Cell and Molecular Biology
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Week 07
Concepts of Genetics (Part 1)
Lecture - 26
Law of Inheritance (Part 2)

Hello, everyone. This is Dr. Vishal Trivedi from the Department of Biosciences and Bioengineering at IIT Guwahati. And what we were discussing was the laws of genetics. So in this particular module, in the previous lecture, what we have discussed so far is the history or the development of the field of genetics. And then we also discuss how Gregor John Mendel performed different types of experiments with simple plants, like peas.

And then what are the different characters that he has used? Based on these experiments, he actually formulated the different types of laws that are famously known as the law of inheritance. And in the previous lecture, we discussed the first law and the law of dominance. And then we also discussed the law of segregation. So in the previous lecture, we discussed that when you focus only on one particular type of genotype and a particular trait related to it, it actually governs the rule or law of dominance, where one particular genotype or trait is dominant over the other traits.

And that's why the trait that is going to be expressed in the first generation is called a dominant trait, whereas the trait that is going to be expressed or not shown as a phenotype is called a recessive trait. Now, in the second generation, when these first-generation individuals are crossbred, there will be a segregation of the genotype, and as a result, it will actually show you the dominant traits as well as the recessive traits. Now, considering this, we have also discussed the exceptions to these laws, such as when we discussed incomplete dominance. We have discussed the core dominance, and so on. And we have taken various examples that are actually exceptions to this particular law.

Right. So we took an example of the blood groups, and we have also taken an example of, you know, the mixing of the red and white colors, and so on. Now, in today's lecture, we are actually going to discuss another interesting aspect, assuming that the phenotype is controlled by more than one gene, or studying how the law will apply or how the system will behave when we are actually dealing with it. With the two genes right or the two particular types of genotypes with a single genotype, it is easy to understand because you are going to say, "Okay, the dominant trait is going to take over the recessive traits," but when it is a two-gene situation, the system becomes more and more complicated, and that's how you are actually going to discover the new law, and that's how you are actually

going to. And that is what we are going to discuss in today's lecture.

And in continuation of that, we are also going to discuss what the applications of these laws are and how these laws can be used to explain the different types of genetic variations observed in different types of organisms. Now, when you have the two genes, right? So remember that when we were talking about it in the previous lecture, we said that it is actually a law that is inherited for a single gene. Now we are going to move on to the more complicated system where we will understand how the inheritance of two genes or more than two genes will behave, right? Because you know that no type of phenotype is governed by a single gene in any organism, except in very simple organisms where there is a very small genotype, right? So when we talk about the inheritance of two genes, you are actually not going to deal with a single gene, but with the cross products of these two genes. Let's understand the two genes. So the inheritance of the two genes is actually going to follow different types of laws.

Right? So Mendel analyzed a number of crosses in which the two pairs of alternative traits were involved. In each case, he obtained the same results, didn't he? So, from these experiments, he proposed his second law, which is the principle of independent assortment, stating that the factors for different pairs of traits assort independently of one another. What this law means is that suppose you are, you know, dealing with two different types of traits. One is for the tall, and the other is for the color. So if you have the TT and YY, which is like YY for the yellow color, right? Then the TT will not have any influence over the YY, and the YY will not have any influence over the TT, right? So that's why the factor was significant, because at the time of Mendel's experiments, he was not very sure about genes and all these genetic materials and so on.

So he actually used the term "factor" to define these genotypes. So the factors for different pairs of traits assort independently, which means that when there is cell division, the TT will assort separately, and the YY will assort completely. There will be no influence of TT on YY or YY on TT. So, in modern terms, this means that the pair of alleles for one gene on different chromosomes segregate independently in the form of gametes. Consider an example: you have the seed shape and the surface.

The surface can be smooth or wrinkled. So, the pair of traits would be yellow and green seed color, right? And remember that yellow is dominant over green, and when Mendel made the cross between the two breeding smooth and yellow plants, which means capital S, capital S and capital Y, capital Y, to the wrinkled and green plant, right? Remember that in the previous lecture, we were talking only about one gene, which is either the yellow plants or the smooth seeds, and all that. But now we are talking about the two genes, right? So he got the result, which is given like this, right? When you are doing a

cross between the original plant, which is the parent generation, you have smooth yellow seeds or wrinkled green seeds. So the genotypes for these two would be SSYY and yy. So at the genotypic level, you are actually going to have the SS, which is for smooth, and the YY, which is for yellow.

And similarly, you are going to use the small ss and the small yy, which are for the wrinkled green seeds. Right now, if you do the crossbreed correctly and you are going to produce the first generation, there are no problems. All that you know is that you are going to produce a smaller capital Y and a small y, which means that in the F1 generation, it will actually follow the same law of dominance, right? And you are actually going to show the dominant traits. And what are the dominant traits? The dominant traits are smooth and yellow seeds. This means that in the F1 generation, you will produce all the seeds that are smooth and yellow.

Now, when the F1 is crossed with the F1, you will produce the F2 generation. This means the smooth yellow seeds are smooth yellow seeds, but the genotype is different; for example, the small capital S, small s, capital Y, small y is going to breed with this, then you are actually going to produce combinations that are not going to be influenced by the other genotype. So, what will happen in the F1 generation? You are actually going to produce four different types of gametes. You are going to produce four gametes. And when these four gametes come together, for example, if one and one come together, you will produce this particular genotype.

When one and two come together, you are going to produce this particular genotype. When the 1 and 3 come, you are going to produce. So, this analysis is called the checkerboard analysis, right? Where you are actually putting the genotype on one side and the phenotype on the other side, and then you are putting a checkerboard, right? So, if the SY-SY is meeting with SY-SY, then you are going to produce this. If the 1 and 1, this is it.

1 and 2, this. 1 and 3, this. 1 and 4, this. Similarly, 2 is to 1 as this is. 2 is to 2 as this; 2 is to 3 as this; 2 is to 4 as this. Because when you are engaging in sexual reproduction, there is no reason that one will not breed with all four of these, right? And similarly, the 3, 3 is going to, you know, mix with 1; then you are going to have this.

3 is going to meet with 2; then you are going to have this. 3 with 3 is this, and 3 is 3, similarly with the 4. Remember that 4 is actually the small s, small y, right? So a small "s," a small "y," when it matches with this, it will have this. 4 to 2 is this, 4 to 3 is this, and 4 to 4 is this, right? Now, this is the genotype. This is the genotypic region, right? Now, if you talk about the phenotypic, then remember, these are the 16 offspring, right,

in the X2 generation.

Out of the 16, 9 are going to be the smooth and yellow seeds. Now this could be pure smooth and yellow seeds, or it could be a hybrid. For example, this is the pure one, isn't it? These are the hybrid ones, right? So this is the pure one for smooth, but the hybrid for the yellow, right? Similarly, this is the hybrid for the smooth one and the pure for the yellow one, right? So even if the S is present singly or doubly, it is actually going to show you a phenotype that is smooth and yellow, right? Similarly, for this one as well, right? See the SS, capital S, capital S, but Y is Y, capital Y, small y. So whether the S is capital S is present alone, which means whether it is present like this or whether it is present like this, it is actually going to give you the smooth seeds. Similarly, for the Y, whether it is present as a capital Y or a lowercase y, it is actually going to show you the yellow seeds, right? So, by keeping this in consideration, out of the 16 seeds you are going to produce in the F2 generation, nine will be yellow and smooth seeds.

Similarly, out of 16, you are going to produce the smooth and green plant seeds. You will produce only when it is going to show this particular type of phenotype, which means it is actually going to display this particular type of phenotype. So smooth, you will produce whether the S is present singly or mixed with the small s, right? So smooth, you will produce even here, and smooth you are going to produce here, right? So, for example, this one, right? This one is going to be a wrinkled yellow seed, right? This is because the small "s" is coming together. This corresponds to the wrinkled one. Similarly, you are going to have it the other way around, right? You are going to have, like, for example, this one; this is going to be wrinkled and yellow, right? So, keeping this in mind, right? There are going to be smooth, green seeds.

Similarly, there are going to be three wrinkled yellow seeds and one wrinkled green seed. Right. So that means out of the 16, you are going to have nine that are smooth and yellow. Three, you're going to have it smooth and green. Three, you're going to have a wrinkled yellow one, and one, you're going to have a wrinkled green one.

So wrinkled green means yellow. You're going to have a small s, small s, and small y, small y. So that is this one. This is only going to be one. So if I tell you about the genotypic ratios, it is actually going to be 9 to 3 to 3 to 1.

Into the phenotypic ratio. And you are going to measure all of this, and then you are going to tell me the genotypic ratio. So what it says is that although we are talking about the two particular genes, one is for the smooth surfaces and one is for the color, it is not going to influence the segregation; it is not going to influence the assortment. So all the F1 seeds from this cross were smooth and yellow as a result of the monohybrid cross, as

predicted, because this is going to uphold the law of dominance. Then, when these F1 generations are going to self-breed, they are heterozygous for two pairs of alleles from the two different loci. Such individuals are called dihybrids.

A cross between two of these dihabits is called a dihabit cross. So when Mendel self-pollinated the dihybrid F2 plant to produce the F2 generation, there were two possible outcomes. One, the alleles determining the seed shape and seed color in the original parents would be transmitted together to the progeny. In this case, an affinity ratio of three to one is going to be predicted. So what it says is that if there is a law of dominance and there is no segregation, there is no independent assortment, then the same phenotype will actually go into the next generation, and as a result, it is going to maintain the same ratio of phenotypic appearances, which is 3 to 1, right? But that is not the case, so another possibility is that alleles determining seed shape and seed color would be inherited independently of one another, and in this case, the dihybrid F1 will produce all sorts of genotypes.

And the phenotypic appearances, right? And as a result of that, you're going to have nine smooth yellow, three smooth green, three wrinkled green, and one wrinkled yellow. And this is going to be pure. So, this is the phenotypic ratio. This is the genotypic ratio, right? So that's why it is actually going to maintain a phenotypic ratio of 9:3:3:1, right? Now, according to the rule of probability, if the alleles for the two pairs of traits are inherited independently in a dihybrid cross, then the F2 from the F1 to F1 cross will give a 9:3:3:1 ratio of the four possible phenotypic cases. Such a ratio is the result of the independent assortment of the two pairs of alleles for the two genes, right? And so the 9 to 3 to 1 ratio may be considered as two separate 3 to 1 ratios multiplied together, the multiplication being done because of the products of the independent events.

So if this is the 3 to 1 cross by 3 to 1, that is actually going to give you the 9 to 1, right? So, basically, it is doing the same thing. It is actually working like a single gene, with each gene behaving independently. So, 3 to 1 is for the single gene, right? Remember that in the F2 generation, you will have a phenotypic ratio of 3 to 1. So, since we are talking about the two genes, it is going to be 3 to 1 multiplied by 3 to 1. And that's how you are actually going to have a phenotypic ratio of 9:3:1.

So, further independent assortment in one example means that both pairs of traits involving the seed, seed shape, and seed color are independent of one another, in terms of the genes involved and how gene function generates the phenotype. So this prediction was met in all the dye habits Mendel crossed, whatever he used, as he remembered that he had used seven different types of traits. So a combination also does not give any other ratio worth like 9 to 3 to 3 to 1, right? So in every dihybrid cross, it is going to give you

this particular ratio, and this particular ratio is coming from 3 to 5, 3 to 1, and 3 to 1, right? So, for example, he counted 315 smooth yellow, 1,058 smooth green, 101 wrinkled yellow, and 32 wrinkled green, and he was very close to the predicted ratio. So, Mendel this result means that the factor determining the two pairs of threads can analyze the transmitted independently. Thus, in fact, Mendel rejected the possibility that the factor for the two pairs of traits was inherited independently together.

So, this is all about Mendel's law, right? Now people will think that if this is all the case, then how is the inheritance actually working, right? So there are multiple theories that actually explain the phenomenon of inheritance, right? How the dominance is, you know, working against the recessive, and so forth. So one of these theories is called the chromosomal theory of inheritance. So, what the chromosomal theory of inheritance is, correct? So the chromosomal theory of inheritance came very late because, at that time when Mendel was doing all these experiments, he was not very sure about what chromosomes and DNA were. Remember that he was using a term called "factor," correct? So factor means something that is, you know, carrying information from one generation to the next because even he was not aware of the genome. So, around the turn of the 20th century, cytologists had established that within a given species, the total number of chromosomes was constant, right? Whereas the chromosome number varies widely among species, For example, humans have 46 chromosomes, whereas cats have 38 chromosomes.

So in 1902, Walter and Theodore independently recognized that the transmission of chromosomes from one generation to the next closely parallels the pattern of inheritance of the Mendelian factors from one generation to the next. This correlation has become known as the chromosomal theory of inheritance. So basically, what the chromosomal theory is saying is that you are actually carrying the chromosomes, and these chromosomes are the genetic material that is passed from one generation to the next. Right. So the chromosomal theory states that genes are located on chromosomes and that the two alleles of a genotype segregate during anaphase I of meiosis when the homologous chromosomes separate.

The alleles may also segregate during anaphase II of meiosis if crossing over takes place. So this is exactly what it says. So you are actually going to have heterozygous chromosomes. So, if two alleles are present, then it is going to be called heterozygous. If the same type of alleles are present, then they are going to be called homologous.

So then in the S phase, it is going to replicate, right? So, you are actually going to have the RR and the small RR, right? And then you are actually going to have three different possibilities, right? So if there won't be any crossing over, is that right? Then it will

remain as a pure strain, right? And during the anaphase, RR is going to be separated, forming one gamete, and the small r small r is also going to be segregated. And then ultimately it is going to give you, after anaphase two, this is meiosis, right? So you are going to have the four gametes: one which is for the capital R, the other one is for the capital R, and then you are going to have the small r small r, right? So if there is a crossing over, then there will be some portion of this and some portion of this, some portion of R and some portion of small r that are going to be mixed with one another. And that's what we discussed when we talked about the recombinations, crossing over, and so on. In the previous lecture, right? So, it is actually going to give you a hybrid genotype, right? Rr, right? And when this separates, it will actually give you the Rr; irrespective of that, the capital R portion is smaller here, and the small r portion is smaller. But then in anaphase 2, you are going to have the pure R, you're going to have the small r, and you're going to have some portion of the capital R.

Similarly, you're going to have the Capital R, where you are going to have a small portion of the small r, and similarly, you're going to have this right, and then this is actually going to, you know, continue, and it is actually going to transmit the information from one generation to the next generation, right? So, as the crossing over is actually bringing more and more genetic variation. And whereas if you see that there is no crossing over, it is actually going to remain as the pure, pure strains. Right. So R is going to remain as R instead of having a small r. Right? And small r is also going to remain as small r.

It does not have any contamination from the capital R, and so on. So crossing over is actually bringing additional diversity. Right. Now, the second question is how sex determination works, right? Some organisms are male, while others are female. So that has always been done by a special class of chromosomes called sex chromosomes.

So the chromosomal theory also explains how sex is determined in all different types of organisms. So the chromosomes in eukaryotes, which are not represented differently in the two sexes, are called autosomes. So in any organism, you actually have two different types of chromosomes. One, the chromosomes that are not different between males and females are called autosomes. Whereas the chromosomes that are actually going to be different, these are called the sex chromosomes.

So, whereas the sex chromosomes and the autosomes are found in all cells, So, there is a misconception that sex chromosomes are found only in gametes, but that is not true. Sex chromosomes have also been found in the somatic cells, but there you don't perform any kind of development, right? Because the somatic cells only give you tissue, It's not going to give you any kind of gametes, and only gametes can actually participate in

reproduction, right? So six chromosomes were discovered in 1900 by Carolus, Mecklen, and Nitti-Stevens. And Wilson, right? All experiments with the insects independently obtained evidence that the particular chromosome determines the sex of an organism. And in the year 1905, Stephen found that in a grasshopper, the female has an even number of chromosomes, while the male has an odd number of chromosomes. So there are two copies of the chromosome in females and one copy in males.

And Stephen called that extra chromosome the Y chromosome. Since this chromosome is directly related to the sex of the organism, the X chromosome is an example of a sex chromosome. The sex of the progeny crosshopper is then determined by whether a sperm contains the X chromosome or does not contain it. So, if it contains the X chromosome, it is going to be female. If it does not contain the X chromosome, it is going to be male.

So all eggs have one X chromosome. If the sperm carries an X chromosome, then the resulting fertilized egg will have a pair of X chromosomes, and that will give rise to a female. If the sperm does not have an X chromosome, the fertilized egg will have the unpaired X, and that will give rise to a male. Unlike grasshoppers, some insects have two different types of X chromosomes. For example, Stephen found that in common mealworms like the Tenebrio molitor, the males have a partner chromosome pair for the X chromosomes. So that partner is much smaller than the clearly distinguishable X chromosome.

And it's even called the partner chromosome, like the X chromosome. And, like the X chromosome, it is a sex chromosome. So, sperm cells of the wheelworm contain either the X chromosome or the Y chromosome. And the sex of the offspring is determined by the type of sperm that fertilizes the X chromosome bearing the Y chromosome. So, if the XXXX chromosomes are female and the XYXX chromosomes are male.

So, similar XYXX chromosome complements are found in other organisms, including humans and the fruit fly, Drosophila melanogaster. In some cases, the females have two X chromosomes, and they are XX with respect to the X chromosome, while the male has an X chromosome and a Y chromosome; that's why it has been called XY. So that is what it is going to show here, right? In the P generation, there are parent one and parent two. And this is an example of the fly, isn't it? So a female actually has a genotype of XX, whereas a male has a genotype of XY.

So remember that we are only talking about the sex chromosomes. There will be another set of chromosomes, but that is not going to be different between males and females. Now, when the progeny comes, right? So, it is actually going to have either the XX or the XY chromosome, right? Because XX is going, when there is meiosis, it is going to form

two different types of gametes, correct? This one is also going to form two different types of gametes, right? And the F, which is matching with X, it is going to produce this. If X matches with Y, then it is actually going to produce this, right? So the progeny genotype would be half XY and half XX. And that's why there will be a 50% probability that you are going to have females and a 50% probability that you will have males, right? Because what genotype you are going to get, you are going to get XX, XY, XX, XY, right? That means 50% male and 50% female, right? So the pattern of transmission of the X and Y chromosomes from generation to generation is very straightforward, right? In this figure, the X is represented by a straight structure, much like a forward slash mark, and the Y is represented by a similar structure, a hook, right? So, the female produces only X within varying limits, and the male produces both X and Y. So, the random fusion of male and female gametes produces progeny with XX and XY chromosomes.

There is another form of phenomenon that is called the six linkage. So evidence supporting the chromosomal theory of inheritance came in 1910 when Thomas Hunt Morgan of Columbia University reported the results of a genetic experiment with Drosophila. So Morgan received the Nobel Prize for his discovery concerning the role that chromosomes play in heredity. So, in one of his true-breeding strains, Clamorgan found a male fly that had a white eye instead of the brick-red eye characteristic of the wild type. The term wild type refers to a strain in an organism that is most prevalent in the wild, correct? So the population of the organism is in respect to the genotype and phenotype.

For example, a Drosophila strain with all wild-type alleles of the gene that determines eye color has brick-red eyes, right? Variation of white light strain also arises from the mutation theory, which involves mutational changes of the wild-type alleles that produce the mutant alleles resulting in the mutant characteristics. So mutant alleles may be recessive or dominant in comparison to the wild-type alleles. For example, the mutant alleles that cause the white eyes are recessive to the wild-type alleles. So Morgan crossed the white-eyed male with a red-eyed female from the same strain and found that all the F1 flies were red-eyed.

He concluded that the white-eyed trait is recessive. Next, he allowed the F1 progeny to interbreed and counted 3,470 red-eyed and 782 white-eyed flies in the F1 generation. The number of individuals with the recessive phenotype was too small to fit the Mendelian 3:1 ratio. Later, Morgan determined that the lower-than-expected number of flies with the recessive phenotype was the result of the lower viability of the white-eyed flies. So, in addition, Morgan noted that the white-eyed flies were all males, right? So, this is a novel result. This results in all genetic crosses performed with the other mutants to date: the mutant phenotype has never been confined to just one sex.

So this is what is shown here, right? So in the P1 generation, the red-eyed flies are bred with the white flies. And in the F1 generation, what you are going to produce are X, W, Y, and X, W. Right? Whereas this one. Right. And they are all going to have red eyes because red is dominant over white.

Right. And as a result of this, the F1 genotype would be half, you know, the XY, XX, and XY, and all these are going to be half female, right? So where W indicates the white eye alleles and W+ indicates the red eye, right? So it's going to be all red-eyed, right? Similarly, when you take the F1 generation and perform the dihybrid cross, or if you're going to do the cross in the F1 generation, then it is actually going to have the XW plus or XW right versus the XW plus and Y. So this X is for females. And so in this one, what you see here is that it is actually going to follow the phenotype of three to one.

Right. Because three have red eyes and one has white eyes. Right. So white has always appeared with the Y chromosome, which means it is actually going to be male. All of these are females, right? So this is also female. And it's also going to be made, right? So, in the F2 genotype, you are actually going to have all these kinds of genotypes, right? So you're going to have one as the WW, one as W plus WW, this is going to be the W plus Y, and this is going to be one W small y, right? So in the F1 phenotype, three-fourths are going to have red eyes, and there are going to be two males and one female, whereas one-fourth with white eyes is going to be female, right? So this is all about the, you know, the X-linked trait, right? So then we also studied the X-linked inheritance of the red eye and the white eye in Drosophila melanogaster, right? And what he found is that, based on these experiments, Morgan proposed that the gene for the red-eye variant is located on the X chromosome. So the condition of an X-linked gene in males is said to be hemizygous because the gene is present only once in the organism, and there is no homologous gene on the X chromosome. So, for example, the white-eyed Drosophila male has an X chromosome with a white allele and no other alleles of that gene in its genotype.

So, these males are hemizygous for the white allele. Because the white alleles of the gene are recessive, the original white-eyed male must have had the recessive allele for the white eye on his X chromosome, right? So, the red-eyed female came from two breeding strains. So both of the X chromosomes must have carried the dominant alleles for the red eye, which is W plus, right? The F1 flies are produced in the following manner. The male receives his only X chromosome from his mother and hence has the W plus allele and is a red shape. Whereas the F1 females receive a dominant W plus allele from their mother and a recessive w allele from their father, they also have red eyes, right? Then we have the F2. In the F2 produced by the interbreeding of the F1 slice, the males that receive an

X chromosome with a Y allele from their mothers have white eyes.

Those who receive the X chromosome with a W+ allele have red eyes. The gene transmission shown in the cross from a male parent to a female offspring to a male grandchild is called criss-cross inheritance. Morgan also crossed a two-breeding white-eyed female that is homozygous for the W allele with a red-eyed male hemizygous for the W allele, and the cross is the reciprocal cross of Morgan's first cross, which is the white male to the red female. All the F1 females receive a W plus bearing X from their father and a W plus bearing Y from their mother. Consequently, they are heterozygous; that is, W plus W, and have red eyes because red is the dominant color versus white, which is a recessive color. All the F1 males receive a W chromosome from their mother and a Y chromosome from their father.

So they have white eyes, don't they? So basically, this is the trait that is linked to the X chromosome, and that's why if they are receiving a W, which is an X from the mother, and a Y from the father, because this particular trait is not present on the Y chromosome, it is only present on the X chromosome, it is actually going to show you the Y types. Furthermore, all the results obtained are different from the normal results of a reciprocal cross because of the inheritance pattern of the X chromosome. So, the inbreeding of the F1 flies involved a W capital Y male and a W plus W female, giving approximately equal numbers of male and female red and white-eyed flies in the F2 generation. This ratio is different from the 3 to 1 ratio of red-eyed versus white-eyed flies obtained in the first cross, in which none of the females and approximately half of the males exhibited the white-eyed phenotype. The difference in the phenotypic ratio between the two sets of crosses reflects the transmission pattern of sex chromosomes and the genes they contain.

So Morgan's cross of Drosophila involved the eye color characteristic, and we now know that the codex for it is found only on the X chromosome. So basically, the red eye color indicates that the characteristics or the phenotype are controlled by a gene that is only present on the X chromosome. So if it is the X present on the X chromosome, then it is only going to be expressed. So these characteristics and the gene that gives rise to them are X-linked, or more correctly, the X-linked trait, because the gene locus is present only on the X chromosome. So, X-linked inheritance is the term used for the pattern of hereditary transmission of X-linked genes.

When the results of reciprocal crosses are not the same and different ratios are observed from the two sexes of an offspring, the sex-linked trait may also be involved. By comparison, the results of the reciprocal cross are always the same when they involve the genes located on the autosomes, with the same distribution of the dominant and recessive phenotypes in males and females. Most significantly, Morgan's results that the

inheritance pattern of a W gene paralleled the inheritance pattern of the X chromosome strongly support the hypothesis that the genes are located on the chromosome. Morgan found many other examples of the gene on the X chromosome in Drosophila and other organisms, thereby showing that his observations were not confined to a single species. And it is actually a general phenomenon, isn't it? So the general phenomenon is that if the genes are present on a particular type of sex chromosome, whether it is an X chromosome or a Y chromosome, we have taken an example only of the X-linked characteristic.

It is going to be transmitted as X goes from one generation to the next. Now this transmission is always been linked to the linkage and as well as the recombination. So what is meant by the linkage? Genes on the non-homologous chromosomes assort independently during meiosis, don't they? So, in many instances, certain genes are inherited together because they are located on the same chromosome. So, genes that are on the same chromosome are called syntenic, right? So genes that do not appear to assort independently because they are located on the same chromosome exhibit linkage and are called linked genes. And these genes belong to the linkage group, right? So, genetic analysis is the detection of the structures and functions of genetic material. In classical genetic analysis, progeny from the crosses between parents with different genetic characteristics is analyzed to determine the frequency with which the different parent alleles are associated in a new combination.

The progeny showing the parental combination of alleles is called parentals, and the progeny showing the non-parental combination is called recombinants. So basically, the linkage is a phenomenon where the movement of two genes from one generation to the next is linked to each other because they are all present on the same chromosome. Remember that when there is a transmission of a chromosome from one generation to the next, you're not going to get 50 chromosomes from a single chromosome; you will get a single 50 percent of the total chromosomes, but the single chromosome, like chromosome number 11, for example. You will get a total of eleven. It's not like you will get 11 divided by 2, right? So if the particular gene is present on the 11th chromosome, you will actually be going to the two genes that will move together.

And that's how they are actually called, the linked gene. Right. So the process by which the recombinants are produced is called genetic recombination. This is anyway we have discussed in detail, isn't it? And through the test process, we can determine which genes are linked to each other and then construct a linkage map or the genetic map of each chromosome, right? So, when you do these kinds of test crosses and the dominant cross and those kinds of crosses, you will know which genes are moving together, and that's how you can make the particular type of map that shows these linked genes and their linkage. So, classical genetic mapping has provided information that is useful in many

aspects of genetic analysis. For example, knowing the location of a gene on a chromosome has been useful in recombinant DNA research in experiments directed toward understanding the DNA sequence in and around genes.

Genetic maps are constructed using both gene markers and DNA markers. A marker or genetic marker is another name for a mutation or variation that gives a distinguishable phenotype. In other words, it is an allele that makes up a chromosome or a gene. Gene markers are alleles of the gene, whereas DNA markers are the molecular markers that represent the DNA regions in the gene that are polymorphic and can thus be detected by the molecular analysis of DNA. Genes on the same chromosomes are like passengers on a charter bus.

Right? So they travel together and ultimately arrive at the same destination. So this is a very important and classic example. If you and your friend are traveling on a bus, that's right. And if you are both sitting on the same bus, you know, wherever this bus is going, right, whether it is going to one organism or whether it is not, you will both actually go and travel together, right? As long as the destination is the same, right? So the destination is the same for both of these, right? How does a gene occasionally switch from one homologous chromosome to another through the process of crossing over? So crossing over produces recombination. It breaks the association of the gene imposed by the linkage. So it happens that you are sitting on this bus, right? And another person is sitting on a different bus.

And over the course of time, when it is actually stopped, you know, at one stop. Right. Then you basically go from this place to that place. And that is what is being called the crossing over, right? So, basically, you can transfer from this bus to that bus. And that's how you can actually break the linked genes. Right. One linked gene is sitting here, and it was both together, right? But at this stoppage, there's a crossing over, right? So these two buses were going together, right? Imagine that this is bus number one and this is bus number two.

So one of the genes goes from this place to this place. And that's how these two people are now going to be on an independent route. Right? So this particular bus is going somewhere else. This bus is going somewhere else. Right? So basically, once the crossing over happens and the linked genes are separated from each other, their movement from one generation to the next will not be together.

They will be separate. So crossing over refers to the exchange of genes between non-sister chromatids. With the understanding of how the linkage affects heredity, we can analyze the crosses for linked genes and successfully predict the types of progeny that

will be produced. For example, if you have the two particular types of homologous chromosomes, one has the capital A and capital B, and the other has the small a and small b, is this correct? So you have one chromosome; you have another chromosome. So here you have the A, B, A, B.

This is homologous to two pairs of chromosomes. Similarly, you have another similar type of chromosome. So, if there is cross-breeding, right? Then A will get the A from here, and B will get the B from here, right? And that's how you are actually going to generate the progeny, the genotype; this is what you will generate in the F1. Now, in the if, each allelic pair, that is the A and small a, is always on different homologous chromosomes, so they must be written on opposite sides of the line. Thus, a genotype like AA or aa is incorrect, as A and a cannot be on the same chromosome. Always keep the same gene order on both sides of the line. Writing something like AB by small s is correct, as it wrongly suggests that A and B are allelic at the same time.

So this is all shown here. So this is the F1 generation; this is the situation. So you basically have to write like this, right? Right. So, crossing over with the linked gene, right? Linkage is rarely complete. Usually, there is some crossing over between the linked genes. and producing a new combination of traits. Crossing over, which takes place in prophase I of meiosis, is the exchange of genetic material between non-sister chromatids.

After a single crossing over has taken place, the two chromatids that did not participate in crossing over remain unchanged. Gametes that receive these chromatids are non-recombinants. The other two chromatids that did participate in crossing over now contain the new combination of alleles; gametes that receive these chromatids are called recombinants, correct? So basically, what happened is that you're going to have, for example, if you are going with bus number one or bus number two, right? And if there is a change of, you know, passengers between the two buses, right? Then you have two possibilities. One, this bus remains as it is, right? And there is no exchange of buses. But if there is an exchange of passengers between this and that, then you are actually going to have another set of chromosomes, where you are actually going to have some genes from this chromosome and some genes from that chromosome.

And that's how you are after crossing over. So this is actually going to be the wild type. And this is actually going to be a recombinant strain. So this is going to be a new strain because it has the passenger from this side, and it's also going to have the passenger on its own, right? So that's why it is actually going to show you the new phenotype, because this is going to have two different types of genes or gene segments. Right. And so, in each meiosis, a single crossing over takes place, and then the two non-recombinant

gametes and the two recombinant gametes are produced. Remember that you are actually going to produce the four gametes in meiosis, right? So, four gametes can come together and can give you the two non-recombinant ones and the two recombinant ones, right? This result is the same as that produced by independent assortment.

So when crossing over between the two loci occurs in meiosis, it is impossible to determine whether the genes are linked and crossing over took place or whether the genes are on a different chromosome. So this is what is shown here. So, if these are the two chromosomes, right? So this is actually bus number one. This is bus number two, right? And this bus actually contains different types of genes. So if there is no crossing over, it will remain as this, and it is actually going to produce the gametes like 1, 1, and 2, 2.

This means it is going to produce pure gametes of four types. One belongs to this blue one, and the two that belong to this one, right? Similarly, if there is crossing over, then there will be an exchange of material between these two individual chromosomes. And as a result of this, it is actually going to produce the one, which is the pure one; two, which is the pure one. But these two are actually participating in the crossover. So this is actually going to be one, two. And this is going to be 2 to 1, right? Because this one is actually a larger portion of one and a very small portion of two; similarly, here you are going to have the larger portion of two and the small, so this is actually going to be a new species.

Or new molecules, right? Or new organisms? These are going to be wild-type organisms, and these are going to be new organisms because crossing over is taking place. So assume that we have linked genes and that some crossing over takes place between them. Suppose a geneticist carried out the care, right? So you are actually going to have these, are you? You are going to have the capital M versus the small m and the capital D versus the small d. And if you do a crossover, right, if the crossover takes place, then the genes for the leaf type and the height, two of the four gametes produced, will be recombinant. If there is no crossing over, all four resulting gametes will be non-recombinant, which means that it will actually follow classical mammalian genetics and will give you pure non-recombinants.

Thus, the majority of gametes will be nonrecombinant. These gametes then unite with those produced by the homozygous recessive parents, which contain only the recessive alleles, resulting in mostly non-recombinant progeny and a few recombinant progeny. So this is what is shown here, correct? So in this cross, you see that 55 of the test cross progeny have normal leaves and are all tall, while 53 have mottled leaves and are dwarfs. The plants are non-recombinant progeny containing the original combination of the traits that are present in the parents. So, of the 123 progeny, that is what is shown here. So, out

of the 123 progeny, what is shown here? So if there is no crossing over, it is actually going to maintain the pure gametes, M and D, and small m and small d.

But if there is a crossing over, then the MD, small d, M small d, and small m small d will actually produce different types of variations. And as a result, it is actually going to produce the non-recombinant progeny, where you will have the pure organisms. But when there is a recombination, it is actually going to produce both the dwarf and the tall plants. So this is going to be a normal leaf, but it is going to be a dwarf plant.

But it is going to be a malted leaf; it's going to be tall because there will be recombination. So this is exactly what is shown here, right? So, if there are 123 progeny, 15 will have the new combination that was not seen in the parents. The normal leaf and the dwarf are 8. And seven are the mortal leaves and the tall ones. So these plants are the recombinant progeny, right? So out of 123, a very small portion is going to show you the recombination. So only 15 is going to show you the recombinations, where eight are going to be the normal leaves and the drop, whereas seven are actually mortal leaves and the tall ones.

So, a test cross for the two independently assorted genes is expected to produce a 1:1:1 phenotypic ratio in the progeny. The progeny of this cross clearly do not exhibit such a ratio, so we might suspect that the genes are not assorting independently. When the linked genes undergo crossover, the result is mostly non-recombinant progeny and fewer recombinant progeny. The results thus show that we observe among the progeny of the test cross that two genes provide evidence of linkage on the same chromosome. So this is an example of how you can calculate the recombination frequency. So, to calculate the recombinant frequency, you will divide the number of recombinant progeny by the total number of progeny and multiply by 100, right? Which is simple, isn't it? Whatever the number of progeny you got as the recombinant, multiply that by, for example, 15.

That is what we found in the previous example, divided by 123 and multiplied by 100. And that is what is shown here, isn't it? So this is the eighth one, and seven, right? So 15 is the recombinant one, and that's when you multiply by the 12 percent, which is the recombination frequency. So that's 12 percent, which is the recombination frequency. This is very simple and easy, right? Then we also have multiple gene inheritances, right? So, how are the multiple genes, right? So far, we have discussed the single genes. We discussed the two genes. Now imagine a situation where you are actually going to have multiple genes, right? Are there more than two genes? So how does the inheritance of more than two genes actually work? So in polygenic inheritance, it is commonly known as quantitative inheritance and multiple-gene inheritance.

Where you are going to monitor multiple parameters, such as height, skin pigmentation, eye color, hair color, and milk and egg production, the phenotypic characteristics present in plants and animals. So many traits and phenotypic characteristics are inherited from the alleles present at different loci, such as in polygenic inheritance. It is a type of internet controlled by more than one gene, where the dominant alleles have cumulative effects, and each dominant allele expresses a part of the unit of the traits. For example, the skin color, right? The skin color is controlled by many types of genes, right? So every gene produces one product, and when multiple genes come together, the mixture of these products is actually going to determine the color of the skin, right? The combined effect of these genes shows a significant effect, but a single gene may have little effect on the phenotype. Thus, fruit is called the dominant allele, which supersedes in the father of phenotypic inheritance, known as Kohlenter and Nell, and was discovered in the East as polygenic inheritance.

For example, the kernel color of wheat is important. So how multiple genes act on a characteristic can produce a continuous range of phenotypes. Let us examine the first demonstration of polygenic inheritance. So Nelson actually studied the kernel color in wheat and found that the intensity of the red pigmentation was determined by three unlinked loci, each of which had two alleles. Then the several homozygous variations of the wheat that differed in color, for example, Mendel, performed crosses between these homozygous variants and studied the ratio of the phenotypes in the progeny.

In one experiment, he crossed a variety of wheat that possessed a white kernel with a variety that produced purple. kernel and obtain the following results. So this is the parent generation where you are going to have either the plant with the white kernel or the plant with the purple kernel, right? Remember that in the F1 generation, you will have the plant that shows you the red-colored kernel, right? And in the F2 generation, there will again be an assortment, right? So it is actually going to show you 16, right? It is going to show you one plant that has a purple kernel, which means it is the wild type.

This is going to show you the parents. Then 4 out of 16 are going to be dark red-colored kernels. Then six out of these are red. Then, kernels 4 to 16 are light red colored, and kernels 1 to 16 will be white. So, this is actually going to be the purebred, just like its parents. This is also going to be pure, which is just like, you know, how the parents are. And these three are actually the different combinations in which the various types of genes are present, right? Now, the scientist interprets the phenotypic ratio as a result of the segregation of alleles at the two loci.

So, he found that the alleles of the three loci that affected the kernel color were the two variations used in this process. So, differently, only on two of the loci. So he proposed

that there are two alleles at each locus, one that produces the red pigment and the other that produces no pigment, right? So he will design the allele that encodes the pigment to be A positive and B positive, and the allele that encodes no pigment is called A negative and B negative, right? So this is going to be a genotype where you have A positive, B positive, A negative, and B negative, right? The effect of these genes was additive, wasn't it? So each gene seems to contribute equally to color. So the overall phenotype could be determined by adding the effects of all the genotypes, as shown in the table, correct? So if there are A plus A plus B plus B, then it is going to have four, right? That means it is going to give you the purple-colored kernels. If A and B are actually coming together, then they are going to give you the pigmentation, which is going to be dark red.

So this actually says that you are going to have four of A and four of B. This means you are putting in more of, you know, the A phenotype. So it is actually going to give you a dark red color. Similarly, if you are adding more of this, right? A minus, A minus, and B minus. Then it is actually going to lower the color, and that's how it will give you the red color. If you keep increasing the, you know, because A minus, A minus B minus is actually for the no color; A plus and B plus are actually for the red color, right? So if you combine them, it will actually tell you what color it is going to form.

So if the A positive and B positive are less, and A- and B- are more, then it is actually going to show you a light red color. If none of the A- and B- is present, and only minus minus is present, then it is actually going to give you a white color or no color at all. So, from these results, we see that the five phenotypes are possible when the alleles of the two influence the phenotype and the effects of the genes are additive. When alleles at 1-2 loci influence the phenotype, more phenotypes are possible, and this makes the color appear to be very continuous between white and purple. So there are multiple combinations that could be possible depending on the amount of genes that are present in a particular genotype, and that actually is going to decide the final color. The environmental factor has influenced the characteristics of individuals with the same genotype, and that's how it is actually going to affect, you know, the appearances of the different types of color.

And these environmental effects are always being studied in a separate field called epigenetics, where you actually study how environmental factors regulate the appearance of different types of phenotypes, right? Then the environment played a small role in determining the color, didn’t it? And a few loci encoded color. So Nelson was distinguished among the different types of phenotypic characteristics. This ability allowed them to see the Mendelian nature of the traits. So this is all about Mendel's laws of inheritance.

What we have discussed so far is how inheritance law actually governs the phenomena of the two genes, inheritance, and so on. And then we also discussed the different types of sex-linked traits. We have also discussed how the X-linked character is expressed whenever there is an X chromosome present and so on. And we also discussed polygenic inheritance; then we also discussed the chromosomal theory of inheritance. So, with this brief discussion about the Mendelian law of inheritance, I would like to conclude the lecture. In our subsequent lecture, we will discuss some more aspects of genetics. Thank you.