Cell and Molecular Biology
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Week 06
Genetic Material in Cells
Lecture - 23
Organization of Genome (Part 2)

Hello everyone, this is Dr. Vishal Trivedi from the Department of Biosciences and Bioengineering, IIT Guwahati. And in the current module, we are discussing the genetic material. What we have discussed so far is the discovery of genetic material through different types of experiments. So initially, there were two prominent candidates for genetic material: one is nucleic acid and the second is proteins, and there was a long debate about which material would actually serve the purpose of having the potential to be genetic material. We have discussed the different types of experiments through which scientists have proved that it is actually the genetic nucleic acid that is the most acceptable material for genetic material.

So within the nucleic acid, it could be DNA or RNA. Mostly, the cells actually have the genetic material in the form of DNA, whereas in some organisms, such as viruses, you are also going to have RNA as the genetic material. Then in the previous lecture, we discussed the genomic organizations and how the genetic material is actually organized in the different types of organisms. So we have discussed the organization of the genome in the prokaryotic cell, and we have discussed how the different types of materials are required for genomic organization in prokaryotes.

What are the properties of the genome in prokaryotic structures? We have taken an example of E. coli and how the compaction is happening inside the E. coli cell, and so on. Now in today's lecture, we are going to discuss the genomic organization of the eukaryotic cell and how the different types of chromosomes are found. So in the genomic organization, when we talk about the genomic organization in the eukaryotic cell, we have the genomic genome, which is present in two places within the eukaryotic cell.

One is the nucleus, and the second is the organelles. So within the organelle, you can have the two different types of organelles where the genomic content is going to be present. One is called the mitochondrion and the second is the chloroplast. So, the genome is actually organized within the eukaryotes in the nucleus. So, within the nucleus, you're going to have the different types of chromosomes.

And within the mitochondria, you are also going to have the mitochondrial chromosome

and the chloroplast chromosomes, and the summation of this DNA material is actually going to be called the genome within the organisms. Now, within the genome organization in eukaryotes, the eukaryotic genome is linear and conforms to the Rusten-Crete double-helix structure model. It is embedded in the nucleosome complex, a DNA and protein structure that packs together to form the chromosomes. Eukaryotic genomes have the 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. A human haploid cell consists of 23 different chromosomes, and one mitochondrial chromosome contains more than 3.

2 billion DNA base pairs. Remember that in the case of the prokaryotic structure we were talking about the number of chromosomes being in the millions, but here the number of chromosomes is going to be in the millions; that's why a higher level of compaction is required so that particular DNA can fit. into the small tiny nucleus. Now, as far as the chromosomes go, eukaryotic chromosomes are usually linear structures. So this is one of the eukaryotic chromosomes, and a typical chromosome is tens of millions to hundreds of millions of bases in length.

Eukaryotic chromosomes occur in sets. Many species are deployed, which means that the somatic cells contain two sets of chromosomes. So you're going to have the chromosomes that are present in the sets. So a double set is present inside the cell. 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 a centromere; right, this is a centromere, and this is the place that 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 chromosome. So these are the telomeres, which are going to be two telomeres. So, these are the specialized sequences that are present on the tails or the corners of the chromosomes.

Then we have the repetitive sequences which are found near the centromeric regions. So these are the DNA or the genes, and how the genes are actually organized onto the chromosome. For example, this is a classical example of how the MSC proteins or MSC genes are being organized onto the chromosomes. And you see that you have HLA typing and all of that. And this is a particular type of chromosome.

What is the chemical composition of the chromosome and the chromatin? So you're going to have the DNA. You're going to have the RNA, and then you're also going to

have the proteins. So you're going to have the DNA, which is 20 to 40%. So the most important constituent of the chromatin. Then you're going to have the RNA, which will be 5 to 10%.

It is associated with the chromatin as transfer RNA, messenger RNA, and ribosomal RNA. So it is actually a part of the expression machinery. And then you're also going to have the protein. So that is going to be 50 to 60%. So mostly, the chromatin is actually made up of DNA plus protein, and it is mostly that 40% is actually going to be DNA and 60% is actually going to be protein.

Within the protein, you're going to have two different types of proteins: the histone proteins and the non-histone proteins. Histone proteins, which are very basic, constitute about 60 percent of the total protein. They are present in a one-to-one ratio with the DNA, and there are five different types of histone proteins: H1, H2A, H2B, H3, and H4. Similarly, you are going to have the non-histone protein. They comprise 20% of the total chromatin protein and are required for the nucleosomal assembly proteins such as NAP and other histone chromatin remodeling complexes.

And then you are going to have the structural proteins such as actin, tubulin, and myosin, the contractile protein, and all the enzymes. So the contribution of the non-histone protein is very, very little compared to that of the histone protein. Histone proteins are 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 proteins and that's why they are actually going to have an instant attraction for the negatively charged DNA. So this is the DNA, right? You know that DNA is negatively charged because of the phosphate backbone. So histones are found in all eukaryotic cells. The commonly present histones in eukaryotic cells are H1, H2A, H2B, H3, and H4. Then all five histones are categorized into two structural regions.

One is called the core histone; the other one is called the linker histone. So the H2A, H2B, H3, and H4 are part of the core histones, whereas the H1 is actually called a 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're going to have the H-2A, H-2B, H-3, and H-4. Whereas the linker histone is not part of the core protein, it is associated with the linker DNA, which links the two nucleosomes.

So, within the histone, you're going to have the core histones and the linker histone. The core histone consists of two copies of 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,

right? So it's going to have a clear attraction because all these histones are going to be positively charged. So its surface is actually going to be positively charged. And that's how they are actually going to have a very high affinity for the DNA.

Similarly, you're going to have the linker histone, which is H1. So how are these histone proteins or what are the different properties of the histone proteins? So, histones are closely associated with the negatively charged DNA. They have a 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 has a molecular weight of 14 kilodaltons and is actually lysine-rich.

Similarly, you can have the H-2B. It's going to be approximately 14 kilodaltons, and it is slightly lysine-rich. Okay, then we have the H3; H3 is going to be 15 kilodaltons, and it's going to be lysine-rich. Then 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's going to be 20 kDa; it is also arginine-rich.

So H3 and H4 histones are first formed as a heterodimer and then come together to form a tetramer with the two other molecules of H3 and H4. H2 and H2B form heterodimers. So this is the sequence in which the histones are actually going to be organized with each other, and that's how they are actually going to form the nucleosomal assembly. So the assembly of nucleosomes involved the ordered association of histones with the DNA. So first the H3, the two molecules of H3 and the two molecules of H4 are actually going to come together, and that's how they are actually going to form a tetramer, which means you are going to have it like this, right? So you're going to have a tetramer that is going to be formed.

Then this tetramer is actually going to have a positive charge, right? So it's going to have a positive charge on top, right? And then it is actually going to bind to the DNA. This means this ball is actually going to have DNA, okay? And then after binding the DNA, the H2A and H2B form a dimer, which means they are actually going to join the H3H4 DNA complex. And that's how it is actually going to have a nucleosome. So this is actually one ball that is going to have the H3H4 DNA. And on top of this, you're going to have the H2A, H2B, then 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 it's 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 amino acid extensions called tails because they lack a defined structure and do not

participate in the association of DNA with the histone octamer; the tails are extensive sites for post-translational modifications, including methylation.

Acetylation and phosphorylation. The assembly of nucleosomes involves the ordered association of histones with DNA. This is anyway we have discussed, right? H3 and H4 are followed by the binding of DNA and the binding of H2A and H2B, and that's how the nucleosome is going to be formed. So the nucleosome is the starting building block for higher-order organizations. So neglossom is actually the building block of the chromosome.

So, this is the DNA. Then it is actually going to form the nucleosomes. Then it is actually going to organize into chromosomes. And then it is actually going to organize in the nucleus. So a human cell contains 3 times 10 to the power of 9 base pairs per haploid set of chromosomes. The average thickness of each base pair is 30.

4 angstroms. This is actually the thickness of the DNA. So, therefore, if the DNA molecule in a haploid set of chromosomes is laid end to end, the total length of the DNA molecule would be approximately one meter. For a diploid set, the length is actually double, which is two meters. As the diameter of a typical human nucleus is about 10 to 15 micrometers, it is obvious that the DNA must be compacted by many orders of magnitude to fit into such a small space. The compaction in the human nucleus is done by nucleosome formation through the association of DNA with histones.

Nucleosomes are packed into successively higher ordered structures. So the nucleosome model is a scientific model that explains the organization of DNA and associated proteins into chromosomes. It also further explains the exact mechanism of the folding of DNA into the nucleus. This model was proposed by Kornberg in 1974, and it is the most accepted model of chromatin organization. The model was further confirmed by the peer audit in 1975.

What are the features of the nucleosomal model? In eukaryotic DNA, the DNA is tightly bound to histone proteins, which leads to the formation of DNA-protein particles called nucleosomes. Nistone plays a very important role in the packaging of such a long DNA molecule in the form of a nucleosome into the nucleus, which is only a few micrometers in diameter. Therefore, the nucleosomes are called fundamental packaging unit particles of chromatin, and they give a beach onto a string appearance, which means if you look very closely, you will see that the DNA is being packed like this. And this packaging is called the beads on a string because this is the linker DNA, and this is actually the core structure of the histone. And that's how these are actually going to fold onto each other.

So it is actually going to be folded like this, and that's how you're going to have beads, and then it's going to be folded like this. And that's how it is actually going to keep condensing, and that's how you're going to have the higher organizations of the packaging. Each nucleosome is a disc-shaped particle with a diameter of 100 nanometers and a height of 5.7 nanometers, containing two copies of each of the four nucleosome histones, such as H2A, H2B, H3, and H4. This histone octamer forms a protein core around which the double-stranded DNA is wrapped 1.

6 times, containing the 146 base pairs. Each nucleosome bead is separated from the next by linker DNA, which is generally 54 base pairs and contains a single H1 protein. This is what I was talking about, right? You have DNA, and then it's actually going to be arranged. On average, the nucleosome repeats at an interval of 200 base pairs. Folding of the DNA, so once the nucleosome is formed, there will be a folding of the DNA, and that's how you're going to have the higher compaction of the DNA. The assembly of DNA begins with a newly produced tetramer, H3H4, that is particularly modified to form a sub-nucleosomal particle.

The two HbH tumors are then added. The results in the formation of a nucleosomal core particle with 146 base pairs of DNA bound to the histone octamer. The nucleosome is made up of a central component and the connecting DNA. In order to create the nucleofilament, the nucleosome core must be spaced regularly, which is accomplished during the maturation stage that requires ATP. The newly integrated stones are deacetylated at this stage. Next, the incorporation of linker stone is accomplished by folding the nucleofilament into the 30-nanometer fiber, the structure of which remains to be elucidated.

Two principal models exist: one is the solenoid model, and the other is the zigzag model, which explain how the DNA is going to be folded after forming the nucleosome to form the higher-order organizations. Last but not least, the further subsequent folding process results in a higher level of structure and distinct domains within the nucleus. So these are some of the organizations you are going to start with the DNA. DNA is actually going to be folded 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's how you're actually 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's how you're 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, in which these solenoids are actually going to be again folded onto each other, and that is how you are going to have these 300-nanometer fibers. Then this 300-nanometer

fiber is actually going to be condensed, and that is how it is 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 chromosome.

So you are going to have the chromosomes. So you started with DNA; you ended with the chromosome. So this is the first, and this is the last binding style, okay? Now, in this, 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 organism, and the bigger the genome, the more you are actually going to have. The more information you carry, the higher your flexibility in modulating that information, and that is how you will have more properties to handle. So, genome size is related to the complexity of that particular organism, right? Because the more information you have, the better you are actually going to manipulate that information. And that's why you're going to have complexity in the system.

This means you can actually have the freedom to modify these proteins. You can actually synthesize the proteins and so on. So if you see very clearly, what you are going to see is that you are going to have the prokaryotic species and the eukaryotic species. Within the prokaryotic species, you will see that the genome size is very small, and that's why the number of genes or the number of proteins is actually going to be very small. This means they are actually going to produce a smaller number of proteins.

And if you are producing a smaller number of proteins, you are actually going to have lower order freedoms to manipulate those proteins because you cannot have the multi-step process. You can have only a one or two-step process because if you are going to produce as many processes, you should actually have the proteins to regulate these steps. So that is basically a drawback, or I would say simplicity in the system. More and more, you are actually going to have a genome size. For example, in the case of yeast, you will have the genome size, which is 12 megabytes.

And then you will see that the number of genes is going to be significantly higher compared to the mycoplasma. And more and more, you actually see that these are the plant species, right? So they are very, very high, and the number of genes you see here is very high. This means they are actually able to have the potential of producing a large number of proteins, and that's how these large numbers of proteins can be utilized in such a way that you are actually going to have an event that is tightly regulated at each step, and that's how you can actually have 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 a spermatozoon, is used to describe the genome size in eukaryotes. Because the size is

essentially consistent within the species, it is known as the C-value or the cot.

The mismatch between the c-value and the presumed amount of genetic information contained within the genome is called the c-value paradox. Since we cannot assume that a species processed less 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 an excess amount of DNA, you can have the flexibility of producing a greater number of proteins, and that's why instead of having the three-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 gene glycolysis is a 10-step process, the grape cycle also has multiple steps, and because they have multiple steps, you can actually have the entry and exit of the metabolites at every stage, and that's how you are actually going to have very complex biochemical reactions. Now the first question is whether there is a requirement for protein production.

For example, if there is a requirement for protein production, the DNA should be free for transcription and translation. So now the question comes: how can you unpack the DNA and how can you have the DNA available for doing other kinds of molecular biology activities such as replication, transcription, and translation? So, the way we have discussed the packaging of DNA, the histones are the crucial proteins that actually participate in the unpackaging or unbinding of DNA. So histones actually have a tail region, right? Remember that the tail region is important for histones to be assembled with each other, and that's how they are actually going to bind to the DNA. This tail region has the modification sites for acetylations, phosphorylations, and methylations. Now, when you have the acetylation, you are actually going to produce the negative charge.

When you have phosphorylation, you are going to induce a negative charge. And when you have methylation, that is also going to modulate the surface properties of that particular protein. So as soon as you have the acetylation and phosphorylation, you are going to have the unwinding of the chromatin structures, and DNA becomes more accessible for the other kinds of downstream applications or activities, such as replication, transcription, and translation. Acetylation takes place at the lysine residues of K4 and K5 in H4.

It takes place through an enzyme called histone acetyltransferase or AT. The acetylated chromatins are more open. This means they are actually going to be active in terms of replication and transcription. It is accessible for transcription factors and polymerases. Deacetylation takes 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's how it is actually going to form the relaxed chromatin. Once the relaxation is over and that process is complete, you are actually going to increase the HDAC activity, which means the histone deacetylation, and then it is actually going to result in closed chromatin. And that's what these are: the things that are actually going to occur simultaneously or to, just to, you know, unwind the DNA, make it accessible so that you can use that DNA, and then, after that, once that process is over, then you can actually close that DNA. The same is true for the phosphorylations. So you're going to have the kinase activity, which is actually going to convert the closed chromatin into relaxed chromatin.

And then you have the phosphatases, which are actually going to remove the phosphate groups. And that's how it is actually going to reverse the event. Then the third is methylation. So it occurs on the side chains of lysine and arginine. The methylation does not alter the charge, but it actually changes the charge that is present on those particular residues.

So lysine can be mono-methylated, di-methylated, or tri-methylated. Methylation is done by the histone lysine methyltransferase and the histone lysine demethylase. So here also you're going to have the methyltransferase and the demethylase, and when you have the methyltransferase, the coarse chromatin is going to be converted into the relaxed chromatin, and the same is going to be reversed by the histone lysine demethylase. So these are about the normal chromosomes. This is the information that is required for the normal chromosomes. But when people were discussing or when we started investigating the different types of chromosomes, they could find that some are specialized chromosomes which are present in some of the organisms.

So let's discuss these specialized chromosomes, how the DNA is packed into them, and what the different properties of these specialized chromosomes are. So the first one is polytene chromosomes. So, what are polytene chromosomes? Polytene chromosomes, which are gigantic chromosomes that grow from smaller developing chromosomes, frequently appear in the salivary glands of dipteran flies such as Drosophila melanogaster. They are also known as the slave grand chromosome because they were found in slave glands. The Balbini found the polytene chromosome in the grand nuclei of the larva in 1881.

Due to the presence of several chromatins in them, they are known as the polytene chromosomes. Now the question is how these polytene chromosomes are found. So most polytene chromosomes are located in the interphase nucleus of a few cells in the dipteran

fly larva. Each chromosome component is successfully duplicated as it grows from the chromosome of the duplicated nucleus. After each DNA doubling, the later stages of mitosis are eliminated, leading to the development of a polytene chromosome.

As a result, the cell cycle is divided into the S phase and G phase. In Drosophila melanogaster, this polytenization cell cycle develops during mid-embryogenesis. DNA strands do not separate in the final stage of each S-phase. Rather, they remain accompanied by one another, generating the polytene chromosomes. The process of endoreduplications or multiple chromosome DNA replication without adequate karyokinesis and cytokinesis results in the polyteny of gigantic chromosomes; as a result, the giant chromosomes are produced, which are 70 to 100 times longer than the typical metaphase chromosomes.

Morphological features of the palatine chromosomes are observed. So the palatine chromosome is a very important thing actually because this is a kind of exception or a kind of structure that is found in specific organisms. So there are numerous partially duplicated chromosomes that are almost intervening with each other, making up the polytene chromosomes. The heterochromatized centromeres of all chromosomes fuse in a centromere. The polytene chromosomes are found in the form of six radiating arms around the chromocenter. You can have the X chromosome, you can have the two chromosomes, the left arm and right arm of the second chromosome, the right arm and left arm of the third chromosome, then you can have the fourth chromosome, which is the shortest arm, and then you can have the Y chromosomes, and so on.

So an altered pattern of bright and dark is seen when these chromosomes are stained and examined under a microscope. Interband refers to a light pattern, while bands refer to the dark pattern. So this is a specific polytene chromosome where you are going to have the right arm, you are going to have the left arm, and within the left arm, you are going to have the left arm of chromosome 2 and the left arm of chromosome 3; similarly, you can have the right arm of chromosome 3, and so within this place, your centromere, you are going to have the divergence, and that's how you're going to have the X chromosome and Y chromosomes, and so on. Then you can have some of the classical characteristics of these chromosomes, such as the Balbini rings. The band undergoes morphological and biochemical changes related to its 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 bands located elsewhere in the chromosome. Puffs are active genes of transcription. So these are the puffs, the chromosomal puffs, and these are the active regions of gene expression. What

is the function of polytene chromosomes? The nuclei of each cell enlarge in size, leading to cell growth. The metabolic benefit of having numerous copies of a gene allows for a higher expression of gene expressions.

The chromosome in Drosophila melanogaster undergoes numerous rounds of endoreduplications in order to generate a significant amount of glue prior to population. The bar phenotype, which includes the kidney-shaped eyes, results from the tandem duplication of the severe polytene bands that are close to the centromere of the X chromosomes. Due to the fact that the polytene chromosomes are interphase chromosomes and are thus transcribed, it offers a chance to investigate transcription through direct observation, and the transcriptional response to certain stimuli can be observed. So apart from the polytene chromosomes, you can also have another kind of chromosome, which is called Lambrus chromosomes. Lambreche chromosomes are transcriptionally active chromosomes that are mainly found in the germinal vesicles of large courses of many vertebrates and invertebrates.

The Lamb-Brush chromosomes derive their name from the lateral loop that excludes the chromosome at a certain point. They are very transcriptionally active as the emerging DNA from a certain point is rich in RNA polymerases. These chromosomes were first observed by Fleming and Ruckerts in 1882 in Ursus of the amphibians. Where do these chromosomes occur? The Lambreche chromosome occurs in the diplotin stage of prophase I of the first meiotic division in the primary oocyte of all animals.

And the structure of the Lambrus chromosomes. So each RNA polymerase is attached to the nascent RNA and associated proteins, generating the visible brush-like appearance. It can be visualized easily that lambrus chromosomes are held in a stretched-out form during the diplotene stage of prophase I of the first meiotic division. The axis of lambrus chromosomes contains an array of beads from which the loops are protruding outward called chromosomes. They exist as meiotic bivalents to homologous chromosomes held together by the creasmeter. So in this lambrus chromosome, you are going to have the chromosomes, then you are going to have the RNA polymerase, which is protruding towards.

This is actually going to be a region of single chromosomes, and it is actually going to be transcriptionally very active because these are the regions that are actually going to be available for transcription and translation. So they contain symmetrical loops of chromatin in a chromosome, their absence of lesions in the centromere region, and each loop bears an axis that is made up of a single DNA molecule that unfolds during RNA synthesis. What is the function of the Lambrus chromosomes? Loops are useful in chromosomal mapping. Then it is extremely helpful in the visualization of gene

expression and also in the changes associated with transcription. It provides great proof for eukaryotic gene amplification, which plays a crucial role in oocyte development, and it is helpful in the hybridization results.

Now, at the end, we are going to discuss the comparison of the prokaryotic and eukaryotic genomes. Many of these properties we have already discussed. Right. So, the comparison of the prokaryotic and eukaryotic genomes. So the prokaryotic genome is small in size.

It is going to be large in the case of the eukaryotic genome. The genome is going to be a DNA and a few proteins in a simpler manner, whereas in the case of eukaryotic cells, the genome is present and many proteins are involved, such as the histone proteins and so on. It contains a single set of chromosomes, whereas in eukaryotes, you can have multiple sets of chromosomes. The amount of DNA is going to be small in the case of a prokaryotic genome. It is going to be a typically very large number of DNA molecules that are present. Then, the prokaryotic genome is polycistronic, whereas in the case of the eukaryotic genome, it is monocistronic.

Then most of their DNA encodes the protein. So it's actually that there's no useless DNA, right? There's no DNA that is not going to be transcribed or that is not going to be translated to protein. Whereas most of the DNA does not code for proteins, right? It is a very small portion of the genome that is actually coding for the protein. The rest are all non-coding regions.

Then RNA processing is not an option. So RNA processing allows for several of these genome variations. Because you have the non-coding regions, these non-coding regions must be separated from the coding region. And that's why RNA processing is required. Messenger RNA has a short lifespan, whereas messenger RNA has a long life because the eukaryotic cell requires the continuous synthesis of a protein for several days. So these are some of the properties of the genome. We have discussed the prokaryotic genome and the organization of the prokaryotic genome, and we have also discussed the eukaryotic genome and eukaryotic genome organizations.

We have discussed the organization of the different proteins involved in nucleosomal assembly and how nucleosomal assembly is formed, and so on. So, with this brief discussion about the genetic material, we are going to conclude our lecture here. Thank you.