Biochemistry –I
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Nucleic Acids II

We continue our discussion on nucleic acids. What did we learn last time was how we have these specific bases the purines and the pyrimidine's interact to form with double bonded, a hydrogen bonded structures, how they form complementary bases basically. What we have here is if we look at nucleic acids, we know that they are now comprised of this pentose sugar of phosphate and a nitrogen containing base.

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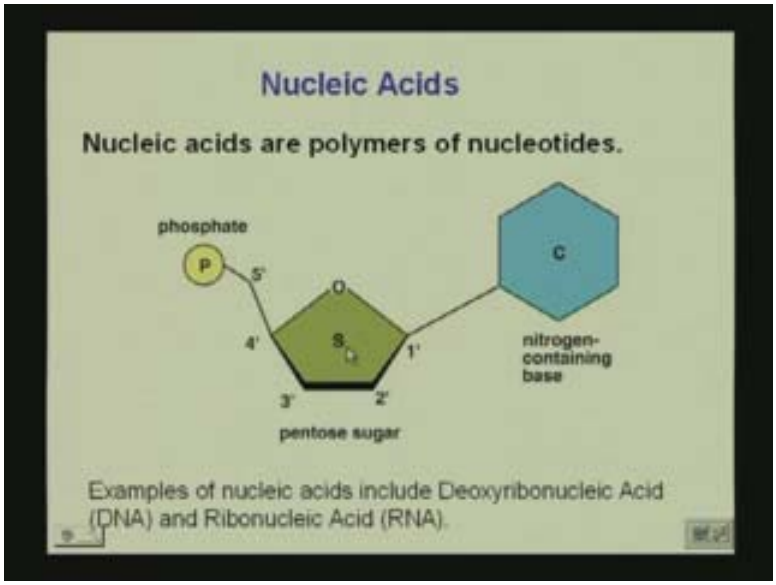

We know that this pentose sugar can be of 2 kinds either a deoxy kind or a ribose. Deoxy ribose or a ribose depending on the type of nucleic acids that you are considering. Obviously we have these 2 types the deoxyribonucleic acid where what is missing at the $2^{'}$ position. The OH is missing at the prime position and we have the sugar and the phosphate. The base families are the purines and the pyrimidines and what do they do they interact with hydrogen bonding, a purine and a pyrimidine to form a basic. Two basis coming together in hydrogen bonded network. There is an additional factor that has to be considered here that is a tautomerization possibility of the bases.

If we look at the adenine consideration here, what do you have here? You have a NH_2 group. What can happen to that NH_2 group? You all know about keto enol tautomerization. What happens in keto enol tautomerization? What happens there, you have a C=O and that is converted to an OH from an adjacent HCH_2. You have a keto enol tautomerization. We are having an amino type and an imino type.

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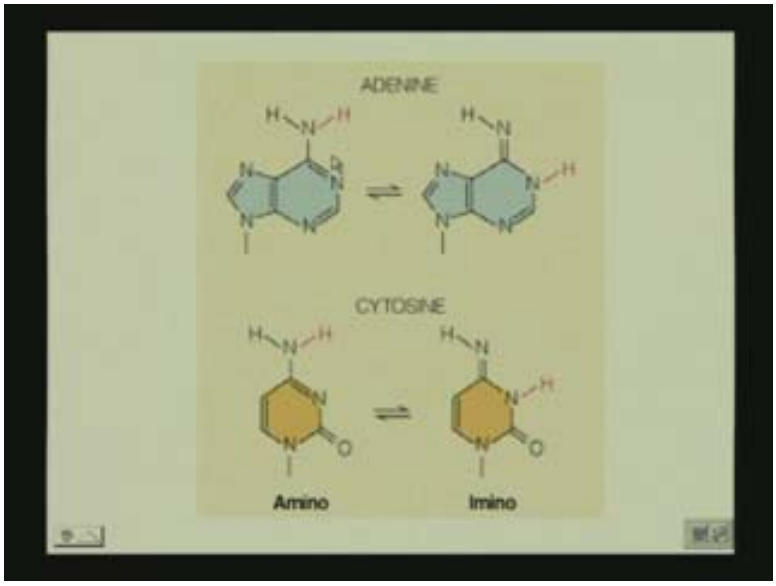

The basic idea is the same where you are shifting this hydrogen in the case of adenine to the adjacent nitrogen. In the keto enol tautomerization, what do you do? You have the H shifted from the carbon to the oxygen, where you have a keto enol tautomerization but what we are talking about here is an amino and imino case which is possible in adenine and cytosine. We have the adenine structure, now where is this attached? This is attached to the sugar ring and what type of bond is this? β and glycosidic bond.

We have the adenine and the imino form. This is the amino form and this is the imino form. The same case with cytosine we have an amino form and an imino form. So we have now two other basis that we also have to look into. They are guanine and thymine but what is the type of tautomerization. It is a keto enol type of tautomerization. When we are looking at the bond here, what do we have? We have the =O going to an OH. That is the difference in the type of tautomerization that you can see in A and C. What is the type of tautomerization you see here? It is an amino imino type of tautomerization where hydrogen is shifted from the amine group to form an imine.

We have this H shifted, this H shifted in cytosine so when we have A and C, we have amino imino type of tautomerization. But when we are talking about guanine and thymine, we have keto enol type of tautomerization where the keto group here becomes OH in guanine in this purine and in thymine the pyrimidine again we have the =O the adjacent H goes to the keto C=O to form the enol.

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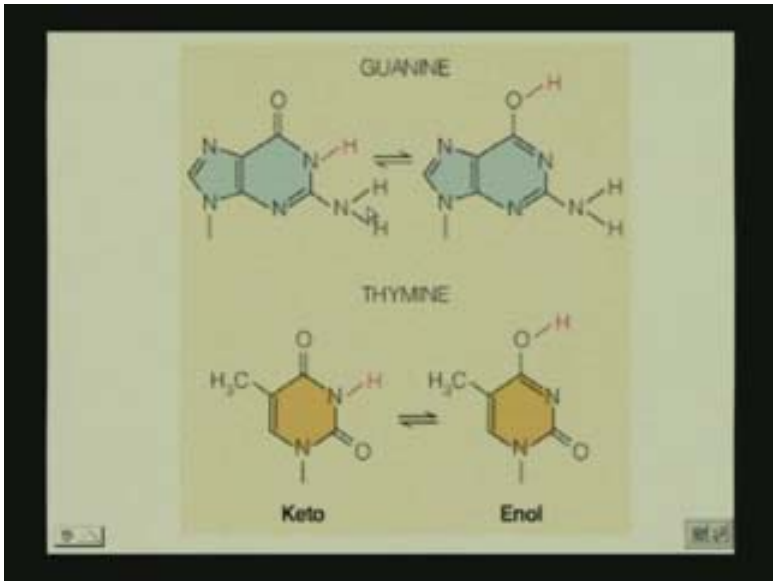

This is you understand that since we are talking about the hydrogen bonding between the bases this becomes an important factor. This is why we have to consider the tautomerization because what you are doing is you are shifting the position of the hydrogen. Now in shifting the position of the hydrogen, what are you doing, you are either disrupting a hydrogen bond or you are making hydrogen bond feasible in a sense. If we look at the linkages, I will show you the hydrogen bond formation in a minute. But we consider the polymer formation in our last class. What did we find? We find that this $3^{'}$ end? What happens to the free OH? What does this free OH do? It goes in attacks a tri phosphate the α phosphate of the tri phosphate releasing the pyrophosphate and attaching the next nucleo type. What are you doing then?
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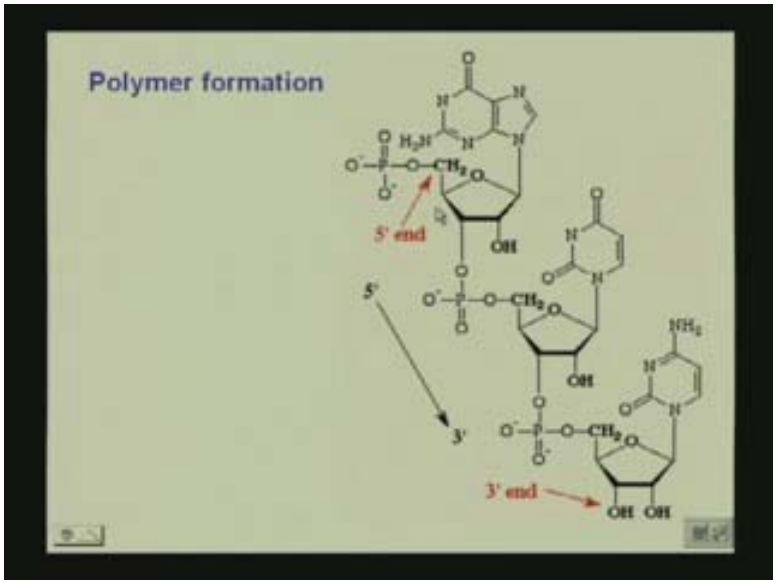

This mononuclear type we are building up our poly nucleotide. We go from the $5'$ to the $3'$ end. We will see how the other strand of DNA is the opposite of this. The $5'$ is at the bottom and the $3'$ up there and then we have the complement addicting of the strands that is what we are going to look today.

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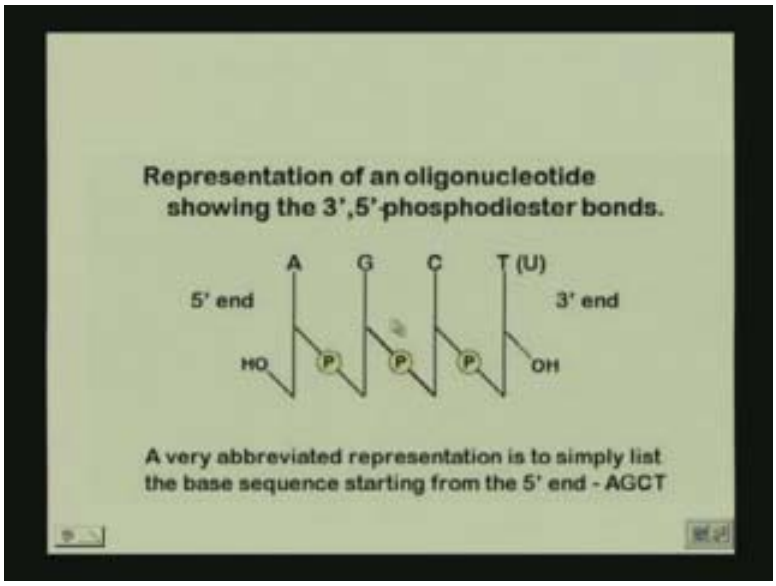

Now in this do we have common here? I mentioned this last time we have, what is this orientation that has been shown here? Is it a syn orientation or an anti orientation? It is a syn orientation. The anti orientation will have a rotation about which bond? The β and glycosidic bond, do you remember we mentioned about types of flexibility the types of angles of rotation that we can have. We can have a χ rotation about this β and glycosidic bond that is going to render the base either in the syn orientation or in the anti orientation. Usually we have the anti orientation to prevent any steric clashes and also to a system the hydrogen bonding in the complementary base of the other strand. The features that we are looking at here is the strand build up from the $5'$ to the $3'$ end.

The addition of a mono nucleotide in each case to form the poly nucleotype. What we know is each of these have a common back bone the sugar phosphate backbone. Usually when we represent it (Refer Slide Time: 07:52), we have a prime end and a $3'$ end and this is 3 prime $5'$ phosphor diester bonds. What do we mean by that? This is the $3'$ position and this is the $5'$ position, so when we mention the phospho diester bond it is a $3'$ $5'$ phospho diester bond. Because what we are going to look at later is that we are going to look at cleavages. How there are certain amino certain enzymes that will break only this bond? There are certain enzymes that will break only this bond. So there was going to be specific, what type of enzymes do you expect the name the nomenclature to be in this case.

You are working on nucleic acids so what is the enzyme going to be? A nuclease. You have done and studied the mechanism of nuclease before. What did that work on? That worked on RNA ribonucleic acid, so when we are going to cleave or going to look at the cleavage of the nucleases. If it is going to cleave ribonucleic acid, then we will have a ribo nuclease. If it is going to cleave a deoxyribonucleic acid, what are we going to have? A deoxyribo nuclease. What is the structure that I have here? Is it a DNA or RNA? Why it is RNA, because the OH is there.

When we have a representation, you know what the $3'$ $5'$ phospho diester bond means? This is the phospho diester bond $3'$ $5'$. If you have an addition, it is going to be added on this side. Just similar to how we had the poly peptide nomenclature. You have the amino terminal and you have the C terminal here. You have what is called a $5'$ end and a $3'$ end. Usually you know that you have a sugar and phosphate. Even though this is a certain representation that is easier to understand how the cleavage actually occurs. You usually do not even write this. You just write the bases like I mentioned last time instead of the poly peptide sequence with the peptide bonds and so on and so forth.

You do not write the peptide bonds. You just write the specific amino acids that are linked to one another because you know they are all linked in the same fashion. The same goes for the nucleic acids. You know that they are all linked by $3'$ $5'$ phospho diester bonds. So there is no need to write the sugar or the phosphate so all you essentially do simply list what is called the base sequence instead of just like you would list in an amino acid sequence. This is something we looked at last time where we have a guanine and a cytosine, we have a thymine and an adenine and we have in this case 3 hydrogen bonds possible.

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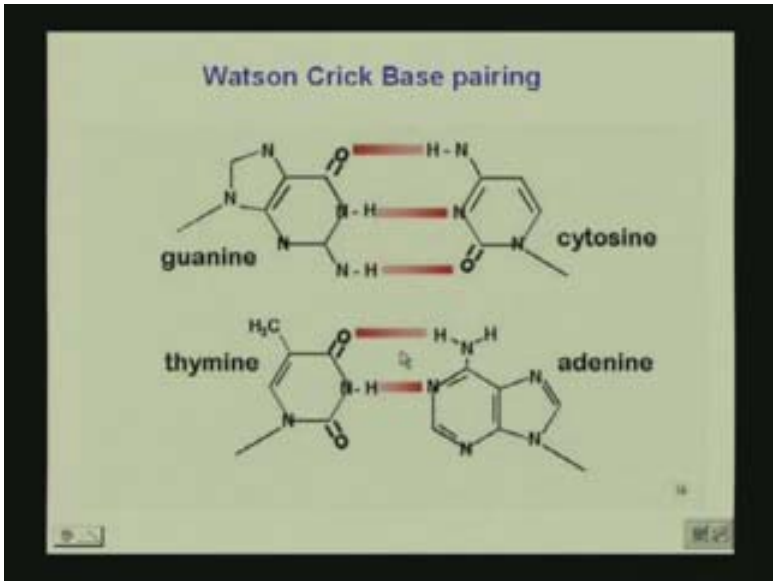

In this case we have 2 such hydrogen bonds possible. We also looked at the Hoogsteen Base pairing where we have a different phase for the base pairing and we also have in this case. What is this? We have 2 purines linked together, where in the normal the Watson Crick case, you could always have a purine linked with a pyrimidine. We have a purine linked with a pyrimidine and if you notice what we see is this 6 member ring of adenine is involved in the Watson Crick base pairing.
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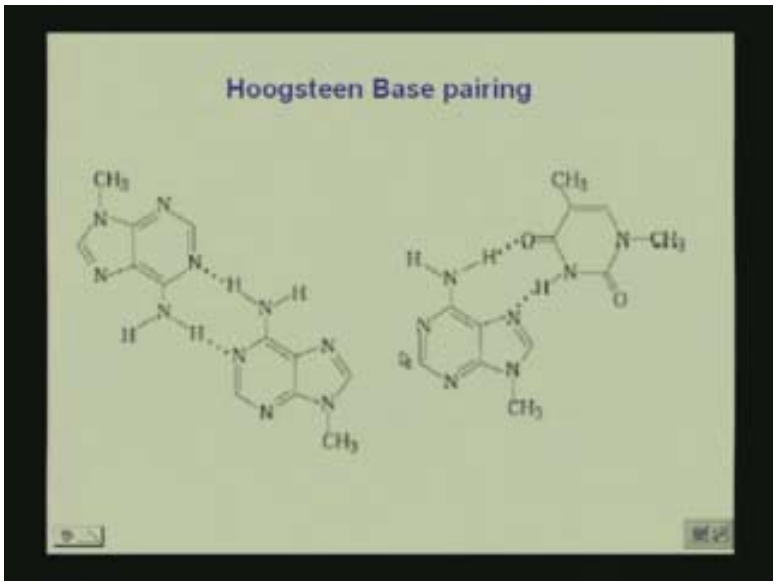

Whereas in the Hoogsteen pairing the one nitrogen of the 5 member ring also take part in the hydrogen bonding between another base. This is what is called the Hoogsteen face and this is what we call the Watson Crick base and this would be an example of an A U pair.
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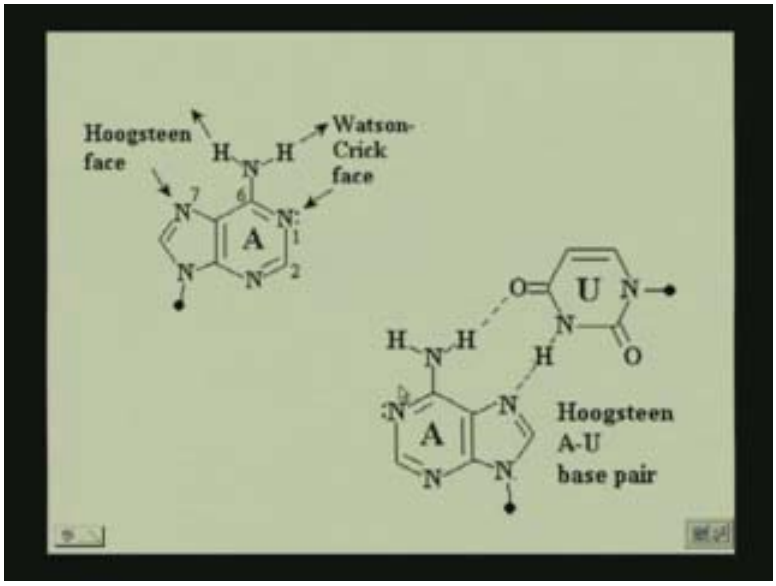

Where would you see an A U pair, In RNA because uracil is a base in RNA. When we are looking at a hydrogen bonding situation like this, we know we are looking at RNA. We know that we are not looking at a Watson Crick base pairing, because you can straight away see that the base pairing is between nitrogen of a 5 membered ring and the nitrogen of the amino group of the 6 membered rings. As soon as you this you know that this is a Hoogsteen base pair. This is what I mentioned quite quickly last time but it is extremely important in the two strands coming together.

What do we have here? We have a Watson crick base pairing. Why because we have the 6 member ring of the adenine of the purine involved in the hydrogen bonding. This is Watson crick hydrogen bonding. We have the 2 hydrogen bonds between A and T. We are talking about DNA now. The distance which is extremely important when we consider how the DNA structure is in its double helical conformation. The distance between the C $1^{'}$ of the purine and the pyrimidine, where it is actually 10.5 Å but you could call it 11 Å. This distance is constant.

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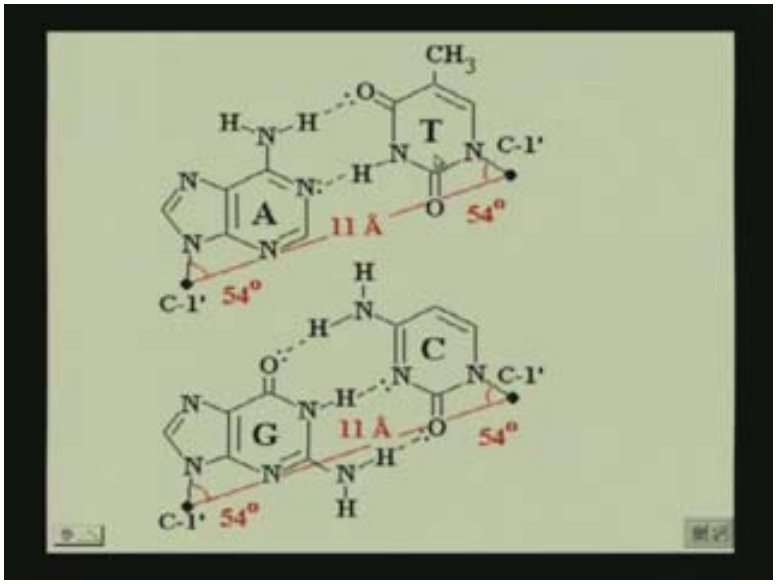

It is also the same when you link G and C together. That is extremely important if you consider the double helix as I mentioned last time because when you have the pairing of the ribbons of the double helix. They have to be equidistant from one another. We have the pairing come like this and then we have the twisting of the helix, the double helix that it is called. What is going to happen? You are going to have a constant distance so what is that going to ensure. That is going to ensure a constant distance of the sugar phosphate backbone, because you have a constant distance of the sugar phosphate backbone. How do you get that? It is because these 2 base pairings coming together are giving you that constant distance of 10.85 Å. That is extremely important you understand in its structural aspects. What we have here is in the hydrogen bonding, where we have 2 hydrogen bonds for the A and T case. We have 11 Å again when we have the hydrogen bonding for this purine pyramindine set. We also have 11 Å.

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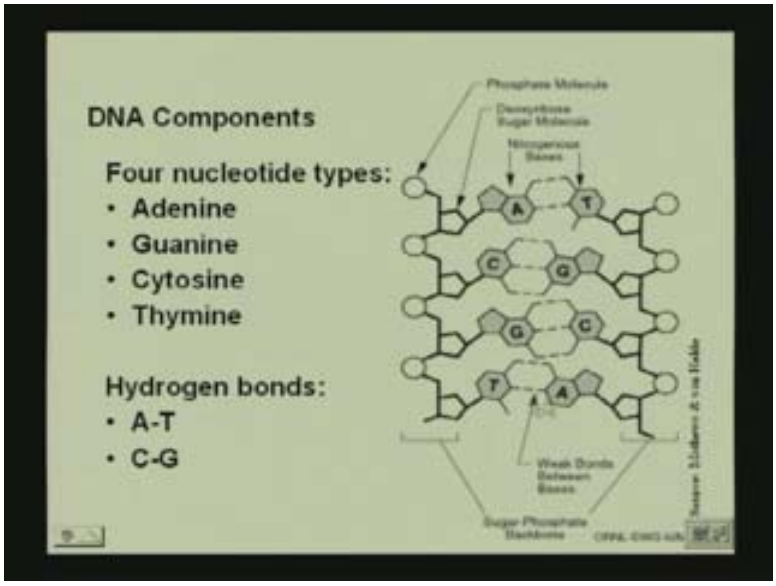

What we have is in the DNA components? We have our 2 strands. What is this? This is the sugar. These circles are the phosphates. We have the sugar phosphate backbone and sticking out from the sugars are all the different bases. We have the complementary basis on the other side. We know now that the distance between the C_1 of this and the C_1 of this is 11 Å, so what do I have? I have a constant distance and parallel orientation here. I have a parallel absolutely parallel set of back bones. Why do you have this? Whether you have the A T set or the G C set, it is the same because the distance is 11 Å and because you are linking a purine and a pyrimidine. You are linking one fused 6 and 5 membered ring. You are linking it with another 6 membered ring.

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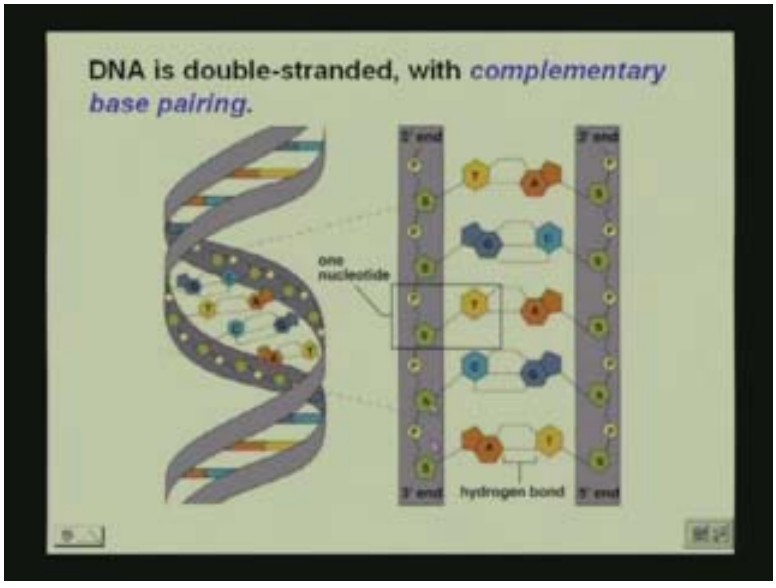

The hydrogen bonds are between the A and T. Two hydrogen bonds and 3 hydrogen bonds between the G and the C. This is what we have. This is what is usually called a ladder conformation because it looks like a ladder. We have a ladder conformation and the $5'$ end to the $3'$ end is what is actually synthesized. This is called the template strand. It is called a coding strand. The sense strand rather this is called the anti-sense strand, it goes from the $3'$ to $5'$. Let me just reiterate that. We have a coding strand that goes from the 5 prime to the 3 prime.

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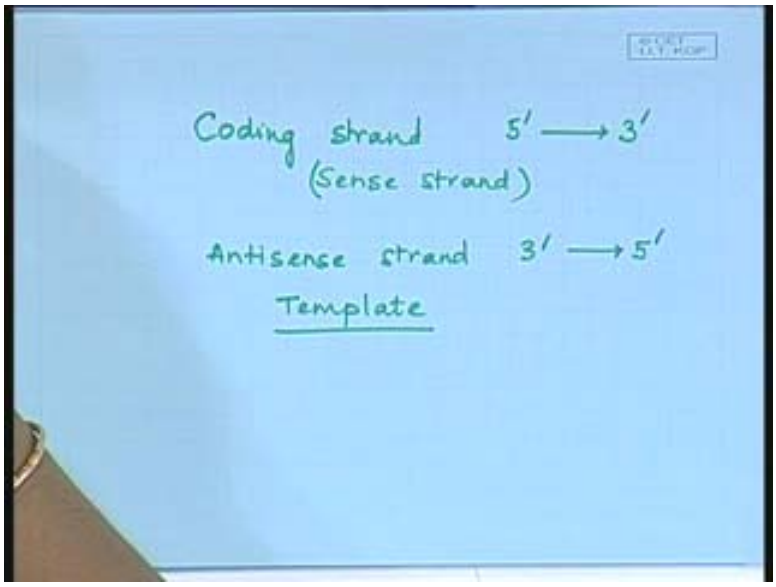

This is also known as the sensed strand because that actually has the information. What information am I talking about here? What information does this DNA strand have? It has the information that is going to go from the DNA to the RNA and then going to decide what protein has to be made. This has the sense in it basically the first strand here, then we are talking about the other strand which is the anti sense strand. The anti sense strand goes from the $3'$ to the $5'$ and this also known as the template strand because it provides the template for the mRNA, the messenger RNA which we will see in a moment.

If we go back to the slides here we have the ladder conformation where we have one nucleotide specified. What does this nucleotide have? It has a sugar, base and phosphate. When we consider the double helical structure, this is the double helical structure where this parallel, this set of parallel strands are twisting around one another. So what we have is we have a constant distance here throughout and a twisting so it is called a double helical structure, where two forms there twisting around one another. What do we have? We have complementary base pairing, 2 hydrogen bonds for A T and 3 for G C. This is what it would like.

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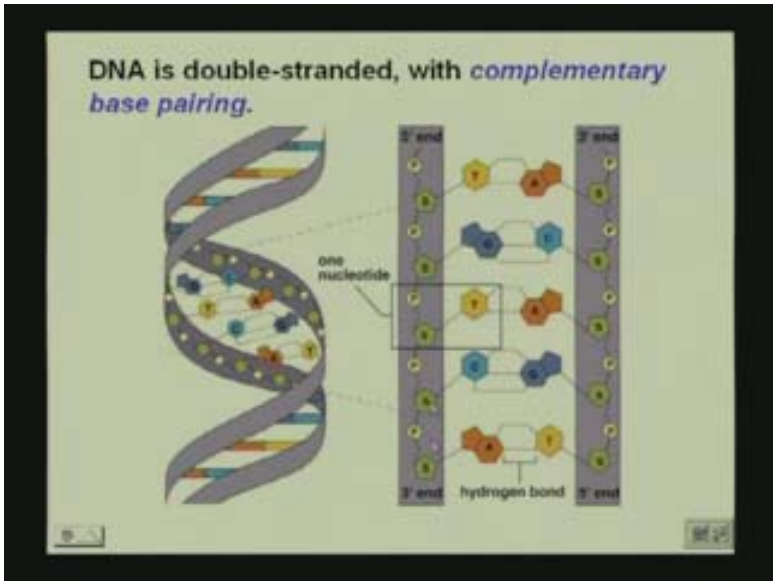

We have a sugar phosphate backbone and we have the bases. When we look at this double helical structure, we see that there is a large gap here. This large gap is alternating, because of the orientation other way the structure is we have these grooves. This is what is called the major groove. This is called a minor groove. We have a major groove of DNA and a minor groove of DNA. There are certain interactions between proteins between other compounds that either set in the minor groove of DNA or they set in the major groove of the DNA depending upon what sort of interactions and obviously the sizes of the compounds of the molecules that we are talking about. If we look at the structure, we have a major groove of DNA and a minor groove of DNA.

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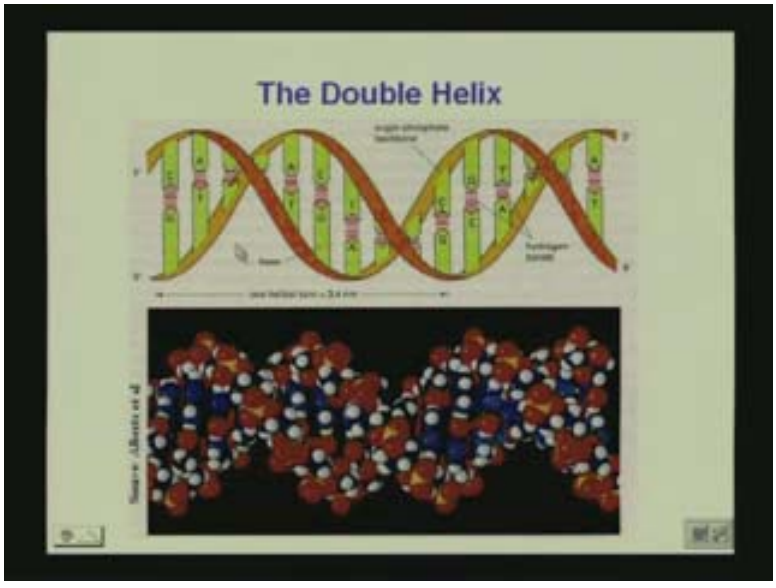

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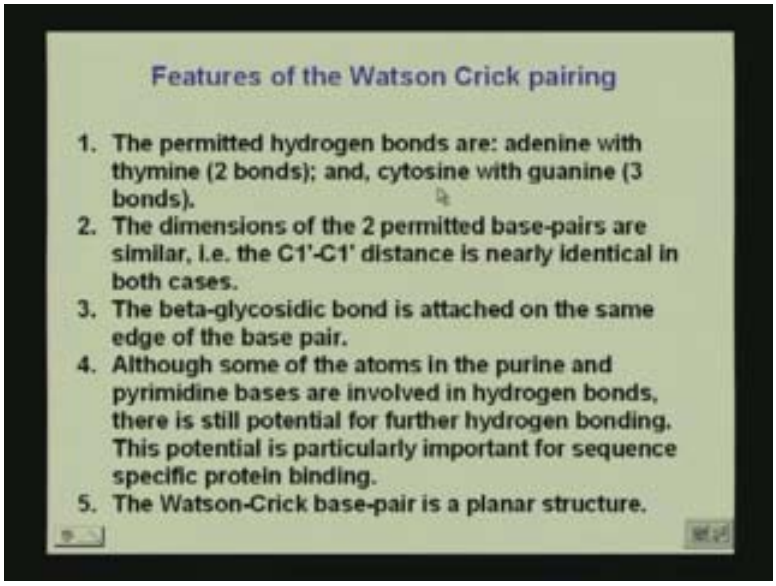

I have just listed here the features of the Watson Crick base pairing because it is going to help us in looking at the distances. We have 2 permitted hydrogen bonds between adenine and thymine and 3 permitted hydrogen bonds between cytosine and guanine. This is something we have seen. The dimensions of the 2 permitted base pairs are similar the $C1^{'}$ to $C1^{'}$ distance is nearly identical in both cases. The beta glycosidic bond is attached on the same edge of the base pair and even though we have the specific hydrogen bonds that are shown for the normal Watson Crick base pairing. You recall that there are other nitrogens also available. For example the Hoogsteen pair looks at other nitrogen all together. It means there are still other potential hydrogen bonding partners available.

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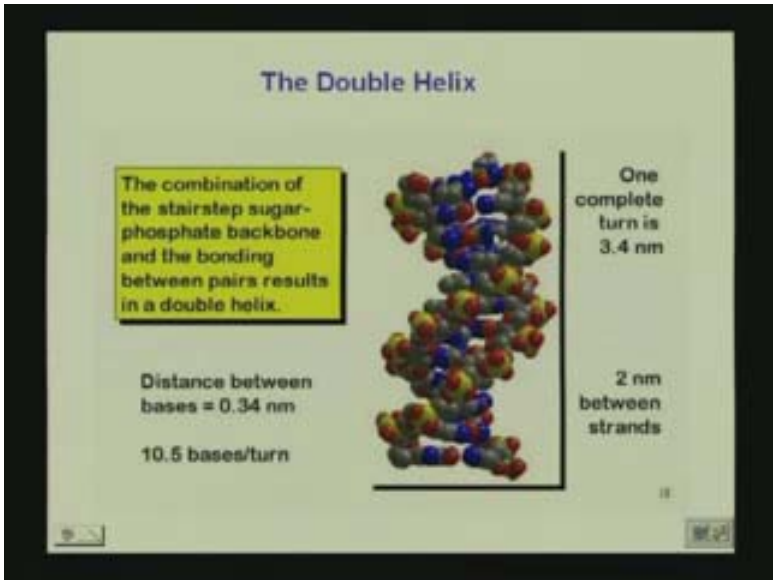

This is important because later on these may be involved in interactions with proteins or interactions with other compounds. Another important thing about Watson Crick base pair is a planar structure. This going to have certain implications in the stacking of the bases in the structure of DNA. These are features we have gone through. All of these features and we know that the structure of the DNA looks like this. The double helix, we have 2 nanometers distance between the strands. We have one complete turn that is 3.4 nanometers and the distance between the bases is 0.34 nano meters. We have a major groove and a minor groove.

These are the essential features of the double helix, apart from the Watson Crick base pairing which is obviously extremely important in its structural aspects. We also have considerations of the major groove and the minor groove what is called the pitch and what is called the distance between the two strands which are constant because the base pairing complementary base pairings are constant. So these are feature that we have to consider. Another feature that we can look at here is the one this part on the right. What groove is this? This is the major groove and so this is the minor groove. If you look at these are actually water molecules. There is other hydrogen bonding possibilities due to what is known as the water spine.

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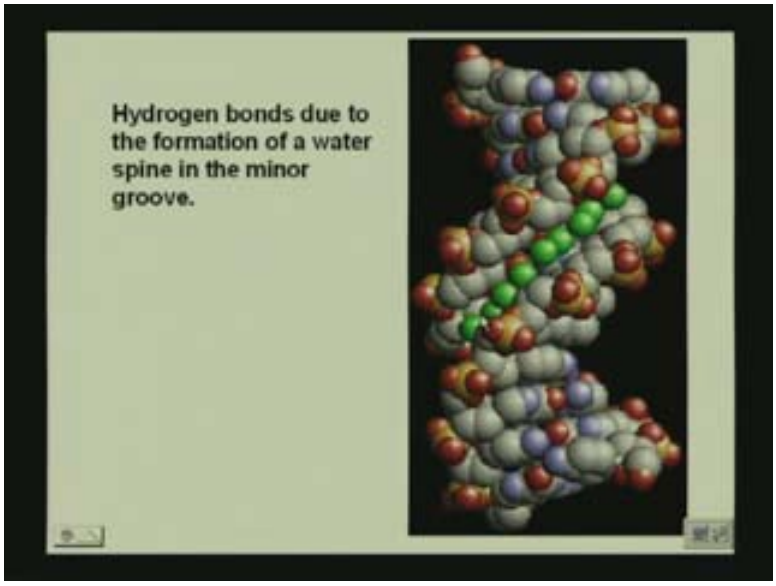

The water spine that follows through the minor groove, we have a spiraling water spine that goes through the minor groove of DNA. The major groove is probably too large for this water molecule to sit in there. This is a part that was also interacting with the other compounds and the other DNA protein interactions that occur. We have extra hydrogen now. How can we have these extra hydrogen bonds? What other units do we have? We have other hetro atoms present. We have phosphates and the phosphor diester bonds present that also have oxygen. Then we have the nitrogen of the bases but the bases are within so we can also have what is called intercalation.

Let me just go where we can have intercalation. If we have the bases like this, you see how they are stacked on one another. We have like a stacking part here, so when we have the stack of the DNA base pairs we have them like this stack one on the other and you can have intercalation.

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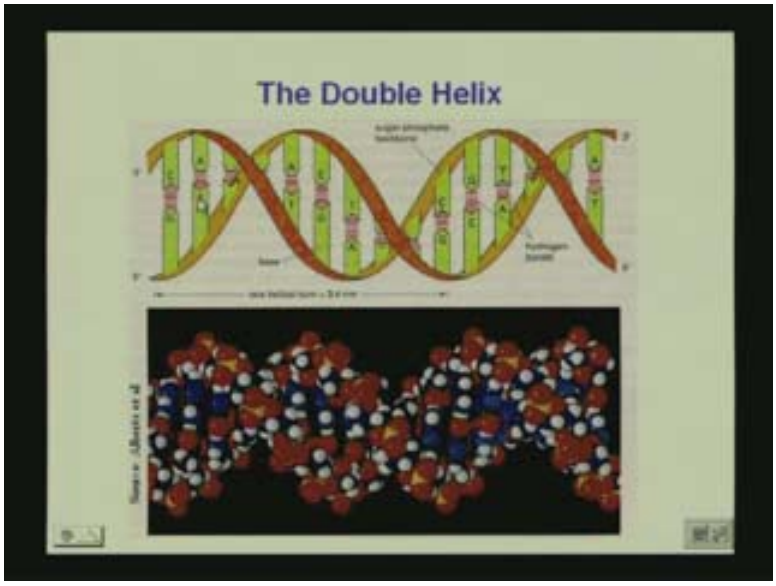

What is intercalation mean? Something that is going to set itself in between, this is very important if you want to design any drug that is going to cleave the DNA. Any drug that you want to know, what is going to happen if you cleave the DNA? If you chop up this DNA what is going to happen? It is not going to prepare the proper RNA and that RNA will not be able to form the protein. So essentially you are going two steps back into preventing a protein formation. That is a lot of research activities going on in this department. What we have here? You have intercalating agents, when we speak of intercalating agents we are talking of agents that are going to disrupt certain interactions. What happens when you have a protein?

When you heat a protein, you add urea to the protein what is happening to it? You are denaturing the protein. You are rendering it inactive in this case. What you are doing? You are rendering the DNA inactive in a sense that when you have these intercalating agents it will prevent the proper stacking. It will prevent the proper interactions that are to be there and prevent the proper protein expression. There are 3 types of DNA. The original Watson and Crick model which just completed 50 years. It was first discovered in 1953 and the paper is available on the net where you can look at the original paper of Watson and Crick that came out in Nature. You have B DNA that is actually the most prominent form of DNA.

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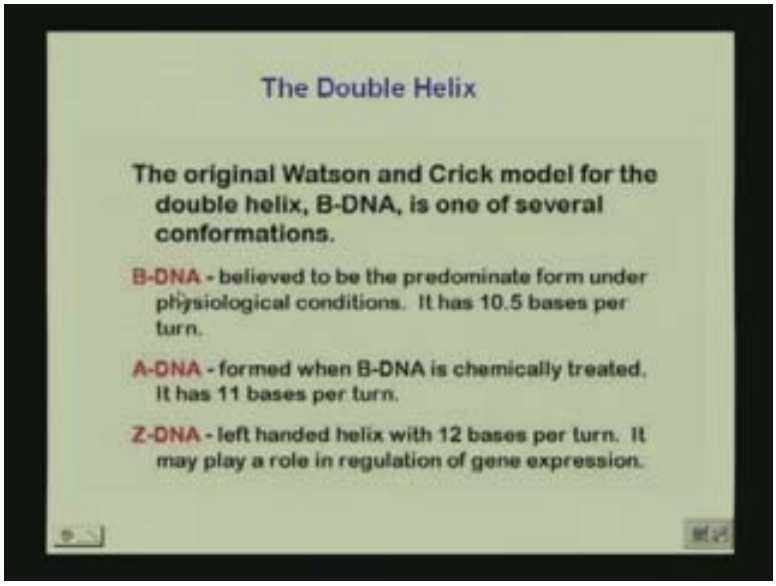

It has 10.5 bases per turn. What are we talking about here? We are talking about the single turn of the double stranded helix that goes up and there are 10.5 bases per turn just like we had a certain pitch of the α helix. It is similar to some thing like that. When we have the A DNA, this is formed when B DNA is chemically treated. Basically it doesn't have those water molecules in the water spine. That is what A DNA is and it has 11 bases per turn. The Z DNA as it is called is a left handed helix with 12 bases per turn and it usually plays a role in gene expression.

These are the 3 forms of the DNA and the most common by far is the B DNA. These are some of the features of the A DNA, B DNA and Z DNA. We have a pitch. What is this pitch? The distance covered by one rotation so the A DNA pitch is 2.8 nano meters, the B DNA is 3.4 nanometers and the 4.5 nanometers for Z DNA. The base pair repeats are 11 bases per turn, 10 bases per turn and 12 bases per turn. The twist per base pair, you realize that there is a slight twist. As you have a base pair like you would also have angle disposition for the α helix. These are the twists per base pair. We have slight base pair tilt which is not very much in the B DNA just 4^0. That is a slight base pair tilt. The 3DNAs, the B DNA, the A DNA and the Z DNA and the most common structure that we will be considering is just the B DNA.

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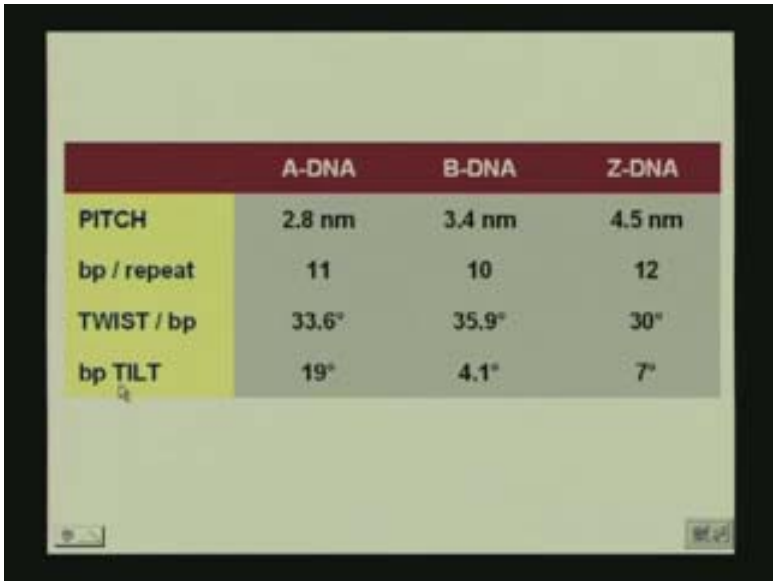

That has about 10 base pairs per turn 3.4 nanometers and base pair tilt of 4^0. The double helix of DNA is actually well, it wouldn't be a secondary structure that is the structure of DNA but there are other forms of DNA also. Studies have shown that the native intact form of DNA can be linear and circular. If you look at the double helix here, if it goes straight up and straight down we would have a linear structure.

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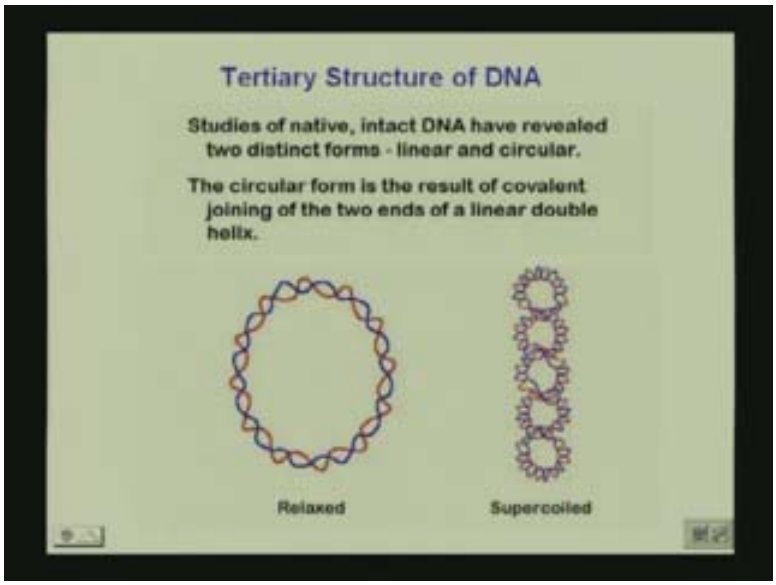

What happens is if the 2 ends are covalently joined together so if we chuck this up we are going to get a linear form, so when we have a covalent joining of the two ends of a linear double helix, we will obviously get a circular helix.

The circular helix remains actually in these two forms. This is the tertiary structure of the DNA. We have a relaxed form and a super coiled form. In this super coiled form, there are certain terminologies that I used, something that you just probably need to know so that we have a linking number. We have a twist and we have what is called a writhe. This is referred to as L T and W. What happens here is? You have here something like that. That is formed from this. You can even have this go even further. You are basically going to have now.

You have to remember that each of these is also a double stranded part. This I drawn here is actually this, is the linear part of the DNA that has covalently linked the ends to form this. It is actually something like that, which you joined together to form this circular DNA that has then further twisted itself. Writhe is like a ringing motion that you have when you suppose, you are squeezing your clothes or something.

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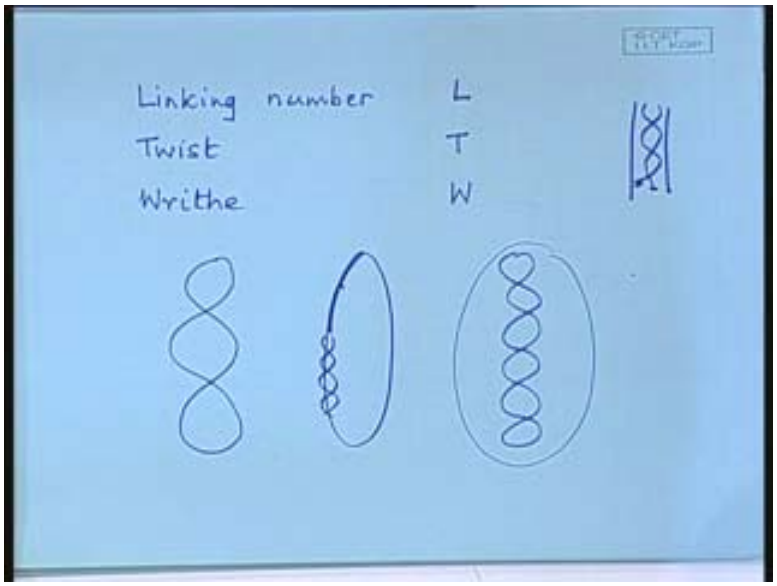

You would have a link a twist and a writhe but the reason why I am telling you this is when we consider the tertiary structure of DNA, as you combine this, you can get smaller and smaller. Smaller parts mean structural aspects of DNA. What you have is this is useful for the storage of DNA you cannot have a linear strands all around. What happens is you have this super coil DNA, which is actually the way you would have the DNA being stored because the DNA has to be stored.

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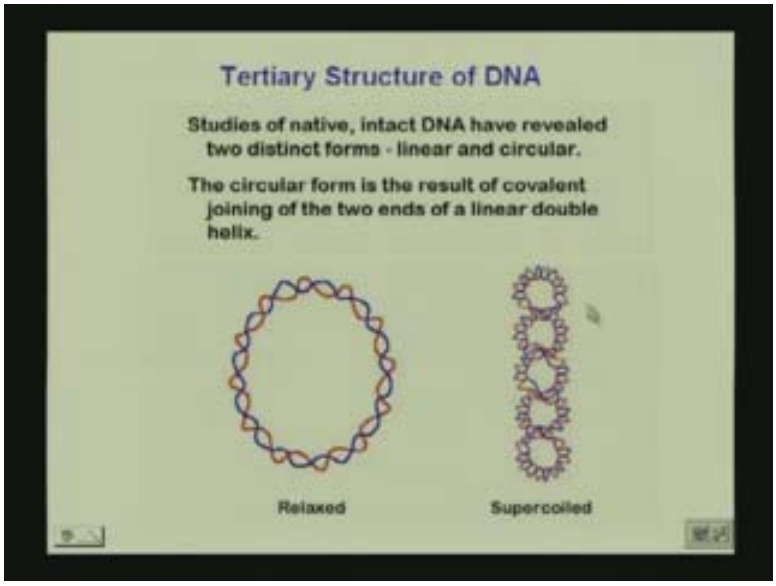

There has to be this DNA, gets to RNA transfer its information to RNA and this information has to be stored in the DNA. Because this linear strand does not remain as such we have what is called super coiled DNA. This is when you have DNA duplication you have these 2 strands what is this. What is this region? This is the major groove of DNA and this is the minor groove of DNA. When we have DNA duplication, part of the strand unwind and we have the ones in blue here are the dotted DNA blue molecules. So what is happening here? You again have a similar strand formed here. If this is A what was it traditionally linked to in the DNA double helix? It is T. When we have the new strand being formed, it will also be linked to a T so what do I have, I have a replication.

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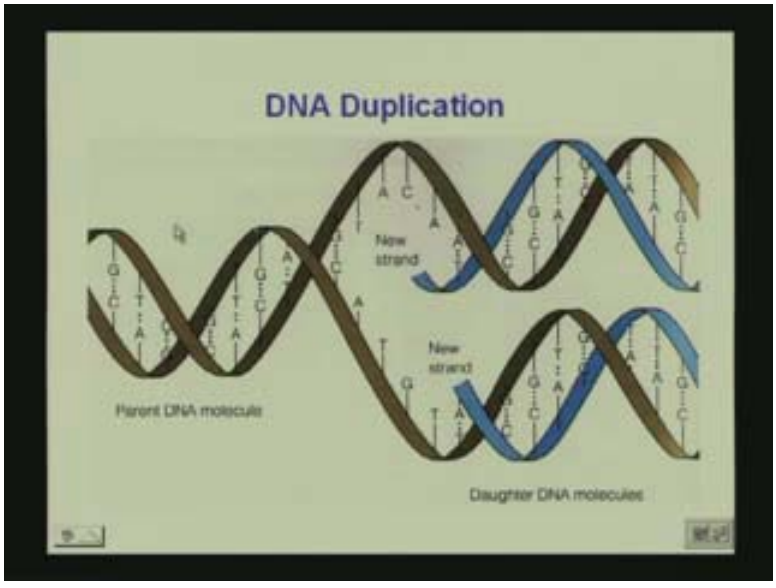

Don’t I have a replication, I am just doubling up the DNA that I have, so it is duplication. Duplication is probably the correct terminology that should be used so we have a duplication of the DNA, where I had one strand. I have new strands so I have my dotted DNA molecules also formed from the parent DNA molecules. RNA, now considering that the DNA structural aspects, we always have as a double helix. In RNA it exists as single stranded molecules.

These single stranded molecules usually do not take on an extended secondary structure like DNA in the form of a double helix. You understand that, in this case there is no necessity for a complementary base pairing. We do not have to maintain a distance because we do not have to maintain that linear polymer, the parallel ladder like structure. In this case the strands usually fold in a uniform periodic pattern and we have several structural elements that are observed. We have what are called bulges and helices and so on and so forth which we will see in a moment.

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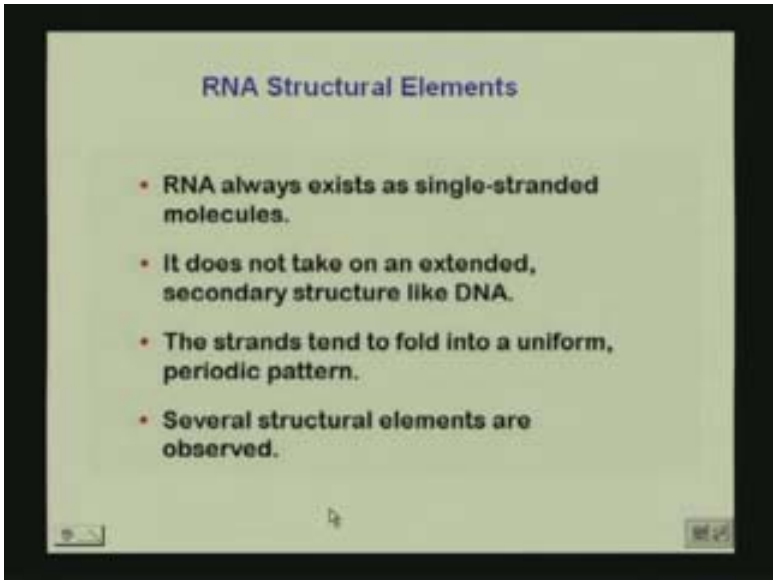

The basic differences here are that, we do not have an extended linear double helical structure like DNA has. It usually is single stranded and it folds and while it folds it forms different types of structural elements. What are these? These are hairpin turns. Hairpin turns are loops in the chain that bring together complementary base pairs. So when we talking about RNA actually we have a single strand. I may have an A, G, C and a U here.

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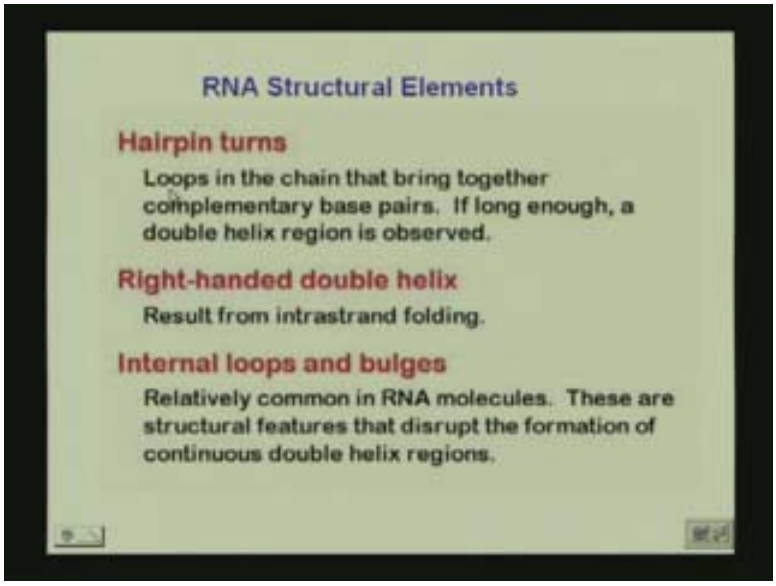

Another A and C here so on and so forth. What might happen in certain cases? We know that this G form hydrogen bonding with C, so in some cases we may have complementary base pairing. What is that going to result? It is going to bring part of these 2 structures close to one another. You are going to have probably something shaped like that. It is not as regular as what you see in DNA at all. It is just parts, bits and pieces of the structure coming together into forming different types of structural elements that are either what are called hairpin turns.

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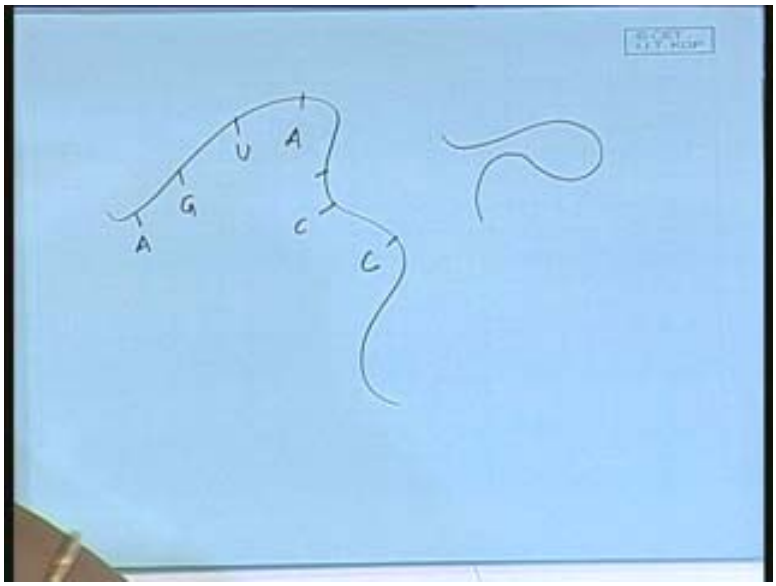

Hairpin turns a right handed double helix at times and internal loops and bulges. These are very common in RNA structures and usually they do not allow the formation of the double helical region of RNA. This is because you do not have any complementary base pairing there, so if you look at the structure it is something like this we have a bulge. We have an internal loop. Why do we have this internal loop because we do not have any complementary base pairing possible here. We can have helical segments, an unpaired loop at the tip. We have partial helicity here and we have bulges say it is probably such so, now you understand in these case there is a possibility for a Hoogsteen pair to occur which is unlikely in the Watson Crick base pairing for DNA. But here you can have a different type of base pairing because you do not have to have any regularity in the structure.

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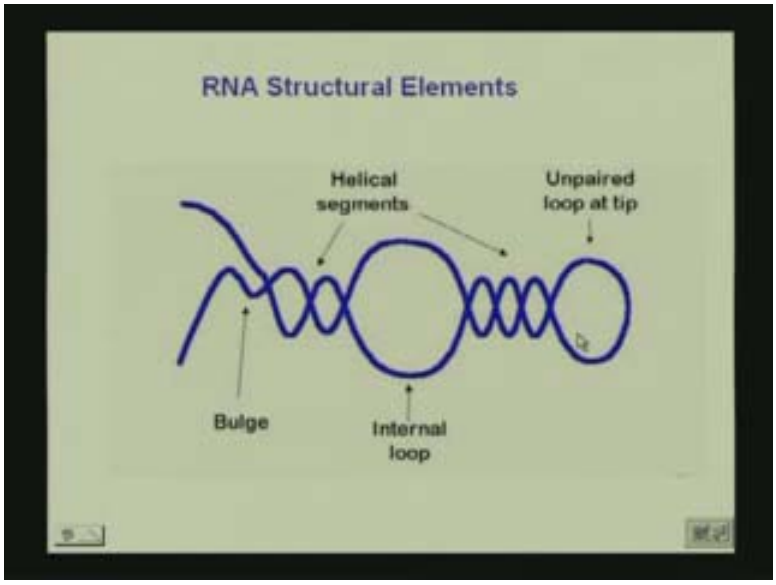

For the DNA double helix to form there has to be this constant distance of 11 Å between the C1 C 1' atoms in the double helix but that there is no such restriction in the RNA. We have this single structure, the single stranded RNA but just have all these helical segments and the loops and bulges and so on and so forth. RNA is basically an adaptor molecule that translates the information between, it translates from information in DNA and protein. When we go from DNA to RNA, it is called transcription, RNA and to protein it is called translation. We have 3 types of RNA. This is something probably be that you studied in school. You have messenger RNA. Messenger RNA is a transcription, a process of DNA going to RNA is called transcription and this transcription of the information of the DNA and it carries the information in a temporary format from the DNA.

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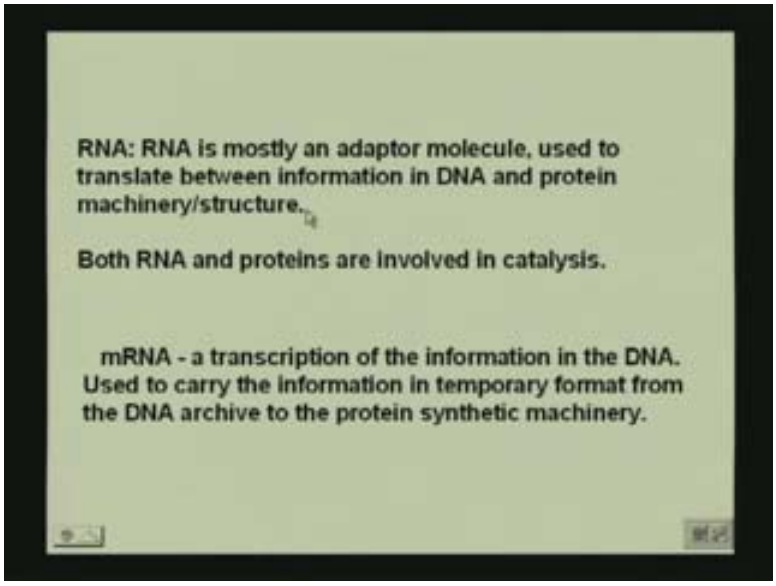

How does this occur? If you look at the previous thing that I was showing you here. This coding strand suppose, we have this from $5'$ to $3'$, the anti sense strand which is the template strand which is used by mRNA is the $3'$ to $5'$ strand. What happens in this case? Say our coding strand is A T G G A A something like that, then what is the anti sense strand going to be, what am I going to have here? T A C C T T. This is my sense strand that goes from $5'$ to $3'$. This is my anti sense strand that $3'$ to $5'$ then I have my mRNA which actually is linked to the anti sense strand. What is the code for the mRNA going to be? What is it going to be? It is going to be complementary to this now. What am I going to get? A then U G G A A.

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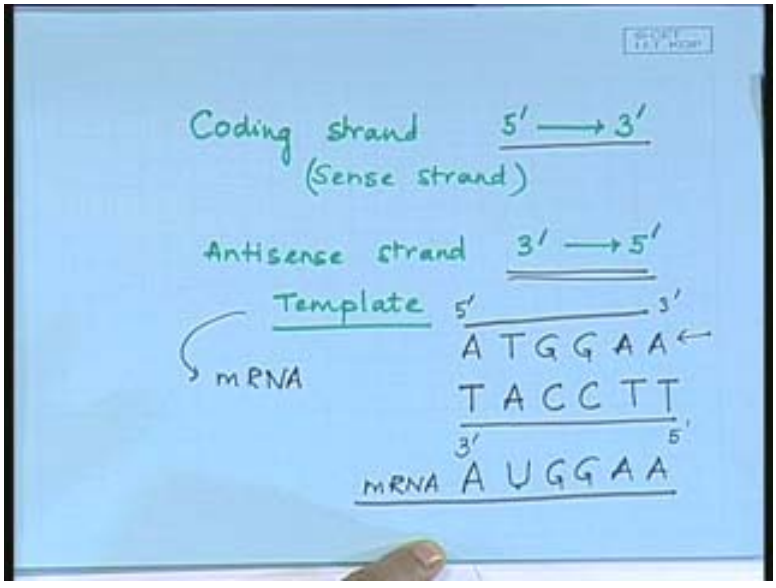

Why U because now I am speaking of mRNA. So now when this is going to form the next so but this information, it has taken from this. You understand that, this is the sense strand the coding one. This is the template, this is the mRNA that is what it does in transcripting the information from the DNA. So it has taken the information from the DNA now. We have ribosomal RNA this actually forms a core of large molecular machine which makes the proteins.
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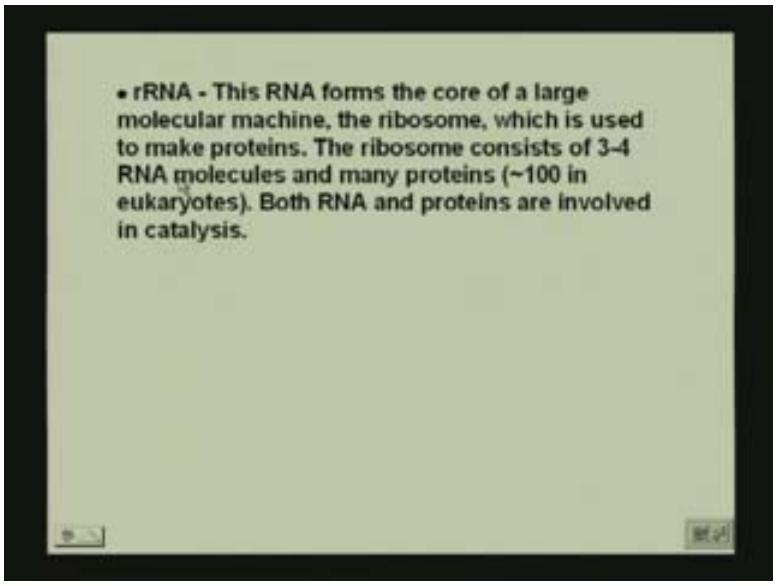

It has a huge number of proteins not all of the structures have been solved yet. And remember you looked at the RNA structure where you had part. What did you have? You had part helices, part bulges and so on so forth, this looks a lot more complicated when we look at the ribosomal RNA.
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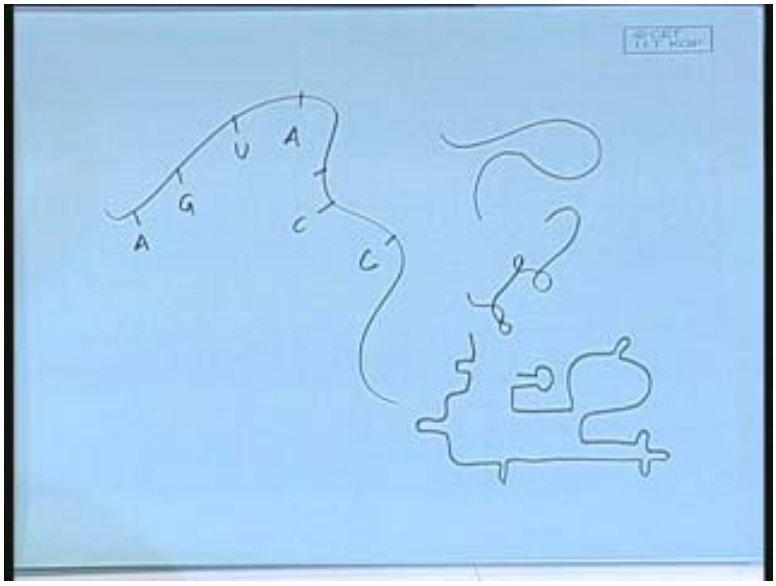

You will have some bits and pieces like this and then you have loops like this. If you look at a picture of, I couldn't get a proper picture. So it will look like this something and they are huge. They have associated with them proteins. These are ribosomal RNA's are actually formed in the ribosomes where they are used to make the proteins. We won't see actually the process of making the proteins but it is extremely interesting. If you go through the internet and you type in protein animation. Just animation of the synthesis of proteins, you can see how the mRNA and the rRNA and the tRNA which we speak about in the women. All walk in tangent to get you the peptide, poly peptide chain.

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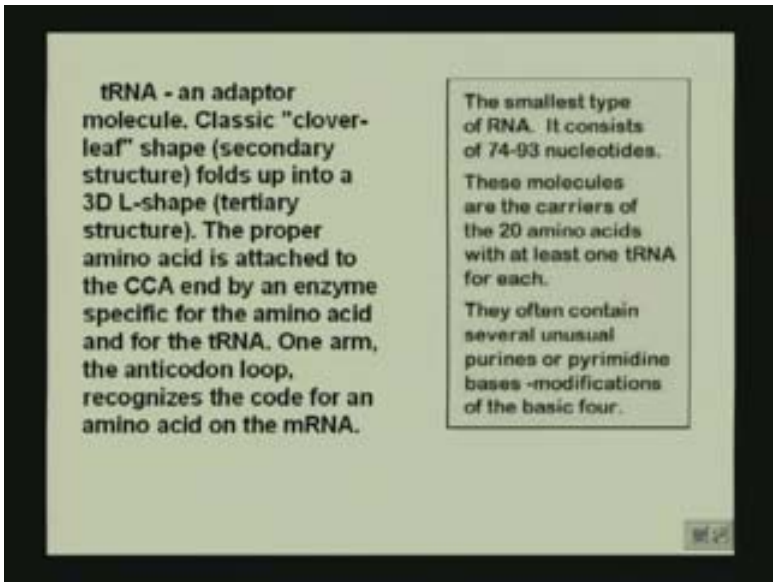

The transfer RNA is smallest type of RNA that has just 64 to 93 nucleotides. It has what is called a clover leaf structure which I will show you in a moment and it is folded up into an L shaped tertiary structure. We have attached to each tRNA a specific amino acid. This amino acid is required for the protein chain to grow. The information present in the tRNA will tell us from the genetic code which amino acid it is supposed to bring to attach to the poly peptide chain I will show you that in a moment.

What we have here is, we have the smallest type of RNA, the tRNA. It has its classic clover leaf structure. This is what is called the classic clover leaf. This clover leaf has 1 2 3 looks like that. What do we see here a specific complementary base pairing, but we have these bulges at the two ends. This is what is called as the anticodon. What happens here in the anti-codon is this is the part that links on with the RNA to get the information as to which poly peptide chain or which amino acid has to be brought.

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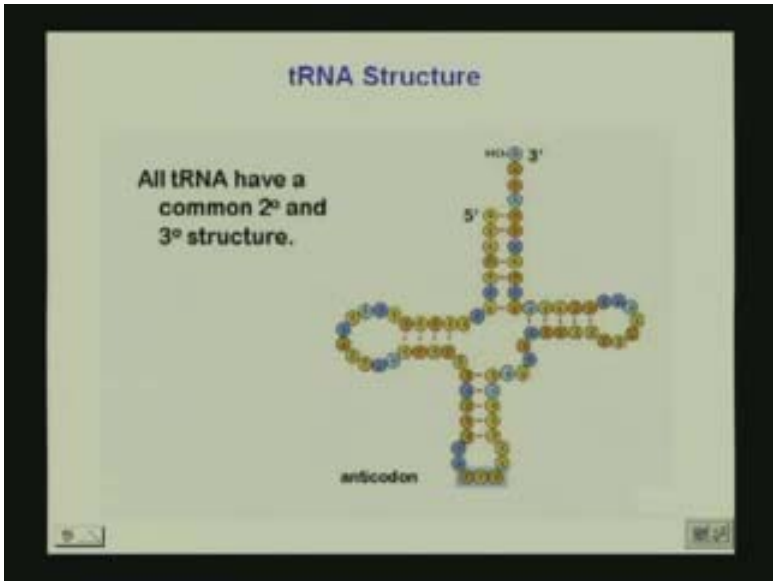

Now what I want to show you is, let me just go back here once. This is what is called the genetic code. In the genetic code I will just show you what it means. We have something like this. This is the first base pair. Let me just get this straight here. We have T C A and G here. We have say T here we have again T C A G. We have C, again T C A G this is something that was found by Hargobind Khurana. What we have here is this is the first the second and the third. What is the first T T T? We have T T T, the second one will be T T C T T C and third is going to be T T A T T G. In this case we have T C T because the first one is T this is the first one this is the second one and this is the third position, so we have T C T. The next one is going to be T C C, this one T C A T C G and so on and so forth.

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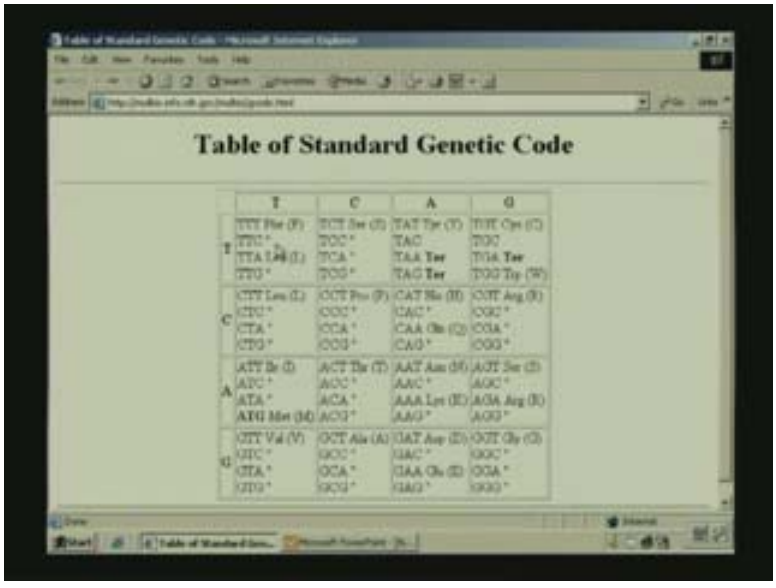

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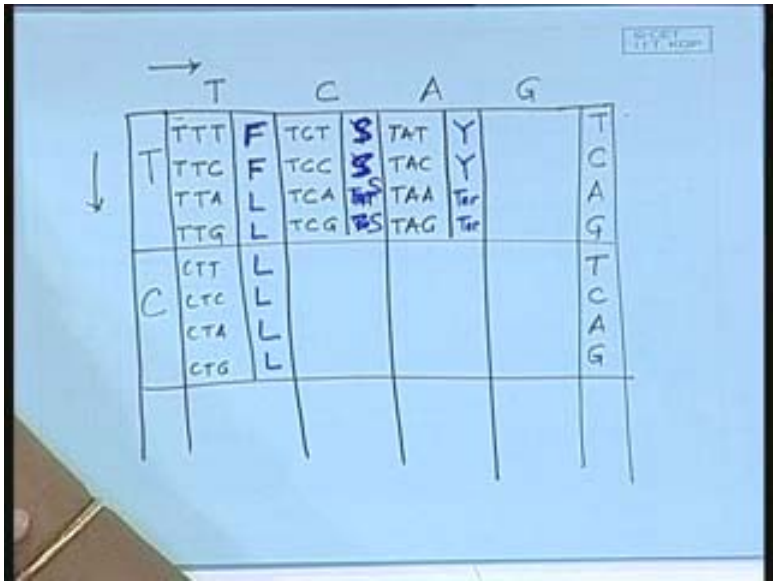

This is what your genetic code is, so this is CTT CTC CTA CTG. Now each of these codes for an amino acid. We have triplet codons. These are triplet codons. The triplet codons will code for an amino acid. These two code for phenylalanine, I think we should write this in a different color so that you can see it better. This code is for phenylalanine, these codes for leucine, this code is for tyrosine and this code is for tyrosine. This is actually your terminal codon. This is serine. All of these are serine. The A ones are your terminal codons. So you have TAT, TAC, TAA, TAG and what do we have? This is where we have tyrosine terminal.

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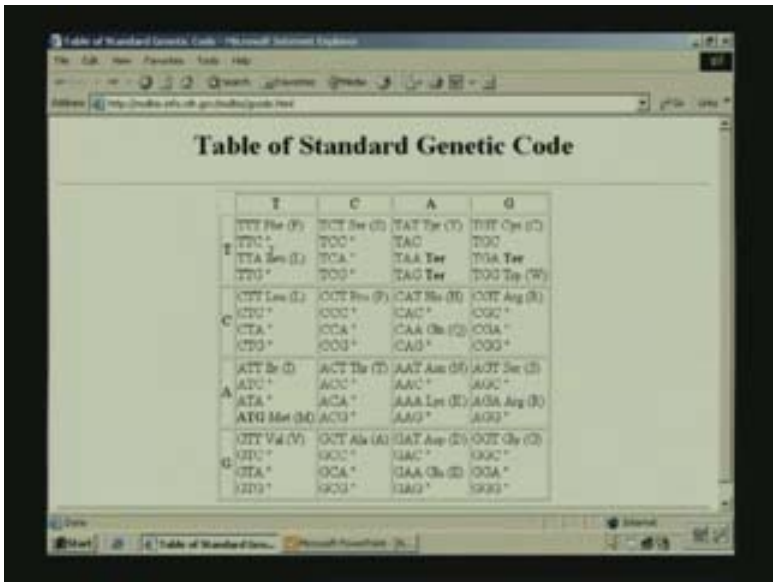

So you understand how many codes I am going to get like this, 64. They will code for 20 amino acids. We have an initiation codon and a terminal codon. This is how if we go back to what we have here; this is what we have seen if you can see this. Then we have you get this as I have just got this from the internet you have this coding for phenylalanine. This is for leucine and so on and so forth. The interesting thing here is that you see for this case, the third base actually does not matter. Why does the third base does not matter? If you look at the leucine codes just look at them, the CTT, CTC, CTA, CTG, all give you leucine.

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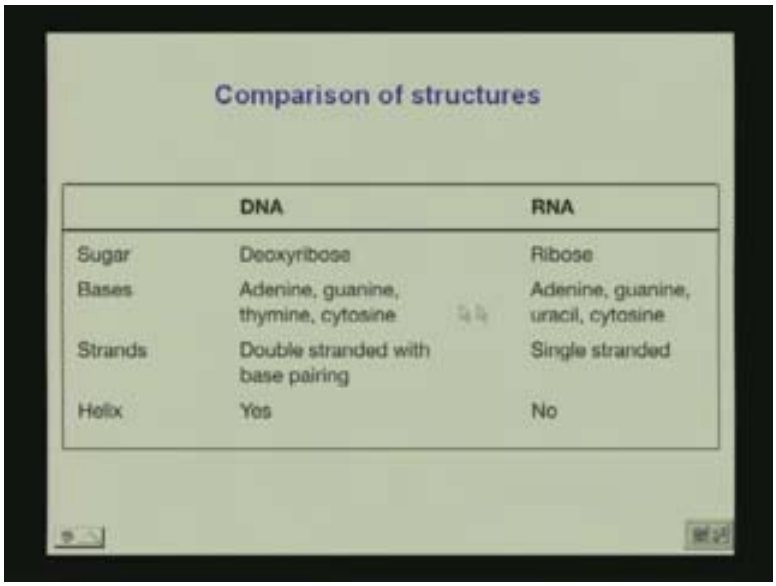

It means that this base may be something else. Where is this base? This base is in our part here. This is the triple codon. It is the anti-codon for that triplet that is for the specific amino acid. What did we see in the genetic code? We had the triplet that corresponds to an amino acid. That amino acid is what is used for your poly peptide chain or rather your protein synthesis. If we just summarize here in a comparison of the structures, we have the sugar for DNA, the deoxyribose and ribose for RNA. The bases are A G T C and here A G U C the strands are double stranded with base pairing here RNA is single stranded. This forms a helix, this does not.