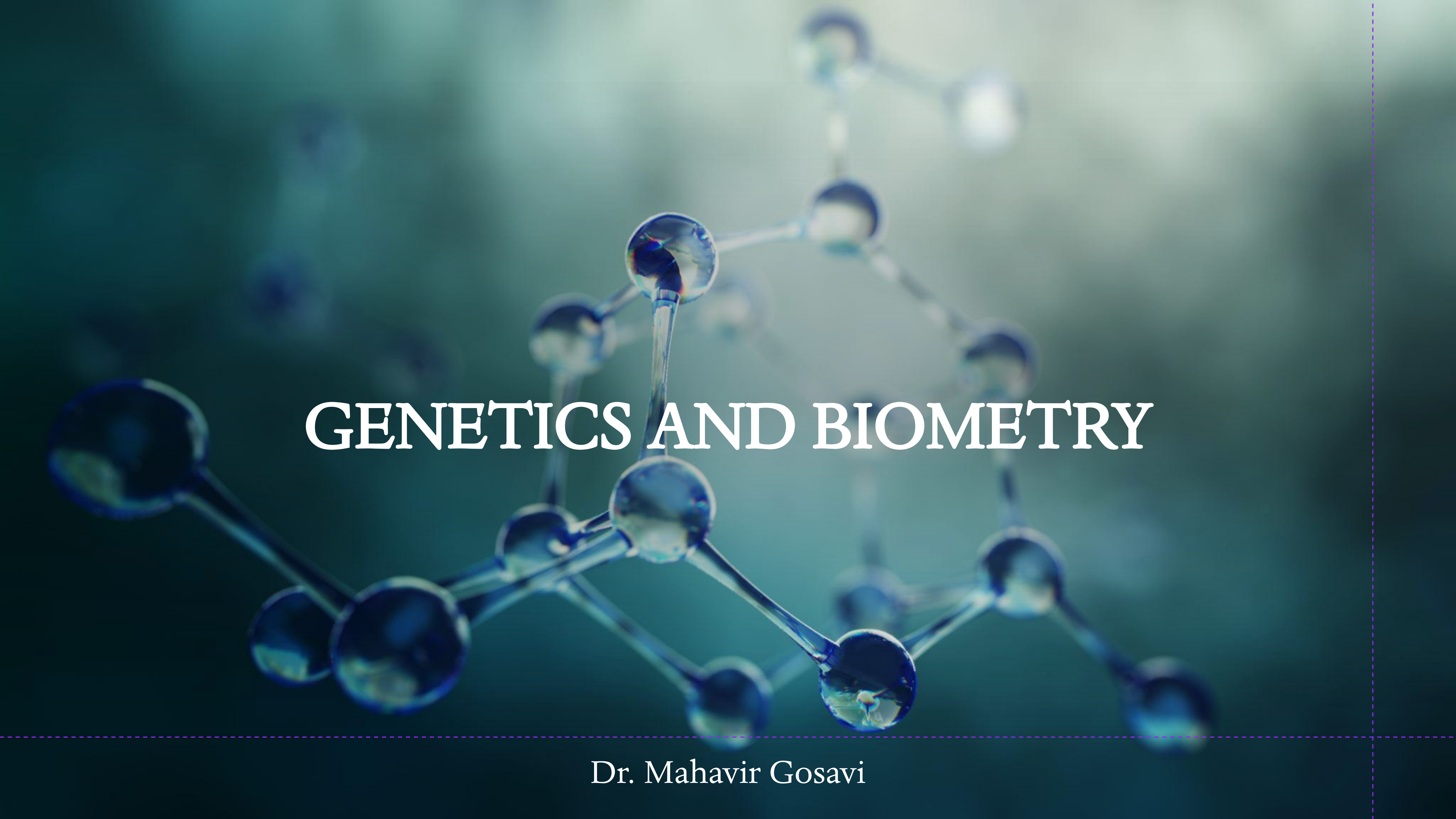
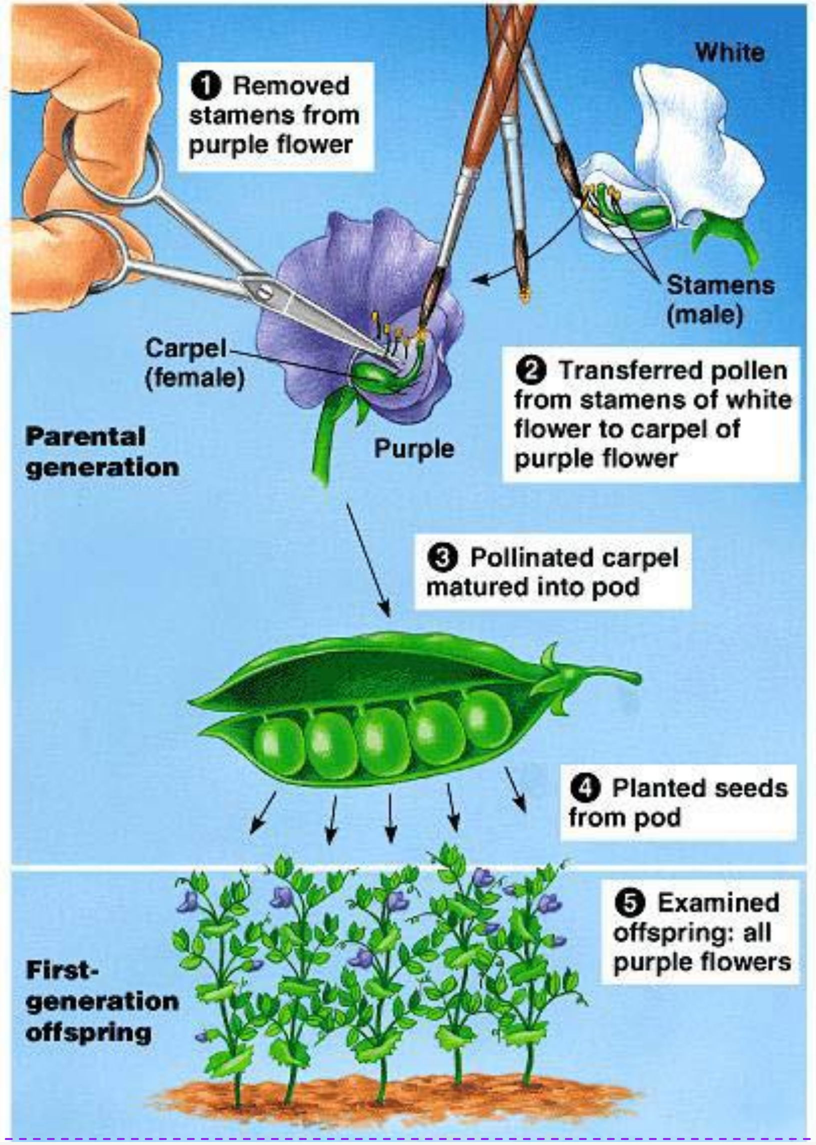


GENETICS AND BIOMETRY

Dr. Mahavir Gosavi

Mendelian concept of hereditary

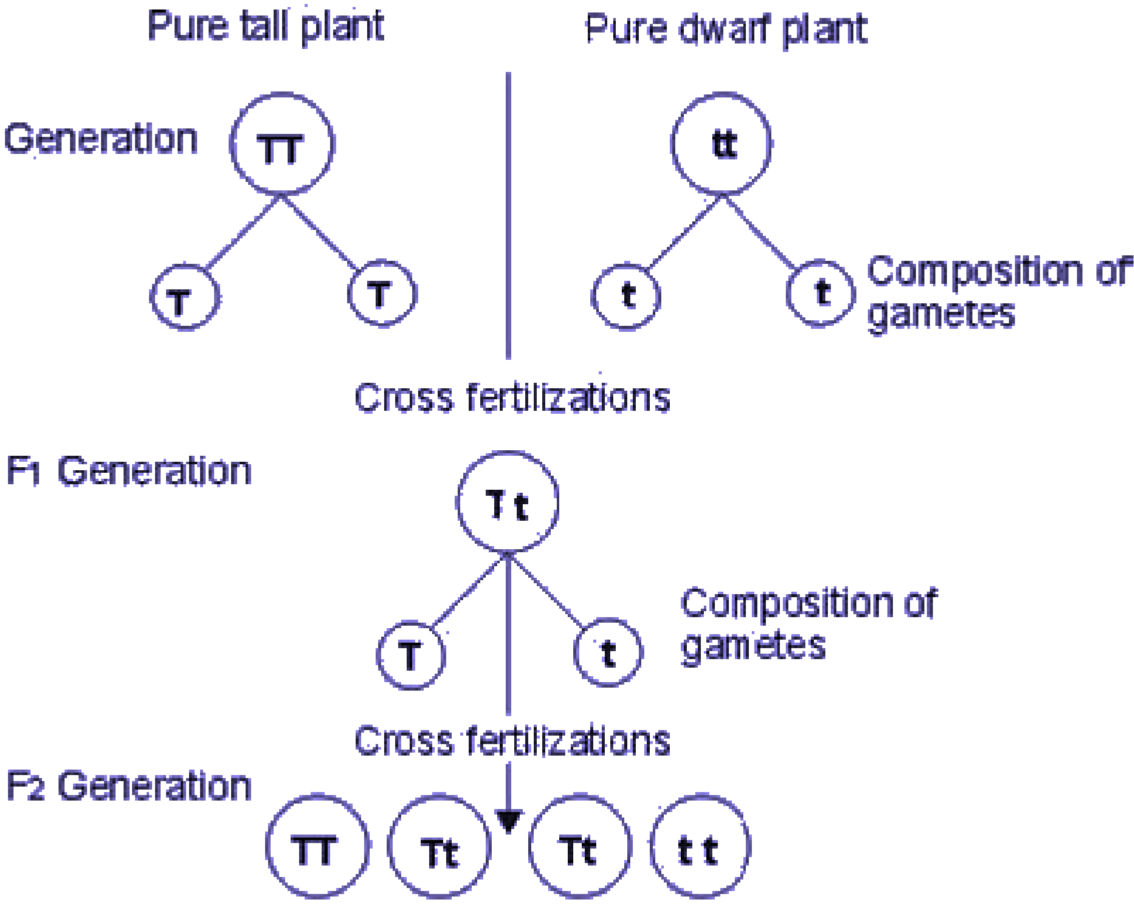


- The laws of inheritance were derived by Gregor Mendel, a 19th century monk conducting hybridization experiments in garden peas (*Pisum sativum*).
- Between 1856 and 1863, he cultivated and tested some 29,000 pea plants.
- From these experiments he deduced two generalizations which later became known as *Mendel's Laws of Heredity* or *Mendelian inheritance.*
- He described these laws in a two-part paper, "Experiments on Plant Hybridization" that he read to the Natural History Society of Bruno on February 8 and March 8, 1865, and which was published in 1866.

- His findings helped other scientists to predict the expression of traits based on probabilities.
- Main cause of his success is his decision to cross only true-breeding plants.
- He also measured only absolute characteristics, such as colour, shape, and position rather than quantitative characteristics.
- He expressed his results numerically and subjected them to statistical analysis. His method of data analysis and his large sample size gave credibility to his data.
- He also had the foresight to follow several successive generations (F_2, F_3) of pea plants and record their variations.
- Finally, he performed "test crosses" (backcrossing descendants of the initial hybridization to the initial true-breeding lines) to reveal the presence and proportion of recessive characters.
- Based on his work, he postulated 4 principles: (1) Principles of Paired Factors (2) Principle of Dominance (3) Law of Segregation or Law of Purity of Gametes (Mendel's First Law of Inheritance) and (4) Law of Independent Assortment (Mendel's Second Law of Inheritance).

1. Principles of Paired Factors

- A character is represented in an organism (diploid) by at least two factors.
- The two factors lie on the two homologous chromosomes at the same locus.
- They may represent the same (homologous, e.g., TT in case of pure tall pea plants) or alternate expression (heterozygous, e.g., Tt in case of hybrid tall pea plants) of the same character.
- Factors representing the alternate or same form of a character are called alleles or allelomorphs.



2. Principle of Dominance

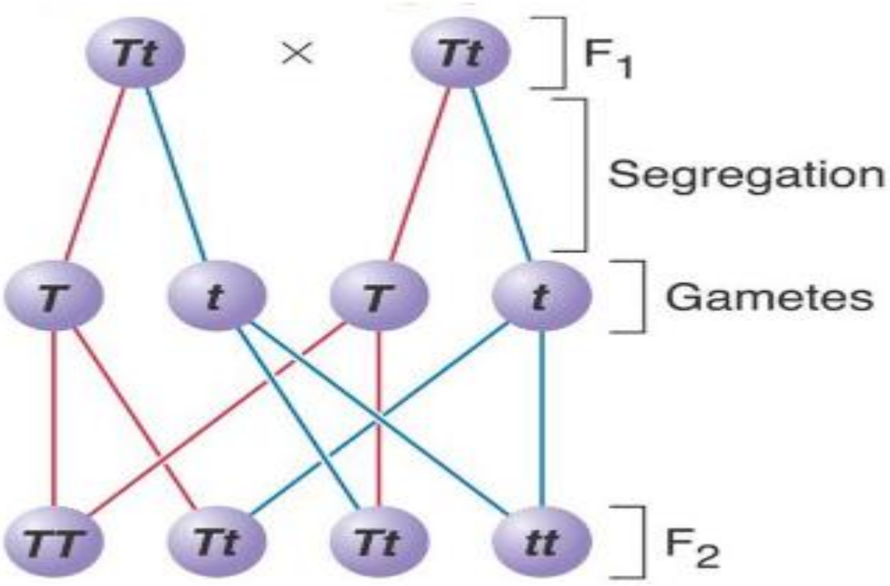
- "When two homozygous individuals with one or more sets of contrasting characters are crossed, the characters which appear in the hybrids of F_1 generation are always the dominant characters and those do not appear in F_1 offspring are always the recessive characters".
- During investigations of the principles of inheritance, Mendel crossed plants of a variety of *Pisum sativum* 6" tall with plants of a variety 1" in height on an average.
- When the seeds from this cross were planted, they produced plants not intermediate between the two parents, as might be expected, but all tall, like the 6" parent.

Parents: **Tall** **X** **Dwarf**

Genotype: TT tt

Gametes: (T) (t)

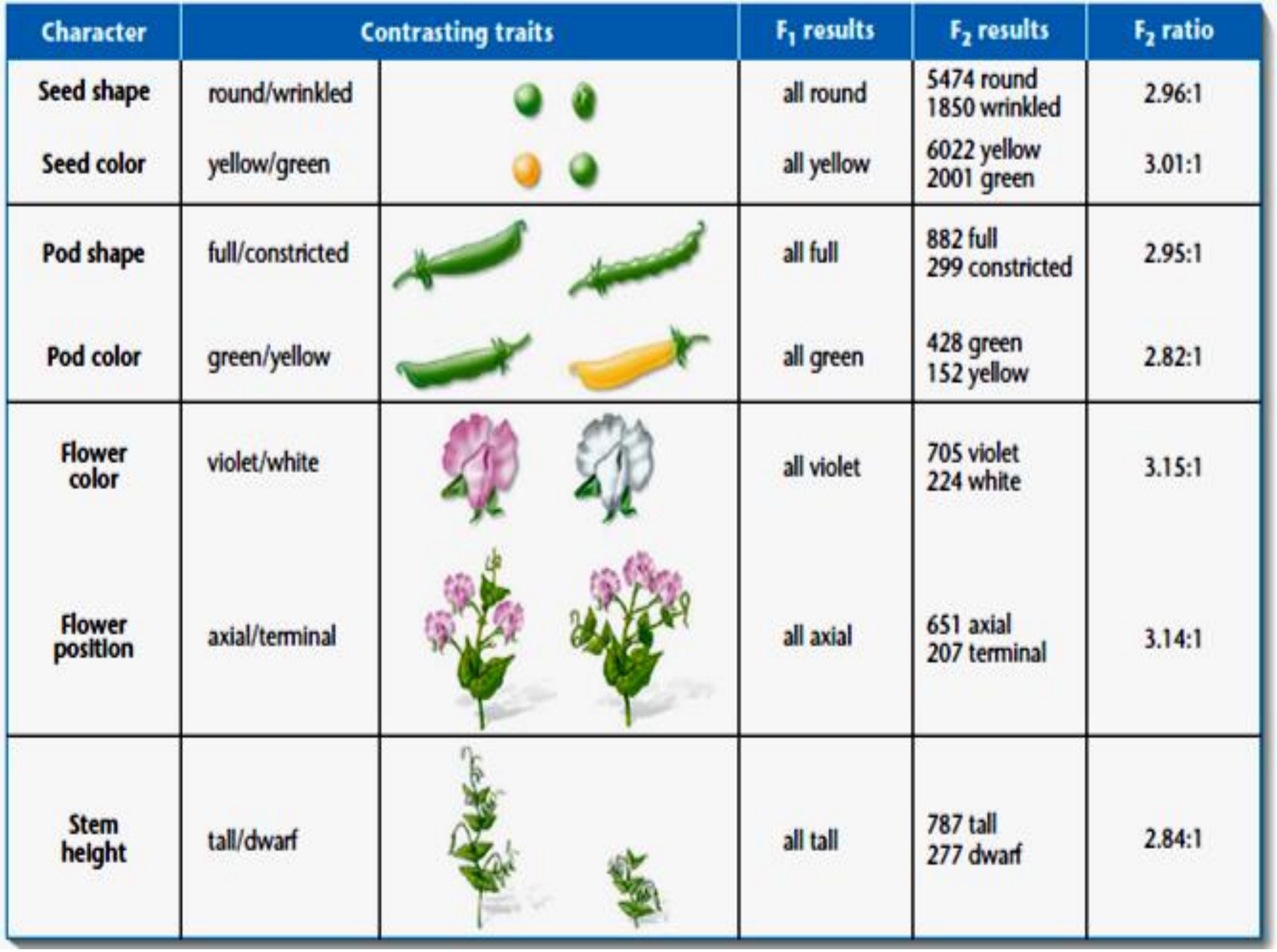
F_1 generation: Tt (Tall)



Mendel made crosses to study the inheritance of six other sets of characters and observed that in every case the hybrid resembled one of the parents with respect to the character.

It follows then that one factor or gene in a pair masks or inhibits the expression of the other.

Thus, in the cross described, the tall factor masks, or inhibits the expression of the dwarf factor in the F_1 ; therefore, the tall factor is called the dominant factor, and the dwarf factor is referred to as the recessive factor, or gene.

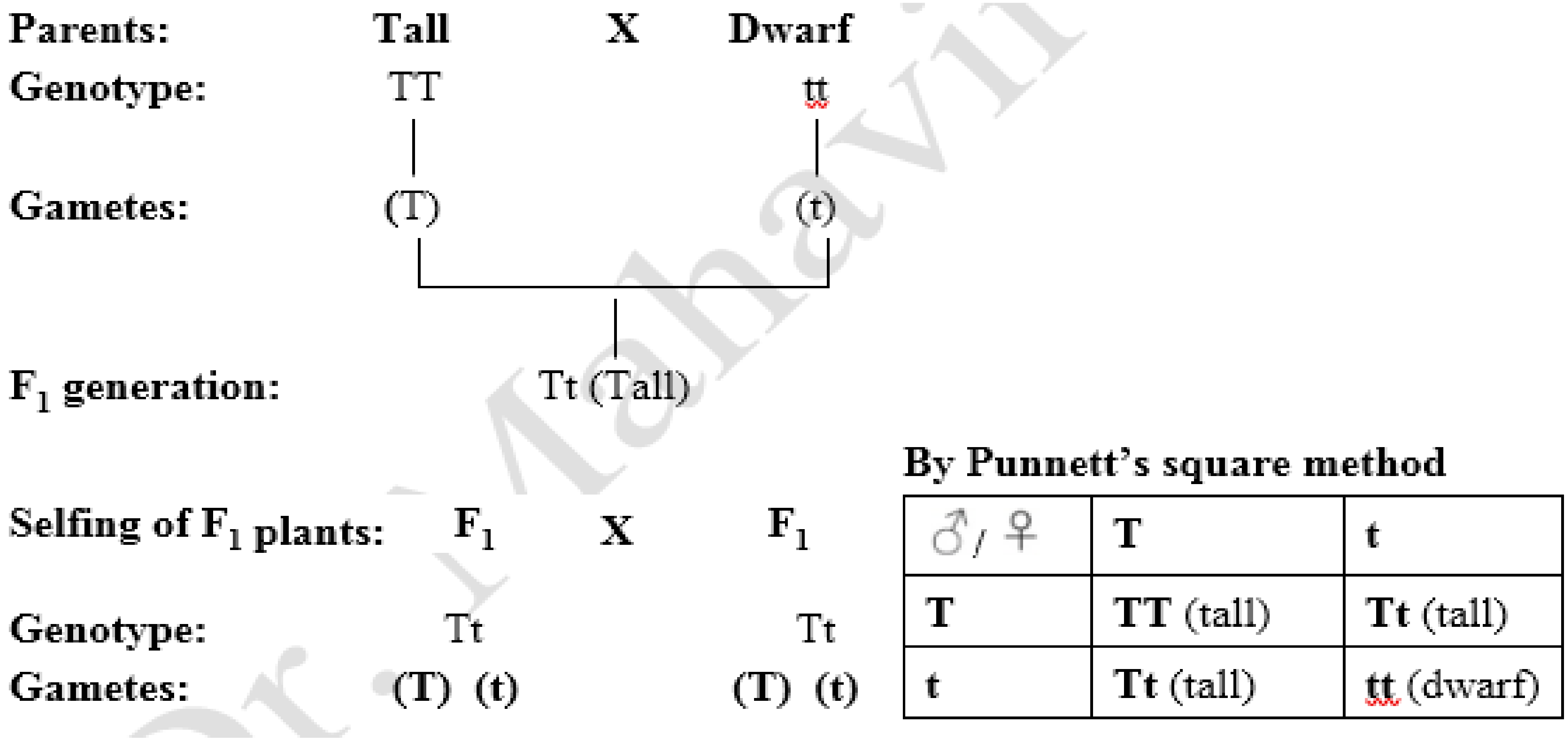


Character	Contrasting traits		F_1 results	F_2 results	F_2 ratio
Seed shape	round/wrinkled		all round	5474 round 1850 wrinkled	2.96:1
Seed color	yellow/green		all yellow	6022 yellow 2001 green	3.01:1
Pod shape	full/constricted		all full	882 full 299 constricted	2.95:1
Pod color	green/yellow		all green	428 green 152 yellow	2.82:1
Flower color	violet/white		all violet	705 violet 224 white	3.15:1
Flower position	axial/terminal		all axial	651 axial 207 terminal	3.14:1
Stem height	tall/dwarf		all tall	787 tall 277 dwarf	2.84:1

7 sets of characters that Mendel studied and classified as dominant and recessive

Monohybrid ratio

- When 2 pure plants differing in 1 character are crossed with each other, the cross is called monohybrid cross and its ratio in F_2 generation is monohybrid ratio which is always 3:1.
- Mendel crossed a tall plant of *Pisum sativum* with a dwarf plant; both were homozygous. All F_1 plants produced were tall (Heterozygous).
- When F_1 plants were selfed, F_2 generation were obtained. In the F_2 generation, out of 1064 plants observed, 787 were tall & 277 were dwarf, i.e. , 75% plants were tall & 25% plants were dwarf.
- Thus, the tall & dwarf plants occurred in the ratio 3:1. The character tallness is dominant as it appears in F_1 generation. So, the gene (factor) responsible for tallness is the dominant gene (T) while dwarfness is recessive as it is not seen in F_1 generation. So, the gene responsible for dwarfness is the recessive gene (t).



Parents: Tall X Dwarf

Genotype: TT tt

Gametes: (T) (t)

F_1 generation: Tt (Tall)

Selfing of F_1 plants: F_1 X F_1

Genotype: Tt Tt

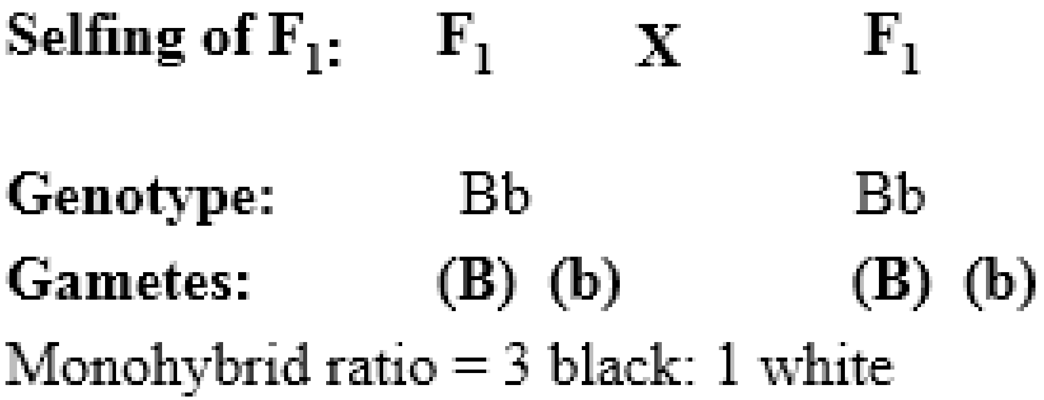
Gametes: (T) (t) (T) (t)

By Punnett's square method

♂/ ♀	**T**	**t**
T	**TT** (tall)	**Tt** (tall)
t	**Tt** (tall)	**tt** (dwarf)

- Phenotypic monohybrid ratio = 3:1, 3tall: 1 dwarf
- Genotypic monohybrid ratio = 1:2:1, 1pure tall: 2 hybrid tall: 1 pure dwarf

- The principle of monohybrid inheritance is not only applicable to plants but to the animals also. For e.g. , Coat colour in guinea pigs.
- **Parents:** **Black** **X** **White**
- **Genotype:** BB bb
- **Gametes:** (B) (b)
- **F_1 generation:** Bb (Black)

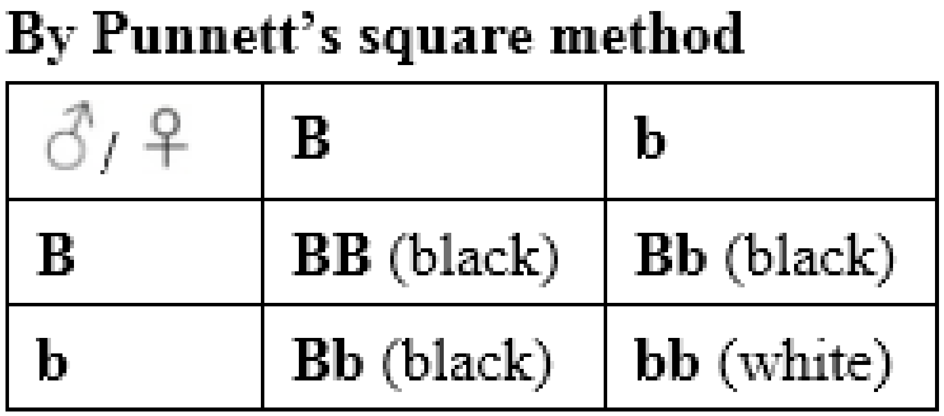


Selfing of F_1: **F_1** **X** **F_1**

Genotype: Bb Bb

Gametes: **(B) (b)** **(B) (b)**

Monohybrid ratio = 3 black: 1 white

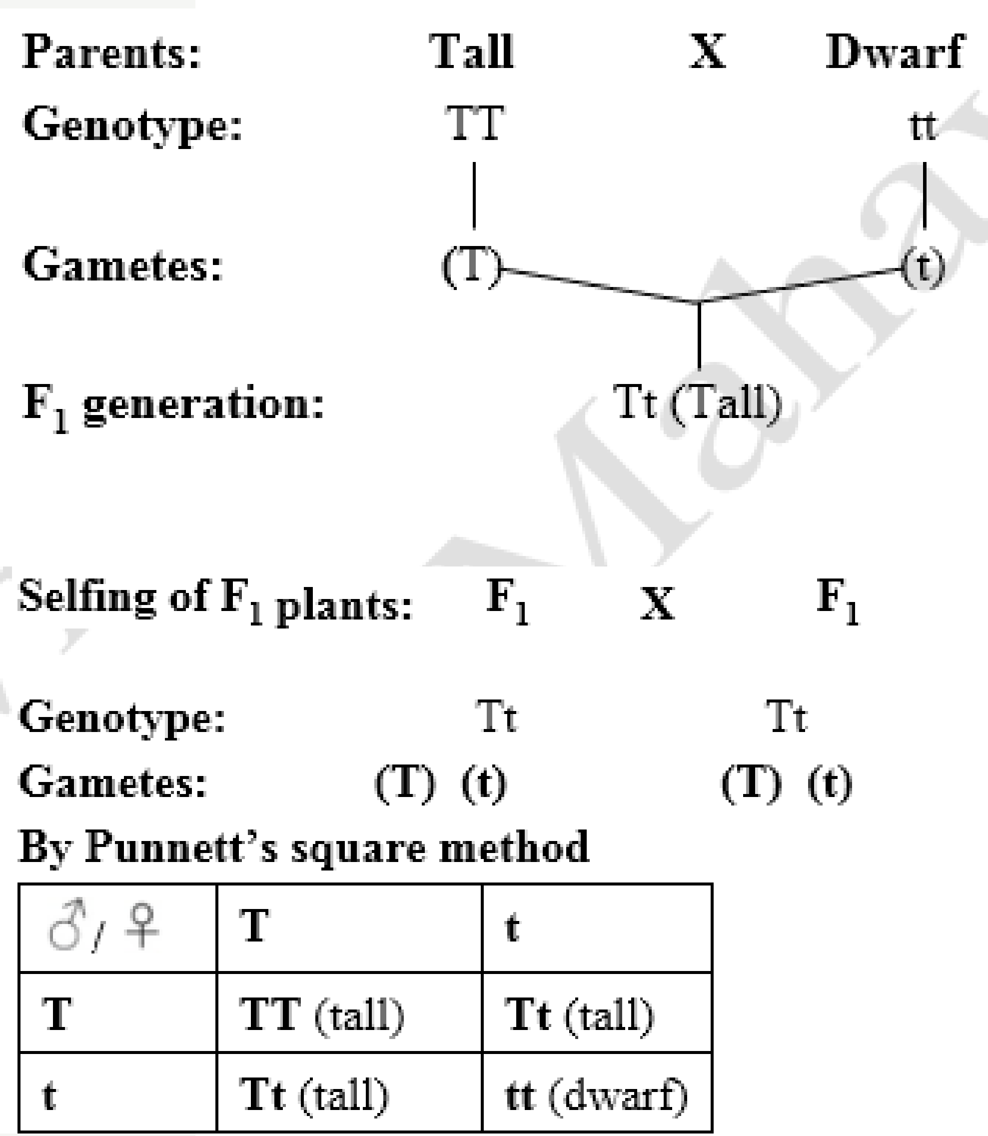


By Punnett's square method

♂/♀	**B**	**b**
B	**BB** (black)	**Bb** (black)
b	**Bb** (black)	**bb** (white)

3. Law of Segregation or Law of Purity of Gametes (Mendel's First Law of Inheritance)

- The two factors (alleles) of a trait which remain together in an individual do not get mixed up but keep their identity distinct, separate at the time of gametogenesis (i.e., gametes formation) or sporogenesis (i.e., spore formation), get randomly distributed to different gametes and then get paired again in different offspring's as per the principle of probability. Since two alleles remain together in pure form without mixing, affecting or blending each other, the law of segregation is also known as "law of purity of gametes".
- **Explanation:** When a dominant and a recessive allele of a gene come together in a hybrid after crossing between two plants having contrasting characters, they do not mix or blend together. They separate into different gametes in equal number. Each gamete has only one type of allele (either T or t). Separation of two alleles of a gene during gamete formation takes place usually due to the separation of homologous chromosomes during meiosis.
- The principle of the law of segregation can be explained by means of a monohybrid cross.



Parents: Tall X Dwarf

Genotype: TT tt

Gametes: (T) (t)

F_1 generation: Tt (Tall)

Selfing of F_1 plants: F_1 X F_1

Genotype: Tt Tt

Gametes: (T) (t) (T) (t)

By Punnett's square method

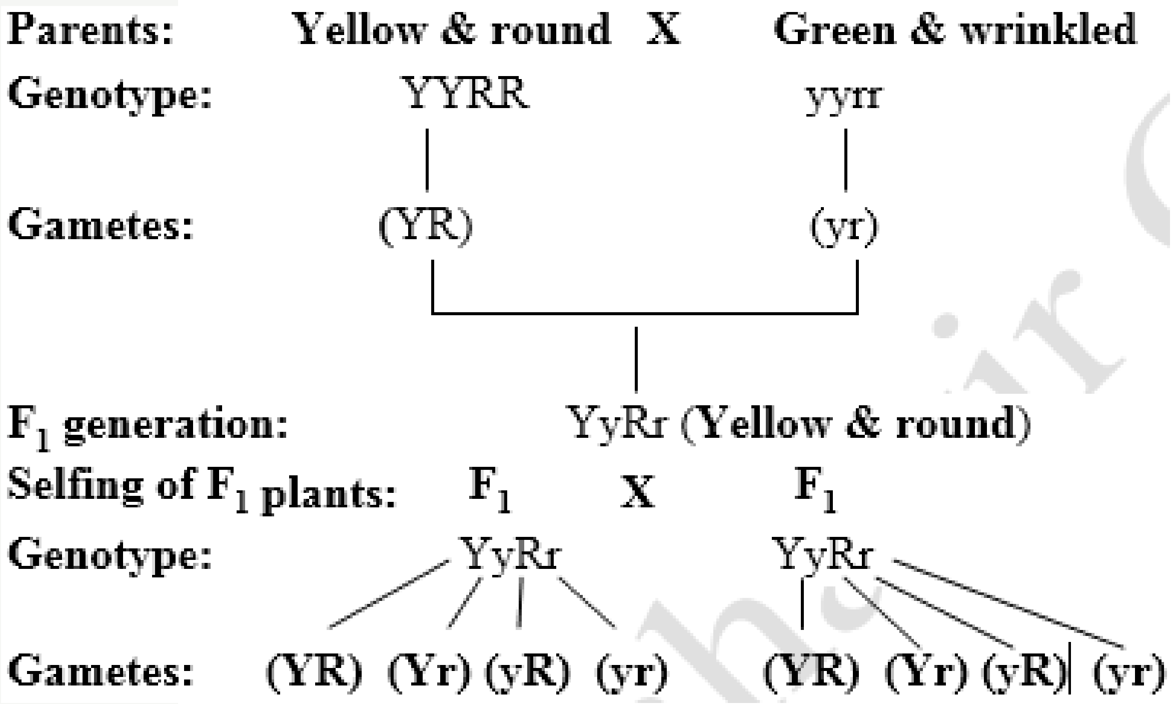
♂/ ♀	**T**	**t**
T	**TT** (tall)	**Tt** (tall)
t	**Tt** (tall)	**tt** (dwarf)

Monohybrid ratio = 3tall: 1 dwarf

- T = gene for tallness & t =gene for dwarfness.
- The factors always occur in pairs. Both plants crossed are "pure" and if self pollinated will always producing only tall and dwarf plants respectively.
- The tall parent (TT) X the dwarf parent (tt).
- Both produce gametes; contain only 1 factor; the tall (T), dwarf (t).
- The fusion of gametes produces a tall plant in the F_1, (Tt) is a heterozygous as it possess 1 allele for tallness and 1 for dwarfness.
- F_1 produce 2 kinds of gamete. 50% with (T) & 50% with (t).
- During fertilization these gametes unite at random & produce F_2 .
- As a result, phenotypic ratio - 3 tall plants : 1 dwarf plant (i.e., 3: 1) is obtained. All plants with TT and Tt are tall, and the plants with tt are dwarf.

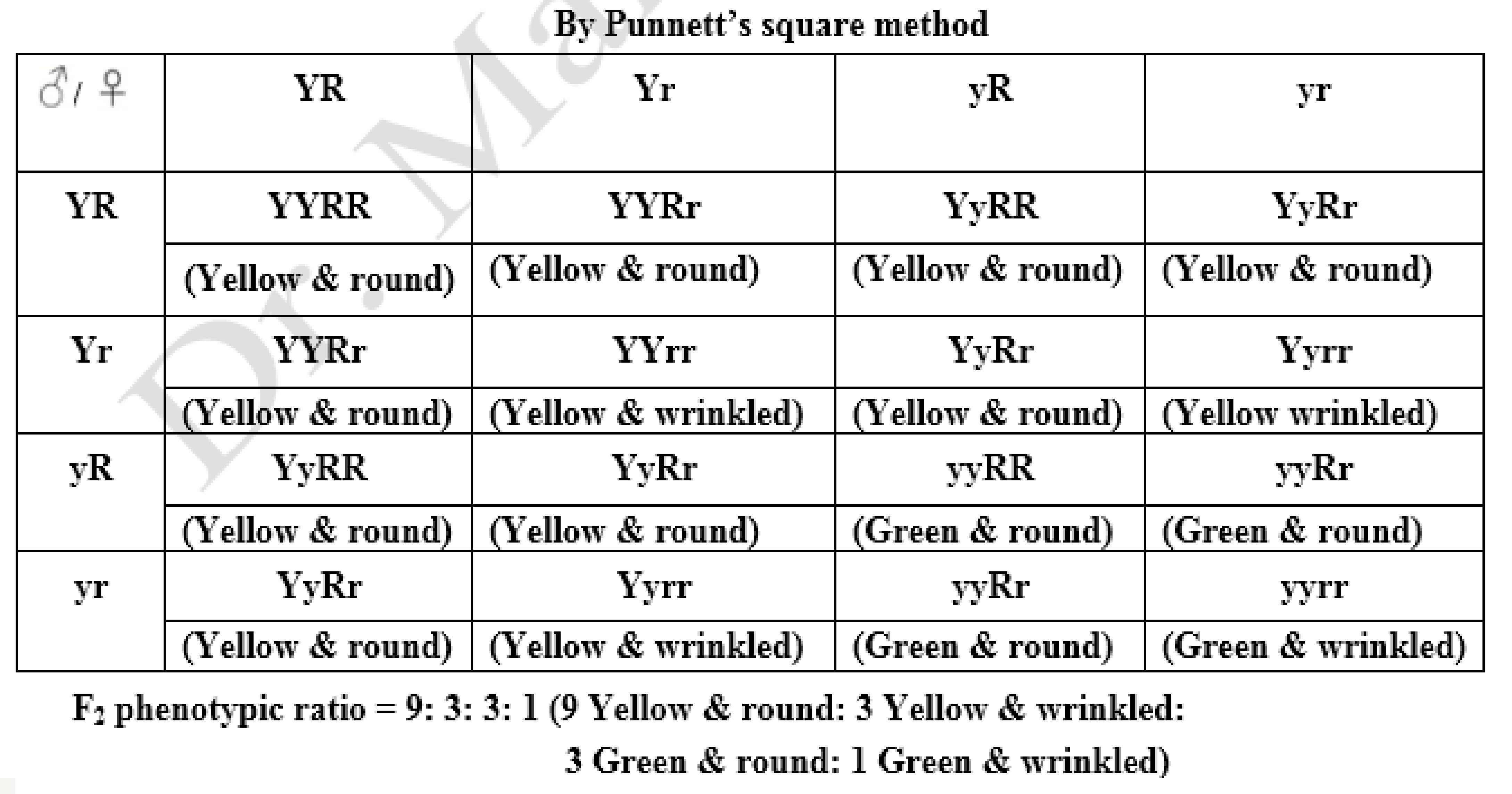
Dihybrid ratio

- When 2 pure plants differing in 2 character are crossed with each other, the cross is called dihybrid cross and its ratio in F_2 generation is dihybrid ratio which is always 9:3:3:1.
- Mendel worked out dihybrid crosses with his sweet pea plants. A cross between pure sweet pea plant having yellow cotyledons & round seeds with a pure sweet pea plant having green cotyledons & wrinkled seeds. It was the first example of dihybrid cross. In this example 2 pairs of contrasting characters viz. a) yellow & green seeds constitutes one pair of contrasting character where yellow seed colour is dominant over green and b) round & wrinkled seeds constitutes one pair of contrasting character where round shape is dominant over wrinkled.



In the dihybrid cross Mendel crossed pure (i.e., homozygous) plants of yellow cotyledons and round seed variety of pea with those having green cotyledons and wrinkled seed. He had already studied these characters and had observed that roundness was dominant over wrinkleless, and yellow colour of the cotyledons was dominant over green colour. One homozygous parent was expressed as YYRR (Yellow cotyledons and Round seed) and the other is expressed as yyrr (green cotyledons and wrinkled seed).

The former, as expected, produced gametes with YR genes, and the latter produced gametes with yr genes. The two kinds of gametes fuse to produce F_1 individual with genetic constitution YyRr. Phenotypically these individuals possess yellow cotyledons with round seeds because yellow colour is dominant over green & roundness is dominant over wrinkleless, and. F_1 individuals are thus heterozygous yellow and heterozygous round.



By Punnett's square method

♂/ ♀	YR	Yr	yR	yr
YR	YYRR	YYRr	YyRR	YyRr
	(Yellow & round)	(Yellow & round)	(Yellow & round)	(Yellow & round)
Yr	YYRr	YYrr	YyRr	Yyrr
	(Yellow & round)	(Yellow & wrinkled)	(Yellow & round)	(Yellow wrinkled)
yR	YyRR	YyRr	yyRR	yyRr
	(Yellow & round)	(Yellow & round)	(Green & round)	(Green & round)
yr	YyRr	Yyrr	yyRr	yyrr
	(Yellow & round)	(Yellow & wrinkled)	(Green & round)	(Green & wrinkled)

F_2 phenotypic ratio = 9: 3: 3: 1 (9 Yellow & round: 3 Yellow & wrinkled:
3 Green & round: 1 Green & wrinkled)

- When Mendel self-fertilized the F_1 individuals, 4 types of gametes were produced viz. YR, Yr, yR & yr due to independent assortment. In F_2 generation he observed plants of four kinds in the following phenotypic frequencies:
- a. Yellow & Round = 315 = 9/16.
- b. Yellow & wrinkled = 108 = 3/16.
- c. Green & Round = 101 = 3/16.
- d. Green & wrinkled = 32 = 1/16.
- Total = 556
- Thus, the four categories of plants appeared in approximate phenotypic ratio of 9: 3: 3: 1. (Called Mendel's dihybrid phenotypic Ratio). The most noteworthy feature of this dihybrid cross that struck Mendel was the appearance of two new categories of plants besides the parental ones i.e., Yellow wrinkled and Green round. These two new categories were in fact the recombination of the parental characters. This led Mendel to postulate the law of independent assortment. **It can also be proved by studying the individual character of seed colour and seed shape separately: Seed colour:** Yellow (9 + 3 = 12): Green (3 + 1 = 4) or 3: 1 & **Seed Shape:** Round (9 + 3 = 12): Wrinkled (3 + 1 = 4) or 3: 1, the result of each character is like the monohybrid ratio.

4. Law of Independent Assortment (Mendel's Second Law of Inheritance)

- According to this law "the 2 factors (genes) of each contrasting character (trait) assort or separate independently of the factors of other characters at the time of gamete formation and get randomly rearranged in the offspring".

- **Explanation:** This law explains simultaneous inheritance of two plant characters. In F_1 when two genes controlling two different characters, come together, each gene exhibits independent dominant behaviour without affecting or modifying the effect of other gene. These gene pairs segregate during gamete formation independently. The alleles of one gene can combine freely with the alleles of another gene. Thus, each allele of a gene has an equal chance to combine with each allele of another gene. Each of the two gene pairs when considered separately, exhibits typical 3: 1 segregation ratio in F_2 generation. This is a typical dihybrid segregation ratio. Random or free assortment of alleles of two genes leads to formation of new gene combinations.

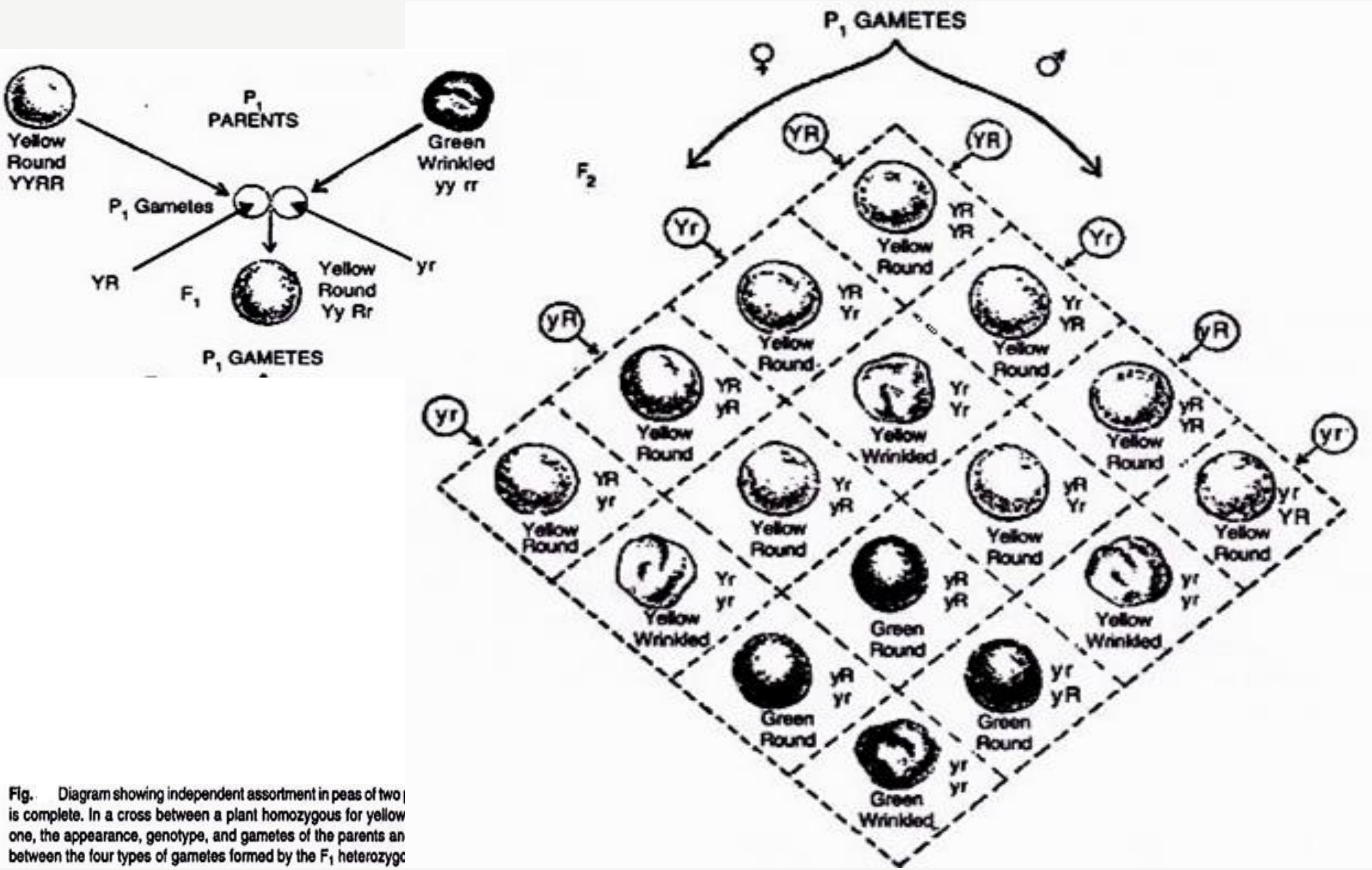


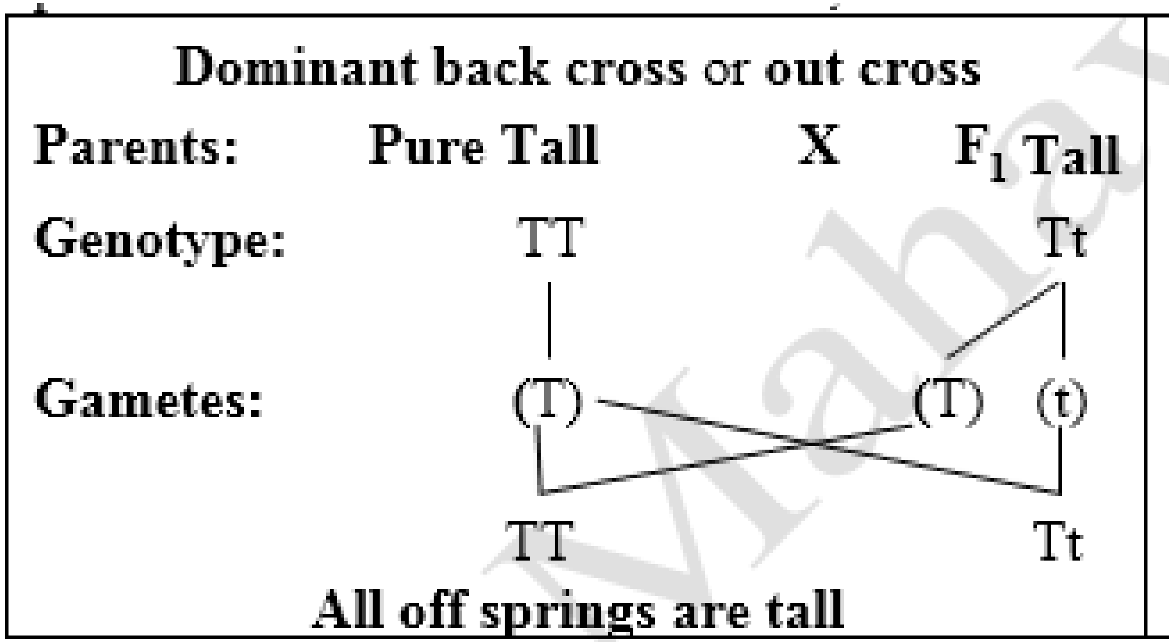
Fig. Diagram showing independent assortment in peas of two p
is complete. In a cross between a plant homozygous for yellow
one, the appearance, genotype, and gametes of the parents an
between the four types of gametes formed by the F_1 heterozygo

Rediscovery of Mendel's work

- Mendel's conclusions were largely ignored. Although they were not completely unknown to biologists of the time, they were not seen as generally applicable, even by Mendel himself, who thought they only applied to certain categories of species or traits.
- A major block to understanding their significance was the importance attached by 19th century biologists to the apparent blending of inherited traits in the overall appearance of the progeny, now known to be due to multigene interactions, in contrast to the organ-specific binary characters studied by Mendel. In 1900, however, his work was "rediscovered" by three European scientists, Hugo de Vries, Carl Correns, and Erich von Tschermak. The exact nature of the "rediscovery" has been somewhat debated.
- Regardless, the "rediscovery" made Mendelism an important but controversial theory. Its most vigorous promoter in Europe was William Bateson, who coined the term "genetics", "gene", and "allele" to describe many of its tenets.
- Many biologists also dismissed the theory because they were not sure it would apply to all species, and there seemed to be very few true Mendelian characters in nature.
- However, later work by biologists and statisticians such as R.A. Fisher showed that if multiple Mendelian factors were involved in the expression of an individual trait, they could produce the diverse results observed.
- Thomas Hunt Morgan and his assistants later integrated the theoretical model of Mendel with the chromosome theory of inheritance, in which the chromosomes of cells were thought to hold the actual hereditary material, and create what is now known as classical genetics, which was extremely successful and cemented Mendel's place in history.

Back cross & test cross

- When heterozygous F_1 individuals are crossed with one of its homozygous parents, across is known as **back cross**. When the F_1 hybrid is crossed with the homozygous dominant parent, then the cross is known as **dominant back cross** or **out cross**. All the resulting off springs will possess the dominant character i.e., 100% dominant character.

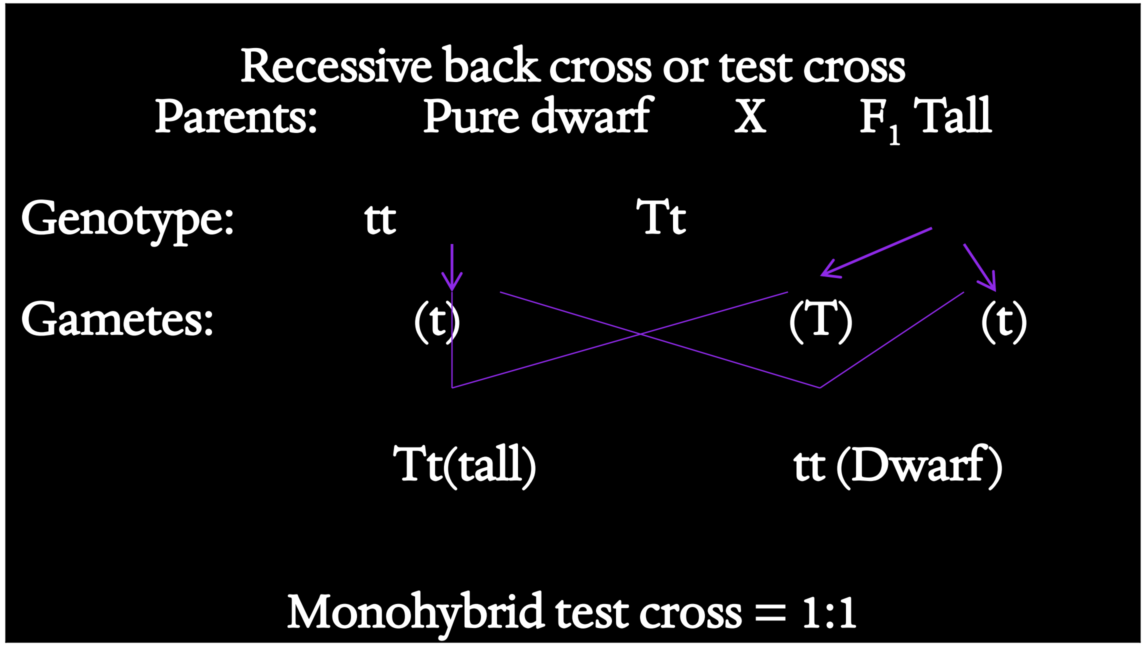


Dominant back cross or out cross

All off springs are tall

Monohybrid test cross

- When the F_1 hybrid is crossed with the homozygous recessive parent, then the cross is known as **recessive back cross** or **test cross**. In this cross 2 types of off springs are obtained in equal numbers i.e., 50% dominant character & 50% recessive character, in the ratio 1: 1. This cross helps to identify the heterozygosity of the hybrid. Hence it is called test cross.



Recessive back cross or test cross

Parents: Pure dwarf X F_1 Tall

Genotype: tt Tt

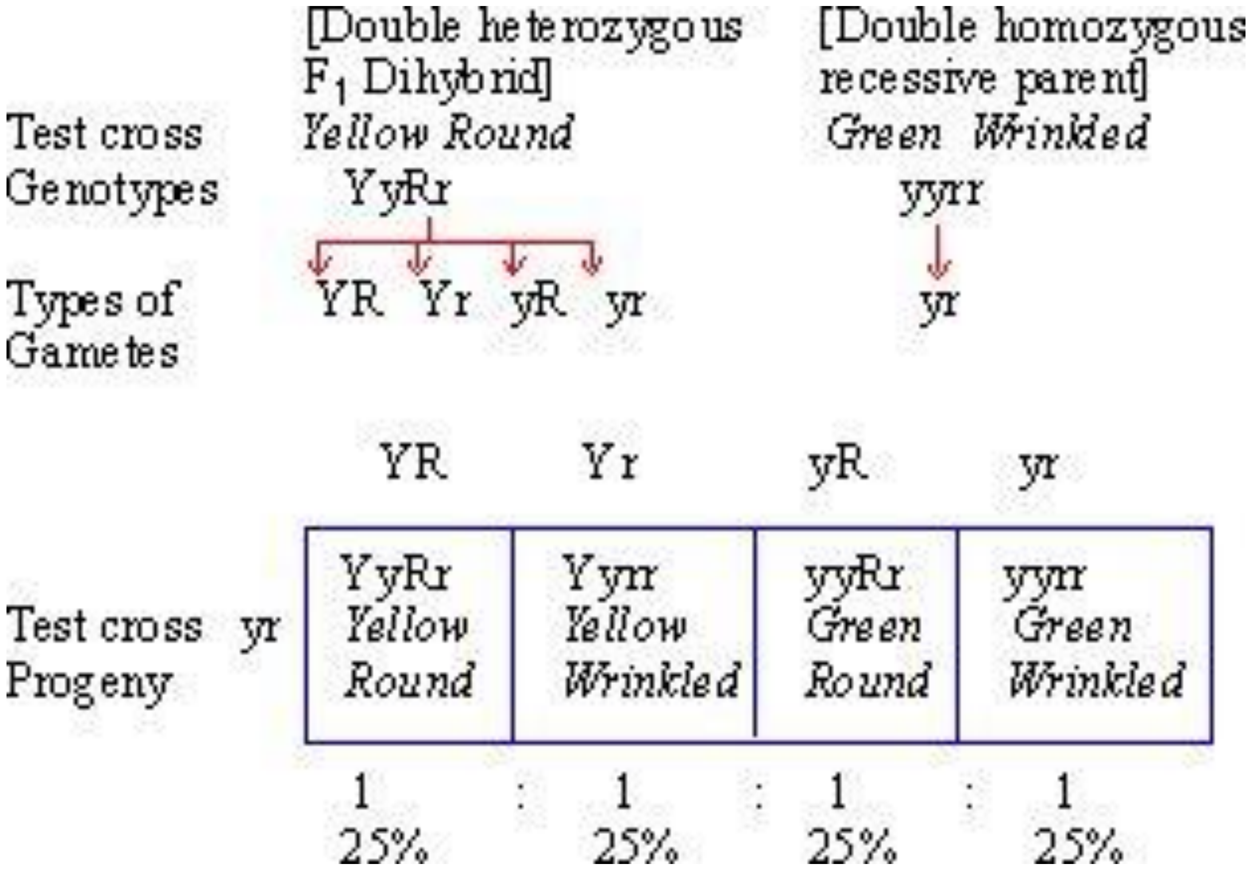
Gametes: (t) (T) (t)

Tt(tall) tt (Dwarf)

Monohybrid test cross = 1:1

Dihybrid test cross

- It involves crossing of F_1 dihybrid with double homozygous recessive parent. For eg., when F_1 dihybrid Yellow & round (YyRr) pea plants are crossed with double homozygous recessive Green & wrinkled pea plants (yyrr). 4 types of off springs are obtained in equal numbers i.e., 25% Yellow & round, 25% Yellow & wrinkled, 25% Green & round & 25% Green & wrinkled, in the ratio 1: 1: 1: 1.



	[Double heterozygous F_1 Dihybrid]	[Double homozygous recessive parent]
Test cross Genotypes	*Yellow Round* YyRr	*Green Wrinkled* yyrr
Types of Gametes	YR Yr yR yr	yr

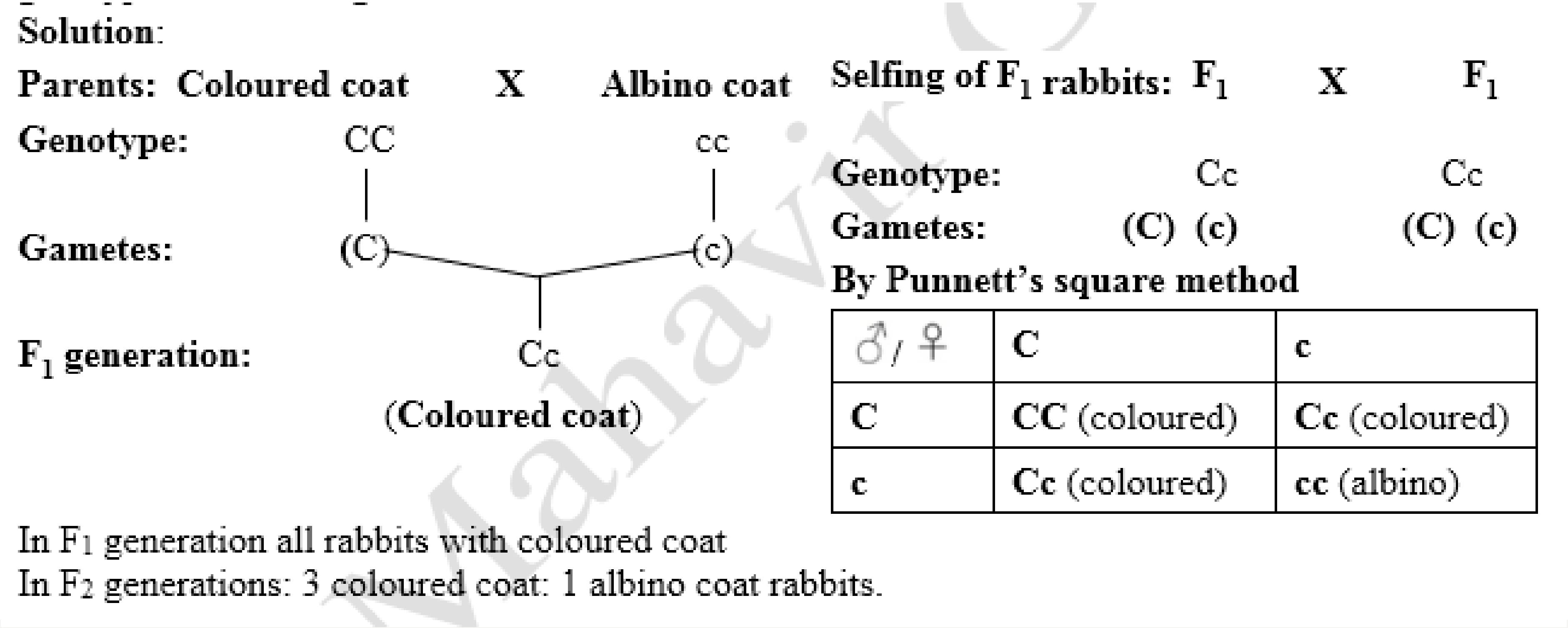
	YR	Yr	yR	yr
Test cross Progeny yr	YyRr *Yellow Round*	Yyrr *Yellow Wrinkled*	yyRr *Green Round*	yyrr *Green Wrinkled*
	1 25%	: 1 25%	: 1 25%	: 1 25%

Significance of test cross

- 1. The test cross method is very useful to breeders & geneticists in determining genotypic constitution of any plant.
- 2. It helps to determine whether the dominant character of F_1 offspring is due to homozygous or heterozygous condition. So, it helps to determine unknown genotype of an individual.
- 3. It helps in determination of linked genes.
- 4. It maintains parental genotype by crossing it back to parents.

Problems based on monohybrid & dihybrid ratio

1) In rabbit, the coloured coat (C) is dominant over albino coat(c). What types of off springs would you expect if you cross a pure line coloured rabbit with an albino rabbit? Show both genotypes in F_1 & F_2 generations.



Solution:

Parents: Coloured coat X Albino coat

Genotype: CC cc

Gametes: (C) (c)

F_1 generation: Cc

(Coloured coat)

Selfing of F_1 rabbits: F_1 X F_1

Genotype: Cc Cc

Gametes: **(C) (c)** **(C) (c)**

By Punnett's square method

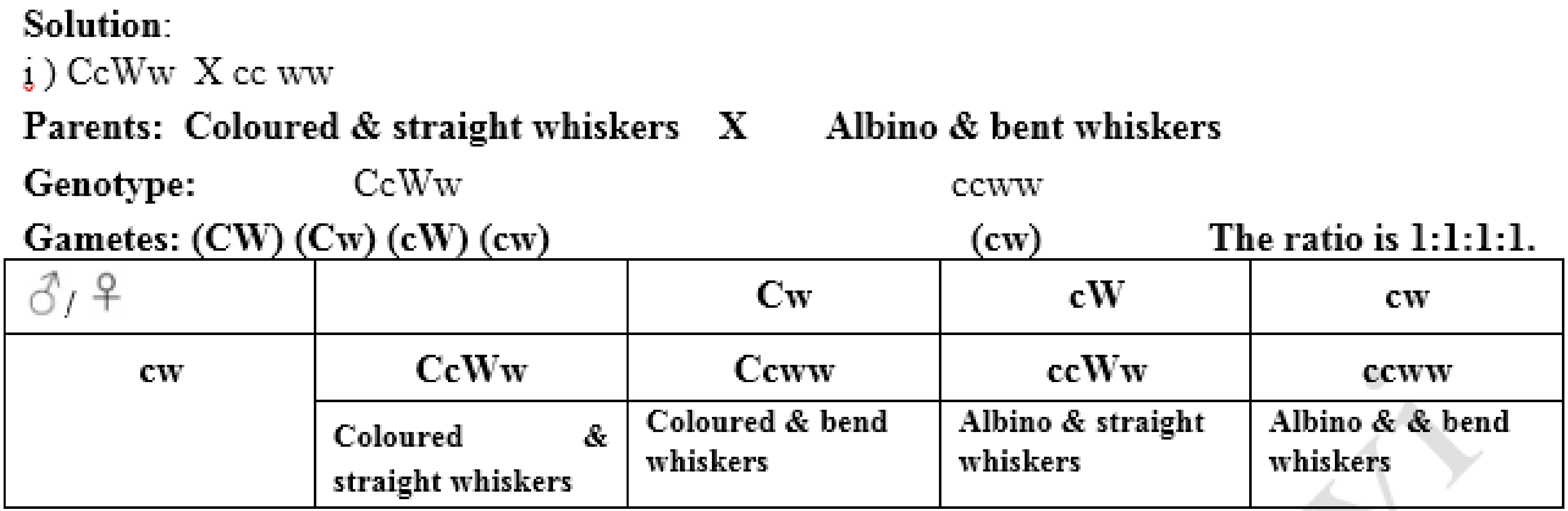
♂/♀	**C**	**c**
C	**CC** (coloured)	**Cc** (coloured)
c	**Cc** (coloured)	**cc** (albino)

In F_1 generation all rabbits with coloured coat

In F_2 generations: 3 coloured coat: 1 albino coat rabbits.

2) In the mice, gene for coloured coat (C) is dominant over albino coat(c) & the gene for straight whiskers (W) is dominant over that for bent whiskers (w). Find out the phenotypes of the following crosses.

i) CcWw X cc ww, ii) Ccww X ccWw, iii) CcWw X CcWw.



Solution:

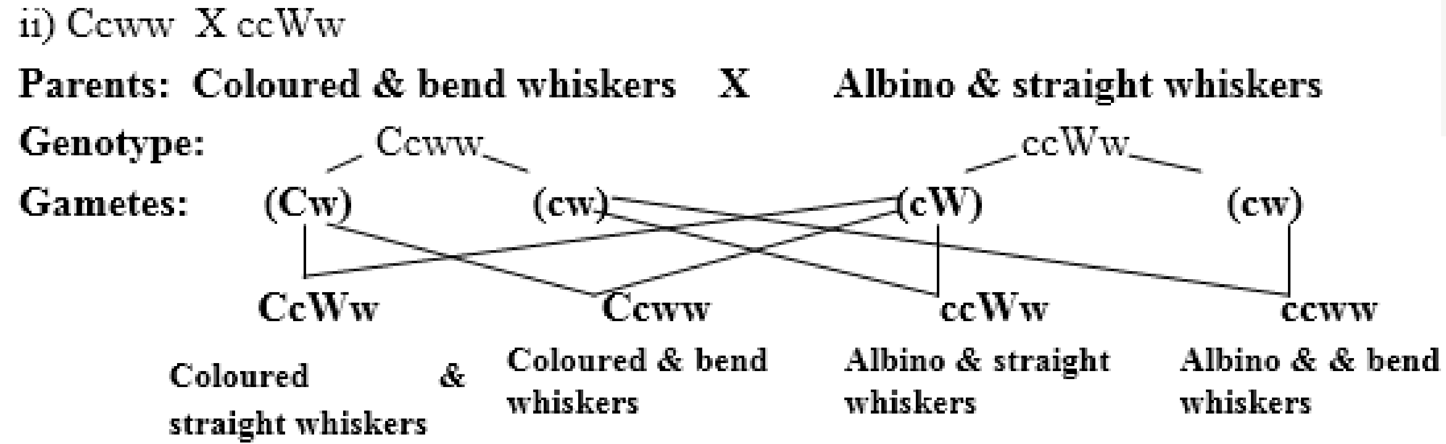
i) CcWw X cc ww

Parents: Coloured & straight whiskers X Albino & bent whiskers

Genotype: CcWw ccww

Gametes: (CW) (Cw) (cW) (cw) **(cw)** **The ratio is 1:1:1:1.**

♂/♀		Cw	cW	cw
cw	CcWw	Ccww	ccWw	ccww
	Coloured & straight whiskers	Coloured & bend whiskers	Albino & straight whiskers	Albino & & bend whiskers



ii) Ccww X ccWw

Parents: Coloured & bend whiskers X Albino & straight whiskers

Genotype: Ccww ccWw

Gametes: (Cw) (cw) (cW) (cw)

CcWw Ccww ccWw ccww

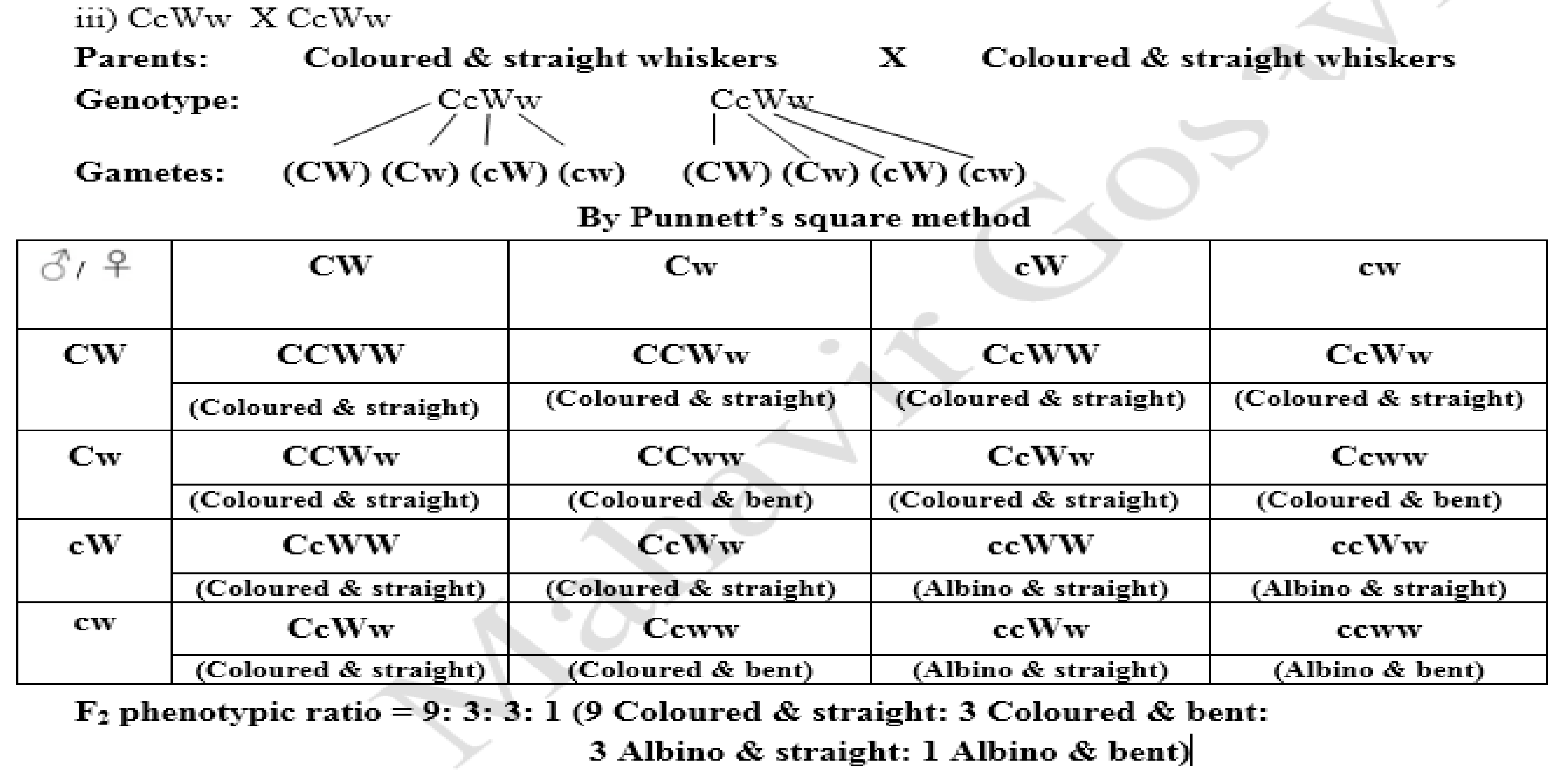
Coloured & straight whiskers

Coloured & bend whiskers

Albino & straight whiskers

Albino & & bend whiskers

The ratio is 1:1:1:1.



iii) CcWw X CcWw

Parents: Coloured & straight whiskers X Coloured & straight whiskers

Genotype: CcWw CcWw

Gametes: (CW) (Cw) (cW) (cw) (CW) (Cw) (cW) (cw)

By Punnett's square method

♂/ ♀	CW	Cw	cW	cw
CW	CCWW (Coloured & straight)	CCWw (Coloured & straight)	CcWW (Coloured & straight)	CcWw (Coloured & straight)
Cw	CCWw (Coloured & straight)	CCww (Coloured & bent)	CcWw (Coloured & straight)	Ccww (Coloured & bent)
cW	CcWW (Coloured & straight)	CcWw (Coloured & straight)	ccWW (Albino & straight)	ccWw (Albino & straight)
cw	CcWw (Coloured & straight)	Ccww (Coloured & bent)	ccWw (Albino & straight)	ccww (Albino & bent)

F$_2$ phenotypic ratio = 9: 3: 3: 1 (9 Coloured & straight: 3 Coloured & bent: 3 Albino & straight: 1 Albino & bent)

More problems for practice

3) What will be the result in F_1 generation when a homozygous white male rabbit (BB) is crossed with a homozygous black female rabbit (bb)? Also work out the test cross.

4) In Drosophila, vestigial wings (*vg vg*) & ebony colour (*eb eb*) are due to 2 separate recessive genes. The dominant alleles are normal (long) wings (vg^+ vg^+) & normal (gray) body colour (eb^+ eb^+). i) What types of off springs are expected in F_1 & F_2 generations from a cross between vestigial ebony female & a homozygous normal male? Show complete genotype & phenotype of both generations. ii) If a vestigial winged female who is heterozygous for gray body colour (*vg vg*, eb^+ *eb*) is crossed with ebony male who is heterozygous for long wings (vg^+ *vg*, *eb eb*), what will be the result of this cross?

5) In tomatoes, yellow fruits (rr) & dwarfed vine (tt) are recessive to red fruits (RR) & tall vine (TT). If pollen from a pure dwarf plant with red fruits (ttRR) is placed on the pistil of a pure tall plant with yellow fruits (TTrr). What types of off springs are expected in F_1 & F_2 generations from a cross?

3) What will be the result in F_1 generation when a homozygous white male rabbit (BB) is crossed with a homozygous black female rabbit (bb)? Also work out the test cross.

- **Parents:** **Black** **X** **White**
- **Genotype:** bb BB
- **F_1 generation:** Bb (white)

Selfing of F_1: **F_1** **X** **F_1**

Genotype: Bb Bb

Gametes: **(B) (b)** **(B) (b)**

♂/♀	B	b
B	BB (white)	Bb (white)
b	Bb (white)	Bb (black)

3 white : 1 black

Test cross

F1 X Homozygous Black parent

(Bb) (bb)

(B) (b) (b)

♂/♀	B	b
b	Bb (white)	Bb (black)

1 white: 1black

4) In Drosophila, vestigial wings (*vg vg*) & ebony colour (*eb eb*) are due to 2 separate recessive genes. The dominant alleles are normal (long) wings ($vg^+\ vg^+$) & normal (gray) body colour ($eb^+\ eb^+$). i) What types of off springs are expected in F_1 & F_2 generations from a cross between vestigial ebony female & a homozygous normal male? Show complete genotype & phenotype of both generations. ii) If a vestigial winged female who is heterozygous for gray body colour (*vg vg*, $eb^+\ eb$) is crossed with ebony male who is heterozygous for long wings ($vg^+\ vg$, *eb eb*), what will be the result of this cross?

Solution i

- Parents: long wings & gray body X vestigial wings & ebony colour
- Genotype: ($vg^+\ vg^+\ eb^+\ eb^+$) (*vg vg eb eb*)
- Gametes: ($vg^+\ eb^+$) (*vg eb*)
- F1 generation: ($vg^+ vg\ eb^+ eb$) = long wings & gray body
- F1 selfed: ($vg^+ vg\ eb^+ eb$) X ($vg^+ vg\ eb^+ eb$)
- Gametes: ($vg^+ eb^+$) ($vg^+\ eb$) ($vg\ eb^+$) (*vg eb*) ($vg^+ eb^+$) ($vg^+\ eb$) ($vg\ eb^+$) (*vg eb*)

♂/♀	$vg^+ eb^+$	$vg^+ eb$	$vg\ eb^+$	$vg\ eb$
$vg^+ eb^+$	$vg^+ vg^+ eb^+ eb^+$ Long wing & gray body	$vg^+ vg^+ eb^+ eb$ Long wing & gray body	$vg^+ vg\ eb^+ eb^+$ Long wing & gray body	$vg^+ vg\ eb^+ eb$ Long wing & gray body
$vg^+ eb$	$vg^+ vg^+ eb^+ eb$ Long wing & gray body	$vg^+ vg^+ eb\ eb$ Long wing & ebony body	$vg^+ vg\ eb^+ eb$ Long wing & gray body	$vg^+ vg\ eb\ eb$ Long wing & ebony body
$vg\ eb^+$	$vg^+ vg\ eb^+ eb^+$ Long wing & gray body	$vg^+ vg\ eb^+ eb$ Long wing & gray body	$Vg\ vg\ eb^+ eb^+$ Vestigeal wings & gray body	$vg\ vg\ eb^+ eb$ Vestigeal wings & gray body
$vg\ eb$	$vg^+ vg\ eb^+ eb$ Long wing & gray body	$vg^+ vg\ eb\ eb$ Long wing & ebony body	$vg\ vg\ eb^+ eb$ Vestigeal wings & gray body	$vg\ vg\ eb\ eb$ Vestigeal wings & ebony body

9 Long wing & gray body : 3 Long wing & ebony body: 3 Vestigeal wings & gray body: 1 Vestigeal wings & ebony body

4. ii) If a vestigial winged female who is heterozygous for gray body colour ($vg\ vg,\ eb^+\ eb$) is crossed with ebony male who is heterozygous for long wings ($vg^+\ vg,\ eb\ eb$), what will be the result of this cross?

Solution ii:

- Parents: vestigial wings & gray body X long wings & ebony body
- Genotype: ($vg\ vg,\ eb^+\ eb$) ($vg^+\ vg,\ eb\ eb$)
- Gametes: ($vg,\ eb^+$) ($vg,\ eb$) ($vg^+,\ eb$) ($vg,\ eb$)

♂/♀	$vg,\ eb^+$	$vg,\ eb$
$vg^+,\ eb$	$vg^+vg,\ eb^+eb$	$vg^+vg,\ eb\ eb$
	Long wing & gray body	Long wing & ebony body
$vg,\ eb$	$vg\ vg,\ eb^+\ eb$	$vg\ vg,\ eb\ eb$
	Vestigeal wings & gray body	Vestigeal wings & ebony body

1 Long wing & gray body : 1 Long wing & ebony body: 1 Vestigeal wings & gray body: 1 Vestigeal wings & ebony body

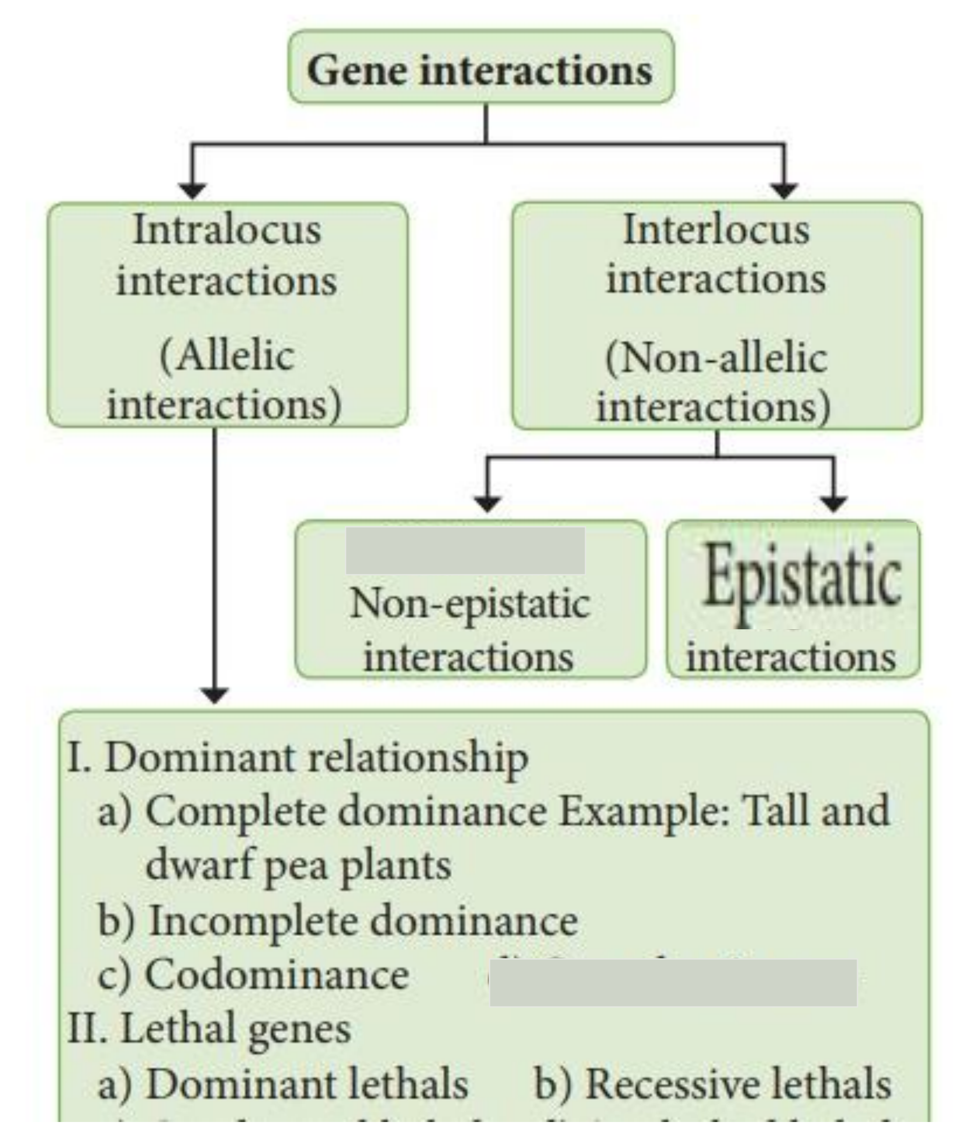
5) In tomatoes, yellow fruits (rr) & dwarfed vine (tt) are recessive to red fruits (RR) & tall vine (TT). If pollen from a pure dwarf plant with red fruits (ttRR) is placed on the pistil of a pure tall plant with yellow fruits (TTrr). What types of off springs are expected in F_1 & F_2 generations from a cross?

- Parents: dwarf plant with red fruits X tall plant with yellow fruits
- Genotype: (ttRR) (TTrr)
- Gametes: (tR) (Tr)

- F1 generation: (*TtRr*) = tall plant & red fruits
- F1 selfed: (*TtRr*) X (*TtRr*)
- Gametes: (*TR*) (*Tr*) (tR) (tr) (*TR*) (*Tr*) (tR) (tr)

♂/ ♀	TR	Tr	tR	tr
TR	TTRR	TTRr	TtRR	TtRr
	Tall plant & red fruits	Tall plant & red fruits	Tall plant & red fruits	Tall plant & red fruits
Tr	TTRr	TTrr	TtRr	Ttrr
	Tall plant & red fruits	Tall plant & yellow fruits	Tall plant & red fruits	Tall plant & yellow fruits
tR	TtRR	TtRr	ttRR	ttRr
	Tall plant & red fruits	Tall plant & red fruits	Dwarf plant & red fruits	Dwarf plant & red fruits
tr	TtRr	Ttrr	ttRr	ttrr
	Tall plant & red fruits	Tall plant & yellow fruits	Dwarf plant & red fruits	Dwarf plant & yellow fruits

9 Tall plant & red fruits: 3 Tall plant & yellow fruits: 3 Dwarf plant & red fruits: 1 Dwarf plant & yellow fruits



Gene interactions

Intralocus interactions (Allelic interactions)

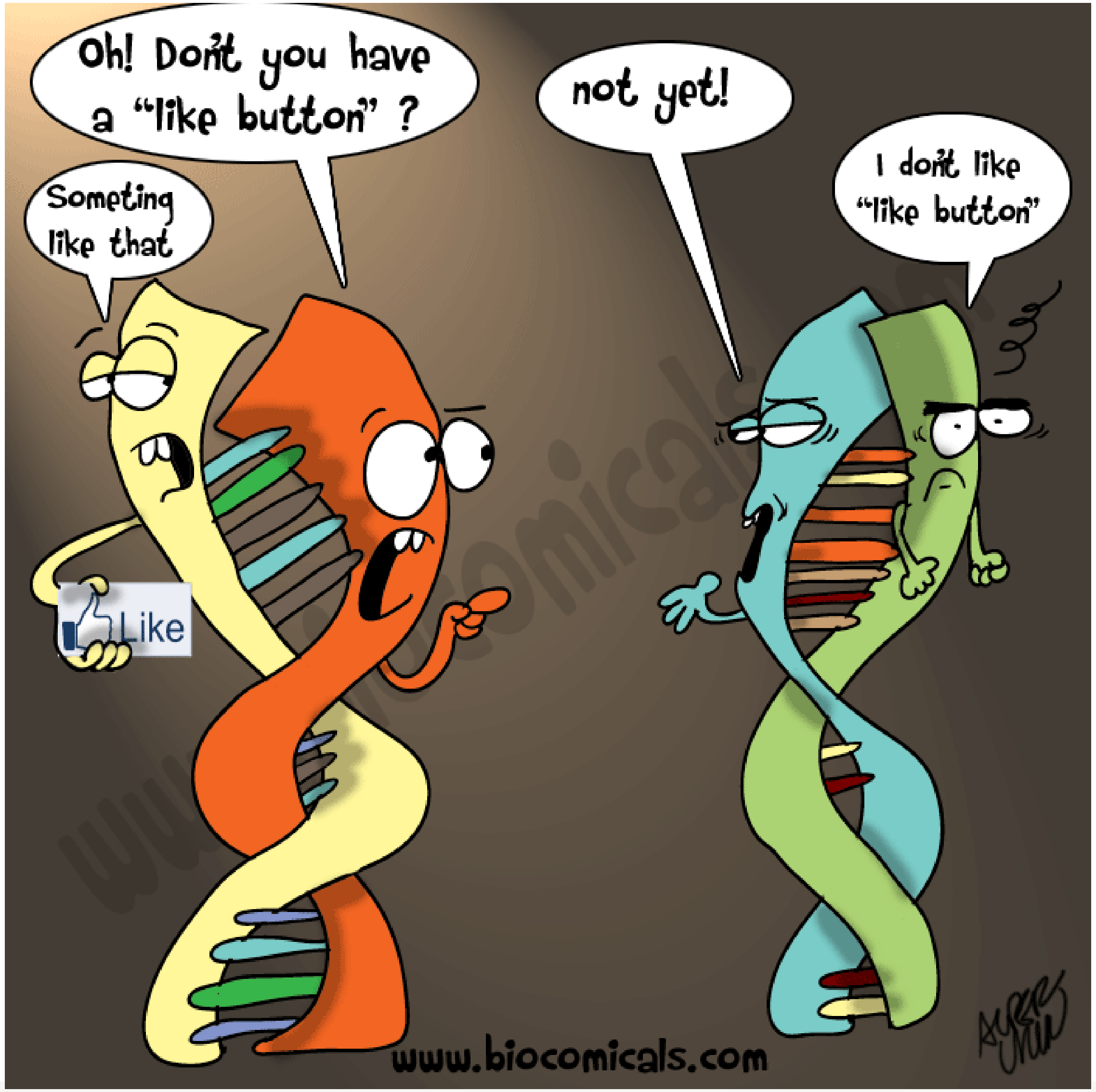
Interlocus interactions (Non-allelic interactions)

[redacted] Non-epistatic interactions

Epistatic interactions

I. Dominant relationship
  - a) Complete dominance Example: Tall and dwarf pea plants
  - b) Incomplete dominance
  - c) Codominance [redacted]

II. Lethal genes
  - a) Dominant lethals
  - b) Recessive lethals



Intra-locus or Inter-locus interaction of genes:

- A gene always occupies a specific position – gene locus within a particular chromosome.
- Phenotypic expression of the gene is due to a specific base sequence of the DNA molecule.
- Alleles found in a particular individual constitute its genotype.
- The interaction of genes may be intra-locus or inter-locus.

Intra-locus (allelic) gene interaction:

- Intra-locus (allelic) gene interaction takes place between genes (alleles) at the same locus; that is between alleles *A* and *a*, B and *b; A_1* and *A_2*, *B_1* and *B_2* or *A_1*, *A_2* and *A_3* etc.
- Intra-locus gene interactions may involve a dominance relationship or Multiple alleles.

Dominance relationships:

- An allele is an alternative form of a gene.
- Alleles contain modified genetic information and often specify an altered gene product.
- The allele that occurs most frequently in a population or one that is considered as normal is called the **wild type allele**.
- Alternative form or forms of wild type allele arises/arise by mutation. The alternative form is the **mutant allele**.
- The **expressivity** of a given allele ranges from **complete dominance** through **co-dominance**, **incomplete** or **partial dominance** to **recessiveness**.
- It is the phenotype of the heterozygote in relation to the phenotype of the two homozygotes that determines the dominance or recessiveness of an allele or the type of dominance relationship.
- In the homozygous condition, the two genes at a locus are identical and express either one or both alleles.
- A heterozygote can express either allele alone (complete dominance) or both the alleles simultaneously (incomplete dominance and co-dominance).

a) Complete dominance:

- In complete dominance intra-locus gene interaction, in the heterozygote only one allele (the dominant allele) expresses itself phenotypically while the other does not.
- The dominant allele expresses itself to the same degree in both the homozygotes and heterozygotes. The expressed trait is known as the dominant trait. A recessive allele expresses itself only in the homozygotes.
- **Examples**
- i. Tall (TT) X Short (tt) pea plants → F_1 – Tall (Tt) plants.
- ii. Yellow (YY) seed coat X Green (yy) seed coat of pea → Yellow (Yy) seed coat.

- In complete dominance the phenotypic ratio is 3:1 while the genotypic ratio is 1:2:1 in F_2 as shown below:

Parents: Yellow seed X Green seed
Genotype: YY yy
Gametes: (Y) (y)
F_1 generation: Yy
(Yellow seed)

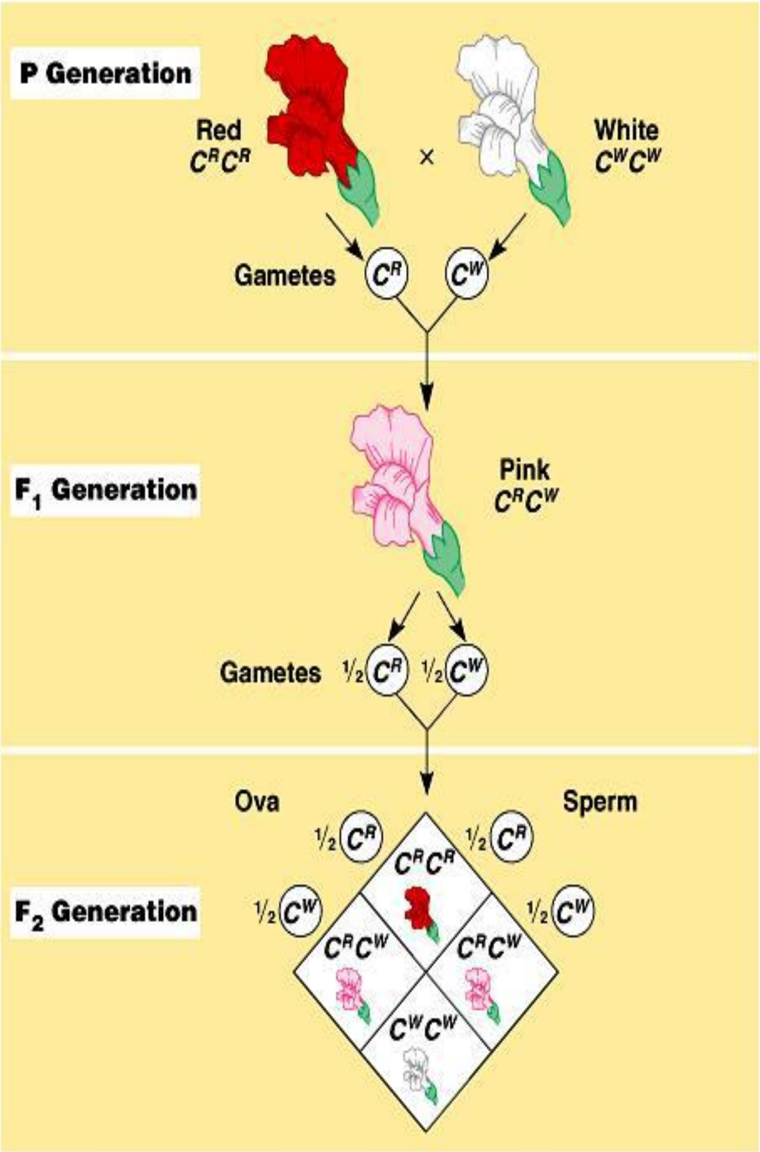
♀

Selfing of F_1: F_1 X F_1
Genotype: Yy Yy
Gametes: (Y) (y) (Y) (y)
By Punnett's square method

♂/ ♀	Y	y
Y	YY (yellow)	Yy (yellow)
y	Yy (yellow)	yy (green)

The phenotypic ratio is 3 yellow: 1 green while
the genotypic ratio is 1 pure yellow: 2 hybrid yellow: 1 pure green.

b) Incomplete dominance:



Incomplete dominance is defined as the expression of both alleles at a locus with the expression of one being more pronounced than that of the other, but still less apparent than in a corresponding homozygote. Sometimes neither of the genes involved is completely dominant or completely recessive. So, the F_1 hybrid is intermediate of both the parents. It is also called as blending effect.

For example, in **four o' clock plant** (*Mirabilis jalapa*) and in Snapdragons there are two types of flower viz., red and white. A cross between red and white flowered plants produced plants with intermediate flower colour i.e., pink colour in F_1 and a modified ratio of 1 red: 2 pink: 1 White in F_2 i.e., **The phenotype ratio is similar to the genotype ratio.**

Parents: Red flower X White flower
Genotype: RR rr
Gametes: **(R)** **(r)**
$F_{1:}$ **Rr (Pink** flower)

F_1 is selfed: **Pink** flr X **Pink** flr
(Rr) (Rr)
Gametes: (R) (r) (R) (r)

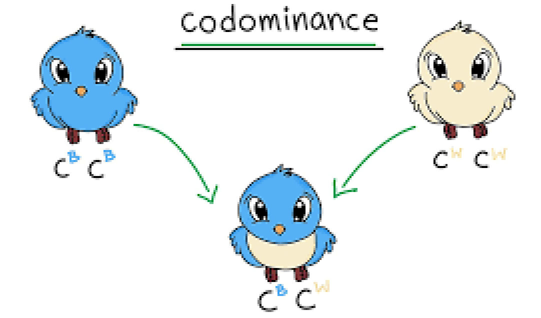
	R	r
R	RR (Red)	Rr (Pink)
r	Rr (Pink)	rr (white)

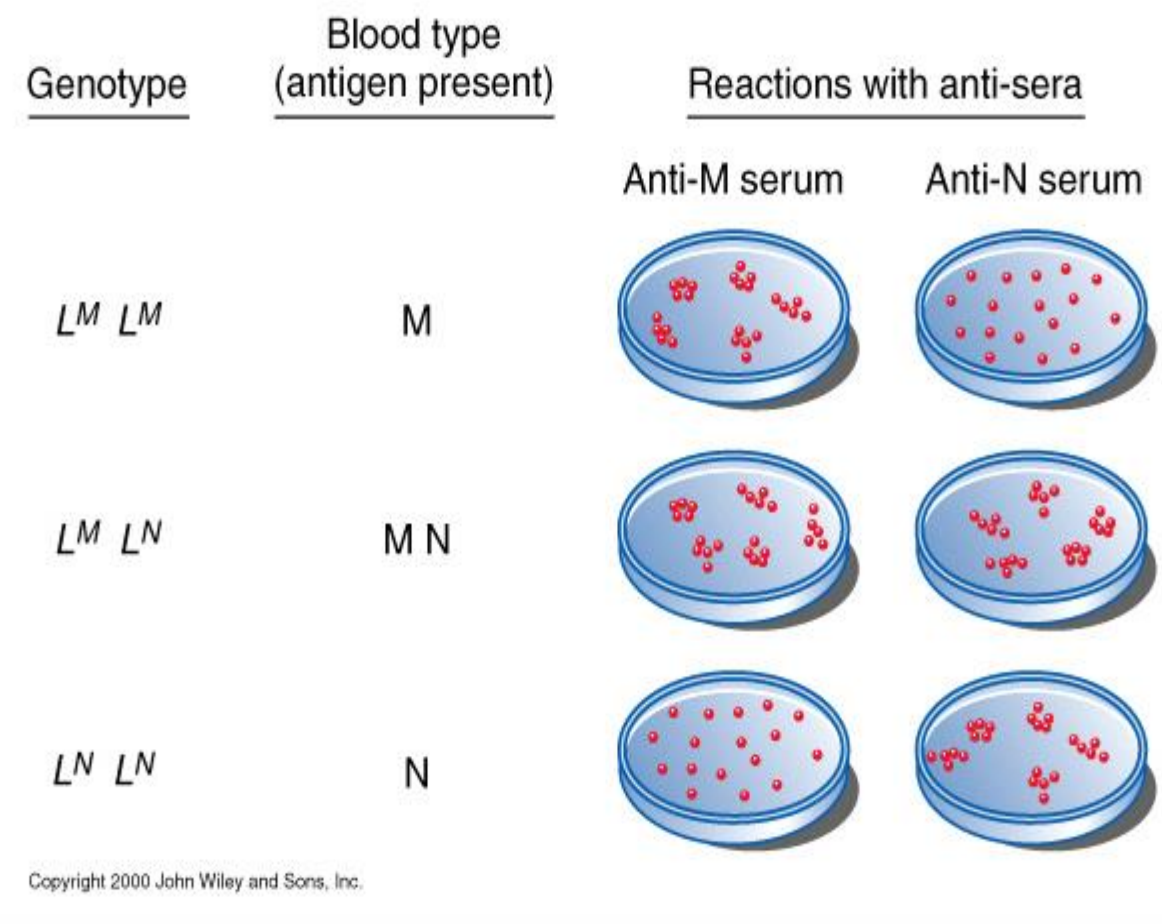
F_2 ratio= 1 Red (RR) : 2 Pink (Rr) : 1 White (rr)

In Radish, the shape of the storage tap root may be long, oval or round.

A cross between a long (l^1 l^1) and round (l^2l^2) radish bearing plants produces F_1 progeny which bears oval radishes (l^1l^2).

Selfing the F_1 produces 1 long: 2 oval: 1 round in the F_2.





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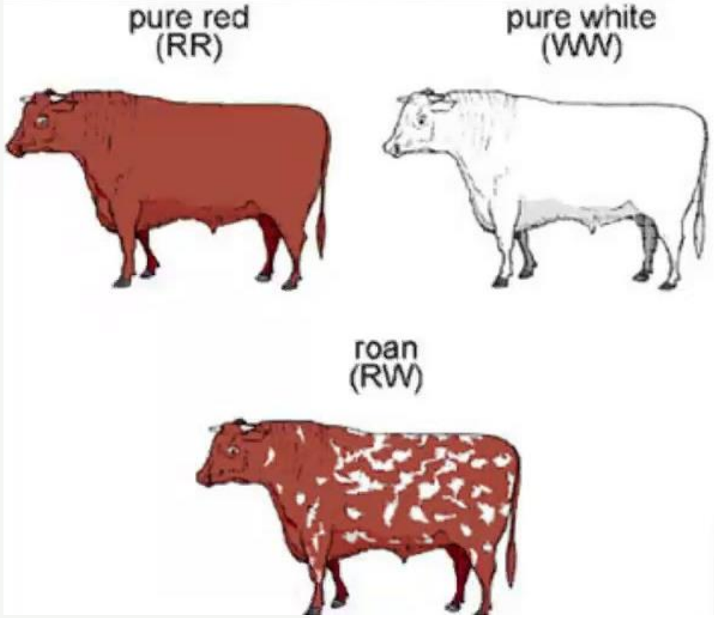
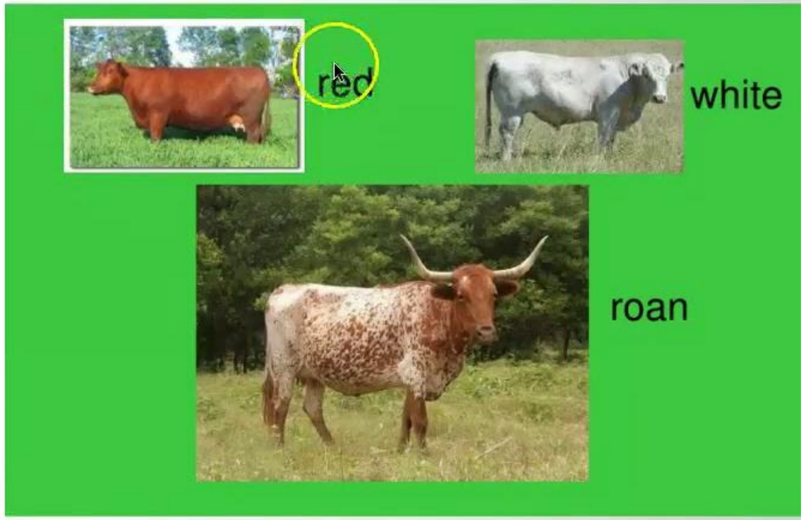
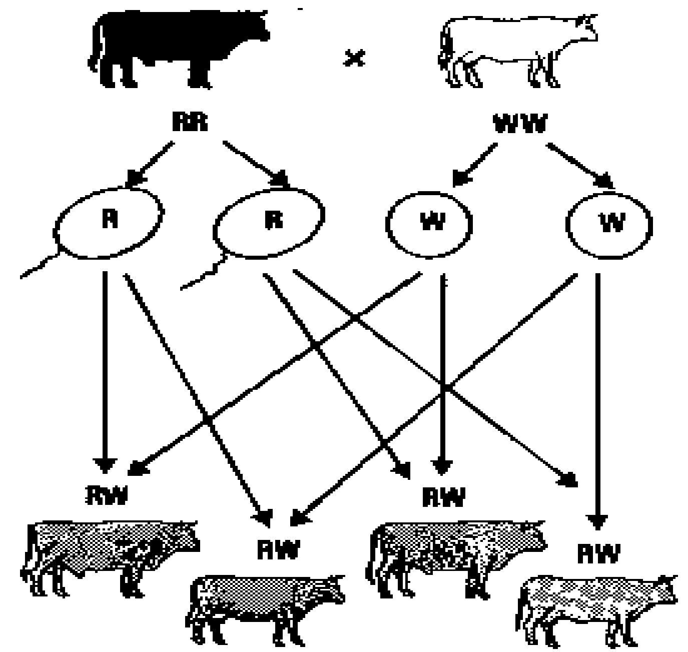
c) Co-dominance:

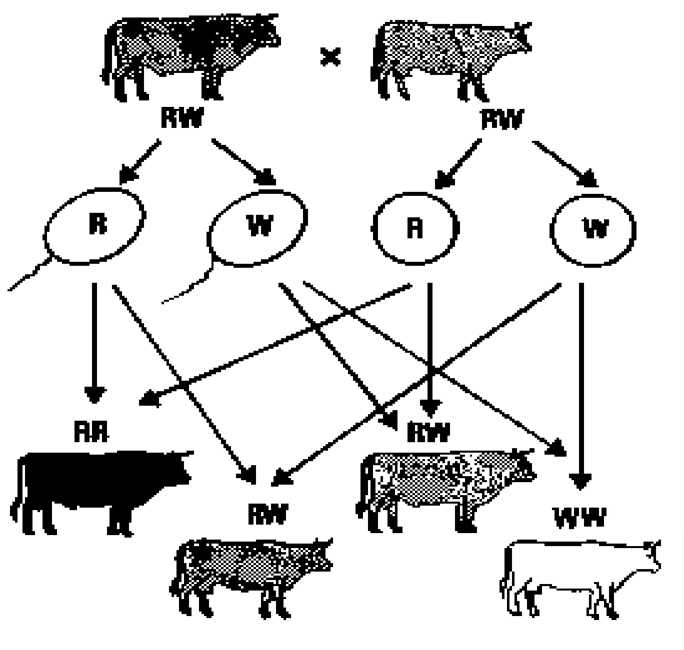
- Here both the alleles of a gene express themselves in the heterozygotes.
- Phenotypes of both the parents appear in F_1 hybrid rather than the intermediate phenotype.
- In human, **MN blood group** is controlled by a single gene. The gene codes for a membrane phenotype, the protein found in plasma membrane of RBCs. The alleles L^M and L^N show co-dominance.
- Father with N blood group (L^N L^N) and mother with M blood group (L^M L^M) will have children with MN blood group (L^M L^N).
- F_2 segregates in the ratio 1M blood group: 2 MN blood group : 1 N blood group.

Codominance Example: Cattle









In *shorthorn breed of cattle,* the homozygous red (RR) and white (WW) cattle when crossed produce reddish-grey or roan (RW) off springs.

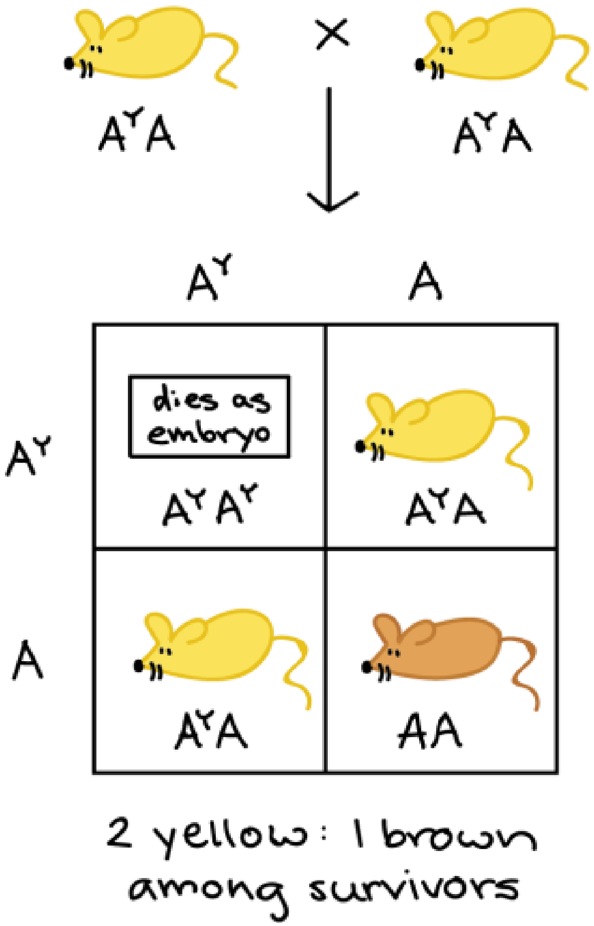
The individual hair of these cattle is actually not reddish grey but is either red or white.

The roan coat is a mixture of red and white hair with both the alleles expressing themselves.

d) Lethal genes:

- Gene, which causes the death of its carrier when in homozygous condition is called lethal gene. Mendel's findings were based on equal survival of all genotypes. In normal segregation ratio of 3:1 is modified into 2:1 ratio.
- Lethal genes have been reported in both animals as well as plants.
- Effect of lethal gene destroys the zygote or embryo.
- Those genes which bring about death of organisms when it reaches reproductive maturity are called sub lethal genes.
- Lethal genes can be recessive, also be dominant, conditional, semi lethal, or synthetic, depending on the gene or genes involved.

i. Dominant lethal genes



- It was discovered by **Cuenot** (1905). In mice allele for yellow coat colour is dominant over grey.
- When a cross is made between yellow and grey a ratio of 2:1 for yellow and gray mice was observed. This indicated that yellow mice are always heterozygous. Because yellow homozygotes are never born because of homozygous lethality.
- As it turned out, this unusual ratio reflected that some of the mouse embryos (A^YA^Y) died very early in development, long before birth. In other words, at the level of eggs, sperm, and fertilization, the colour gene segregated normally, resulting in embryos with a 1:2:1 ratio for A^YA^Y, A^YA & AA genotype. However, A^YA^Y mice died as tiny embryos, leaving a 2:1 genotype and phenotype ratio among the surviving mice.

ii. Recessive lethal genes – eg. Sickle cell anemia

Parents: $(H^N H^S)$ X $(H^N H^S)$

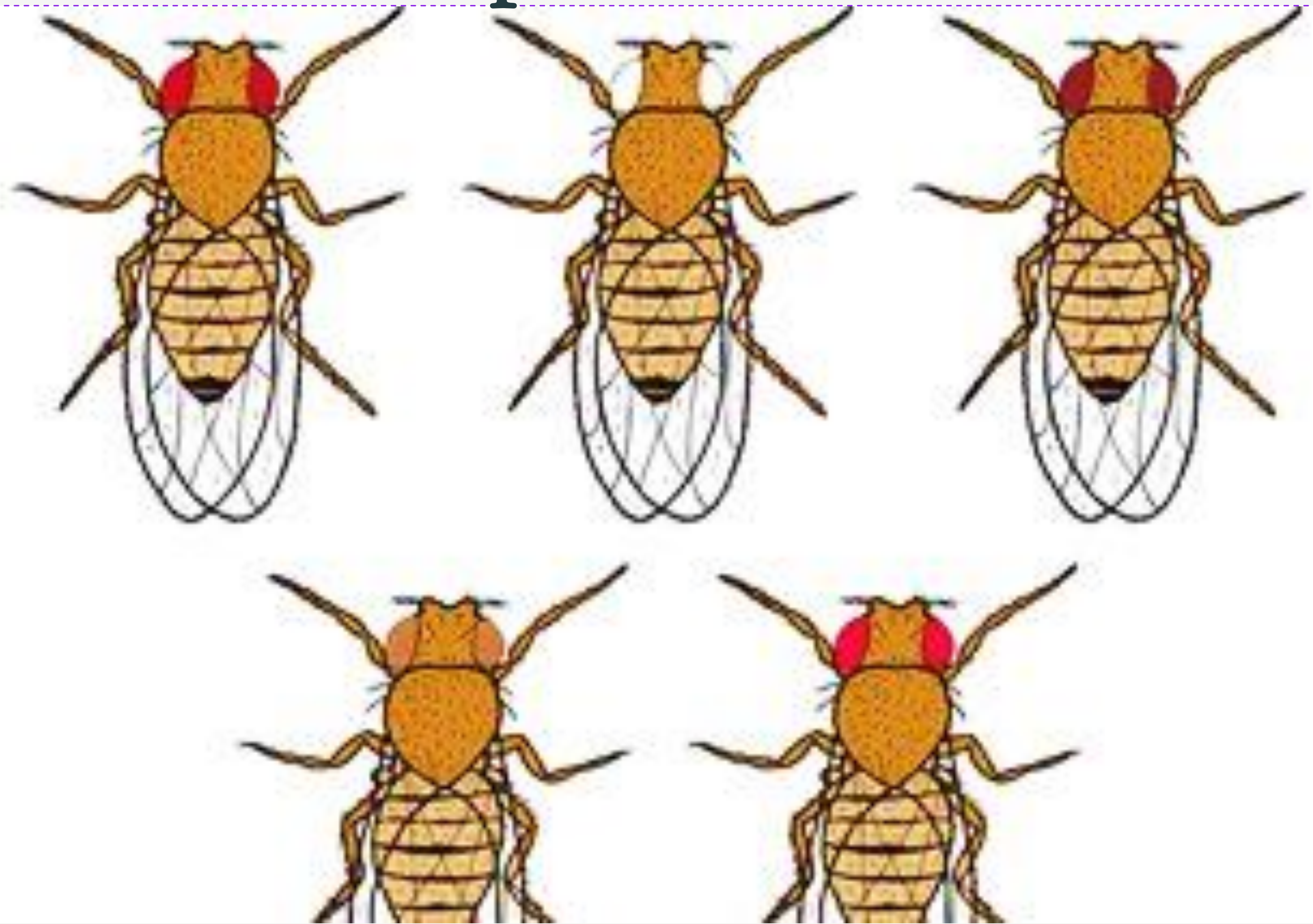
Gametes: (H^N) (H^S) (H^N) (H^S)

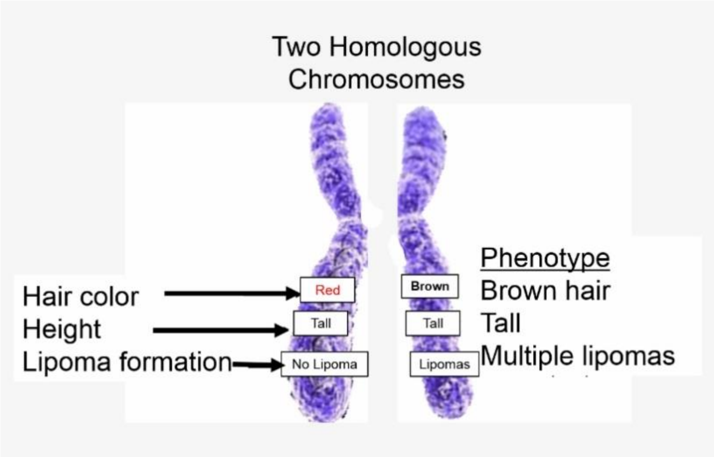
	H^N	H^S
H^N	$H^N H^N$	$H^N H^S$
H^S	$H^N H^S$	$H^S H^S$

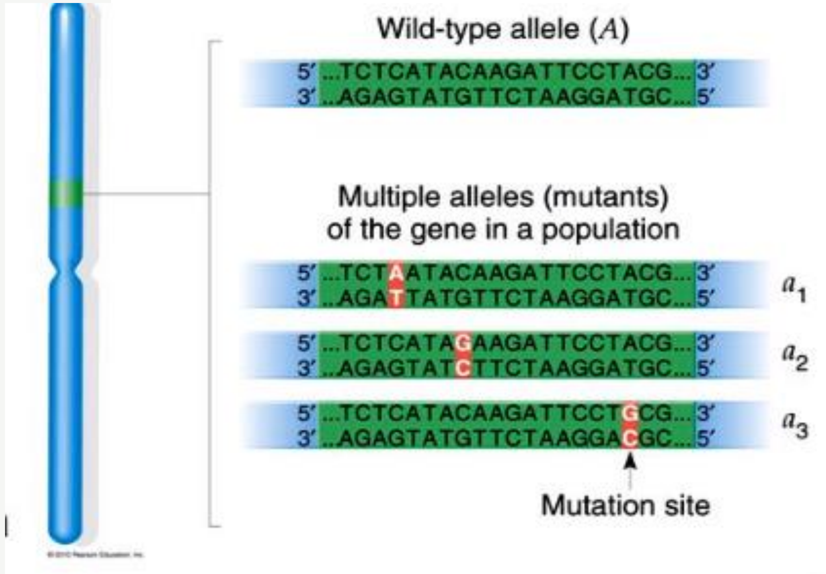
*$H^S H^S$ dies

- Sickle cell anemia is a disease produced due to homozygous recessive gene pair.
- RBCs in this disease become sickle shaped, so they get entangled with each other.
- Due to this, flow of O_2 becomes insufficient.
- It causes death of a child. Suppose both the parents are heterozygous $(H^N H^S)$.

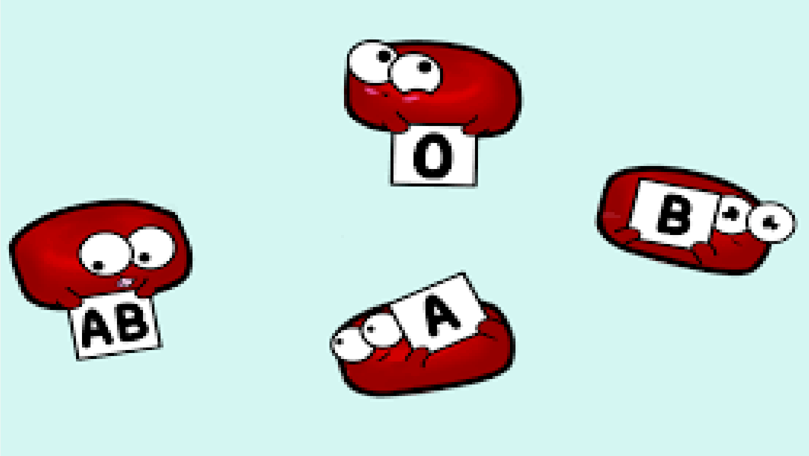
Multiple Alleles







- Mendel proposed that a character is controlled by a single pair of genes.
- These 2 genes are located at the same locus on both homologues; called alleles of each other.
- They can undergo mutation & give rise to three or more kinds of genes occupying the same locus are referred to as **multiple alleles**.
- Although only one of them present on single chromosome & no more than 2 of them could be present in normal diploid organism.
- These mutant alleles express different alternatives of the same character.



- **Definitions:** a) **"Three or more kinds of gene which occupy the same locus are referred to as multiple alleles."** – Altenburg.
- b) Multiple alleles are 3 or more genes occupying the same locus, affecting the same character but effect is different.
- **Symbols for multiple alleles**: A capital letter is used to describe the original dominant gene & corresponding small letters are used for the recessive allele & to designate other alleles which are intermediate in their degree of dominance between these 2 extremes are assigned the lowercase letter with some suitable superscript. (A, a, a', a'', a'''.......)

Characteristics of multiple alleles :

Agouti

CC/Ccch/Cch/ Cc

Chinchilla

cch cch/ cch ch/ cch c

Himalayan

ch ch/ ch c

Albino

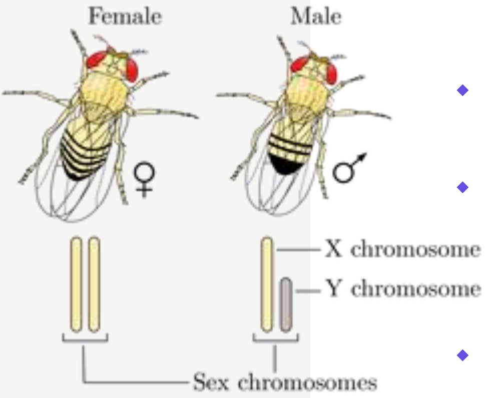
cc

- They always occur at the same locus on the chromosome.
- Within a series of multiple alleles crossing over never occurs.
- They always affect the same trait, but their effect is different – example eye colour in *Drosophila*.
- Among the alleles produced the wild type always dominant over the recessive one. The other mutant alleles in the series may either be dominant, or they produce a phenotypic effect of an intermediate between wild & recessive type.
- A cross between two mutants results in the off springs with a mutant phenotype and never the wild phenotype.
- Further, F_2 generations from such crosses show typical monohybrid ratio for the concerned character.

The order of dominance is *C> cch >ch >c.*

Examples of Multiple Alleles: a) Eye colour in *Drosophila*

- T.H. Morgan (1910) described the first case of multiple alleles of eye colour in *Drosophila*.
- In a vial of flies with normal red eyes he found a fly with white eyes which had arisen due to a mutation in the gene which produces red colour in normal flies.
- The red eyes are due to the gene **W** located on the X chromosome at 1.5 mu from the left end.
- The white eyes are due to **w** gene present at same locus.
- Subsequently many eye colours were found in *Drosophila*, all occupying the same locus.
- While red eye colour is dominant to all eye colours, white colour for the eyes is recessive to all.
- The order of dominance is red (W) > coral (w^{co}) > blood (w^{bl}) > eosin (w^{e}) > cherry (w^{ch}) > apricot (w^{a}) > honey (w^{h}) > buffed (w^{bf}) > tinged (w^{t}) > peach (w^{p}) > ivory (w^{i}) > white (w).



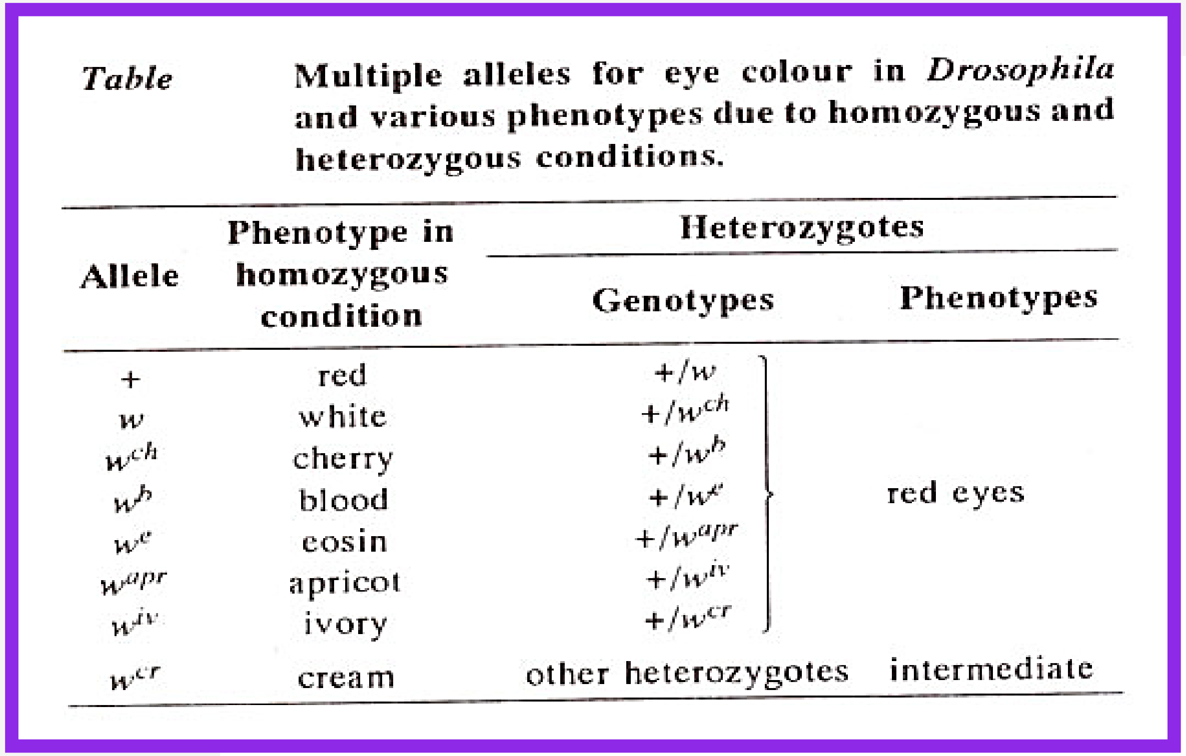
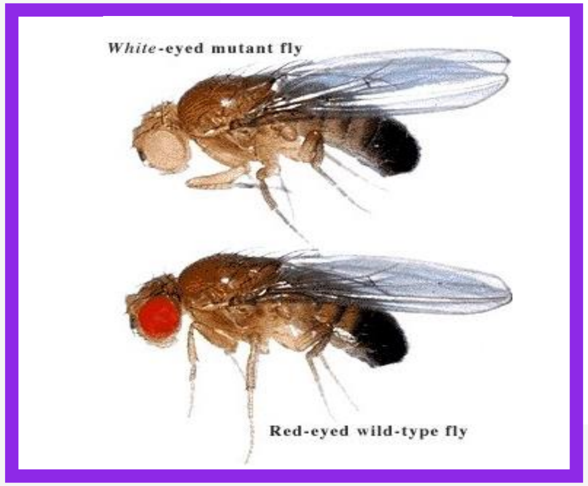
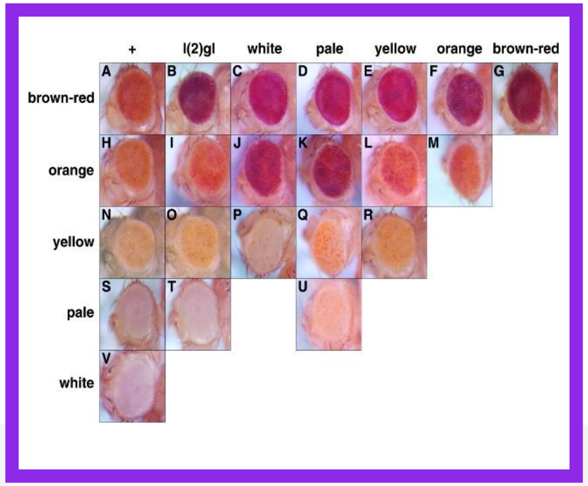
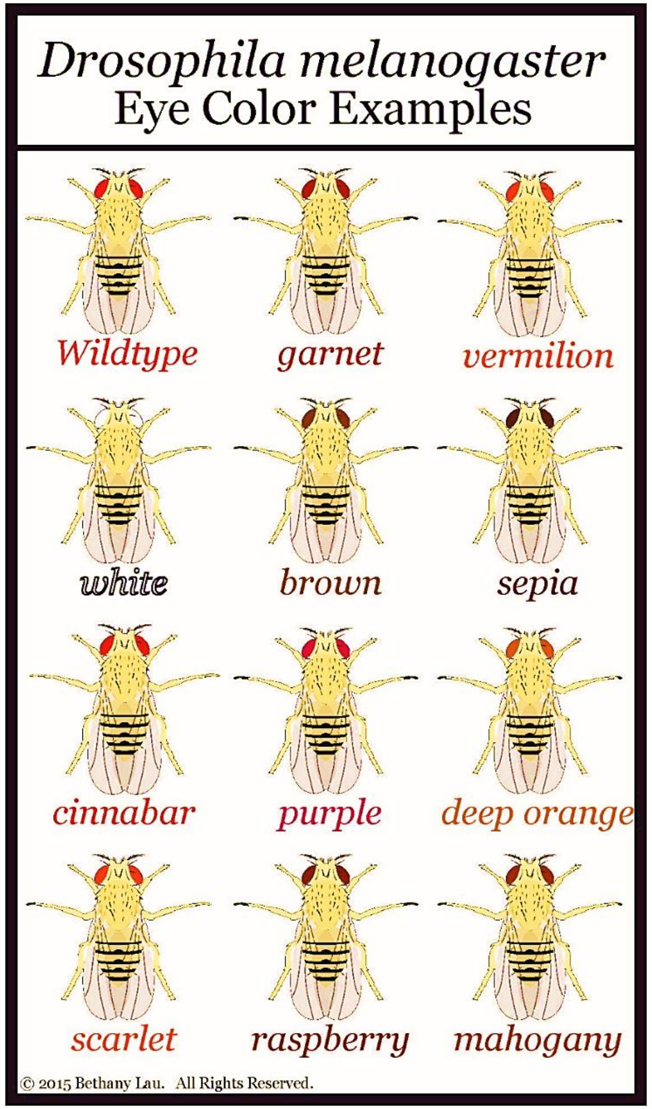


Table **Multiple alleles for eye colour in *Drosophila* and various phenotypes due to homozygous and heterozygous conditions.**

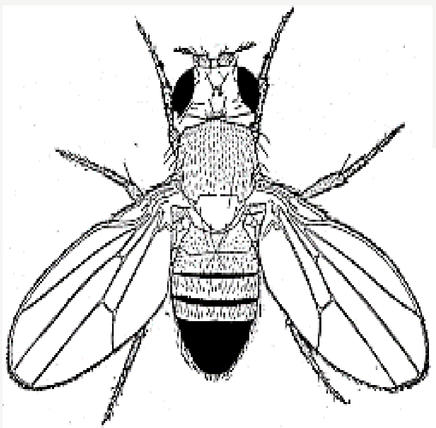
Allele	Phenotype in homozygous condition	Heterozygotes	
		Genotypes	Phenotypes
$+$	red	$+/w$	red eyes
w	white	$+/w^{ch}$	
w^{ch}	cherry	$+/w^{b}$	
w^{b}	blood	$+/w^{e}$	
w^{e}	eosin	$+/w^{apr}$	
w^{apr}	apricot	$+/w^{iv}$	
w^{iv}	ivory	$+/w^{cr}$	
w^{cr}	cream	other heterozygotes	intermediate

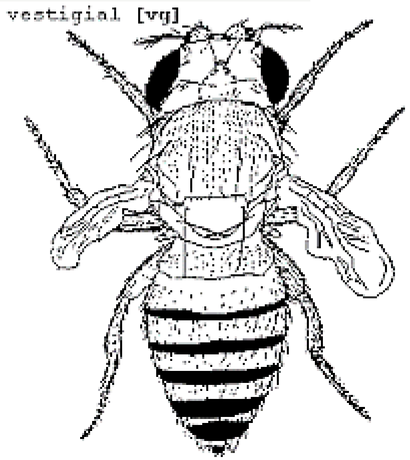


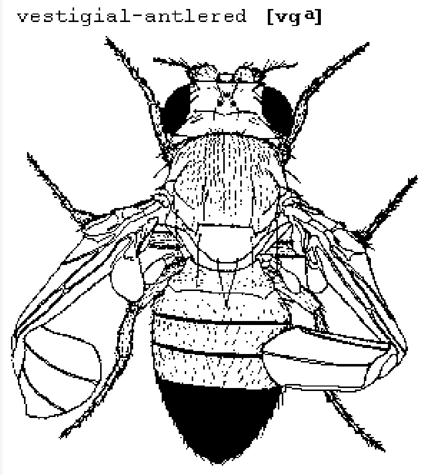




b) Wings of *Drosophila*:







- In *Drosophila* wings are normally long.
- There occurred two mutations at the same locus, one causing vestigial (reduced) wings and other mutation causing antlered (less developed) wings.
- Both vestigial and antlered are alleles of the same normal gene and of each other and are recessive to the normal gene.
- vestigial is represented by (vg) and antlered (vg^a). The normal allele is by the symbol +.
- **Thus, there are three races of Drosophila:**
- (i) Long ++ (+/+), (ii) Vestigial vg vg (vg/vg), (iii) Antlered vg^a vg^a (vg^a/vg^a).
- A cross between a long-winged fly and vestigial winged or antlered winged is represented below:

Parents: long winged vestigial winged
Genotype: (+/+) X (vg/vg)

Gametes: (+) (vg)

F1 : +/vg

F1 selfed : +/vg X +/vg

Gametes: (+) (vg) (+) (vg)

	+	vg
+	+/+ (L)	+/vg (L)
vg	+/vg (L)	vg/vg (vg)

F2 ratio = 3 long : 1 vestigeal

Parents: long winged antlered winged
Genotype: (+/+) X (vg^a / vg^a)

Gametes: (+) (vg^a)

F1 : +/ vg^a

F1 selfed : +/ vg^a X +/ vg^a

Gametes: (+) (vg^a) (+) (vg^a)

	+	vg^a
+	+/+ (L)	+/vg^a (L)
vg	+/vg^a (L)	vg^a/vg^a (vg^a)

F2 ratio = 3 long : 1 antlered

Parents: vestigial winged antlered winged

Genotype: (vg/vg) X (vg^a / vg^a)

Gametes: (vg) (vg^a)

F1 : vg / vg^a (Intermediate)

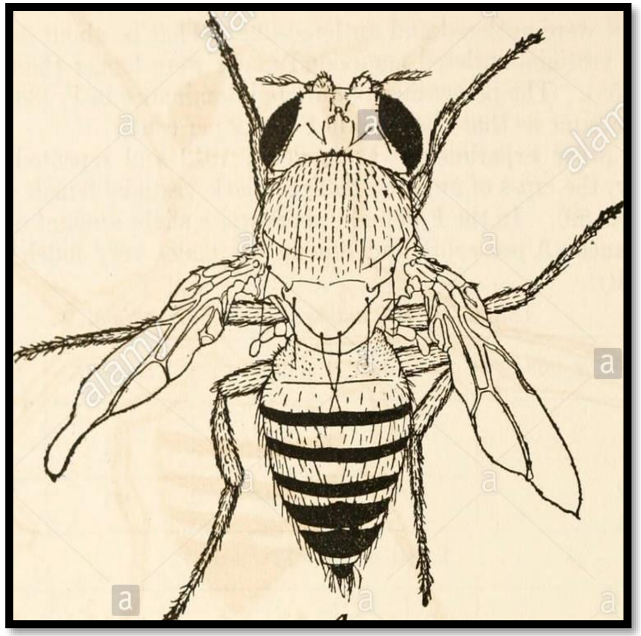
F1 selfed : vg / vg^a X vg / vg^a

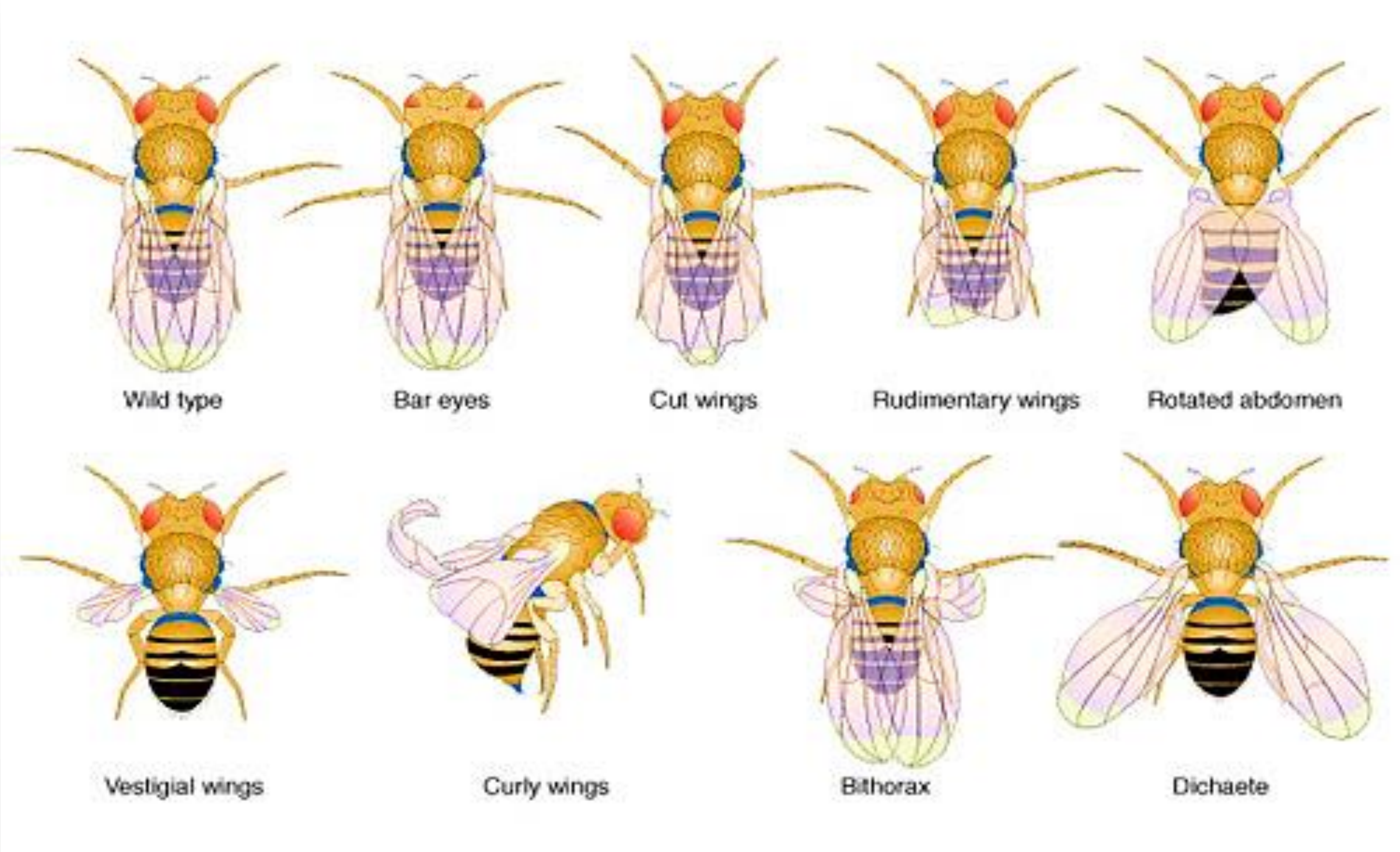
Gametes: (vg) (vg^a) (vg) (vg^a)

	vg	vg^a
vg	vg/ vg (vg)	vg/vg^a (I)
vg^a	vg/vg^a (I)	vg^a/vg^a (vg^a)

F2 ratio = 1 vestigial : 2 Intermediate: 1 antlered

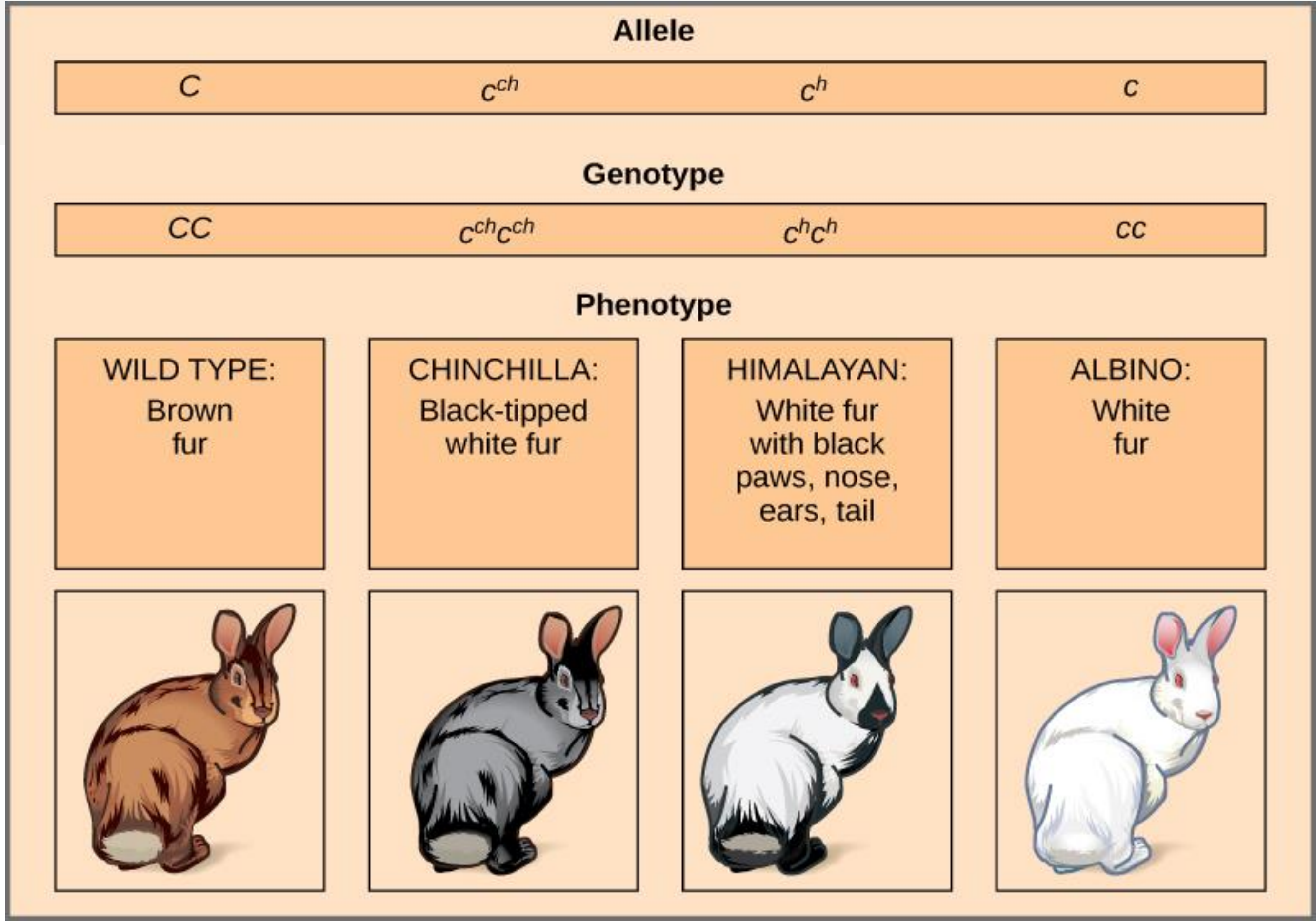
- When a fly with vestigial wing is crossed with another fly having antlered wings, the F_1 hybrids are intermediate in wing length showing that none of the mutated gene is dominant over the other.




Wild type
Bar eyes
Cut wings
Rudimentary wings
Rotated abdomen
Vestigial wings
Curly wings
Bithorax
Dichaete

c) Coat colour in rabbits:

- The wild type coat colour in rabbits is **agouti**, in which each hair has a yellow band just below the tip, giving an overall grey colour. It is due to dominant gene *C* present in homozygous or heterozygous form.
- **Chinchilla** (***cch cch***) in which the coat colour is silver-grey since the hair lacks the yellow band.



Allele			
C	c^{ch}	c^h	c
Genotype			
CC	$c^{ch}c^{ch}$	c^hc^h	cc
Phenotype			
WILD TYPE: Brown fur	CHINCHILLA: Black-tipped white fur	HIMALAYAN: White fur with black paws, nose, ears, tail	ALBINO: White fur

- **Himalayan** (***ch ch***) is characterized by white rabbits with black extremities.
- **Albino** rabbits (***cc***) are full white with red eyes.
- The albino phenotype is recessive to all the phenotypes while agouti is dominant to all.
- The order of dominance is ***C > cch >ch >c.***

Parents	**F1**	**F2**
CC X $c^{ch}c^{ch}$	Cc^{ch}	3 agouti : 1 chinchilla
CC X $c^{h}c^{h}$	Cc^{h}	3 agouti : 1 himalayan
CC X cc	Cc	3 agouti : 1 albino
$c^{ch}c^{ch}$ X$c^{h}c^{h}$	$c^{ch}c^{h}$	3 chinchilla : 1himalayan
$c^{h}c^{h}$ X cc	$c^{h}c$	3 himalayan : 1 albino
$c^{ch}c^{ch}$ X cc	$c^{ch}c$	3 chinchilla : 1 albino

Pattern of inheritance of coat colour in rabbits

d) The ABO blood group system

In humans, discovered by Landsteiner (1901) is a classical example of multiple alleles.

- If blood transfusions were made between persons of two incompatible blood groups, the transfused cells were likely to clump and shut out the capillaries in the recipient, sometimes resulting in death.
- It was found that all persons could be classified in to four groups about the antigen property of the blood cells.
- The antigens which are proteins localized on the surface of RBCs are coded by a series of multiple alleles.
- The gene encoding the proteins are denoted by the symbol **I.**

Bl gr	Genotype	Antigen	Antibody
A	$I^A I^O$ or $I^A I^A$	A	B
B	I^BI^O or $I^B I^B$	B	A
AB	$I^A I^B$	AB	Nil
O	$I^O I^O$	Nil	A, B

- Depending on the allele, antigen A or B is encoded by gene I^A for A and I^B for B. If the individual is I^A I^B both the antigens A and B are produced. I^o does not encode for any antigen. The following table gives genotype, antigen and antibody for the various blood groups.

Parents		**Children**	
Phenotypes	Genotypes	Phenotypes	Genotypes
O X O	$I^O I^O$ x $I^O I^O$	O	$I^O I^O$
O X A	$I^O I^O$ x $I^A I^A$ / $I^A I^O$	O, A	$I^O I^O$, $I^A I^O$
O X B	$I^O I^O$ x $I^B I^B$ / $I^B I^O$	O, B	$I^O I^O$, $I^B I^O$
O X AB	$I^O I^O$ x $I^A I^B$	A, B	$I^A I^O$, $I^B I^O$
A X A	$I^A I^A$/ $I^A I^O$ x $I^A I^A$/ $I^A I^O$	A, O	$I^A I^A$, $I^A I^O$, $I^O I^O$
A X B	$I^A I^A$/ $I^A I^O$ x $I^B I^B$/ $I^B I^O$	A, AB, B, O	$I^A I^O$, $I^A I^B$, $I^B I^O$, $I^O I^O$
A X AB	$I^A I^A$/ $I^A I^O$ x $I^A I^B$	A, AB, B	$I^A I^A$, $I^A I^O$, $I^A I^B$, $I^B I^O$
B X B	$I^B I^B$/ $I^B I^O$ x $I^B I^B$/ $I^B I^O$	B, O	$I^B I^B$, $I^B I^O$, $I^O I^O$
B X AB	$I^B I^B$/ $I^B I^O$ x $I^A I^B$	A, B, AB	$I^A I^O$, $I^B I^B$, $I^B I^O$ $I^A I^B$
AB X AB	$I^A I^B$ x $I^A I^B$	A, B, AB	$I^A I^A$, $I^B I^B$, $I^A I^B$

Problems based on multiple alleles:

1. In rabbits, chinchilla coat colour (c^{ch}) is dominant over Himalayan (c^{h}). The gene for albino coat (c) is recessive to both chinchilla and Himalayan. Further, all the three genes are recessive to the full coat colour agouti (C). What phenotypic ratios would be obtained from the following crosses:

(a) CC X $c^{ch}c^{ch}$, (b) CC X $c^{h}c^{h}$, (c) CC X cc, (d) $c^{ch}c^{ch}$ X $c^{h}c^{h}$, (e) $c^{h}c^{h}$ X cc, (f) $c^{ch}c^{ch}$ X cc.

2. Couples preparing for marriage have their blood types as follows:

(a) O X O, (b) O X A, (c) O X B, (d) O X AB, (e) A X A, (f) A X B, (g) A X AB, (h) B X B, (i) B X AB, (j) AB X AB. What will be the blood groups of their future off springs?

Inter-locus (non allelic) gene interaction

- When alleles at different loci (i.e., non-allelic genes) interact to affect a phenotype such gene interaction is an inter-locus one.
- Results in a variation of the dihybrid cross from the 9:3:3:1 F_2 ratio.
- This interaction may be non-epistatic or epistatic.
- If a gene present at one locus interferes with the expression of a gene at another locus on the same or on a different chromosome, then the type of interaction is an epistatic one.
- On the other hand, if genes at different loci interact to produce a different phenotype affecting the same trait, then the type of interaction is a non-epistatic one.


Rose


Pea


Walnut

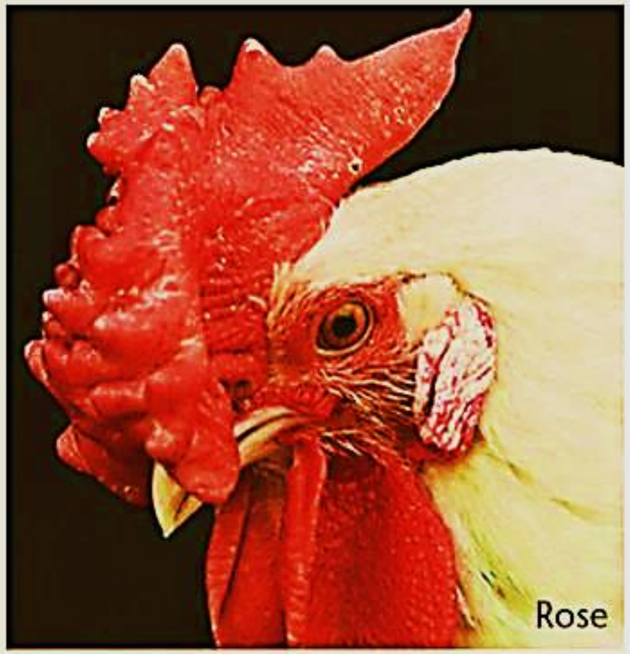

Single

Non-epistatic interaction: (Single character governed by 2 pairs of alleles/ Interaction between dominant genes/ Inheritance of comb in poultry):-

- Sometimes 2 dominant genes controlling the same character produce a new phenotype in F_1 when they come together from 2 different parents.
- Bateson and his colleagues (1900) studied inheritance of comb shape in fowls. There are 4 types of combs in fowls: rose, pea, walnut and single.
- Bateson first performed a cross between rose and single. In F_1 all hens had a rose comb and F_2 ratio for rose, and single was 3 : 1. It indicates that rose and single comb are controlled by a single gene and that rose is dominant over single.
- In the second cross chickens with pea comb were mated with single comb, the F_1 progeny had pea comb, and F_2 had pea and single in the proportion 3 : 1. Obviously, the gene for pea comb is dominant over single.

- This raises an interesting question—is the genes for rose and pea comb same or different?
- Bateson then crossed rose and pea. Surprisingly, the F_1 birds had an altogether different comb of the walnut type!
- An F_2 progeny raised by inbreeding the walnut type consisted of four types of chickens—walnut, rose, pea and single in the ratio 9 : 3 : 3 : 1. As this ratio is typical for dihybrid inheritance it became clear that rose and pea combs were controlled by two pairs of genes.
- The appearance of walnut comb in F_1 of cross between rose and pea shows that both are the independent dominant genes P and R are jointly responsible for the walnut comb.
- When present together in the zygote, P and R genes interact to produce the walnut comb.
- When present alone, they produce rose or pea comb.
- The recessive alleles of rose and pea combs produce the fourth type of chicken with the single comb.

Walnut (R_P_)



Rose (R_pp)

Pea (rrP_)

Single (rrpp)

Parents: **Rose comb** **X** **Pea comb**

Genotype: RRpp rrPP

Gametes: (Rp) (rP)

F_1 generation: RrPp (**Walnut comb**)

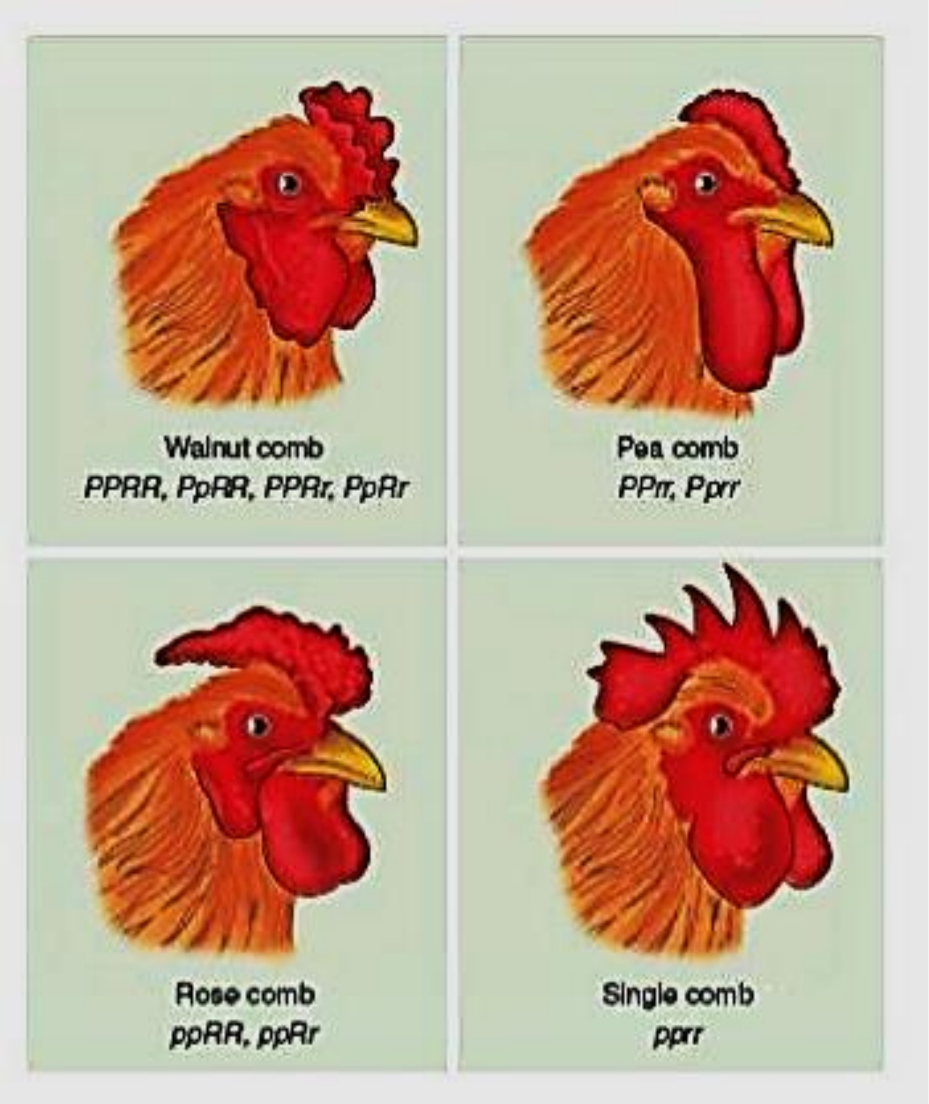
Selfing of F_1 : **F_1** **X** **F_1**

Genotype: RrPp RrPp

Gametes: **(RP) (Rp) (rP) (rp)** **(RP) (Rp) (rP) (rp)**

Try this cross!

♂ / ♀	RP	Rp	rP	rp
RP				
Rp				
rP				
rp				



By Punnett's square method

♂ / ♀	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 phenotypic ratio = 9: 3: 3: 1 (9 walnut: 3 rose: 3 pea: 1 single)

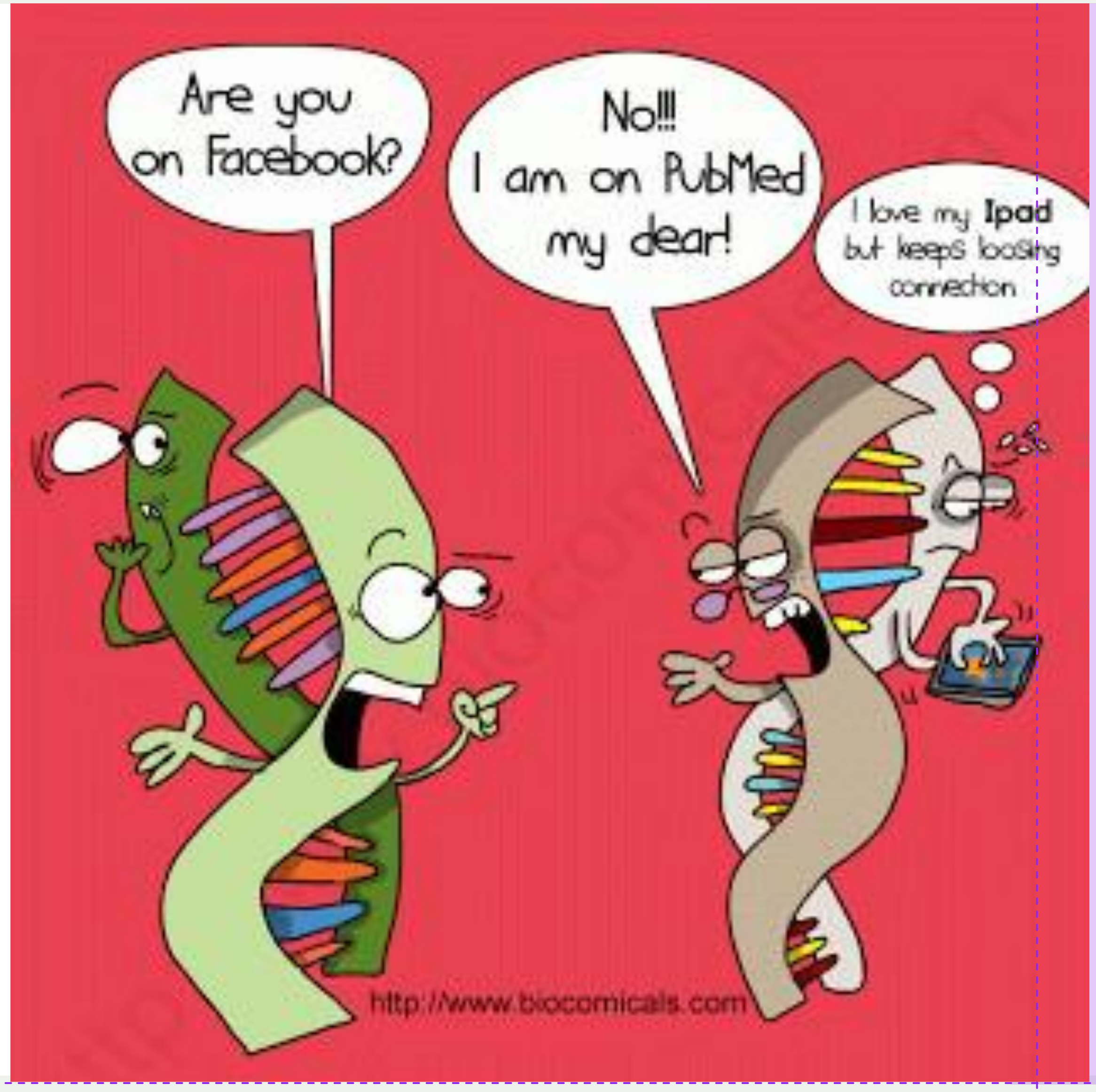
Epistatic interaction:

- Epistasis is a Greek word means suppression.
- A gene at one locus on a chromosome suppresses or masks the expression of a gene at another locus (nonallelic).
- The gene that inhibits the expression of another non allelic gene is said to be epistatic to that gene & the gene which get masked is said to be hypostatic.
- (Epistatic genes may be inactive genes that produce defective enzymes or no enzymes and thus block particular reactions and mask the phenotype of hypostatic genes).

Epistatic Interactions

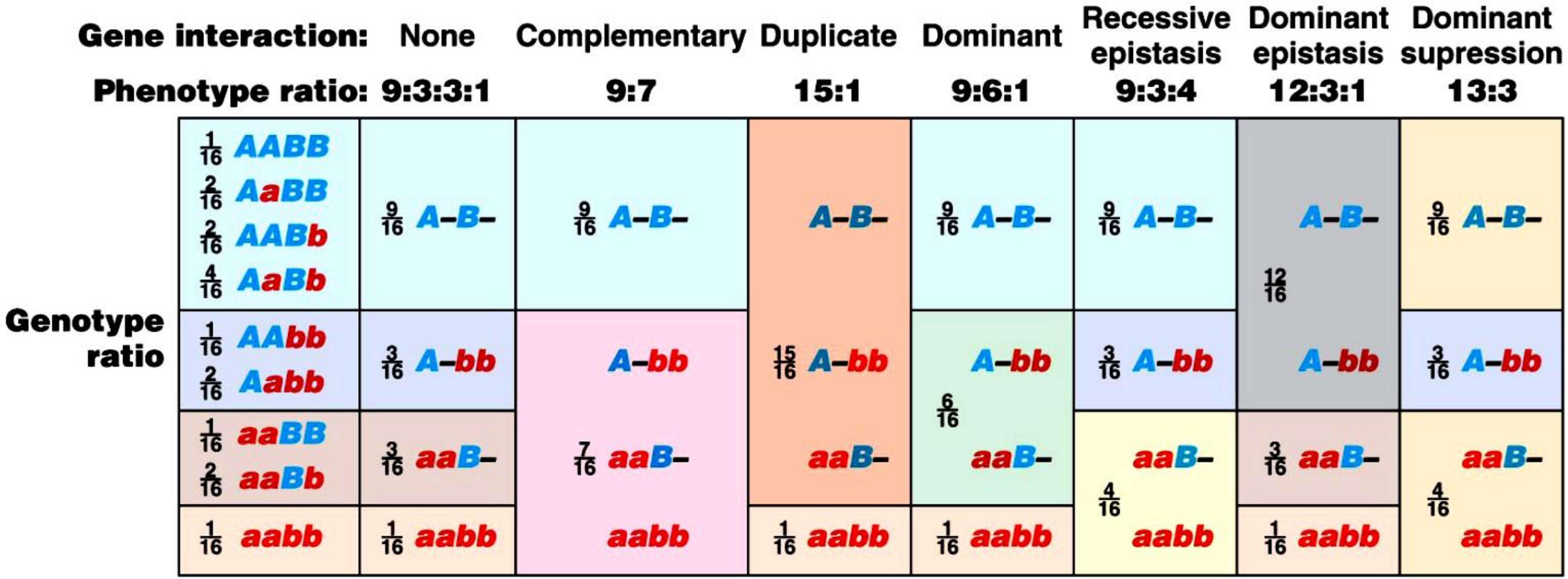
A minimum of 2 genes are required for **epistatic interactions;** these usually participate in the same pathway.

There are six ways epistasis could affect the predicted 9:3:3:1 dihybrid ratio.



Epistatic Interactions

Gene interaction alters the classic 9:3:3:1 ratio seen in the F2 progeny of the dihybrid cross!



	Gene interaction:	None	Complementary	Duplicate	Dominant	Recessive epistasis	Dominant epistasis	Dominant supression
	Phenotype ratio:	9:3:3:1	9:7	15:1	9:6:1	9:3:4	12:3:1	13:3
Genotype ratio	$\frac{1}{16}$ AABB $\frac{2}{16}$ AaBB $\frac{2}{16}$ AABb $\frac{4}{16}$ AaBb	$\frac{9}{16}$ A–B–	$\frac{9}{16}$ A–B–	A–B– $\frac{15}{16}$ A–bb aaB–	$\frac{9}{16}$ A–B–	$\frac{9}{16}$ A–B–	A–B– $\frac{12}{16}$ A–bb	$\frac{9}{16}$ A–B–
	$\frac{1}{16}$ AAbb $\frac{2}{16}$ Aabb	$\frac{3}{16}$ A–bb	A–bb $\frac{7}{16}$ aaB– aabb		A–bb $\frac{6}{16}$ aaB–	$\frac{3}{16}$ A–bb		$\frac{3}{16}$ A–bb
	$\frac{1}{16}$ aaBB $\frac{2}{16}$ aaBb	$\frac{3}{16}$ aaB–				aaB– $\frac{4}{16}$ aabb	$\frac{3}{16}$ aaB–	aaB– $\frac{4}{16}$ aabb
	$\frac{1}{16}$ aabb	$\frac{1}{16}$ aabb		$\frac{1}{16}$ aabb	$\frac{1}{16}$ aabb		$\frac{1}{16}$ aabb	

Types of epistasis: 1. Dominant Epistasis (12 : 3 : 1 Ratio):

(Y_ww)

(yyww)

(W_Y_/W_yy)

When a dominant allele at one locus can mask the expression of both alleles (dominant and recessive) at another locus, it is known as dominant epistasis.

In other words, the expression of one dominant or recessive allele is masked by another dominant gene. This is also referred to as simple epistasis.

An example of dominant epistasis is found for **fruit colour in summer squash**.

There are 3 colours of fruit, viz., white, yellow and green.

Yellow colour is due to a **dominant** gene (**Y**).

The **green** fruits are produced in a **recessive condition** (**yy**).

White colour is controlled by a **dominant** gene (**W**), white is **dominant over both yellow and green**. Thus, gene **W is epistatic to** the gene **Y**.

(Y_ww =Yellow fruits, yyww = green fruits, W_Y_/W_yy = white fruits).

- **Parents:** **White fruit** **X** **Yellow fruit**
- **Genotype:** WWyy wwYY
- **Gametes:** (Wy) (wY)
- **F_1 generation:** WwYy (**White fruit**)

Selfing of F_1 : **F_1** **X** **F_1**

Genotype: WwYy WwYy

Gametes: **(WY) (Wy) (wY) (wy)** **(WY) (Wy) (wY) (wy)**

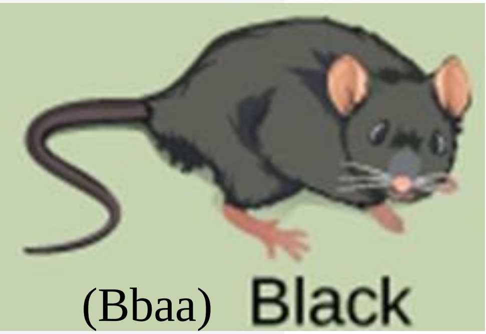
By Punnett's square method

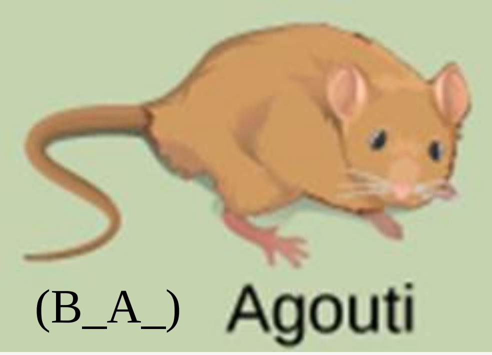
♂ / ♀	WY	Wy	wY	wy
WY				
Wy				
wY				
wy				

♂ / ♀	WY	Wy	wY	wy
WY	WWYY	WWYy	WwYY	WwYy
	(White)	(White)	(White)	(White)
Wy	WWYy	WWyy	WwYy	Wwyy
	(White)	(White)	(White)	(White)
wY	WwYY	WwYy	wwYY	wwYy
	(White)	(White)	(Yellow)	(Yellow)
wy	WwYy	Wwyy	wwYy	wwyy
	(White)	(White)	(Yellow)	(Green)

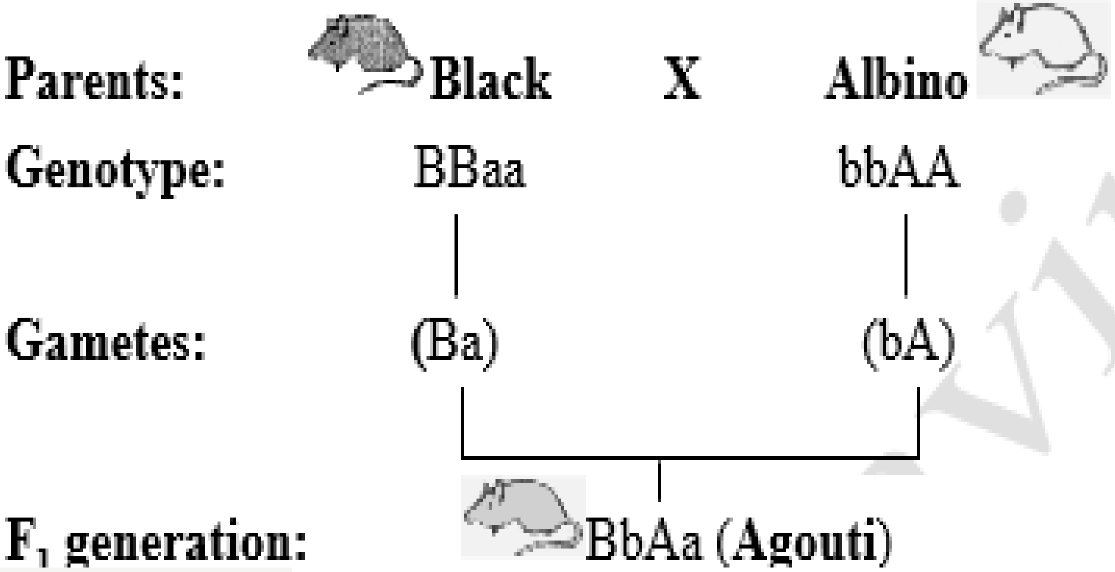
F_2 phenotypic ratio = 12: 3: 1 (12 White: 3 Yellow: 1 Green)

2. Recessive Epistasis/ Supplementary gene (9:3:4 Ratio):

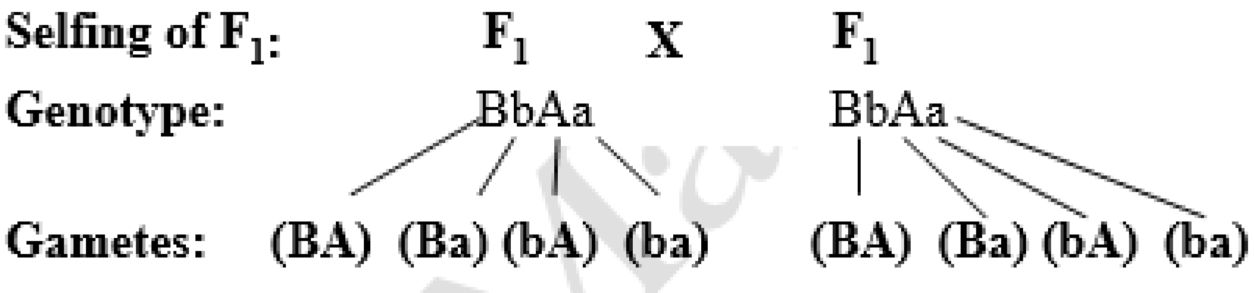




- When one dominant gene produce its effect irrespective of presence or absence of other gene.
- But the second gene can produce its effect in presence of the first, then it is known as recessive epistasis, also known as supplementary epistasis. A good example is **Coat colour in mice**.
- Dominant gene (B) produces black coat colour (BBaa). In presence of another dominant gene (A) agouti coat colour (hair black at base followed by yellow band followed by black or brown tip) is produced (B_A_). But albino coat is produced in absence of dominant gene B (bb_ _).
- When a black mouse is mated at an albino (both true breeding) the F_1 produces all agouti by gene interaction.



Parents: Black X Albino
Genotype: BBaa bbAA
Gametes: (Ba) (bA)
F_1 generation: BbAa (Agouti)



Selfing of F_1: F_1 X F_1
Genotype: BbAa BbAa
Gametes: (BA) (Ba) (bA) (ba) (BA) (Ba) (bA) (ba)

By Punnett's square method

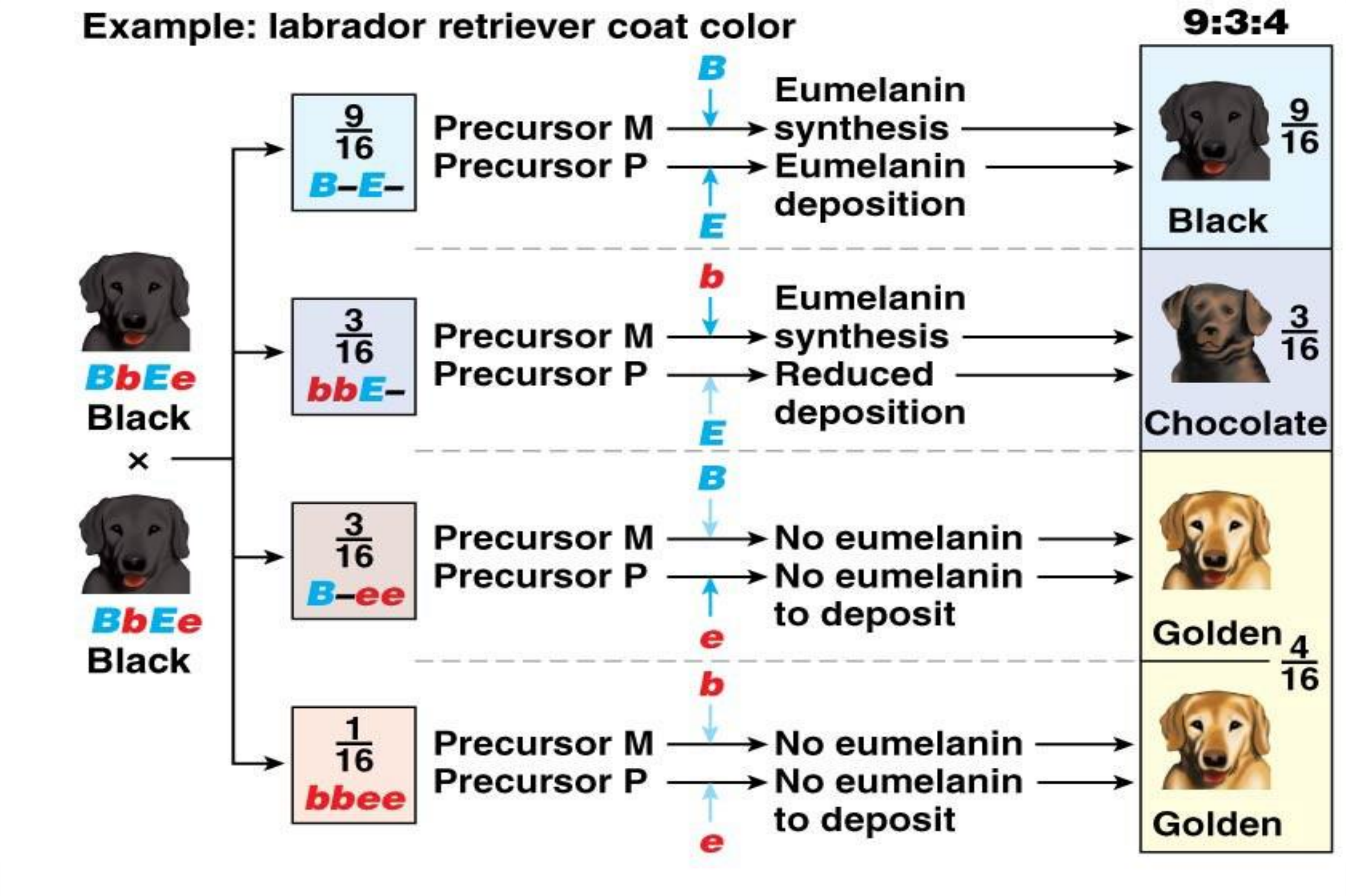
♂/♀	BA	Ba	bA	ba
BA				
Ba				
bA				
ba				

In this case gene B is supplements A. Since A and B both are needed for agouti colour. Absence of A in the dominant form promotes the expression of B and when the recessive aa alleles are present the mice are albinos.

Black colour develops only in the presence of recessive gene aa and at least one dominant gene B.

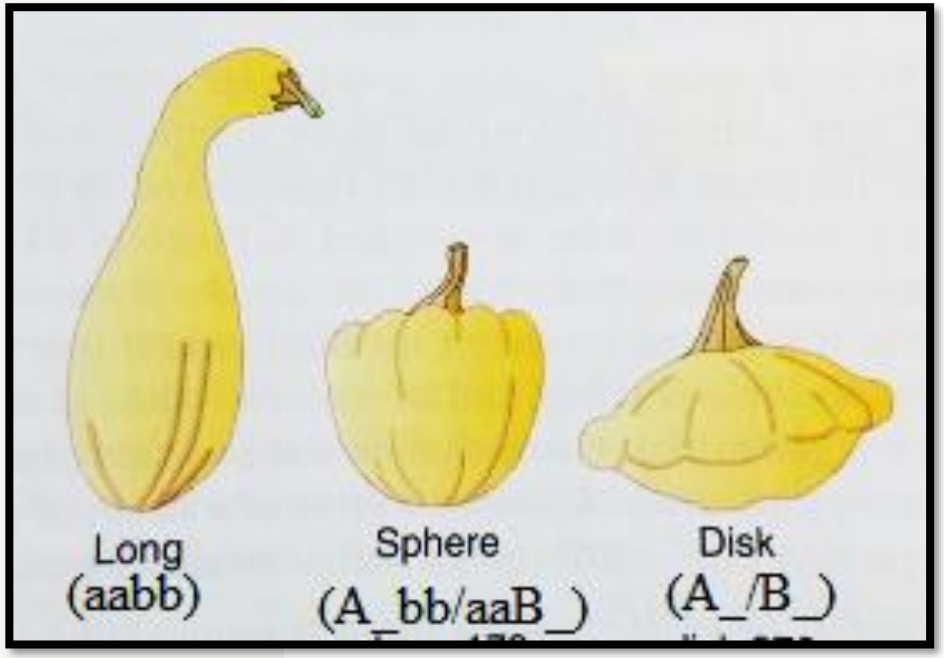
♂ /♀	BA	Ba	bA	ba
BA	BBAA	BBAa	BbAA	BbAa
	(Agouti)	(Agouti)	(Agouti)	(Agouti)
Ba	BBAa	BBaa	BbAa	Bbaa
	(Agouti)	(Black)	(Agouti)	(Black)
bA	BbAA	BbAa	bbAA	bbAa
	(Agouti)	(Agouti)	(Albino)	(Albino)
ba	BbAa	Bbaa	bbAa	bbaa
	(Agouti)	(Black)	(Albino)	(Albino)

F_2 phenotypic ratio = 9: 3: 4 (9 Agouti: 3 Black: 4 Albino)


Example: labrador retriever coat color
9:3:4
BbEe
Black
×
BbEe
Black
9/16
B–E–
Precursor M
Precursor P
B
E
Eumelanin synthesis
Eumelanin deposition
Black
9/16
3/16
bbE–
Precursor M
Precursor P
b
E
Eumelanin synthesis
Reduced deposition
Chocolate
3/16
3/16
B–ee
Precursor M
Precursor P
B
e
No eumelanin
No eumelanin to deposit
Golden
4/16
1/16
bbee
Precursor M
Precursor P
b
e
No eumelanin
No eumelanin to deposit
Golden

3. Duplicate genes with cumulative/additive effect/Polymeric Gene Interaction (9:6:1 Ratio):

2 dominant alleles have similar effect when they are separate but produce enhanced effect when they come together. It is known as polymeric gene interaction. The joint effect of 2 alleles appears to be additive or cumulative, but each of the two genes shows complete dominance, hence they cannot be considered as additive genes. In case of additive effect, genes show lack of dominance.



A well-known example is **fruit shape in summer squash** (*Cucurbita pepo*). There are 3 types of fruit shape, viz., disc, spherical and cylindrical.

The disc shape is controlled by 2 dominant genes (A and B), the spherical shape is produced by either dominant allele (A or B) (Spherical fruits = Aabb/ AAbb/ aaBa/ aaBb) and long fruits are developed in double recessive (aabb) plants.

Inter-mating of F$_1$ plants produced plants with disc, spherical and long shape fruits in 9 : 6 : 1 ratio in F$_2$. This can be explained as follow:

- **Parents:** **Disc fruit** **X** **Long fruit**
- **Genotype:** AABB aabb
- **Gametes:** (AB) (ab)
- **F_1 generation:** AaBb (**Disc fruit**)

Selfing of F_1 : **F_1** **X** **F_1**

Genotype: AaBb AaBb

Gametes: **(AB) (Ab) (aB) (ab)** **(AB) (Ab) (aB) (ab)**

By Punnett's square method

♂ / ♀	AB	Ab	aB	ab
AB				
Ab				
aB				
ab				

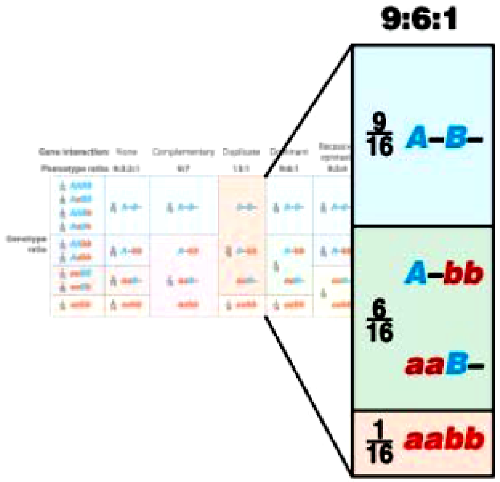
Plants with A_B_ genotypes produce disc fruits, those with A_bb_ and aaB_ genotypes produce spherical fruits, and plants with aabb genotype produce long fruits.

Thus, in F_2, normal dihybrid segregation ratio 9:3:3: 1 is modified to 9: 6: 1 ratio. Similar gene action is also found in barley for awn length.

♂ / ♀	AB	Ab	aB	ab
AB	AABB	AABb	AaBB	AaBb
	(Disc)	(Disc)	(Disc)	(Disc)
Ab	AABb	AAbb	AaBb	Aabb
	(Disc)	(Spherical)	(Disc)	(Spherical)
aB	AaBB	AaBb	aaBB	aaBb
	(Disc)	(Disc)	(Spherical)	(Spherical)
ab	AaBb	Aabb	aaBb	aabb
	(Disc)	(Spherical)	(Spherical)	(Long)

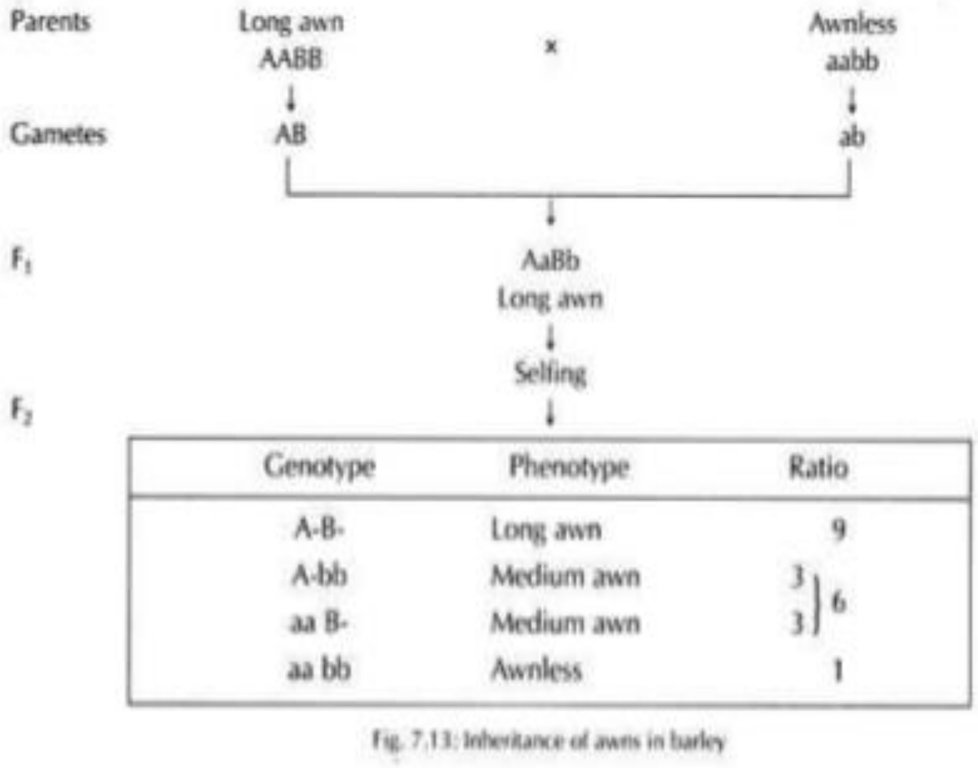
F_2 phenotypic ratio = 9: 6: 1 (9 Disc: 6 Spherical: 1 Long).

③ Dominant gene interaction



Dominant gene interaction occurs between genes that each contribute to a phenotype producing one. One phenotype if dominant alleles are present at each gene, a second phenotype if recessive alleles are homozygous for either gene, and a third phenotype if recessive homozygosity occurs at both genes.

Eg: Awn length in barley



Parents Long awn AABB × Awnless aabb

Gametes AB ab

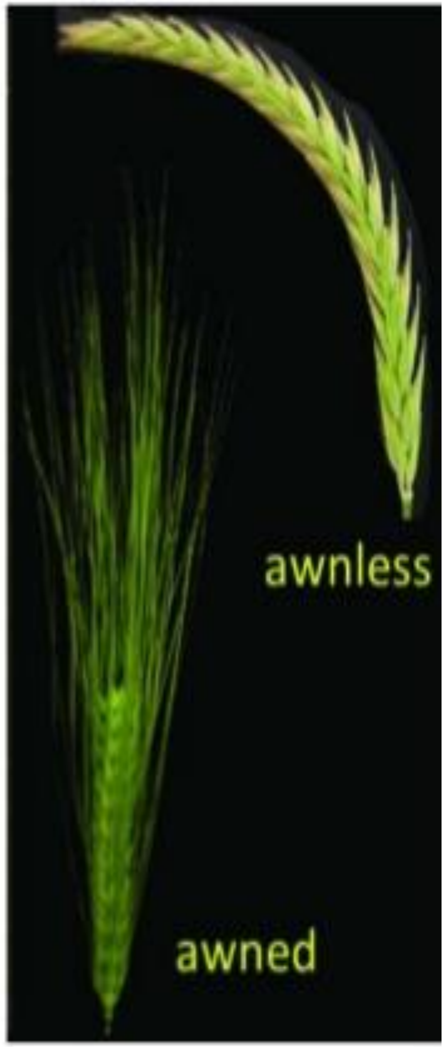
F₁ AaBb Long awn

Selfing

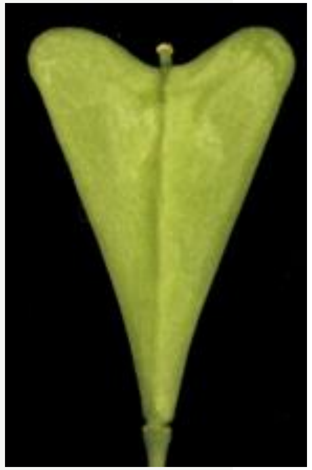
F₂

Genotype	Phenotype	Ratio
A-B-	Long awn	9
A-bb	Medium awn	3 } 6
aa B-	Medium awn	3
aa bb	Awnless	1

Fig. 7.13: Inheritance of awns in barley



4. Duplicate Dominant Epistasis (15 : 1 Ratio):



Triangular
(A _ B_/A_ _ _/_ _B_)

Spindle
(aabb)

When a dominant allele at either of 2 loci can mask the expression of recessive alleles at the 2 loci, it is known as duplicate dominant epistasis. This is also called duplicate gene action.

A good example is **fruit shape in *Capsella***.

Development of fruit is controlled by 2 dominant duplicate genes (A and B). Presence of any of these 2 alleles can produce triangular fruits. The spindle fruit develops only when both these genes are in homozygous recessive state (aabb).

A cross between triangular and spindle fruit produced triangular fruits in F_1. Inter-mating of F_1 plants produced triangular and spindle fruits in 15: 1 ratio in F_2 generation. This can be explained as follows:

- **Parents:** **Triangular fruit** **X Spindle fruit**
- **Genotype:** AABB aabb
- **Gametes:** (AB) (ab)
- **F_1 generation:** AaBb (**Triangular fruit**)

Selfing of F_1 : **F_1** **X** **F_1**

Genotype: AaBb AaBb

Gametes: **(AB) (Ab) (aB) (ab)** **(AB) (Ab) (aB) (ab)**

The A is epistatic to B/b and all plants having A will develop triangular fruits.

Another dominant allele B is epistatic to A/a. Individuals with this allele also will develop triangular fruits.

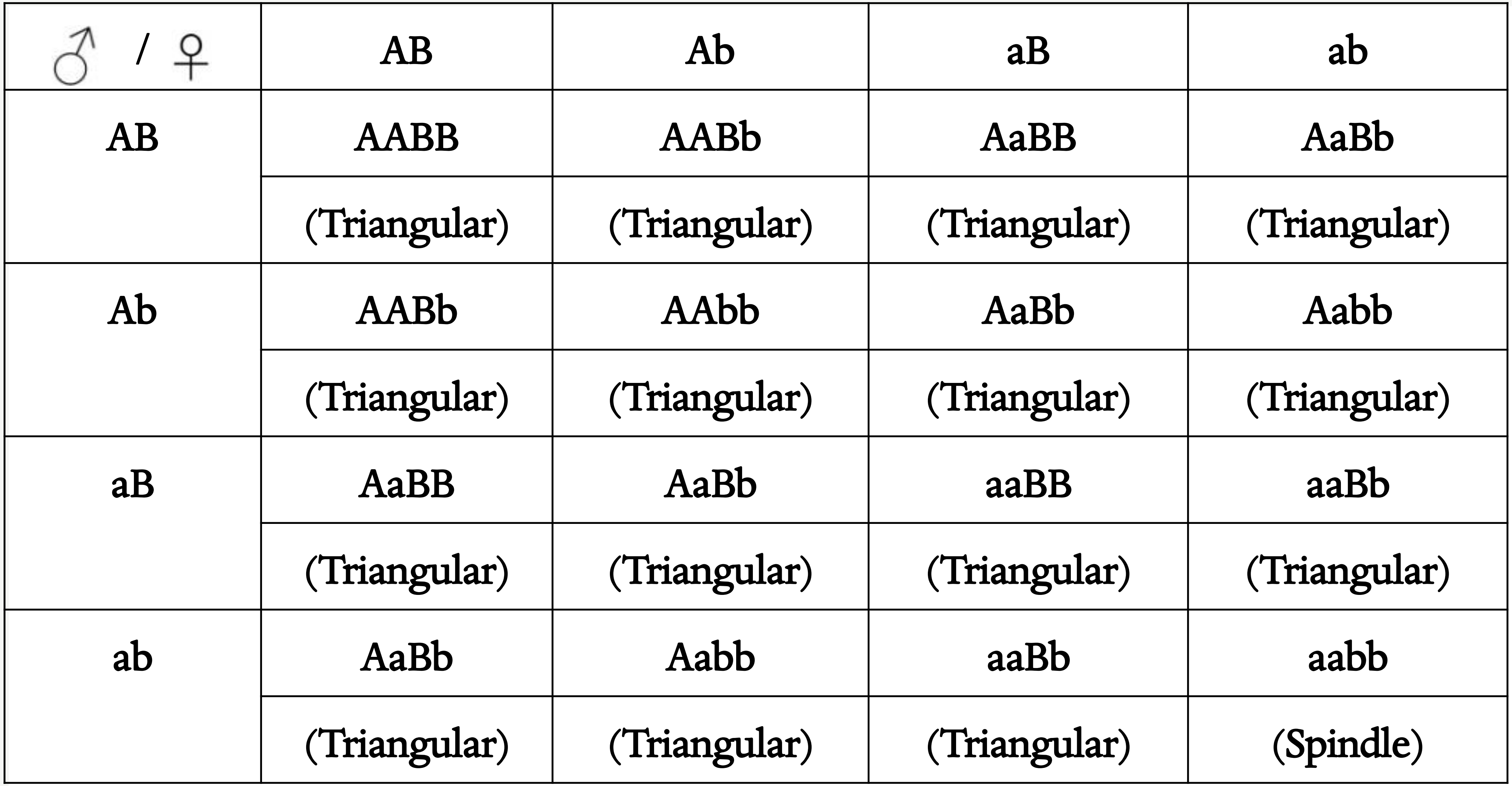
Hence in F_2, plants with A_B_, A_bb and aaB_ genotypes will develop triangular fruits. The spindle fruits will develop only in double recessive (aabb) genotype.

In this way only two classes of plants are developed and the normal dihybrid segregation ratio 9: 3: 3: 1 is modified to 15: 1 ratio in F_2.

Similar gene action is found for nodulation in peanut and development of awn in rice.

By Punnett's square method

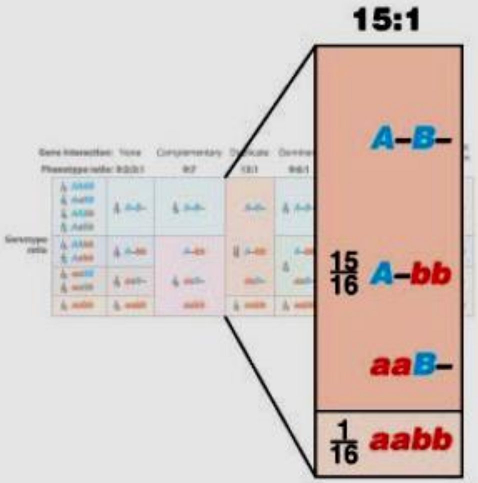
♂ / ♀	AB	Ab	aB	ab
AB				
Ab				
aB				
ab				



♂ / ♀	AB	Ab	aB	ab
AB	AABB	AABb	AaBB	AaBb
	(Triangular)	(Triangular)	(Triangular)	(Triangular)
Ab	AABb	AAbb	AaBb	Aabb
	(Triangular)	(Triangular)	(Triangular)	(Triangular)
aB	AaBB	AaBb	aaBB	aaBb
	(Triangular)	(Triangular)	(Triangular)	(Triangular)
ab	AaBb	Aabb	aaBb	aabb
	(Triangular)	(Triangular)	(Triangular)	(Spindle)

F_2 phenotypic ratio = 15: 1 (15 Triangular: 1 Spindle).

② Duplicate gene interaction



15:1

A–B–

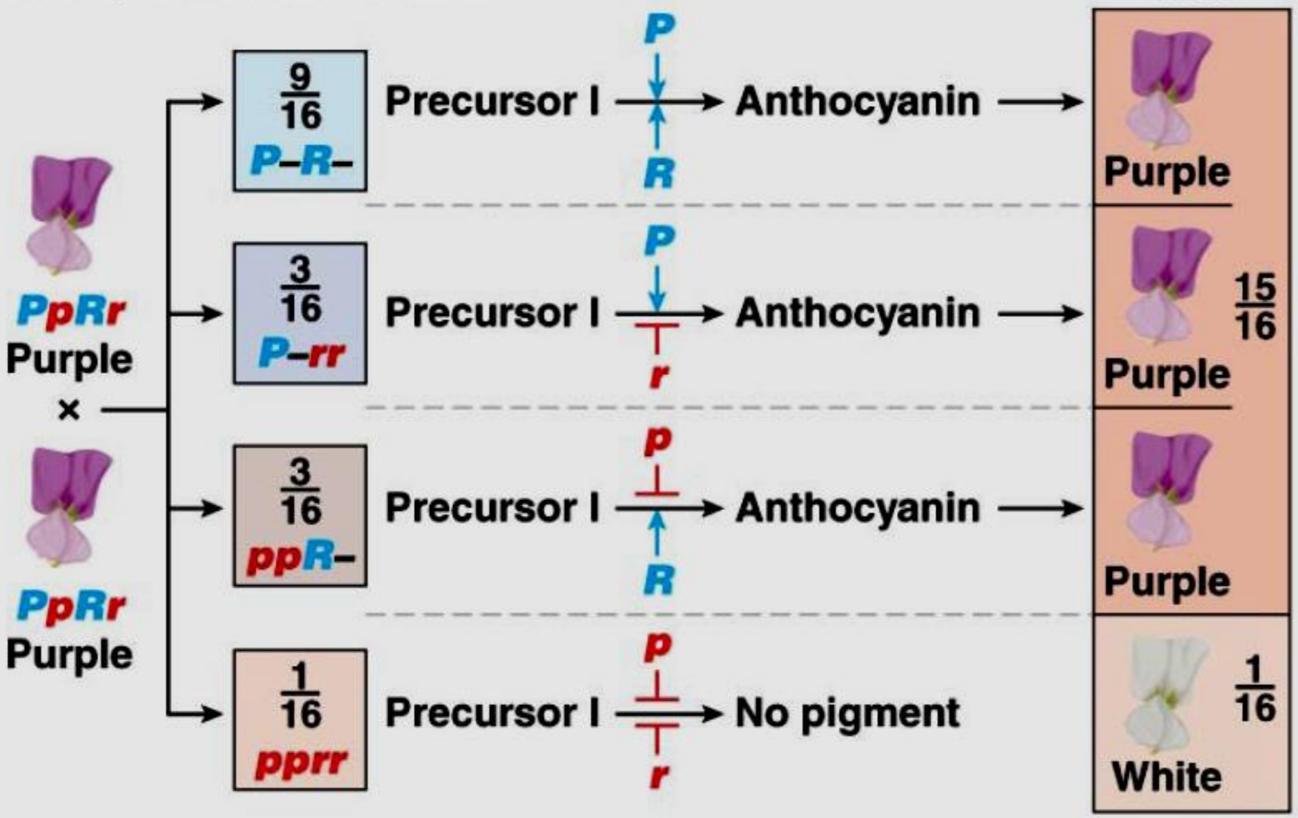
15/16 A–bb

aaB–

1/16 aabb

Duplicate gene interaction allows dominant alleles of either duplicate gene to produce the wild-type phenotype. Only organisms with homozygous mutations of both genes have a mutant phenotype.

Example: bean flower color



15:1

PpRr Purple × PpRr Purple

9/16 P–R–: Precursor I → Anthocyanin (P, R) → Purple

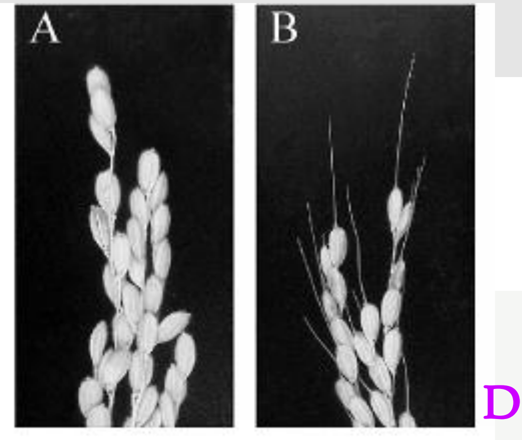
3/16 P–rr: Precursor I → Anthocyanin (P, r) → Purple

3/16 ppR–: Precursor I → Anthocyanin (p, R) → Purple

1/16 pprr: Precursor I → No pigment (p, r) → White

15/16 Purple

1/16 White



Development of awn in rice.

5. Duplicate Recessive Epistasis / Complementary gene (9 : 7 Ratio):

(C_P_ = Purple)

(CCpp / Ccpp / ccPP/ ccPp/ ccpp = white)

When recessive alleles at either of the 2 loci can mask the expression of dominant alleles at the 2 loci, it is called duplicate recessive epistasis or complementary epistasis. The best example is **flower colour in sweet pea** (*Lathyrus odoratus*).

The flowers of the wild type are purple and dominant over white.

Both the 2 dominant genes C and P are essential to produce purple colour. The formation of the pigment involves the conversion of the precursor to an intermediate compound with the help of an enzyme synthesized by gene C and the conversion of this intermediate compound to the pigment with the help of another enzyme synthesized by gene P.

Thus, the absence of either gene prevents the development of anthocyanin pigment, and the flowers are white. (C_P_ = Purple flowers; CCpp / Ccpp / ccPP/ ccPp/ ccpp = white flowers)

Bateson and Punnet crossed two white flowers and obtained purple flowers in F_1 when the F_1 were allowed to inbreed, the F_2 had 9 purple and 7 white flowers (9 : 3 : 3 : 1 modified to 9 : 7).

- **Parents: White X White**
- **Genotype:** CCpp ccPP
- **Gametes:** (Cp) (cP)
- **F_1 generation: CcPp (Purple)**

Selfing of F_1 : F_1 X F_1

Genotype: CcPp CcPp

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

Here recessive c is epistatic to P/p and mask the expression. Another recessive p is epistatic to C/c and masks their expression.

Hence in F_2, plants with C_P_ genotypes will have purple flowers, and plants with CCpp / Ccpp / ccPP/ ccPp/ ccpp genotypes produce white flowers.

Thus only 2 phenotypic classes, viz., purple and white are produced.

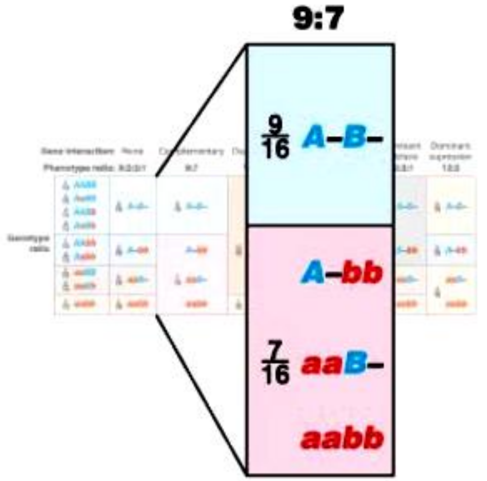
Another example of duplicate recessive epistasis is the inheritance of deafnessin humans.

♂ / ♀	CP	Cp	cP	cp
CP				
Cp				
cP				
cp				

♂ / ♀	CP	Cp	cP	cp
CP	**CCPP**	**CCPp**	**CcPP**	**CcPp**
	(Purple)	(Purple)	(Purple)	(Purple)
Cp	**CCPp**	**CCpp**	**CcPp**	**Ccpp**
	(Purple)	(White)	(Purple)	(White)
cP	**CcPP**	**CcPp**	**ccPP**	**ccPp**
	(Purple)	(Purple)	(White)	(White)
cp	**CcPp**	**Ccpp**	**ccPp**	**ccpp**
	(Purple)	(White)	(White)	(White)

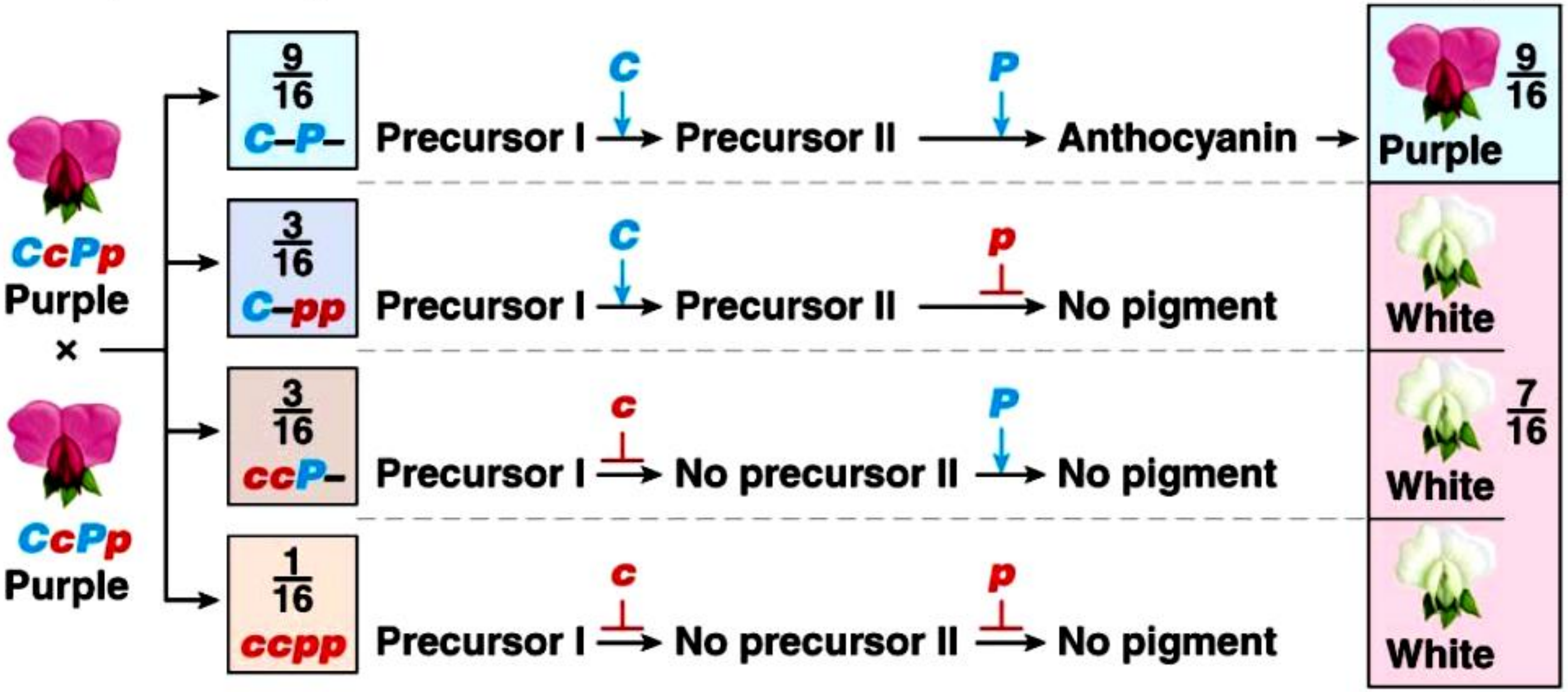
F_2 phenotypic ratio = 9: 7 (9 Purple: 7 White).

① Complementary gene interaction



Complementary gene interaction occurs when genes must act in tandem to produce a phenotype. The wild-type action from both genes is required to produce the wild-type phenotype. Mutation of one or both genes produce a mutant phenotype.

Example: sweet pea flower color



6. Dominant – recessive interaction /Inhibitory or suppressor genes (13 : 3 Ratio):

- A dominant allele at one locus can mask the expression of both (dominant and recessive) alleles at second locus. Also known as **inhibitory gene interaction**.
- e.g., **Anthocyanin pigmentation in rice.**
- The green colour of plants is due to gene I which is dominant over purple colour. The purple colour is controlled by another dominant gene P.
- When a cross was made between green (IIpp) and purple (iiPP) colour plants, the F_1 was green. Inter-mating of F_1 plants produced green and purple plants in 13 : 3 ratio in F_2.
- Here the allele I is epistatic to alleles P and p. Hence in F_2, plants with I_P_, I_pp and iipp genotypes will be green because I will mask the effect of P or p. Plants with iiP_ will be purple, because I is absent.
- In this way the normal dihybrid segregation ratio 9: 3: 3: 1 is modified to 13: 3 ratio. Similar gene interaction is found for grain colour in maize, plumage colour in poultry and certain characters in other crop species.

Parents: Green X Purple
Genotype: IIpp iiPP
Gametes: (Ip) (iP)

F_1 generation: IiPp (Green)

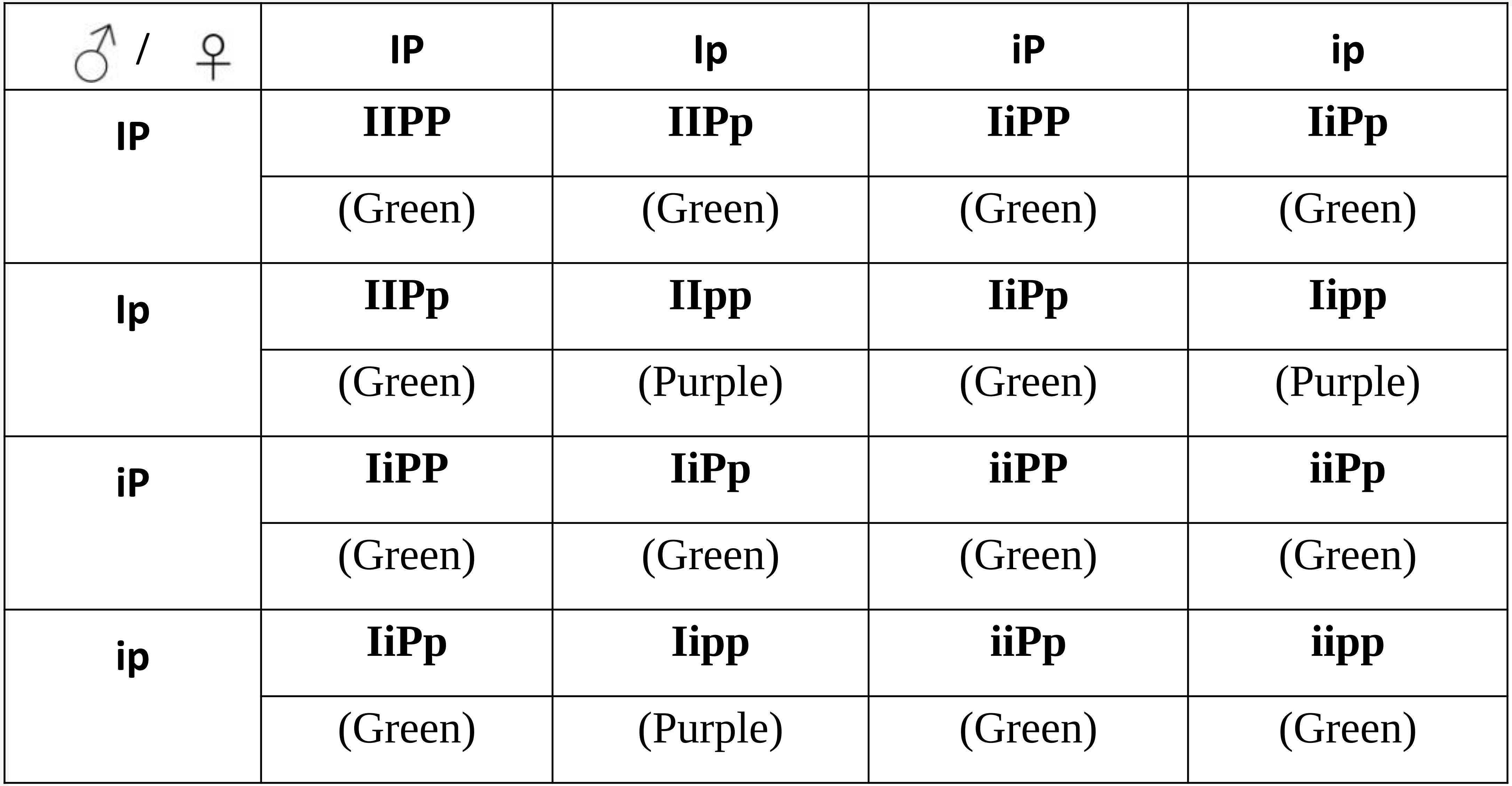
Selfing of F_1 : F_1 X F_1
Genotype: IiPp IiPp
Gametes: (IP) (Ip) (iP) (ip) (IP) (Ip) (iP) (ip)

By Punnett's square method:-

Green
I_P_, I_pp and iipp

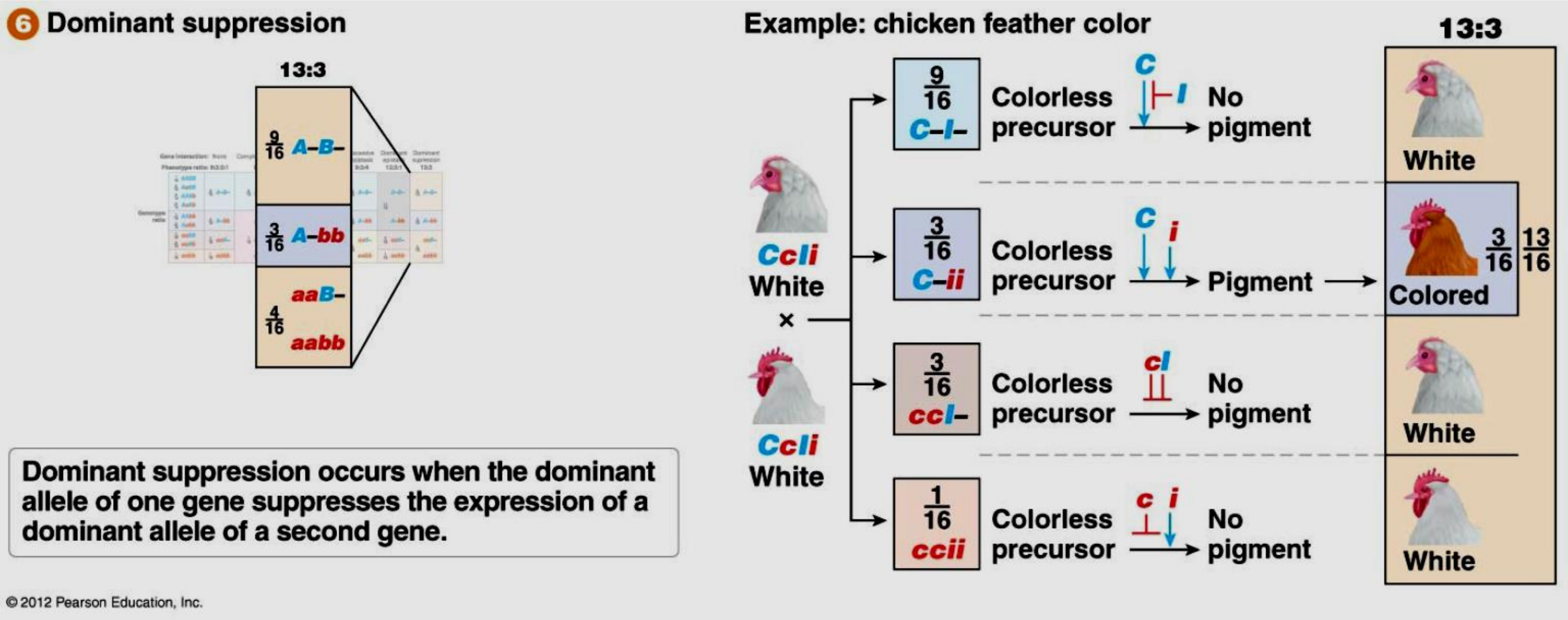
Purple
iiP_

♂ / ♀	IP	Ip	iP	ip
IP				
Ip				
iP				
ip				



♂ / ♀	IP	Ip	iP	ip
IP	IIPP	IIPp	IiPP	IiPp
	(Green)	(Green)	(Green)	(Green)
Ip	IIPp	IIpp	IiPp	Iipp
	(Green)	(Purple)	(Green)	(Purple)
iP	IiPP	IiPp	iiPP	iiPp
	(Green)	(Green)	(Green)	(Green)
ip	IiPp	Iipp	iiPp	iipp
	(Green)	(Purple)	(Green)	(Green)

F_2 phenotypic ratio = 13: 3 (13 Green : 3 Purple).



6 Dominant suppression

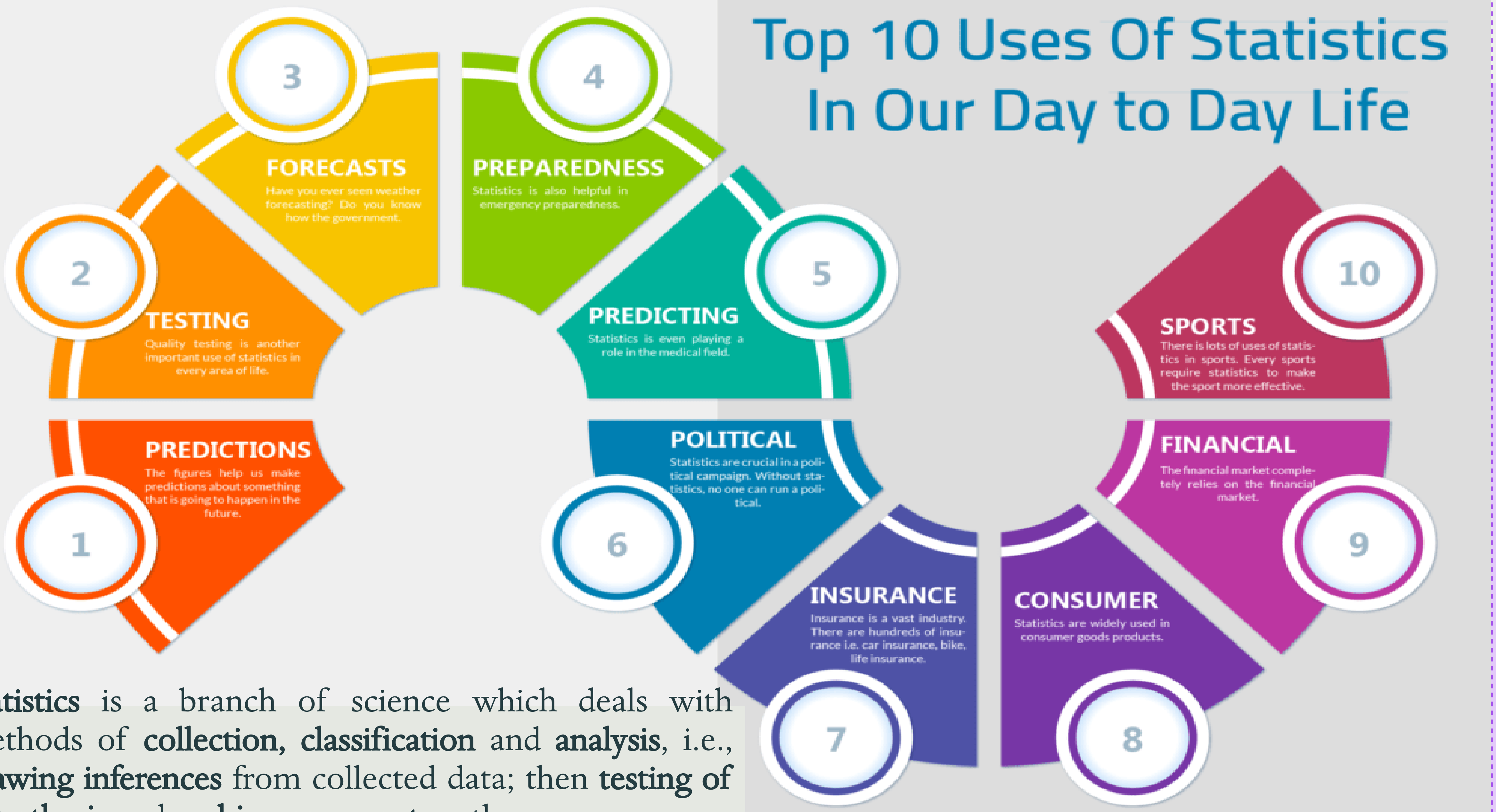
Dominant suppression occurs when the dominant allele of one gene suppresses the expression of a dominant allele of a second gene.

bi·o·sta·tis·tics

bīōstə'tistiks

noun

the branch of statistics that deals with data relating to living organisms.



Top 10 Uses Of Statistics In Our Day to Day Life

PREDICTIONS
The figures help us make predictions about something that is going to happen in the future.

TESTING
Quality testing is another important use of statistics in every area of life.

FORECASTS
Have you ever seen weather forecasting? Do you know how the government.

PREPAREDNESS
Statistics is also helpful in emergency preparedness.

PREDICTING
Statistics is even playing a role in the medical field.

POLITICAL
Statistics are crucial in a political campaign. Without statistics, no one can run a political.

INSURANCE
Insurance is a vast industry. There are hundreds of insurance i.e. car insurance, bike, life insurance.

CONSUMER
Statistics are widely used in consumer goods products.

FINANCIAL
The financial market completely relies on the financial market.

SPORTS
There is lots of uses of statistics in sports. Every sports require statistics to make the sport more effective.

Statistics is a branch of science which deals with methods of **collection, classification** and **analysis**, i.e., **drawing inferences** from collected data; then **testing of hypothesis** and **making comment** on these.

Biostatistics (Biometry)

- It is the theoretical & practical application of statistical concepts and techniques to topics in biology. Because biology is such a broad field — studying all forms of life from viruses to trees to fleas to mice to people.
- Biostatistics covers a very wide area, including designing biological experiments, safely conducting research on human beings, collecting and verifying data from those studies, summarizing and displaying that data, and analyzing the data to draw meaningful conclusions from it and the interpretation and presentation of the results of those analyses.

- **Biostatistics is a branch of statistics dealing with use of its theories and methods for collection, analysis and interpretation of biological data. One of the most important purposes of biometry is to provide statistical methods to analyze biological data.**

Characteristics of biostatistics:

i. Numerical data should be aggregates of facts.

ii. Data should be affected to a marked extent by multiplicity of causes.

iii. Data should be numerically expressed.

iv. Data should be enumerated or estimated according to reasonable standards of accuracy.

v. Data should be collected in a systematic manner.

vi. Data should be collected for a predetermined purpose.

vii. Data should be placed in relation to each other.

Numerical data should be aggregates of facts.

- In the plural sense, statistics refers to data, but data to be called statistics must consist of aggregate of certain facts.
- A single and isolated fact or figure like, 60 Kgs. weight of a student or the death of a particular person on a day does not amount to statistics.
- The data must be in the form of a set or aggregate of certain facts, viz. 50, 65, 70 Kgs. Weight of students in a class is liable to be affected by multiplicity of causes.
- Only those facts which are capable of being studied in relation to time, place or frequency can be called statistics.
- e.g., data relating to I.Q. of a group of students, academic achievement of students, etc. can be studied in relation to each other.

Data should be affected to a marked extent by multiplicity of causes.

- It is not easy to study the effects of one factor only by ignoring the effects of other factors. So, the effects of all the factors on the phenomenon should be studied, because effects of the factors can change with change of place, time or situation.
- For example, we can say that result of class XII in board examination does not depend on any single factor but collectively on standard of teachers, teaching methods, teaching aids, practical's performance of students, standard of question papers and as well as of evaluation.
- Similarly scores on memory test of a group certainly depend on meaningfulness of learning materials, maturity of the students, methods of learning, motivation, interest of the students, etc.

Data should be numerically expressed.

- Qualitative phenomena which cannot be numerically expressed, cannot be described as statistics e.g., honesty, goodness, ability, etc.
- But if we assign numerical expression, it maybe described as statistics.
- It means that the data or the fact to constitute statistics must be capable of being expressed in some quantitative form as weights of 60, 70, 100 and 90 Kg. or profits of Rs. 10,000, Rs. 20,000 etc.
- Thus, these data must contain numerical figures so that those may be called as numerical statement of facts.

Data should be enumerated or estimated according to reasonable standards of accuracy.

- The standard of estimation and of accuracy differs from enquiry to enquiry or from purpose to purpose. There cannot be one standard of uniformity for all types of enquiries and for all purposes.
- A single student cannot be ignored while calculating I.Q. of 100 students in group whereas 10 students can be easily ignored while finding out I.Q. of students of whole country.
- Similarly, we can ignore 10 deaths in a country, but we cannot ignore even a single death in a family.
- The amount of time and resources at disposal also determine the amount of accuracy in estimates.

Data should be collected in a systematic manner.

- In order to have reasonable standard of accuracy statistics must be collected in a very systematic manner.
- Any rough and haphazard method of collection will not be desirable for that may lead to improper and wrong conclusion.
- Accuracy will also be not definite and as such cannot be believed.
- A proper plan should be made, and trained investigators should be used to collect data so that they may collect statistics.
- So, to get correct results the data must be collected in a precise manner.

Data should be collected for a predetermined purpose.

- The investigator must have a predefined purpose.
- Data collected without any purpose is of no use.
- Suppose we want to know intelligence of a section of people, we must not collect data relating to income, attitude and interest.
- Without having a clear idea about the purpose, we will not be able to distinguish between necessary and unnecessary data.

Data should be placed in relation to each other.

- Statistics is a method for the purpose of comparison etc.
- It must be capable of being compared, otherwise, it will lose much of its value and significance.
- Comparison can be made only if the data are homogeneous.
- Data on memory test can be compared with I.Q. not with salary status of parents.
- It is with the use of comparison only that we can depict changes which may relate to time, place, frequency or any other character, and statistical devices are used for this purpose.

Application of Biostatistics:

1. To study the distribution or inheritance of given character e.g., height of organism, etc.
2. To study correlation of two characters in a population. Such as height and weight—whether weight increases or decreases proportionately with height.
3. The laws of probability are of importance in genetics for forecasting the chance from a cross and elucidating the operation of genetic principle.
4. Study of alleles of genes in populations and the factors which maintain or change the frequencies of particular genotype in populations can be studied.
5. In case of plant breeding whether Mendelian Genetics is being followed or not, can be tested.

Application of Biostatistics:

6. The application of fertilizers or irrigation or any kind of cultural practice can be effectively justified by application of test of significance.
7. To find the action of drug—a drug is given to animals or humans to see whether the changes produced are due to the drug or by chance.
8. To compare the action of two different drugs or two successive dosages of the same drug.
9. To identify signs and symptoms of a disease or syndrome.
10. For designing research experiments, selecting methods of collection, analysis & interpretation of data, also drawing conclusions.

Limitation of Biometry:

(a) All the conclusions about statistical analysis depend on the availability of sample data. If the sampling is biased, the analysis will be erotic.

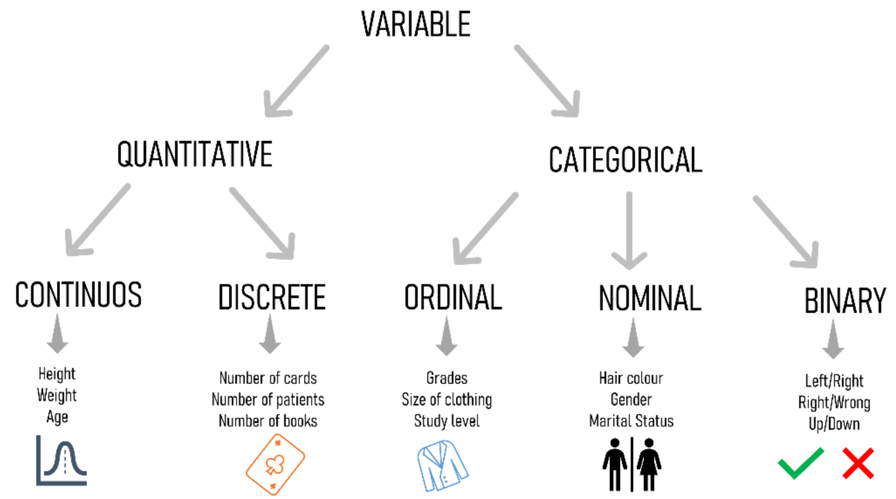
(b) Statistics can be used and applied only on collective data, not on individual data.

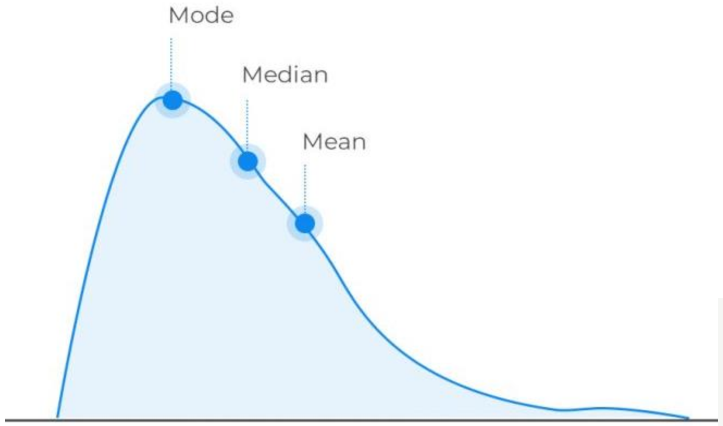
(c) Statistical laws are always true in case of large population on the average, not on the small sample.

Common Statistical Terms:

1. **Variable**: A characteristic that takes on different values in different persons, places or things. A quantity that varies within limits such as height, weight, blood pressure, age, etc. It is denoted as X and notation for orderly series as $X1$, $X2$, $X3$, …. Xn. The suffix n is symbol for number in the series. Σ (sigma) stands for summation or results or observation.

2. **Constant**: Quantities that do not vary such as $\pi = 3.1416$, $e = 2.7183$. They do not require statistical study. In biostatistics, mean, standard deviation, standard error, correlation coefficient and proportion of a particular population are considered as constant.

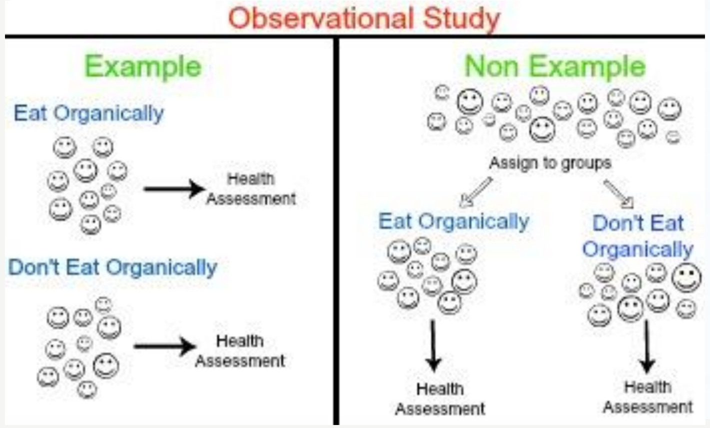


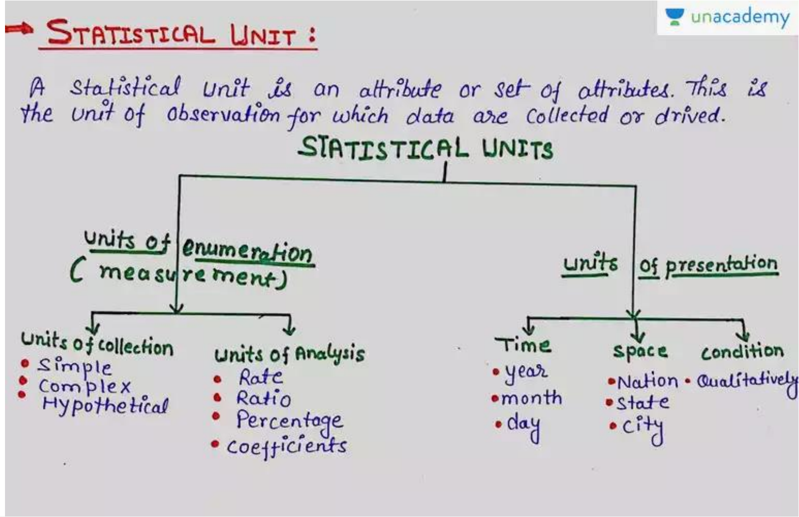


3. **Observation**: An event and its measurements such as blood pressure (event) and 120 mmHg (measurement).

4. **Observational unit**: The source that gives observations such as object, person, etc. In medical statistics the term individuals or subjects is used more often.

5. **Data**: A set of values recorded on one or more observational units. Data are raw materials of statistics.





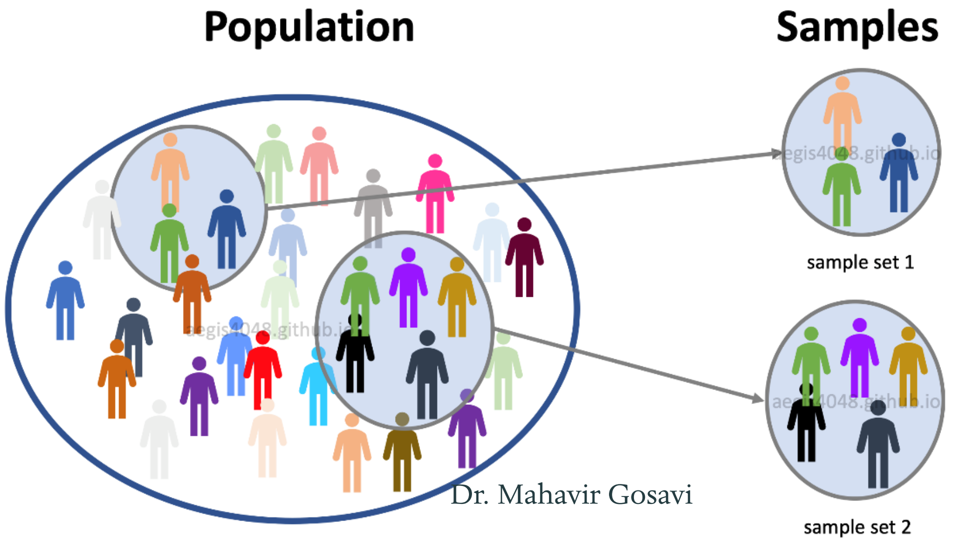
STATISTICAL UNIT :

A Statistical unit is an attribute or set of attributes. This is the unit of observation for which data are Collected or drived.

6. **Population**: It is the entire group of study specimens or individuals having some common characteristic or parameter to be analyzed.

7. **Sample**: It is relatively small group of study specimens or individuals of a definite number. It is drawn from population and considered as representative of the entire population. Sample analysis helps to throw light on the entire population characteristics or parameters understudy.

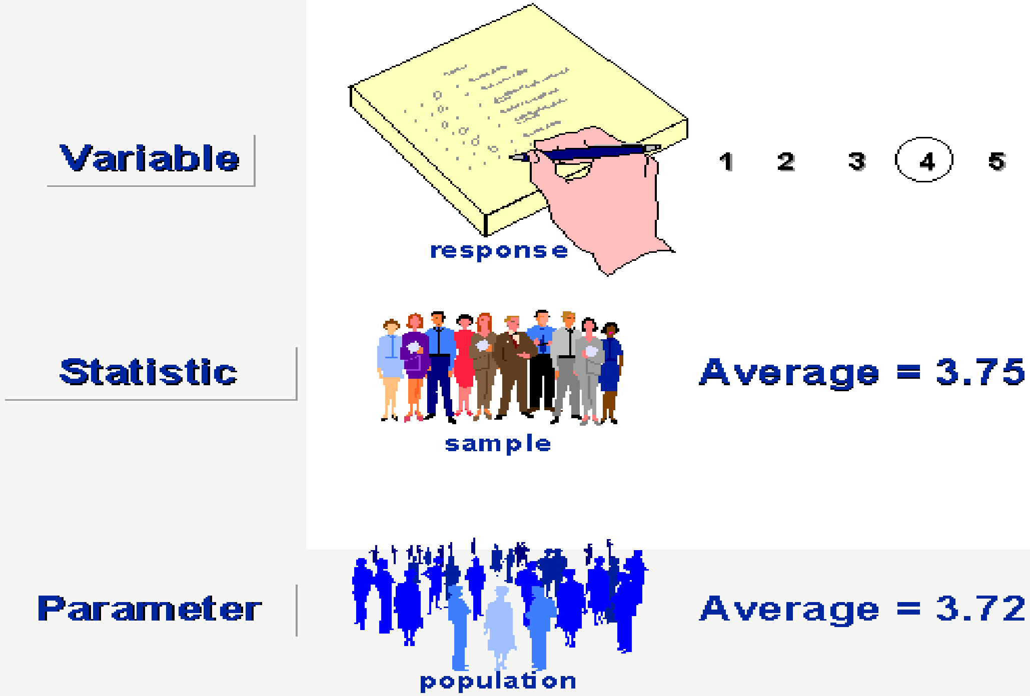
8. **Random sampling**: It involves random selection of sample (individuals or study specimens) from the population so that every individual in the population will get equal opportunities of getting included in the sample.

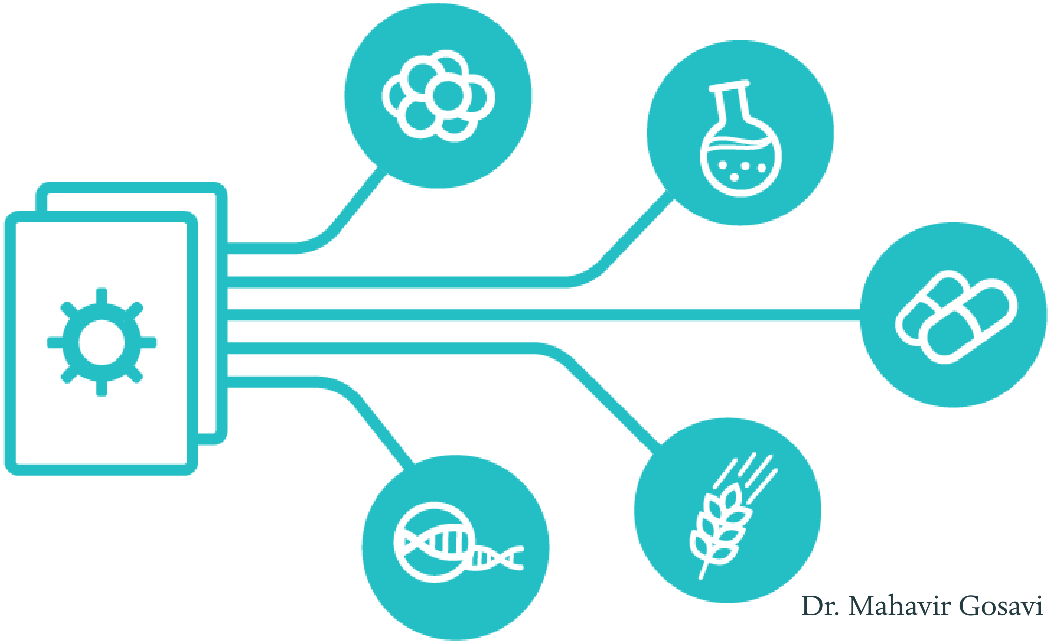


9. **Parameter**: It is a summary value or constant of a variable that describes the sample such as its mean, standard deviation, standard error, correlation coefficient, proportion, etc. This value is calculated from the sample and is often applied to population but may or may not be a valid estimate of population. Though not desirable, parameter and statistic are often used as synonyms.

10. Biological data: It is the collections of observations carried out by studying biological specimens. The collection is carried out either by survey or by simple counting or enumeration and the data is expressed in numerical values.

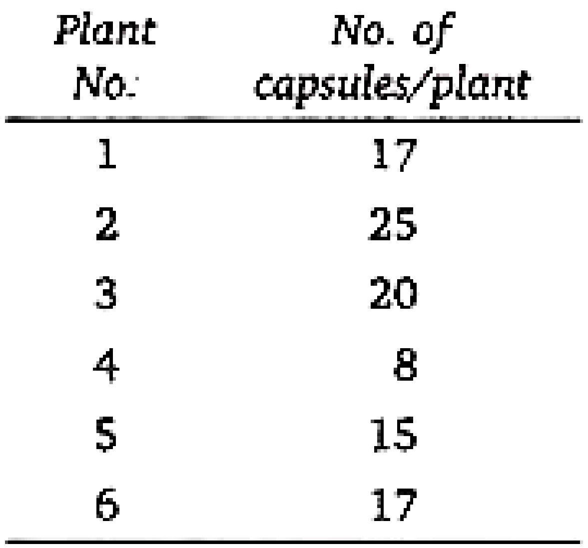
11. Variables: These are the numerical values or quantities obtained by studying biological data and they differ from individual to individual or specimen to specimen. The variables can be continuous or discontinuous.



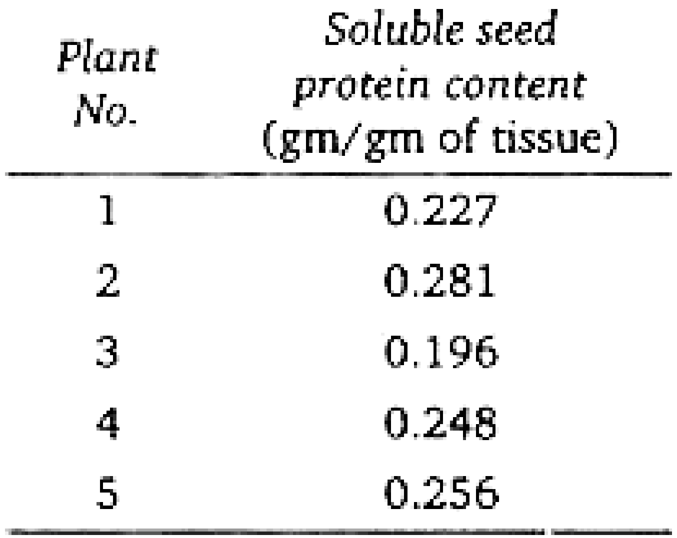


Data can be of 2 types, such as:

- **Qualitative**, e.g., flower colour, leaf shape, pupil colour of eye, etc., these are non-numerical characters.
- **Quantitative**, e.g., plant height, number of branches per plant, seeds per capsule, fish yield, etc. The item representing the quantitative characters is known as variable, that is, a character differing in value from one organism to another, from one sample to another.
- Again, variable may be **discrete or continuous**.
- Discrete the units are obtained by counting and such variables are always represented as integers.



Plant No.	*No. of capsules/plant*
1	17
2	25
3	20
4	8
5	15
6	17



Plant No.	*Soluble seed protein content* (gm/gm of tissue)
1	0.227
2	0.281
3	0.196
4	0.248
5	0.256

Measures of central tendency—averages:

Measures of ***central tendency*** and ***dispersion*** are common descriptive measures for summarizing numerical data.

1. Measures of central tendency: are measures of the location of the middle or the center of a distribution. The most frequently used are the ***mean***, ***median*** and ***mode***.

The ***mean*** is obtained by summing the values of all the observations and dividing by the number of observations.

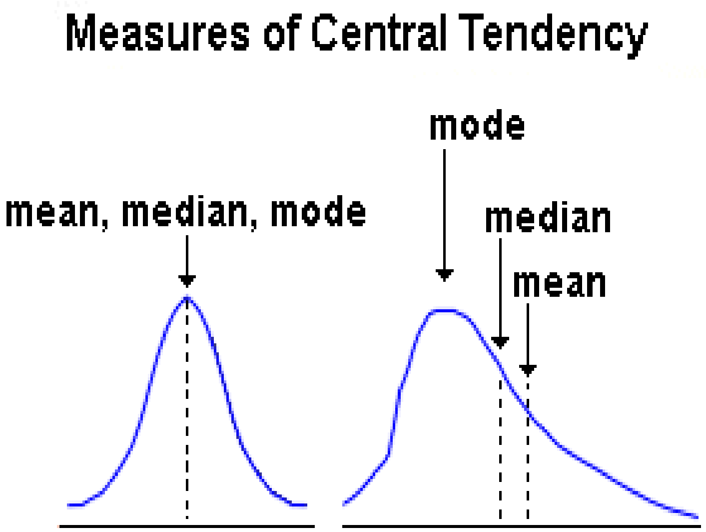
The ***median*** is the middle value in a sample of ordered values. Half the values are above the median and half are below the median.

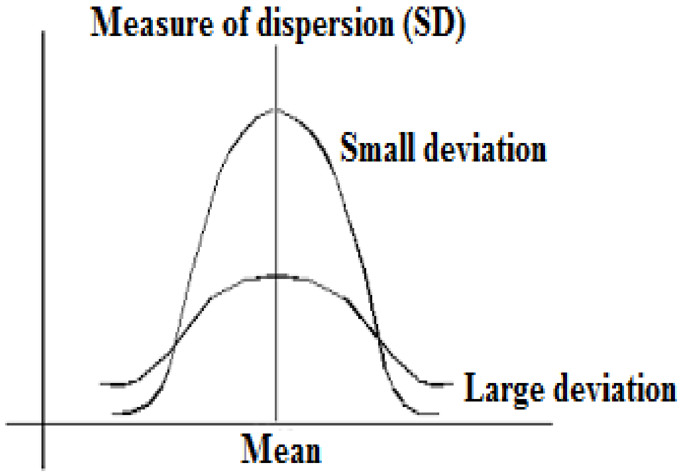
The ***mode*** is a value occurring most frequently. It is rarely of any practical use for numerical data.

The mean, median and mode are similar when the distribution is symmetrical. When the distribution is skewed the median is more appropriate as a measure of central tendency.

2. Measures of dispersion: is a numerical value describing the amount of variability present in a data set.

The **standard deviation (SD)** is the most commonly used with it we can measure dispersion relative to scatter of the values about their mean.





a) Arithmetic mean:

It is popularly known as average. It is calculated by dividing the sum of all the individual observations by the total number of observations. The Arithmetic mean is **represented by $\bar{X}$** and calculated by using following formula:

$\bar{X} = \sum x/n$ or $\bar{X} = \sum x/n$

- Where,
  - n = Total no. of observations
  - X = Single observation
  - Σ = Summation (total)
  - f = Frequency
- m = class mid-value

Examples: Calculate the arithmetic mean of marks obtained in Botany by 10 students out of 100 in Sem I.

Roll no.	1	2	3	4	5	6	7	8	9	10
Marks	67	69	66	68	72	63	76	65	70	74

Solution:

Roll no.	Marks
1	67
2	69
3	66
4	68
5	72
6	63
7	76
8	65
9	70
10	74
n= 10	**$\sum x = 690$**

$$\bar{X} = \sum x/n$$

$$= \frac{690}{10}$$

$$= 69$$

Thus, arithmetic mean of marks obtained in Botany by 10 students is 69.

Calculation of mean from grouped data

ii) The marks obtained by 30 students of FYBSc in a Botany paper consisting of 100 marks are presented in table below. Find the mean of the marks obtained by the students.

Marks obtained	10	20	36	40	50	56	60	70	72	80	88	92	95
No. of students	1	1	3	4	3	2	4	4	1	1	2	3	1

Solution: Let us convert the ungrouped data into grouped data by forming class-intervals of 15. While allocating frequencies to each class-interval, students falling in any upper class-limit would be considered in the next class.

$$X = \Sigma fm / \sum f = \frac{1860}{30}$$

$=$ 62, Thus, mean of marks obtained in Botany by 10 students is 62.

Class Intervals (x)	Mid Value (m)	Tally marks	Frequency (f)	Frequency × Mid value (fm)
10 – 25	17.5	||	2	35.0
25 – 40	32.5	|||	3	97.5
40 – 55	47.5	卌 ||	7	332.5
55 – 70	62.5	卌 |	6	375.0
70 – 85	77.5	卌 |	6	465.0
85 – 100	92.5	卌 |	6	555.0
			$\sum f = 30$	=1860

Merits of Mean:

1. It can be easily calculated.
2. Its calculation is based on all the observations.
3. It is easy to understand.
4. It is rigidly defined by the mathematical formula.
5. It is least affected by sampling fluctuations.
6. It is the best measure to compare two or more series of data.
7. It does not depend upon any position.

Demerits of Mean :

1. It may not be represented in actual data, so it is theoretical.
2. It is affected by extreme values.
3. It cannot be calculated if all the observations are not known.
4. It cannot be used for qualitative data i.e., love, beauty, honesty, etc.
5. It may lead to fallacious conditions in the absence of original observations.

Uses of Mean :

1. It is extremely used in medical statistics.
2. Estimates are always obtained by mean.

b) Median and median class

Middle value of a data when arranged either in ascending or descending order, represented as **'Me'**. It is the class which has approximately half of the cumulative frequency of that of the class having highest cumulative frequency.

Calculation of median from ungrouped data –

Arrange the values in ascending or descending order.

When the number of observations N, is odd, the middle most value –i.e., the $(N+1)/2$ th value in the arrangement will be the median.

When N is even, the A.M of $N/2$ th and $(N+1)/2$ th values of the variable will give the median.

* ESRs of 7 subjects are 3,4,5,6,4,7,5. Find the median.

Ans: Let us arrange the values in ascending order. **3,4,4,5,5,6,7**. Since N is odd then median will be the (N+1)/2 th value i.e., the 4th observation i.e., 5 is the median in this series.

* ESRs of 8 subjects are 3,4,5,6,4,7,6,7. Find the median.

Ans: Let us arrange the values in ascending order. **3,4,4,5,6,6,7,7.** Since N is even then median will be the Mean of $N/2$ th and $(N+1)/2$ th values. In this series the median is the mean of 4th and 5th Observations is 5 + 6 = 5.5 is the median in this series.

Median is calculated from ungrouped data by using following formula,

$$Me = l + \frac{\left(\frac{n}{2}\right) - c.f.}{f} \times i$$

- Where,
- l = Lower limit of median class
- n = Total no. of observations
- c.f. = Cumulative frequency of the class preceding the median class
- f = frequency of median class
- i = Class interval

Class Intervals (x)	Mid Value (m)	Tally marks	Frequency (f)	Frequency × Mid value (fm)	Cumulative frequency (cf)	
10 – 25	17.5	||	2	35.0	2	
25 – 40	32.5	|||	3	97.5	5	
40 – 55	47.5	𝍸 ||	7	332.5	12	
55 – 70	62.5	𝍸 |	6	375.0	18	Median class
70 – 85	77.5	𝍸 |	6	465.0	24	
85 – 100	92.5	𝍸 |	6	555.0	30	
			$\Sigma f = 30$	$\Sigma fm = 1860$		

- **Let us calculate median from the data given problem ii.**

$$Me = l + \frac{\left(\frac{n}{2}\right) - c.f.}{f} \times i$$

$$= 55 + \frac{\frac{30}{2} - 12}{6} X\ 15 \quad = 55 + \frac{15 - 12}{6} X\ 15 \quad = 62.5$$

Thus, median of the given data is 62.5.

Merits of Median:

1. It is very simple measure of the central tendency of the series.
2. It is Free from the effect of extreme values.
3. Median values are always a certain specific value in the series.
4. Median value is real value as compared to arithmetic mean average, the value of which may not exist in the series at all.
5. The median value can be estimated also through the graphic presentation of data.
6. Median can be estimated even in the case of certain incomplete series.

Demerits of median:

1. Median is of limited representative character as it is not based on all the items in the series.
2. When the median is located somewhere between the two middle values, it remains only an approximate measure, not a precise value.
3. Arithmetic mean is capable of further algebraic treatment, but median is not.

Uses of Median:

1. It is quite a commonly used measure in the case of such series which are related to qualitative observation as health of the student.

c) Mode and modal class

It is the value that occurs most frequently in data set. It is symbolized as **‘Mo’.** The data can be unimodal, bimodal or multimodal. Modal class is the class which shows the presence of highest frequency.

* ESRs of 9 subjects are 3,4,5,6,4,7,6,7,6. Find the mode.

Ans: Let us arrange the values in ascending order. 3,4,4,5,6,6,6,7,7. Since mode is the most frequent value from the data series then 6 is the mode in this series.

* ESRs of 7 subjects are 3,4,5,6,4,7,5. Find the median.

Ans: Let us arrange the values in ascending order. 3,4,4, 5,5,6,7. Since mode is the most frequent value from the data series then 4 & 5 are the modal values in this series. So, the data is **bimodal**.

- **Mode is calculated from grouped data by using following formula:**

$$Mo = l + \frac{(f1 - f0)}{(f1 - f0) + (f1 + f2)} x\, i$$

- Where,
- l = Lower limit of median class
- f_0 = Frequency of the class preceding modal class
- f_1 = Frequency of the modal class
- f_2 = Frequency of the class succeeding modal class
- i = Class interval

Let us calculate mode from the data given problem ii.

$$Mo = l + \frac{(f1 - f0)}{(f1 - f0) + (f1 + f2)} x\, i \quad = 55 + \frac{7 - 3}{(7 - 3) + (7 + 6)} X\, 15$$

$$= 55 + \frac{4}{17} X\, 15 \quad = 58.53$$

Thus, mode of the given data is 58.53.

Class Intervals (x)	Mid Value (m)	Tally marks	Frequency (f)	Frequency × Mid value (fm)	Cumulative frequency (cf)	
10 – 25	17.5	||	2	35.0	2	
25 – 40	32.5	|||	3	97.5	5	
40 – 55	47.5	𝍸 ||	7	332.5	12	Modal class
55 – 70	62.5	𝍸 |	6	375.0	18	Median class
70 – 85	77.5	𝍸 |	6	465.0	24	
85 – 100	92.5	𝍸 |	6	555.0	30	
			$\sum f = 30$	$\Sigma fm = 1860$		

Merits of Mode:

1. Mode is readily comprehensible and easy to calculate.
2. Mode is not at all affected by extreme values.
3. Mode can be conveniently located even if the frequency distribution has class-intervals of unequal magnitude provided the modal class and the classes preceding and succeeding it are of the same magnitude.

Uses of Mode: Mode is useful for qualitative data.

Demerits of Mode:

1. Mode is ill-defined. Not always possible to find a clearly defined mode.
2. It is not based upon all the observations.
3. It is not amenable to further mathematical treatment.
4. As compared with mean, mode is affected to a great extent by fluctuations of sampling.
5. When data sets contain two, three, or many modes, they are difficult to interpret and compare.

d) Standard deviation (S.D.)

Standard deviation is a statistical measure of the variability of the sample around the mean to determine standard deviation of the sample. When the value of standard deviation is less than the mean value, it is said to be negative and when the value of standard deviation is more than the mean value, it is said to be positive. Standard deviation is found out by using following formula, (Mean is 62)

Standard deviation (S.D.) $\sigma = \sqrt{\frac{\Sigma f d^2}{\Sigma f}}$

Class Intervals (x)	Mid value (m)	Frequency (f)	fm	Deviation of x from mean ($d = m - \bar{x}$)	d^2	fd^2
10 – 25	17.5	2	35.0	- 44.5	1980.25	3960.5
25 – 40	32.5	3	97.5	- 29.5	870.25	2610.75
40 – 55	47.5	7	332.5	- 14.5	210.25	1471.75
55 – 70	62.5	6	375.0	0.5	0.25	1.5
70 – 85	77.5	6	465.0	15.5	240.25	1441.5
85 – 100	92.5	6	555.0	30.5	930.25	5581.5
		$\sum f = 30$	$\Sigma fm = 1860$			$\sum fd^2 = 15067.5$

Standard deviation (S.D.) $\sigma = \sqrt{\dfrac{\Sigma fd^2}{\Sigma f}} = \sqrt{\dfrac{15067.5}{30}} = \underline{+}22.41$

Result: Standard deviation (S.D.) for give data is $\underline{+}$ 22.41

Merits of SD:

1. SD is rigidly defined measure, and its value is always fixed.
2. SD is based on all the items in the series. So, it is the best measure of dispersion.
3. SD is least affected by the sampling fluctuations than other measures.
4. SD can be used for mathematical operations and algebraic treatments. It is also applicable in statistical analysis.

Demerits of SD:

1. SD is complex to compute and difficult to understand as compared to other measures of dispersion.
2. SD is highly affected by the extreme values in the series.
3. SD cannot be obtained for open end class frequency distribution.

Uses of standard deviation:

1. It summarizes the deviations of a large distribution from mean in one figure used as a unit of variation.
2. Indicates whether the variation of difference of an individual from the mean is by chance, i.e., natural or real due to some special reasons.
3. Helps in finding the standard error which determines whether the difference between means of two similar samples is by chance or real.
4. It also helps in finding the suitable size of sample for valid conclusions.

THANK YOU

IT’S ALL

Problem for practice

1) The length of 25 different leaves were measured in cm for Ashoka tree and the data is presented in table below. Find the mean, median & mode for length of the leaves, also calculate SD for the same.

10.2	16.8	15.5	17.9	16.0
14.3	11.2	18.1	15.9	12.3
11.6	13.9	14.8	13.4	14.6
17.9	15.2	12.5	15.6	10.3
18.3	16.8	14.9	13.6	11.9

10.2	16.8	15.5	17.9	16.0
14.3	11.2	18.1	15.9	12.3
11.6	13.9	14.8	13.4	14.6
17.9	15.2	12.5	15.6	10.3
18.3	16.8	14.9	13.6	11.9

Solution: Let us convert the ungrouped data into grouped data by forming class-intervals of 2. While allocating frequencies to each class-interval, leaves falling in any upper class-limit would be considered in the next class.

Class Intervals (x)	Mid Value (m)	Tally marks	Frequency (f)	Frequency × Mid value (fm)
10 – 12	**11**	~~||||~~	**5**	**55**
12 – 14	**13**	~~||||~~ |	**6**	**78**
14 – 16	**15**	~~||||~~ |||	**8**	**120**
16 – 18	**17**	||||	**4**	**68**
18 – 20	**19**	||	**2**	**38**
			$\sum f = 25$	$\Sigma fm = 359$

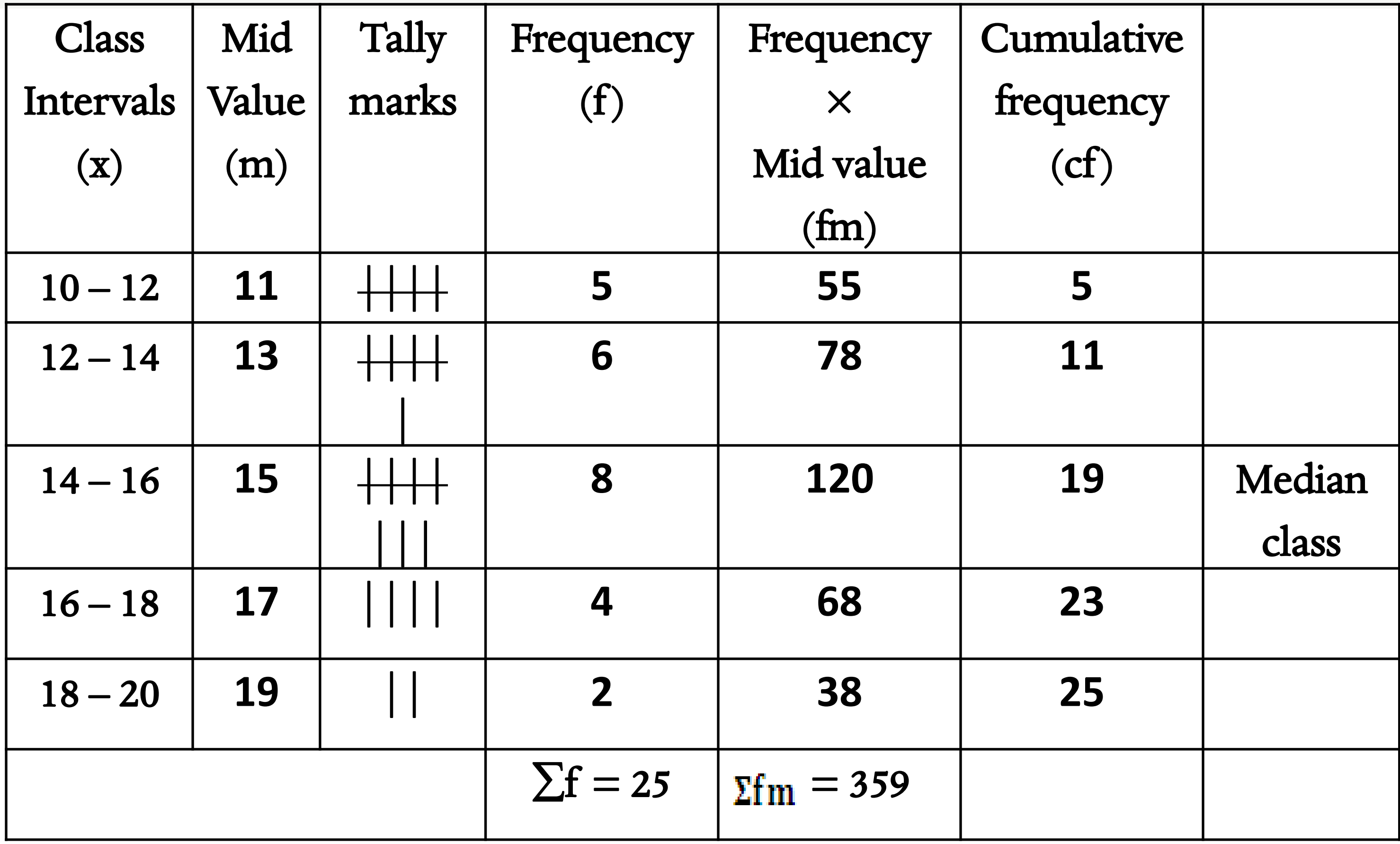
$\bar{X} = \Sigma fm / \sum f = \frac{359}{25}$

= **14.36cm**, Thus, mean of leaves of 25 Ashoka leaves is 14.63cm.

Median is calculated from ungrouped data by using following formula,

$$\text{Me} = l + \frac{\left(\frac{n}{2}\right) - \text{c.f.}}{f} \times i$$

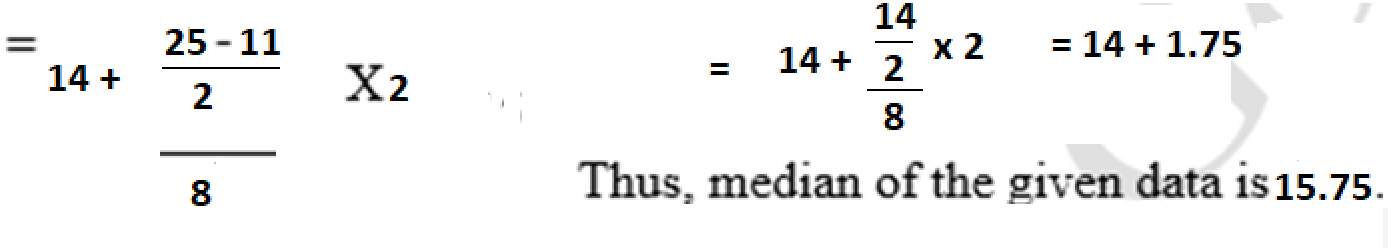
- Where,
- l = Lower limit of median class
- n = Total no. of observations
- c.f. = Cumulative frequency of the class preceding the median class
- f = frequency of median class
- i = Class interval



Class Intervals (x)	Mid Value (m)	Tally marks	Frequency (f)	Frequency × Mid value (fm)	Cumulative frequency (cf)	
10 – 12	11	𝍸	5	55	5	
12 – 14	13	𝍸 |	6	78	11	
14 – 16	15	𝍸 |||	8	120	19	Median class
16 – 18	17	||||	4	68	23	
18 – 20	19	||	2	38	25	
			$\sum f = 25$	$\Sigma fm = 359$		

- **Let us calculate median from the data given problem ii.**

$$\text{Me} = l + \frac{\left(\frac{n}{2}\right) - \text{c.f.}}{f} \times i$$



$$= 14 + \frac{\frac{25-11}{2}}{8} \text{ X} 2 \qquad = 14 + \frac{\frac{14}{2}}{8} \times 2 \qquad = 14 + 1.75$$

Thus, median of the given data is 15.75.

- **Mode is calculated from grouped data by using following formula:**

$$Mo = l + \frac{(f1 - f0)}{(f1 - f0) + (f1 + f2)} x\ i$$

- Where,
- l = Lower limit of median class
- f_0 = Frequency of the class preceding modal class
- f_1 = Frequency of the modal class
- f_2 = Frequency of the class succeeding modal class
- i = Class interval

Let us calculate mode from the data given problem ii.

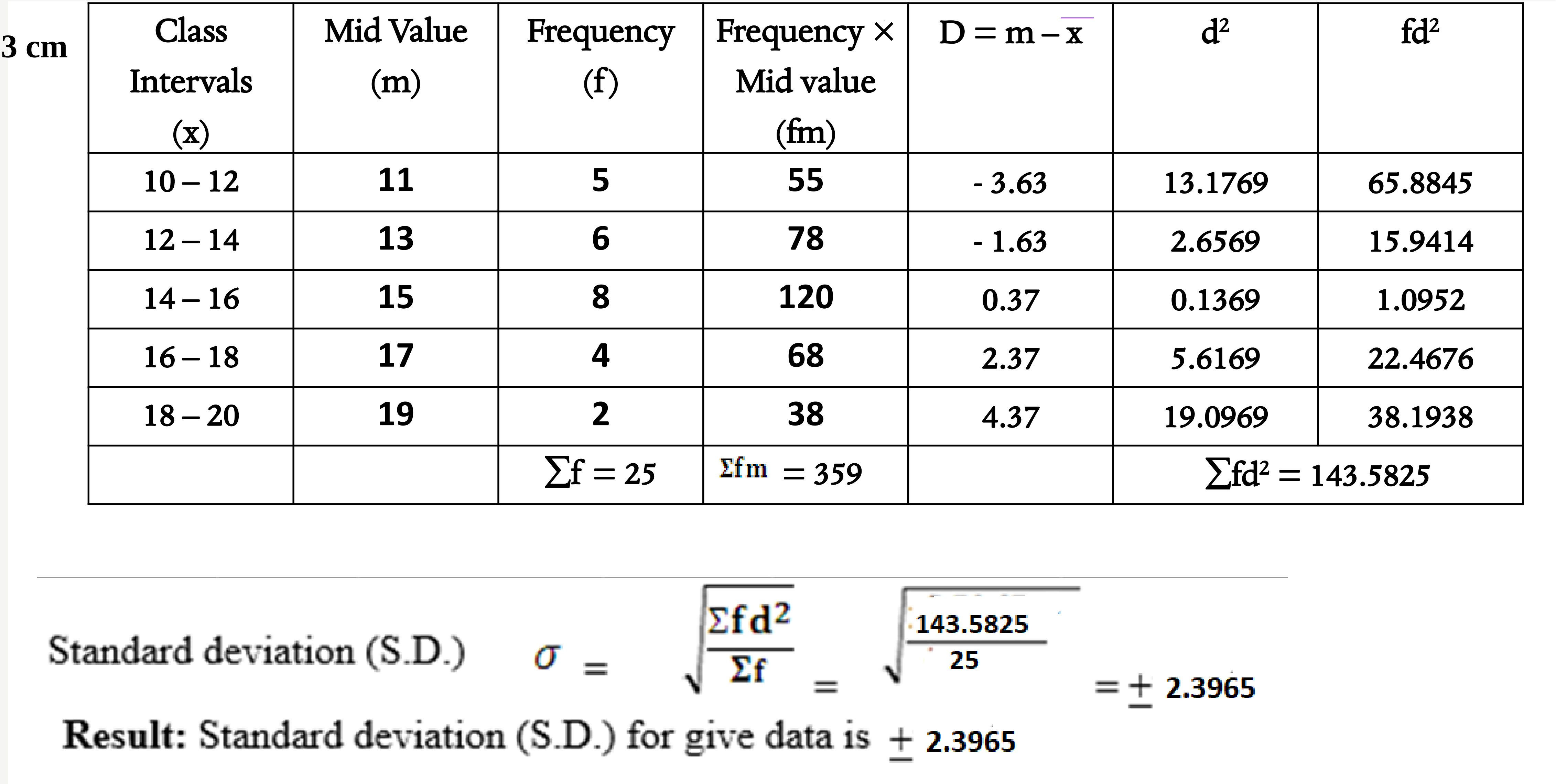
Class Intervals (x)	Mid Value (m)	Tally marks	Frequency (f)	Frequency × Mid value (fm)	Cumulative frequency (cf)	
10 – 12	11	𝍸	5	55	5	
12 – 14	13	𝍸 |	6	78	11	
14 – 16	15	𝍸 |||	8	120	19	Modal/ Median class
16 – 18	17	||||	4	68	23	
18 – 20	19	||	2	38	25	
			$\sum f = 25$	$\Sigma fm = 359$		

$$Mo = l + \frac{(f1 - f0)}{(f1 - f0) + (f1 + f2)} x\ i \quad = \quad 14 + \frac{8 - 6}{(8-6) + (8+4)}\ X\ 2$$

$$= 14 + \frac{2}{14}\ X\ 2 \quad = \quad 14.29$$

Thus, mode of the given data is 14.29.

Mean is 14.63 cm



Class Intervals (x)	Mid Value (m)	Frequency (f)	Frequency × Mid value (fm)	$D = m - \bar{x}$	d^2	fd^2
10 – 12	**11**	**5**	**55**	- 3.63	13.1769	65.8845
12 – 14	**13**	**6**	**78**	- 1.63	2.6569	15.9414
14 – 16	**15**	**8**	**120**	0.37	0.1369	1.0952
16 – 18	**17**	**4**	**68**	2.37	5.6169	22.4676
18 – 20	**19**	**2**	**38**	4.37	19.0969	38.1938
		$\sum f = 25$	$\Sigma fm = 359$		$\sum fd^2 = 143.5825$	

Standard deviation (S.D.) $\sigma = \sqrt{\frac{\Sigma fd^2}{\Sigma f}} = \sqrt{\frac{143.5825}{25}} = \pm 2.3965$

Result: Standard deviation (S.D.) for give data is ± 2.3965