele frequencies (especially in small populations);Gene flow – movement of genes between populations.

Natural Selection and how it brings about Evolution

Natural selection is the process by which individuals with advantageous traits survive and reproduce more successfully than those without them. Over time, these advantageous traits increase in frequency within the population, leading to evolutionary adaptation.

Steps in Natural Selection

1. Variation exists in a population (due to mutations, genetic recombination).
2. Environmental pressure (e.g., predators, climate, and competition) acts on the population.
3. Individuals with favorable traits survive and reproduce ("survival of the fittest").
4. Favorable traits are passed to offspring.
5. Over many generations, the population becomes adapted to its environment.

Examples

- Peppered moths during the industrial revolution: light moths were camouflaged on clean bark, but after pollution darkened tree trunks, dark moths had a survival advantage.
- Antibiotic resistance in bacteria: bacteria with resistant genes survive antibiotics and pass resistance to future generations.

ISOLATION MECHANISMS

Isolation mechanisms are barriers that prevent interbreeding between populations, thus reducing or blocking gene flow and leading to the formation of new species. They are grouped into two categories, namely;

1. **Pre-zygotic barriers.**
2. **Post-zygotic barriers.**

Pre-zygotic isolation mechanisms (before fertilization):

These are isolating mechanisms that prevent fertilization from occurring between individuals of different species. They act before the formation of a zygote, meaning that they stop mating or fertilization from taking place. The types of pre-zygotic barriers include:

(a) Geographical isolation: This occurs when species/populations are separated by physical barriers which prevents them from meeting to mate such as mountains, rivers, oceans, or deserts.

(b) Ecological (habitat) isolation: This occurs when species/populations occupy or live in different habitats within the same area and thus rarely meet to mate. (e.g., one in trees, another on the ground).

(c) Temporal (Seasonal) isolation: This occurs when species breed/reproduce at different times of the day, season, or year. For example two plant species flowering in different seasons.

(d) Behavioral (Ethological) isolation: This occurs when organisms exhibit differences in courtship, mating calls, or behaviors which prevent them from mating. For example, two birds with different mating calls or dances.

(e) Mechanical isolation: This occurs when structural differences in reproductive organs prevent successful mating. The genitalia of the two groups may be incompatible thus preventing mating. For example, it may be impossible for the penis of the male to enter a female's vagina.

(f) Gametic isolation: This happens in a way that even if mating occurs, the gametes (sperm and egg) of one species cannot fuse successfully due to incompatibility.

Post-zygotic isolation mechanisms (after fertilization):

These are isolating mechanisms that operate after fertilization has occurred, preventing the development of fertile, viable offspring. They do not stop mating or fertilization but simply prevent hybrid offspring from surviving or reproducing successfully. Therefore, they act after the formation of a zygote and reduce hybrid survival, fertility or future generations' viability. They include:

1. **Hybrid inviability**: This occurs when the fertilized egg (zygote) fails to develop properly into a viable organism or dies at an early stage. The genes of different parent species may interact in ways that impair the hybrid's development or survival in its environment.
2. **Hybrid sterility**: This occurs when the hybrids survive and grow to maturity but are sterile thus cannot reproduce. This is because the chromosomes of the two parent species differ in number or structure and therefore they cannot allow for complete pairing of chromosomes during meiosis e.g. the mule (2n =63) results from a horse 2n=60 and donkey (2n=66).
3. **Hybrid breakdown**: This occurs when the first-generation hybrids are fertile, but subsequent generations are weak, abnormal or infertile.

How isolation mechanisms contribute to evolution

Isolating mechanisms drive evolution by restricting gene flow. Therefore isolating mechanisms help populations to stop interbreeding with each other/prevents gene mixing/restricts gene flow. When groups of the same species are separated by time, place, behavior or genetics, they can't share genes. Overtime, each group changes in its own way because of mutations, natural selection and adaptation to its environment. These changes or differences can become so big/build-up to the extent that the groups turn into or emerge into new species.

SPECIATION

Speciation is the evolutionary process by which new species arise from existing ones. It occurs when populations become genetically isolated and diverge over time.

Types of speciation:

1. **Allopatric speciation**: This occurs when populations are geographically isolated, leading to genetic divergence. In some cases, commonly in flowering plants, two species may give rise to a new species; this is known as interspecific hybridization.
2. **Sympatric speciation**: This occurs when the new species evolve within the same geographical area due to ecological or behavioral isolation. It occurs when the whole population is occupying the same geographical area.

Causes of speciation

- Cross-fertilization between two individuals of different species leading to formation of sterile hybrid.
- **Isolation**-Reproductive or geographical leading to demes evolving along different lines
- **Natural selection**-Operating differently in the different gene pools/subpopulation due to differences in climate or ecology.
- **Other drivers** occurring differently in the different demes causing upset in the allele frequencies, that's to say Mutation, Genetic drift and Non-random mating.

Steps in speciation:

- Isolation of populations.
- Accumulation of genetic differences through mutation, natural selection, and genetic drift.
- Reproductive isolation develops.
- Formation of new species.

Evolutionary advancements in key life processes

Living organisms have evolved various structural and functional adaptations that enhance their survival and reproduction in diverse environments. Over time, evolutionary pressures such as competition, predation, climate change, and availability of resources have shaped key life processes like circulation, reproduction, gaseous exchange, coordination, movement, and excretion across the different species. These advancements illustrate the transition from simple to complex organisms, ensuring efficiency, specialization, and suitability for survival.

Evolutionary advancements in Key life processes across different species:

Life process	Evolutionary advancement across species
Circulation	**(a) Protozoa & Sponges (Porifera):** These have no circulatory system. They rely on simple diffusion and water currents for transport of gases and nutrients. **(b) Cnidarians & Platyhelminthes (flatworms):** These have no true circulatory system, but have a gastrovascular cavity for distribution of nutrients. **(c) Nematoda:** These have a pseudocoelomic fluid which circulates materials. **(d) Annelida (Earthworms):** These have a closed circulatory system with blood vessels and pumping hearts. They also have a transport pigment called Hemoglobin in blood which improves oxygen transport. **(e) Arthropods & Molluscs:** These have an open circulatory system blood (hemolymph) flows into body cavities supplying nutrients to the body cells. However, some members to phylum arthropoda like Crustaceans evolved more efficient gill circulation. Some members to phylum Mollusca like Cephalopods (e.g., octopus) have evolved a closed circulatory system, efficient for active lifestyles. **(f) Vertebrates:** These have evolved a closed circulatory system which meets the demand of a large complex organisms. **For example;** • Fish have a closed, single circulation consisting of a 2-chambered heart. • Amphibians have a closed, double circulation consisting of a 3-chambered heart, but there is some mixing of oxygenated & deoxygenated blood.

	• Reptiles have a closed, double circulation with most having a 3-chambered heart with partial septum, reducing mixing while a few reptiles like crocodiles have a 4 chambered heart. • Birds & Mammals have closed, double circulation consisting of a 4-chambered heart, where oxygenated and deoxygenated blood is completely separated. It is highly efficient for warm-blooded metabolism.
Reproduction	**(a) Protists & Sponges**: These undergo asexual reproduction such as by Binary fission, budding, fragmentation. This form of reproduction allows rapid multiplication without gametes, ensuring survival in stable environments. **(b) Cnidarians & Platyhelminthes (flatworms):** These show alternation in their modes of reproduction between asexual (budding) and sexual stages. **(c) Nematodes & Annelids:** In these, sexual reproduction becomes dominant and internal fertilization occurs in some members. **(d) Arthropods & Molluscs:** Most show sexual reproduction, with internal fertilization common in terrestrial species. **(e) Vertebrates:** These undergo sexual reproduction. For example; • Fish: Show mostly external fertilization and external development. • Amphibians: Show external fertilization (in water), indirect development with larval stage. • Reptiles: Show internal fertilization, amniotic egg evolved – allowed reproduction independent of water. • Birds: Show internal fertilization, amniotic egg with shell, parental care, incubation. • Mammals: Show internal fertilization, viviparity (live birth in most), placenta for nourishment, intensive parental care.
Gas exchange	**(a) Protozoa, Sponges and Cnidarians:** These rely on simple diffusion through body surface due to possession of a large surface area to volume ratio. **(b) Platyhelminthes & Nematodes:** These rely on simple diffusion, but flattened body improves efficiency. **(c) Annelids:** Gas exchange through moist skin. **(d) Arthropods:** The aquatic forms have gills for gas exchange. Terrestrial insects have a tracheal system, which allows direct air delivery to tissues. **(e) Molluscs:** These have gills (ctenidia) in aquatic species; mantle cavity in some terrestrial snails. **(f) Vertebrates; such as;** • Fish: Have gills with for gas exchange. Bony fish rely on counter-current exchange system, highly efficient in extracting O_2 from water while cartilaginous fish rely on parallel flow exchange system.

	• Amphibians: These have gills in larvae stages, while the adult forms use lungs, skin and lining of mouth cavity for gas exchange. • Reptiles: These have a more advanced lungs with folded internal surface area. • Birds: Have a highly efficient unidirectional airflow in lungs, with air sacs ensuring continuous oxygen supply. • Mammals: Have alveolar lungs, with a large surface area, diaphragm for ventilation.
Coordination	a) **Protozoa:** These depend on simple responses via chemical or ionic changes in the cytoplasm. b) **Cnidarians:** These have a nerve net without centralization. c) **Platyhelminthes**: The bilateral symmetry evolved allowed introduction of cephalization (concentration of nerve cells in head region). d) **Annelids:** Have a ventral nerve cord with segmental ganglia. e) **Arthropods & Molluscs:** These have advanced ganglia and brains; complex sensory organs (compound eyes in insects, camera-type eyes in cephalopods). f) **Vertebrates:** These have a central nervous system (CNS) with brain and spinal cord. • Fish: These have relatively simple brains. • Amphibians: These have a slightly more developed forebrain. • Reptiles: These have enlarged cerebrum for improved sensory processing. • Birds: These have a large cerebellum for balance and flight coordination. • Mammals: These have a highly developed cerebral cortex, capable of learning, memory, and complex behavior. **Note: Hormonal coordination:** Simple chemical messengers in much used in invertebrates but vertebrates have a fully developed endocrine systems.
Movement	(a) **Protozoa:** The movement in some members may involve use of pseudopodia, cilia, flagella. (b) **Sponges:** The adult forms are sessile while the larval stages move using cilia. (c) **Cnidarians:** These have contractile fibers and hydrostatic skeleton. (d) **Flatworms & Nematodes:** These have muscles working with hydrostatic skeleton for wriggling. (e) **Annelids:** These have circular and longitudinal muscles with hydrostatic skeleton, peristaltic movement. (f) **Arthropods:** These have exoskeleton, and specialized locomotion (walking, flying, and swimming). Provides protection and attachment for muscles but limits growth (molting required). (g) **Molluscs:** Some have a muscular foot like the snails), jet propulsion (squid).

	(h) Echinoderms: These have unique water vascular system for movement. **(i) Vertebrates:** These have endoskeletons which provides internal support, allows continuous growth, and supports larger body size. They show special locomotory structures such as; • Fish: These have fins for swimming. • Amphibians: These have limbs adapted for land/water. • Reptiles: These have limbs for crawling; snakes lost limbs but adapted muscles for slithering. • Birds: These have wings for flight. • Mammals: These have limbs which show a wide diversity for special forms of movement like running, swimming, and flying in bats.
Excretion	**(c) Protozoa:** These carry out excretion by diffusion and contractile vacuoles. **(d) Sponges & Cnidarians:** These remove nitrogenous waste, ammonia by simple diffusion across body surface. **(e) Platyhelminthes:** These have special excretory structures called flame cells (protonephridia) for osmoregulation and excretion. **(f) Annelids:** These have special excretory structure called Metanephridia – more advanced tubular excretory structures. **(g) Arthropods:** some members like insects and arachnids have special excretory structures called Malpighian tubules while crustaceans have evolved Green glands. **(h) Molluscs:** These have special excretory structure called Nephridia for removal of nitrogenous waste. **(i) Echinoderms:** These depend on simple diffusion via tube feet and body surfaces. **(c) Vertebrates:** These have special excretory organs for excretion such as; • Fish have simple kidneys, to excrete ammonia (ammonotelic). • Amphibians have kidneys for urea excretion (ureotelic). • Reptiles & Birds have kidneys for uric acid excretion (uricotelic), thus conserves water. • Mammals have advanced kidneys with nephrons, for urea excretion, regulation of water and salts.

Significances of the evolutionary advancements in the life processes for survival

The evolutionary advancements in the different life processes have all increased efficiency, adaptability and survival of organisms in different environments. They allowed organisms to grow larger, become more active, reproduce more successfully and colonize new habitats, thus shaping biodiversity.

Life Process	Significance of Evolutionary Advancements for survival
Circulation	Development of more developed and complex circulatory system ensured; **(i)** Efficient transport of oxygen, nutrients, and wastes which offers support to larger, more complex organisms with high metabolic rates. For example; • Closed systems maintain higher blood pressure, enabling rapid delivery of materials. • Double circulation separates oxygenated and deoxygenated blood, allowing higher metabolic rates and thus supports endotherms.
Reproduction	Development of more advanced reproductive organs and reproductive strategies ensured species continuity in diverse and changing environments. For example; **(b)** Use of sexual reproduction increased genetic variation which enhanced adaptability to their environment. **(c)** Development of internal fertilization protects gametes and embryos from desiccation and predation hence increasing the chances of survival. **(d)** Formation of amniotic eggs among the birds allowed colonization of land. **(e)** Development of placenta which ensures continuous nourishment and protection also improved survival among the placental mammals.
Gaseous Exchange	Development of more advanced and specialized gas exchange system ensured more efficient exchange of respiratory gases, which supported aerobic respiration thus enabling more active lifestyles and increased survival in different habitats. For example; **(a)** Development of tracheal system in insects allows direct delivery of oxygen to body tissues. **(b)** Use of lungs in birds with one-way air flow maximizes oxygen uptake, thus supporting sustained flight at high altitudes with low oxygen partial pressures.
Coordination	**(a)** Development of more advanced coordination systems facilitated quick responses to stimuli, which aided in predator avoidance and prey capture. **(b)** Also the complex nervous system enabled development of more complex behaviors, learning, and adaptability which increased survival chances in the environmental.
Movement	**(a)** Development of more advanced locomotory structures enabled escape of organism from predators, acquisition of food, mates, colonization of new habitats, and adaptation to diverse environments.

	(b) The development of exo- and endo-skeletons also provided support ad leverage, allowing attainment of larger body sizes and faster locomotion
Excretion	**(a)** Development of more advanced excretory system allowed efficient maintenance of internal environment (homeostasis) by removal of toxic wastes, efficient regulation water and salt balance, thus allowing colonization and survival in varied conditions (e.g., deserts, freshwater, marine).

Natural selection in action

This refers to the day-to-day observations of natural selection or examples of natural selection.

Examples include the following.

- Insects' resistance to insecticides/pest resistance to pesticides, like flies and mosquitoes to Dichlorodiphenyltrichloroethane (**DDT**).
- Resistance to antimalarial drugs.
- Antibiotic resistance by pathogens e.g. bacteria to penicillin and methicillin.
- Heavy metal tolerance in grass and other plants.

Antimicrobial and pesticide resistance

Antimicrobial resistance refers to the ability of microorganisms (bacteria, viruses, fungi or parasites) to survive and multiply despite the presence of drugs (antibiotics, antivirals, antifungals or antimalarial) that normally kill them or stop their growth.
Pesticide resistance refers to the ability of pests (insects, rodents) to survive chemical treatments that are designed to kill or control them.

Causes of resistance:

- Overuse or misuse of antibiotics or pesticides.
- Under dosing or incomplete treatment courses.
- Repeated use of the same chemical.
- Poor pest or infection management practices.

How does does the resistance arise?

Resistance usually develops or rises through natural selection. Within the pest or microorganism population, some individuals may naturally carry mutations or traits or genetic variations that make them less affected to a drug or pesticide/which allows them to survive after exposure to antimicrobial drugs or pesticides. Continuous exposure of such antimicrobials or pesticides to the pest or microbial populations creates a directional selective pressure which results into individuals that have susceptible traits/less adapted forms/non-mutant forms to die while the resistant forms/mutant forms (those carrying mutant genes that make them resistant to the drug) to survive and reproduce rapidly, passing on the resistant traits to the next generations. Overtime, the population becomes dominated by resistant individuals.

Note:

Mutations that confer resistance usually already exist naturally in the population due to random genetic variations. Therefore, continuous exposure to pesticides does not

directly induce mutations; instead it selects for individuals that already carry resistant traits. ***"Pesticides induce mutations implies chemicals causes resistance mutations, which is not true in most cases"***. The process is by natural selection, not mutation induction.

Bacterial populations can easily become resistant because of the same following reasons:

- They have a haploid DNA such that in case of a mutation, the resistant allele is instantly expressed phenotypically due to absence of the non-resistant copy
- They reproduce rapidly by binary fission hence the number of resistant individuals' increases so rapidly that soon the whole population becomes resistant.
- Ability of individual bacteria to exchange resistant alleles. This is called **plasmid exchange** leading to a rapid spread of resistance in a population.

Solutions to resistance

- Rotate or combine pesticides/chemicals to reduce resistance.
- Follow correct dosages as prescribed by a qualified health professional.
- Use of integrated pest management (IPM) such as combining biological, cultural and mechanical methods.
- Development of resistant crop varieties to pests or diseases.
- Development of new antibiotics and alternative therapies.

Mass extinction

Mass extinction refers to a large-scale, rapid decrease in the biodiversity on Earth, where a significant percentage of species (large number of species, usually more than 50%) become extinct in a relatively short geological period. Usually mass extinction events are catastrophic and often reset ecosystems. At least five major mass extinctions have occurred in Earth's history.

Factors that contribute to mass extinction:

The causes of mass extinctions include drastic environmental changes, catastrophes, and biological causes.

1. **Environmental factors:** As a result of sudden or extreme environmental changes, some species may fail to adapt quickly resulting into mass extinction. These environmental changes include:
   - Climate change such as global warming, extreme weather events
   - Sea level fluctuations.
   - Catastrophes such as volcanic eruptions releasing toxic gases.
2. **Extraterrestrial impacts** such as asteroid or large meteorite impacts causing fires, dust clouds, and blocking sunlight can cause large scale extinctions of species.
3. **Biological factors:** These are processes within the biosphere that may disrupt ecosystems and cause widespread extinctions of species. They include:
   - Competition between species: when two or more efficient species evolve, they can outcompete the older ones for food, space or other resources and so the weaker ones or the less adapted species becomes extinct.
   - Over predation and herbivory: Evolution of new predators with better hunting adaptations (like speed, venom, teeth) or excessive predation can wipe out all the

prey populations. For example, introduction of new predatory species into islands by humans often leads to extinction of native species. Similarly, new herbivores may destroy plant species or entire ecosystems if grazing is excessive.

- Spread of new diseases/Epidemics: Outbreak of pathogens can decimate species with little resistance. Therefore, spread of diseases in dense populations can lead to mass extinction.
- Introduction of invasive species: The invaders may have better adaptations that allow them to outcompete or prey on the native species, driving them to extinction.

4. **Human activities/factors:** Modern extinctions is being caused mainly by human activities that drastically alter the ecosystems. These include:
   - **Habitat destruction:** Human activities such as deforestation, urbanization, mining, settlements, road constructions, agricultural expansions etc can cause destruction of habitats resulting into species losing their homes, food sources and breading grounds.
   - **Pollution:** discharge of pollutants into air, water and soil/land affects the health of the organisms resulting into their death.
   - **Overexploitations** such as Overhunting, overfishing, and poaching or illegal wildlife trade can result into large scale decline in the populations faster than they can recover.
   - **Introduction of invasive species**: Human transport species intentionally or accidently to new areas which species may have no natural predators or may have better adaptations than the native species allowing them to outcompete or prey on the native species.

The major extinctions, their timelines, key events involved and their causes

The major mass Extinctions are:

Mass extinction	Approximate time/ Timelines	Key events	Probable causes
1. **Ordovician -Silurian extinction**	~440 million years ago (Mya)	About 85% of marine species lost. Major decline in trilobites, brachiopods, bryozoans	• Global cooling and glaciation. • Sea level fall (regression). • Reduced habitat for shallow marine life.
2. **Late Devonian extinction**	~375 million years ago	~70-80% of species lost. Major impact on marine life, especially reef-building organism (corals), loss of many jawless fish	• Linked to climate change, Global cooling. • Possible asteroid impact. • Low oxygen in oceans (ocean anoxia).

			• Rapid plant expansion altering carbon cycle.
3. Permian–Triassic extinction (The great dying)	~250 million years ago	About 96% of marine species and 70% of terrestrial species were wiped out. The largest known extinction event that led to collapse of many ecosystems.	• Massive volcanic eruptions (Siberian traps). • Methane release from seafloor. • Global warming (climate shifts) and ocean acidification. • Anoxia in oceans
4. Triassic–Jurassic extinction	~200 million years ago	~70-75% of the species were lost. Many reptiles, amphibians and marine species became extinct. This cleared the way for dinosaurs to dominate.	• Likely due to volcanic activity. • Climate change and ocean acidification. • Sea level fluctuations.
5. Cretaceous –Paleogene extinction	~65 million years ago	~75% of species were lost. Many marine reptiles and ammonites became extinct/ wiped out non-avian dinosaurs, but mammals diversified afterward.	• Caused by asteroid impact (Chicxulub crater). • Massive volcanic eruptions. • Climate change. • Disruptions in food chains
6. Holocene/ Anthropocene extinction	~10,000 years ago	Rapid loss of large mammals, birds, amphibians and fish. Significant human driven extinctions.	• Habitat destructions and deforestation. • Overhunting and overfishing. • Climate change due to human activity. • Introduction of invasive species.

Effects of mass extinctions

The major impacts of mass extinctions are;

- **Loss of biodiversity:** Mass extinctions lead to sudden disappearance of a large proportion species across habitats resulting into a reduction in species richness and ecosystem complexity, many ecological niches become empty affecting interdependent species and loss of specialized species that had unique ecological roles.
- **Can lead to collapse of ecosystems:** The disappearance of key species destabilizes ecosystems resulting into breakdown of food chains leading to secondary extinctions and disruptions of nutrient cycles.

- **Can lead to emergence and radiation of new species (adaptive radiation)/evolutionary opportunities:** Mass extinctions create empty ecological niches allowing surviving species to diversify. The adaptive radiation or rapid evolution of new species allows some species to exploit the available niches; emergence of dominant new species groups as well as evolution of novel traits to adapt to post-extinction environments.
- **Contributes to reshaping of ecosystems:** Mass extinctions fundamentally restructure ecosystems. This allows emergence of ecosystems with novel structures and interactions.
- **Human/scientific implications:** Studying past mass extinctions informs us about current biodiversity crises. This provides insights/lessons into conservation strategies for conservation and biodiversity protection.

Contribution/the role of mass extinction to Evolution

Mass extinction, though destructive, is a driving force of evolution. Therefore, it prevents evolutionary stagnation by allowing new life forms to emerge and thrive.

- Mass extinction acts as a driving force for adaptive radiation, which leads to evolution through creating empty ecological niches as a result of removing dominant species which allows surviving species rapidly diversify to fill empty niches. When many species disappear, ecological niches (specific roles or habitats) within ecosystems become vacant allowing the surviving species to colonize the new niches. This reduces completion and allows surviving species to diversify rapidly/evolve rapidly to fill the empty niches.
- It also acts as a selection pressure on survivors: Mass extinctions create extreme environmental pressures such that only species with favourable adaptations survive, they reach reproductive age and pass on their genes to the next generation. This leads to evolution of new traits.
- Acceleration of speciation: Following mass extinction, speciation rates often increase. This is because after mass extinctions, empty niches encourage divergence of surviving lineages. Thus, the rapid appearance of new species enhances biodiversity recovery