# Molecular Biology
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## Module - 04
## Central Dogma of Molecular Biology
## Lecture-19 Genetic Material (Part 3)

Hello everyone, this is Dr. Vishal Thevedi from department of biosciences and bioengineering IIT, Guwahati. And in the current module, we are discussing about the genetic material. What we have discussed so far, we have discussed about the discovery of genetic material by doing the different types of experiments. So, initially there were two prominent candidate for the genetic material, one is the nucleic acid, the second is the proteins. And there was long debate about which material is actually going to serve the purpose of having a potential to be genetic material.

We have discussed about the different types of experiments through which the scientists have, you know, proved that it is actually the genetic nucleic acid which is actually been the most acceptable material for genetic material. So within the nucleic acid, it could be DNA or the RNA. Mostly the cells are actually having the genetic material in the form of DNA, whereas in some of the organisms such as viruses, you also going to have the RNA as the genetic material. Then in the previous lecture, we have discussed about the genomic organizations and how the genetic material is actually going to be organized in the different types of organisms.

So, we have discussed about the organization of the genetic genome organization in the prokaryotic cell and we have discussed about how the different types of materials are required for genomic organization in the prokaryotes, what are the properties of the genome into the prokaryotic structures. We have taken an example of E. coli and how the compactation is happening inside the E. coli cell and so on. Now in today's lecture, we are going to discuss about the genomic organization into the eukaryotic cell and how the different types of chromosomes are being found.

So in the genomic organization, when we talk about the genomic organization in the eukaryotic cell, we are having the genomic genome which is present in two places in the eukaryotic cell. One is the nucleus and the second is the organelles. So if it is a plant cell, it is actually so within the organelle, you can have the two different types of organelle where the genomic content is going to be present. One is called as the mitochondria and the second is the chloroplast. So you can genomic genome is actually been organized within the eukaryotes in the nucleus.

So within the nucleus, you are going to have the different types of chromosomes and within the mitochondria also you are going to have the mitochondrial chromosome and the chloroplast chromosomes and summation of these DNA material is actually going to be called as the genome within the organisms. Now within the genome organization in the eukaryotes, so the genome eukaryotic genome is linear and confirmed with western crete double-clicked cell structure model. It is embedded in the nucleosome complex DNA and protein structure that packed together to form the chromosomes. Eukaryotic genome have unique feature of exon-intron organization of the protein coding genes representing the coding sequence and the intervening sequences that represent the functionality of the RNA inside the genome. One haploid cell consists of the 23 different chromosomes and one mitochondrial chromosomes contain more than 3.

2 billion DNA base pairs. Remember that in the case of the prokaryotic structure, we were talking about the number of chromosome in the case of millions, but here the number of chromosomes are going to be in millions that is why there is a more higher level of compactation is required so that that particular DNA is going to be fit into the small tiny nucleus. Now as far as the chromosomes, so eukaryotic chromosomes are usually linear structure. So this is the eukaryotic one of the eukaryotic chromosomes and a typical chromosome is 10 of millions to hundreds of millions of bases where in length. Eukaryotic chromosomes occurs in set many species are deployed which means that the somatic cells contain two set chromosomes two sets of the chromosomes right.

So you are going to have the chromosomes which are present in the sets right and so double set is present inside the cell and during the duplications or during the division one set is actually going to be shared with the daughter cells. Each chromosome contains a centromere that forms the recognition site for the kinetochore complex. So this is the centromere right this is the centromere and this is the place which is actually going to be recognized by the kinetochore proteins. Then we have the telomeres which contain the specialized sequences located at the end of the linear chromosomes. So these are the telomeres which are going to be two telomeres.

So and this is the specialized sequences which are present on the tails or the corners of the chromosomes. Then we have the repetitive sequence which are found in near the centromeric regions. So these are the DNA or the genes how the genes are actually been organized onto the chromosomes. For example this is a classical example how the MSC proteins are or MSC genes are been organized onto the chromosomes within and you see that you have HLA typing and all that and this is a particular type of chromosomes. What is the chemical composition of the chromosome or the chromatin? So you are going to have the DNA you are going to have the RNA and then you also going to have the proteins.

So you are going to have the DNA which is 20 to 30 percent. So most important constituent of the chromatin then you are going to have the RNA which is going to be 5 to 10 percent. It is associated with the chromatin as the transfer RNA messenger RNA or ribosomal RNA. So it is actually be a part of the expression machinery and then you also going to have the proteins so that is going to be 50 to 60 percent. So mostly the chromatin is actually made up of the DNA plus protein and it is mostly the 40 percent is actually going to be DNA and 60 percent is actually going to be the protein.

Within the protein you are going to have the two different types of proteins you are going to have the histone proteins or the non histone proteins. So histone proteins very basic proteins constitute about 60 percent of the total protein almost it is present in the 1 is to 1 ratio with the DNA and you are going to have the five different types of histone proteins H1, H2A, H2B, H3 and H4. Similarly you are going to have the non histone proteins they are 20 percent of the total chromatin protein and they are required for the nucleosomal assembly proteins such as NAP and the other histone chromatin remodeling complexes and then you are going to have the structural proteins such as actin, tubulin and myosin and the contractile protein and all the enzymes. So the contribution of the non histone protein is very very little compared to the histone protein histone protein is required for packaging. So histone is a positively charged protein so these are the basic proteins which means they are actually going to be positively charged protein and that is why they are actually going to have the instant attraction for the negatively charged DNA.

So this is the DNA you know that the DNA is negatively charged because of the phosphate backbone. So the histones are found in all the eukaryotic cells they are commonly present in the histone commonly present histone in the eukaryotic cells are H1, H2A, H2B, H3 and H4. Then these all the five histones are being categorized into the two structural regions one is called as the core histone the other one is called as the linker histone. So the H2A, H2B, H3 and H4 are part of the core histone whereas the H1 is actually being called as the linker histone. So core histone the two copies of the core histone form the protein core around which the DNA is wrapped and within this you are going to have the H2A, H2B, H3 and H4 whereas the linker histone it is not the part of the core protein but it is associated with the linker DNA which links the two nucleoside.

So within the histone you are going to have the core histone and the linker histone. The core histone you are going to have the two copies of the H2A, H2B, H3 and H4 which are actually going to form the core of the nucleosome and then this core is actually going to wrap the DNA. So it is going to have the clear attraction because all these histones are going to be positively charged so their surface is actually going to be positively charged

and that is how they are actually going to have the very high affinity for the DNA. Similarly you are going to have the linker histone which is going to be H1. So how these histone proteins are or what are the different properties of the histone proteins.

So histones are closely associated with the negatively charged protein DNA. They have the high content of positively charged amino acids such as lysine and arginine. So you have the core histones and you have the linker histones. Core histone H2A you are going to have the molecular weight of 14 kilo Dalton and it is actually going to be a lysine rich. Similarly you can have the H2B is going to be approximately 14 kilo Dalton and it is the slightly lysine rich.

Then we have the H3, H3 is going to be 15 kilo Dalton and it is going to be lysine rich and you have the H4 which is going to be 11 KDA and it is going to be arginine rich. Then we have the linker histone which is H1 and it is going to be 20 KDA and it is also arginine rich. So H3 and H4 histones are first formed the heterodimer then come together to form a tetramer with the two other the molecule of H3 and H4. H2 and H2B form the heterodimers. So this is the sequence in which the histones are actually going to be organized with each other and that is how they are actually going to form the nucleosomal assembly.

So the assembly of nucleosome involved the ordered association of histone with the protein and DNA. So first the H3 the two molecule of H3 and the two molecule of H4 are actually going to come together and that is how they are actually going to form a tetramer which means you are going to have the like this. So you are going to have a tetramer which is going to be formed. Then this tetramer is actually going to because this tetramer is going to have the positive charge. So this is going to have a positive charge on the top right and then it is actually going to bind the DNA.

This means this ball is actually going to have the DNA. And then to after binding the DNA then the H2A and H2B is dimer which means is actually going to join the H3H4 DNA complex and that is how it is actually going to have the nucleosomal So this is actually one ball which is going to have the H3H4 DNA and on top of this you are going to have the H2A H2B and H2A H2B like that. So DNA is actually going to be present inside this particular core. So this one copy of nucleosome is actually going to communicate with another nucleosome right so this is going to have another copy and this is the region where the H1 is actually going to bind. So this is the lingered region which is actually going to bind.

The core histones have the amino acid extensions called as TALE because it lacks the defined structure and do not participate in association of DNA with the histone octamer.

The TALEs are the extensive site for a post translational modification including the methylation, acetylation and the phosphorylation. The assembly of the histone involves the ordered association of the histone with the DNA. This is anyway we have discussed right H3H4 followed by the binding of DNA followed by the binding of the H2A H2B and that is how the nucleosome is going to be formed. So the nucleosome is the starting building block for the higher order organizations.

So nucleosome is actually the building block of the chromosome right so this is the DNA right then it is actually going to form the nucleosome then it is actually going to organized into the chromosomes and then it is actually going to organize into the nucleus. So a human cell contains 3 into 10 to power 9 base pair per haploid set of the chromosome. The average thickness of each base pair is 3.4 angstrom this is the thickness of the DNA actually. So therefore if the DNA molecule in a haploid set of chromosome were lay out end to end the total length of the DNA molecule would be approximately 1 meter.

For a diploid set the length is actually the double which is the 2 meter as the diameter of a typical human nucleus is about 10 to 15 micrometer it is obvious that the DNA must be compacted by many order of magnitude to fit into such a small space. The compactation in human nucleus is done by the nucleosome formation by the association of the DNA with the histone. Nucleosomes are packed into successively high ordered structures. So nucleosome model is scientifically model which explains the organization of the DNA and associated protein into the chromosome. It also further explains the exact mechanism of the folding of the DNA into the nucleus.

This model was proposed by the Kornberg in 1974 and it is the most acceptable model of the chromatin organization. The model was further confirmed by the Pea audit in 1975. What are the features of the nucleosomal model? In eukaryotic DNA in eukaryotes the DNA is tightly bound to the histone protein which leads to the formation of DNA protein particles called nucleosome. Neustones play a very important role in packaging of such a long DNA molecule in the form of a nucleosome into the nucleus only a few micrometer in diameter. Therefore the nucleosomes are called fundamental packaging unit particle of chromatin and it gives a beads on to a string appearances which means if you see very clearly you will see that the DNA is being packed like this.

And this packaging is called as the beads on a string because this is the linker DNA and this is actually the core structure of the histone and that is how these are actually going to be you know fold on to each other. So it is actually going to be fold like this and that is how you are going to have a beads and then it is going to be fold like this and that is how it is actually going to be condensing and that is how you are going to have the higher

organizations of the packaging. Each nucleosome is a disk shaped particle with a diameter of 100 nanometer and 5.7 nanometer in height containing two copies of each four nucleosome histones such as H2A, H2B, H3 and H4. This histone octamer forms a protein core around which the double standard DNA is wrapped to 1.

6 times containing the 146 base pair. Each nucleosome bead is separated from the next by a linker DNA which is generally 54 base pair and contains the single H1 protein. This is what I was talking about right you have a DNA and then it is actually going to be arranged. On average the nucleosome repeat at an interval of 200 base pair. So folding of the DNA so once the nucleosome is formed there will be a folding of the DNA and that is how you are going to have the higher compactation of the DNA. The assembly of DNA begins with a newly produced tetramer which is H3H4 that is a particularly modified to form a sub nucleosomal particle the two Hb-HTM are then added.

Results in the formation of a nucleosomal core particle with a 146 pair DNA bound to the histone octamer the nucleosome is made up of this central component and the connecting DNA. In order to create the nucleo filament the nucleosome core must be spaced regularly which is accomplished during the maturation stage which requires the ATP. The newly integrated stones are deacetylated in this stage. Next the incorporation of linker stone is accomplished by folding of the nucleo filament into the 30 nanometer fiber the structure of which remain to be elucidated. Two principle model exist one is the solenoid model and the other is the zigzag model actually to explain how the DNA is actually going to be folded after forming the nucleosome to form the higher order organizations.

Last but not least further subsequent folding process results in a higher level of structure and distinct domain within the nucleus. So these are the some of the organizations so you are going to start with the DNA. DNA is actually going to be fold into the so if you start with the 2 nanometer then you are actually going to form the beads on a string form and that is how actually you are going to have the nucleosomes. Then these nucleosomes are actually going to be organized and refolded the DNA is actually going to be folded again and that is how you are going to have the 30 nanometer chromatin fibers. Then these 30 nanometer chromatin fibers are actually going to be further organized and they are actually going to form the 300 nanometer fibers and in which these solenoids are actually going to be again folded onto each other and that is how you are going to have this 300 nanometer fibers.

Then this 300 nanometer fiber is actually going to be condensed and that is how it is actually going to form the 1700 nanometer fiber and you are going to have the condensed region of the chromosome and from this you are going to have the further condensation

and as a result it is actually going to form the 1400 nanometer for chromosomes. So you are going to have the chromosomes so you started with DNA you ended with the chromosomes. So this is the first and this is the last binding style. Now in this is the packaging of the genome into the eukaryotic system and the genome has a very significant impact on the properties of that particular organisms and the bigger the genome you are actually going to have the more of the information what you are going to carry and that is how you are actually going to have the higher flexibility of modulating that information and that is how you are going to have the more properties to handle. So genome size is related to the complexity of that particular organisms because higher the information you have the higher you are actually going to manipulate that information and that is how you are going to have the complexity into the system.

This means you are going to you can actually have the freedom to modify the proteins you can actually be able to synthesize the proteins and so on. So if you see a very clearly what you are going to see is you are going to have the prokaryotic species and you are going to have eukaryotic species. Within the prokaryotic species you will see that the genome size is very small and that is why the number of genes or number of proteins are actually going to be very small. This means they are actually going to produce the less number of proteins and if you are producing the less number of proteins you are actually going to have the lower order freedoms to manipulate those proteins because you cannot have the multi step process you can have only the one or two step process because you if as many number of process you are going to produce you can actually should have the proteins to regulate these steps. So that is basically a drawback or I will say simplicity in the system right.

More and more you are actually going to have genome size for example in the case of yeast you are going to have the genome size which is 12 megabyte right and then you will see that the number of genes are going to be significantly very high compared to the mycoplasma and more and more actually you see that these are the plant species right. So they are very very high and the number of genes what you see here is very high this means they are actually being able to have the potential of producing the large number of proteins and that is how these large number of proteins can be utilized in such a way that you are actually going to have an event which is tightly regulated at each step and that is how you are actually going to have the you can actually be able to have the more control over the process. So the C value or the cot values or the quantity of DNA per haploid genome such as that seen in the nucleus of S. permatozone is used to describe the genome size in the eukaryotes because the size is essentially consistent within the species it is known as the C value or the characteristics. The mismatch between the C value and the presume amount of genetic information contained within the genome was called C value paradox.

Since we cannot assume that a species processed less the DNA than the quantity required to specify its vital function we have to explain why many species contain this amount of excess DNA. This is very simple actually if you have excess amount of DNA you can have the flexibility of producing more number of proteins and that is how you can have the instead of having the 3 step process you can have the 20 step process because if you increase the number of steps you are actually going to have the flexibility. You have seen that the glycolysis is a 10 step process. Grape cycle also has a multiple steps and because they have the multiple steps you can actually have the entry and exit of the metabolites at every stage and that is how you are actually going to have the very very complex biochemical reactions. Now the first question comes if there is a requirement of the protein production for example if there is a requirement of protein production that is required that the DNA should be free for doing the transcription and translation.

So now question comes how you can be able to unpack the DNA and how you can be able to have the DNA which is available for doing the other kinds of molecular biology activities such as replication, transcription and translations. So unpackaging of DNA so the way we have discussed about the packaging of the DNA the same way the histone has the crucial protein which are actually going to participate into the unpackaging of the DNA or the unwinding of the DNA. So histone are actually having the tail region right remember that tail region is important for histone to be assembled with each other and that is how they are actually going to bind the DNA. This tail region has the modification site for acetylations, for phosphorylations and the methylations. Now when you have the acetylation you are actually going to have you are going to produce the negative charge.

When you have the phosphorylation you are going to induce the negative charge and when you have a methylation that also is going to modulate the surface property of that particular protein. So as soon as you have the acetylation and phosphorylation you are going to have the unwinding of the chromatin structure and DNA becomes more accessible for the other kinds of downstream applications or other kinds of downstream activities such as replication, transcription and translations. So acetylations, so acetylation take place at the lysine residue of K4, K5 in the H4. It takes place through an enzyme which is called as histone acetyltransferase or AT. The acetylated chromatin are more open this means they are actually going to be active in terms of the replication and transcription.

It is accessible for transcription factor and polymerases. Deacetylation take place by the histone deacetylase or HDAC. The acetyl group donor is acetyl-CoA. So you are going

to have the closed chromatin and when you have the activity of the histone acetylase it is actually going to acetylate the chromatin and that is how it is actually going to form the relaxed chromatin. So once the relaxation is over when that process is over then you are actually going to put the HDAC activity which means the histone deacetylate and then it is actually going to be closed chromatin and that is how these are the things which are actually going to occur simultaneously or you know to just to you know unwind the DNA make it all accessible so that you can be able to use that DNA and then after that once that process is over then you can actually be able to close that DNA.

Same is true for the phosphorylation. So you are going to have the kinase activity which is actually going to convert the closed chromatin into the relaxed chromatin and then you have the phosphatases which are actually going to remove the phosphorylations and that is how it is actually going to reverse the events. Then third is methylation. So it occurs on the side chain of the lysine and arginine. The methylation does not alter the charge but it actually changes the charge what is present on to that particular residues. So lysine can be mono methylated di or tri methylated methylation done by the histone lysine methyl transferase and the histone lysine methyl D methylase.

So you are here also you are going to have the methyl transferase and the D methylase and when you have the methyl transferase the closed chromatin is going to be convert into the relaxed chromatin and same is going to be reversed by the histone lysine D methylase. So these are the about the normal chromosome. These are the information which is required for the normal chromosomes but when people were discussing about or when we started investigating the different types of chromosomes they could found some are the specialized chromosome which is present in the some of the organisms. So let us discuss about this specialized chromosomes and how the DNA is packed into the specialized chromosome and what are the different properties of these specialized chromosomes.

So the first is polytine chromosomes. So what are polytine chromosomes? Polytine chromosomes which are gigantic chromosome that grew from a smaller developing chromosomes frequently appear into the slavery gland of the pterian flies such as Drosophila melirulogaster. They are also known as slavery gland chromosome because they were found in slavery glands. The Balbini found a polytine chromosome in the slavery gland nuclei of the larva in the 1881 due to the presence of several chromatin in them they are known as the polytine chromosomes. Now the question is how these polytine chromosomes are being found? Though the most polytine chromosomes are located in the interface nucleus of a few cell in the pterian fly larva each chromosome component is successfully duplicated as they grow from the chromosome of the duplicated nucleus. After each DNA doubling the later stage of the mitosis are

eliminated leading to the deployment of a polytine chromosome as a result the cell cycle is divided into the S phase and G phase in Drosophila melirulogaster.

This polytineation cell cycle is developed during the mit embryogenesis. DNA strands do not separate at the final stage of each S phase rather they remain accompanied to one another generating the polytine chromosomes. The process of endor duplications or multiple chromosome DNA replication without adequate kyrokinases and cytokinesis results into the polytine of gigantic chromosomes as a result the giant chromosomes are produced which are 70 to 100 times longer than the typical metasource chromosomes. Morphological features of the polytine chromosomes. The polytine chromosome is a very important thing actually because this is a kind of an exception or kind of the structure what is been found in a specific organisms.

So there are numerous partially duplicated chromosomes that are almost intervened with each another making up the polytine chromosomes. The heterochromatized centromere of all chromosome fuse in a centromere. The polytine chromosomes are found in the form of 6 radiating arms from the chromo center you can have the X chromosome you can have the 2 chromosomes, 2 chromosomes left arm right arm, third chromosome right arm, left arm then you can have the fourth chromosome which is the shortest arm then you can have the Y chromosomes and so on. An altered pattern of bright and dark is seen when these chromosomes are stained and examined under a microscope. Inter-band referred to a light pattern which band referred to the dark pattern.

So this is a specific polytine chromosomes where you are going to have the right arm you are going to have left arm within the left arm you are going to have the left arm of chromosome 2, left arm of chromosome 3 similarly you can have the right chromosome of arm 3 and so on. So within this place your centromere you are going to have the divergence and that is how you are going to have the X chromosome and Y chromosomes and so on. Then you can have the some of the classical characteristics of these chromosomes such as you are going to have the Balbini rings to the band undergoes morphological and biochemical changes related to their gene activity and the activation of the genes of a band causes the compact chromatin strands to uncoil and expand outward resulting in a chromosomal puff. The puff contains the DNA loops that are less condensed and the DNA of band elsewhere in the chromosome puffs are active gene of the transcription. So these are the puffs so chromosomal puff and these are the active region of the gene expressions.

What is the function of the polytine chromosomes? The nuclei of each cell enlarge in size leading to a cell growth. The metabolic benefit of having a numerous copy of a gene allow for a higher expression of gene expressions. The chromosome in Drosophila

menagaster undergoes numerous round of endoreduplications in order to generate the significant amount of glue prior to pupillations. The bar phenotype which includes the kidney shape eyes occurs from the tandem duplication of the severe polytine bands that are close to the centromere of the X chromosomes due to the fact that the polytine chromosomes are interface chromosomes and are thus transcribed. As a result it offers a charge to investigate transcription by the direct observation and transcriptional response to the certain stimuli can be observed.

So apart from the palatine chromosomes you can also have the another kind of chromosome which is called as Lambrech chromosomes. So Lambrech chromosomes what are Lambrech chromosomes? Lambrech chromosomes are transcriptionally active chromosome which are mainly found in the germinal vesicle of large courses of many vertebrate and the invertibate. The Lambrech chromosomes derive their name from the lateral loop that exclude from the chromosome at a certain point. They are very much transcriptionally active as the emerging DNA from the certain point are rich in RNA polymerases. These chromosomes were first observed by the Fleming and Ruckerts in 1882 in oocyst of the amphibians.

Where do these chromosomes occur? The Lambrech chromosomes occur in the diplodin stage of the prophase I of the first meotic division in the primary oocyst of all the animals and the structure of the Lambrech chromosomes. So each RNA polymerase is attached to the nascent RNA and associated protein generating the visible brush like appearance. It can be visualized easily that Lambrech chromosomes are held in a stretched out form during the diplodin stage of the prophase I of the first meotic division. The axis of Lambrech chromosome contain array of beat from which the loops are protruding onward called chromosomes. They exist as meotic bivalent homologous chromosomes held together by the Crease meta.

So these are the so in this Lambrech chromosomes you are going to have the chromosomes then you are going to have the RNA polymerase which is protruding towards. So this is actually going to be a region of singly chromosomes and so on. And it is actually going to be transcriptionally very active because these are the region which are actually going to be available for transcription and the translation. So they contain the symmetrical loops one each other chromatin in a chromosome their absence of lesion in the centromere region each loop and each loop bears an axis which made up of single DNA molecule that is unfold during the RNA synthesis. What is the function of the Lambrech chromosomes? Prokaryotes are useful in chromosomal mapping then extremely helpful in visualization of gene expression and also the change associated with the transcription.

It provides a great proof for the eukaryotic gene amplification which play a crucial role in the oocyte development and it is helpful in the hybridization results. Now at the end we are going to discuss the comparison of the prokaryotic as well as the eukaryotic genome. Many of these properties we have already discussed right. So the comparison of the prokaryotic as well as the eukaryotic genome. So prokaryotic genome is small in size it is going to be large in the case of eukaryotic genome.

Genome is going to be a DNA and a few protein in a simpler manner whereas, DNA in the case of eukaryotic cell the genome is going to be present and many proteins are involved such as the histone proteins and so on. It contains a single set of chromosome whereas, in the eukaryotes you can have the multiple set of chromosomes. The amount of DNA is going to be small in the case of prokaryotic genome it is going to be typically very large number of DNA which is present. Then the prokaryotic genome is polycystronic whereas, in the case of eukaryotic genome it is monocystronic. Then most of the DNA encodes for the protein so it is actually there is no useless DNA right there is no DNA which is not going to be transcribed or which is not going to be translated to the protein whereas, most of the DNA does not code for the protein right.

It is very a small portion of the genome which is actually coding for the protein rest all is non-coding regions. Then RNA processing not an option right so RNA processing allows for the several of these genome because you have the non-coding regions is non-coding region has to be separated from the coding region and that is why the RNA processing is required. And messenger RNA has a short life span whereas, the messenger RNA is long life because the eukaryotic cell requires the continuous synthesis of a protein for several days right. So these are the some of the properties of the genome we have discussed about the prokaryotic genome and the organization of the prokaryotic genome and we have also discussed about the eukaryotic genome and eukaryotic genome organizations. We have discussed about the organization of the proteins of the different protein which are involved in the nucleosomal assembly and how the nucleosomal assembly is being formed and so on.

So with this brief discussion about the genetic material we are going to conclude our lecture here in our subsequent lecture we are going to discuss some more aspects related to molecular biology. Thank you.