
CHAPTER

22

VARIATION AND GENETICS

Animation 22:: Variation and Genetics
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GENES, ALLELES AND GENE POOL

Hereditary characteristics pass from parents to offspring through genes in their gametes. Gene is the basic unit of biological information. In fact DNA stores all sorts of biological information coded in the sequence of its bases in a linear order, and genes are actually parts of DNA comprising its base sequences. The position of a gene on the chromosome is called its locus.

Genes are responsible for producing startling inherited resemblances as well as distinctive variations among generations. When these pass in the form of intact parental combination between generations, inherited similarities are conserved; but when these shuffle, mutate or juggle with each other, variations emerge. Genes form pairs on pairs of homologous chromosomes. One member of a gene pair is located on one homologue, and the other member on the other homologue. Partners of a gene pair are called alleles. Each allele of a gene pair occupies the same gene locus on its respective homologue. Both alleles on one locus may be identical, or different from each other. (Fig. 22.1).

Animation 22: Gene Pool
Source & Credit: GIF SOUP

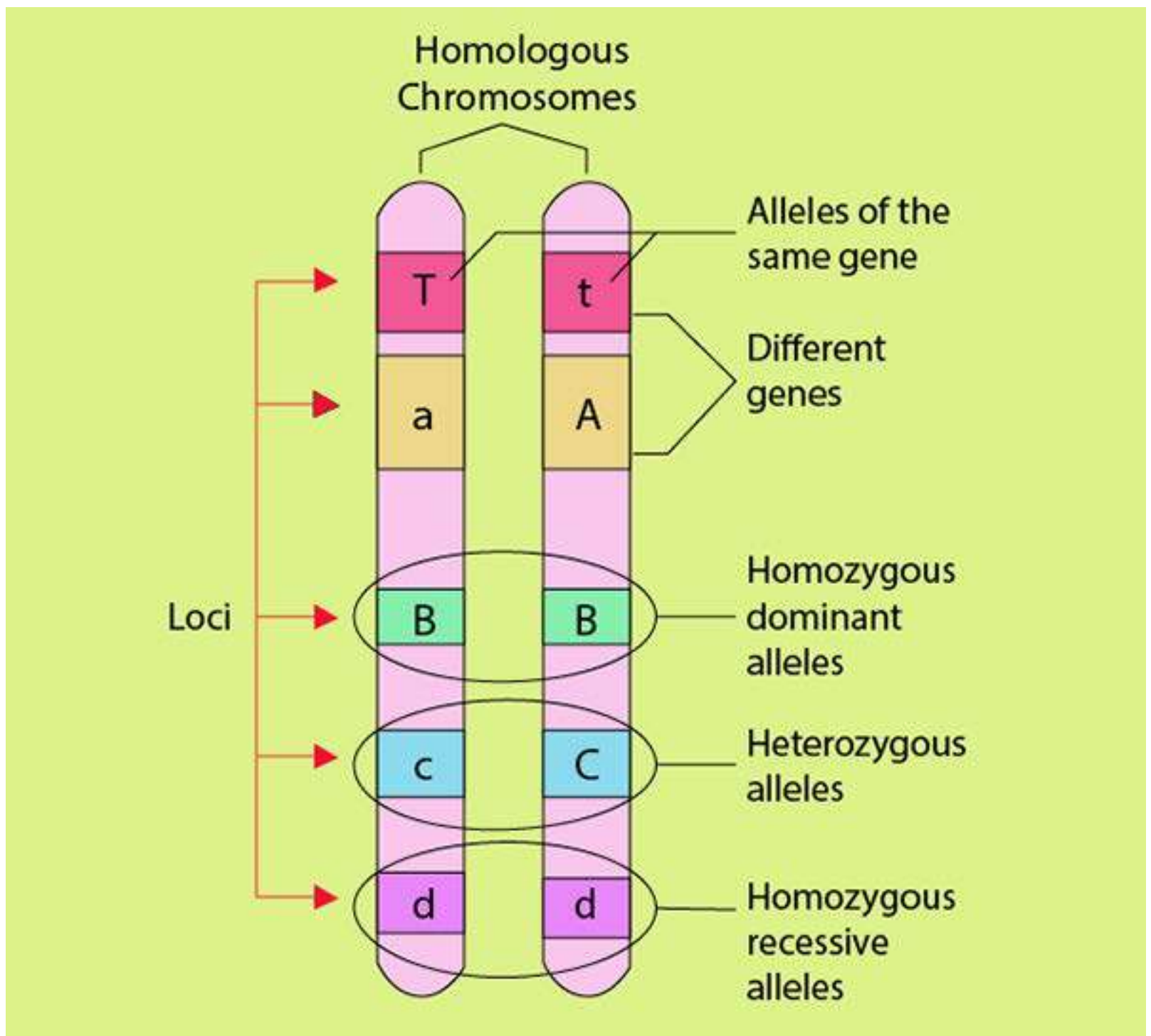


Fig 22.1 Allelic pairs on a homologous pair of chromosomes

Phenotype is the form of appearance of a trait. Genotype is the genetic complement i.e., the genes in an individual for a particular trait. A flower may be red or white in colour. Flower colour is a trait and red and white are its two phenotypes. Each form of expression is determined by a different allele of the colour gene. Allele “R” is the determiner for redness, while “r” is the determiner for whiteness.

GENE POOL

Any group of interbreeding organisms of the same species that exist together in both time and space is called a population. All the genes/alleles found in a breeding population at a given time are collectively called the gene pool. It is the total genetic information encoded in the total genes in a breeding population existing at a given time.

If we imagine population not as a group of individuals, but as a group of individually segregating and randomly assorting alleles, we can understand the concept of “beanbag genetics”. The alleles are like beans in a beanbag. The entire beanbag full of beans is the gene pool of the population. In the beanbag approach we can imagine the entire gene pool comprising all the alleles for all the different traits at once, or we can just focus on some subset, such as all the alleles for a single trait.

Jumping genes do not settle peacefully on their loci, they keep on hopping on different loci on the same chromosome or other chromosomes.

For convenience, we can focus on the gene pool for a single particular trait. A sample population of 100 diploid plants, some of which bear red flowers, others bearing white flowers has a sum total of 200 of all the different alleles (R or r) for flower colour trait as its gene pool.

MENDEL'S LAWS OF INHERITANCE

Gregor Johann Mendel (1822 - 1884) laid the foundation of classical genetics by formulating two laws of heredity; law of segregation and law of independent assortment. He was a priest. He performed series of breeding experiments on garden pea, *Pisum sativum* in his monastery garden for eleven years (1854 — 1865). *Pisum sativum* was easy to cultivate and it grew well in his garden. Its flowers were hermaphrodite. It was normally self-fertilizing, but could also be cross-fertilized. As the time gap between generations was short, Mendel could raise many generations of pea within a short time. Pea had many sharply distinct traits. Each trait had two clear cut alternative forms or varieties; e.g., seed shape had a round or wrinkled phenotype, plant height was either tall or short, seed colour could be yellow or green. Mendel called them contrasting pair of a trait. He focussed on seven such pairs (Fig. 22.2).

He first established true-breeding lines or varieties for each trait. A true - breeding variety upon self - fertilization always produced offspring identical to the parents, e.g., a true breeding “round” seed plant produced only “round” seeds. Similarly, a true breeding “wrinkled” seed plant produced only “wrinkled” seeds.

After establishing 14 pure - breeding lines of seven characters, he cross-fertilized plants that differed in one character only. The offspring of such a cross were called monohybrids. He cross-fertilized a true breeding round-seeded male plant with a true breeding wrinkled-seeded female plant (Fig. 22.3).

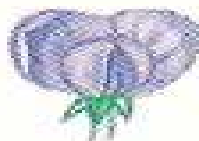
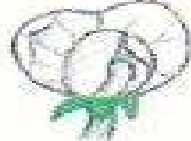
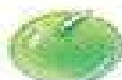
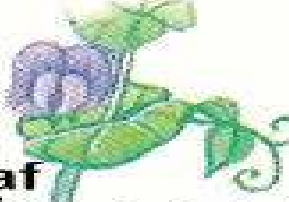
Trait	Dominant vs. recessive	
Flower color	 Purple	 White
Seed color	 Yellow	 Green
Seed shape	 Round	 Wrinkled
Pod color	 Green	 Yellow
Pod shape	 Round	 Constricted
Flower position	 At leaf junction Axial	 At tips of branches Top
Plant height	 (6-7feet) Tall	 Short (inche 9-18)

Fig 22.2 Seven traits of garden pea studied by Mendel.

He called it first parental generation (P_i). Their offspring were called F_i or first filial generation. All F_i offspring were round like one of the parents. Wrinkled phenotype did not appear at all. Round dominated wrinkled. Its dominance was complete because no offspring intermediate between parents was found. He called the trait that appeared in F_i as dominant; while the trait, which was masked, as recessive.

Then Mendel allowed self-fertilization among F_i monohybrids to raise F₂ progeny. As a result of monohybrid cross 3A of F₂ were round and 1A wrinkled.

Mendel got similar results and the same 3:1 ratio in offspring of monohybrid crosses for all the seven contrasting pairs of traits. Mendel proceeded a step ahead. He self-fertilized F₂ plants to raise F₃. He noted that 1/3 of F₂ round produced only round, while 2/3 of F₂ round produced both round and wrinkled in 3:1 ratio; but F₁ wrinkled produced only wrinkled.

He concluded that 1/3 of F₂ rounds were true-breeding like P_i round, and 2/3 of F₂ rounds were monohybrids like F_i round.

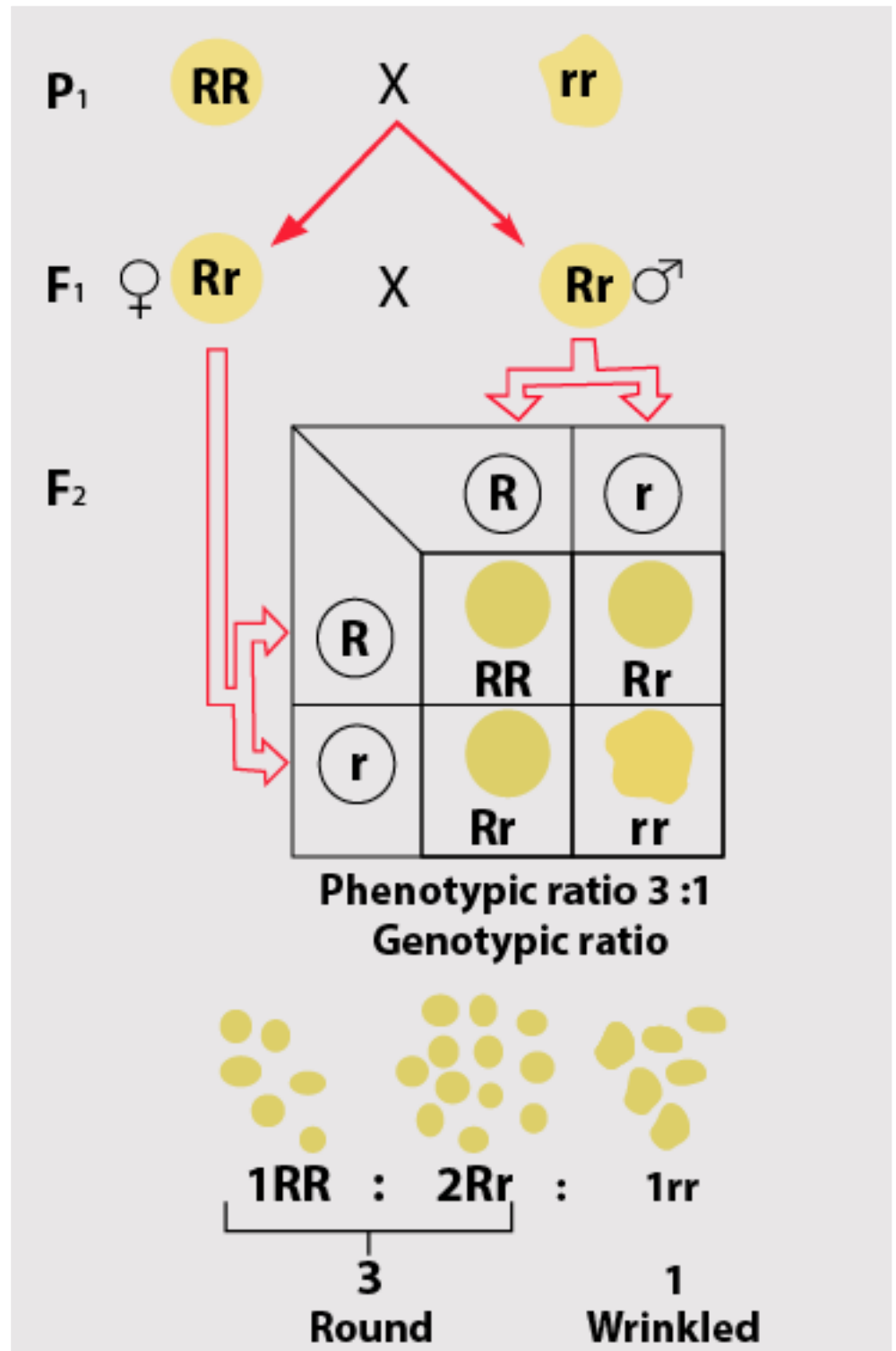


Fig 22.3 Mendel's cross to study single trait inheritance in pea.

Mendel's Interpretations

Mendel proposed that each contrasting form of a trait, e.g., roundness or wrinkledness of seed was determined by particulate hereditary factors, which he called 'elementen'. These factors carrying hereditary information were transmitted from parents to offspring through gametes. Each pea plant had a pair of these factors, one derived from male parent and the other from female parent. Both of these factors together controlled expression of a trait. He designated dominant factor with a capital letter and recessive factor with a small letter; e.g., R for roundness factor and r for wrinkledness factor. Johannsen renamed them as 'genes'.

The true - breeding round seed plant of P₁ generation carried 'RR' alleles while the true - breeding wrinkled seed plant of P₂ carried 'rr' alleles. When both the alleles of a gene pair in an organism are same, the organism is homozygous for that gene pair. An individual with a homozygous genotype is a homozygote.

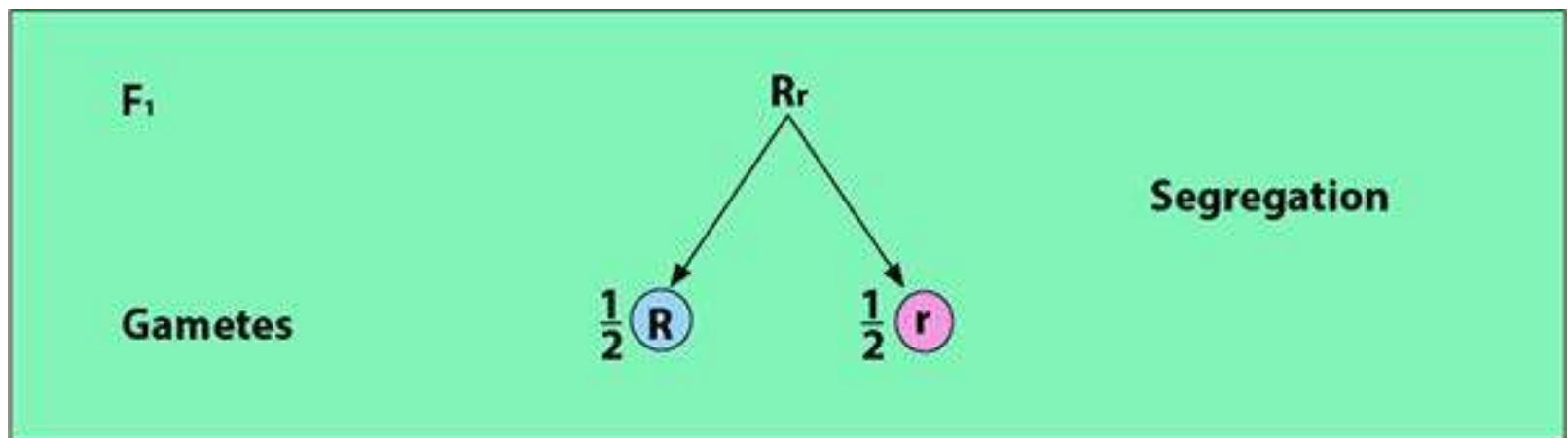


Fig 22.4 Segregation of alleles during gamete formation

Mendel inferred that the factors of a pair (alleles) separated from each other during gamete formation so that each gamete got only one factor (allele) for each trait. So half the gametes got one allele, and the other half carried the other allele. Fertilization was random. When male gamete carrying factor (R) fertilized female gamete with factor (r), the complete set of the two factors (Rr) for the trait was restored in zygote.

The zygote developed into F₁ offspring that was heterozygous 'Rr', because the two alleles of its gene pair were different from each other. An individual with a heterozygous genotype is a heterozygote. F₁ offspring (Rr) was a monohybrid for seed shape; it was round in phenotype but heterozygous in genotype. Its alleles also segregated during gamete formation (Fig. 22.4).

Punnett square indicates that 1/4 of F₂ progeny would have been 'RR' (homozygous round), 1/2 Rr (heterozygous round), and 1/4 rr (wrinkled).

Mendel actually observed 3 : 1 phenotypic ratio in F₂. His phenotypic data of F₃ can also be explained on the basis of 1 : 2 : 1 genotypic ratio of F₂. Mendel compared the results of all the seven separately studied characters, and found them strikingly similar to formulate law of segregation.

Law of Segregation : According to law of segregation, the two coexisting alleles for each trait in an individual segregate (separate) from each other at meiosis, so that each gamete receives only one of the two alleles. Alleles unite again at random fertilization of gametes when zygote is formed.

Test Cross

Mendel devised a cross called test cross, which is used to test the genotype of an individual showing a dominant phenotype. It is a mating in which an individual showing a dominant phenotype is crossed with an individual showing its recessive phenotype. This cross finds out the homozygous or heterozygous nature of the genotype (Fig. 22.5).

Case 1	Case 2
If the seed is homozygous round(RR) it will grow into a pea plant that forms all gametes with only `R` allele. Wrinkled seed plant is always homozygous recessive. it will form all gametes with `r` allele. Fertilization will result in 100% round seed progeny.	If the seed is heterozygous round (Rr), it will grow into a plant that forms half the gametes, with `R` and half with `r` allele. Wrinkled seed plant will form only `r` type of gametes. Fertilization will result into 50% round and 50% wrinkled seed progeny. Even a single wrinkled seed in the progeny is a convincing proof for Heterozygous nature of the round parent.

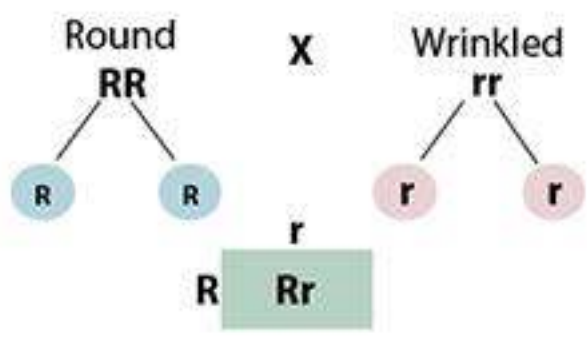
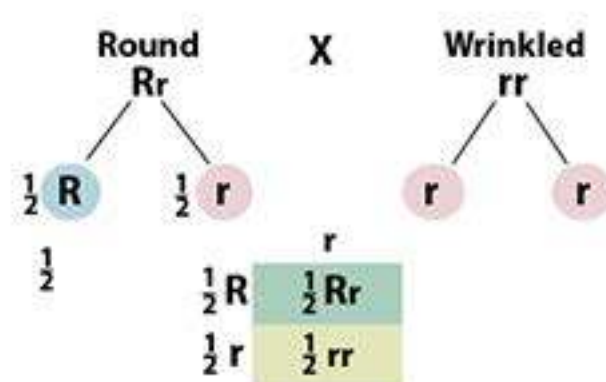
 Result : All round seed progeny . The tested phenotypically dominant individual is homozygous.	 Result : 1/2 round seed and 1/2 wrinkled seed progeny. The tested phenotypically dominant individual is heterozygous .
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Fig 22.5 Test cross of a round seed

Dihybrid and Dihybrid Cross

After thoroughly studying each trait separately, Mendel decided to study the inheritance of two simultaneously, e.g., seed shape and seed colour. Seed shape could be round or wrinkled. Similarly, seed colour could be yellow or green. He crossed true breeding round and yellow seed plants with true breeding wrinkled and green seed plants. All F_1 **dihybrid** were round and yellow seeded due to dominance. Then he made a **dihybrid cross** by allowing self-fertilization among F_1 dihybrids. The results were quite surprising. Seeds produced as F_2 progeny were not only in the two **parental combination** i.e., round yellow and wrinkled green, but also in two **new phenotypic combination** i.e., round green and wrinkled yellow. A clear cut 9:3:3:1 phenotypic ratio was found in F_2 . Appearance of these new recombinant phenotypes of F_2 indicated that some sort of shuffling of alleles had occurred during gamete formation. Mendel inferred the mechanism of this shuffling as **independent assortment of alleles** into gametes. He concluded that the alleles for seed shape and colour were not bound to remain in parental combination forever, i.e., 'R' with 'Y' and 'r' with 'y'; rather these were free to assort independently. R could go with Y or y in any gamete with equal chance.

Animation 22: Dihybrid Cross
Source & Credit: GIF SOUP

Similarly, r could go with y or Y in any gamete with equal probability. Four types of gametes, i.e., RY, Ry, rY and ry were formed in equal number in a perfect ratio of 1:1 : 1:1. When these gametes randomly fertilized each other, a 9:3:3:1 phenotypic ratio was produced among F2 progeny (Fig 22.6).

Mendel formulated Law of Independent Assortment : “When two contrasting pairs of traits are followed in the same cross, their alleles assort independently into gametes.” Alleles of one pair inherit independently of alleles of the other pair. The distribution of alleles of one trait into gametes has no influence on the distribution of alleles of the other trait. Thus the chance for a plant to be round or wrinkled is independent of its chance of being yellow or green.

Probability is the chance of an event to occur. Inheritance of seed shape is an independent event. In F2 offspring of a monohybrid cross the independent chance for a seed to be round is $\frac{3}{4}$, or it to be wrinkled is $\frac{1}{4}$. Inheritance of seed colour is another separate event. The independent chance in F2 of a monohybrid cross for a seed to be yellow is $\frac{3}{4}$ or it to be green is $\frac{1}{4}$. When two independent events are occurring simultaneously like in Dihybrid cross, the ratio of each joint phenotypic combination can be obtained by multiplying the probabilities of individual phenotypes. It is called

product rule.

The joint probability that both of the independent events will occur simultaneously, is equal to the product of individual probabilities of each event.

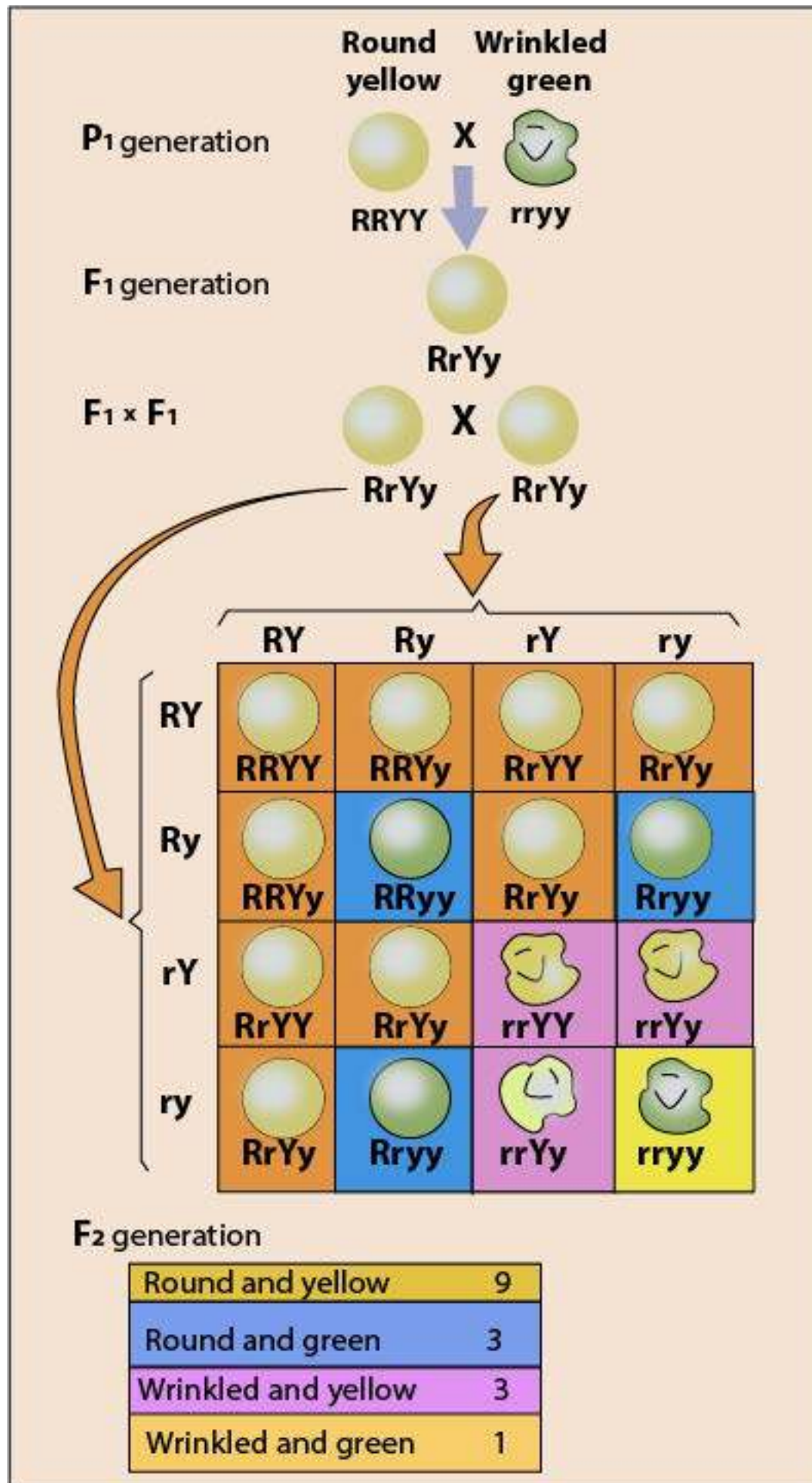


Fig 22.6 Dihybrid cross produces parental as well as recombinant types.

Event No. 1	Event No. 2	Both events at a time
Seed shape	Seed colour	Seed shape and colour
Independent probability to be:	Independent probability to be:	Joint probability to be:
Round = Round = Wrinkled = Wrinkled =	yellow = green = yellow = green =	Round yellow = $9/16$ Round green = $x = 3/16$ Wrinkled yellow = $x = 3/16$ Wrinkled green =

Genes are located at specific loci on chromosomes. Independent assortment of genes depends upon independent assortment of their chromosomes. All the genes present on a homologous pair of chromosomes are linked to each other in the form of a linkage group. These cannot assort independently. Those traits assort independently whose alleles are riding on non homologous chromosomes. Pea has seven homologous pairs of chromosomes. Mendel knew nothing about chromosomes. The traits he studied were confined to only four chromosomes. He reported independent assortment of those traits whose genes were either on different homologous chromosomes, or were so far away from each other on the same chromosome that they appeared to assort independently due to crossing over.

Mendel presented his findings to Brunn Society for the study of Natural Science in 1865. His work was published in the proceedings of the society in 1866. That laid the foundation of classical genetics. His work lay neglected for 34 years. In 1900, 16 years after his death, three botanists; Correns, De Vries and Tschermach independently rediscovered and acknowledged his work.

Activity: Normal individuals have melanin pigment in their skin, hair and eyes. Albinos totally lack pigment in their bodies. Albinism is a recessive trait in humans. Two normal parents have an albino child. What is the probability that their next child will also be an albino?

DOMINANCE RELATIONS

Dominance is a physiological effect of an allele over its partner allele on the same gene locus. There are four types of dominance relations among alleles, each indicating a different style of their functional effect upon each other.

1. Complete dominance
2. Incomplete dominance
3. Codominance
4. Over dominance

Complete Dominance

When one allele (R) is completely dominant over the other (r), presence of the recessive allele is functionally hidden, so the heterozygote (Rr) has the same round phenotype as (RR) homozygote.

The contrasting pairs of alleles for all the seven characters chosen by Mendel showed complete dominance. After Mendel, further breeding experiments were carried out on different plants and animals. Many novel phenotypes and phenotypic ratios were observed that could not be explained on the basis of complete dominance.

Incomplete Dominance

In 1899 Carl Correns was working on a flowering plant named 4 O'clock. When he crossed a true breeding red flowered plant with a true breeding white flowered 4 O'clock, all the F₁ hybrids had pink flowers. This new phenotype had a shade intermediate between those of the parents due to an intermediate amount of pigment in petals. When Correns self-fertilized F₁ pink, the F₂ showed all three phenotypes of flowers in the ratio of 1 red : 2 pink : 1 white. Red was homozygous for red alleles, and white was homozygous for white alleles. But when allele for red and allele for white were present together in the same plant, neither of them masked the effect of other; rather these alleles showed incomplete dominance in the form of pink colour.

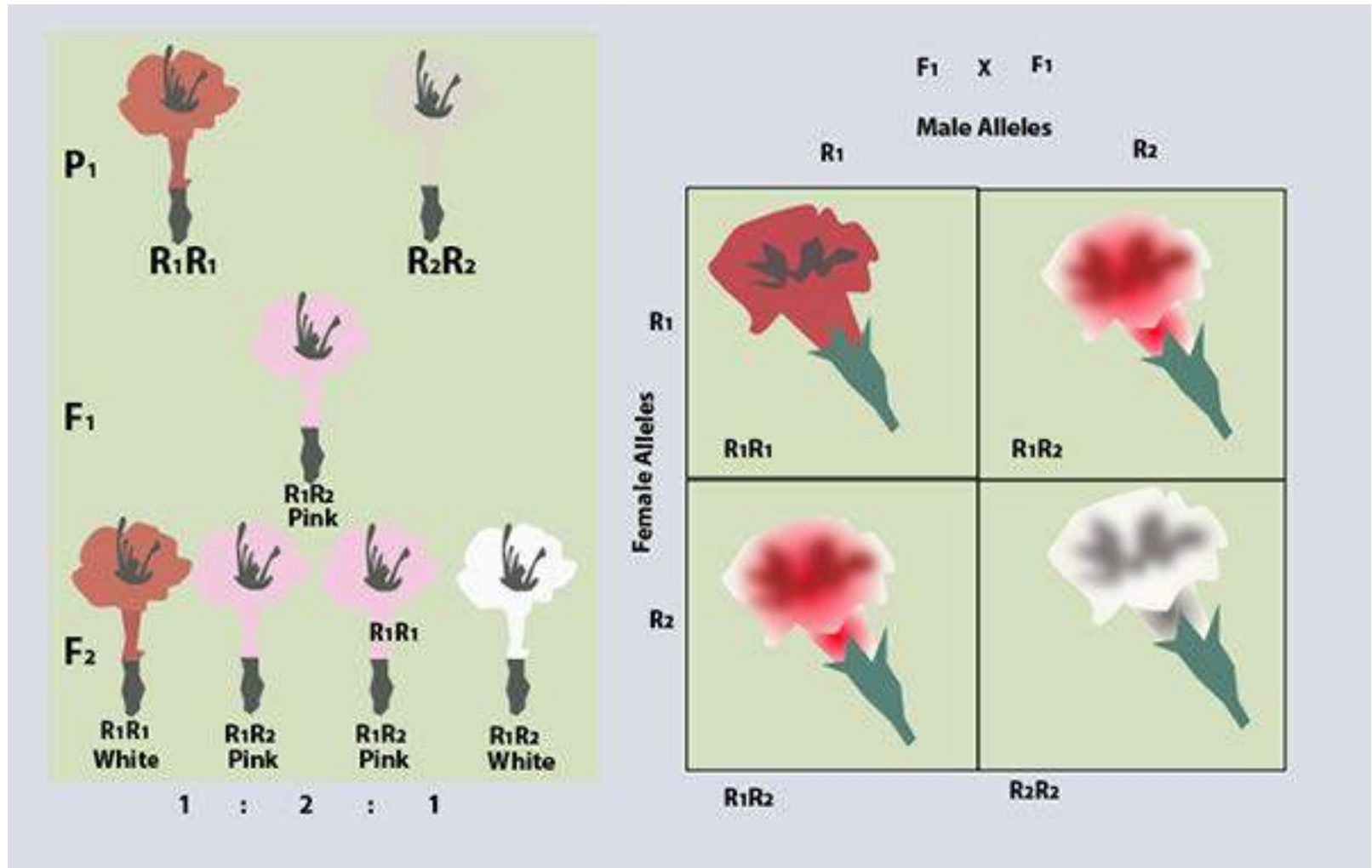


Fig 22.7 Incomplete dominance in 4 O'clock

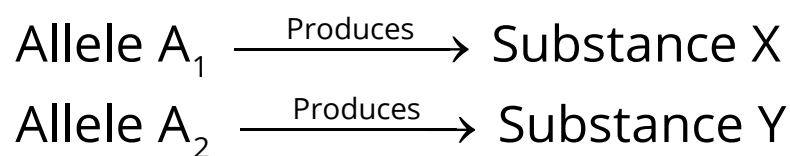
When the phenotype of the heterozygote is intermediate between phenotypes of the two homozygotes, it is called **incomplete or partial dominance**.

As there is no truly dominant allele, the usual capital and small letter distinction for dominant and recessive trait is not necessary. Both the alleles are represented by the same letter 'R' but are numbered differently to distinguish white from red. Allele for red is designated as R_1 , and the allele for white as R_2 (Fig. 22.7).

Punnett square indicates that the phenotypic ratio is the same as the genotypic ratio. There is absolutely no need of a test cross. Do these results make Mendel's principles invalid? The flower colour does show blending at phenotypic level in F_1 , which is quite contrary to what Mendel observed. But the re-appearance of red and white flowers in F_2 confirms that blending does not occur at genetic level.

Codominance

The phenotype of heterozygote is distinct in quality from those of the two homozygotes. It is not an intermediate quantitative expression like incomplete dominance. Each allele of the gene pair is associated with a different substance, e.g.,



Codominance occurs when both the alleles express independently in heterozygote; (A_1A_2) and form their respective products X and Y. The codominant heterozygote would have both substances at the same time.

Different alleles of a gene that are both expressed in a heterozygous condition are called **codominant**.

MN BLOOD TYPE OR BLOOD GROUP SYSTEM

Human blood groups can be of many types, e.g. ABO, MN, MNSs, Rh etc. Landsteiner and Levine discovered MN blood types in man on the basis of specific antigens present on RBC. These RBC antigens induce production of their specific antibodies. There are three general phenotypes; M, N and MN. M phenotype has antigen M which is produced by gene LM. N phenotype has antigen N that is produced by its allele LN. MN phenotype has both M and N antigens, simultaneously produced by their alleles LM and LN

Phenotype	Genotype	Antigens on RBC
M	$I^M I^M$	M
N	$I^N I^N$	N
MN	$I^M I^N$	M and N

If a man of M blood group marries a woman of N blood group, all their children will have MN blood group (Fig. 22.8)

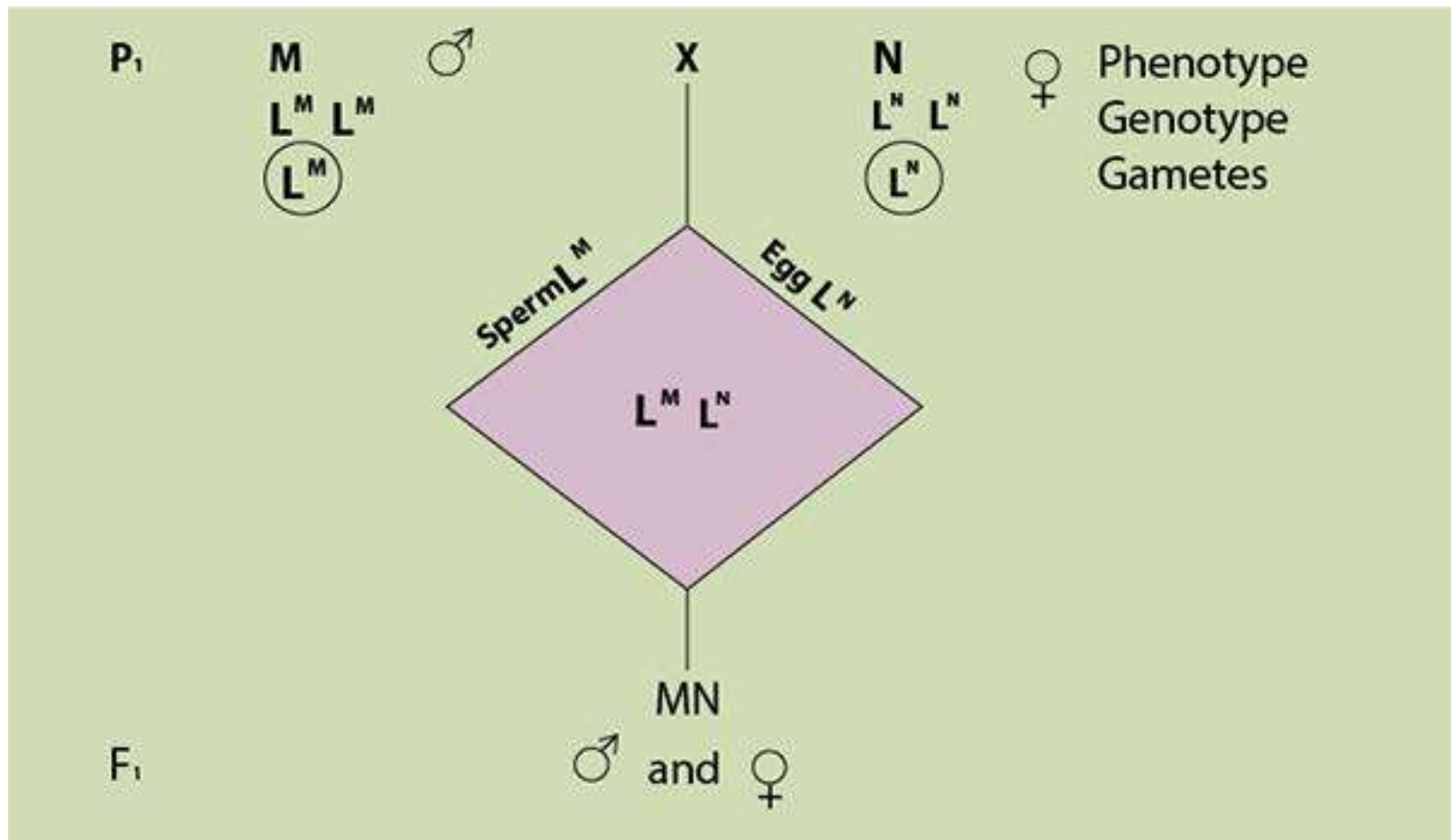


Fig 22.8 Codominance in MN Blood group alleles.

Over Dominance

This dominance relation is fascinating because the over dominant heterozygote exceeds in quantity the phenotypic expression of both the homozygotes. In fruit fly *Drosophila* the heterozygote (w^+ / w) has more quantity of fluorescent pigments in eyes than wild (W^+ / W^+) Or white eye (w / w) homozygotes.

MULTIPLE ALLELES

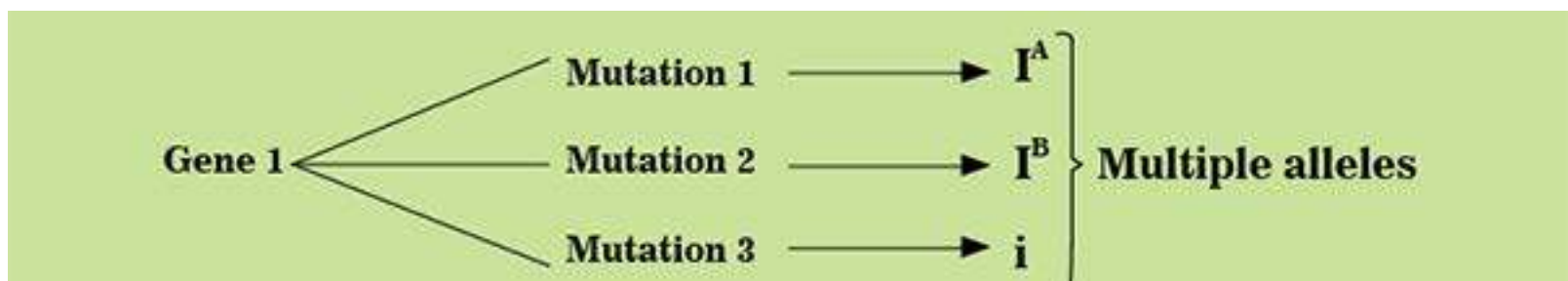
Gene mutations may produce many different alleles of a gene. Some genes may have as many as 300 alleles. All such altered alternative forms of a gene, whose number is more than two, are called multiple alleles. Any two of these multiple alleles can be present in the genome of a diploid organism, but a haploid organism or a gamete can have just one of them in its genome.

ABO - The First Discovered Multiple Allelic Blood Group System in Man

ABO blood group system was discovered by Karl Landsteiner in 1901. ABO system has four different phenotypes which are distinct from each other on the basis of specific antigens on the surface of RBC. A person having antigen A has blood group A; a person having antigen B has blood group B; a person having both the antigens A and B has blood group AB; but a person having neither antigen A nor B would have blood group O.

Bernstein explained the genetic basis of ABO system in 1925. This blood group system is encoded by a single polymorphic gene I on chromosome 9. It has three multiple alleles I^A , I^B , and i .

Allele I^A specifies production of antigen A, and allele I^B specifies production of antigen B, but allele i does not specify any antigen. Their dominance relations are interesting too. Alleles I^A and I^B are codominant to each other, because each expresses equally in $I^A I^B$ heterozygote to produce AB phenotype. But allele i is recessive to both I^A and I^B . Therefore $I^A I^A$ or $I^A i$ genotypes will produce phenotype A. Similarly $I^B I^B$ or $I^B i$ produces phenotype B. The homozygous ii will produce phenotype O.



The blood group alleles start their expression at early embryonic stage and keep on expressing themselves till death. Therefore the blood group phenotype of a person never changes throughout life.

Anti-A and anti-B antibodies appear in plasma during the first few months after birth. They are naturally occurring in the absence of corresponding antigen. The blood serum of A phenotype contains anti-B antibodies. They will agglutinate or clump any RBC which have B antigens on them. B phenotype contains anti-A antibodies in the serum and agglutinate any RBC with antigen A. Phenotype AB has neither anti-A nor anti-B antibodies in the serum. The serum of O blood type contains both anti-A and anti-B antibodies. The blood serum containing anti-bodies is called antiserum.

Any blood transfusion is ideally safe if it does not cause agglutination in the recipient. Agglutination leads to serious results because clumped cells cannot pass through fine capillaries. The blood samples of the donor and the recipient are cross matched for compatibility before giving transfusion. If incompatible blood is transfused, dangerous hemolytic reaction occurs. Either the antibodies of the recipient destroy the RBC of donor or the antibodies of the donor hemolyze the RBC of the recipient.

Blood group A can be transfused only into A and AB recipients because they do not have anti - A antibodies. Blood group B can be transfused only into B and AB recipients as they do not have anti - B antibodies. AB blood can be transfused only into AB recipients because they have neither anti - A, nor anti B antibodies. O blood has neither A nor B antigen, but it does have anti - A and anti-B antibodies. An O recipient can only be given transfusion from a donor O. Phenotype O can also be used as donor for small transfusions to A, B and AB recipients because donor's antibodies are quickly absorbed by other tissues or greatly diluted in the recipient's blood stream. O blood group individuals are called universal donors. AB blood group individuals are called universal recipients because they can receive transfusions of blood from any of the four blood groups.

A and B antigens can also be present in saliva and other body fluids of some persons called secretors. Secretors have dominant secretor gene "Se" on chromosome 19.

Genetic analysis on the basis of blood groups helps in solving cases of disputed parentage. It can only be used to prove that an individual is not the parent of a particular child, e.g. a child of AB phenotype (IA IB) can not be the child of a parent of phenotype O (ii). Similarly a man of B phenotype cannot be father of a blood type A child, whose mother is of phenotype O. His father could either be A or AB phenotype.

Activity : Two new born babies get mixed up in the nursery of a hospital. Baby I is. type B and baby II is of type O. Determine their parentage from the phenotypes of these two couples. Mr. Haris is type A and Mrs. Haris is type AB. Mr. and Mrs. Bilal are both of type A.

Rh Blood Group System

ABO blood type is further differentiated by a + or - sign. This positive or negative sign refers to the presence or absence of another blood group system antigen called Rh factor. Rh blood group system is defined on the basis of **Rh factor** present on the surface of RBC. This system is named Rh after Rhesus monkey, because its antigen was first discovered in it by Landsteiner in 1930s.

Rh blood group system is encoded by three genes C, D and E, which occupy two tightly linked loci. Alleles of gene D occupy one locus called locus D, while genes C and E alternatively occupy the other locus. The D locus is of prime importance.

Gene D has two alleles, D and d. D is completely dominant over d. Persons having genotype DD or Dd have Rh factor on their RBC and are Rh+. Persons with genotype dd do not have Rh factor and are Rh-. Unlike the naturally occurring anti - A and anti - B antibodies of ABO system, anti - Rh antibody production requires a stimulus by the human Rh antigen itself. An Rh- person does not produce anti - Rh antibodies unless he is exposed to Rh antigen. Rh+ donor is totally incompatible for Rh- recipient. If an Rh- person receives Rh antigen through wrong Rh+ blood transfusion, he will begin to produce anti - Rh antibodies against Rh antigens. Rh- blood, clear of any anti - Rh antibody from a donor who has never been exposed to Rh antigen can be transfused to Rh+ recipient.

Erythroblastosis foetalis : Maternal-foetal Rh incompatibility Maternal-foetal incompatibility results when an Rh- woman, married to an Rh+ man conceives a child who is Rh+. If the man's genotype is DD, all of their offspring (Dd) will be Rh+. If the man's genotype is Dd, half of their offspring with Dd genotype will be Rh+. If RBC of Rh+ foetus cross the placental barrier and enter into Rh- mother's blood stream, the mother's immune system reacts to the foetal Rh antigen stimulus by producing a large number of anti - Rh antibodies. When mother's anti - Rh antibodies seep through placenta into blood circulation of foetus, they start hemolysis (break down / bursting) of RBC of foetus. As this destruction continues, the foetus becomes anaemic. The anaemic foetus starts to release many -immature erythroblasts into his blood stream. That is why this hemolytic disease of the new bom is called erythroblastosis foetalis. This anaemia may lead to .abortion or still birth. Even if the pregnancy continues, the liver and spleen of the foetus swell as they rapidly produce RBC. The breakdown product of RBC called bilirubin also accumulates in the foetus. Bilirubin damages his brain cells and turns his skin and whites of the eye yellow. This condition is jaundice. So the baby if born alive, suffer from severe hemolytic anaemia and jaundice. Such baby's blood should be immediately replaced by Rh'' blood free of anti - Rh antibodies. The first Rh incompatible pregnancy may not face much problems if very few of foetal antigens cross placenta into maternal circulation and the amount of maternal antibody production is not very high. But when placenta detaches at birth, a large number of foetal cells enter mother's blood stream and stimulate production of large amount of anti - Rh antibodies by the mother. These anti - Rh antibodies persist in mother's blood for a long time and are persistent risk for the next Rh+ foetus. Rh sensitization of Rh' mother is avoided by a simple therapy. She is given an injection of Rh antiserum during early pregnancy and immediately after birth. The Rh - antibodies in the Rh antiserum will destroy Rh+ RBC of the foetus before they stimulate production of maternal anti - Rh antibodies. The injected antiserum disappears before the next pregnancy

Sometimes a mild ABO incompatibility protects the baby against a more severe Rh incompatibility. If O' mother conceives A+ or B+ baby, any^ foetal A or B type RBC entering the mother's blood are quickly destroyed by her anti - A or anti - B antibodies, before she can form anti - Rh antibodies.

Activity: An Rh⁻ woman is married to an Rh⁺ man whose father was also Rh⁻. What is the probable risk of erythroblastosis foetalis in their babies?

EPISTASIS

When an effect caused by a gene or gene pair at one locus interferes with or hides the effect caused by another gene or gene pair at another locus, such a phenomenon of gene interaction is called epistasis. Epistasis must not be confused with dominance. Dominance is the relationship between alleles of the same gene occupying the same locus, but epistasis is the interaction between different genes occupying different loci.

Bombay Phenotype

The expression of ABO blood type antigens by I^A or I^B gene depends upon the presence of another gene H. ABO locus is on chromosome 9, while H locus is on chromosome 19. H gene changes a precursor substance into substance H. It produces an enzyme that inserts a sugar onto a precursor glycoprotein on the surface of RBC. Only then antigen A or antigen B specified by I^A or I^B gene could attach to this sugar of substance H. The recessive allele h cannot insert sugar molecule to glycoprotein. Therefore, hh individuals lack the site of attachment for antigen A or antigen B. Thus A and B antigens cannot adhere to their RBC and fall away. Their RBC lack A and B antigens although they do not lack I^A and I^B genes. They are phenotypically like O, but are not genotypically O. Their phenotype is called Bombay phenotype (Fig. 22.9).

Activity: A student, of biology learns about ABO blood types. He knows that he's type O, and his father is type A and mother is type AB. He wonders how his blood type could have arisen. Suggest how type A and AB parents could produce a child of blood type O.

PLEIOTROPY

When a single gene affects two or more traits, the phenomenon is called pleiotropy. Such a gene with multiple phenotypic effect is called **pleiotropic**.

Examples:

1. White eye gene in *Drosophila* also affects the shape of sperm storing organs (spermathecae).
2. Genes that affect growth rate in humans also influence both weight and height.
3. In cats, the dominant allele *W* not only makes fur pure white but also causes deafness. In *ww* homozygous normal pigmented cats, melanocytes produce pigment of fur and also contribute to 'hair cells in inner ear that sense sound. When a cat gets *W* allele, its melanocytes fail to develop properly. Melanocyte failure causes both phenotypes, i.e. white fur and deafness.

CONTINUOUSLY VARYING TRAITS

Genotype interacts with environment to produce phenotype. Phenotypic expression of traits has two aspects:

- (i) Qualitative
- (ii) Quantitative

Qualitative differences are large and more obvious, but quantitative variations are small and less striking. Some traits, like pea seed shape, show discontinuous qualitative variations with two sharply distinct phenotypes, round or wrinkled; others like 4 O'clock flower colour can have three phenotypes, red, pink and white; still others like ABO blood group system have four qualitatively different phenotypes A, B, AB and O. But many traits like height, weight, intelligence and skin colour in humans, and grain colour in wheat exhibit continuous quantitative variation over a range of many phenotypes. Mendel focused on traits that showed only two qualitatively different phenotypes which could be determined by just two alternate alleles of a single gene. Darwin observed small continuous variations within individuals of a population. Such a range of phenotypic spectrum of a trait cannot be traced to a single gene with two alleles. Even a few multiple alleles of a single gene cannot make such a wide range of phenotypes.

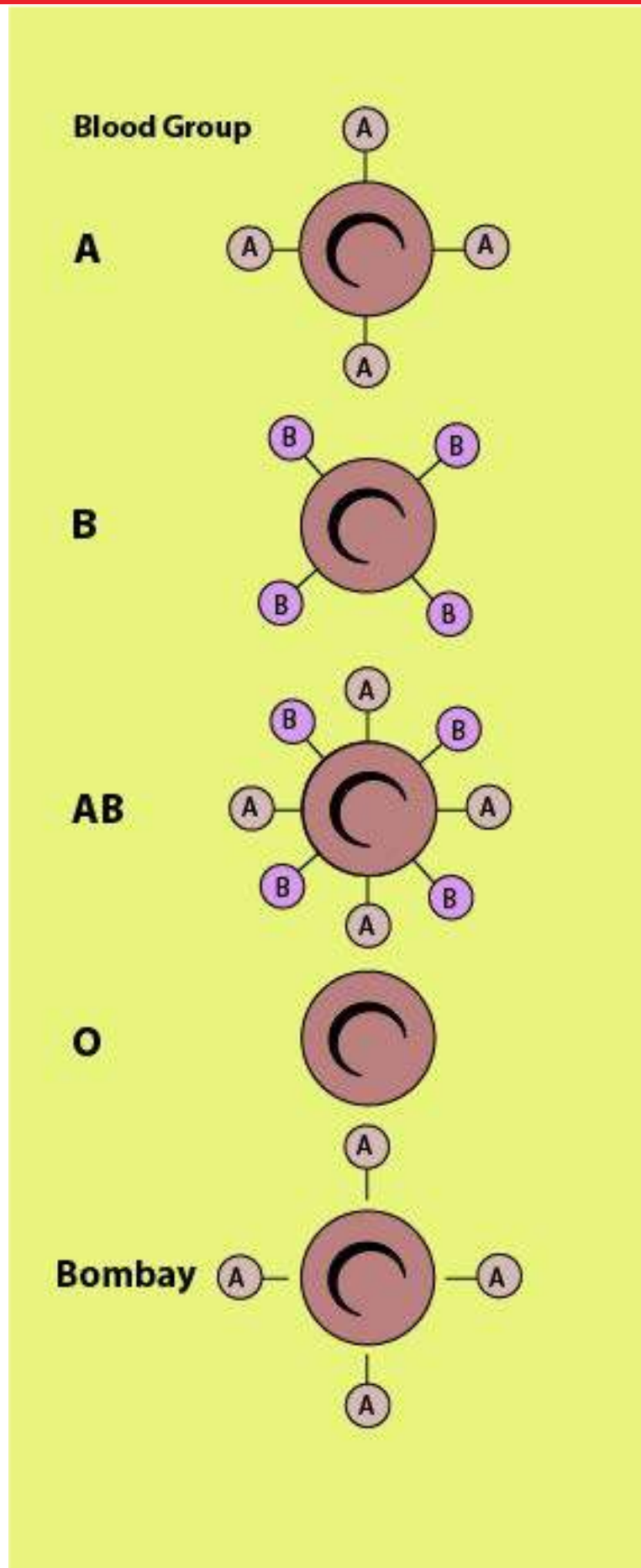


Fig 22.9 Bombay phenotype results from epistasis

A continuously varying trait is encoded by alleles of two or more different gene pairs found at different loci, all influencing the same trait in an additive way. These quantitative traits, are called **polygenic traits**, and their genes are **polygenes**. Each polygene has a small positive or negative effect on the character. Polygenes supplement each other and sum of positive and negative effects of all individual polygenes produce quantitative phenotypes of a continuously Varying trait.

Wheat grains vary in colour from white to dark red. This trait shows a continuous spectrum of colour variation. (Fig 22-10). Some grains are white, some are deep red but most grains have shades in between from light pink to moderately dark red. Nilsson - Ehle studied the genetics of wheat grain colour. When he crossed a true breeding dark red grain plant with a true breeding white grain plant, all F₁ grains had light red colour, intermediate between two parental shades. It seemed as if it was a case of incomplete dominance. But when F₁ grains were grown to mature plants and crossed with each other, F₂ grains had exactly seven shades of colour in the ratio of 1 dark red : 6 moderately dark red : 15 red : 20 light red : 15 pink : 6 light pink : 1 white (Fig. 22-11).



Fig 22.10 Colour variation in wheat grains is a polygenic traits.

Three different gene pairs, i.e. Aa, Bb, Cc at three different loci contribute to the wheat grain colour. Each individual would contain six alleles for the trait. Alleles A, B and C code for an equal amount (dose) of red pigment, which is a positive effect. But none of a, b and c encode red pigment, which is a no (zero) dose negative effect. If all the six alleles code for red pigment (AABBCC), the grain is dark red; when none of the six alleles encode red pigment (aabbcc), the grain is white. When a grain has one allele for red pigment (Aabbcc or aaBbcc or aabbCc) its colour is light pink; if it has two alleles for the pigment (AaBbcc or aaBbCc or AabbCC) it is pink, if it has three pigment alleles (AaBbCc or AABbcc or AabbCC), it will be light red. Similarly four alleles colour dose (AABBcc or aaBBCC or AAbbCC) will make red and five alleles colour dose (AABBcC or AABbCC or AaBBCC) will produce moderately dark red grain. Thus the colour phenotype of the grain is the sum of the individual effects of all the six alleles. Environmental factors like light, water and nutrients also influence the amount of grain colour. Environmental variations make the distribution of phenotypes more smooth and continuous.

Human skin colour is also a quantitative trait which is controlled by three to six gene pairs. The greater the number of pigment specifying genes, the darker the skin. A child can have darker or lighter skin than his parents.

Human height is a more complex polygenic trait. The perfectly continuous variation in range of human heights produces a smooth bell - shaped curve (Fig 22-12). A few people are very tall or very short, but most individuals fall in the average or mean value. This trait is controlled by many pairs of genes at different loci. Even multiple alleles may be possible at each locus. More the number of alleles for shortness, the shorter the height will be. Similarly greater the number of alleles for tallness, the taller

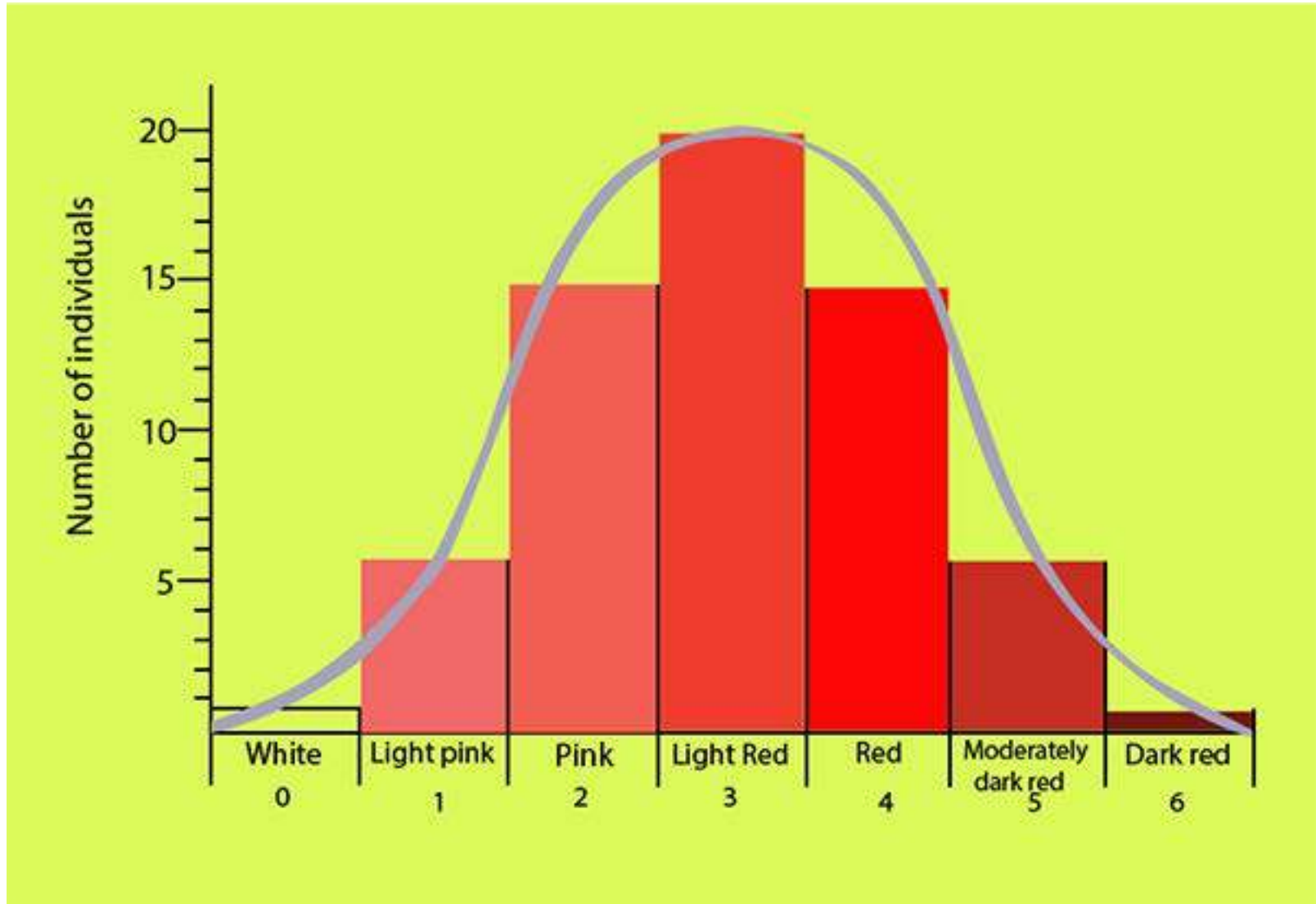


Fig 22.11 Number of pigment - contributing alleles in F2

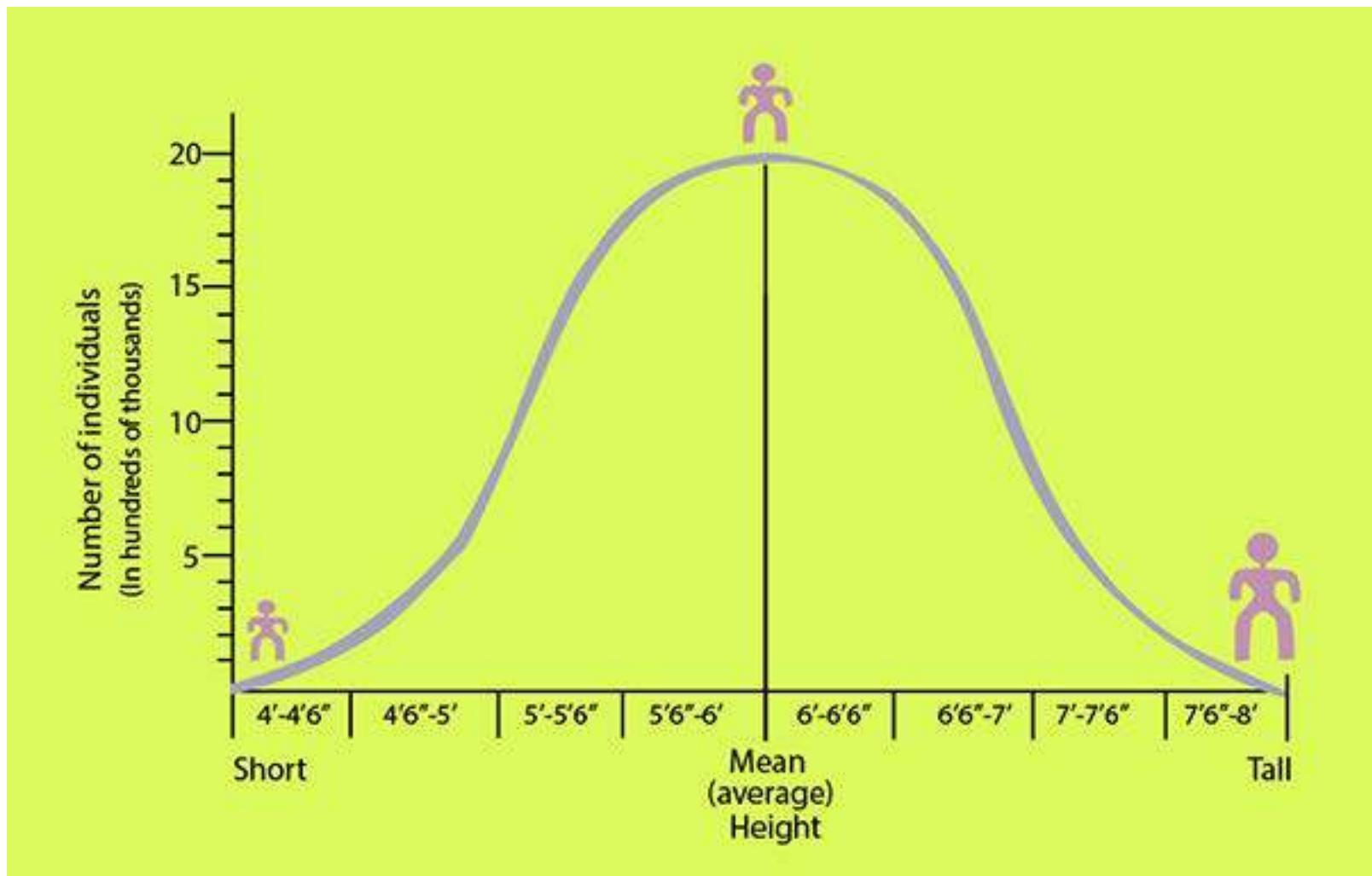


Fig.22.12-Human hight is a continously varying trait

the height will be. Environment also has a strong influence on height, intelligence and skin colour in humans. Constant exposure to sun darkens skin. Poor nutrition prevents achieving genetically determined height. Healthy and encouraging social environment promotes intelligence.

Activity : Study continuous variations in height and discontinuous variation in tongue rolling ability Of man and record your observations as histograms.

Frequency histograms illustrate variations. A frequency histogram is a simple graph. The horizontal or X axis indicates the range of different phenotypes of a trait within a population. The vertical or Y axis indicates the number of individuals or their percentage in the population.

Some people can roll their tongue into a distinct U shape when they extend it out of their mouth. They are called rollers (Fig 22.13). This ability is due to a single dominant gene. It is a discontinous variation inherited in simple Mendelian fashion. Its frequency diagram forms asymmetric distribution curve, with much greater frequency of phenotypes at one end than at the other.



Human height is a continuously varying trait. If we plot a frequency diagram of heights of humans in a large population, so many phenotypes are found with categories blending into one another. It forms a smooth bell shaped normal distribution curve. Measure the heights of a fairly large number of students in your college in cms, each to the nearest centimeter. Also note the ability of each student as roller or non roller. Record your observation in a table like this.

Sr.NO	Name	Height in cm	Roller/ Non-Roler

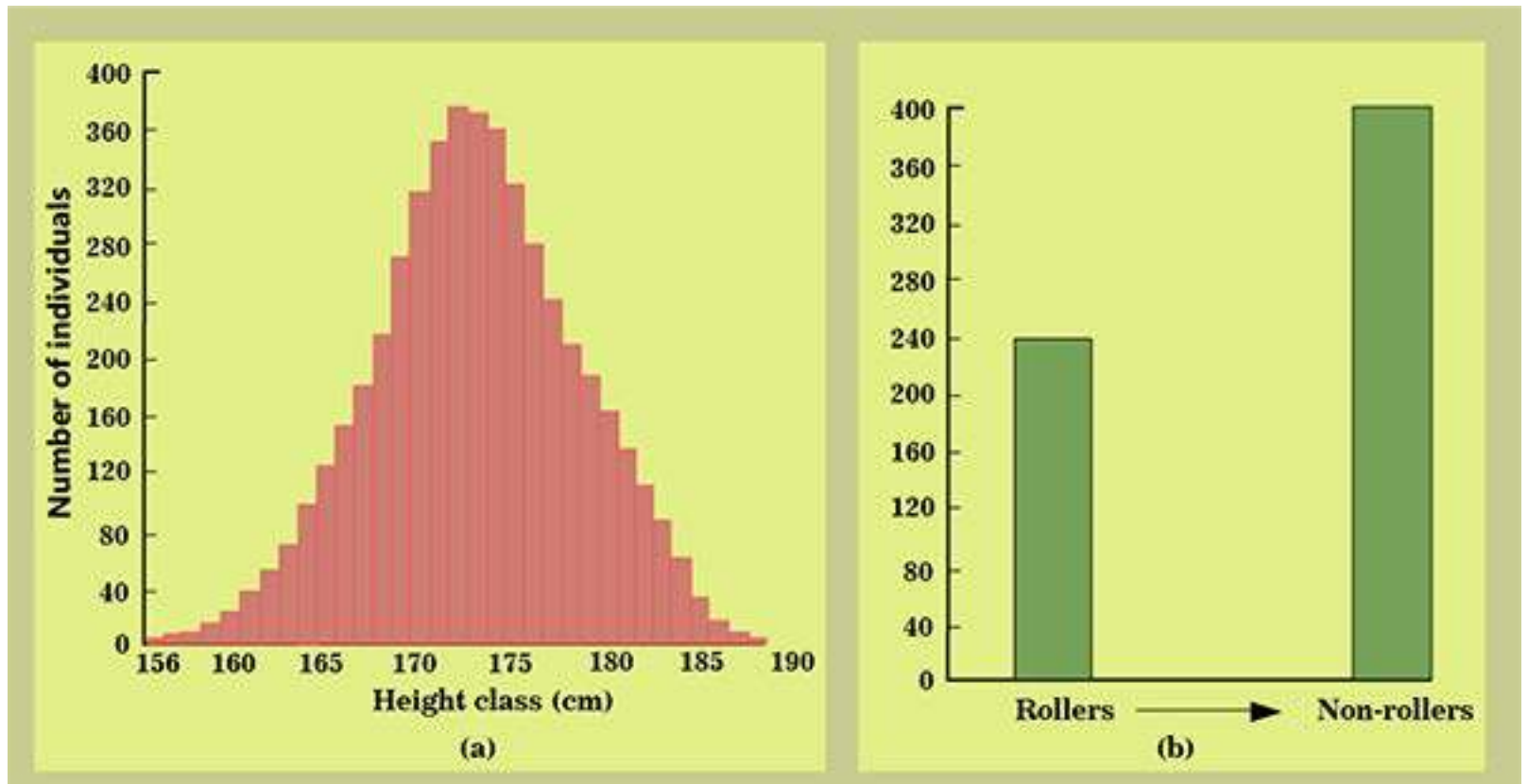


Fig 22.14 Comparison of a continuous and a discontinuous variation in human

Representing each measurement class as a bar with its height proportional to the number of individuals in each class, plot the graph (Fig 22-14).

GENE LINKAGE

Every organism possesses numerous characters controlled by thousands of genes, but the number of chromosomes is limited. .Therefore, each chromosome must carry many genes on it. All the genes located on the same chromosome are linked to each other. This phenomenon of staying together of all the genes of a chromosome is called linkage. Gene linkage is a physical relationship between genes. A chromosome carries its linked genes en bloc in the form of a **linkage group**. The number of linkage groups corresponds to the number of homologous pairs of chromosomes. Man has 23 linkage groups. Genes for colour blindness, haemophilia, gout etc form one linkage group on human X - chromosome. Similarly, gene for sickle cell anaemia, leukemia and albinism make another linkage group on human chromosome 11. Linked genes whose loci are close to each other do not obey Mendel's law of independent assortment, because these cannot assort independently during meiosis. Gene linkage also minimizes the chances of genetic recombination and variations among offspring.

Animation 22: Gene Linkage
Source & Credit: Point Pleasant Beach High School

CROSSING OVER

Linked genes can be separated by crossing over. Closer the two gene loci, more strongly are their genes linked. The farther apart two genes lie, greater are chances of their separation through crossing over. Crossing over is an exchange of segments between non-sister chromatids of homologous chromosomes during meiosis.' Let us visualize crossing over by considering only one pair of homologous chromosome (Fig. 22-16). The homologous chromosomes pair up lengthwise, point to point and locus to locus. One homologue carries genes 'A' and 'B' \ the other homologue has 'a' with 'b'. Chiasmata are formed at many places between non-sister chromatids of homologous chromosomes. Crossing over occurs at 4 strand stage between non-sister chromatids. It may take place at more than one place along a chromosome. Exchange of chromosome segments logically means exchange of DNA, i.e. genes or alleles. As alleles of non-sister chromatids are different, an exchange between their segments results in recombination of genes. Allele 'b' crosses over to homologue containing allele 'A'; and allele 'B' comes on the homologue of 'a'. Then homologous chromosomes separate by opening up chiasmata. The sister chromatids also separate from each other and each becomes an independent chromosome to move singly in each of the four haploid gametes. Four types of gametes are formed; two with parental combinations of linked genes, i.e. AB and ab, and two with recombination of genes, i.e. Ab and aB. If crossing over does not occur, only the two parental types of gametes are formed. Parental types of gametes produce parental types of offspring, while recombination gametes produce recombinant types of offspring.

$$\text{Recombination frequency} = \frac{\text{Recombination types}}{\text{Sum of all combinations}} \times 100$$

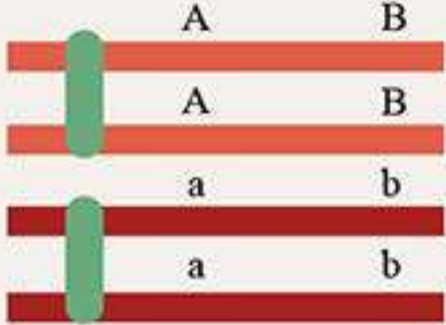
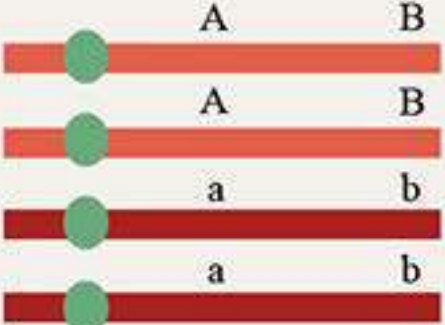
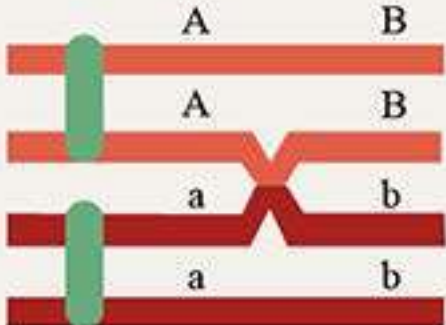
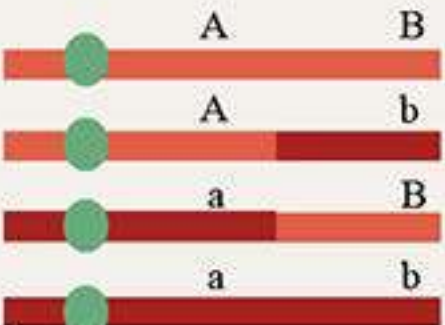
	Meiotic chromosomes	Meiotic products	
Meiosis with no crossover between the genes			Parental
			Parental
			Parental
			Parental
Meiosis with crossover between the genes			Parental
			Recombinant
			Recombinant
			Parental

Fig 22.16 Crossing over recombine genes.

Cross Over or Recombination Frequency

It is the proportion of recombinant types between two gene pairs as compared to the sum of all combinations.

The recombination frequencies between two linked genes can be calculated by backcrossing the heterozygote to a homozygous double recessive (Fig. 22-17).

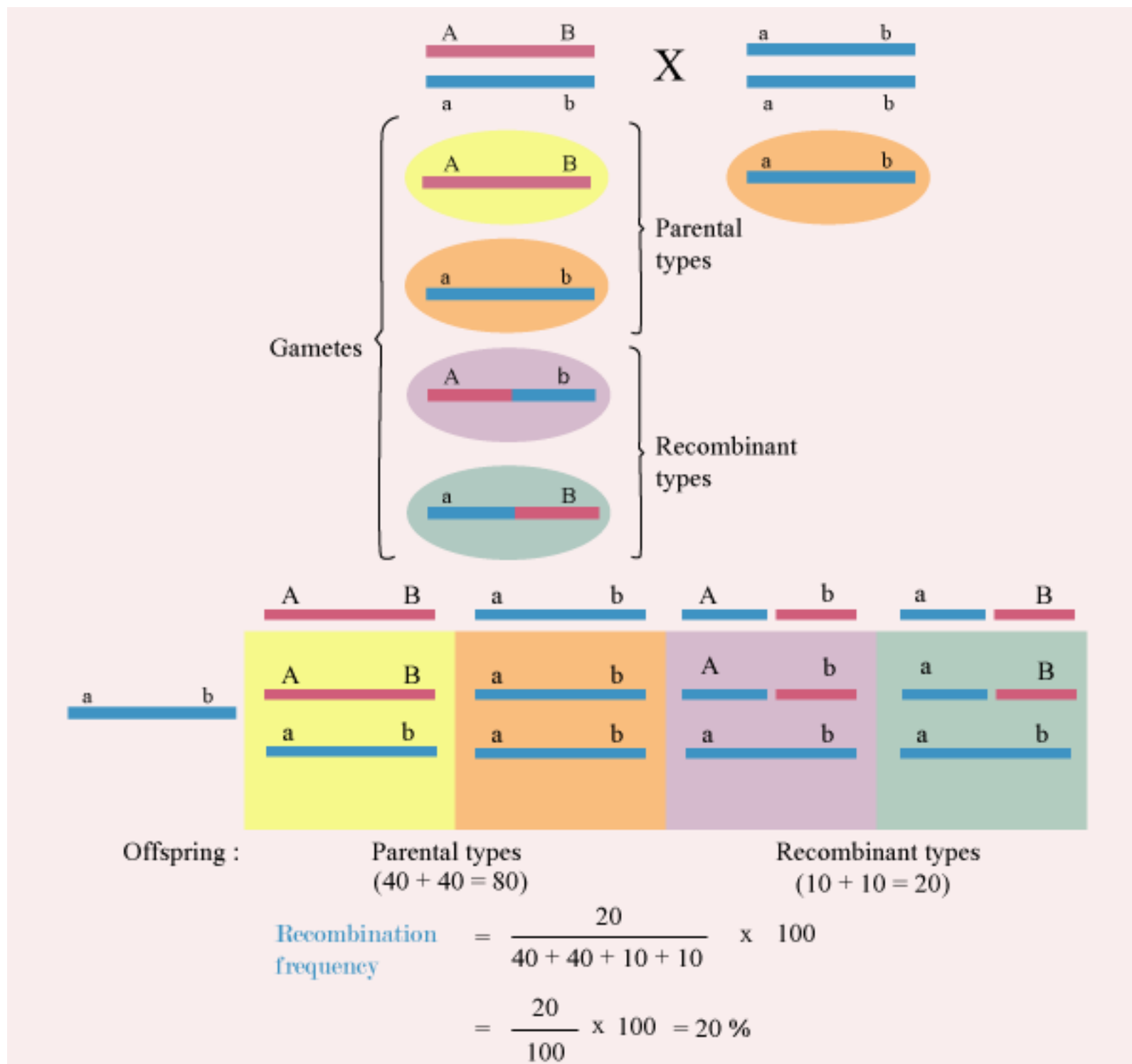
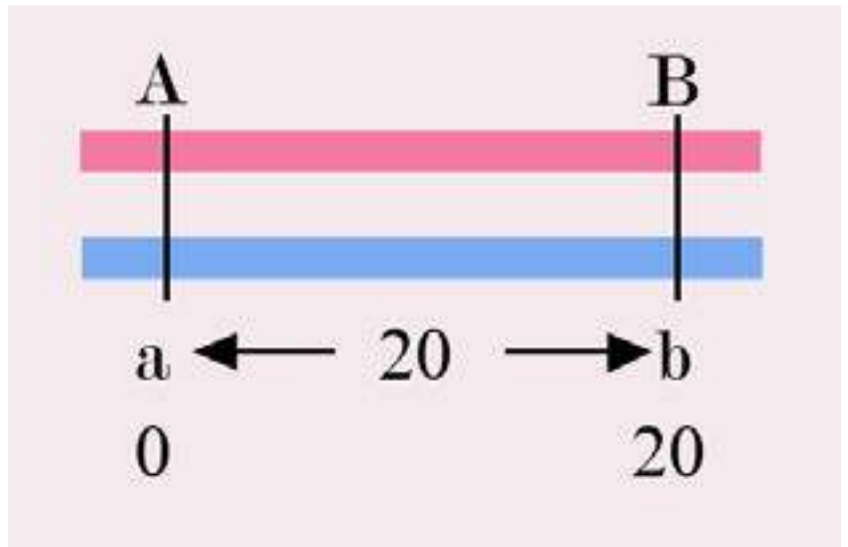


Fig 22.17 Recombination frequency between two linked genes.

The recombination frequency is directly proportional to the distance between the linked gene loci. Genes can be mapped on a chromosome on the basis of their recombination frequencies. If 1% of recombination frequency is equal to 1 unit map distance, the two linked genes A and B with a 20% recombination frequency must be 20 units apart.



Crossing over produces genetic variations among offspring. Genetic variations lead to tremendous variations in their traits. Variations provide raw material for evolution by letting them adapt successfully to the changing environment.

SEX DETERMINATION

Sex Chromosomes

The search for mechanism of inheritance of sex started after discovery of Mendel's work in 1900. A clear picture of the genetic basis of sex determination emerged after the discovery of sex chromosomes.

The fruit fly, *Drosophila melanogaster* has eight chromosomes in the form of four homologous pairs. T.H. Morgan (1911) noticed a peculiar difference in the chromosomes of male and female *Drosophila* (Fig 22-18). The chromosomes of the three homologous pairs were similar in both of the sexes, but the fourth pair was very different. The female had two similar rod shaped X-chromosomes in the fourth pair, while the male had one rod shaped X-chromosome but the other a morphologically different, J-shaped Y chromosome in the fourth heteromorphic pair. X and Y chromosomes are called sex-chromosomes because these have genes for determination of sex. Chromosomes of the other three pairs are autosomes. All chromosomes other than sex-chromosomes are called autosomes. Autosomes do not carry any sex determining gene.

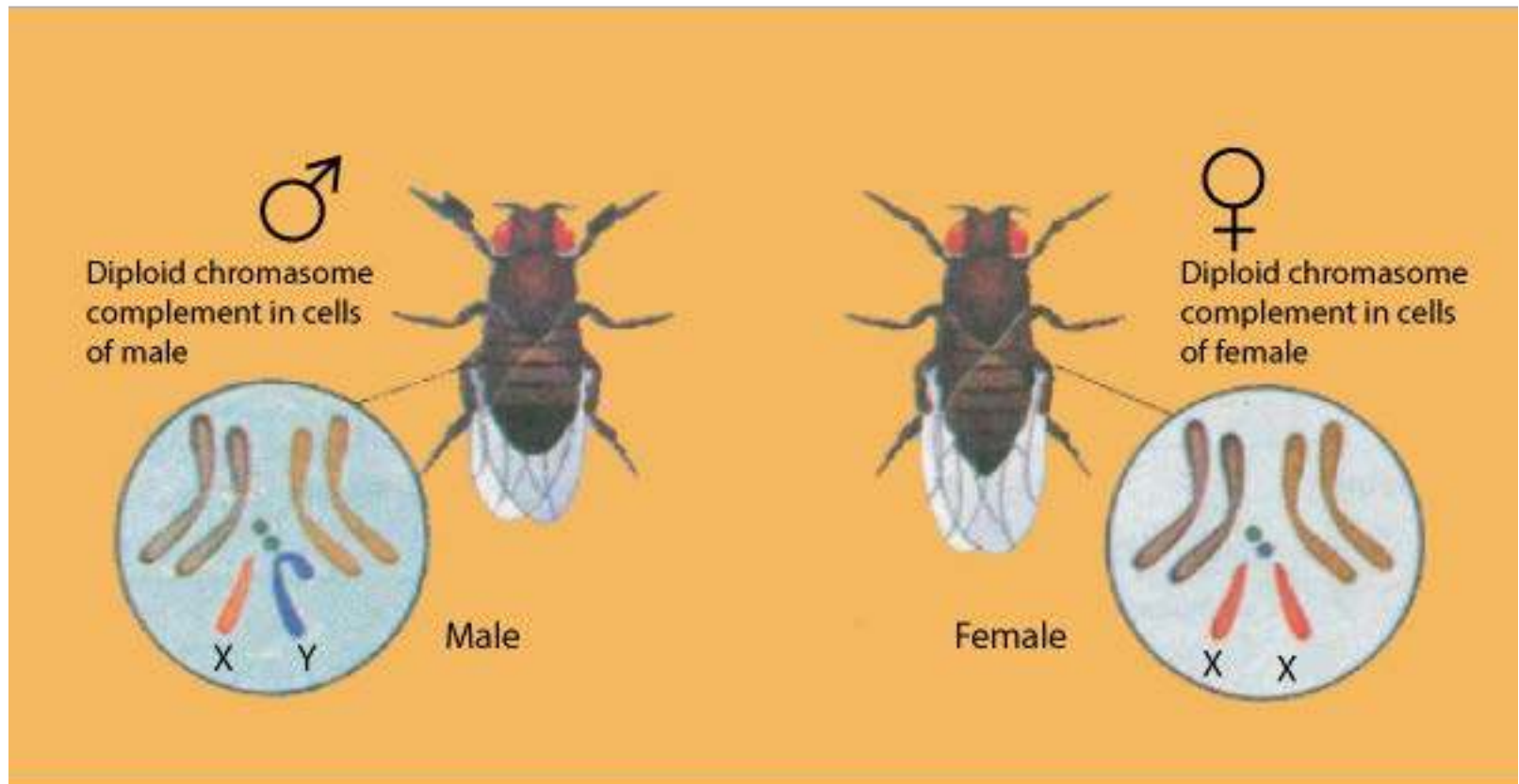


Fig 22.18 Chromosomes of *Drosophila melanogaster*.

Humans have 46 chromosomes in the form of 23 pairs. 22 pairs are of autosomes and one pair is of sex-chromosomes. Autosome pairs are common in both the sexes but the 23rd sex chromosome, pair is very different in males and females (Fig. 22-19). A woman has two similar X chromosomes in her 23rd pair but a man has an X chromosome along with a much shorter Y chromosome in his 23rd pair. The 23rd pair in man is heteromorphic. She is XX but he is XY.

SRY is the male determining gene. It is located at the tip of short arm of Y-chromosome. Its name SRY stands for "Sex determining regions of Y."

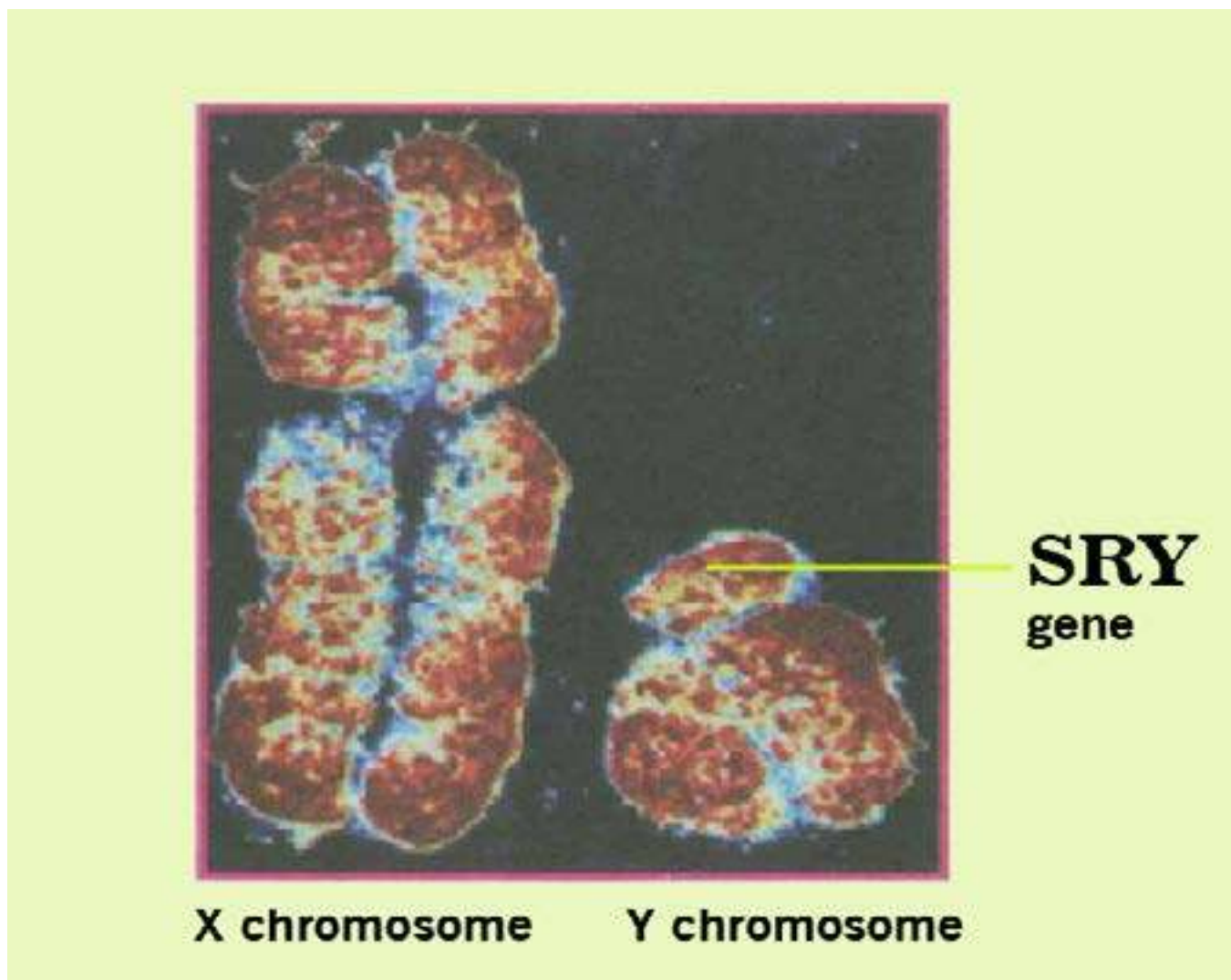


Fig 22.19 Sex Chromosomes of a man

In some grasshoppers males and females have different number of chromosomes. The female has 24 chromosomes in the form of 11 pairs of autosomes and a pair of X chromosomes. But the male grasshopper has 23 chromosomes. He has 11 pairs of autosomes and only one X chromosome. The other member for sex chromosome pair is entirely missing in male. Thus male is XO and female is XX.

Patterns of Sex Determination

There is a wide variety of sex determining ' mechanisms but three patterns are more, common.

1. XO - XX Type This pattern of sex determination is found in grasshopper and Protenor bug. Male is XO because it has only one X chromosome. The other sex chromosome is missing entirely. Male is heterogametic because it forms two types of sperms; half the sperms have X chromosome while the other half are without any sex chromosome. A gamete without any sex chromosome is called nullogamete.

Some species have compound sex chromosomes. They maintain many X or Y or both XY chromosomes of more than one kind that act together as a single sex-determining group. That is why the difference in number of chromosomes between male and female is very large. In the round worm *Ascaris incurva*, the female has 42 chromosomes in the form of 8 pairs of compound X along with 13 pairs of autosomes (16+26). Its male has 35 chromosomes comprising 8X plus one Y along with 13 pairs of autosomes (8+1+26).

Female is XX, because it has two X-chromosomes. It is homogametic, it forms only one type of eggs. Every egg carries an X chromosome. Sex of the offspring depends on the kind of sperm that fertilizes the egg. If an X-carrying sperm fertilizes the egg, an XX female offspring is produced. If the nullogamete sperm fertilizes the egg, an XO male offspring is produced (Fig. 22-20). Sex ratio between male and female offspring is 1:1.

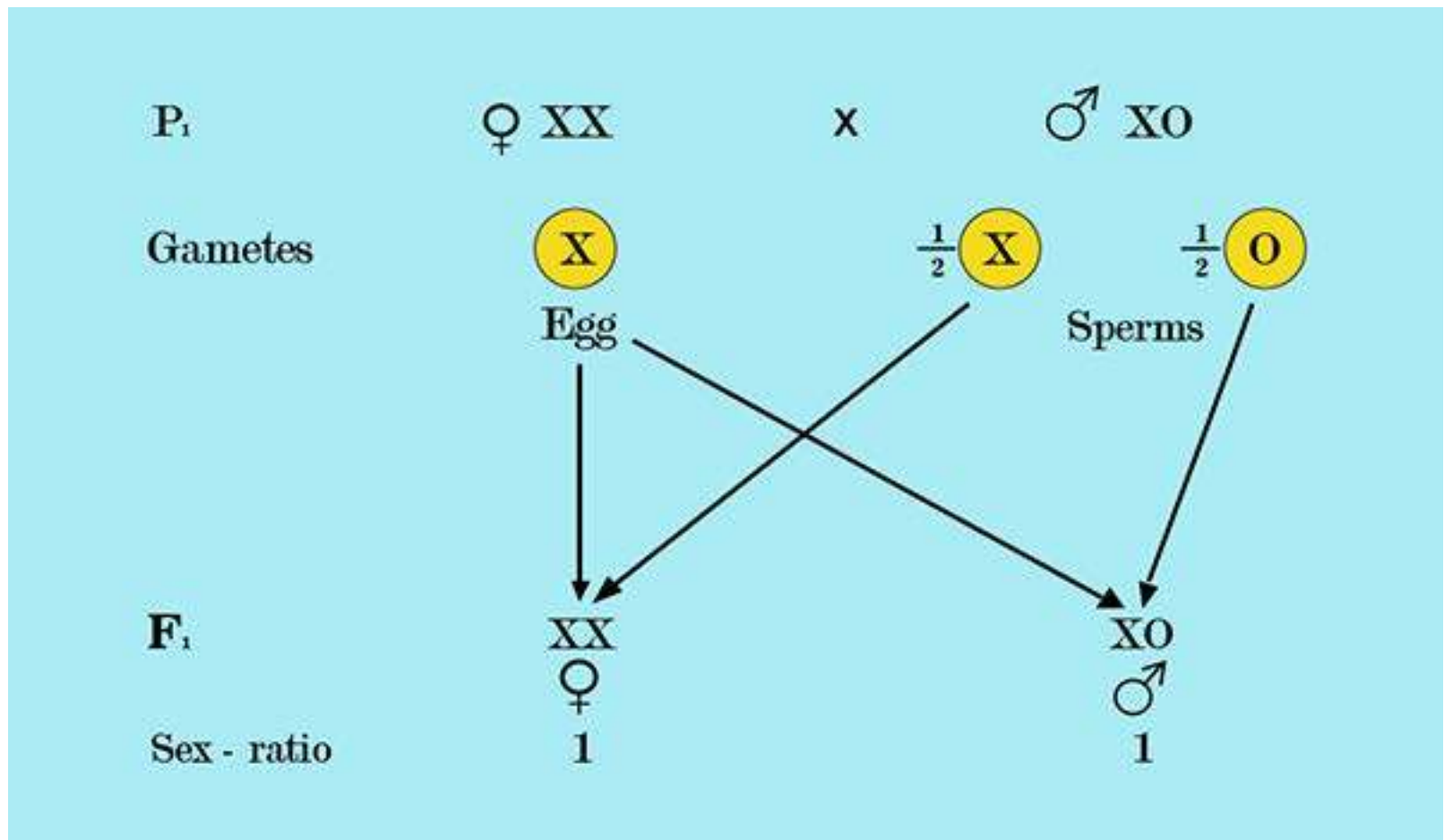


Fig 22.20 Sex determination in grass hopper and Protenor bug.

2. XY-XX Type: This pattern of sex determination is found in *Drosophila*, man and many other organisms. Male is XY and female is XX. Male being heterogametic produces two types of sex-determining sperms. Half the sperms carry X-chromosome and the other half carry Y - chromosome. Chances for both types of sperms are equal.

Female being homogametic produces only one type of eggs, each with an X chromosome. Sex of the offspring is determined by the type of sperm. If an X - carrying sperm fertilizes the egg, the zygote will be XX, and a female offspring is produced. If a Y - carrying sperm fertilizes the egg, the zygote will be XY, and a male offspring will be produced. The sex-ratio between male and female offspring is 1:1. Sex ratio indicates chances of the sex of the offspring. Chances for a son or daughter in human birth are equal (Fig. 22.21).

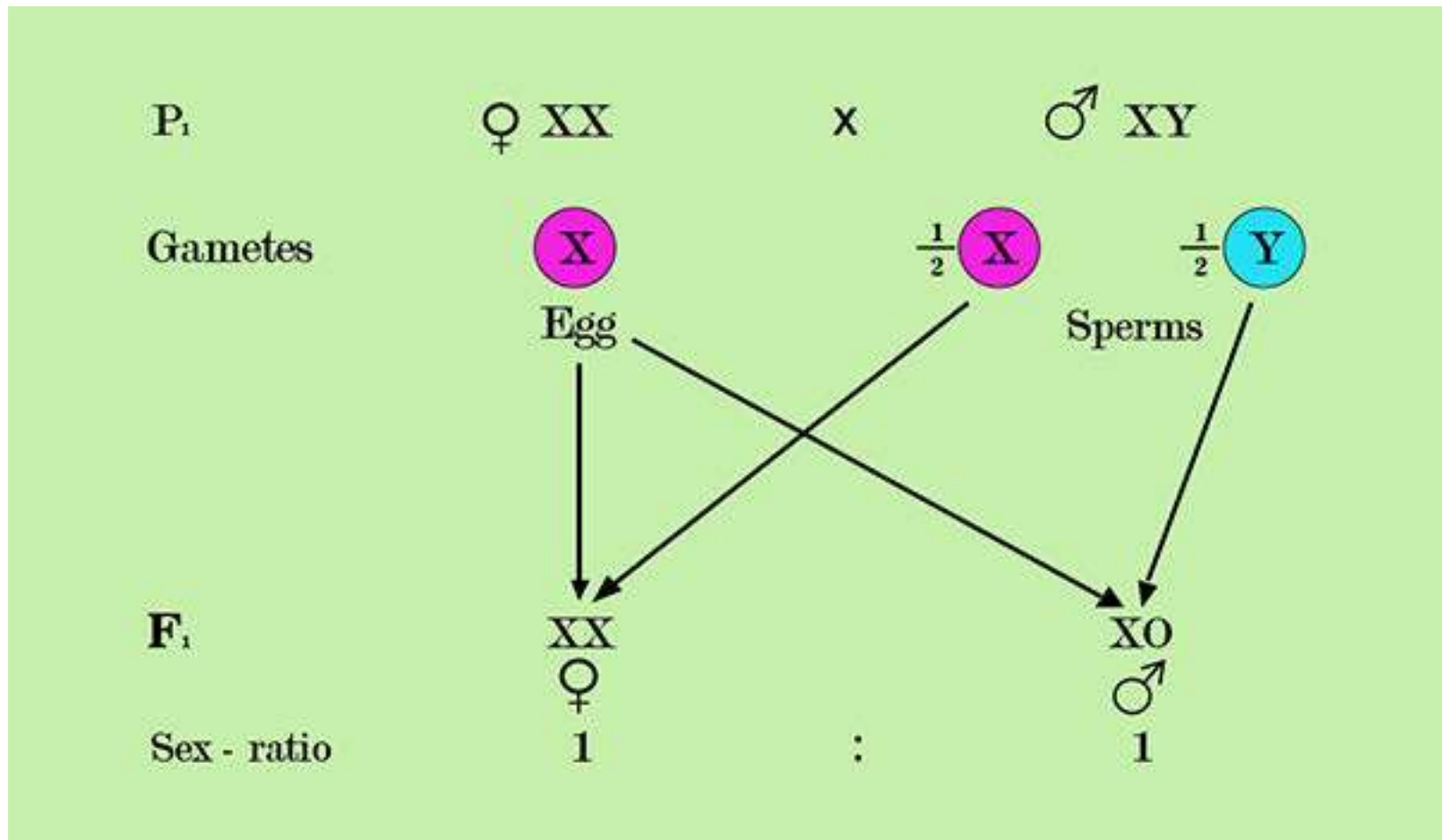


Fig 22.21 Sex Determination in man and Drosp

3. ZZ - ZW Type : This type of sex - determination pattern is common in birds, butterflies and moths. It was discovered by J. Seiler in 1914 in moth. It is the reverse of XY - XX system. Here the female is heterogametic ZW but the male is homogametic ZZ. Female produces two kinds of eggs Z and W in equal proportions. All sperms are alike, each carrying a Z - chromosome. It is the kind of egg that determines the sex of offspring. When a Z - carrying egg is fertilized by the sperm, a male offspring is produced, but when a W - carrying egg is fertilized by the sperm a female offspring is produced. Sex ratio is 1:1 (Fig. 22.22).

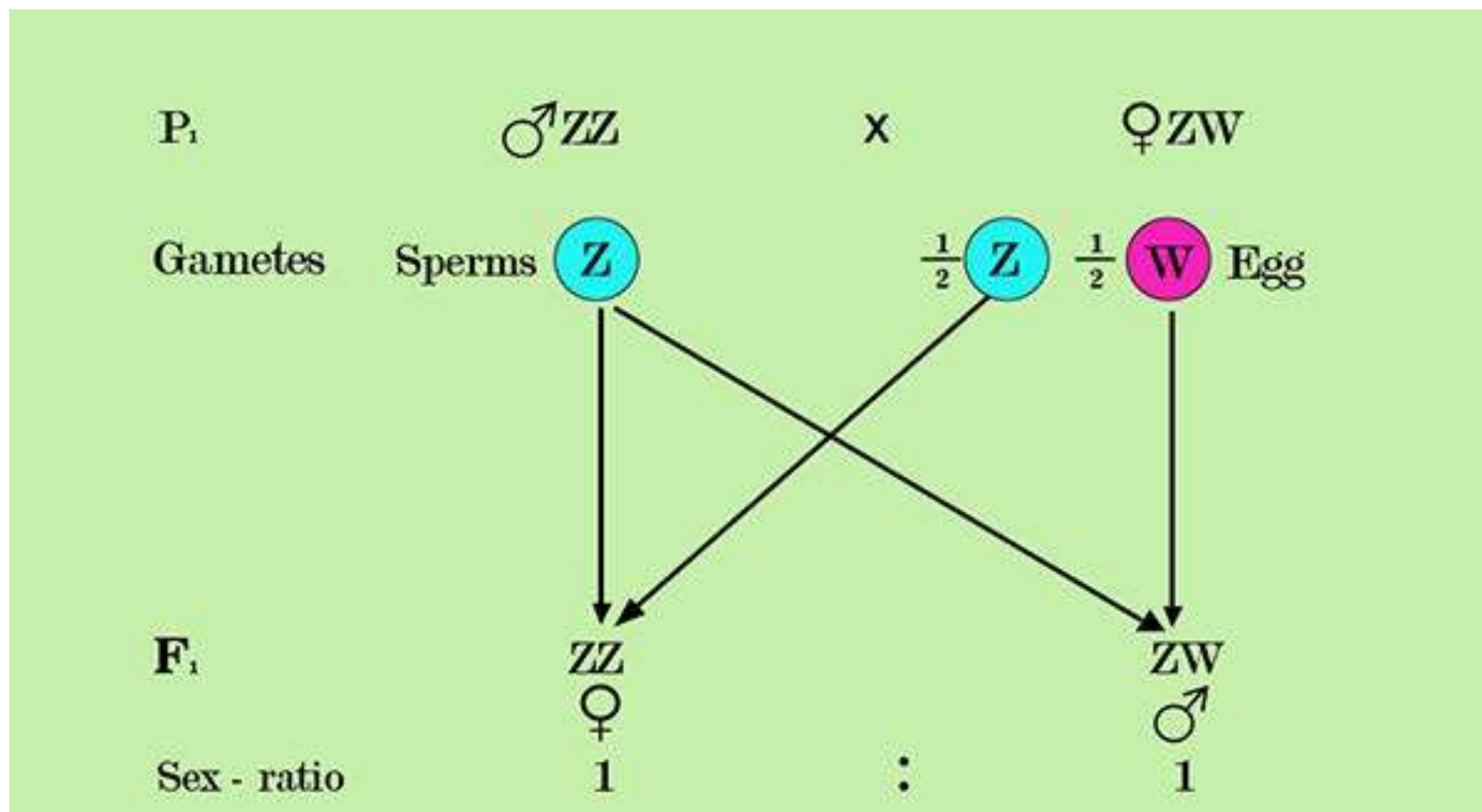


Fig 22.22 Sex determination in birds and butterflies.

Comparison of chromosomal determination of sex between *Drosophila* and Humans

Although both *Drosophila* and humans follow the same XY - XX sex determining pattern, yet there is a basic technical difference between the two. Presence of 'SRY' gene on Y chromosome is essential for triggering the development of maleness in humans. Absence of Y chromosome simply leads to the female development path. XO Turner's syndrome in humans produced through non-disjunction is a sterile female. But in *Drosophila* XO is a sterile male. Similarly XXY individual produced through non disjunctional gametes in humans is a sterile male called Klinefelter's syndrome, but the same XXY set of chromosomes in *Drosophila* produces a fertile female (Fig. 22-23).

Species	XX	XY	X0	XXY
<i>DROSOPHILA</i>	♀	♂	♂	♀
Humans	♀	♂	♀	♂

Fig 22.23 Comparison of sex determination in man and *Dorsophila*

There is a close genic balance between genes of different chromosomes. *Drosophila* has an X chromosome-autosome balance system. Its Y chromosome appears to have very little influence on sex. Here actually the X chromosome is female determining and the autosomes are male determining. Sex of an individual depends more on the number of X chromosomes relative to the number of sets of autosomes. An X : A ratio of 1.00 or higher produces female whereas an X : A ratio of 0.5 or lower produces males.

Sex Determination in Plants

Plants show a variety of sexual situations. Some species like Ginkgo are dioecious having plants of separate sexes. Male plants produce flowers with only stamens and female plants produce flowers with only carpels. Some dioecious plants have a difference of sex chromosomes between the sexes. These have an X - Y system. These plants typically exhibit an X - chromosome - autosome balance system for sex determination. Many other sex - determining mechanisms are also seen in dioecious plants. Correns (1907) discovered that pollens of certain plants were sex - determining. All eggs are of one type. Pollens of the two types are produced in equal number. One kind of pollen after fertilizing the egg produces male plant whereas the other kind of pollen after fertilization produces female plant (Fig. 22-24).

Many species of eukaryotic microorganisms like yeast do not have sex chromosome. These depend on genic system for determination of sex. In this system the sexes are specified by simple allelic differences at a small number of gene loci e.g., *a* and *A* are the two mating types (sexes) of yeast, controlled by MAT *a* and MAT *A* alleles respectively.

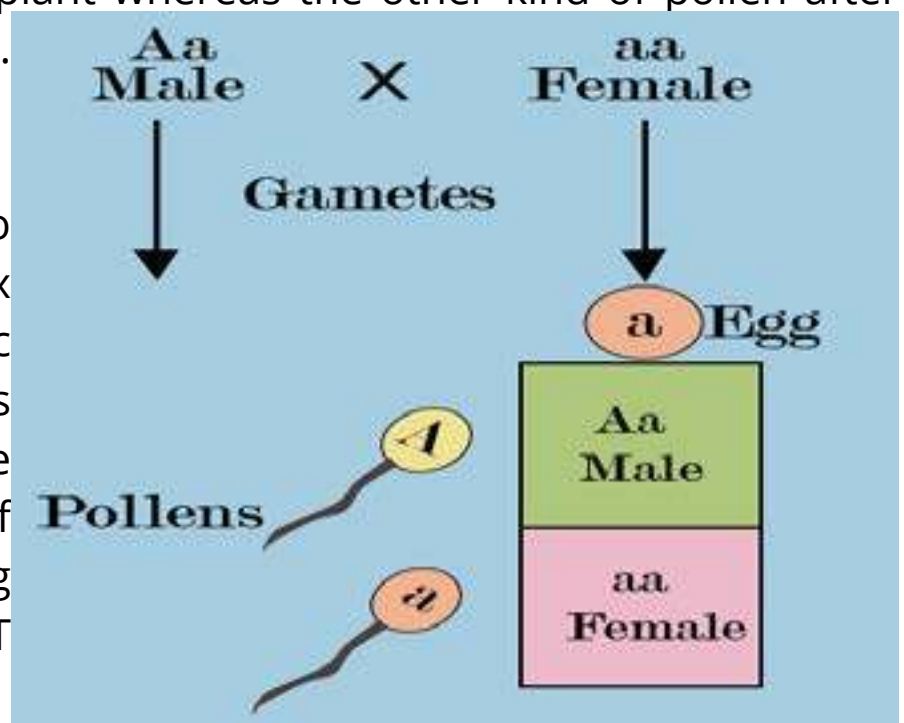


Fig 22.24 Pollens determines Sex

SEX LINKAGE**Sex Linkage in Drosophila**

Thomas Hunt Morgan (1910) provided experimental evidence in support of chromosomal theory of heredity through discovery of sex linkage in fruitfly *Drosophila*.

Drosophila is a very useful organism for genetic studies for many reasons: *

1. The tiny fly is often seen hovering over rotten fruits. It can be easily collected and cultured on mashed banana and other fruits. It does not need large spacious cages. It lives happily in ordinary glass bottle of jams and marmalades. It eats yeast that grows on mashed banana.
2. Male and female *Drosophila* show sexual dimorphism i.e. these are morphologically distinct from each other. Male is smaller in size with black rounded abdomen. Female is larger with pointed abdomen. Male has sex combs on front legs.
3. *Drosophila* has a generation time of just two weeks. It lays a large number of eggs which hatch out into fertile offspring. Many generations can be raised in a relatively short time.
4. *Drosophila* is perfectly suited for genetic studies. It shows fairly large number of distinct contrasting traits. Morgan and his colleagues studied pattern of inheritance of more than 85 traits of *Drosophila*. Its larvae are excellent material for dissection for chromosome study. It has only eight chromosomes in four homologous pairs that can be conveniently studied under a microscope. Its salivary gland cells have giant chromosomes in their nuclei. These giant chromosomes have characteristic banding patterns corresponding to genes.
5. The entire genome of *Drosophila* has been successfully sequenced as part of human genome project.

Morgan raised cultures of *Drosophila* flies to study different traits, such as colour of the eye. Normal fruit flies, the wild type, have bright red eyes. One of his coworkers Calvin Bridges, observed an unusual white eye mutant male fly. (Fig. 22.25).

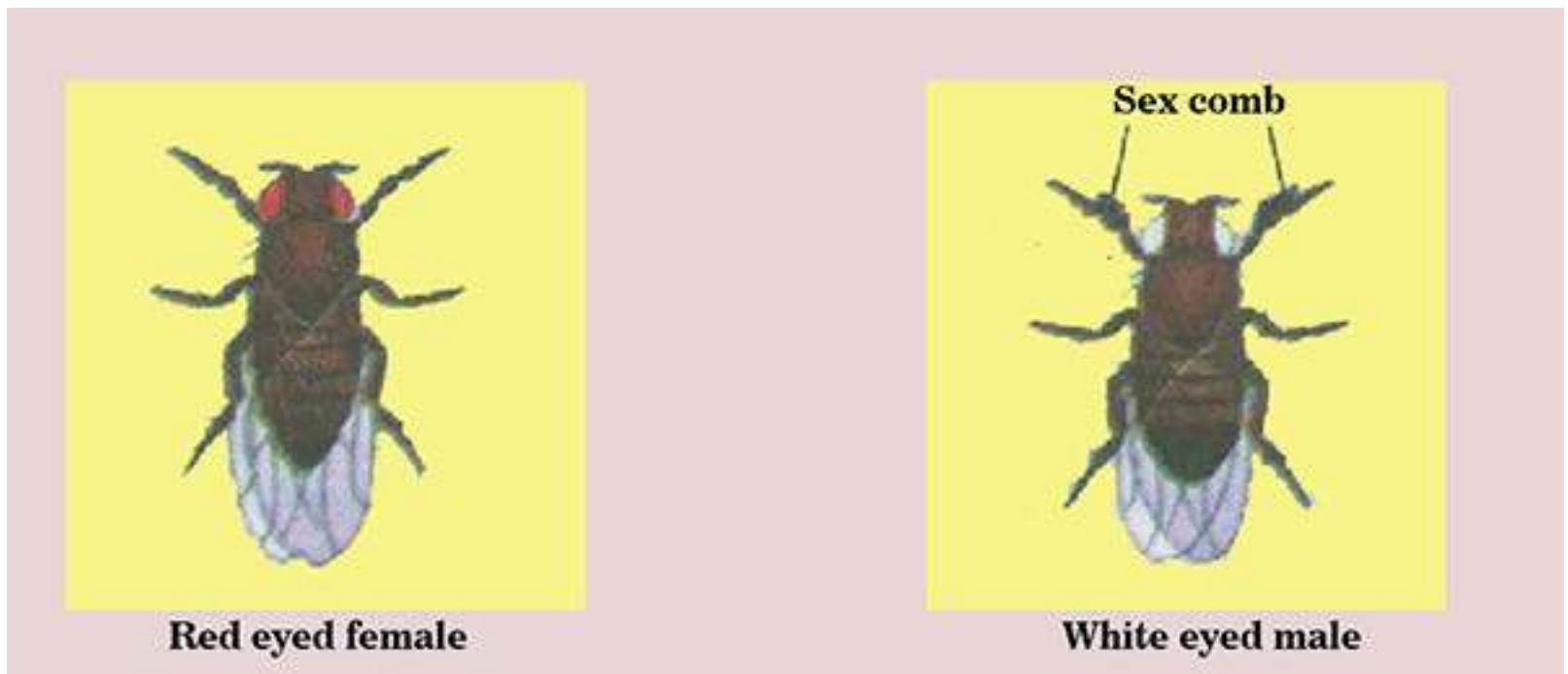


Fig 22.25 Wild type red eyed female and mutant white eyed male *Drosophila*

Morgan mated this white eyed male with a wild type red eyed female. All 1237 offspring of this cross had red eyes. Morgan concluded that red eye is a dominant trait (Fig 22-26a).

Morgan allowed males and females of F₁ generation to mate and produce F₂ generation. He counted 2459 red-eyed females, 1,011 red-eyed males and 782 white eye males among F₂ (Fig. 22.26b).

The proportion of 3470 red eyed to 782 white eyed flies did not perfectly fit into Mendelian 3 : 1 ratio. The number of recessive phenotype individuals was too small. There was another peculiarity in this result. All the white-eyed flies were only males. There was no white eye female in F₂ generation.

The inheritance of eye colour somehow seemed to be related to the 'sex' of the offspring. Morgan proposed that:

(i) The gene for eye colour is located on X chromosome, (ii) the alleles for eye colour are present only on X chromosome. There is no corresponding allele for this trait on Y chromosome.

Thus even a single recessive allele on X chromosome can express itself in males because Y chromosome is empty for that gene. Males are hemizygous as they carry just one allele on their only X chromosome. Females have two X chromosomes, each carrying an allele of the trait. Females can be homozygous or heterozygous.

Symbol "w" represents the recessive allele for white eye, and "w+" designates its wild type allele for red eye. The genotypes of the parents of P₁ cross were: Xw⁺ Xw⁺ for red eye female, and Xw Y for the white eye male.

Morgan's hypothesis explained clearly why all the white eyed flies in F₂ generation were only males.

Step 3: Test cross : Morgan wanted to test his hypothesis (Fig. 22-26c). He crossed the P₁ white eyed male (XWY) with one of its own daughters, the red eyed heterozygous female from F₁ generation. This test cross produced 129 red-eyed females, 132 red-eyed males, 88 white-eyed females and 86 white eyed males. White-eyed flies were less viable than red-eyed flies. Half the female offspring in fact had red eyes and half had white. Similarly half the males had red eyes and half had white.

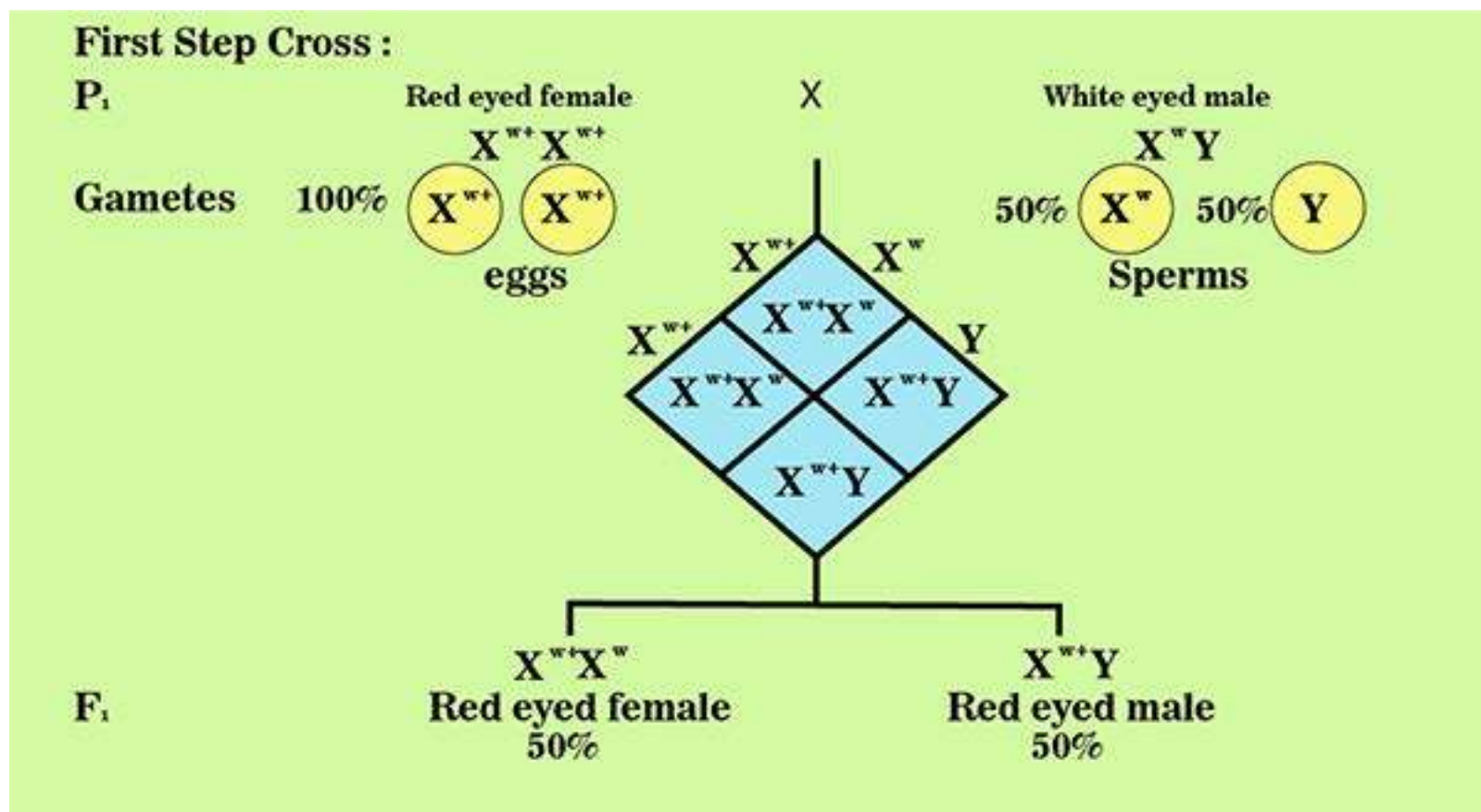


Fig 22.16(a)

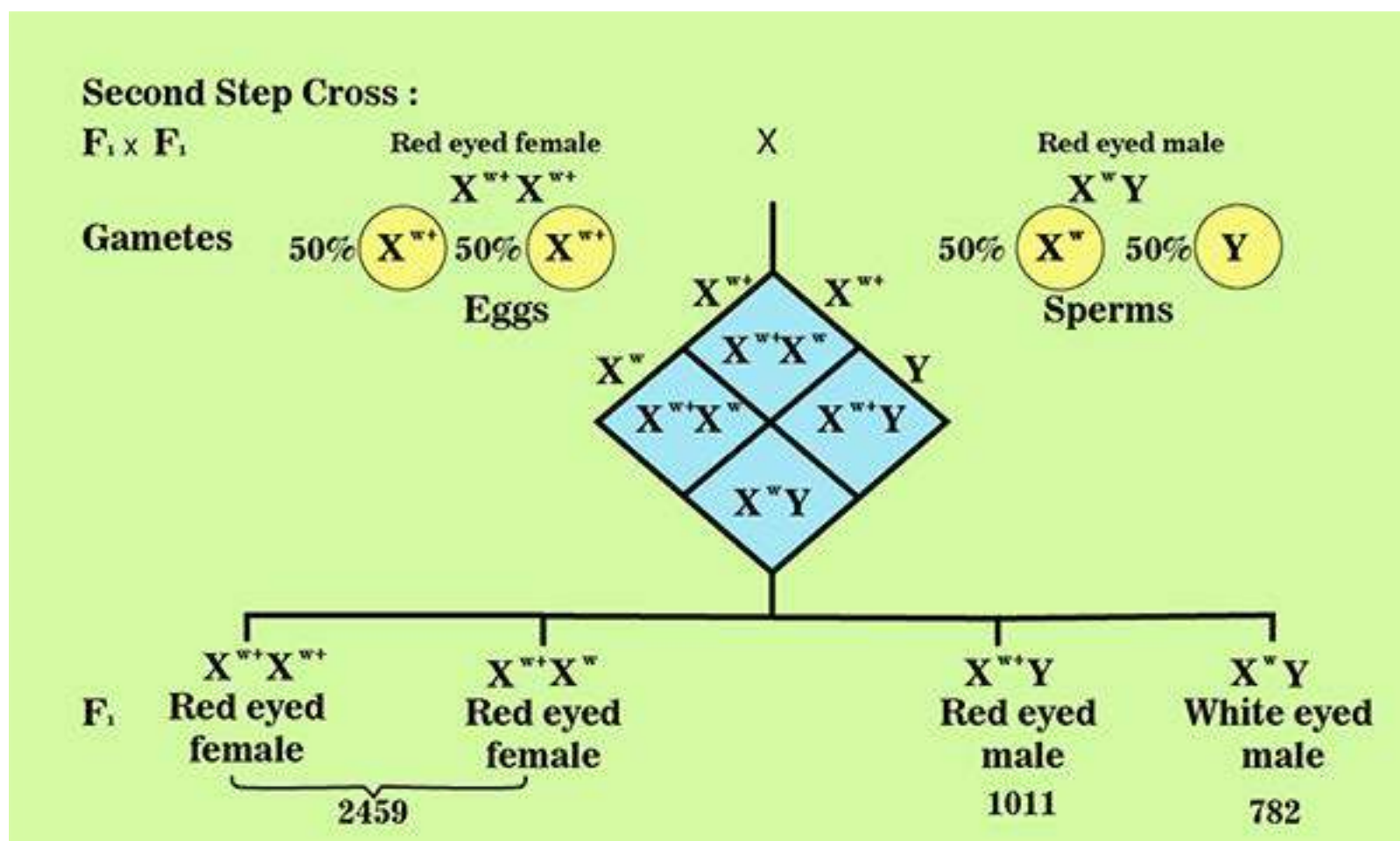


Fig 22.26(b)

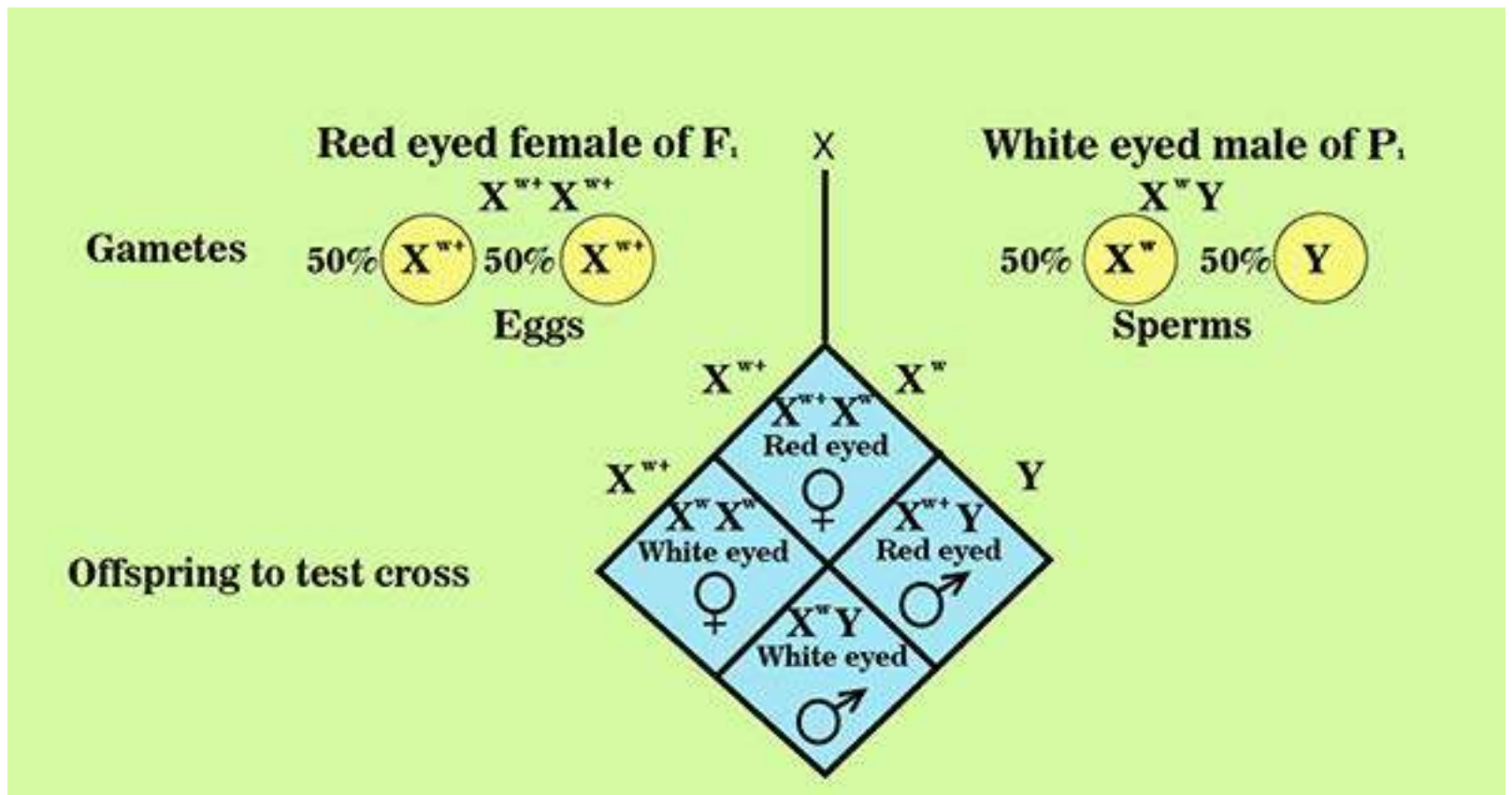


Fig 22.26(c)

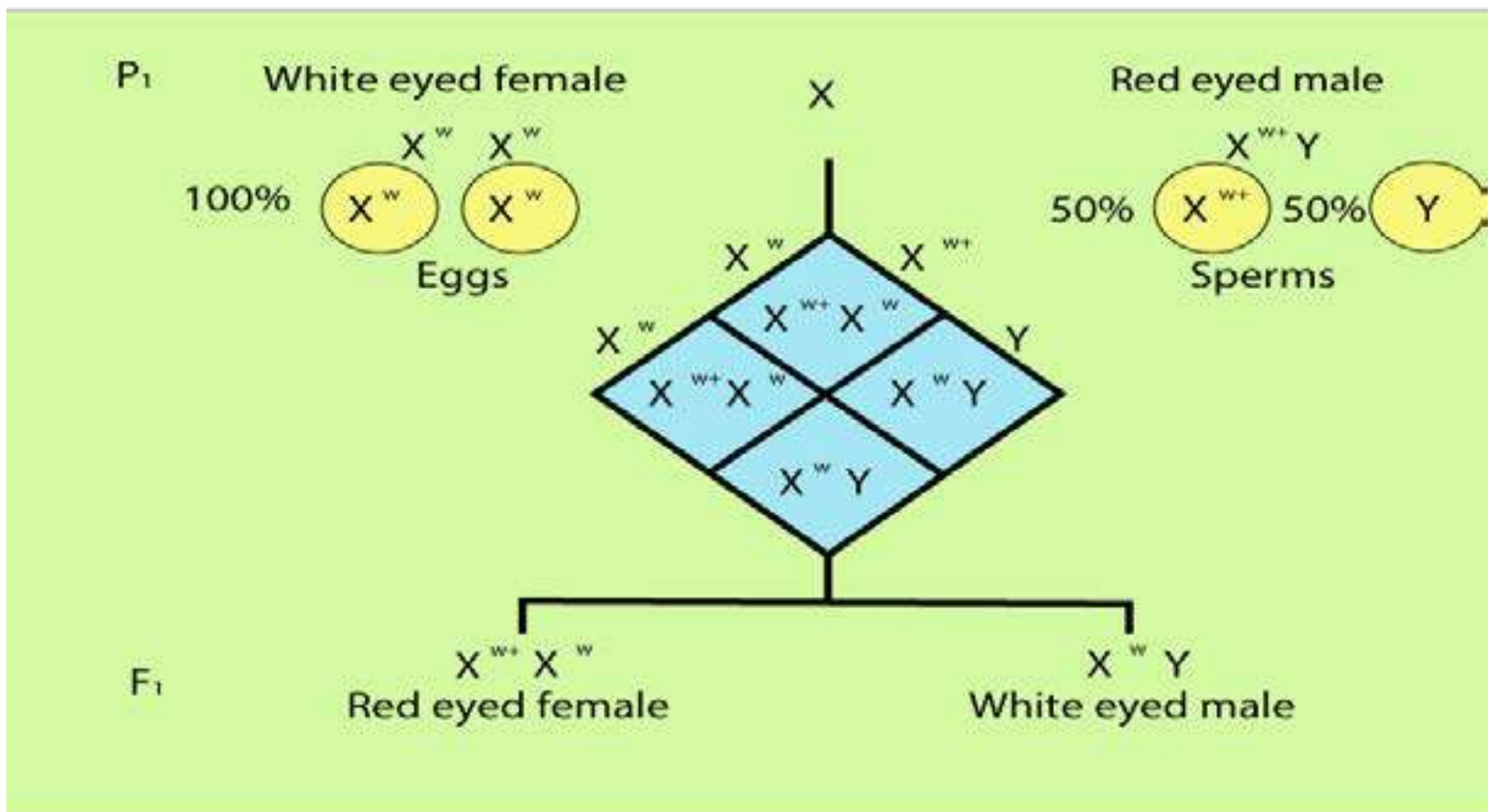


Fig 22.26(d)

Step 4: Reciprocal cross as a confirmatory test: Appearance of white eyed female provided an opportunity for a further confirmatory test. Morgan mated a white eyed female with a red-eyed male (Fig. 22.26d). All female offspring had red eyes, and all male offspring had white eyes. Then these F₁ red eyed females and white eyed males were mated to produce F₂. Half of the F₂ females had red eyes, half had white. Similarly half of the F₂ males had red eyes and half had white. This F₁ x F₁ cross was exactly like step 3 test cross.

A trait whose gene is present on X chromosome is called **X - linked trait**. X - linked traits are commonly referred as **sex-linked traits**. A gene present only on X chromosome, having no counterpart on Y chromosome, is called **X - linked gene**.

Sex-linked inheritance follows a very specific pattern. As a son inherits his X chromosome only from his mother, and a daughter gets an X chromosome from each parent, an X - linked trait passes in a crisscross fashion from maternal grandfather (P_i) through his daughter (F_i) to the grandson (F₂). It never passes direct from father to son because a son inherits only Y chromosome from father.

Morgan's discovery of sex-linked inheritance was a great contribution to the understanding of genes and chromosome. In 1933, T. H. Morgan was awarded a Nobel Prize for his contributions to genetics.

Y chromosome is not completely inert. It does carry a few genes which have no counterpart on X chromosome. Such genes are called **Y-Linked genes** and their traits are called Y-linked traits e.g. SRY gene on Y chromosome of man determines maleness. Y - linked traits are found only in males. These traits directly pass through Y chromosome from father to son only. As females do not normally inherit Y chromosome, such traits can not pass to them. Some genes like bobbed gene in *Drosophila* are present on X and Y both. These are called **X - and - Y linked genes**. These are also called pseudoautosomal genes because their pattern of inheritance is like autosomal genes.

Sex - Linkage in Humans

Humans have many X-linked traits of which some like haemophilia and colour blindness are recessive while others like hypophosphatemic or vitamin D resistant rickets are dominant. X-linked dominant is a trait which is determined by an X-linked dominant gene, while X-linked recessive is a trait that is determined by an X-linked recessive gene. Their patterns of inheritance are very different from each other.

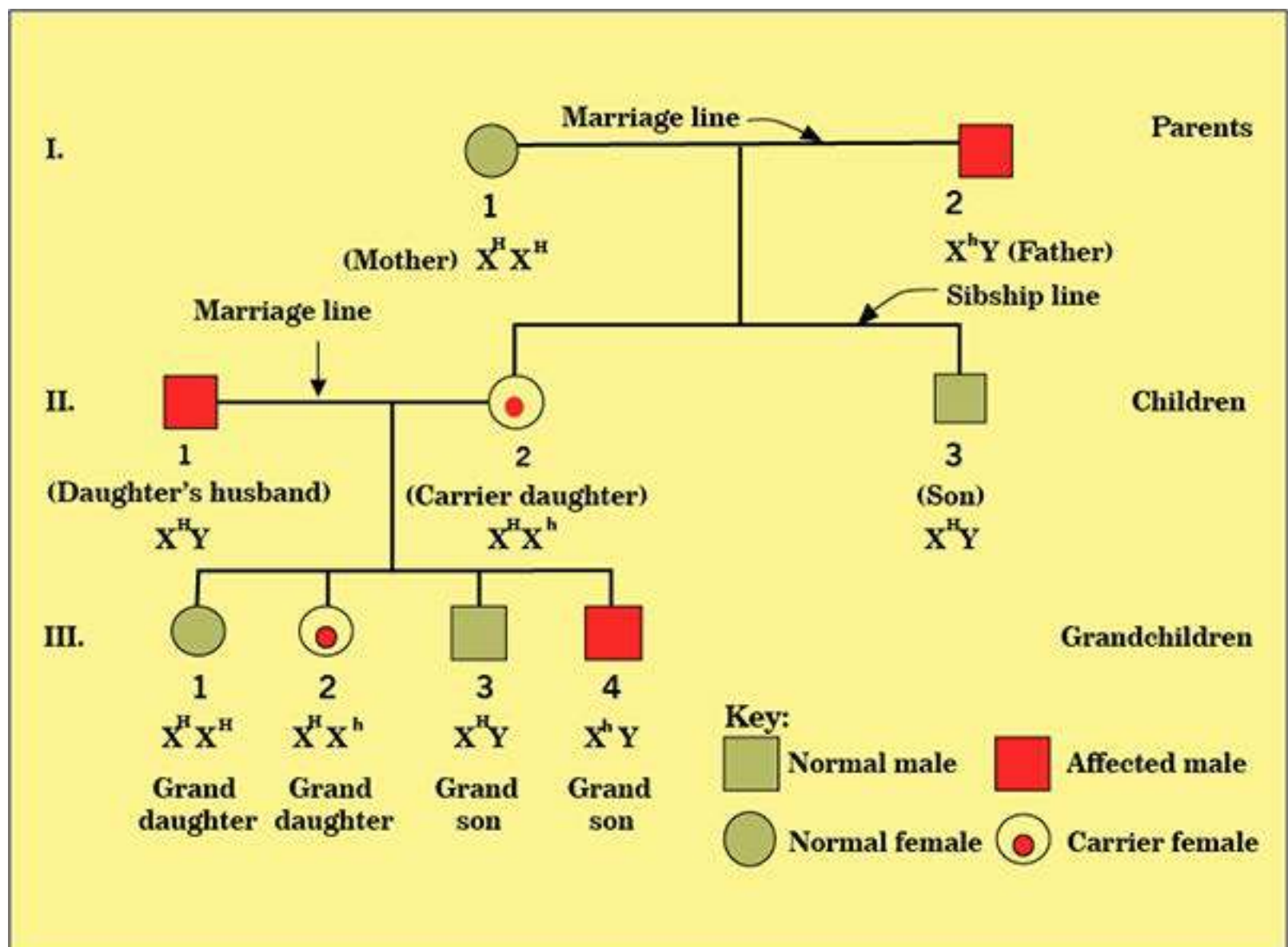


Fig 22.27 Transmission of X-linked recessive traits (haemophilia) in humans.

X - linked recessive inheritance: Experimental matings are not practically possible in humans. Mode of inheritance of human traits can be traced through pedigrees.

Genetics of Haemophilia: Haemophilia is a rare X—linked recessive trait. Haemophiliac's blood fails to clot properly after an injury, because it has either a reduction or malfunction or complete absence of blood clotting factors. It is a serious hereditary disease because a haemophiliac may bleed to death even from minor cuts. Haemophilia is of three types: A, B and C. Haemophilia A and B are non - allelic recessive sex - linked, but haemophilia C is an autosomal recessive trait. 80% haemophiliacs, suffer from haemophilia A due to abnormality of factor VIII, about 20% suffer from haemophilia B due to disturbance in factor IX, but less than 1% suffer from haemophilia C due to reduction in factor XI. Being X - linked recessives, haemophilia A and B affect men more than women, but haemophilia C affects both the sexes equally because it is autosomal. Chances for a man to be affected by haemophilia A and B are greater than a woman. A woman can suffer from haemophilia A or B only when she is homozygous for the recessive allele, but a man with just one recessive allele will display the trait. Haemophilia A and B zigzag from maternal grandfather through a carrier daughter to a grandson. It never passes direct from father to son. Gene for normal is H. Gene for haemophilia A is h. In generation I of this pedigree (Fig. 22.27) a man (I - 2) suffering from haemophilia A marries a normal woman (I - 1). He passes haemophilia gene to his daughter (II - 2) through his X chromosome. He cannot pass this gene to his son (II - 3) because the son receives only Y chromosome from him. His daughter (II - 2) also receives another X but with normal dominant allele from her mother (I - 1).

The daughter looks phenotypically normal, but she is heterozygous and a carrier for the recessive gene. When she marries a normal man (II - 1) she passes her father's trait to one of her two sons (III - 4) who inherits grandfather's X from her. The single recessive allele for haemophilia expresses successfully in the hemizygous son because his Y chromosome does not carry its counterpart. The other son (III - 3) is normal as he

Many X - linked traits in man are also found X - linked in other mammals like mouse, rabbit, dog, sheep, horse, donkey, cattle, kangaroo and chimpanzee. Was the mammalian X chromosome conserved throughout mammalian evolution?

inherits grand mother's X with normal gene, One daughter (III - 1) with both normal X is normal, but the other daughter (III - 2) is carrier like her mother.

Activity: Cases of Haemophilia A are reported in Queen Victoria's family. Pedigree of Queen Victoria's family (Fig. 22.28) indicates that Queen Victoria was a carrier mother, because she gave birth to an affected son Prince Leopold. Prince Leopold passed on this recessive X - linked trait in typical zigzag fashion through his carrier daughter (III - 1) to his grandson Rupert (IV - 1). Assign genotype to each individual. Can you explain how Alexis (IV - 3) became haemophiliac?

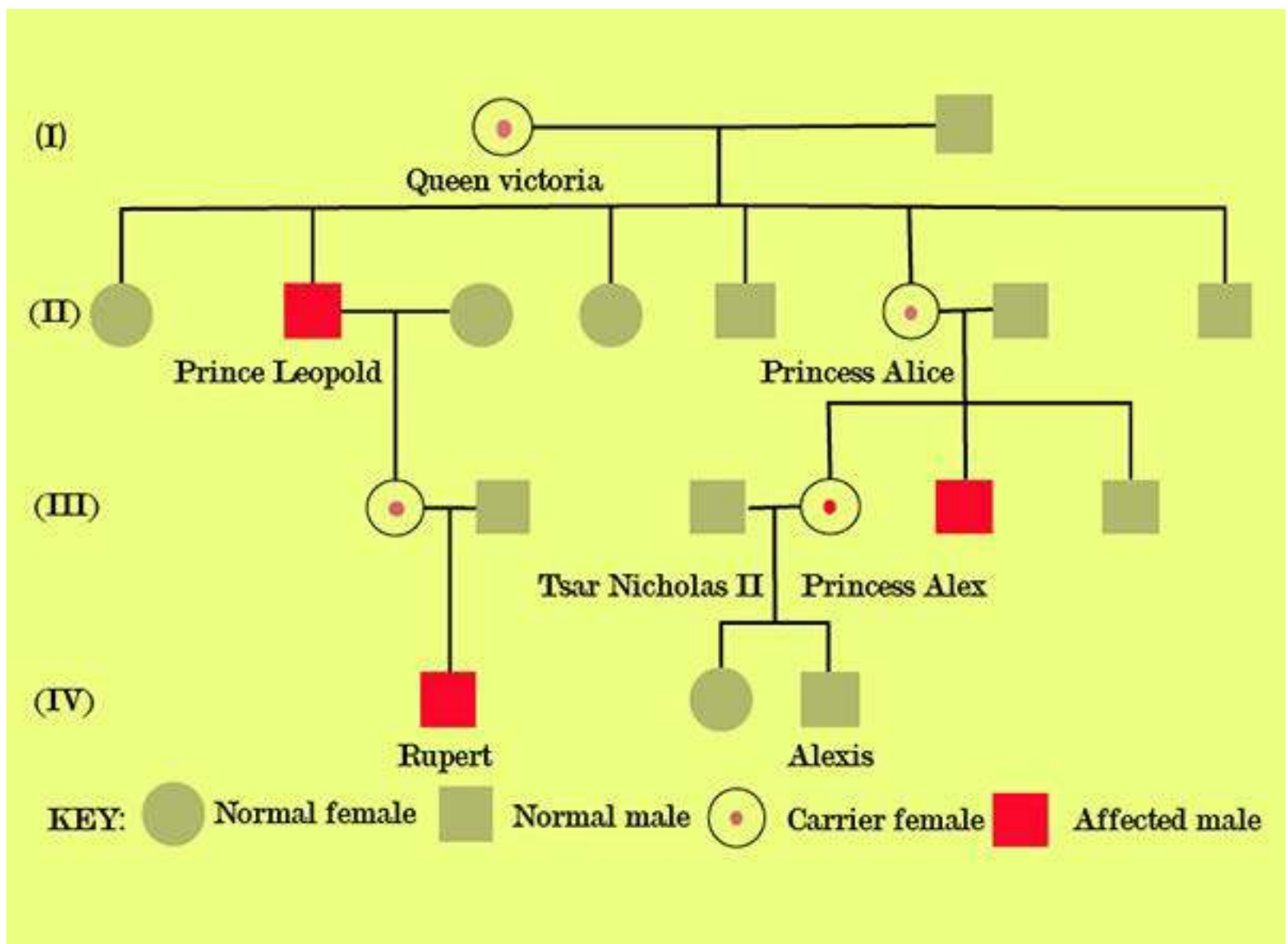


Fig 22.28 Pedigree of Queen Victoris's family showing cases of Hemolhilia A.

:Genetics of colour-blindness

Normal trichromatic colour vision is based on three different kinds of cone cells in the retina, each sensitive to only one of the three primary colours, red, green or blue. Each type of cone cell has specific light absorbing proteins called opsins. The genes for red and green opsins are on X chromosome, while the gene for blue opsin is present on autosome 7. Mutations in opsin genes cause three types of colour-blindness. A **dichromat** can perceive two primary colours but is unable to perceive the one whose opsins are missing due to mutation. **Protanopia** is red blindness, deuteranopia is green blindness, while tritanopia is blue blindness. Some people can detect red and green but with altered perception of the relative shades of these colours. They have abnormal but still partially functional opsins. They are protanomalous and deuteranomalous for red and green weakness respectively. A **monochromat** can perceive one colour. Monochromacy is true colour-blindness. Blue cone monochromacy is an X - linked recessive trait in which both red and green cone cells are absent. That is why it is also called red - green colour-blindness. It is a common hereditary disease. Like any sex - linked recessive trait, it also zigzags from maternal grandfather through a carrier daughter to a grandson. It never passes direct from father to son. This type of colour-blindness is more common in men than women, because chances for a male to be affected by it are much more than a female.

Testicular feminization syndrome is a rare X-linked recessive trait. Although the persons affected by this trait have a male set of XY chromosomes, yet the *tfn* gene on their X chromosome develops them physically into females. They have breast, female genitalia, a blind Vagina but no uterus. Degenerated testis are also present in abdomen. Such individuals are happily married as females but are sterile. It is an androgen insensitivity syndrome. Male sex hormone testosterone has no effect on them.

Activity: A sex-linked recessive allele “c” produces red - blindness. Its normal dominant allele is “C”. A normal woman whose father was red-blind, marries a red-blind man. What proportion of their children can have normal colour vision?

X - linked dominant inheritance : Pattern of X - linked dominant inheritance is different from X - linked recessive. It is more common in females than males. All daughters of an affected father, but none of his sons are affected. Any heterozygous affected mother will pass the trait equally to half of her sons and half of her daughters (Fig. 22.29). Hypophosphatemic rickets is an X - linked dominant trait. It is a rare hereditary disease. It is different from common dietary rickets, which could be cured by taking vitamin D. It does not result from vitamin D deficiency but its cause is a genetic communication failure at molecular level. The genes encoding bone proteins never receive vitamin D's message to function.

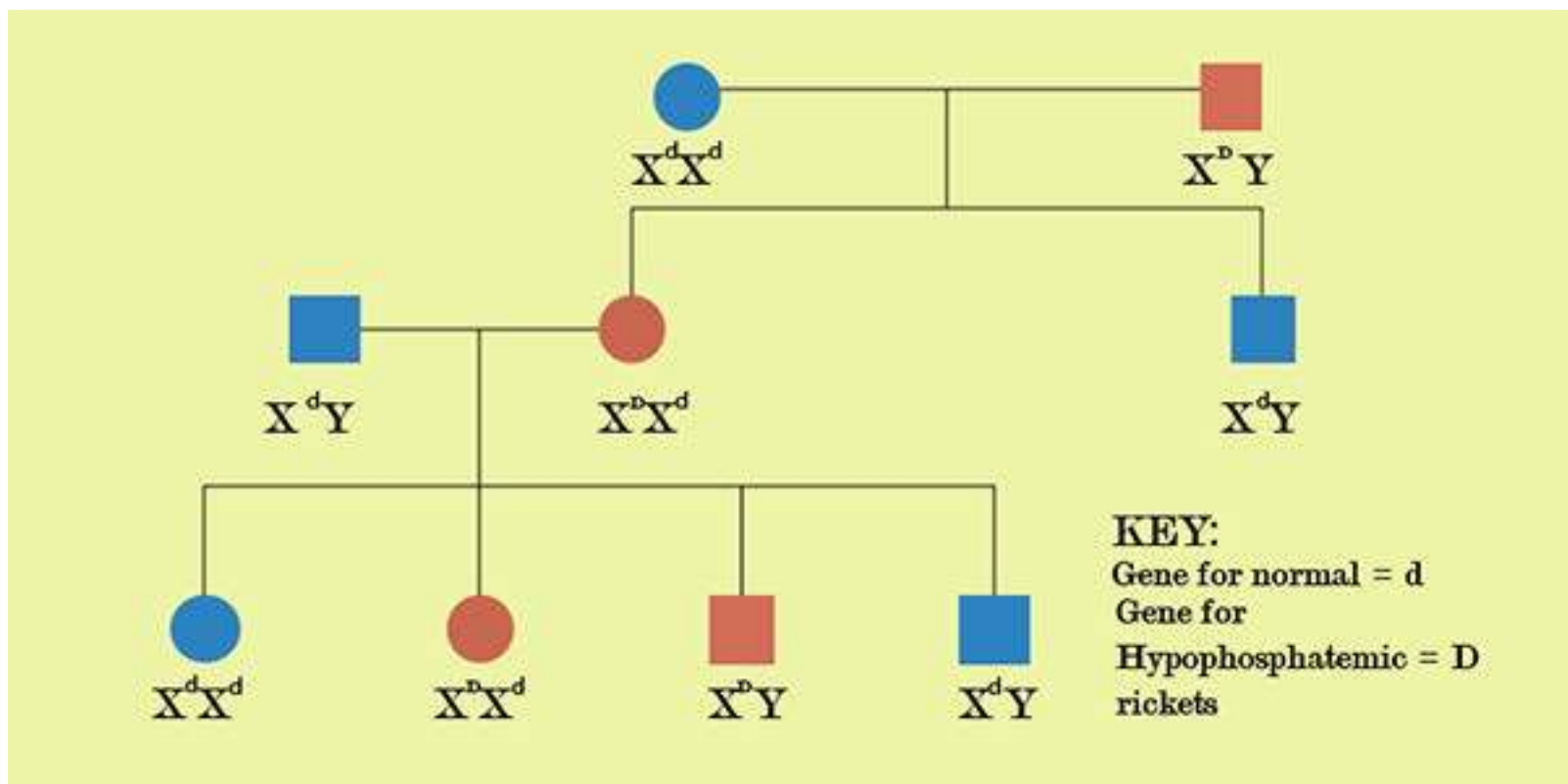


Fig 22.29 Transmission Of X-linked dominant traits in humans.

Y - Linked inheritance : Pattern of Y - linked inheritance is very peculiar. Maleness is a Y - linked trait. Y - linked trait passes through Y - chromosome from father to son only. Such traits cannot pass to daughters because they do not inherit Y - chromosome. All sons of an affected father are affected by a Y - linked trait (Fig. 22.30). SRY' gene on Y chromosome determines maleness in man. It is male sex switch which triggers developmental process towards maleness after 6 week pregnancy.

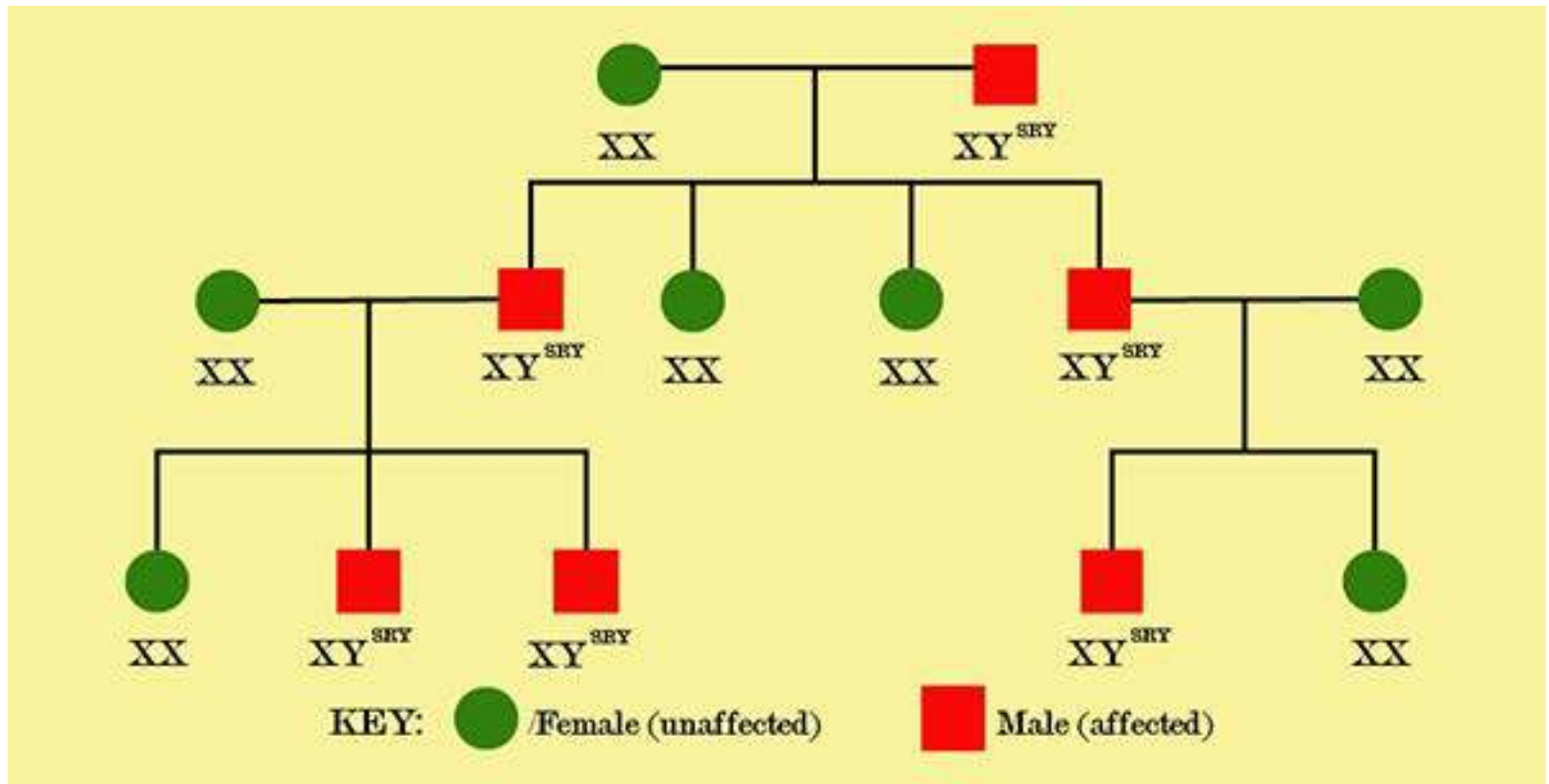


Fig 22.30 Y-linked inheritance in man

Sex Limited Trait

A sex-limited trait is limited to only one sex due to anatomical differences. Such trait affects a structure or function of the body present in only males or only females. These traits may be controlled by sex-linked or autosomal genes. Genes for milk yield in dairy cattle affect only cows. Similarly beard growth in humans is limited to men. A woman does not grow a beard herself but she can pass the genes specifying heavy beard growth to her sons.

Sex Influenced Trait

Sex influenced trait occurs in both males and females but it is more common in one sex. It is controlled by an allele that is expressed as dominant in one sex but recessive in the other. This difference in expression is due to hormonal difference between the sexes. Pattern baldness is a sex influenced trait. Many more men than women are bald. It is inherited as an autosomal dominant trait in males but as an autosomal recessive trait in females. A heterozygous male is bald but a heterozygous female is not. A woman can be bald only when she is homozygous recessive.

Activity: A man is 45 years old and bald. His wife also has pattern baldness. What is the risk that their son will lose his hair?

DIABETES MELLITUS AND ITS GENETIC BASIS

Diabetes mellitus is a hereditary disease. It is actually a heterogeneous group of disorders which are characterized by elevated blood sugar level. Diabetics are unable to metabolise blood sugar in their body. They pass glucose in their urine. Diabetes is the leading cause of kidney failure, adult blindness, lower limb amputation and heart disease.

There are two major types of diabetes: Type I is IDDM or insulin dependent diabetes mellitus. Type II is NIDDM or non insulin dependent diabetes mellitus. Type I is also called Juvenile diabetes because it usually occurs in early age before 40. It arises due to deficiency of pancreatic hormone insulin that normally routes blood glucose to cells for use. Type I is an auto immune disorder. The immune system backfires and manufactures auto antibodies against body's own cells. Sometimes, specific viral infections activate auto immune response. T - cells of immune system attack pancreas and destroy insulin producing (β - cells. As a result, pancreas does not produce insulin. Diabetics of type I must receive exogenous (from outside source) insulin to survive.

Progress is being made in understanding the genetic basis of this disease. The insulin gene is located on short arm of chromosome 11. Polymorphism and genetic variations within this locus is responsible for diabetes type I susceptibility. But today, it is no more just a recessive single gene trait, rather it is a multifactorial (polygenic with environmental influence) inheritance associated with several alleles.

Diabetes mellitus type II is non insulin dependent. It accounts for 90% of all diabetic patients. These persons produce some endogenous insulin themselves, but their body cells gradually fail to respond to insulin and cannot take up glucose from blood. They develop a sort of insulin resistance. It occurs among people over the age of 40, and is more common among the obese. Obesity increases insulin resistance. As exercise reduces obesity it indirectly increases insulin sensitivity and improves glucose tolerance.

There, definitely exists a genetic component in the form of an underlying tendency to develop diabetes under certain environmental conditions. About 2% - 5% of type II diabetics get the disease early in life, before 25 years of age. It is called maturity onset diabetes of the young (MODY). MODY can be inherited as an autosomal dominant trait. About 50% of cases of MODY are caused by mutations in glucokinase gene. Glucokinase enzyme usually converts glucose to glucose - 6 - phosphate in pancreas. MODY can also be caused by mutations in any of the four other genes which encode transcription factors involved in pancreatic development and insulin regulation. But these four MODY genes do not play any significant role in adult - onset type II.

Blood pressure is also an example of multifactorial trait. There is a correlation between systolic and diastolic blood pressure of parents and their children. This correlation is partly due to genes common in them. Blood pressure is also influenced by environmental factors such as diet, stress and tension.

Exercise**Q1 Fill in the blanks.**

1. _____ is the basic unit of biological information.
2. A sudden change in the structure of a gene is called _____
3. _____ is the chance of an event to occur.
4. A cross among monohybrids is a _____ cross.
5. An individual with a homozygous genotype is called _____.
6. Different alleles of a gene that are both expressed in a heterozygote are called _____
7. When a heterozygote exceeds the phenotypic expression of both the homozygotes the phenomenon is called _____.
8. When a single gene affects two or more traits, the phenomenon is called _____
9. A gene with multiple phenotypic effect is called _____.
10. The phenomenon of staying together of all the genes of a chromosome is called _____
11. _____ minimizes the chances of genetic recombination.
12. _____ is an exchange of segments between non-sister chromatids of homologous chromosomes during meiosis.
13. All chromosomes other than sex chromosomes are called _____.
14. _____ is the maleness determining gene in man.
15. Type _____ of diabetes mellitus is non insulin dependent.
16. Polygenic inheritance with environmental influence is called _____ inheritance.

Q.2 Short questions.

1. In grasshopper, the male has XY and the female has XX types of sex chromosomes.
2. Pea is normally a self fertilizing plant.
3. Dihybrids are offspring of the parents who differ in one contrasting pair of trait.
4. X - linked traits pass direct from father to son.
5. A person suffering from Blue cone monochromacy can not see blue colour.
6. In birds and moths eggs determine sex.
7. A homozygote forms all gametes of the same type.
8. The allele for a sex limited trait is dominant in one sex but recessive in the other.

9. Pattern baldness is a sex influenced trait.
10. Carriers of haemophilia show no symptoms of the disease.

Q.4 Short Questions.

1. Differentiate between:

Phenotype and genotype	Gene and allele
Homozygous and heterozygous	Monohybrid and dihybrid
Autosome and sex chromosome	Dominance and epistasis
Allele and multiple allele	X-linked trait and Y-linked trait
Incomplete dominance and codominance	Sex limited and sex influenced trait
Continuous and discontinuous variations	Dominant trait and recessive trait
	Wild type and mutant

2. What is a gene pool?
3. Was pea a lucky choice for Mendel? What would have happened if he had studied an eighth character?
4. What is a test cross? Why did Mendel devise this cross?
5. What would happen if alleles of a pair do not segregate at meiosis? How would it affect the purity of gamete?
6. If the alleles do not assort independently, which type of combination is missing in the progeny.
7. Why has each gamete equal chance of getting one or the other allele of a pair?
8. Does the dominant allele modify the determinative nature of its recessive partner?. What sort of relationship do they have?
9. Which type of traits can assort independently?
10. Why does the blood group phenotype of a person remain constant throughout life?
11. What is a universal blood donor?
12. How can you protect the baby against Rh - incompatibility?
13. Which type of genes do not obey law of independent assortment?
14. How can linked genes be separated from each other ?
15. What is multifactorial inheritance?
16. What is MODY?
17. Can a child have more intelligence (IQ score) than his parents?

Q.4 Extensive Questions

1. What is incomplete dominance? Explain it with an example.
2. Define Mendel's law of segregation. Explain it with an example.
3. Define Mendel's law of independent assortment. Explain it with an example.
4. Define probability. Derive 9:3:3:1 F₂'ratio of independent assortment through product rule.
5. What is codominance? Explain the phenomenon of codominance with an example.
6. Define multiple alleles. Describe multiple allelic blood group system of man.
7. What is Rh factor? Describe the genetic basis of Rh - blood group system of man.
8. What is erythroblastosis foetalis? Discuss this adverse effect of Rh incompatibility? Also suggest a therapy to avoid Rh sensitization of an Rh⁻ mother married to an Rh⁺ man.
9. Define epistasis. Explain epistatic gene interaction with an example.
10. What is a pleiotropic gene? Discuss pleiotropy with examples.
11. What are polygenes? Explain polygenic inheritance.
12. What is crossing over? Define recombination frequency and explain its significance.
13. What are sex-chromosomes? Discuss the chromosomal patterns of sex determination in organisms.
14. Compare chromosomal determination of sex between Drosophila and humans.
15. Define gene pool. Explain the concept of gene pool in a sample population.
16. What is sex linkage? Explain T. H. Morgan's study of sex - linkage in Drosophila.
17. Compare the pattern of inheritance of an X - linked dominant trait with an X - linked recessive trait in humans.
18. Explain diabetes mellitus and its genetic basis.
19. Discuss the genetics of colour-blindness or haemophilia.