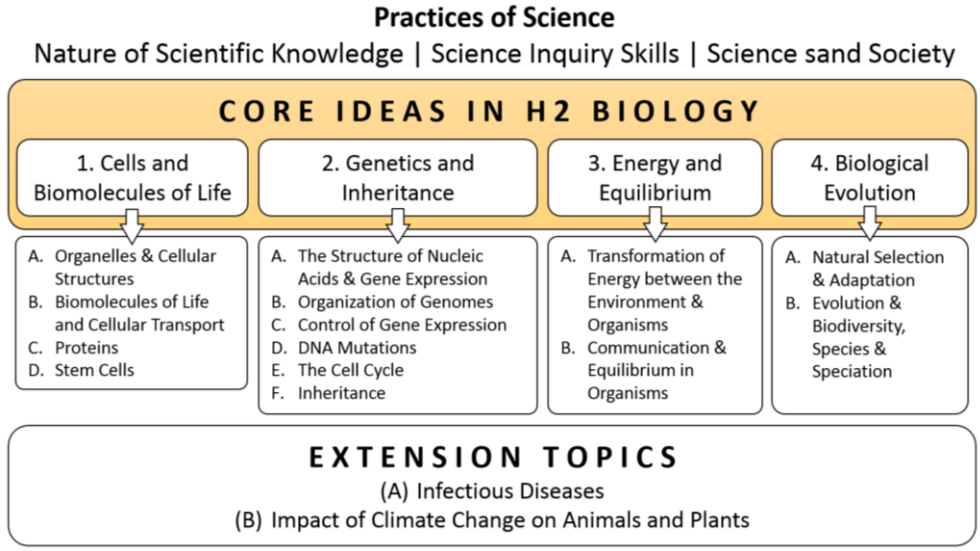
11. Genetics & Inheritance (VIII) – Inheritance



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

TOPIC SYNOPSIS

An understanding of *Genetics and Inheritance* that would help make sense of the transition from molecular to organismal level. *Genetics and Inheritance* provides the molecular basis to the understanding of how variations in populations arise and this is important in the study of biological evolution. At the cellular level, expression of genes involves cellular structures such as the nucleus, endoplasmic reticulum and ribosome. Many essential products of gene expression are enzymes involved in biochemical pathways which control physiological functions. As such, mutation of genes may give rise to dysfunctional proteins which in turn could result in diseases. Sickle cell anemia and cancer are raised as examples of a monogenic and a multi-genic disease respectively.

The following questions should help students frame their learning:

- How does the genetic make-up of an organism and the environment influence the organism's appearance, behavior and survival?
- How does the inheritance of genetic information ensure the continuity of human as a species?

Mutation arises from imperfect replication of genetic information; together with other biological processes, such mutations increase genetic variation

Mutation, meiosis and sexual reproduction give rise to genetic variation within a population. Besides these, environmental factors are known to influence the phenotype of organisms. There are two kinds of genetic variations: continuous variation involves many genes, which have an addictive effect in controlling a characteristic; discontinuous variation involves one or just a few genes in controlling a characteristic. Besides these, environmental factors are known to influence the phenotype of organisms.

Expression of genes gives rise to functional products that affect biochemical reactions and physiological functions of organisms. This demonstrates how the genotype and phenotype of an organism are related. Besides its genotype, the environment also plays a role in determining the phenotype of an organism and this is related to the field of epigenetics. Some environmental factors include availability of nutrients and changes in temperature.

The chromosomal basis of inheritance sheds light on the pattern of transmitting genes from parents to offspring

When Gregor Mendel first started his investigations into inheritance, the concept of genes had not been used. He used the term 'traits' in place of genes. By using genetic diagrams, the phenotypic and genotypic ratios of filial generations can be predicted for crosses involving monohybrid or dihybrid inheritance. In line with Mendelian genetics, pedigree diagrams can be used to predict the probability of inheriting genetic diseases, such as haemophilia and Huntington's disease.

Non-Mendelian inheritance involves more complex traits. For example, alleles of some genes exhibit co-dominance or incomplete dominance and some genes have multiple alleles or are found on the sex chromosomes. Furthermore, phenotypes may depend on interactions between two or more genes, e.g. epistasis. In addition, inheritance of linked genes does not follow Mendelian laws; in predicting the phenotypic and genotypic ratios of filial generations for linked genes, the occurrence and frequency of crossing over has to be considered.

LEARNING OUTCOMES

Core Idea 2F: Inheritance
This concept includes both Mendelian and non-Mendelian inheritance. Besides genetics, the environment also plays a role in determining the phenotype of an organism. Statistical tests, such as the chi-squared test, allow scientists to test the significance of differences between observed and expected results of genetic crosses.

Candidates should be able to:

a) Explain the terms: locus, allele, dominant, recessive, codominant, incomplete dominance, homozygous, heterozygous, phenotype, genotype and linkage.

b) Explain how genes are inherited from one generation to the next via the germ cells or gametes.

c) Explain how genotype is linked to phenotype.

d) Use genetic diagrams to solve problems in dihybrid crosses, including those involving codominance, incomplete dominance, multiple alleles, sex linkages, autosomal linkage and epistasis.

e) Use genetic diagrams to solve problems involving test crosses.

f) Explain the meaning of the terms linkage and crossing-over and explain the effect of linkage and crossing over on the phenotypic ratios from dihybrid crosses.

g) Describe the interaction between loci (epistasis) and predict phenotypic ratios in problems involving epistasis. (Knowledge of the expected ratio for various types of epistasis is not required; focus of this section is on problem solving).

h) Explain how the environment may affect the phenotype (including how diet affects the differentiation of honey bees and how temperature affects fur color of Himalayan rabbits).

i) Explain the difference between genetic variation that is continuous (many, additive, genes control a characteristic) and discontinuous (one or few genes control a characteristic).

j) Use the chi-squared test to test the significance of differences between observed and expected results.

LECTURE OUTLINE

1. Introduction
- 1.1 Definition of terms
- 1.2 Historical background

2. Mendelian Genetics
- 2.1 Monohybrid Inheritance and Mendel's First Law – Law of Segregation
- 2.2 Dihybrid Inheritance and Mendel's Second law – Law of Independent Assortment
- 2.3 Summary of Mendel's Hypothesis

3. Interaction between Alleles of a Gene
- 3.1 Codominance
- 3.2 Incomplete dominance
- 3.3 Multiple alleles

4. Linkage
- 4.1 Autosomal linkage
  - 4.1.1 Crossing Over
  - 4.1.2 Genetic diagrams involving linked genes
- 4.2 Sex determination in humans and other organisms
- 4.3 Sex Linkage
  - 4.3.1 Haemophilia
  - 4.3.2 Red-green Colourblindness
  - 4.3.3 Eye colour of *Drosophila* and Reciprocal Cross

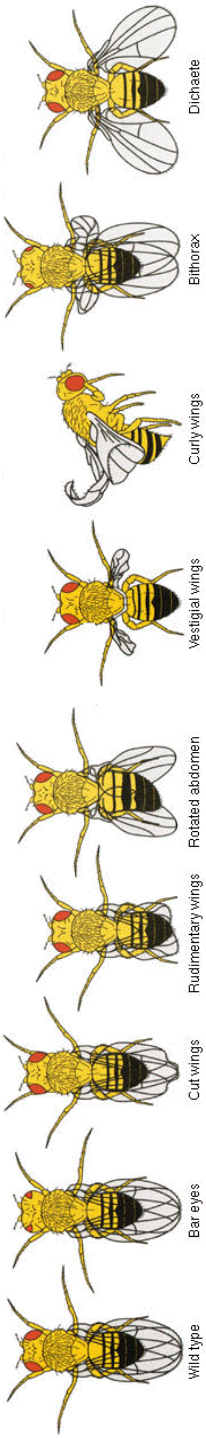
5. Pedigree Chart
- 5.1 Background and Symbols used
- 5.2 Identifying Inheritance Patterns

6. Gene Interactions
- 6.1 Two-gene interaction can produce a 9:3:3:1 ratio
- 6.2 Epistasis produces modified 9:3:3:1 ratios
  - 6.2.1 Coat colour in mice – 9:3:4 ratio
  - 6.2.2 Plumage colour in chicken – 13:3 ratio
  - 6.2.3 Colour of summer squash – 12:3:1 ratio
  - 6.2.4 Flower colour in sweet peas – 9:7 ratio
  - 6.2.5 Fruit shape of summer squash – 9:6:1 ratio
  - 6.2.6 Seed capsule shape of Sherphard's Purse – 15:1 ratio

7. The Chi-squared Test

8. Variation
- 8.1 Discontinuous Variation
- 8.2 Continuous Variation
- 8.3 Sources of Variation
  - 8.3.1 Gene reshuffling
  - 8.3.2 Gene Mutations (*covered in Genetics & Inheritance III*)
  - 8.3.3 Chromosomal Aberrations (*covered in Genetics & Inheritance III*)

9. Effect of Environment on Phenotypes



1. Introduction

Learning Outcome:

a) Explain the terms: locus, allele, dominant, recessive, codominant, incomplete dominance, homozygous, heterozygous, phenotype, genotype and linkage.

b) Explain how genotype is linked to phenotype.

1.1 Definitions of terms

a) Homologous chromosomes

- A **diploid** organism has two sets of chromosomes, **one from each parent** (Fig. 1.1).

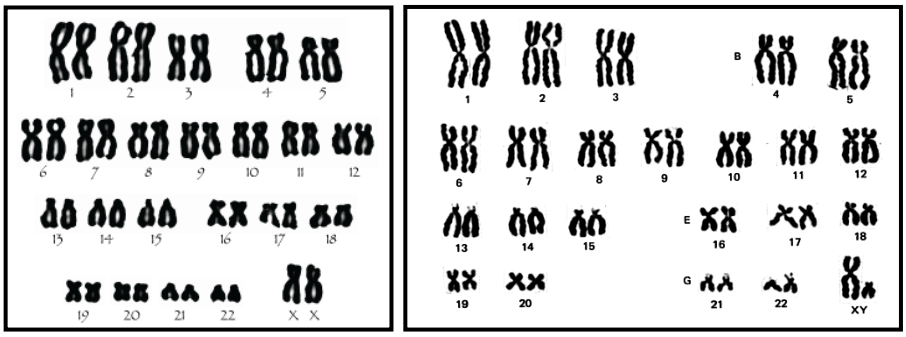


Fig. 1.1: A karyotype of a female (left) and a male (right) human. Note that in female, there are 23 pairs of homologous chromosomes, which includes the XX sex chromosomes. In male, there are 22 pairs of homologous chromosomes and XY sex chromosomes which are not homologous. Short segments at either end of the Y chromosome are the only regions that are homologous with the corresponding regions of the X. These homologous regions allow the X and Y chromosomes in males to pair and behave like homologous chromosomes during meiosis in the testes

- Chromosomes of a homologous pair:
  - **pair with each other** during **prophase I** of meiosis
  - have exactly the **same order of gene loci**
  - have **centromeres** in the **same position** and **arms** of the **same length**

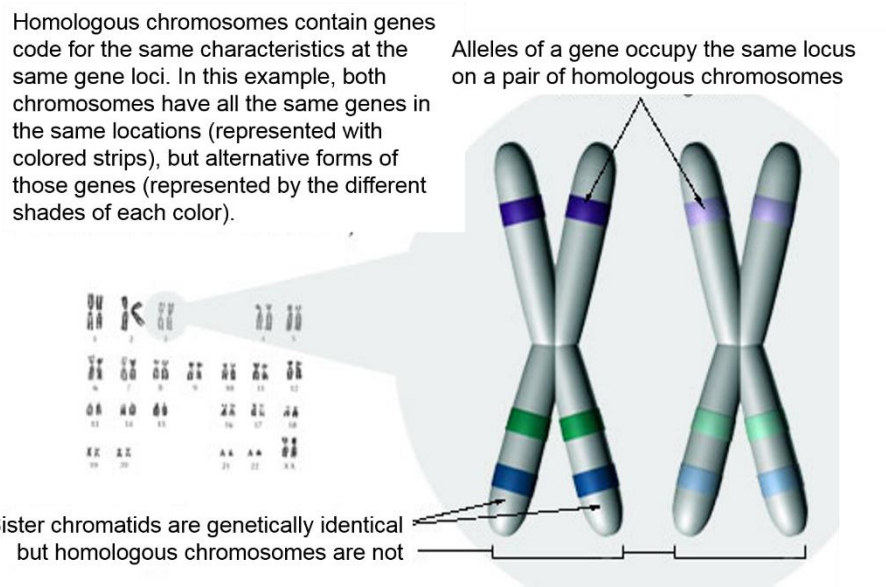


Fig. 1.2: The left is a karyotype of a female human and the right is a cartoon representation and description of homologous chromosomes

- Any two chromosomes which determine the **same characteristics** (e.g. eye colour, blood group) are called **homologous chromosomes** (or homologs).

- Although homologous chromosomes determine the same characteristic, they **need not be genetically identical** (Fig. 1.2). E.g. a gene on a homologous chromosome could be blood group. The allele on one of the chromosomes may code for protein that gives rise to blood group A and the allele on the other chromosome may code for protein that gives rise to blood group B.

b) Gene

- A gene is a discrete unit of hereditary information.

- It is a **specific sequence of nucleotides** (Fig. 1.3) in the DNA molecule which **codes for a RNA** (e.g. tRNA, rRNA, telomerase RNA) or **polypeptide** (e.g. amylase).

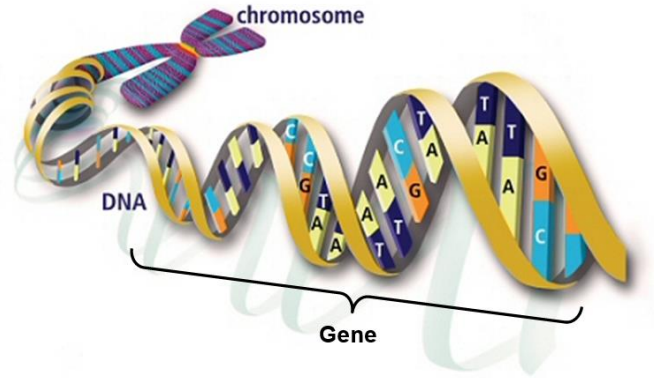


Fig. 1.3: A gene is a segment of DNA of specific nucleotide sequence that codes for a specific RNA or protein.

c) Gene locus (plural: loci)

- The **position** occupied by a gene on a chromosome (Fig. 1.4).

- E.g. the locus of gene *B* is towards one end of the chromosome while the locus of gene *A* is more at the middle.

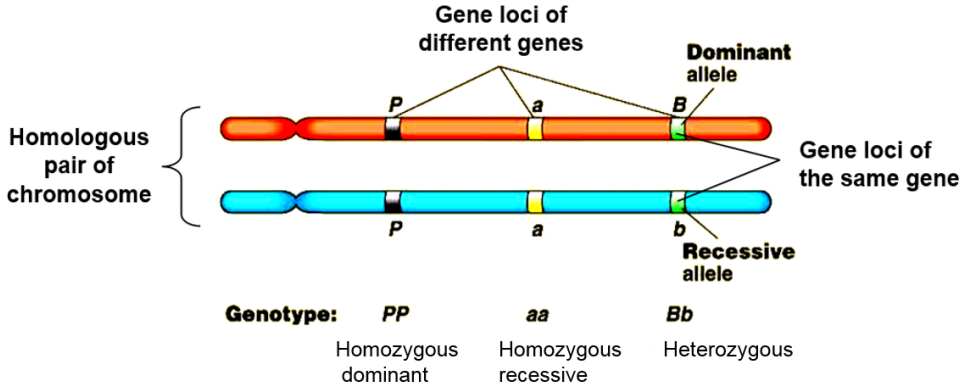


Fig. 1.4: A diagrammatic explanation of gene loci, dominant/recessive alleles, homozygous dominant, homozygous recessive and heterozygous

d) Allele

- Allele is an **alternative form of the same gene** responsible for variation in a particular characteristic.

- **Alleles of a gene** occupy the **same gene locus** on homologous chromosomes (Fig. 1.4).

- Alleles cause variation due to a **slight difference in the nucleic acid sequence**, which give rise to **different forms of the protein**. E.g. normal haemoglobin allele and mutated haemoglobin allele (Fig. 1.5a).

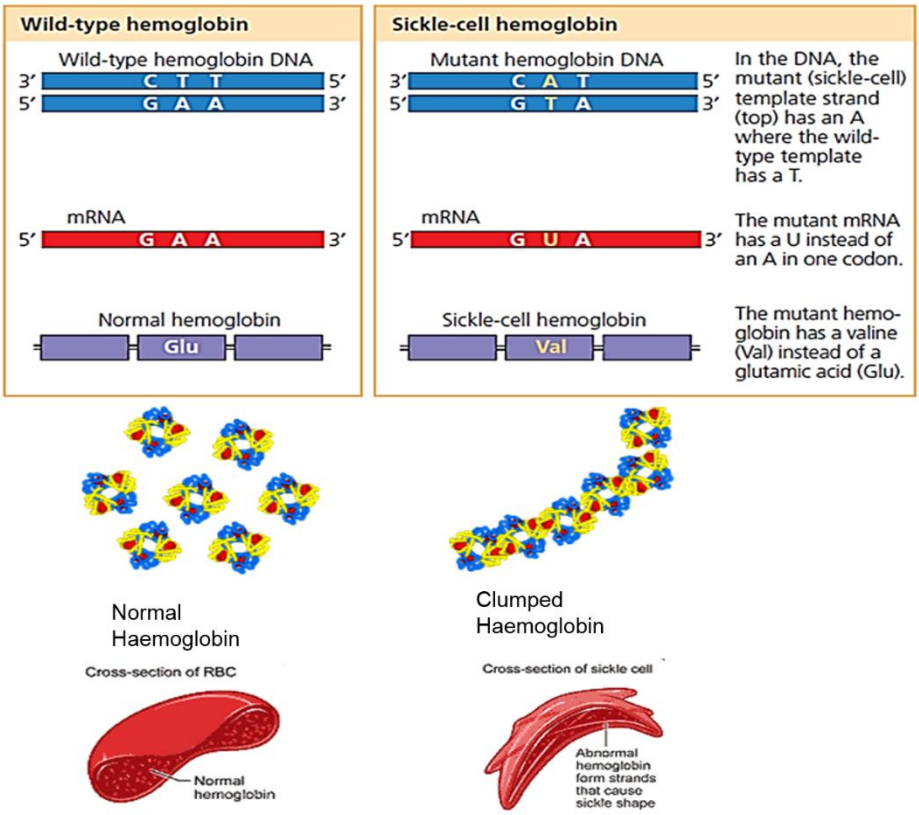


Fig. 1.5a: The mutated haemoglobin allele is a result of a single-base substitution that causes glutamic acid (GAA) to be replaced by valine (GUA). This change in amino acid sequence causes haemoglobin molecules to crystallize when oxygen levels in the blood are low. As a result, red blood cells sickle and get stuck in small blood vessels.

- Alleles occur in **pairs** in a **diploid individual**, and only **one of a pair** is represented in a **gamete**.

- Dominant allele
  - An allele that is **fully expressed** in the **phenotype** even in the presence of an alternative allele, i.e. expressed **in both homozygous and heterozygous condition**. The allele is said to be **completely dominant** over the other.
  - In a genetic diagram, this is often represented by an upper case letter (Fig. 1.4, PP for homozygous condition and Bb for heterozygous condition).

- Recessive allele
  - An allele which is expressed in the **phenotype** only in the presence of another identical allele, i.e. expressed **only in homozygous condition**.
  - The expression of the recessive allele is **masked** in a **heterozygote**.
  - In a genetic diagram, this is often represented by *lower* case letter (Fig. 1.4, aa for homozygous recessive and Bb for heterozygous condition).

- Multiple alleles (*details in Section 3.3*)
  - Gene that exists in **more than two allelic forms** in a **given population**.
  - Regardless of the number of different alleles, **only two** of which can be present in a **diploid** organism.
  - E.g. the gene responsible for the ABO blood group of the human population exists in three forms – I^A, I^B and I^O (Fig. 1.5b).

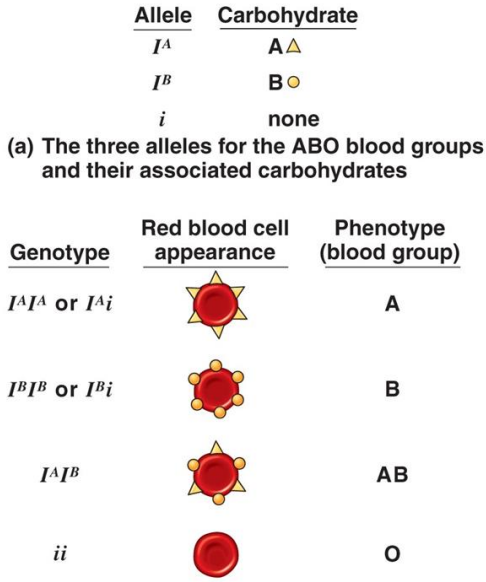


Fig. 1.5b: Codominance of allele I^A and I^B in the ABO blood group of humans and how the genotypes translates into the respective phenotypes. Note: I^O can be written as i

e) Codominance (*details in Section 3.1*)

- The phenomenon in which two alleles which are **expressed equally in the phenotype** of a heterozygote. They are said to be **codominant** with each other.

- E.g. blood group AB in humans is due to the expression of both the I^A and I^B alleles (Fig. 1.5).

f) Incomplete dominance (*details in Section 3.2*)

- The phenomenon in which one allele for a specific trait is **not completely dominant** over the other allele, resulting in heterozygote offspring having a **phenotype** which is **intermediate** of that of the homozygous parents.

- E.g. crossing red snapdragon plants (RR) with white ones (rr) results in pink offspring (Rr).

- The presence of only one allele (R) does not provide enough pigment to give the flower a fully red colour, but only enough pigment to give the flower pink colour of the heterozygote (Rr).

g) Genotype

- Genotype of the **genetic makeup of an organism** with respect to the alleles under consideration.

- Genotype of an organism can either be:
  - Homozygous – It is the diploid condition at which the **alleles at a given locus** are **identical** (Fig. 1.4: *PP* and *aa*, Fig. 1.5b: I^AI^A, I^BI^B and I^OI^O)
  - Heterozygous – It is the diploid condition at which the **alleles at a given locus** are **different** (Fig. 1.4: *Bb*, Fig. 1.5b: I^AI^O and I^BI^O)

h) Phenotype

- Phenotype is the **observable characteristics of an individual**. This is dependent on the genotype. In some cases, expression of the phenotype is determined by the interaction between the genotype and the environment (e.g. height). However, in others, environment does not affect the expression (e.g. eye colour).

i) Pure line / breed true / pure breeding / truebreeding

- Members of a pure line are **homozygous at the gene loci** and are said to **breed true** (Fig. 1.6).

- The individual is either homozygous dominant or homozygous recessive, and **never heterozygous**. E.g. AABB, AAbb, aaBB.

j) F_1 generation

- First filial generation produced by crossing 2 parental stocks (Fig. 1.6).

k) F_2 generation

- Second filial generation produced by crossing two different F_1 organisms or by self-fertilization of the same F_1 organism (Fig. 1.6).

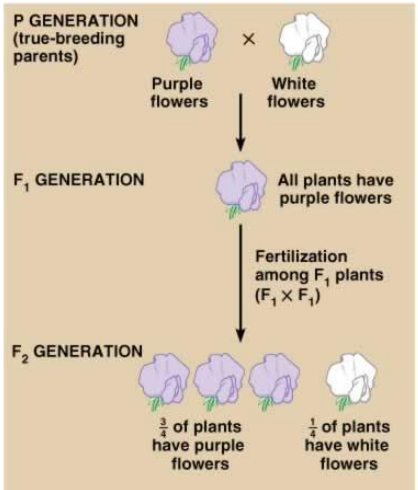


Fig. 1.6: Crossing two true-breeding parents results in F_1 generation all exhibiting the dominant trait and F_2 generation exhibiting dominant and recessive traits in the ratio of 3:1

l) Test cross

- An organism which shows the effect of a dominant allele can have two possible genotypes.
- For example, a pea plant which produces smooth seeds could either be homozygous dominant (SS) or heterozygous (Ss) for the gene.
- It is often necessary to determine the genotype accurately. This can be achieved by a **test cross**.
- A test cross is the **crossing of an organism having an unknown genotype with a homozygous recessive organism to determine the unknown genotype within one breeding generation**.
- A homozygous recessive individual is used because all its gametes will contain the recessive allele at the gene locus, which will not have any effect on the phenotype of the offspring.
- The phenotypic ratio of offspring from a cross involving a homozygous dominant individual and a heterozygote is different (Fig. 1.7).

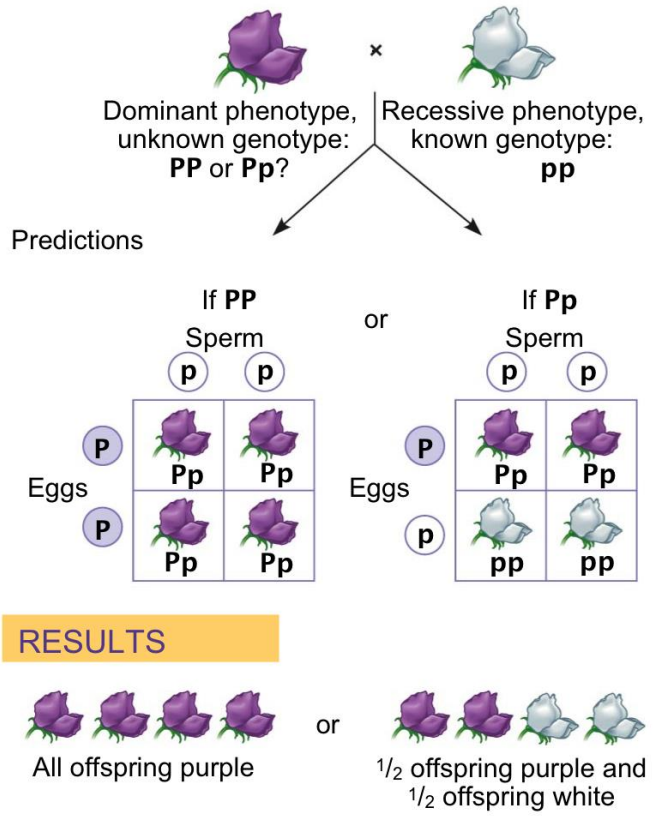


Fig. 1.7: A test cross reveals if a pea plant that produces purple flower is homozygous (PP) or heterozygous (Pp) by determining the phenotypic ratio of the offspring

m) Reciprocal cross (*Details in Section 4.3.3*)

- A cross where the same genetic features are used but the **sexes are reversed**.
- A reciprocal cross is carried out **to determine whether the trait is sex-linked**. For sex-linked genes, reciprocal crosses give different F_1 results whereas for autosomal genes, the same F_1 results are expected.

1.2 Historical background

- Johann Mendel Gregor was born in Heinzendorf, Moravia in 1822. During his childhood, he worked as a garderner.

- In 1843, he entered the Augustinian Abbey of Saint Thomas in Brno, where he took the name Gregor.

- In 1851, he was sent to University of Vienna to study natural history and mathematics before returning to the monastery in 1853 as a teacher.

- Between 1856 and 1863 Mendel cultivated and tested some 29 000 pea plants (*Pisum sativum*). He established that it had the following advantages over other species:

    1. There were several varieties available, which had quite **distinct characteristics**. Many traits occur in two alternate forms that are easy to distinguish. For example, stem length, seed shape, seed colour, pod colour, pod shape, flower colour and flower position (Fig. 1.8).

    2. The plants were **easy to cultivate** and **produce many offspring**.

    3. **Short generation time** - develop quickly hence results can be seen within a short time.

    4. The reproductive structures were completely enclosed by the petals, which **ensure self-pollination**. This led to pure breeding, whereby the same characteristics are produced generation after generation.

    5. **Artificial cross-breeding** between varieties was possible (Fig. 1.9), resulting in hybrids that were completely fertile.

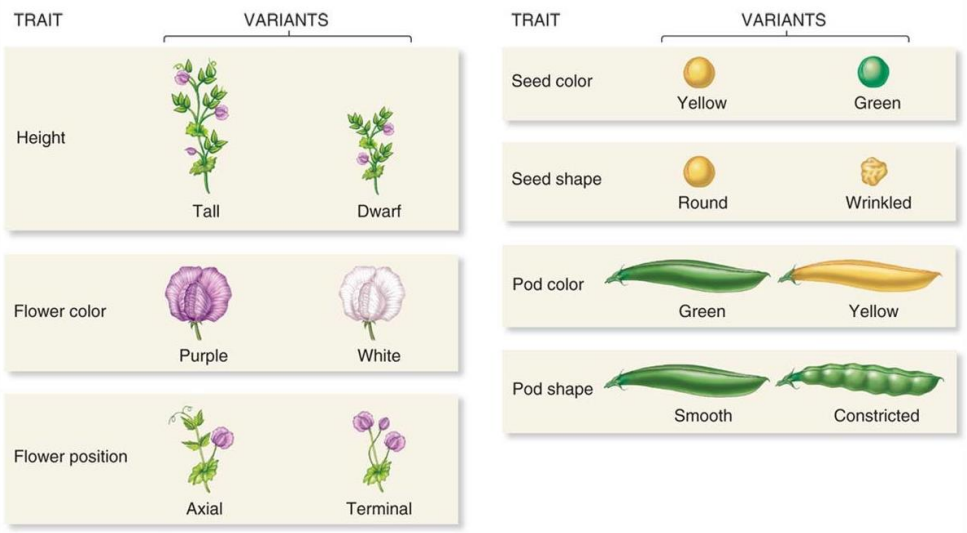


Fig. 1.8: Seven pea plant traits that Mendel examined

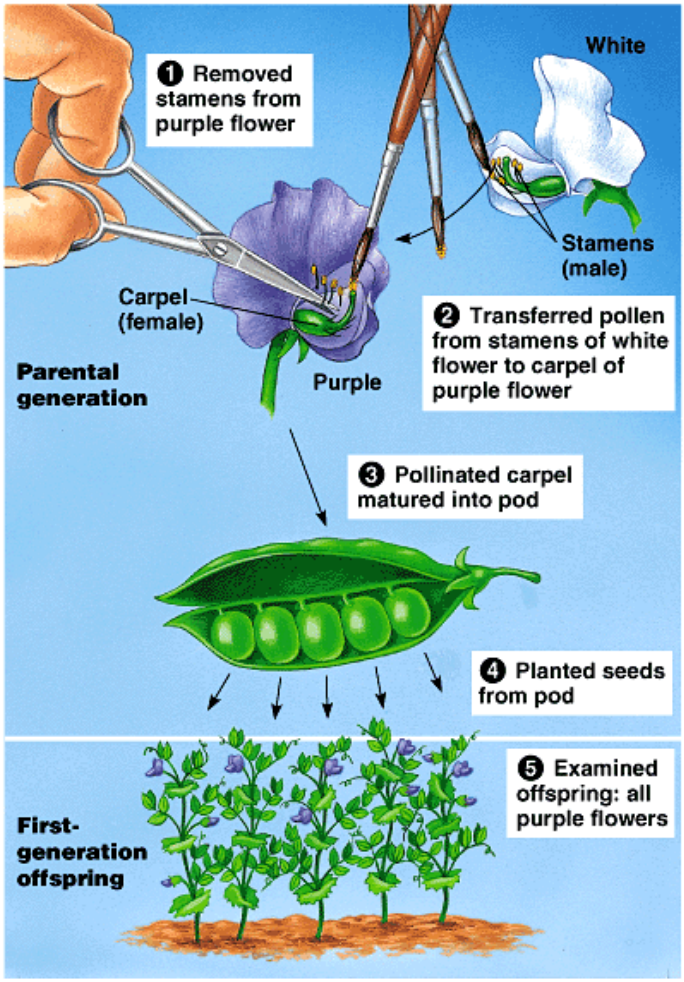


Fig. 1.9: Artificial cross breeding between varieties of pea plants

- From the data gathered, he published his paper “Experiment in Plant Hybridization” in 1866.
- Initially, his work was not well-received and created little impact. It was only in 1900, when his work was rediscovered by Hugo de Vries and Carl Correus, which led to the revelation of the **two fundamental principles of Heredity**. They are now known as the **Law of Segregation** and the **Law of Independent Assortment**.

2. Mendelian Genetics

Learning Outcome:
d) Use genetic diagrams to solve problems involving test crosses.

2.1 Monohybrid inheritance & Mendel's 1st law – Law of Segregation

- Monohybrid inheritance: The inheritance of **one characteristic** controlled by alleles of **one gene**.

Key Concept 1:
- The law of segregation or **Mendel's First Law** (Fig. 2.1) states that:
  - **Each pair of alleles of a gene segregates** and **each gamete receives one of each pair of alleles**.

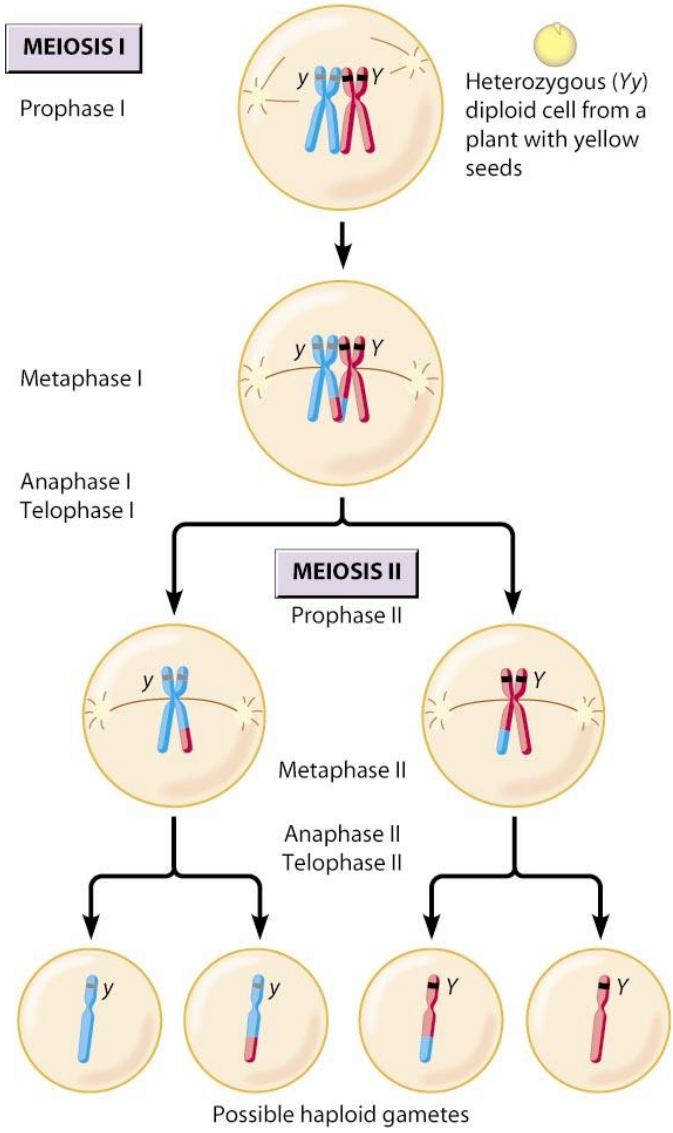


Fig. 2.1: Mendel's First Law – Law of Segregation

- In Mendel's experiment (Fig. 2.2)
    - A pure-breeding tall pea plant was crossed with a pure-breeding short pea plant. This is referred to as the parent generation.
    - Seeds from the above cross were sown.
    - The seeds germinated and developed into tall offspring. This is referred to as the first filial generation (F_1 generation).
    - The F_1 plants were selfed.
    - Seeds resulting from the selfing of F_1 were sown and the offspring were examined, classified and counted. This is called the second filial generation (F_2 generation).

- Results of Mendel's experiment:
    - All the F_1 offspring were tall.
    - About 75% of the F_2 generation were tall and 25% were short. In other words, the ratio of tall to short plants was approximately 3:1.
    - About 25% of the F_2 offspring were of genotype TT, 50% were Tt and 25% were tt.

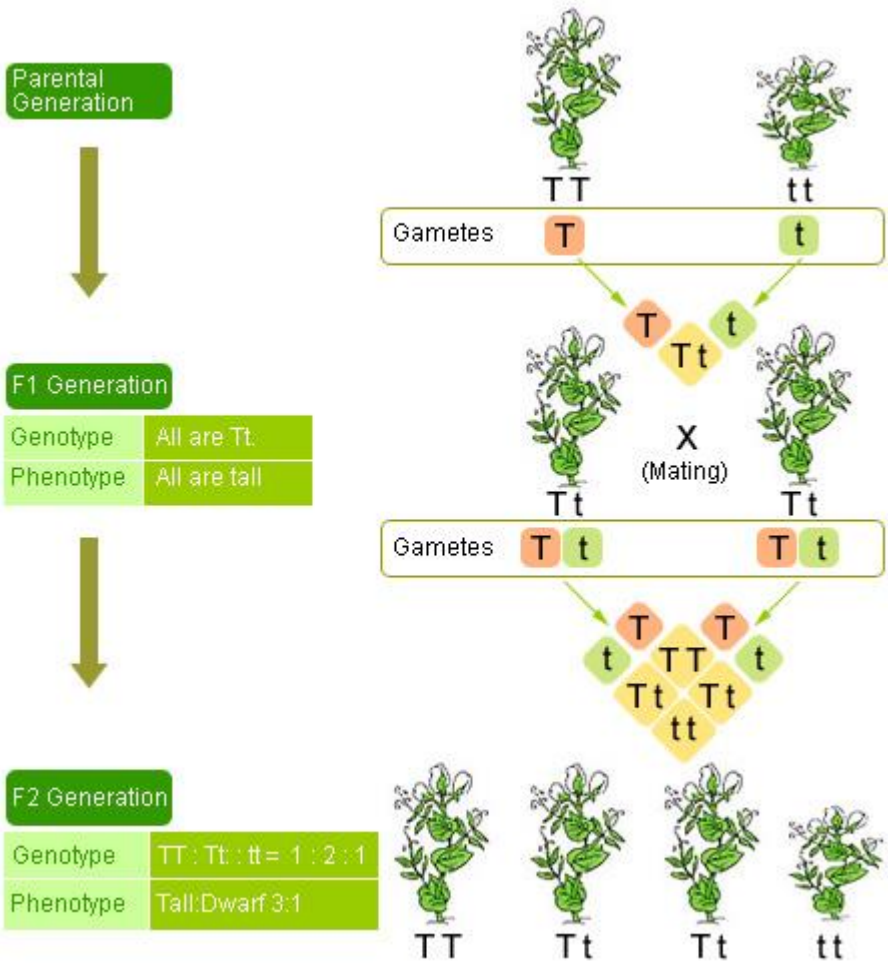
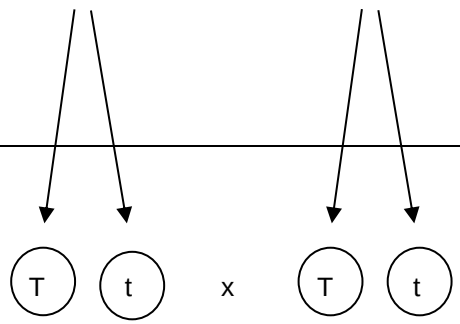


Fig. 2.2: Mendel's pea experiment

- **Example 2.1a:** Genetic diagram illustrating the Law of Segregation
  In the garden pea, *Pisum sativum*, the allele for tallness is dominant to that for shortness. A pure-breeding tall plant was crossed with a pure-breeding short plant, producing the first generation offspring. Selfing of the first generation plants produced the second generation offspring.
  Using suitable symbols, construct a genetic diagram to show the results of selfing the first generation plants. [5]

<table>
<tr><th>Genetic Statements</th><th>Working</th><th>Remarks (for your understanding)</th></tr>
<tr><td>Key</td><td>T represents the allele for tallness.
t represents the allele for shortness.
The allele for tallness is dominant to the allele for shortness</td><td>This has to be determined at the start if the symbols have not been given by the question.
The capital letter represents the dominant allele and the lower-case letter represents the recessive allele.</td></tr>
<tr><td>Parental phenotype</td><td>Pure Breeding Tall Plant x Pure Breeding Short Plant</td><td>The phenotype of the both parents is stated. There are usually two diploid parents involved / mated / crossed.</td></tr>
<tr><td>Parental genotype (2n)</td><td rowspan="2">TT x tt
T T x t t</td><td>The genotype (diploid) of both parents is stated. Here, one parent is homozygous dominant and the other is homozygous recessive.</td></tr>
<tr><td>Meiosis</td><td>Formation of gametes in each parent occurs during meiosis in their reproductive organs. The two alleles of the gene pair each separate into one gamete.</td></tr>
<tr><td>Gametes (n)</td><td></td><td>Because the parents are homozygous at this gene locus, only one type of gamete is produced by each parent with respect to the T/t locus.
The resulting gametes produced are haploid, i.e. only one allele per gene locus.
Note: Gametes must be circled in genetic diagrams.</td></tr>
<tr><td>F_1 genotype (2n) and phenotype</td><td>
<table>
<tr><td>♂ \ ♀</td><td>t</td><td>t</td></tr>
<tr><td>T</td><td>Tt
Tall</td><td>Tt
Tall</td></tr>
<tr><td>T</td><td>Tt
Tall</td><td>Tt
Tall</td></tr>
</table>
</td><td>When fertilisation occurs between the gametes of the two parents, the diploid state of the offspring is restored.

The genotype and phenotype of the offspring are stated so that they can be counted to determine the ratio.</td></tr>
<tr><td>F_1 phenotypic ratio</td><td>All tall plants</td><td>The phenotype of the offspring is then stated and given as a ratio.</td></tr>
</table>

<table>
<tr><th>Genetic Statements</th><th>Working</th><th>Remarks (for your understanding)</th></tr>
<tr><td colspan="2">Selfing of F_1 generation</td><td>Meaning both male gametes and female gametes came from the same parent. This is possible with plants.</td></tr>
<tr><td>F_1 phenotype</td><td>Tall Plant x Tall Plant</td><td></td></tr>
<tr><td>F_1 genotype (2n)</td><td rowspan="2">Tt x Tt
 
T t x T t</td><td>The genotype (diploid) of both F_1 is stated. Here, both are heterozygous.</td></tr>
<tr><td>Meiosis</td><td>Formation of gametes in each F_1 occurs during meiosis in their reproductive organs. The two alleles of the gene pair each separate into one gamete.</td></tr>
<tr><td>Gametes (n)</td><td></td><td>Significance of Mendel’s First Law of Segregation:
In each F_1, during meiosis, the homologous chromosomes carrying alleles T and t respectively segregated at anaphase I and anaphase II. The homologue carrying allele T ended up in one gamete while the homologue carrying allele t ended up in the other gamete.
This results in 50% of gametes carrying allele T and the other 50% carrying allele t.</td></tr>
<tr><td>F_2 genotype (2n) and phenotype</td><td><table><tr><td>♂ \ ♀</td><td>T</td><td>t</td></tr><tr><td>T</td><td>TT
Tall</td><td>Tt
Tall</td></tr><tr><td>t</td><td>Tt
Tall</td><td>tt
Short</td></tr></table></td><td>When fertilisation occurs between the gametes of the two F_1, the diploid state of the offspring is restored.

The genotype and phenotype of the offspring are stated so that they can be counted to determine the ratio.</td></tr>
<tr><td>F_2 phenotypic ratio</td><td>3 tall : 1 short</td><td>The resulting ratio is 3:1 as TT and Tt gives tall plants.</td></tr>
</table>

- Test cross
  - For an organism displaying a dominant phenotype, its genotype may be homozygous (e.g. TT) or heterozygous (e.g. Tt).
  - For an organism displaying a recessive phenotype, it must have a genotype which is homozygous for the recessive allele (i.e. tt)
  - It may be of interest to a breeder to know the genotype of an organism displaying a dominant phenotype and the only way the genotype can be determined is to carry out a test cross.
  - **Test cross is the crossing of an organism having an unknown genotype with a <u>homozygous recessive organism</u>** to determine the unknown genotype within one breeding generation.

- **Example 2.1b**: Test cross
  From Mendel's experiment on the height of pea plants, the genotype of tall plants could either be TT or Tt. Explain, using a genetic diagram, how the results of a test cross allowed Mendel to determine if a tall plant is homozygous (TT) or heterozygous (Tt).

  Scenario 1: If the genotype of a tall pea plant is TT…

  Gentoype TT x tt

  Gametes (T) (T) x (t) (t)

  Genotype and phenotype of offspring Tt, tall

  Phenotypic ratio All Tall

  Scenario 2: If the genotype of the tall pea plant is Tt…

  Gentoype Tt x tt

  Gametes (T) (t) x (t) (t)

  Genotype and Phenotype of offspring

♂ \ ♀	(T)	(t)
(t)	Tt Tall	tt Short
(t)	Tt Tall	tt Short

  Phenotypic ratio 1 Tall **:** 1 Short

- ***Practice Question 2.1a***
  A breeder wanted to know the genotype of a black spotted female Dalmatian. In Dalmatian dogs, the allele for black spots is dominant to the allele for brown spots. The black spotted female was crossed with a brown spotted male, and a litter of 2 black puppies was produced. The breeder concluded that the female Dalmatian was homozygous for black spots.

  Explain if the breeder's conclusion was correct.

Genetic diagram:

Key: **B** represents the allele for black spot
b represents the allele for brown spot
The allele for black spot is dominant to the allele for brown spot

Scenario 1

Parental phenotype:

Parental genotype (2n):

Meiosis:

Gametes (n):

F_1 genotype (2n):

F_1 phenotype:

F_1 phenotypic ratio:

Scenario 2

Parental phenotype

Parental genotype (2n):

Meiosis:

Gametes (n):

F_1 genotype (2n):

F_1 phenotype:

F_1 phenotypic ratio:

Conclusion

- **Practice Question 2.1b**
  A species of poppy plant may have plain petals or petals with a large black spot near the base.
  (a) If any two plants with spotted petals were crossed, the offspring always have spotted petals.
  (b) If an unspotted plant is crossed with a spotted plant, the offspring can either be all unspotted or half will be spotted and half unspotted.

  Explain this phenomenon with genetic diagrams.

For (a), spotted petals must be the recessive trait and hence plain petals the dominant trait.
For (b), the unspotted petal plant could either be homozygous to result in all offspring being unspotted *or* heterozygous to result in half of the offspring spotted or unspotted.

Genetic diagram:

R represents …….
r represents …….

Scenario 1

Scenario 2

Test your learning:

1. A plant of genotype GG was crossed with another of genotype gg. The resulting F_1 plants were self-fertilised to produce the F_2 generation.

   In the F_2, what would be the expected frequency of plants with the genotype Gg?

   A. 3/4
   B. 1/4
   C. 1/2
   D. 3/16

2. Albinism in humans is controlled by a recessive allele. How many copies of this allele will be found at one of the poles of a cell at telophase I of meiosis in an albino person?
   (Hint: It might help if you could draw the relevant events/appearance of the chromosome at the stage indicated.)

   A. 23
   B. 4
   C. 2
   D. 1

2.2 Dihybrid inheritance & Mendel's 2nd law – Law of Independent Assortment

Mendel's Second Law of Independent assortment:
http://www.sumanasinc.com/webcontent/animations/content/independentassortment.html
http://www.sumanasinc.com/webcontent/animations/content/mendelindassort.html

Learning Outcome:
c) Use genetic diagrams to solve problems in dihybrid crosses.

- Dihybrid inheritance involves the inheritance of **two characteristics** which are controlled by **alleles of two genes**, respectively.

Key Concept 2:
- The law of independent assortment or Mendel's Second Law states that the **alleles of one gene segregate independently of the alleles of another gene** during gamete formation (Fig. 2.2).

- Assortment of homologous chromosome pairs at the metaphase plate is **random**. Hence, allele *R* does not necessarily follow allele *Y* during anaphase I. Allele *R* might be separated to the same cell as allele *Y* or *y*.

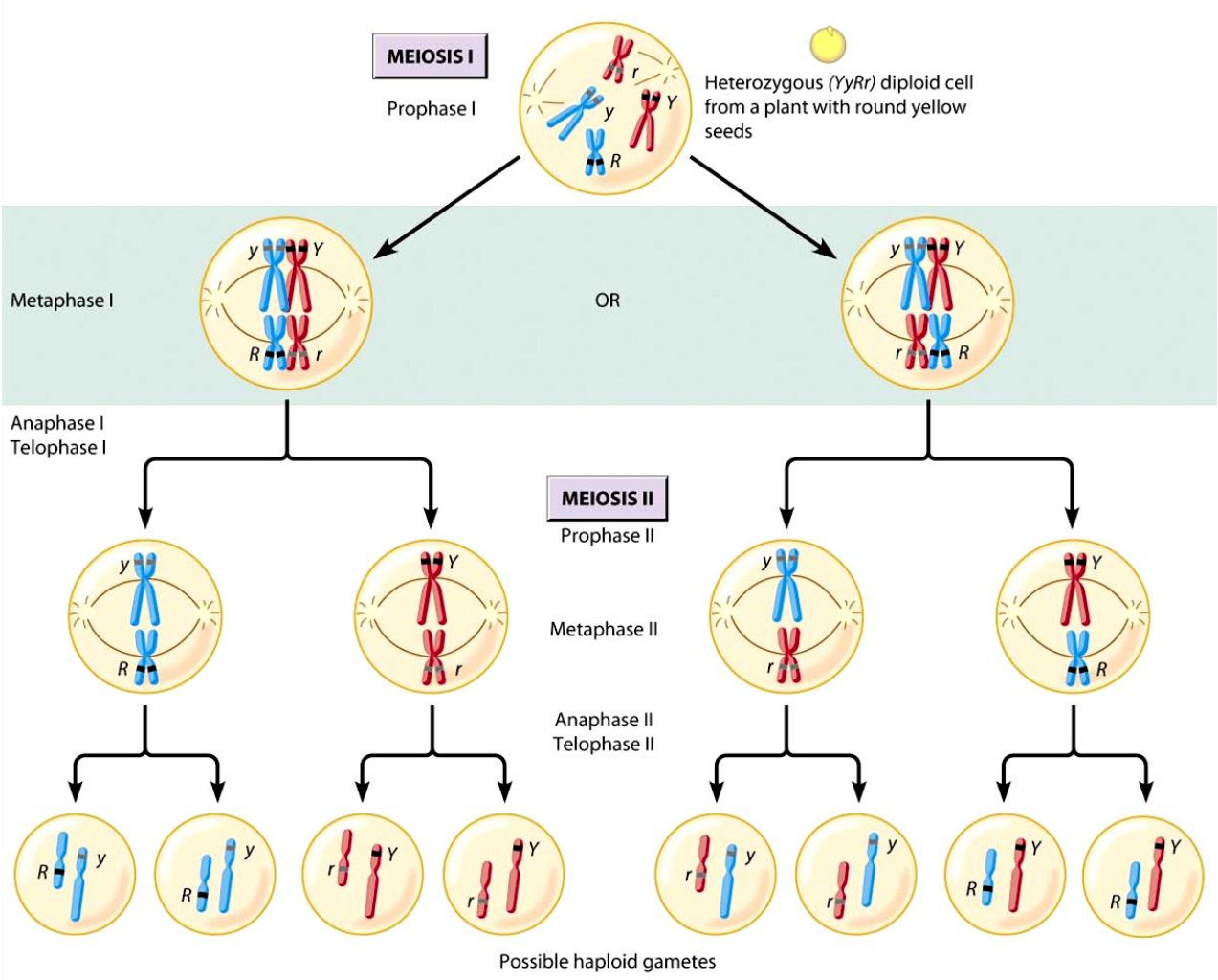
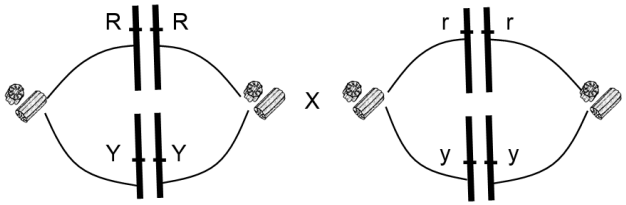


Fig. 2.3: Mendel's Second Law – Law of Independent Assortment. Figure shows movement of chromosomes during meiosis I and II and how the alleles of the two genes segregate independently in the process. The 2 genes, with their respective alleles (i.e. Y & y, R & r) are present on two different pairs of homologous chromosomes.

a) Mendel identified his second law by following **two characteristics at the same time** – seed colour (yellow or green) and seed shape (round or wrinkled). From monohybrid crosses, Mendel knew that the allele for yellow seed is dominant while the allele for green seed is recessive. Similarly, the allele for round seed is dominant to the allele for wrinkled seeds.

- **Example 2.2a:** Genetic diagram illustrating the Law of Independent Assortment
  A pure-breeding round and yellow seed plant was crossed with a pure-breeding wrinkled and green seed plant.

<table>
<tr><th>Genetic Statements</th><th>Working</th><th>Remarks (for your understanding)</th></tr>
<tr><td>Key</td><td>R represents the allele for round seed, r represents the allele for wrinkled seed.
Y represents the allele for yellow colour, y represents the allele for green colour
The allele for round seed is dominant to the allele for wrinkled seed
The allele for yellow seed is dominant to the allele for green seed</td><td>Define the key if not provided by the question.
Stating the symbols and which represent alleles are dominant or recessive.</td></tr>
<tr><td>Parental phenotype</td><td>round, yellow seed x wrinkled, green seed</td><td>As this is a dihybrid cross, two characteristics are stated.</td></tr>
<tr><td>Parental genotype (2n)</td><td>RRYY x rryy</td><td>For a dihybrid cross, two gene loci are being examined. Diploid condition (2n) means that each parent has two alleles per gene locus</td></tr>
<tr><td>Meiosis</td><td> 
</td><td>Gene locus R/r and gene locus Y/y are on two different pairs of chromosomes.

Mendel’s Law of Segregation and Independent Assortment apply during the formation of gametes. Each pair of chromosomes (hence the allele each carries) separate into different gametes.</td></tr>
<tr><td>Gametes (n)</td><td>RY RY x ry ry</td><td>Gametes formed from meiosis, but as the parental plants are homozygous at both gene loci, they produce only one type of gamete.</td></tr>
<tr><td>F_1 genotype (2n) and phenotype</td><td>
<table>
<tr><td>♀ / ♂</td><td>RY</td><td>RY</td></tr>
<tr><td>ry</td><td>RrYy
Round, yellow</td><td>RrYy
Round, yellow</td></tr>
<tr><td>ry</td><td>RrYy
Round, yellow</td><td>RrYy
Round, yellow</td></tr>
</table>
</td><td>As yellow colour in seeds is dominant over green, Rr gives yellow seeds.

As round seed shape is dominant over wrinkled seeds, Yy gives round seeds.</td></tr>
<tr><td>F_1 phenotypic ratio</td><td>All round, yellow</td><td></td></tr>
</table>

<table>
<tr><th>Genetic Statements</th><th>Working</th><th>Remarks (for your understanding)</th></tr>
<tr><td colspan="2">The F_1 generation were self-pollinated.</td><td></td></tr>
<tr><td>F_1 phenotype</td><td>round, yellow seed x round, yellow seed</td><td></td></tr>
<tr><td>F_1 genotype (2n)</td><td>RrYy x RrYy</td><td></td></tr>
<tr><td>Meiosis</td><td>Make drawing to figure out how the alleles end up in each gamete in the next step</td><td></td></tr>
<tr><td>Gametes (n)</td><td>(RY) (Ry) (rY) (ry) x (RY) (Ry) (rY) (ry)</td><td>Mendel’s Law of Segregation and Independent Assortment apply during the formation of gametes. Hence, there are four possible types of gametes</td></tr>
<tr><td>F_2 genotype (2n) and phenotype:</td><td>
<table>
<tr><th>♀ \ ♂</th><th>RY</th><th>Ry</th><th>rY</th><th>ry</th></tr>
<tr><td>RY</td><td>RRYY
Round, yellow</td><td>RRYy
Round, yellow</td><td>RrYY
Round, yellow</td><td>RrYy
Round, Yellow</td></tr>
<tr><td>Ry</td><td>RRYy
Round, yellow</td><td>RRyy
Round, green</td><td>RrYy
Round, yellow</td><td>Rryy
Round, green</td></tr>
<tr><td>rY</td><td>RrYY
Round, yellow</td><td>RrYy
Round, yellow</td><td>rrYY
wrinkled, yellow</td><td>rrYy
wrinkled, yellow</td></tr>
<tr><td>ry</td><td>RrYy
Round, yellow</td><td>Rryy
Round, green</td><td>rrYy
wrinkled, yellow</td><td>rryy
wrinkled, green</td></tr>
</table>
</td><td>A Punnett square is used to show the different combinations of alleles after <u>fertilisation</u> occurs to restore the <u>diploid</u> condition in the offspring.

There are <u>four possible phenotypes</u> after fertilisation.

However, there are a <u>large number of genotypes</u>.

Count them:
1 RRYY 1 RRyy 1 rrYY 1 rryy
2 RRYy 2 Rryy 2 rrYy
2 RrYY
4 RrYy

9 : 3 : 3 : 1

How many genotypes are there? <u>9</u></td></tr>
<tr><td>F_2 phenotypic ratio</td><td>9 round yellow : 3 round green : 3 wrinkled yellow : 1 wrinkled green</td><td></td></tr>
</table>

- Relating Example 2.2a to Mendel's First and Second Laws,

  - Each gamete carries only one allele of every pair of alleles (i.e. one allele for colour, one allele for shape).
    - The gametes of the first parent carry one R allele and one Y allele.
    - The gametes of the second parent carry one r allele and one y allele.

  - The gametes of an F_1 individual come in four possible combinations: RY, Ry, rY, ry. There is a **1 in 4 chance** of a gamete containing any of the four combinations of alleles.

  - From the Punnett square, the probability each of the F_2 phenotype is as follows:
    - round and yellow seeds = 9/16
    - round and green seeds = 3/16
    - wrinkled and yellow seeds = 3/16
    - wrinkled and green seeds = 1/16

- **Example 2.2b** – Dihybrid Test cross
  From the F_2 generation in Example 2.2a, plants with round and yellow seeds may have one of the four possible genotypes (RRYY, RRYy, RrYY, RrYy). What can be done to determine the genotype of these plants? Explain using genetic diagrams.

  Perform a test cross – by crossing the plant with unknown genotype with a homozygous recessive plant with wrinkled and green seeds.

➢ *If there are 4 phenotypes in the offspring in the ratio of 1:1:1:1, what is the genotype of the unknown?*

Phenotype: round, yellow seed x wrinkled, green seed

Genotype (2n): RrYy x rryy

Gametes (n): (RY) (Ry) (rY) (ry) x (ry) *(one combination only)*

Offspring genotype (2n) and phenotye:

♀ \ ♂	(RY)	(Ry)	(rY)	(ry)
(ry)	RrYy Round yellow	Rryy Round green	rrYy wrinkled yellow	rryy Wrinkled green

Phenotypic ratio: round yellow : round green : wrinkled yellow : wrinkled green
1 : 1 : 1 : 1

➢ *If all offspring show the dominant phenotype (round, yellow seeds), what is the genotype of the unknown?*

Results of the test cross: …….. x rryy

↓

All round yellow seeds

➢ *If the offspring is either round yellow seed or wrinkled yellow seed, what is the genotype of the unknown?*

Results of the test cross: …….. x rryy

↓

Round yellow seeds : Wrinkled yellow seeds
1 : 1

➢ *If the offspring is either round yellow seed or round green seed, what is the genotype of the unknown?*

Results of the test cross: …….. x rryy

↓

Round yellow seeds : Round green seeds
1 : 1

- **Practice Question 2.2a**
  A pea plant with axial purple flowers is test crossed with a plant that produces terminal white flowers. Given that axial flowers and purple flower are dominant traits,

  (a) State the possible genotypes of plants with axial purple flowers.

  ……..

  (b) Explain two of the four possible outcomes of the test cross between these two plants.

  Working:

  …… represents the allele for ……

  …… represents the allele for ……

  …… represents the allele for ……

  …… represents the allele for ……

  The allele for …… is dominant to the allele for ……

  The allele for …… is dominant to the allele for ……

Scenario 1

Parental phenotype

Parental genotype (2n)

Gametes (n)

Offspring genotype (2n)
And phenotypes

F_1 phenotypic ratio:

Scenario 2

Parental phenotype

Parental genotype (2n)

Gametes (n)

Offspring genotype (2n)
And phenotypes

F_1 phenotypic ratio:

2.3 Summary of Mendel's hypotheses

The six points below summarize the nature of Mendelian genetics (Fig. 2.3):

1. **Each characteristic** of an organism is **controlled by a pair of alleles**.

2. If an organism has two different alleles for a given characteristic, one may be expressed (**dominant allele**) to the total exclusion of the other (**recessive allele**).

3. During meiosis, **each pair of alleles segregates** and **each gamete receives one of each pair of alleles** [Law of Segregation].

4. During meiosis / gamete formation, **the segregation of a pair of alleles is independent of the segregation of another pair of alleles** [Law of Independent Assortment].

5. **Each allele is transmitted** from generation to generation **as a discrete unchanging unit**.

6. Each organism inherits **one allele** for **each characteristic** from **each parent**.

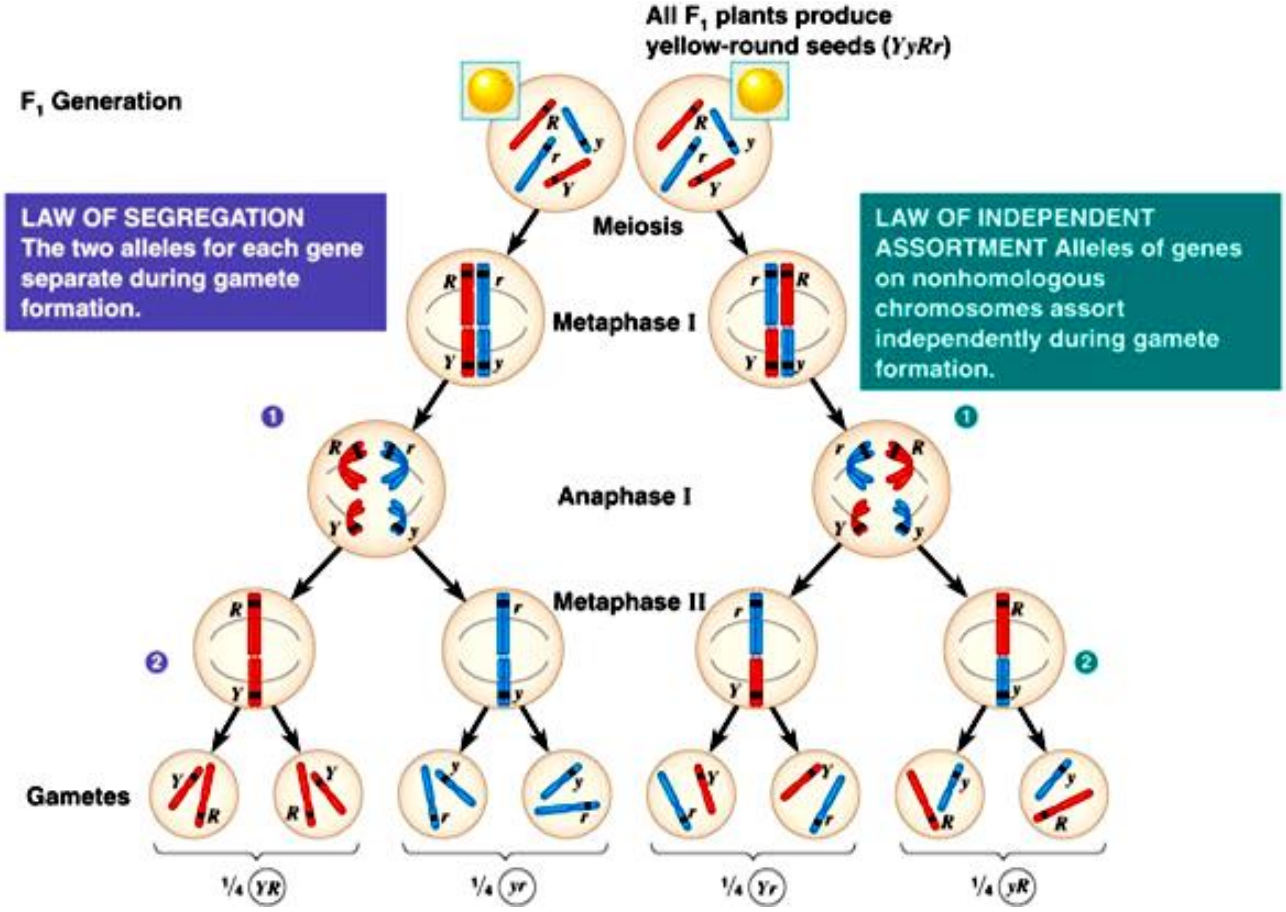


Fig. 2.4: Movement of chromosomes during meiosis I and II and how the alleles are segregated independently in the process.

NOTE: The mechanism of dihybrid inheritance only applies to characteristics controlled by genes on **different** chromosomes (i.e. unlinked genes). Genes situated on the

1. sex chromosome (i.e. sex linkage, *Section 4.3*) and
2. same autosome (i.e. autosomal linkage / linked genes, *Section 4.1*)

do not show this pattern of independent assortment.

3. Interaction between Alleles of a Gene

Learning Outcome:
c) Use genetic diagrams to solve problems in dihybrid crosses, including those involving codominance, incomplete dominance, multiple alleles.

3.1 Codominance

- In *Section 2*, the dominant allele shows complete dominance over the recessive allele. However, for some other genes, alleles may show different degrees of dominance and recessivity in relation to each other.

- Alleles of a gene may be **expressed equally in the phenotype of the heterozygote**. This condition is known as **codominance**.

- Examples include: blood type AB in humans and coat colour in cattle.

- In cases where codominance of alleles exists, the gene should be designated by an upper case letter and the alleles be indicated by appropriate superscript upper case letter.
  - I^A and I^B for the blood antigen A and blood antigen B respectively.
  - C^R and C^W for the red coat and white coat of cattle respectively.

Example 3.1
The molecular basis of the human ABO blood group is shown below:

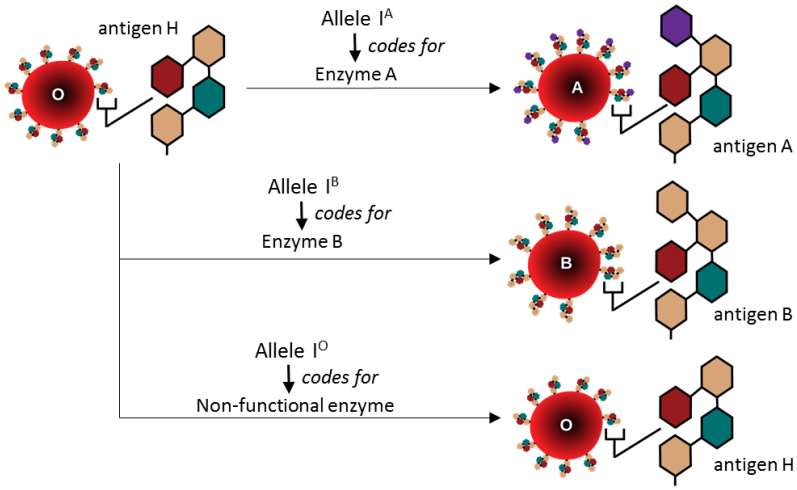


Fig. 3.1: How the ABO blood group works.

A woman with blood group A, whose father is blood group O, marries a man with blood group AB. Construct a genetic diagram to show the blood group of their children.

Genetic diagram:

Parental phenotype:	Blood group AB		X	Blood group A		
Parental genotype:	I^AI^B		X	I^AI^O		
Gametes produced:	I^A	I^B	X	I^A	I^O	
Genotype of offspring:	I^AI^A	I^AI^O		I^AI^B	I^BI^O	
Phenotype of offspring:	Blood grp A	Blood grp A		Blood grp AB	Blood grp B	
Phenotypic ratio:	2A : 1AB : 1B					

Explanation for codominance:

- The four blood groups (A, B, AB and O) is a result of different combinations of 3 alleles I^A, I^B and I^O
- I^A codes for an enzyme the converts antigen H to antigen A on red blood cells
- I^B codes for another enzyme that converts antigen H to antigen B on red blood cells
- I^O codes for a non-functional enzyme. Antigen H remains as it is (blood group O).
- The **alleles I^A and I^B** are **codominant**. A heterozygote (I^AI^B) produces both enzymes, resulting in both antigen A and B on red blood cells.
- Both alleles I^A and I^B are dominant to the I^O allele

3.2 Incomplete dominance

- Incomplete dominance describes the general situation in which the phenotype of a heterozygote is **intermediate** between the two homozygous parents.

- At the molecular level, incomplete dominance is generally caused by a **quantitative effect** of a **wild-type** (normal/non-mutated) **allele**. i.e. the amount of protein synthesized.

- Example: *Snapdragon plant* (Fig. 3.2) – Crossing a red snapdragon plant with a white one results in offspring which are pink.

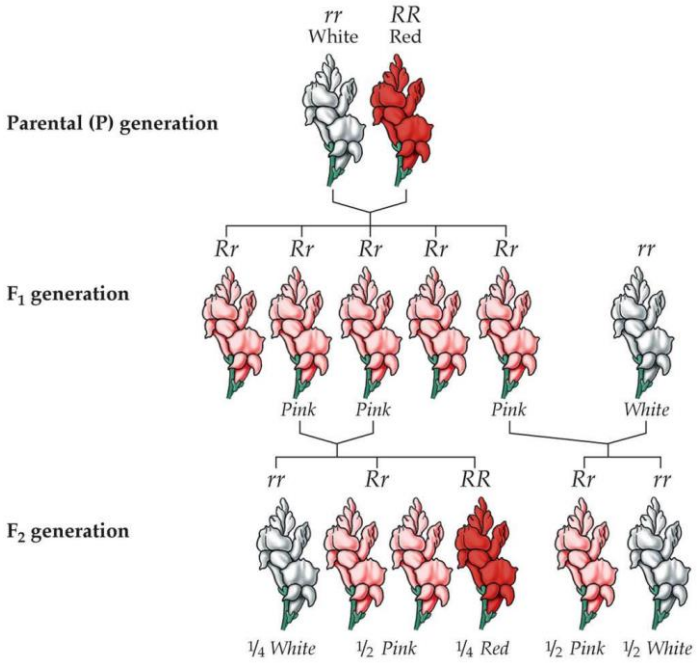


Fig. 3.2: Snapdragon plants as an example of incomplete dominance

- Biochemical basis of incomplete dominance in snapdragon plant:
  - **R** represents the allele that codes for an enzyme that synthesizes red pigment
  - **r** represents the allele that codes for a non-functional enzyme that cannot synthesize any pigment
  - **RR** genotype
    - Sufficient enzymes present → large amount of red pigments synthesized → red colour
  - **Rr** genotype
    - Insufficient enzymes present → small amount of red pigments synthesized → pink colour
  - **rr** genotype
    - No enzymes → No pigments synthesized. Hence, white colour.

3.3 Multiple alleles

- Multiple alleles is a phenomenon where **a gene controlling a single characteristic** has **three or more alleles** in a given population.

- In a **diploid** individual, a **maximum of two of these alleles can be present**.

- Examples of multiple alleles:

1) ABO blood group in humans (Fig. 3.1 and Fig. 3.3)

- The four blood groups (A, B, AB and O) is a result of different combinations of 3 alleles I^A, I^B and I^O
- Since only two of the three alleles may be present in an individual at any one time, an individual may possess any of the following six genotypes:

Genotype	Phenotype	Glycoprotein on surface of red blood cells
I^AI^A	Blood type A	Antigen A present
I^AI^O		
I^BI^B	Blood type B	Antigen B present
I^BI^O		
I^AI^B	Blood type AB	Both antigens A and B present
I^OI^O	Blood type O	Neither antigen present

Mother's Blood Type	Father's Blood Type: A	B	AB	O	Child's Blood type Must Be
A	A or O	A, B, AB, or O	A, B, or AB	A or O	
B	A, B, AB or O	B or O	A, B, or AB	B or O	
AB	A, B, or AB	A, B, or AB	A, B, or AB	A or B	
O	A or O	B or O	A or B	O	

Mother's Blood Type	Child's Blood Type: A	B	AB	O	Father's Blood Type Must Be
A	A, B, AB or O	B or AB	B or AB	A, B, or O	
B	A or AB	A, B, AB or O	A or AB	A, B, or O	
AB	A, B, AB or O	A, B, AB or O	A, B, or AB		
O	A or AB	B or AB		A, B, or O	

Fig. 3.3: The relationship between parents' and child's blood groups

2) Fur colour in rabbits (Fig. 3.4)

- There are 4 alleles governing fur colour in rabbits
- Agouti allele (C) **>** Chinchilla allele (c^{ch}) **>** Himalayan allele (c^h) **>** Albino allele (c)

CC, Cc^{ch}, Cc^h, Cc	$c^{ch}c^{ch}$	$c^{ch}c^h$, $c^{ch}c$	c^hc^h, c^hc	cc
Dark gray	Chinchilla	Light gray	Himalayan	Albino

Fig. 3.4: Different combinations of alleles give rise to different phenotypes

- **Example 3.2** – ABO blood group
  Using a genetic diagram, explain why a child whose parents are both blood group O must have blood group O.

  Genetic diagram:

  Key: I^A represents the allele for production of type A antigen
  I^B represents the allele for production of type B antigen
  I^O represents the allele that produces neither antigen
  I^A and I^B are codominant; I^A and I^B are dominant to the I^O

Parental phenotype:	Blood group O	X	Blood group O
Parental genotype:	I^OI^O	X	I^OI^O
Gametes produced:	I^O	X	I^O
Genotype of offspring:		I^OI^O	
Phenotype of offspring:		All blood group O	

- **Practice Question 3.1** – ABO blood group
  What would be the blood group of the children when two individuals, one of whom is blood group A marry another with blood group O?

  Genetic diagram:

  Possibility 1: The parent with blood group A has the genotype I^AI^A

  Possibility 2: The parent with blood group A has the genotype I^AI^O

- **NOTE:** The genotypes of the children **depend on the genotype of the blood group A parent.**
  - If the blood group A parent is **homozygous (**……..**)**, the children can only have the **genotype** …….. **and be blood group** ……...
  - If the blood group A parent is **heterozygous (**……..**)**, each child has a …….. **% chance of being blood group** …….. **or** ……...

4. Linkage

Learning Outcome:
c) Use genetic diagrams to solve problems in dihybrid crosses, including those involving sex linkages, autosomal linkage.
d) Explain the meaning of the terms linkage and crossing-over and explain the effect of linkage and crossing over on the phenotypic ratios from dihybrid crosses.

4.1 Autosomal linkage

- Mendelian genetics deal with inheritance of genes situated on **different** chromosomes. However, it does not explain inheritance of genes situated on the same chromosome.

Key concept 3:
- Genes situated on the **same chromosome** are said to be **linked**. All genes on a single chromosome form a linkage group and usually pass into the same gamete and are inherited together. As a result of this, **genes belonging to the same linkage group usually do not show independent assortment**.

- ***Example 4.1 – Morgan's experiment*** shows how linkage between genes (i.e. genes on the same chromosome) affects the inheritance of the two different characteristics:

Unlinked genes vs linked genes:
http://bcs.whfreeman.com/thelifewire/content/chp10/1002002.html

  - Morgan studied two characteristics of the fruitfly (*Drosophila melanogaster*), body colour and wing length. The normal flies have the dominant alleles for grey body and normal wings. The mutant flies have the recessive alleles for black body and vestigial wings.

  - When true breeding flies having grey body (b^+) and normal wings (vg^+) were mated with flies having black body (b) and vestigial wings (vg), all F_1 offspring had grey body and normal wings.

  - The female F_1 flies were then mated with a **homozygous recessive** male (a test cross).

  - If the genes for body colour and wing length were <u>located on different chromosomes</u> and <u>assorted independently</u> (i.e. unlinked), explain the expected result of the test cross using a genetic diagram.

***Genetic diagram (test cross)*:**

Parental Phenotype: grey body, normal wing x black body, vestigial wing

Parental Genotype (2n): b^+ b vg^+ vg x b b vg vg

Gametes (n): (b^+ vg^+) (b^+ vg) (b vg^+) (b vg) x (b vg)

Genotype (2n) And phenotype Of offspring:

♀ \ ♂	(b^+ vg^+)	(b^+ vg)	(b vg^+)	(b vg)
(b vg)	b^+ b vg^+ vg Grey body, normal wings	b^+ b vg vg Grey body, Vestigial wings	b b vg^+ vg Black body, normal wings	b b vg vg Black body, vestigial wings

Phenotypic ratio:

Grey body, normal wings	:	Grey body, vestigial wings	:	Black body, normal wings	:	Black body vestigial wings
1	:	1	:	1	:	1

- The actual result from Morgan's experiment, however, differed from the expected Mendelian ratio (Fig. 4.1).
- There were **disproportionately large numbers of offspring with parental phenotypes** – grey body/normal wings and black body/vestigial wings.
- Offspring with **non-parental** (also known as **recombinant**) **phenotypes**, grey body/vestigial wings and black body/ normal wings were **present in small numbers**.

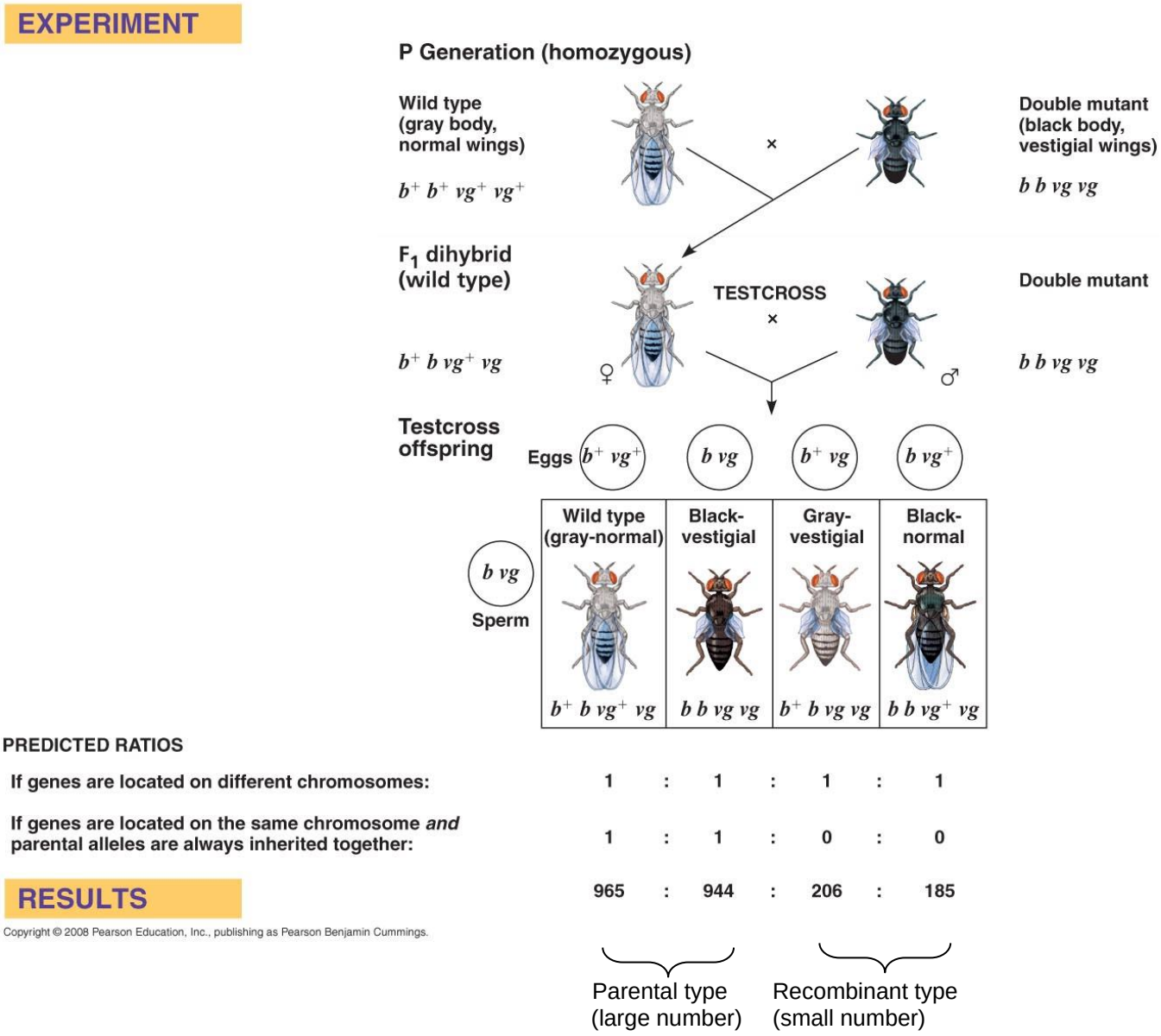


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Fig. 4.1: Results of Morgan's experiment – expected VS observed ratios

- Morgan's explanation:
  - The genes for these 2 characteristics are on the **same chromosome** (i.e. they are **linked**).
  - They are therefore usually **inherited together**.
  - The appearance of the **non-parental (recombinant) phenotypes is due to crossing over during prophase I of meiosis**.
  - There will be **no fixed ratio** for offspring of different phenotypes.

4.1.1 Crossing over

- In 1909, Belgian cytologist Janssens observed the formation of **chiasmata** during prophase I in meiosis. **Chiasma** (plural, chiasmata) is an X-shaped, microscopically visible region formed due to crossing over between chromatids of homologous chromosomes. (Fig. 4.2).

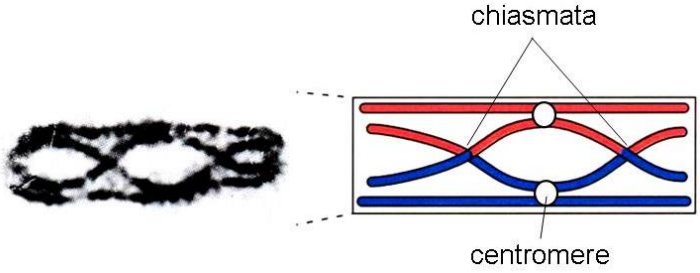


Fig. 4.2: An electron micrograph and its corresponding cartoon depiction of a pair of homologous chromosomes undergoing crossing over during prophase I of meiosis

Meiosis with crossing-over:
http://highered.mcgraw-hill.com/sites/dl/free/0072835125/126997/animation5.html

- All genes on **the same chromosome form a linkage group** and are usually **passed into the same gamete. These genes inherited together**. As a result of this, **genes on the same chromosome usually do not show independent assortment**.

- **Crossing over** is the exchange of corresponding alleles between non-sister chromatids of two homologous chromosomes during prophase I of meiosis (Fig. 4.3).

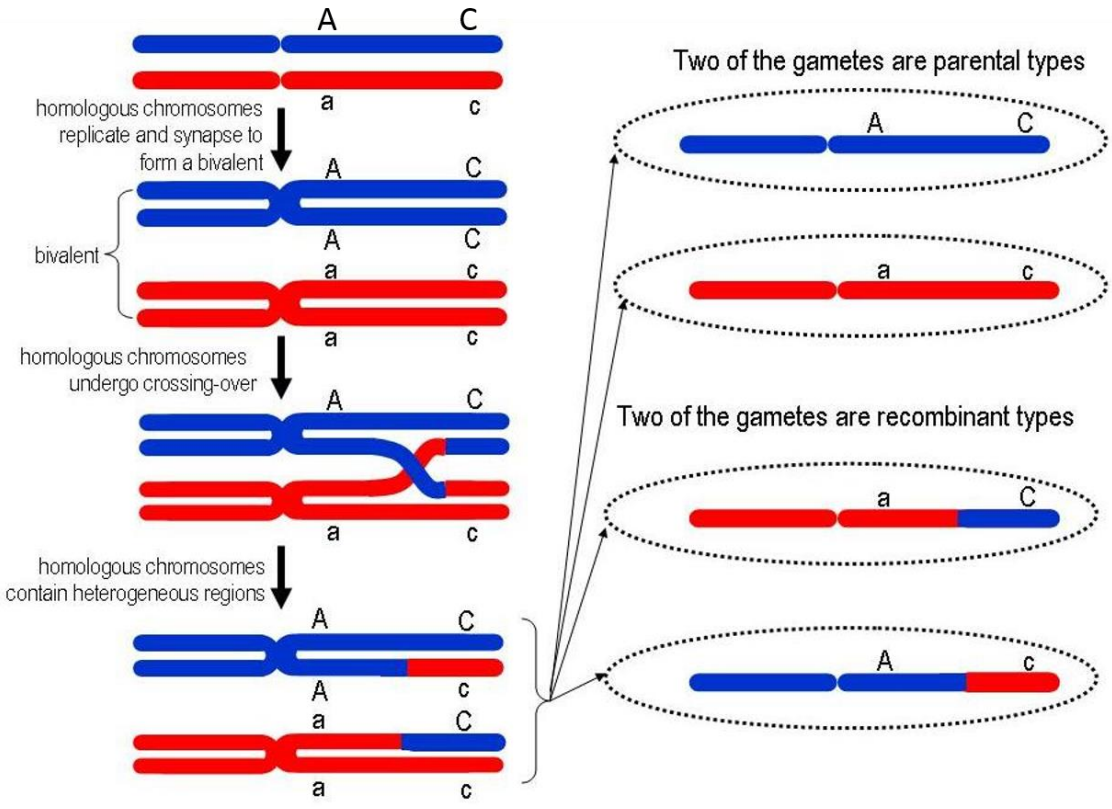


Fig. 4.3: Crossing over results in genetic recombination (genetically non-identical gametes)

- Crossing over results in **genetic recombination**. The gamete that contains the recombinant chromatid is known as **recombinant gamete**. The offspring that exhibits new combinations of characteristics that are different from their parents are known as **recombinant**.

- This sequence of events accounts for the occurrence of recombinant phenotypes in Morgan's test cross.

Key concept 4:

- If the two genes are **tightly linked** (i.e. very close together on the same chromosome), they would be **inherited as one unit**. There would not be recombinants as **crossing over is very unlikely to occur** between the two loci.

Key concept 5:

- The **further apart the linked genes** are on the chromosomes, the **greater the possibility of crossing over** occurring between them. Therefore, the **greater the cross over frequency** (in percentage):

- Based on Morgan's experiment (Fig. 4.1), recombination frequency is calculated by:

$$\frac{\text{No. of individuals showing recombination}}{\text{Total no. of offspring}} \times 100\% = \frac{(206 + 185)}{(965+944) + (206+185)} \times 100\% = \mathbf{17\%}$$

Test Yourself

In a particular species of plants, 'round seeds' and 'hairy leaves' are genes which are **tightly linked** (i.e. adjacent to each other). Pure bred, round-seeded, hairy leaves plants are crossed with pure bred, flat-seeded, hairless plants to produce only round-seeded, hairy plants in the F_1 generation. These F_1 plants were then test-crossed.

Which phenotypic ratio would be expected from the test cross?

	Round seed Hairy	Round seed hairless	Flat seed hairy	Flat seed hairless
A	1	1	1	1
B	9	3	3	1
C	1	0	0	1
D	3	0	0	1

Explanation

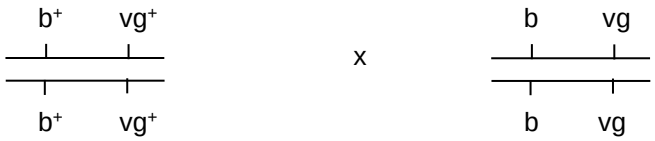
4.1.2 Genetic diagrams involving linked genes

- Linked genes are usually represented by placing them on corresponding positions of two horizontal lines.
  - Symbols on one side of the line represent alleles of the 2 gene loci on one chromosome.
  - Symbols on the other line represent alleles of the same gene loci on the other homologous chromosome.

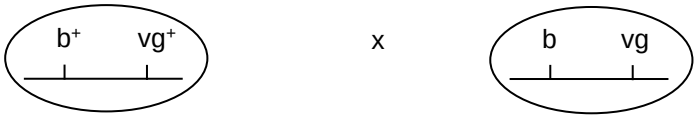
- ***Example 4.1***– Genetic diagram illustrating Morgan's experiment on how linkage between genes affects the inheritance of two different characteristics

Parental phenotype: grey body, normal wing x black body, vestigial wing

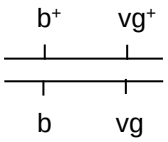
Parental genotype (2n):



Gametes produced (n):



F_1 genotype (2n):

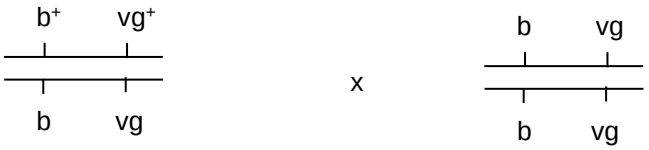


F_1 phenotype: All grey body, normal wing

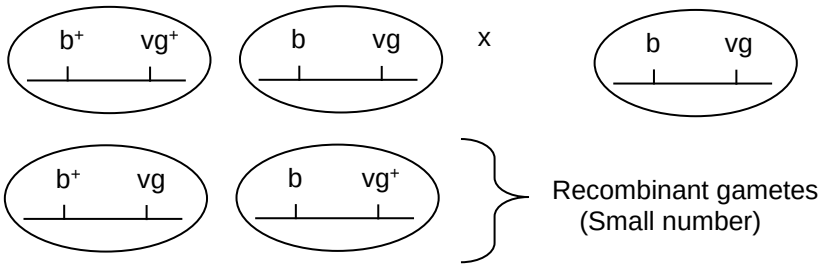
Test Cross

Phenotype of testcross parents: grey body, normal wing x black body, vestigial wing

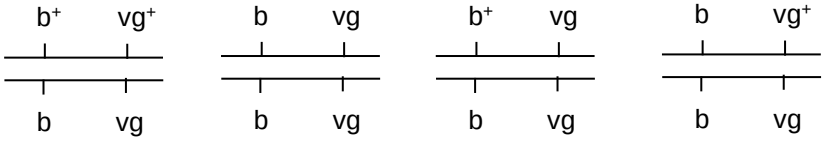
Genotype of testcross parents:



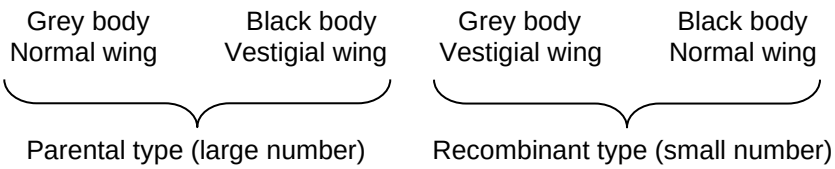
Gametes produced (n):



Genotype of testcross offspring:



Phenotype of testcross offspring:



4.2 Sex determination in humans and other organisms

- Microscopic examinations of the chromosome structure of a range of mammals revealed that males and females showed certain chromosomal differences. Homologous chromosomes are found in all cells except for one pair of chromosomes which always shows differences between the sexes. These are known as the **sex chromosomes** (heterosomes).

- The sex chromosomes (named **X** and **Y**) are involved in sex determination. All other chromosomes are known as **autosomal chromosomes** or **autosomes**.

- In humans, for example, the first 22 pairs of chromosomes are autosomes. In human females, the 23rd pair is a pair of sex chromosomes which are homologous. In human males, however, the sex chromosomes are not homologous (Fig. 1.1 & Fig. 4.4).

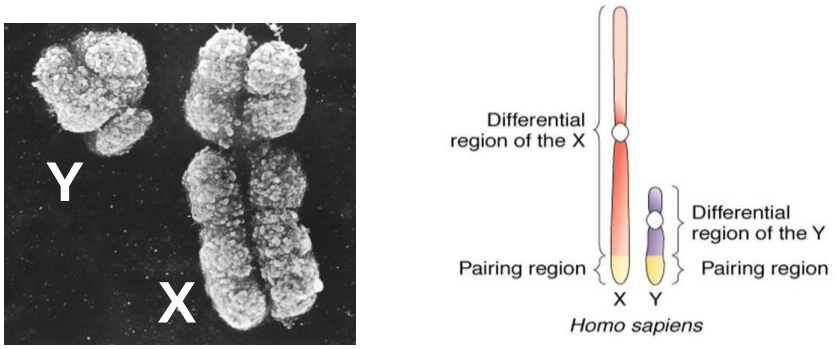


Fig. 4.4: An electron micrograph of XY chromosomes (left) and a diagram (right) depicting the small region of homology between X and Y chromosomes which allows them to behave like a pair of homologous chromosomes and pair up during meiosis.

- In the production of gametes, the sex chromosomes segregate in typical Mendelian fashion (Fig. 4.5).

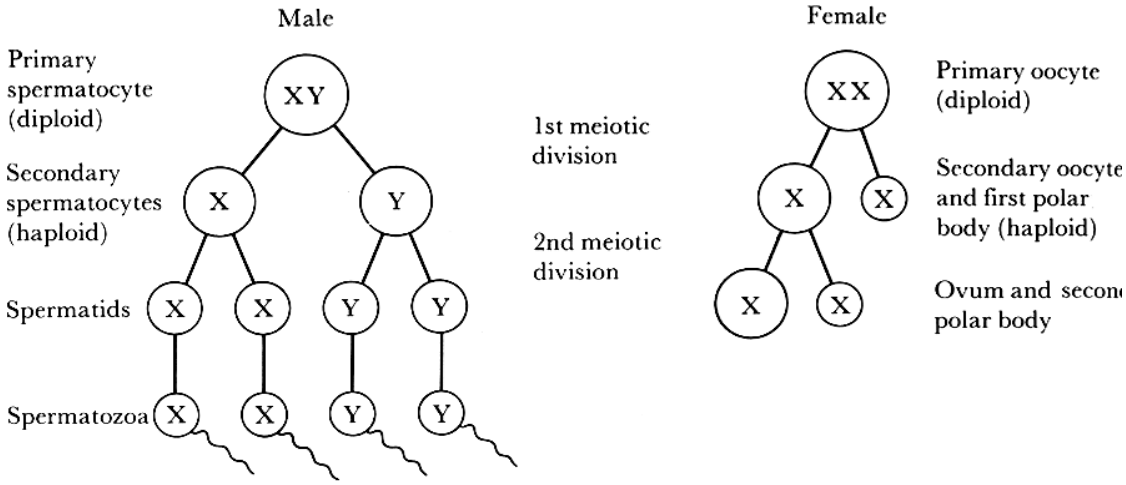


Fig. 4.5: Segregation of sex chromosomes during human gametogenesis

- In the female:
  - There are **two X chromosomes** (genotype XX).
  - During gamete formation, the **female only produces one type of gamete** (with respect to the sex chromosomes) – all the egg cells contain an X chromosome.
  - In humans, the female is the **homogametic sex**.

- In the male:
  - There is **one X chromosome and one Y chromosome**. (Genotype XY).
  - During gamete formation, the **male produces two types of gametes** (with respect to the sex chromosomes) - 50% of the sperms carry the X chromosome and the other 50% carry the Y chromosome.
  - In humans, the male is the **heterogametic sex**.

- Besides the mammalian XY system, three other chromosomal systems for determining sex are shown in Fig. 4.6.

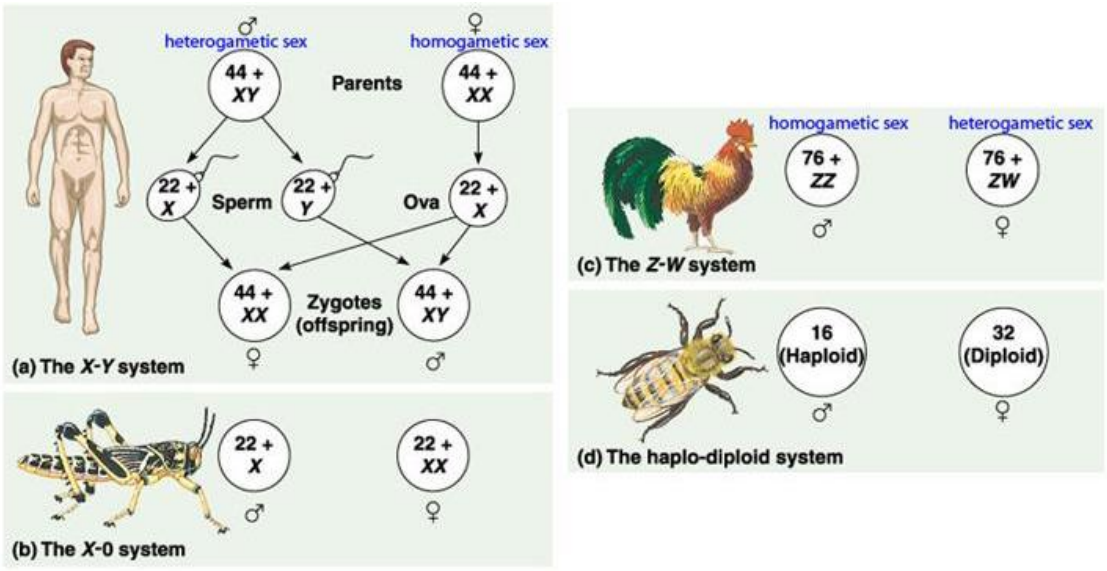


Fig. 4.6: ***(a) The XY system.*** In mammals, the sex of an offspring depends on whether the sperm cell contains an X chromosome or a Y. ***(b) The X-0 system*****.** In grasshoppers, cockroaches and some other insects, there is only one type of sex chromosome, the X. Females are XX. Males have only one sex chromosome (X0). ***(c) The ZW system*****.** In birds, some fishes and some insects, the sex chromosomes are designated Z and W. Females are ZZ and males are ZW. ***(d) The haplo-diploid system*****.** There are no sex chromosomes in most species of bees and ants. Females developed from fertilized eggs and are thus diploid. Males develop from unfertilized eggs and are haploid. Males have no father.

4.3 Sex linkage

- Genes carried on the sex chromosomes are said to be **sex-linked**.

- The Y chromosome is smaller than the X chromosome, and carries very few genes compared to the X chromosome, which carries over 1,000 genes. There is a portion of the X chromosome with no homologous region on the Y chromosome.

- Characteristics that are determined by genes carried on the non-homologous region of the X chromosome will appear in males even if they are recessive (Fig. 4.7). Thus, males have a higher tendency to inherit sex-linked diseases as they only have one X chromosome, whereas females have two X chromosomes.

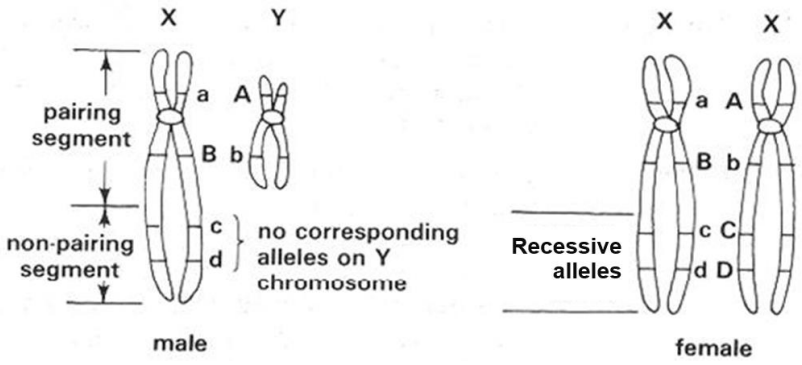


Fig. 4.7: The non-homologous region between X and Y chromosome and the homologous region between two X chromosomes

- Examples of sex-linked conditions:

Organism	Condition
Human	• Red-green colour blindness • Haemophilia • Premature balding
Fruit fly	• Eye colour (red/white)
Cat	• Coat colour (black/ginger/tortoiseshell)

- Representing sex-linked characteristics in a genetic diagram:
  - Capital letters **X** and **Y** represent the sex chromosomes.
  - Superscript capital letter represents a dominant allele carried on the X chromosome (e.g. $\mathbf{X^A}$).
  - Superscript small letter represents a recessive allele carried on the X chromosome (e.g. $\mathbf{X^a}$).

- In all sex-linked traits, **females** who are **heterozygous** are described as **carriers** of the trait. They are **phenotypically normal** but half of their gametes carry the recessive allele.

- The possible genotypes and phenotypes for sex-linked traits:

Genotype		Phenotype
$X^A X^A$	Homozygous Dominant female	Normal
$X^A X^a$	Heterozygous female	Normal (carrier)*
$X^a X^a$	Homozygous Recessive female	Affected*
$X^A Y$	Hemizygous Dominant male	Normal
$X^a Y$	Hemizygous Recessive male	Affected*

**Assumption – the disease-causing allele is recessive*

4.3.1 Haemophilia

- Patients with haemophilia are unable to produce one of the many blood clotting factors [Factor 8 or anti-haemophiliac globulin (AHG)]. Factor 8 increases the rate of blood clotting, and in the absence of Factor 8, blood cannot clot. This will lead to slow but persistent bleeding.

- One remedy is to extract Factor 8 from the blood of a donor and transfuse into the haemophiliacs. This will allow them to live a relative normal life. The trait is rare but the frequency of occurrence can be increased when there's prevalent inbreeding (e.g. European royal families).

- ***Example 4.2*** – A cross between a normal female carrier and a normal male:

Key: X^H represents X chromosome with normal dominant allele
X^h represents X chromosome with recessive allele for haemophilia
Y represents Y chromosome

Parental phenotype:	Normal Female Carrier	x	Normal Male	
Parental genotype (2n):	X^HX^h	x	X^HY	
Gamete (n):	X^H X^h	x	X^H	Y
Offspring genotype (2n):	X^HX^H	X^HY	X^H X^h	X^hY
Offspring phenotype:	Normal Female	Normal Male	Normal Female (Carrier)	Haemophiliac Male

Offspring phenotypic ratio: 2 normal females **:** 1 normal male **:** 1 haemophilic male

- ***Practice Question 4.1***
A normal female carrier for haemophilia marries a haemophiliac male. Explain using a genetic diagram, the phenotypic ratio for their offspring. State the probability
(a) that the first child is a male who is haemophiliac.
(b) that the second child is haemophiliac.

Probability that the first child is a male who is haemophiliac = ……

Probability that the second child is haemophiliac = ……

4.3.2 Red-green colour blindness

- Red-green colour blindness is the inability to distinguish between red and green. The pattern of inheritance of red-green colour blindness is similar to that of haemophilia.

- ***Practice Question 4.2***
  A woman whose father is colour-blind marries a colour-blind man. Their first child is a daughter.
  a) What is the probability that their daughter is colour-blind?
  b) What is the probability that their second child is also a daughter who is colour-blind?

  Key: X^B represents .....

  X^b represents .....

  Y represents .....

  Probability that their daughter is colour-blind = ……..

  Probability that their second child is also a daughter who is colour-blind = ……..

- Observations from the Inheritance of X-linked traits
  - X-linked recessive traits are more common in men than women. Why?
  - Sons inherit X-linked trait from the mother but not the father. Why?

4.3.3 Eye colour of *Drosophila* and reciprocal cross

- A cross where the same **genetic features are used but the sexes are reversed**.
- A reciprocal cross is sometimes carried out **to determine whether the trait is sex-linked**. For sex-linked genes, reciprocal crosses give **different** F_1 results whereas for autosomal genes, the same F_1 results are expected.
- ***Example 4.3*** – Reciprocal crosses of white- and red-eyed *Drosophilia* (Fig. 4.8)

  Key: X^W represents X chromosome with dominant allele for red eye
  X^w represents X chromosome with recessive allele for white eye
  Y represents Y chromosome

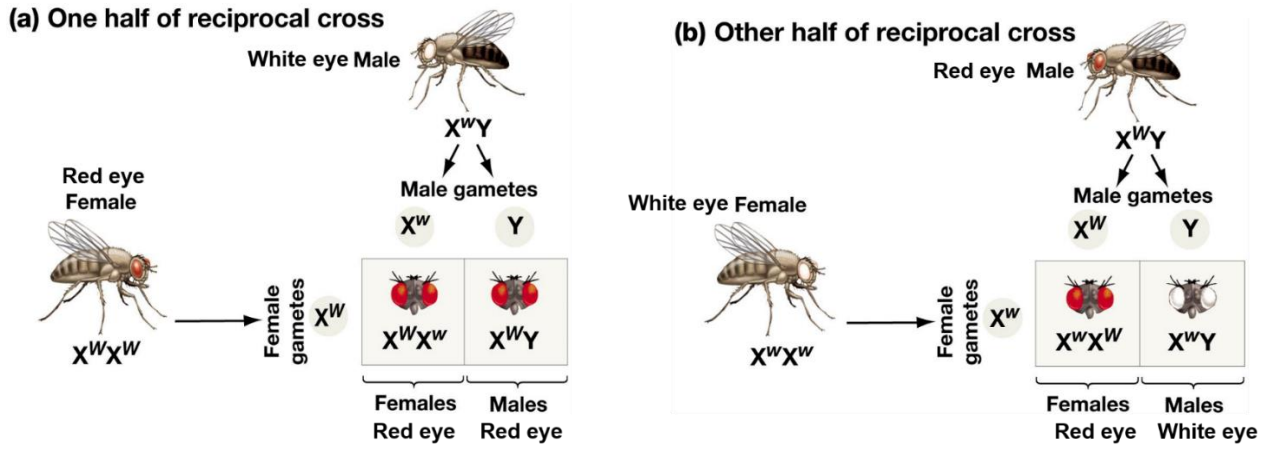
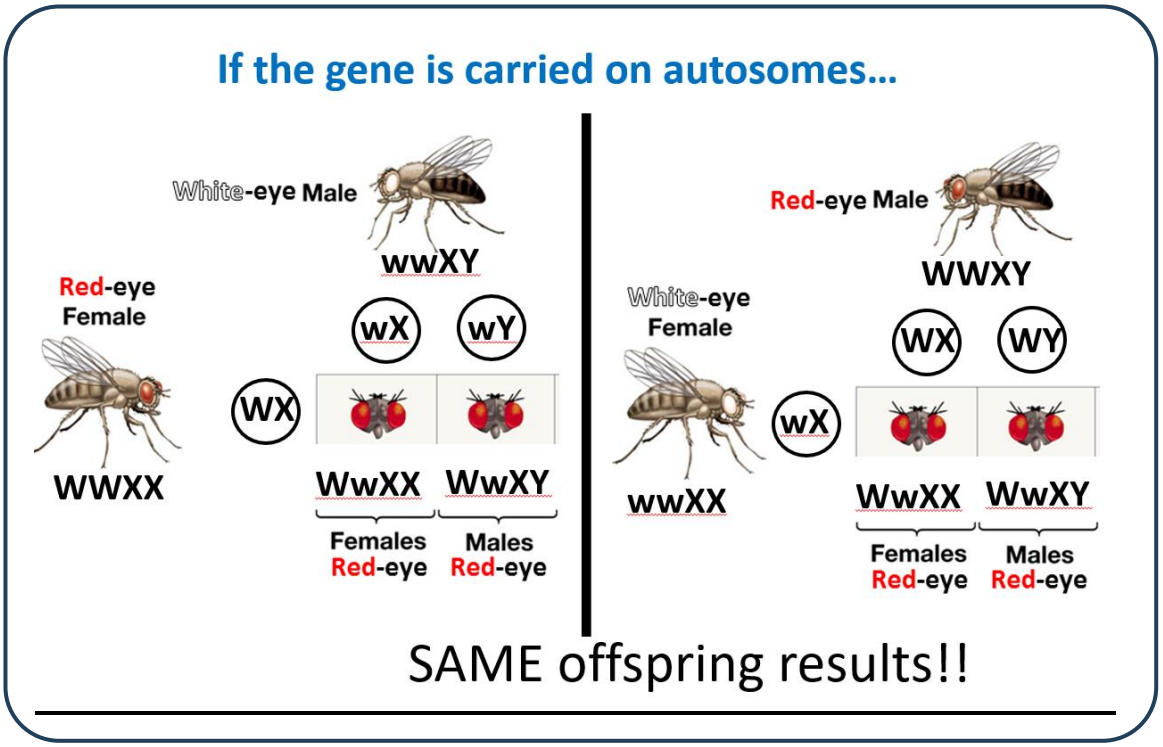


Fig. 4.8: Sex linkage results in different phenotypic ratios in the offspring when reciprocal cross is performed



5. Pedigree Chart

5.1 Background and symbols used

- It is not possible to perform test cross and reciprocal cross on humans. Moreover, F_1 and F_2 generations are too small for statistical analysis and generation time is too long. Instead human genetics are based on study of pedigrees, which show line of descent.

- In pedigree diagrams (Fig. 5.1), males are represented by squares and females by circles. Trait under investigation is shaded if expressed.

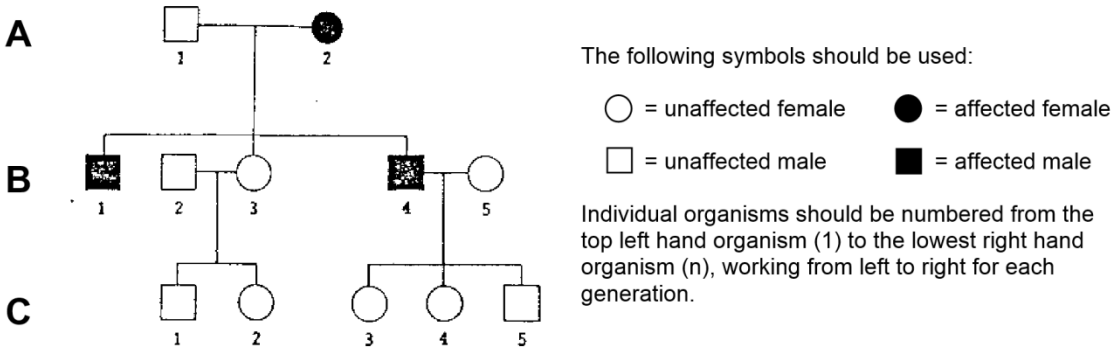


Fig. 5.1: A simple pedigree diagram

- Using pedigree diagrams, it is possible to deduce how a particular gene is inherited. A classic example of the inheritance of haemophilia is illustrated in Fig. 5.2.

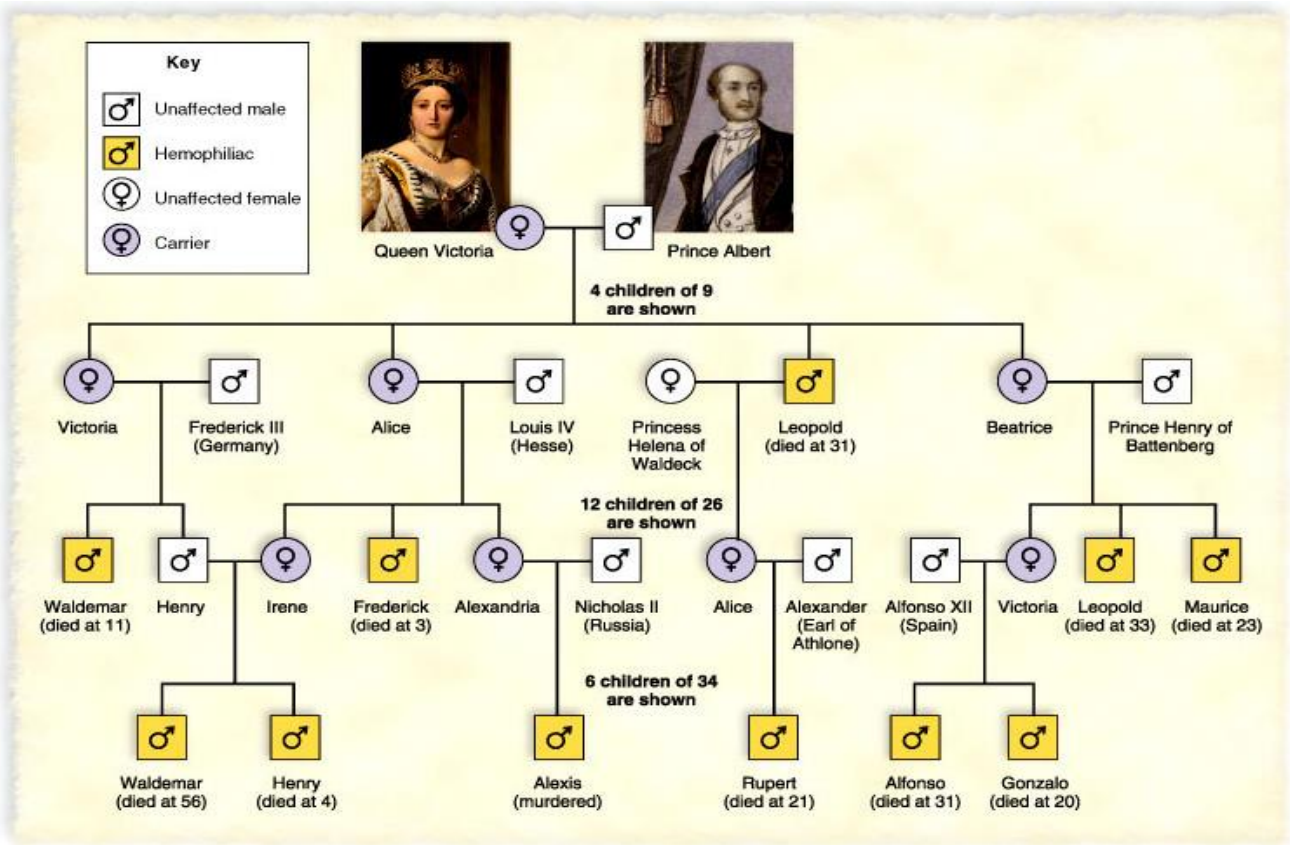


Fig. 5.2: The inheritance of haemophilia in the descendants of Queen Victoria. The ancestry of the British Royal Family is one of the best-documented examples for the study of human pedigree

5.2 Identifying inheritance pattern

a) Autosomal dominant (Fig. 5.3)

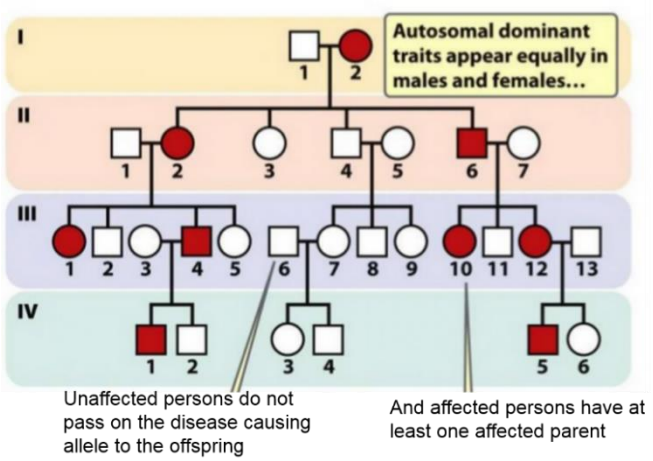


Fig. 5.3: A pedigree showing a pattern of inheritance for an autosomal dominant trait

- This trait is determined by a dominant allele because
  - every affected individual has at least an affected parent
  - it appears in every generation

- This trait is autosomal (i.e. not sex-linked) because
  - equal numbers of males and females are affected
  - male (III-4) passes the trait to his son (IV-1). In sex-linked, father contributes the Y-chromosome to his son hence does not pass on the X-linked disease to his son.

b) Autosomal recessive (Fig. 5.4)

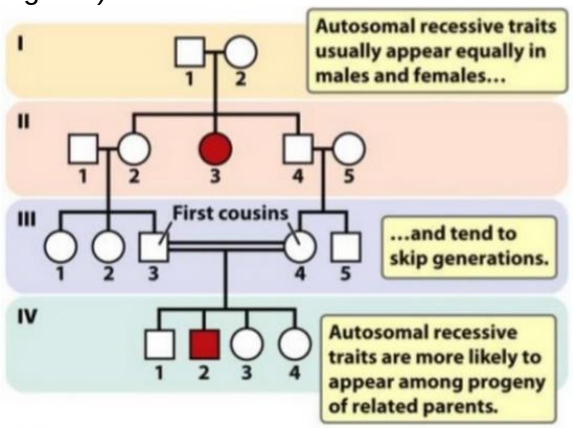


Fig. 5.4: A pedigree showing a pattern of inheritance for an autosomal recessive trait

- This trait is determined by a recessive allele because
  - an affected individual (II-3) may have unaffected parents (I-1 and I-2)
  - the recessive trait skipped a generation

- This trait is autosomal (i.e. not sex-linked) because
  - Unaffected heterozygote parents (I1 and I2) each passed a copy of the recessive allele to the affected daughter (II3). If the recessive allele is sex-linked, the daughter (II3) would **not** be affected as she would inherit the dominant allele on the X chromosome (normal) from the unaffected father (I1).

c) Sex-linked recessive (Fig. 5.5)

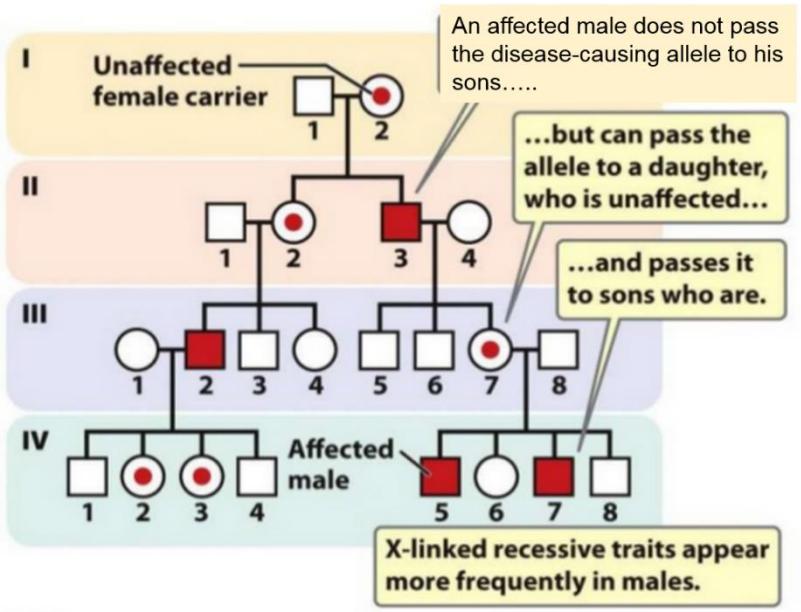


Fig. 5.5: A pedigree showing a pattern of inheritance for a sex-linked recessive trait

- This trait is determined by a sex-linked recessive allele because
  - none of the sons of an affected male (and an unaffected female) is affected
  - sons of an affected female are affected (not shown in Fig. 5.5)
  - more males than females are affected

d) Sex-linked dominant (Fig. 5.6)

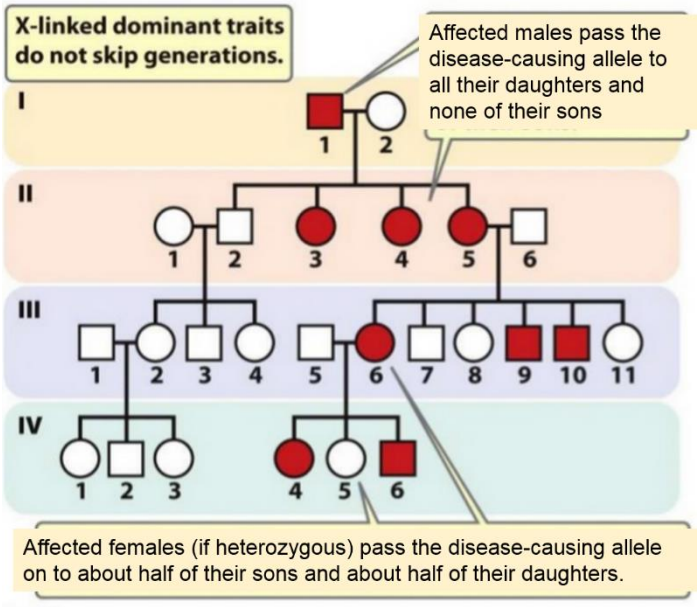
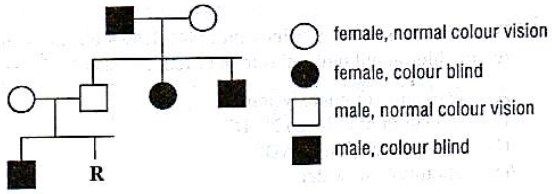


Fig. 5.5: A pedigree showing a pattern of inheritance for a sex-linked dominant trait

- This trait is determined by a sex-linked dominant allele because
  - All daughters of an affected male individual are affected.
  - An affected male does not pass the disease to his sons, since sons receive Y chromosome from their father.

Test your learning:

The diagram shows the inheritance of red-green colour blindness in a family. This condition is caused by a sex linked recessive allele.



What is the probability that individual R will be a colourblind boy?

A. 0
B. 0.125
C. 0.25
D. 0.5

6. Gene Interactions

Learning Outcome:
c) Use genetic diagrams to solve problems in dihybrid crosses, including those involving epistasis.
f) Describe the interaction between loci (epistasis) and predict phenotypic ratios in problems involving epistasis. (Knowledge of the expected ratio for various types of epistasis is not required; focus of this section is on problem solving).

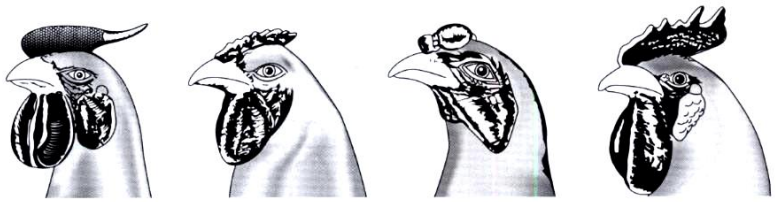
- In the patterns of monohybrid and dihybrid inheritance covered thus far, the focus was on the development of a **single characteristic** governed by **one gene locus** (*monohybrid inheritance*) or **two characteristics** governed by **two gene loci** (*dihybrid inheritance*).

Key concept 6:
- The development of a **single characteristic** may also be due to the interaction between **two or more genes**, rather than just a single gene. This phenomenon is known as **gene interaction**.

6.1 Two-Gene interaction can produce a 9:3:3:1 ratio

- A cross involving a **two-gene interaction** (interaction of their products) can produce a **9:3:3:1** ratio in offspring when **four distinctive phenotypes** of a characteristic/trait are produced.

- ***Example 6.1*** – Inheritance of shape of comb in domestic fowl (*N07/P2/Q5*)



The genotype R–pp gives a rose comb, rrP– gives a pea comb, R–P– gives a walnut comb and rrpp gives a single comb. The dash (–) indicates the presence of either the dominant or recessive allele. List all the genotypes which will produce a walnut phenotype.

.....

Bateson and Punnett demonstrated gene interactions by crossing chickens with rose combs (pure line) with chickens with pea combs (pure line). All the resulting F_1 offspring differed from both the parents and has walnut combs. When pairs of these F_1 offspring were allowed to interbreed, they produced the resulting F_2 ratio:

9 walnut comb **:** 3 pea comb **:** 3 rose comb **:** 1 single comb

Explain the above crosses using a genetic diagram.

Parental phenotype: Rose Comb x Pea Comb

Parental genotype (2n): RRpp x rrPP

Gametes (n): (Rp) x (rP)

F_1 genotype (2n): RrPp

F_1 phenotypic ratio: All Walnut Comb

F_1 generation were mated

F_1 phenotype: Walnut Comb x Walnut Comb

F_1 genotype (2n): RrPp x RrPp

Gametes (n): (RP) (Rp) (rP) (rp) x (RP) (Rp) (rP) (rp)

F_2 genotype (2n):

♀ \ ♂	RP	Rp	rP	rp
RP	RRPP Walnut	RRPp Walnut	RrPP Walnut	RrPp Walnut
Rp	RRPp Walnut	RRpp Rose	RrPp Walnut	Rrpp Rose
rP	RrPP Walnut	RrPp Walnut	rrPP Pea	rrPp Pea
rp	RrPp Walnut	Rrpp Rose	rrPp Pea	rrpp Single

F_2 phenotype: Walnut : Rose : Pea : Single
F_2 phenotypic ratio: 9 : 3 : 3 : 1

Conclusion

- **Two genes** situated on different chromosomes governed the **expression of one characteristic** – shape of comb (unlike Mendelian dihybrid inheritance)

- The alleles of these two genes interact to give rise to four phenotypes:
  - Pea comb is determined by presence of dominant P allele
  - Rose comb is determined by presence of dominant R allele
  - Walnut comb is determined by presence of at least one of each dominant allele for pea and rose comb (i.e. P–R–)
  - Single comb is determined by homozygous recessive condition (i.e. pprr)

6.2 Epistasis produces modified 9:3:3:1 ratios

Key concept 7:

- **Epistasis** is used to describe the situation in which the product of one gene (Gene A) can **inhibit / interfere** with the phenotypic effects of a different gene (Gene B)**.**
    - Gene A is said to be **epistatic** to Gene B.
    - Gene B is said to be **hypostatic** to Gene A.

Key concept 8:

- Many different ratios can result from different cases of epistasis (Fig. 6.1), but they are, in essence, **modified form of the 9:3:3:1 Mendelian dihybrid ratio** when a **cross is conducted between 2 heterozygotes (AaBb X AaBb).**

Organism	Character	A–B–	A–bb	aaB–	aabb	Modified ratio	Type of Epistasis
		9/16	3/16	3/16	1/16		
Mouse	Coat colour	Black	Albino	Brown	Albino	9:3:4	Recessive epistasis *Allele b epistatic to locus A/a*
Chicken	Colour	White	White	Coloured	White	13:3	Dominant epistasis *Allele A is epistatic to locus B/b*
Squash	Colour	White	White	Yellow	Green	12:3:1	Dominant epistasis *Allele A is epistatic to locus B/b*
Sweet pea	Flower colour	Purple	White	White	White	9:7	Duplicate recessive genes
Squash	Shape	Disc	Sphere	Sphere	Long	9:6:1	Duplicate genes with cumulative effect
Shepherd's Purse	Seed capsule shape	Triangular	Triangular	Triangular	Ovoid	15:1	Duplicate dominant genes

Fig. 6.1: The basis of modified dihybrid F_2 phenotypic ratios, resulting from crosses between doubly heterozygous F_1 individuals. The above shows the possible ratios which resulted from gene interactions

6.2.1 Coat colour in mice – 9:3:4 ratio

Fur colour in mice is controlled by two different genes occupying different loci. The gene that determines whether colour pigment will be deposited in the fur has two alleles, colour deposition (C, dominant) and no colour deposition (c, recessive). The other gene determines the nature of colour and its alleles are black (B, dominant) and brown (b, recessive). The mice may have black or brown fur depending upon their genotypes, but this will only appear if accompanied by the allele for color deposition.

When a homozygous black mouse is crossed with an albino mouse, all F_1 offspring were black. When the F_1 offspring were self-crossed, F_2 generation ratio of 9 black **:** 3 brown **:** 4 albino mice are produced. Explain the results using a genetic diagram.

Gene required for deposition of hair pigment (C/c locus)

- Allele **C** represent alleles for pigment deposition in fur
- Allele **c** represent alleles for no pigment deposition (i.e. albino)

Gene coding for colour pigment (A/a locus)

- Allele **B** → black pigment
- Allele **b** → brown pigment

Parental phenotype: Black mouse x Albino mouse

Parental genotype (2n): BBCC x bbcc

Gametes (n): (BC) x (bc)

F_1 genotype (2n): BbCc

F_1 phenotypic ratio: All black mice

F_1 generation were crossed

F_1 phenotype: Black x Black
F_1 genotype (2n): BbCc x BbCc

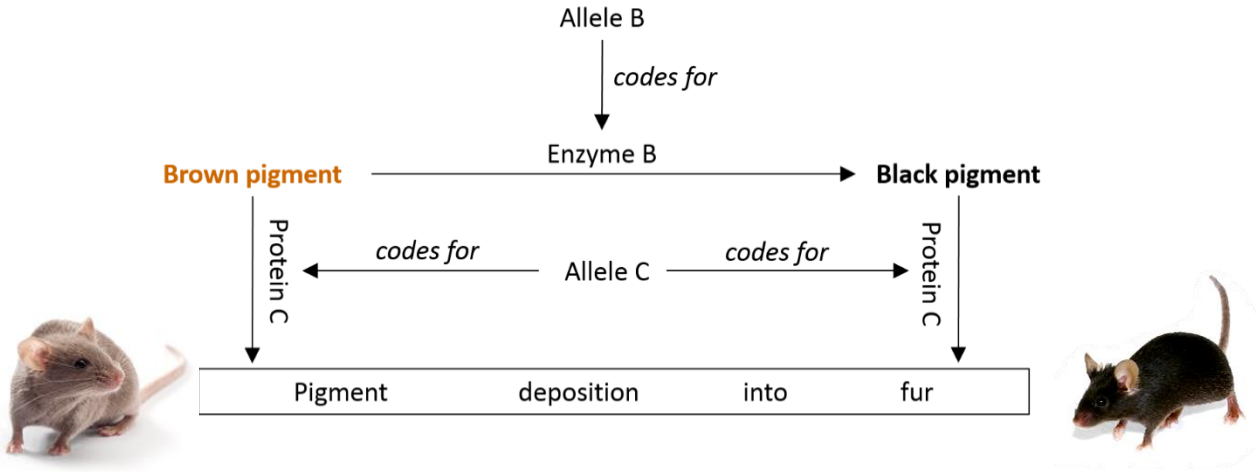
Gametes (n): (BC) (Bc) (bC) (bc) x (BC) (Bc) (bC) (bc)

F_2 genotype (2n) and phenotypes:

♀ \ ♂	BC	Bc	bC	bc
BC	BBCC	BBCc	BbCC	BbCc
Bc	BBCc	BBcc	BbCc	Bbcc
bC	BbCC	BbCc	bbCC	bbCc
bc	BbCc	Bbcc	bbCc	bbcc

F_2 phenotypic ratio: 9 black : 3 brown **:** 4 albino

- Biochemical basis and conclusion:
    - The dominant allele C is necessary for colour deposition into fur.
    - Individuals with genotypes ––CC or ––Cc express coloured fur. Hence, individuals with brown fur have genotypes bbCC or bbCc. Those with black fur have at least one dominant B and one dominant C allele (e.g. B–CC or B–Cc)
    - **Genotype cc** is **epistatic** to the gene coding for fur colour. In the presence of genotype cc, colour is not expressed. This condition is known as **recessive epistasis** (the presence of **two** copies of the epistatic recessive allele interferes with the phenotypic expression of the hypostatic gene).
    - Individuals with genotypes BBcc, Bbcc or bbcc will be albino.
    - Hence, the resulting phenotypic ratio is 9:3:4 (9 black, 3 brown and 4 albino) instead of the expected 9:3:3:1 ratio in a typical Mendelian dihybrid cross.



Organism	Character	A–B–	A–bb	aaB–	aabb	Modified ratio	Type of Epistasis
		9/16	3/16	3/16	1/16		
Mouse	Coat colour	Black B–C–	Albino B–cc	Brown bbC–	Albino bbcc	9:3:4	Recessive epistasis

6.2.2 Plumage colour in chicken – 13:3 ratio

In the inheritance of feather colour in chickens there is an interaction between two autosomal gene loci, **I/i** and **C/c**. Individuals carrying the dominant allele, **I**, have white plumage even if they also carry the dominant allele, **C**, for coloured plumage.

White Leghorn chickens have the genotype **IICC**, while white Wyandotte chickens have the genotype **iicc**. A white Leghorn is crossed with a white Wyandotte.

Use a genetic diagram to show the expected genotypes and phenotypes and their ratios in the F_1 and F_2 generations.

Gene coding for white plumage (I/i locus)

- Allele **I** represent allele for white plumage
- Allele **i** represent allele for coloured plumage

Gene coding coloured plumage (C/c locus)

- Alelle **C** represent allele for coloured plumage
- Alelle **c** represent allele for white plumage

Parental phenotype: White Leghorn x White Wyandotte

Parental genotype (2n): IICC x iicc

Gametes (n): (IC) x (ic)

F_1 genotype (2n): IiCc

F_1 phenotypic ratio: All White Chickens

F_1 generation were crossed

F_1 phenotype: White Chicken x White Chicken

F_1 genotype (2n): IiCc x IiCc

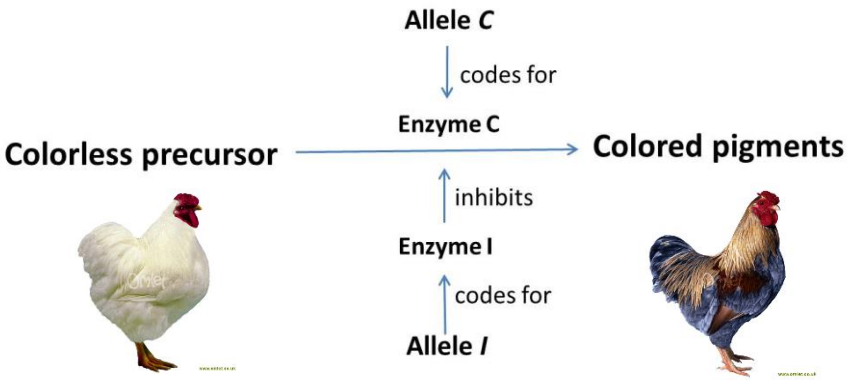
Gametes (n): (IC) (Ic) (iC) (ic) x (IC) (Ic) (iC) (ic)

F_2 genotype (2n) and phenotypes:

♀ \ ♂	IC	Ic	iC	ic
IC	IICC	IICc	IiCC	IiCc
Ic	IICc	IIcc	IiCc	Iicc
iC	IiCC	IiCc	iiCC	iiCc
ic	IiCc	Iicc	iiCc	iicc

F_2 phenotypic ratio: 13 white : 3 coloured

- Biochemical basis and conclusion:
    - The product of allele I inhibits the phenotypic effect of the C allele.
    - Allele I is **epistatic** to the colour gene C. This is known as **dominant epistasis** (the presence of **one** copy of the epistatic dominant allele interferes with the phenotypic expression of the hypostatic gene).
    - Individuals that carry the dominant allele, I, have white plumage even if they carry the dominant allele C for colour (I–C–).
    - Individuals which are homozygous recessive for the colour gene (––cc) will also have white plumage.
    - For coloured plumage to develop, individuals must have genotype iiC–.



    - Precursor means the molecule that comes before the other of the same kind.

Organism	Character	A–B–	A–bb	aaB–	aabb	Modified ratio	Type of Epistasis
		9/16	3/16	3/16	1/16		
Chicken	Colour	White I–C–	White I–cc	Coloured iiC–	White iicc	13:3	Dominant epistasis

6.2.3 Colour of summer squash– 12:3:1 ratio

In the inheritance of fruit colour in summer squash, there is an interaction between two autosomal gene loci, **W/w** and **Y/y**. Plants carrying the dominant allele, **W,** develop white fruits even if they also carry the allele, **Y**, for yellow fruits or **yy** for green fruits.
A plant homozygous dominant for the two genes is crossed with a plant homozygous recessive for the two genes. Predict the phenotypic ratio of the F_2 offspring.

Gene coding for inhibition of colour deposition (W/w locus)

- Allele **W** represent allele for white colour deposition
- Allele **w** represent allele for coloured deposition

Gene coding for coat colour (B/b locus)

- Allele **Y** represent allele for yellow colour
- Allele **y** represent allele for green colour

Parental phenotype: White fruits x Green fruits

Parental genotype (2n): WWYY x wwyy

Gametes (n): (WY) x (wy)

F_1 genotype (2n): WwYy

F_1 phenotypic ratio: All White Fruits

F_1 generation were crossed

F_1 phenotype: White Fruits x White Fruits

F_1 genotype (2n): WwYy x WwYy

Gametes (n): (WY) (Wy) (wY) (wy) x (WY) (Wy) (wY) (wy)

F_2 genotype (2n) and phenotypes:

♀ \ ♂	WY	Wy	wY	wy
WY	WWYY	WWYy	WwYY	WwYy
Wy	WWYy	WWyy	WwYy	Wwyy
wY	WwYY	WwYy	wwYY	wwYy
wy	WwYy	Wwyy	wwYy	wwyy

F_2 phenotypic ratio: 12 White **:** 3 Yellow **:** 1 Green

- Biochemical basis and conclusion:
    - **Dominant epistasis** occurs: Allele W is **epistatic** to the colour gene Y/y.
    - Plants that carry the dominant allele W will have white fruits. This is because the gene product of W allele inhibits expression of the gene coding for yellow or green colour.
    - Plants that carry both recessive w alleles and the dominant Y allele will have yellow fruits (wwY–).
    - Plants that carry both recessive w alleles and both recessive y alleles will have green fruits (wwyy).
    - For coloured fruits (yellow/green) to develop, plants must have genotype ww––.

Organism	Character	A–B–	A–bb	aaB–	aabb	Modified ratio	Type of Epistasis
		9/16	3/16	3/16	1/16		
Squash	Colour	White W–Y–	White W–yy	Yellow wwY–	Green wwyy	12:3:1	Dominant epistasis

6.2.4 Flower colour in sweet peas – 9:7 ratio

In sweet peas, two genes are required for the expression of purple colour flower. If either of these genes are not present, the flower is white. Two different pure line sweet peas plants with white flowers are crossed to obtain F_1 offspring, which all had purple flowers. When these F_1 are self-crossed, the F_2 generation ratio of 9 purple plants **:** 7 white plants are produced. Explain the results using a genetic diagram.

Parental phenotype: White flowers x White flowers

Parental genotype: CCpp x ccPP

Gametes (n): (Cp) (cP)

F_1 genotype: CcPp

F_1 phenotype: All purple flowers

F1 generation was selfed

F_1 phenotype: Purple flowers x Purple flowers

F_1 genotype (2n): CcPp x CcPp

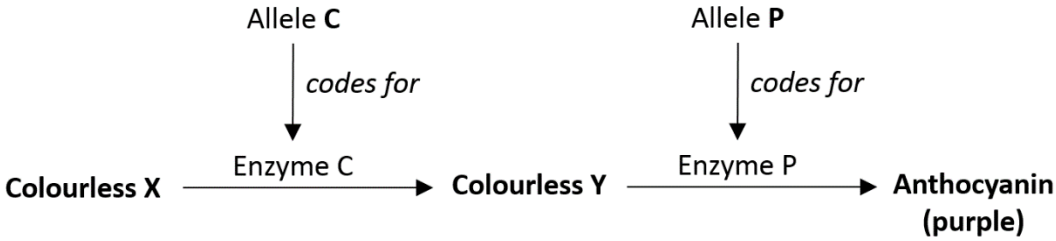
Gametes (n): (CP) (Cp) (cP) (cp) x (CP) (Cp) (cP) (cp)

F_2 genotype (2n) and phenotypes:

♀ \ ♂	CP	Cp	cP	cp
CP	CCPP	CCPp	CcPP	CcPp
Cp	CCPp	CCpp	CcPp	Ccpp
cP	CcPP	CcPp	ccPP	ccPp
cp	CcPp	Ccpp	ccPp	ccpp

F_2 phenotypic ratio: 9 purple **:** 7 white

- Biochemical basis and conclusion:
    - **Duplicate recessive genes** – The same phenotype is produced as long as **one gene locus is homozygous recessive (aa––, ––bb, or aabb).** When dominant alleles of both loci are present together (A–B–), they **complement** each other to produce a different phenotype.
    - The two precursor molecules (X and Y) of the purple pigment authocyanin are colourless.
    - Conversion of X to Y is catalysed by an enzyme C, while conversion of Y to anthocyanin is catalysed by an enzyme P.
    - Synthesis of functional products C and P is directed by alleles C and P respectively. Alleles c and p synthesize non-functional enzymes.
    - Plants with at least one C and one P allele (C–P–) would have purple flowers.
    - Plant with genotype ––pp has white flowers since it cannot produce functional enzyme P.
    - Plant with genotype cc–– has white flowers since it cannot product functional enzyme C.
    - Plant with genotype ccpp has white flowers since both enzymes C and P are non-functional.



Organism	Character	A–B–	A–bb	aaB–	aabb	Modified ratio	Type of Epistasis
		9/16	3/16	3/16	1/16		
Sweet pea	Flower colour	Purple C–P–	White C–pp	White ccP–	White ccpp	9:7	Duplicate recessive genes

6.2.5 Fruit shape in summer squash – 9:6:1 ratio

Shapes of summer squash fruits are spherical, disc-shaped or long. When plants with disc-shaped fruits (**AABB**) are crossed to plants with long fruits (**aabb**), the F1 generation all have disc fruits. However, in the F2 offspring, fruits with a novel shape (sphere) appear, as well as fruit exhibiting the parental phenotypes. They are in the ratio of 9 disc **:** 6 sphere **:** 1 long. Explain the results.

Parental phenotype: Disc x Long

Parental genotype (2n): AABB x aabb

Gametes (n): (AB) x (ab)

F_1 genotype (2n): AaBb

F_1 phenotypic ratio: All disc-shaped

F_1 generation were crossed

F_1 phenotype: Disc x Disc

F_1 genotype (2n): AaBb x AaBb

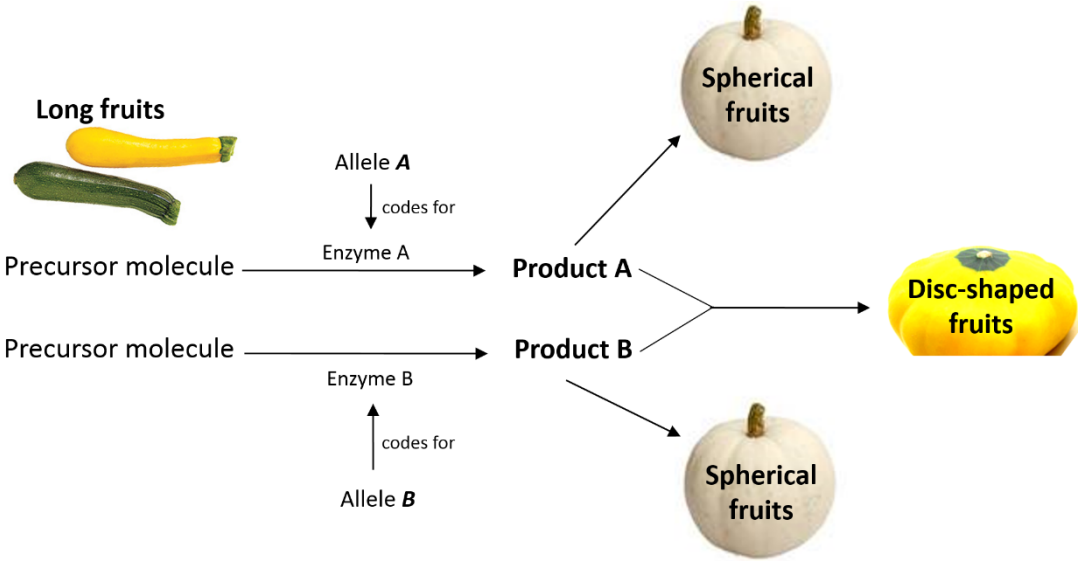
Gametes (n): (AB) (Ab) (aB) (ab) x (AB) (Ab) (aB) (ab)

F_2 genotype (2n) and phenotypes:

♀ \ ♂	AB	Ab	aB	ab
AB	AABB	AABb	AaBB	AbBb
Ab	AABb	AAbb	AaBb	Aabb
aB	AaBB	AaBb	aaBB	aaBb
ab	AaBb	Aabb	aaBb	aabb

F_2 phenotypic ratio: 9 disc **:** 6 sphere **:** 1 long

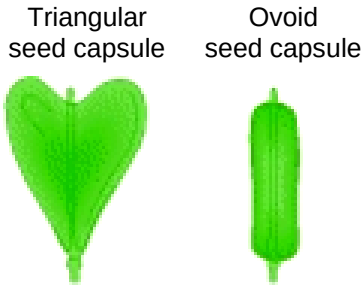
- Biochemical basis and conclusion:
  - Both genes code for enzymes that influence the fruit shape equally.
  - In the absence of dominant alleles (aabb), no enzymes are synthesized to convert the precursor molecules, hence the fruit is long.
  - A **dominant allele at <u>either locus</u>** (A––– or –––B) will code for either enzyme A or B which ensures a sphere-shaped fruit.
  - If the **dominant allele** from **<u>both loci</u> (A–B–)** are present, both enzymes are synthesized to flatten the fruit into a disc shape. This is known as **duplicate genes with cumulative effect**.



Organism	Character	A–B–	A–bb	aaB–	aabb	Modified ratio	Type of Epistasis
		9/16	3/16	3/16	1/16		
Squash	Shape	Disc A–B–	Sphere A–bb	Sphere aaB–	Long aabb	9:6:1	Duplicate genes with cumulative effect

6.2.6 Seed capsule shape of Shepherd's Purse – 15:1 ratio

The seed capsules of a weedy plant called the Shepherd's Purse are either triangular or ovoid in shape. Ovoid capsules are only produced if a plant is homozygous for the recessive alleles of two genes (**aabb**). If the dominant allele of either gene is present, the plant produces triangular capsules. Determine the F2 phenotypic ratio when a plant homozygous dominant for both the genes are crossed with a plant with ovoid seed capsules.



Parental phenotype: Triangular x Ovoid

Parental genotype (2n): AABB x aabb

Gametes (n): (AB) x (ab)

F_1 genotype (2n): AaBb

F_1 phenotypic ratio: All Triangular shape

F_1 generation were crossed

F_1 phenotype: Triangular x Triangular

F_1 genotype (2n): AaBb x AaBb

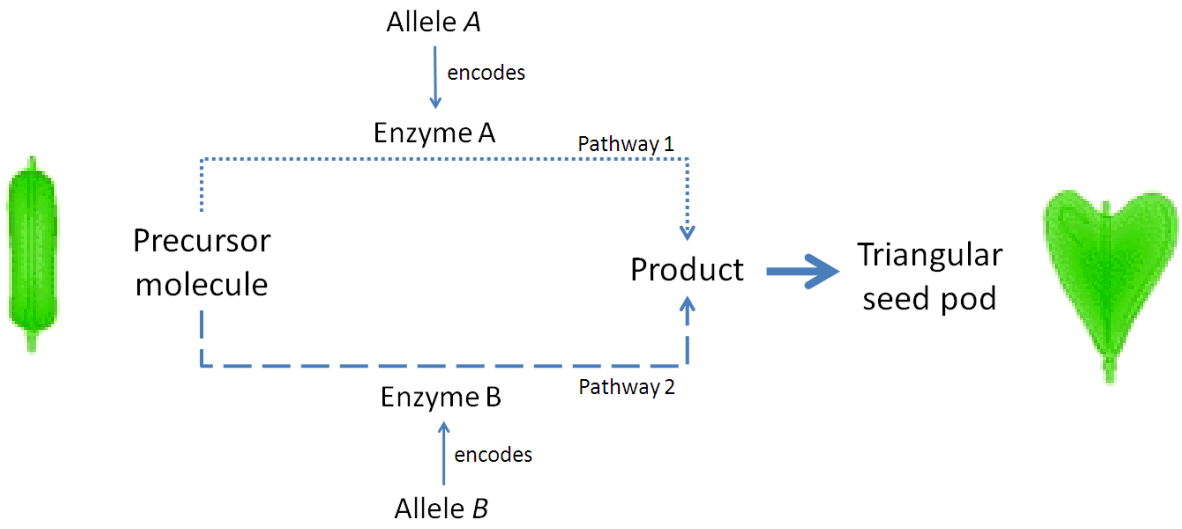
Gametes (n): (AB) (Ab) (aB) (ab) x (AB) (Ab) (aB) (ab)

F_2 genotype (2n) and phenotype:

♀ \ ♂	AB	Ab	aB	ab
AB	AABB	AABb	AaBB	AbBb
Ab	AABb	AAbb	AaBb	Aabb
aB	AaBB	AaBb	aaBB	aaBb
ab	AaBb	Aabb	aaBb	aabb

F_2 phenotypic ratio: 15 triangular : 1 ovoid

- Biochemical basis and conclusion:
    - **Duplicate dominant gene** – The dominant alleles of both loci each produces the same phenotype without cumulative effect.
    - In the presence of **<u>either</u> dominant allele A <u>or</u> allele B** (A––– or –––B), The enzyme coded by **<u>either</u> allele A <u>or</u> allele B** can convert the precursor molecule into a product that leads to a triangular capsule in two different pathways.
    - When both loci are homozygous recessive (aabb), both enzyme A and B are not produced or non-functional. **<u>Both pathways are blocked</u>**, hence the ovoid phenotype but not the triangular phenotype is produced.



Organism	Character	A–B–	A–bb	aaB–	aabb	Modified ratio	Type of Epistasis
		9/16	3/16	3/16	1/16		
Shepherd's Purse	Seed capsule shape	Triangular A–B–	Triangular A–bb	Triangular aaB–	Ovoid aabb	15:1	Duplicate dominant genes

7. The Chi-squared Test

Learning Outcome:
Use the chi-squared test to test the significance of differences between observed and expected results.

- The Chi-squared (χ^2) test is a statistical test that measures the **significance of any deviation between the expected and observed results**, and the **probability that such deviation is due to chance**.

- For genetics experiments, the test is used to **compare if the difference between the observed data and the expected value is significantly different.** In other words, to assess if data **conform to an expected ratio**.

- Simple example:
  - Imagine tossing a coin 100 times. Since the probability of it landing on either heads or tails is 0.5, you would expect it to land heads on 50 occasions and tails on 50 occasions.
  - In an actual attempt, it was found to land heads 55 times, and tails only 45 times.
  - The discrepancy between the expected and the actual results could either be due to **chance**, or to the fact that the coin is **biased** in some way.
  - The χ^2 - test is the means by which the **statistical validity** of such results can be tested.

- This measure of deviation is called the χ^2 value, and is represented by the term χ^2.

$$\chi^2 = \sum \frac{(O - E)^2}{E} \qquad \nu = c - 1$$

where
Σ = sum of the calculation for each category
O = observed value / result for each category
E = expected value / result for each category
ν = number of degrees of freedom
c = number of classes

- Degrees of freedom: For the χ^2 test, this is equal to one less than the number of categories or classes in the sample.

- Performing the χ^2 test

Step 1: Write the Null Hypothesis and the Alternative Hypothesis.

Null Hypothesis:
The difference between the observed and the expected values is <u>not</u> significant

Alternative Hypothesis:
The difference between the observed and the expected values <u>is significant</u>

Step 2: Construct a table and compute the following.

- Observed values (these are the results from the experiment)
- Expected values (E) for each category
- Deviation of observed values from the expected (O-E)
- $(O - E)^2$
- $(O - E)^2 / E$

Phenotype categories	Expected ratio *(if applicable)*	Expected numbers (E)	Observed numbers (O)	(O – E)	$\frac{(O - E)^2}{E}$

Step 3: Calculate the χ^2 value using the formula.

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

Step 4: Determine the degree of freedom (ν).

ν = number of classes (c) – 1

Step 5: Locate the χ^2 value on the χ^2 table.

- The χ^2 table tabulates the χ^2 values that correspond to the numbers of degrees of freedom.
- It also shows the corresponding probabilities (P) that the deviations are due to chance alone.

Degrees of Freedom *(df)*	**Probability** (p)										
	0.95	0.90	0.80	0.70	0.50	0.30	0.20	0.10	0.05	0.01	0.001
1	0.004	0.02	0.06	0.15	0.46	1.07	1.64	2.71	3.84	6.64	10.83
2	0.10	0.21	0.45	0.71	1.39	2.41	3.22	4.60	5.99	9.21	13.82
3	0.35	0.58	1.01	1.42	2.37	3.66	4.64	6.25	7.82	11.34	16.27
4	0.71	1.06	1.65	2.20	3.36	4.88	5.99	7.78	9.49	13.28	18.47
5	1.14	1.61	2.34	3.00	4.35	6.06	7.29	9.24	11.07	15.09	20.52
6	1.63	2.20	3.07	3.83	5.35	7.23	8.56	10.64	12.59	16.81	22.46
7	2.17	2.83	3.82	4.67	6.35	8.38	9.80	12.02	14.07	18.48	24.32
8	2.73	3.49	4.59	5.53	7.34	9.52	11.03	13.36	15.51	20.09	26.12
9	3.32	4.17	5.38	6.39	8.34	10.66	12.24	14.68	16.92	21.67	27.88
10	3.94	4.86	6.18	7.27	9.34	11.78	13.44	15.99	18.31	23.21	29.59
	Nonsignificant								Significant		

Step 6: Determine the probability that the deviations are due to chance alone (P) based on the calculated χ^2 value.

- The "cut-off" point is typically P = 0.05.
- If **P < 0.05 (or 5%)**, the **difference** between observed and expected results is **significant**. **Reject** Null Hypothesis.
- If **P > 0.05**, the difference between observed and expected results is **not significant**. **Accept** Null Hypothesis - the difference is due to chance alone.

Step 7: Conclude.

- Write a statement concluding whether there is any significant difference between the observed and expected results **with respect to the experiment**.
- If the difference is not significant, include in the conclusion this statement – "The difference between observed and expected results is insignificant and is due to chance."

- ***Example 7.1***
  In *Drosophila*, normal (wild-type) wings are dominant to vestigial wings. Suppose we cross two normal-winged individuals both believed to be heterozygous for this character. We should expect a 3:1 ratio of normal wings to vestigial wings. In reality, of 48 offspring produced, 30 have normal wings and 18 have vestigial wings. Is this close enough to a 3:1 ratio to justify the view that both parents were heterozygous?

(Step 1)

Null Hypothesis:
The difference between the observed and the expected values is not significant.

Alternative Hypothesis:
The difference between the observed and the expected values is significant.

(Step 2)

Phenotype categories	Expected ratio	Expected number (E)	Observed number (O)	(O – E)	$\frac{(O-E)^2}{E}$
Normal wings	3	¾ x 48 = 36	30	–6	1.0
Vestigial wings	1	¼ x 48 = 12	18	6	3.0

(Step 3)

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$

$= 1.0 + 3.0$
$= 4.0$

(Step 4)

No. of categories = 2 (normal wing and vestigial wing)
∴ No. of degrees of freedom $\nu = 2 - 1 = 1$

(Step 5)

Check up the χ^2 table, locate the position of the calculated χ^2 value for $\nu = 1$.

Degrees of Freedom (*df*)	**Probability** (p)										
	0.95	0.90	0.80	0.70	0.50	0.30	0.20	0.10	0.05	0.01	0.001
1	0.004	0.02	0.06	0.15	0.46	1.07	1.64	2.71	3.84	6.64	10.83
2	0.10	0.21	0.45	0.71	1.39	2.41	3.22	4.60	5.99	9.21	13.82
3	0.35	0.58	1.01	1.42	2.37	3.66	4.64	6.25	7.82	11.34	16.27
4	0.71	1.06	1.65	2.20	3.36	4.88	5.99	7.78	9.49	13.28	18.47
5	1.14	1.61	2.34	3.00	4.35	6.06	7.29	9.24	11.07	15.09	20.52
6	1.63	2.20	3.07	3.83	5.35	7.23	8.56	10.64	12.59	16.81	22.46
7	2.17	2.83	3.82	4.67	6.35	8.38	9.80	12.02	14.07	18.48	24.32
8	2.73	3.49	4.59	5.53	7.34	9.52	11.03	13.36	15.51	20.09	26.12
9	3.32	4.17	5.38	6.39	8.34	10.66	12.24	14.68	16.92	21.67	27.88
10	3.94	4.86	6.18	7.27	9.34	11.78	13.44	15.99	18.31	23.21	29.59
	Nonsignificant								Significant		

(Step 6)

Given that the number of degrees of freedom = 1, the value of $\chi^2 = 4.0$ is larger than the critical value of 3.84, i.e. probability values smaller than 0.05 (5%).

This means that the probability that the deviation is due to chance is less than 5% (i.e. $P < 0.05$).

The deviation is therefore significant, and not due to chance. Reject Null Hypothesis.

(Step 7)

Conclusion:
There difference between the observed and the expected results is significant.
Hence we cannot assume that the parents are heterozygous.

- ***Example 8.2***
  Domestic chicken with walnut combs were crossed with each other. In the event, the 160 offspring produced 93 individuals with walnut combs, 24 with rose combs, 36 with pea combs and 7 with single combs. Do these results show that the parents were heterozygous?

(Step 1)

Null Hypothesis:
The difference between the observed and the expected values is not significant.

Alternative Hypothesis:
The difference between the observed and the expected values is significant.

(Step 2)

Phenotype categories	Expected ratio	Expected number (E)	Observed number (O)	(O – E)	$\frac{(O-E)^2}{E}$
Walnut comb	9	9/16 x 160 = 90	93	3	0.1
Rose comb	3	3/16 x 160 = 30	24	–6	1.2
Pea comb	3	3/16 x 160 = 30	36	6	1.2
Single comb	1	1/16 x 160 = 10	7	–3	0.9

(Step 3)

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$
$$= 0.1 + 1.2 + 1.2 + 0.9$$
$$= 3.4$$

(Step 4)

No. of categories = 4
$\therefore$ No. of degrees of freedom, $\nu = 4 - 1 = 3$

(Step 5)

Check up the χ^2 table, locate the position of the calculated χ^2 value for $\nu = 3$.

Degrees of Freedom (*df*)	**Probability** (p)										
	0.95	0.90	0.80	0.70	0.50	0.30	0.20	0.10	0.05	0.01	0.001
1	0.004	0.02	0.06	0.15	0.46	1.07	1.64	2.71	3.84	6.64	10.83
2	0.10	0.21	0.45	0.71	1.39	2.41	3.22	4.60	5.99	9.21	13.82
3	0.35	0.58	1.01	1.42	2.37	3.66	4.64	6.25	7.82	11.34	16.27
4	0.71	1.06	1.65	2.20	3.36	4.88	5.99	7.78	9.49	13.28	18.47
5	1.14	1.61	2.34	3.00	4.35	6.06	7.29	9.24	11.07	15.09	20.52
6	1.63	2.20	3.07	3.83	5.35	7.23	8.56	10.64	12.59	16.81	22.46
7	2.17	2.83	3.82	4.67	6.35	8.38	9.80	12.02	14.07	18.48	24.32
8	2.73	3.49	4.59	5.53	7.34	9.52	11.03	13.36	15.51	20.09	26.12
9	3.32	4.17	5.38	6.39	8.34	10.66	12.24	14.68	16.92	21.67	27.88
10	3.94	4.86	6.18	7.27	9.34	11.78	13.44	15.99	18.31	23.21	29.59
	Nonsignificant								Significant		

(Step 6)

Given that the number of degrees of freedom = 3, the value of $\chi^2 = 3.4$ is smaller than the critical value of 7.82, i.e. probability values larger than 0.05 (5%).

This means that the probability that the deviation is due to chance is between 30% to 50% ($0.30<p<0.50$), i.e. $p > 0.05$

The deviation is therefore not significant, and is due to chance. Accept Null Hypothesis.

(Step 7)

Conclusion:
There difference between the observed and the expected results is not significant.
Hence the results showed that the parents are heterozygous.

8. Variations

Learning Outcome:

g) Explain how the environment may affect the phenotype (including how diet affects the differentiation of honey bees and how temperature affects fur color of Himalayan rabbits).

h) Explain the difference between genetic variation that is continuous (many, additive, genes control a characteristic) and discontinuous (one or few genes control a characteristic).

- The term **variation** describes the difference in characteristics shown by organisms belonging to the same natural population or species. Variation contributes to diversity among organisms.

- Variation is a result of genes, environment, and interaction between genes and environment.

- A study of the phenotypic differences in any large population shows that two forms of variation occur, discontinuous and continuous. Studies of variation in a character involve measuring the expression of that characteristic in a large number of organisms within the population, such as height in humans. The results are plotted as histograms or a graph which reveals the frequency distribution of the variations of that characteristic within the population (Fig. 8.1).

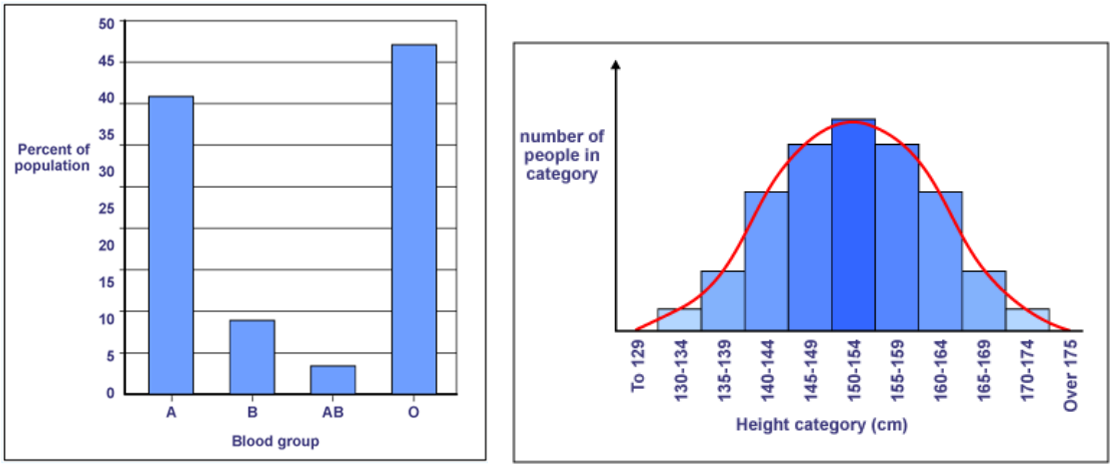


Fig. 8.1: (Left) A bar chart representing frequency distribution of discontinuous variation and (right) a histogram representing continuous variation

8.1 Discontinuous variation

- There are certain characteristics within a population which exhibit variations which are **discrete**. Discrete variation produces individuals **showing clear cut differences with no intermediates** between them. Examples include blood groups in humans, wing lengths in *Drosophila* and sex determination in animals and plants.

- It is usually **controlled by one or two major genes** with 2 or more allelic forms. In discontinuous variation, phenotypic expression is **relatively unaffected by the environment**. It is also known as **qualitative inheritance** and is an important type of inheritance in unravelling the laws of heredity.

8.2 Continuous variation

- **Continuous variation** can be defined as a type of variation where the characteristic shows a **complete gradation** from one extreme to the other without any break. This is illustrated most clearly by characteristics such as mass, height, shape and colour of organs and organisms

- Continuous variation is produced by the **combined effect of many genes (polygenes) and the environment.** The effect of each of these individual genes is too small to be of any significant impression on the phenotype. There is however infinite variety produced by the combined effects of all these genes (polygenes). It is thus known as **quantitative inheritance**.

Features	Discontinuous variation	Continuous variation
Number of genes	Determined by **one or a few** genes and the effects of each gene is discernible. **Different alleles** at a single gene locus have **large effects** Different gene loci have quite different effects on the phenotype.	Determined by **many** genes i.e. polygenic trait. These different gene loci have the same and often **additive effect** on the phenotype. Different alleles at a gene locus have small effects. Hence the phenotypic expression is the result of the combined effect of all these genes (or alleles).
Types of phenotypic classes	Discrete groups	A range of values between two extremes.
Method of measurement	By recognition of **different qualities** and summation of all the traits.	By recognition of **quantity** through measurement e.g. mean, standard deviation.
Type of inheritance	Qualitative	Quantitative
Effects of environment	No effect	Affected by environment Phenotype = Genotype + Environment
Examples	Blood groups, wing length in *Drosophila*, sex determination in animals and plants	Height, number of eggs laid, amount of milk production

Table 8.1: Comparison between discontinuous and continuous variation.

8.3 Sources of variation

As a result of the interaction between continuous and discontinuous variations and the environment, no two organisms will possess identical phenotypes. Many factors contributed to this variation within a population:

- Gene reshuffling
- Gene mutation
- Chromosomal mutation/aberrations

} **Genetic variation** which ultimately results in phenotypic variation

- Environment

} **Phenotypic variation**

8.3.1 Gene reshuffling

- Gene reshuffling is the basis for continuous variation. The mechanisms that contribute to genetic variation during meiosis and fertilization during sexual reproduction include:
  - Crossing over during prophase I of meiosis.
  - Independent assortment and segregation of homologous chromosomes during metaphase I and anaphase I of meiosis respectively
  - Independent assortment and segregation of chromatids during metaphase II and anaphase II of meiosis respectively (if crossing over occurred previously)
  - Random fertilization of gametes

a) Crossing over during prophase I of meiosis

- During prophase I of meiosis:
  - Homologous chromosomes pair up.
  - Chiasmata form between non-sister chromatids of homologous chromosomes.
  - Corresponding non-sister chromatids may break and rejoin at any point along their length where chiasmata formed.
  - As a result, corresponding alleles are exchanged (Fig. 8.2)

- Chiasmata can occur almost anywhere on the chromatids, and the number of chiasmata may vary from zero to as many as eight. The amount of genetic variation resulting from this reshuffling of alleles between homologous chromosomes can be infinite.

- This produces new linkage groups and so provides a major source of genetic recombination of alleles. The exact genotypes produced depend on the number of chiasmata and the positions of the genes relative to the sites of crossing over. (Fig. 8.3)

- Crossing over is **not the same as mutation** as crossing over does not create new genes / alleles. It merely reshuffles the alleles.

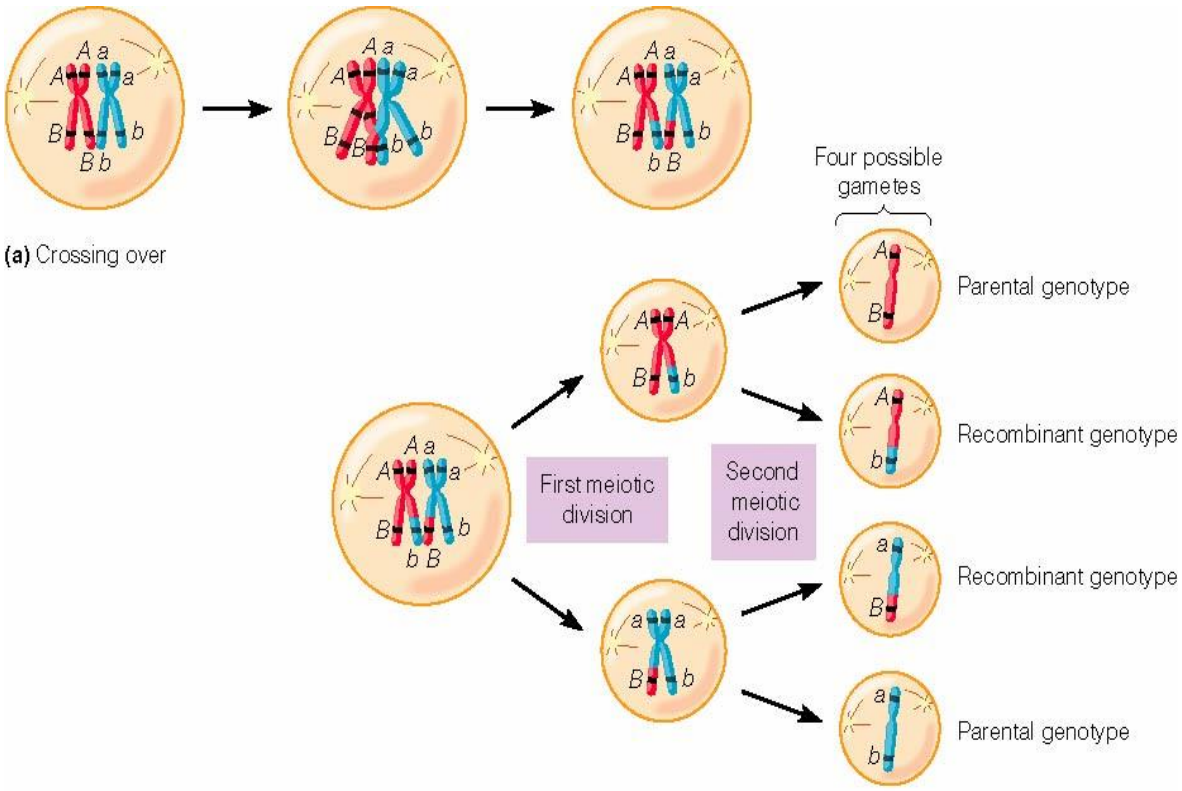


Fig. 8.2: Crossing over during prophase I results in non-genetically identical gametes (parental and recombinant genotypes) at the end of meiosis

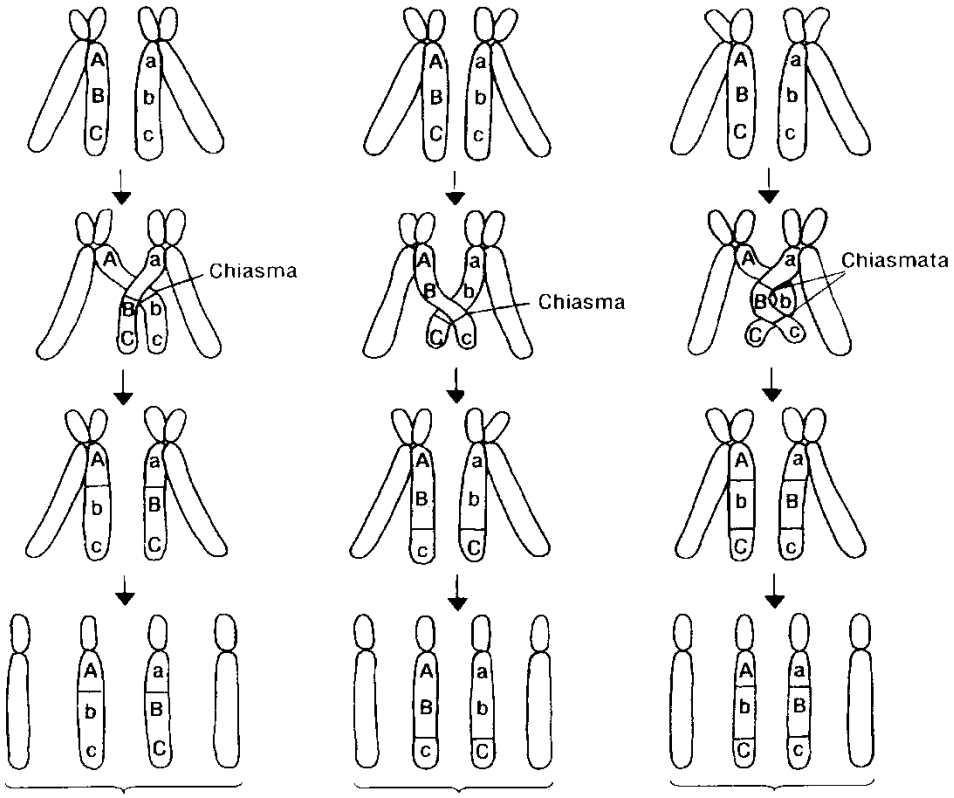


Fig. 8.3: Chiasmata can form at various positions between the two non-sister chromatids, resulting in variation in the genotype of gametes at the end of meiosis

b) Independent assortment and segregation of homologous chromosomes during metaphase I and anaphase I of meiosis respectively (Fig. 8.4)

c) Independent assortment and segregation of chromatids during metaphase II and anaphase II of meiosis respectively (Fig. 8.5)

- The orientation of the homologous chromosomes on the equatorial spindle during metaphase I of meiosis determines the direction in which the homologous chromosomes separate during anaphase I. This orientation of the homologous chromosomes is random.
- During metaphase II, the orientation of pairs of chromatids is also random and determines which chromatids migrate to opposite poles of the cell during anaphase II.
- This gives rise to a large number of different chromosome combinations in the gametes.
- For independent assortment segregation alone, the number of possible combinations of gametes during meiosis is $\mathbf{2^n}$, where n is the haploid number of the organism.
- For humans, the number of possible combinations is 2^{23} (about 8 million). Together with crossing over, the number is far more than 2^{23}.

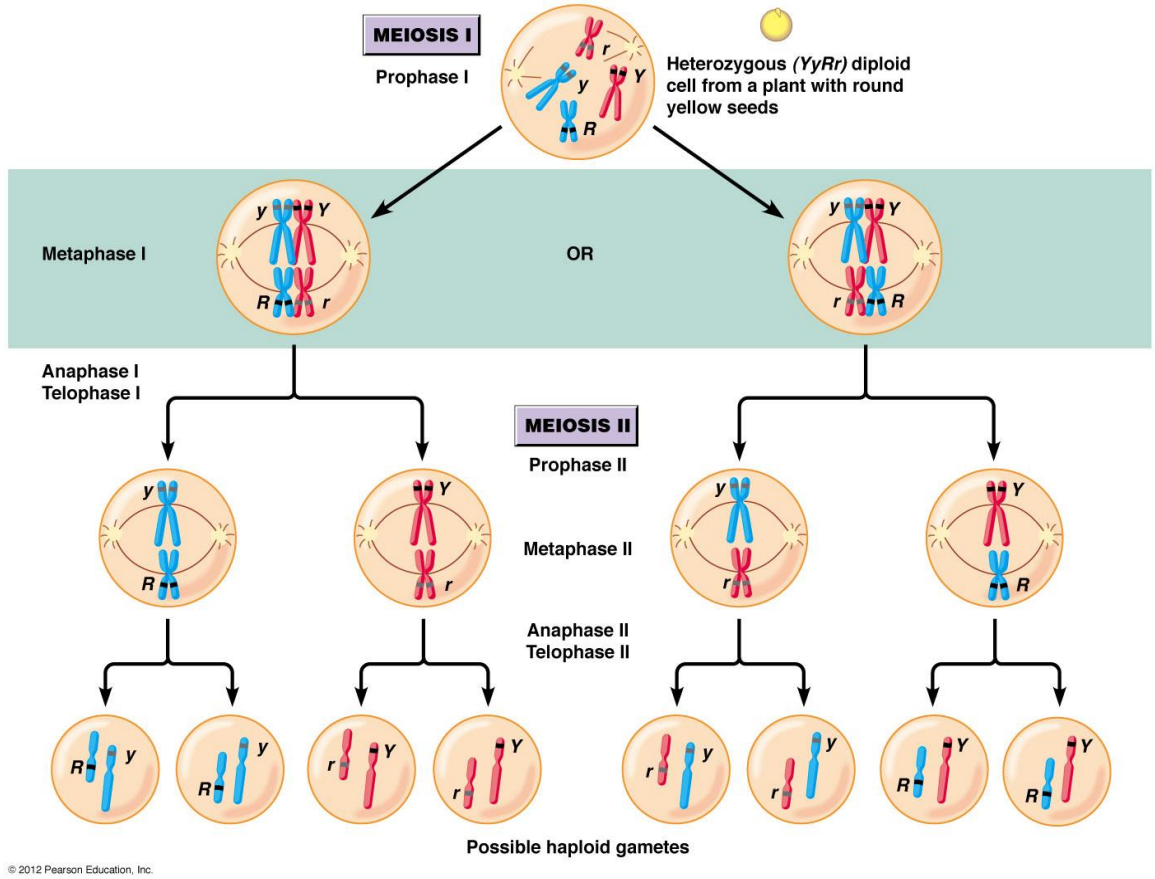


Fig. 8.4: Independent assortment and segregation of homologous chromosomes at metaphase I and anaphase I result in different chromosomal combinations. Crossing over is not depicted in this diagram.

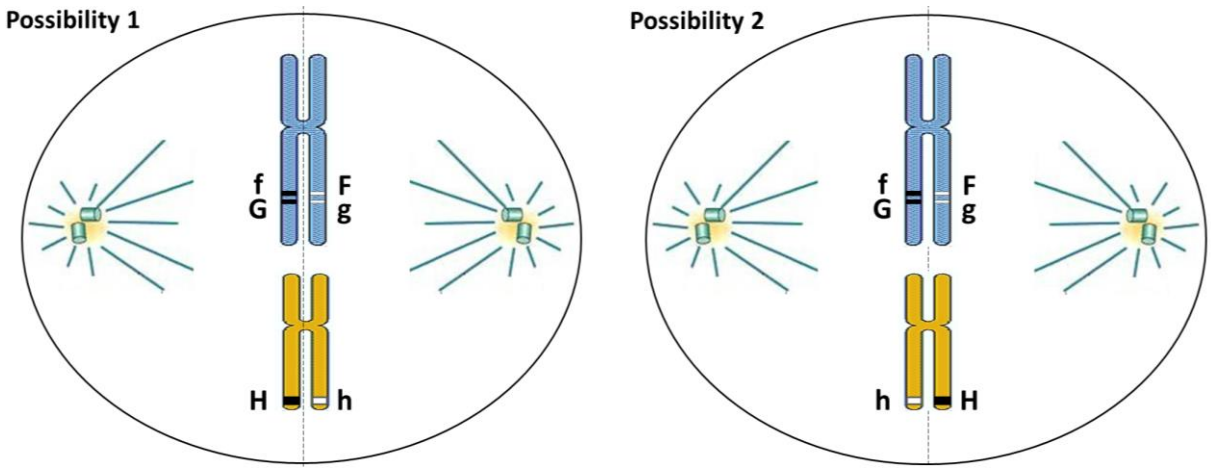


Fig. 8.5: Independent assortment and segregation of chromatids at metaphase II and anaphase II further result in different chromosomal combinations. Note that crossing over has occurred during prophase I.

d) Random fertilization of gametes

- The random nature of fertilization (Fig. 8.6) adds to the genetic variations arising from crossing over and independent assortment and segregation of chromosomes in meiosis.
- A zygote is formed when an ovum (1 of approximately 8 million) is fertilized by a single sperm cell (1 of approximately 8 million possible combinations).
- Without considering crossing over, random fusion of sperm and egg will produce a zygote with any of the over 70 trillion diploid combinations (2^{23} x 2^{23}).
- If crossing over is considered, the number of possibilities is infinite.

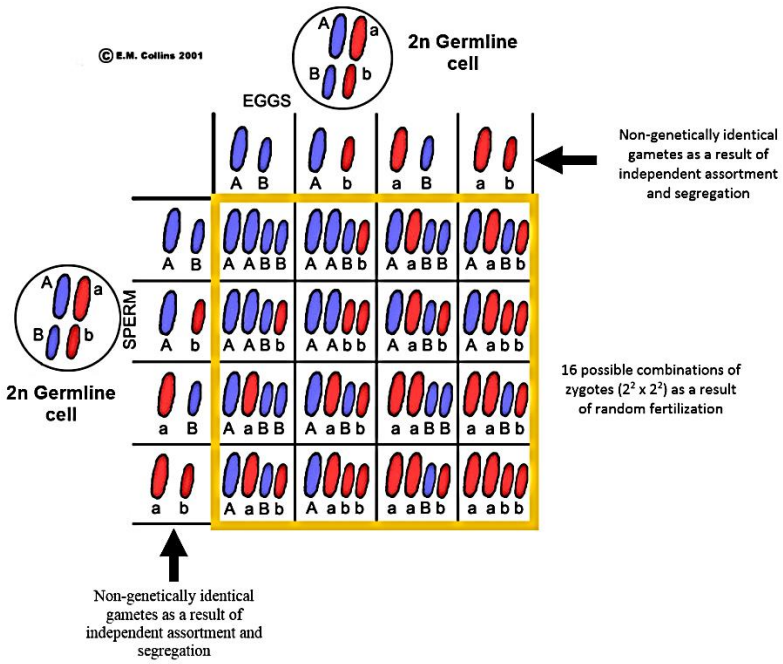


Fig. 8.6: Together with independent assortment and segregation, random fertilization adds on to the genetic variation of offspring. (2n = 4) is used here as an illustration.

8.3.2 Gene mutations

- Gene mutations are the ultimate source of variation as they **give rise to new alleles** which code for potential new traits. They can also result in inheritable / genetic diseases.

- *Refer to Genetics and Inheritance (III) for details*

8.3.4 Chromosomal aberrations

- *Refer to Genetics and Inheritance (III) for details*

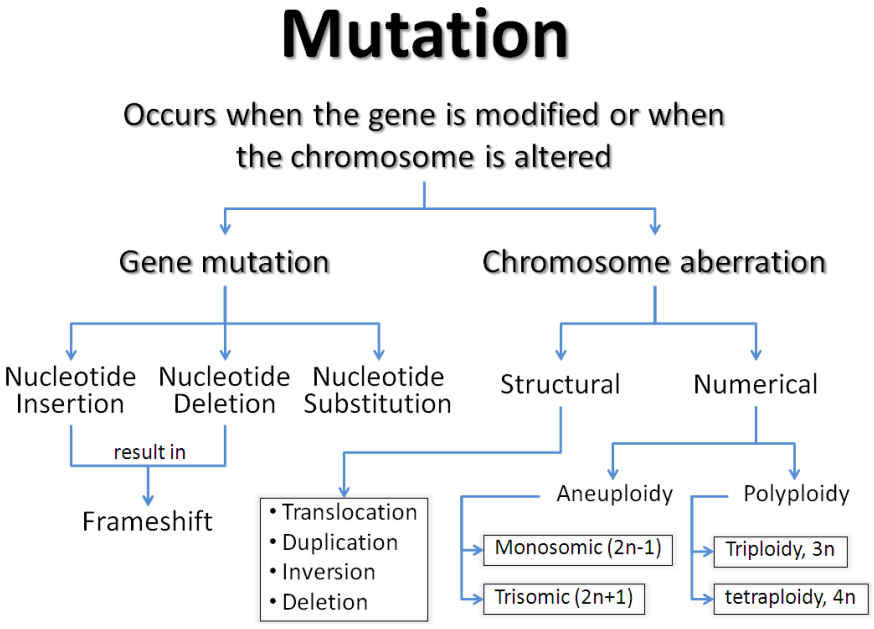


Fig. 8.7: Summary of mutation.

9. Effect of Environment on Phenotypes

- In natural systems, organisms face a multitude of ecological challenges and often respond with phenotypic shifts. Because organisms experience multiple selective and/or inducing agents, observed phenotypes generally reflect the influence of multiple environmental variables, in addition to other evolutionary factors (e.g. gene flow, genetic drift, genetic/developmental constraints).

- Environmental influences on traits can arise via genetically based responses to selection. Regardless of the adaptive nature or the form of genetic basis of phenotypic variation, environmental effects on phenotypes can be complex

- The product of a genotype is generally not a rigidly defined phenotype, but a **range of phenotypic possibilities** over which there may be variation due to **environmental influence**.

- Environment contributes to the quantitative nature of these characteristics (e.g. continuous variation of skin colour). Such characteristics are multifactorial, meaning many factors, both genetic and environmental, collectively influence phenotype.

Case study 1: Honey bees – Workers VS Queen (Nutritional effect)

- In spite of their identical, clonal nature at the DNA level, they are strongly differentiated across a wide range of characteristics including anatomical and physiological differences, the longevity of the queen and reproductive capacity.
- Larva bee fed with royal jelly becomes the queen. Larva bee fed with other diet becomes workers.
- Royal jelly suppresses the expression of DNA methyltransferase (Dnmt3) gene.
- Dnmt3 is needed for DNA methylation, which silences other genes (*Topic 6: Control of gene expression*).
- Hence, genes essential for queen development is not methylated and are expressed in the larva bee who fed with royal jelly.

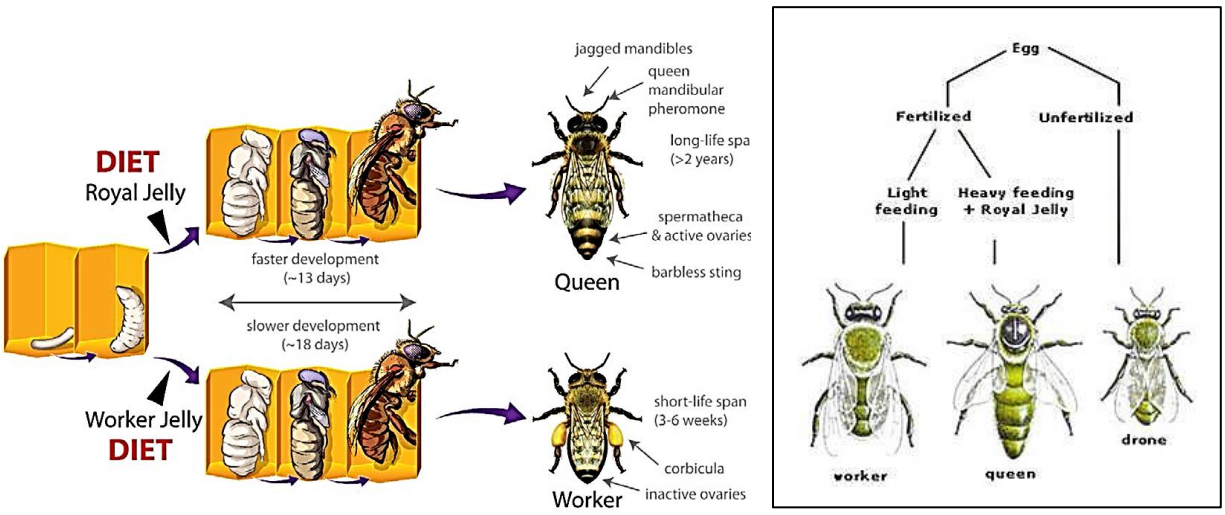


Fig. 9.1: Effect of nutrition on the development of honey bees.

Case study 2: Fur color of Himalayan rabbit (Temperature effect)

- A Himalayan rabbit is completely white at birth. But within weeks, the fur on the rabbit's ears, nose, tail and lower legs darkens.
- The rabbit is homozygous for an allele that encodes for a heat-sensitive enzyme. This enzyme catalyzes a step in the synthesis of the brown pigment melanin.
- In central body region, metabolic heat denatures the enzyme, no melanin is produced, and the fur remains white.
- In cooler body parts, the enzyme is functional, melanin is produced, and the fur is tinted brown.

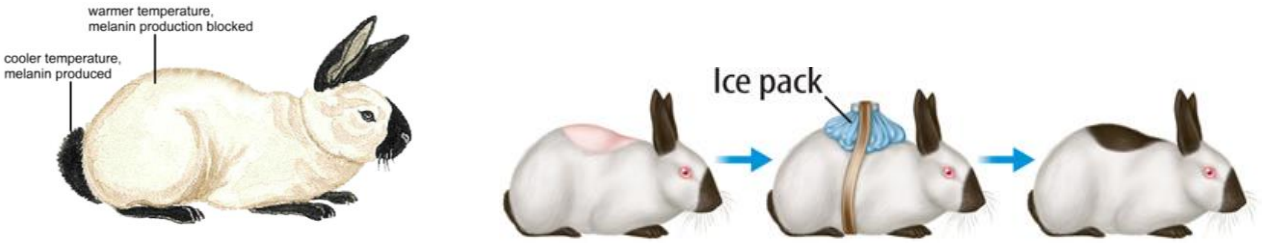


Fig. 9.2: The effect of temperature on fur color can be demonstrated by shaving a patch of fur, and keeping the area cool as it grows back. In the artificially cooled area, the heat-sensitive enzyme remains functional, melanin is produced, and the fur grows back dark.

• THE END •