Biochemistry
Prof. S. Dasgupta
Department of Chemistry
Indian Institute of Technology – Kharagpur

Lecture - 17
Nucleic Acids II

We continue our discussion on nucleic acids. Now what we learnt last time was how we have these specific bases, the purines and the pyrimidines interact to form with double bonded, hydrogen bonded structures, how they form complementary bases basically okay.

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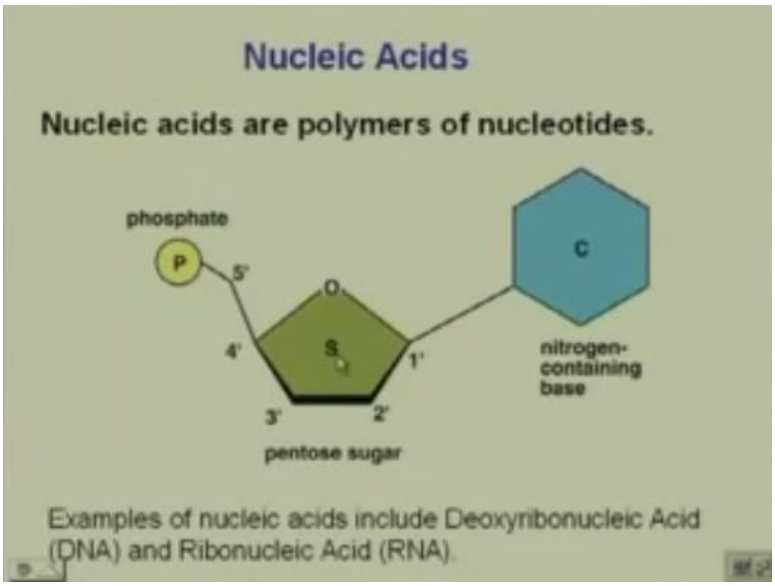

So what we have here is if we look at the nucleic acids we know that they are now comprised with this pentose sugar of phosphate and a nitrogen-containing base right and we know that this pentose sugar can be of two kinds, either deoxy kind or a ribose, a deoxyribose or a ribose depending of the type of nucleic acid that you are considering. Now obviously, we have these two types, the deoxy ribonucleic acid where what is missing at the two prime position, the OH is missing at the two prime position.

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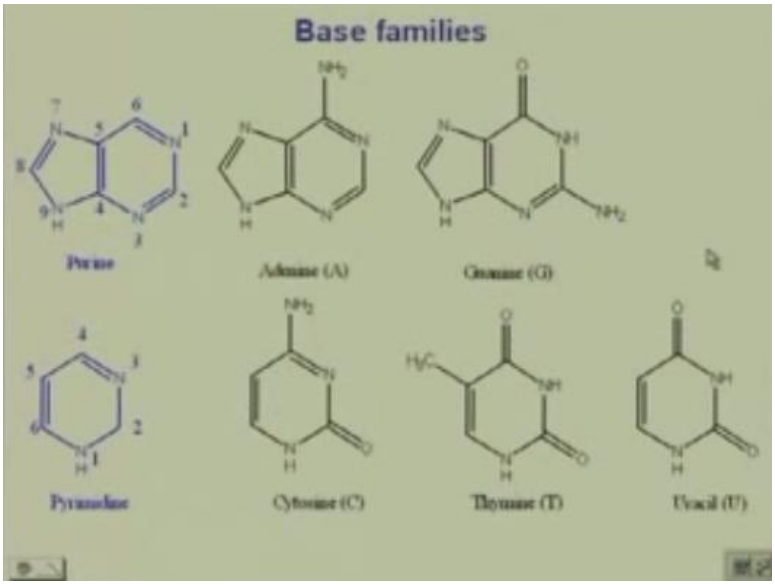

We have the sugar and the phosphate and the base families are the purines and the pyrimidines and what do they do; they interact with hydrogen bonding, a purine and a pyrimidines to form a two bases coming together in a hydrogen-bonded network.

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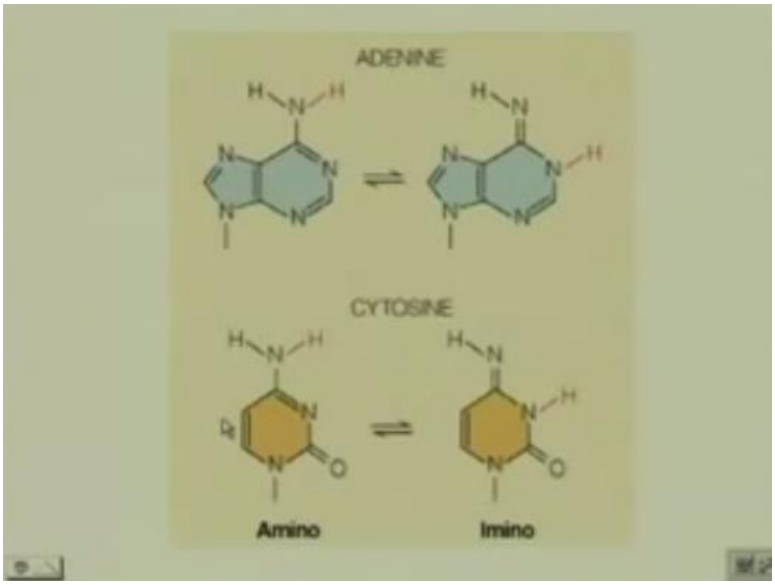

Now there is an additional factor that has to be considered here that is a tautomerisation possibility of the bases okay. Now if you look at the adenine consideration here; what do you have here, you have an NH2 group okay. Now what can happen to that NH2 group is this H can, you all know about keto-enol tautomerisation, what happens in keto-enol tautomerisation, what happens there, you have a C double bond O and that is converted to an OH from an adjacent HCH2 right. So you have a keto-enol tautomerisation.

Here we are having an amino type and an imino type okay, but the basic idea is the same way

you are shifting this hydrogen in the case of adenine to the adjacent nitrogen. In the keto-enol tautomerisation, what do you do, you have the H shifted from the carbon to the oxygen right, where you have a keto-enol tautomerisation, but what we are talking about here is an amino and imino case, which is possible in adenine and cytosine right.

So we have the adenine structure. Now where is this attached, this is attached to the sugar ring and what type of a bond is this, beta N glycosidic bond okay. So we have the adenine and 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 okay.

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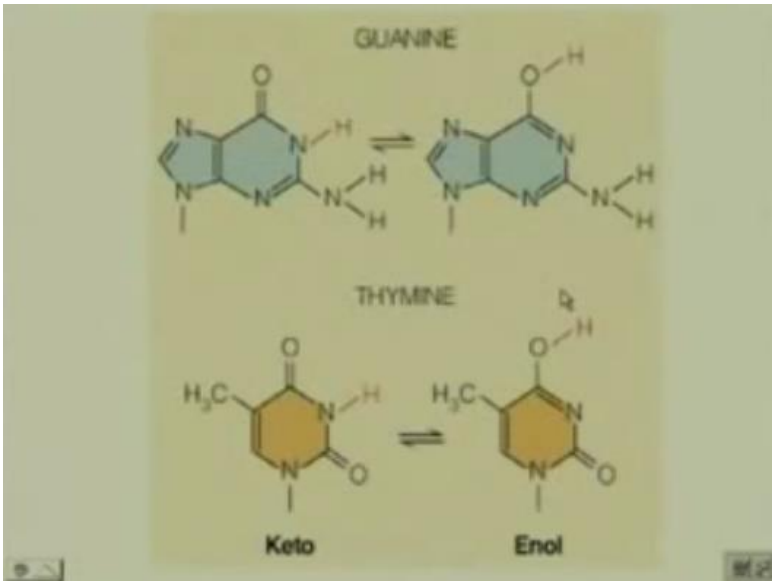

So we have now two other bases that we also have to look into, they are guanine and thymine, but what is the type of tautomerisation here, it is a keto-enol type of tautomerisation okay.

So when we are looking at the bond here; what do we have, we have the double bond O go to an OH. So that is the difference in the type of tautomerisation that you can see in A and C, so what is the type of tautomerisation you see here, it is an amino-imino type of tautomerisation where your hydrogen is shifted from the amine group to form an imine okay.

So we have this H shifted, this H shifted in cytosine. So when we have A and C, we have imino type of tautomerisation, but when we were talking about guanine and thymine, we have keto-enol type of tautomerisation, where the keto group here becomes OH in guanine, in this purine and in thymine, the pyrimidine, again we have the double bond O, the adjacent H goes

to the keto C double bond O to form the enol okay.

So this is, you understand that since we are talking about the hydrogen bonding between the bases, this becomes an important factor okay. This is why we have to consider the tautomerisation 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 a hydrogen bond feasible in a sense okay.

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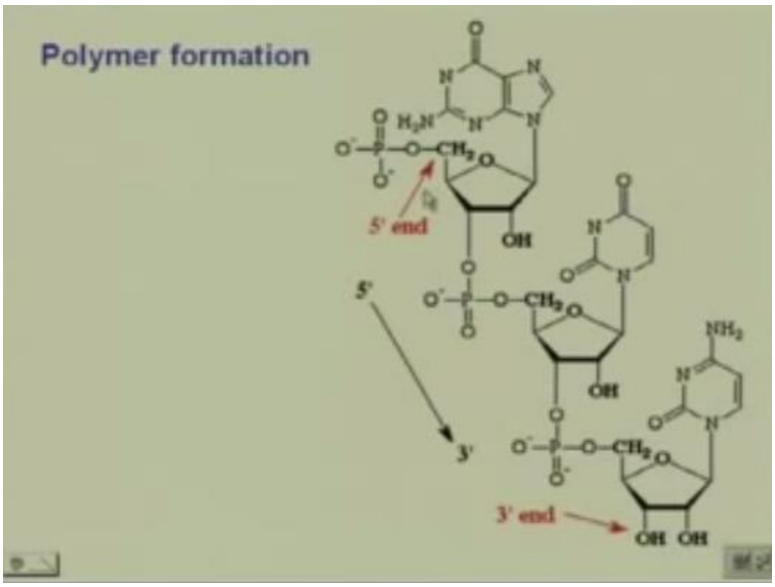

If we look at the linkages, I will show you the hydrogen bond formation in a minute, but we considered the polymer formation in our last class and what did we find, we find that this 3 prime end, what happens to the free OH, what is this free OH do, it goes and attacks the triphosphate, the alpha phosphate of the triphosphate releasing the pyrophosphate and attaching the next nucleotide.

What are we doing then from these mononucleotides we are building up our polynucleotide okay. So we go from the 5 prime to the 3 prime end and we will see how the other strand of DNA is the opposite of this okay. The 5 prime is at the bottom here and the 3 prime up there and then we have the complementarity of the strands that is what we are going to look at today.

Now in this what we do we have common here, I mentioned this last time, we have what is this orientation that has be 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, about the beta

glycosidic bond. Remember we mentioned about the types of flexibility, the types of angles of rotation that we can have right.

We can have a (()) (07:08) rotation about this beta and glycosidic bond that is going to render the base either in the syn orientation or in the anti orientation and usually we have the anti orientation to prevent any steric clashes and also to assist in the hydrogen bonding in the complementary base of the other strand. So the features that we are looking at here is the strand build up from the 5 prime to the 3 prime end, the addition of a mononucleotide in each case to form the polynucleotide.

Now what we know is each of these have a common backbone, the sugar phosphate backbone. So usually when we represent it, we have a 5 prime end and a 3 prime end okay and this is the 3 prime, 5 prime phosphodiester bond. What do you mean by that, this is the 3 prime position and this is the 5 prime position, so when we mention the phosphodiester bond, it is a 3 prime, 5 prime phosphodiester bond, is that clear okay because what we are going to look at later is we are going to look at cleavages okay.

How there are certain enzymes that will break only this bond. There are certain enzymes that will break only this bond, so there is 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 right.

We have studied the mechanism of ribonuclease before, what did that work on, that worked on RNA ribonucleic acid. So when we are going to cleave or we are going to look at the cleavage of the nucleases, if it is going to cleave ribonucleic acid then we will have a ribonuclease. If it is going to cleave a deoxyribonucleic acid, what are we going to have, a deoxy ribonuclease as simple as that okay.

But what is the structure that I have here, is it a DNA or an RNA, it is an RNA why because the OH is there as simple as that okay.

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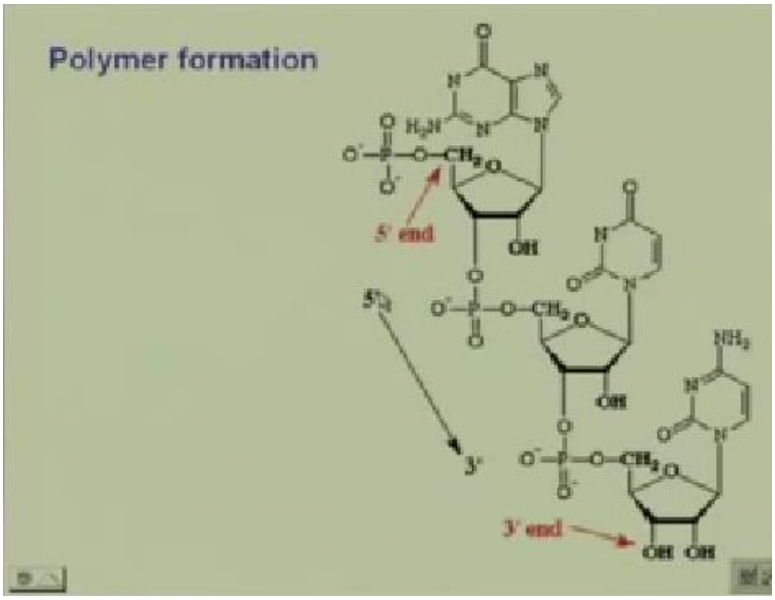

So now when we have a representation you know what the 3 prime, 5 prime phosphodiester bond means. This is the phosphodiester bond 3 prime, 5 prime. If you have an addition, it is going to be added on this side right. Just similar to how we had the polypeptide nomenclature. You have the amino terminal and you have the C-terminal.

Here you have what is called a 5 prime end and a 3 prime end. Now usually you know that you have a sugar and you know that you have a phosphate. So even though this is a certain representation that is easier to understand how the cleavage actually occurs. You usually do not even right this. You just right the bases like I mentioned last time instead of the polypeptide sequence with the peptide bonds and so on and so forth.

You do not right the peptide bonds. You just right 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 nucleic acid. You know that they are all linked by 3 prime, 5 prime phosphodiester bonds. So there is no need to write the sugar or the phosphate. So all you essentially do is simply list what is called the base sequence instead of just like you would list an amino acid sequence.

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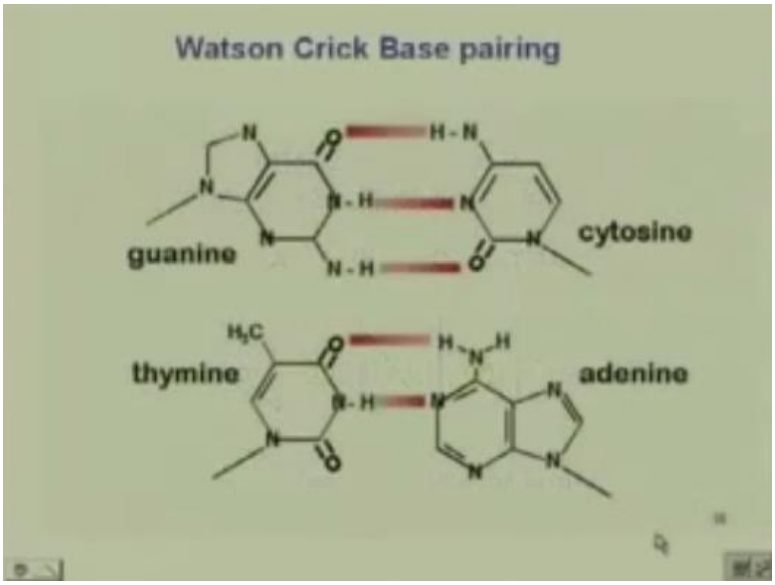

This is something that we looked at last time where we have a guanine and a cytosine; we have a thymine and an adenine okay and we have in this case three hydrogen bonds possible. In this case, we have two such hydrogen bonds possible.

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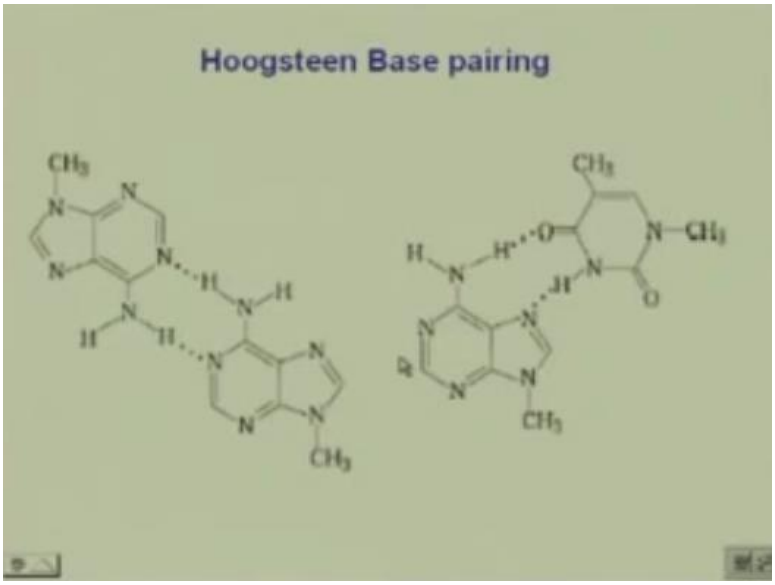

We also looked at the Hoogsteen Base pairing where we have a different phase for the base pairing and we also have in this case, what is this, we have two purines linked together where in the normal case and an Watson Crick case you were always have a purine linked with the pyrimidine. Here again we have a purine linked with the pyrimidine.

If you notice what we see is this six-membered ring of adenine is involved in the Watson Crick Base pairing.

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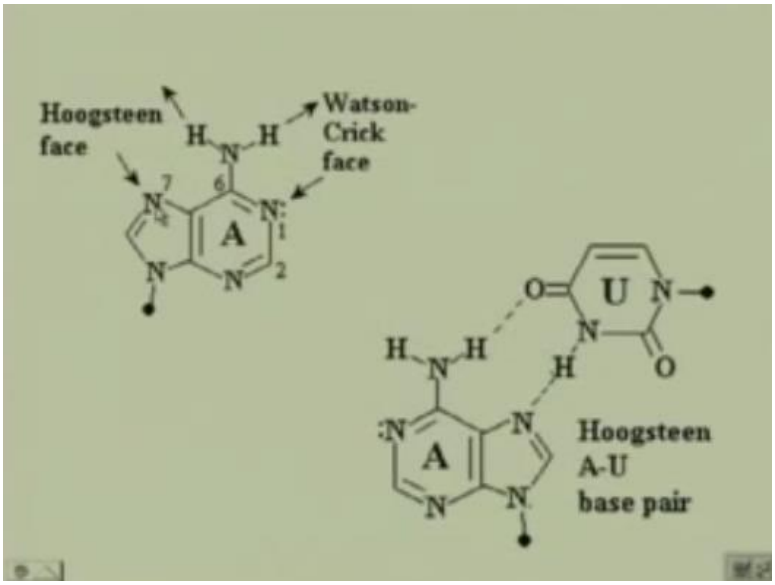

Whereas in the Hoogsteen pairing, we have the one nitrogen of the five-membered ring also take part in the hydrogen bonding between another base okay. So this is what is called the Hoogsteen face and this is what we called the Watson Crick face and this would be an example of AU pair where would you see an AU pair, in RNA because uracil is a base in RNA.

So when we are looking at a hydrogen bonding situation like this, we know we are looking at RNA and we know we are not looking at a Watson Crick Base pairing because you can straightaway see that the base pairing is between the nitrogen of a five-membered ring and a nitrogen of the amino group of the six-membered ring. So as soon as you see this, you know this is a Hoogsteen Base pair okay.

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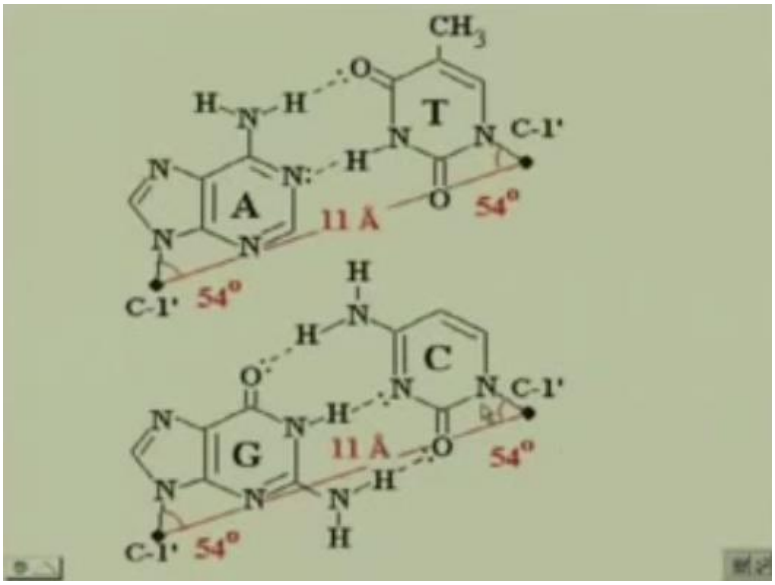

Now this is what I mentioned quite quickly last time, but it is extremely important in the two strands coming together. What do we have here; here we have a Watson Crick Base pairing. Why because we have the six-membered ring of the adenine of the purine involved in hydrogen bonding okay. So this is Watson Crick hydrogen bonding.

We have the two hydrogen bonds between A and T. So 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 C1 primes of the purine and the pyrimidine is where it is actually 10.85 angstroms, but you could call it 11 angstroms. This distance is constant. It is also the same when you link G and C together.

Now 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. So we have the pairing come like this and then we have a twisting of the helix, the double helix that it is called.

What is going to happen is 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 right because you have a constant distance of the sugar phosphate backbone, how do you get that, it is because these two base pairing is coming together are giving you that constant distance of 10.85 angstroms okay.

That is extremely important you understand in its structural aspects. So what we have here is in the hydrogen bonding where we have two hydrogen bonds for the A and T case, we have 11 angstroms. Again when we have the hydrogen for this purine pyrimidine set, we also have 11 angstroms.

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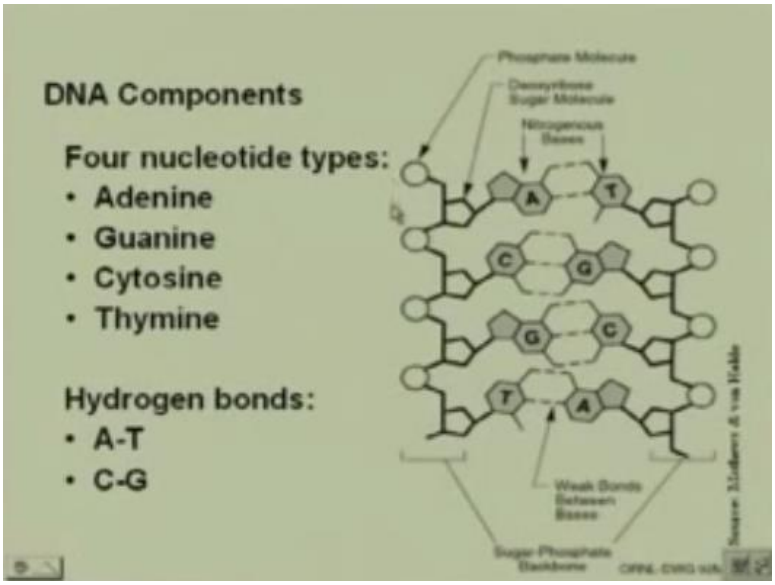

So what we have is, in the DNA components we have our two strands. What is this, this is the sugar and these circles are the phosphates okay. So we have the sugar phosphate backbone and sticking out from the sugars are all the different bases and we have the complementary bases on the other side and we know now that the distance between the C1 of this and the C1 of this is 11 angstroms.

So what do I have, I have a constant distance. So I have a parallel orientation here. I have absolutely parallel set of backbones, is that clear okay. Why do you have this, whether you have the A-T set or the G-C set, it is the same because the distances are 11 angstroms and because you are linking a purine and a pyrimidine. You are linking one fused six and five membered ring and you are linking it with another six-membered ring and the hydrogen bonds are between the A and the T, two hydrogen bonds and three hydrogen bonds between the G and the C.

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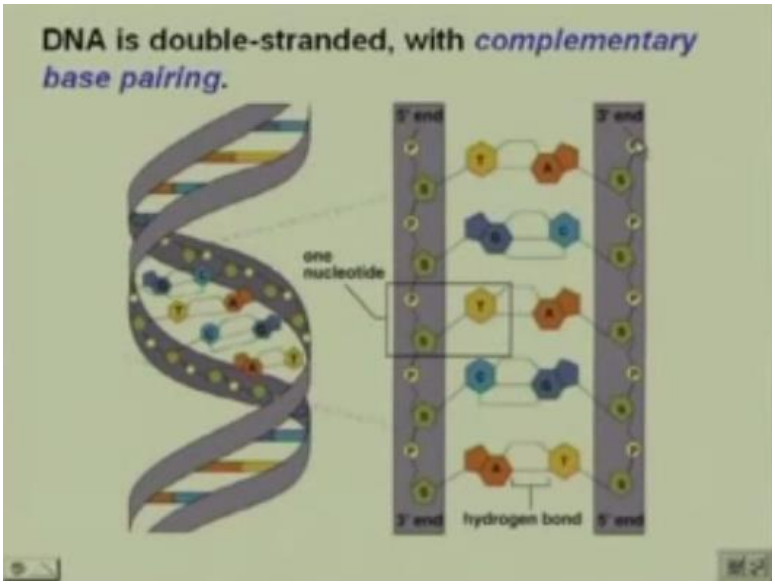

So this is what we have. This is what is usually called ladder conformation because it looks like a ladder. So we have a ladder conformation and the 5 prime end to the 3 prime end is what is actually synthesised okay. This is called the coding strand, the sense strand rather. This is called the antisense strand. It goes from the 3 prime to the 5 prime okay.

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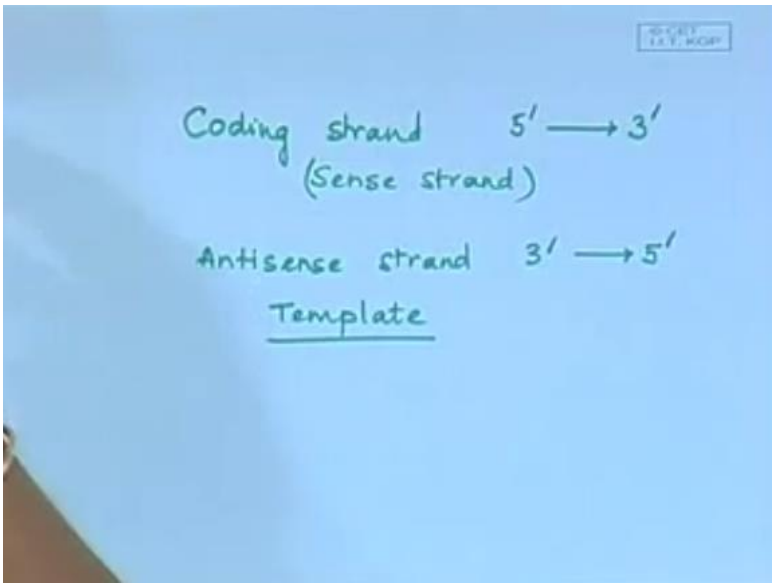

So let me just reiterate that. We have a coding strand that goes from the 5 prime to the 3 prime. This is also known as the sense strand because that actually has the information. What information am I talking about here, what information does this DNA strand have, it has the information that is going to go from the DNA to the RNA that is then going to decide what protein has to be made okay.

So this has the sense in it basically, the first strand here. Then we were talking about the other

strand, which is the antisense strand. The antisense strand, it goes from the 3 prime to the 5 prime and this is also known as a template strand because it provides the template for the M RNA. The messenger RNA, which we will see in a moment okay.

So if we go back to the slides here, we have the ladder conformation here where we have one nucleotide specified, what does this nucleotide have, it has a sugar, it has a base, it has a phosphate okay and when we consider the double helical structure, this is the double helical structure, where this parallel, the set of parallel strands are twisting around one another okay.

So what we have is we have a constant distance throughout and a twisting, so it is called double helical structure. We have two forms there twisting around one and other and what do we have we have complementary base pairing, two for two hydrogen bonds for A-T, 3 of G-C.

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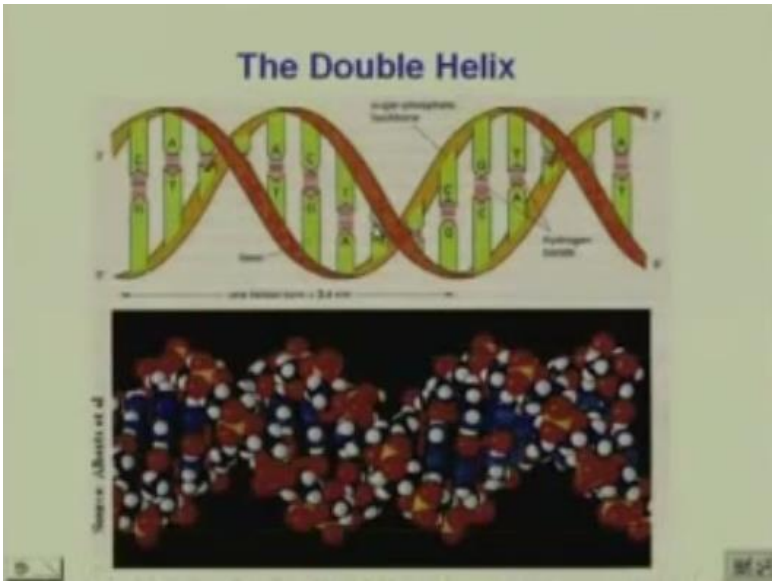

So this is what it would look like. We have a sugar phosphate backbone and we have the bases. Now when we look at this double helical structure, we see that there is a large gap here, this gap, there is a large gap here alternating right, because of the orientation other way the structure is we have these grooves. These are called grooves, this is what is called the major groove okay and this is called the minor groove.

So we have a major groove of DNA, we have a minor groove of DNA and 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 DNA depending upon what sort of interactions and

obviously the sizes of the compounds of the molecules that we are talking about. So if we look at the structure, we have a major groove of DNA and we have a minor groove of DNA okay.

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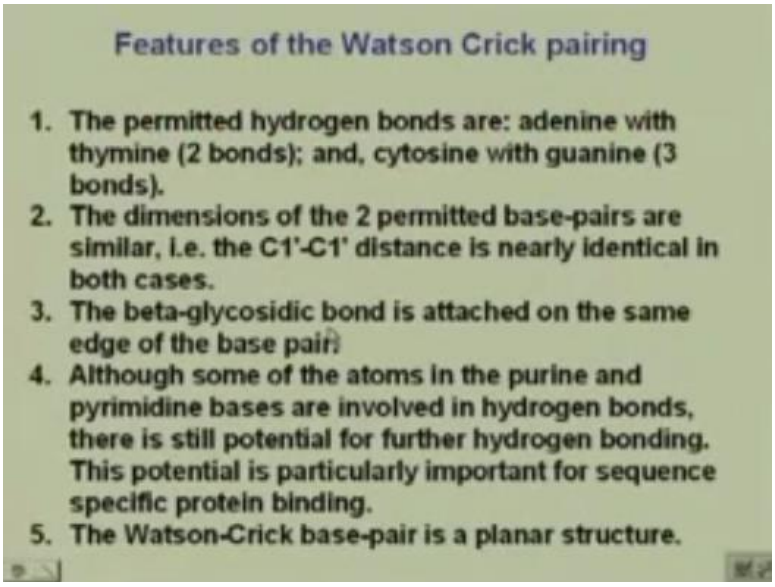

So now I have just listed here the features of the Watson Crick pairing because it is going to help us in looking at the distances. We have two permitted hydrogen bonds between adenine and thymine, three permitted hydrogen bonds between cytosine and guanine. This is something we have seen.

The dimensions of the two permitted base-pairs are similar; the C1 prime to C1 prime 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 pairing, you recalled that there are other nitrogens also available.

For example, the Hoogsteen pair looks at another nitrogen all together right. So it means, there is still potential hydrogen bonding partners available. Now this is important because later on these may be involved in interactions with proteins or interactions with other compounds okay and another thing that is important is that the Watson Crick Base pair is a planar structure and this is going to have certain implications in the stacking of the bases in the structure of DNA okay.

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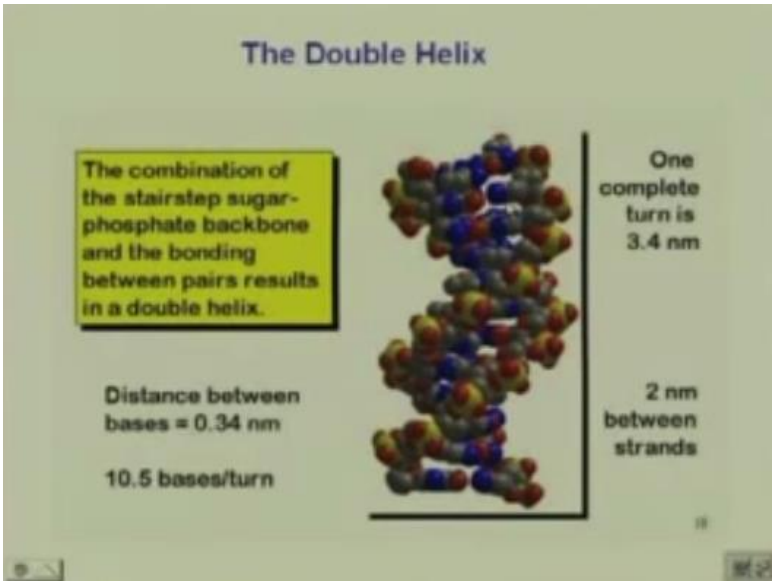

So these are the features we have gone through all of these features and we now know that the structure of DNA looks like this okay. So the double helix we have two nanometres between the strands. We have one complete turn that is 3.4 nanometres and the distance between the bases is 0.34 and we have a major groove and a minor groove. So these are the essential features of the double helix.

Apart from the Watson Click 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 were constant because the complementary base pairings are constant okay. So these are the features that we have to consider.

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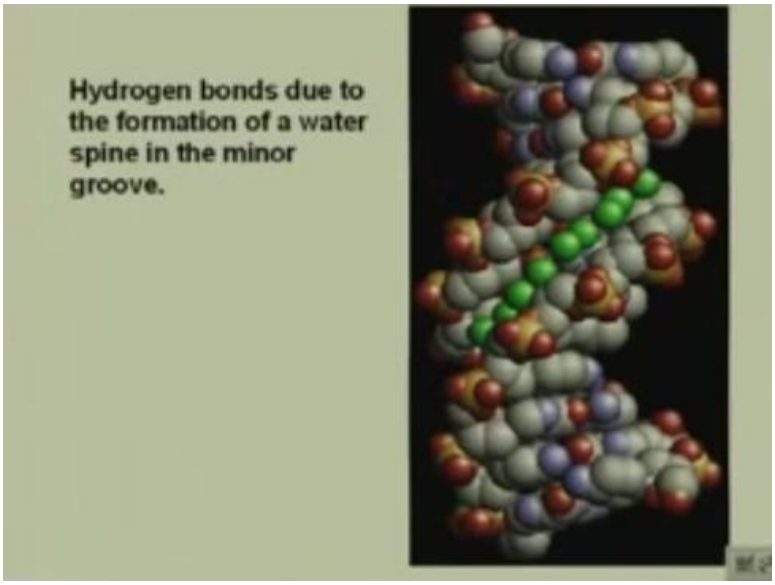

Another feature that we can look at here is the one this part on the right, what groove is this, this is the major groove and so this is the minor groove. Now if you look at these, these are actually water molecules okay. So there is other hydrogen bonding possibilities due to what is known as our water spine okay. The water spine that follows through the minor groove okay, so we have a spiralling water spine that goes to the minor groove of DNA okay.

The major groove actually is probably too large for this water molecule to sit in there and this is a part that also interacting with the other compounds and the other DNA protein interactions that occur okay.

How can we have these extra hydrogen bonds, what other units do we have, we have other heteroatoms present right. We have phosphates; we have the phosphodiester bond present right that has also has an oxygen, then we have the nitrogen of the bases also, but the bases are within so we can also have what is called intercalation okay.

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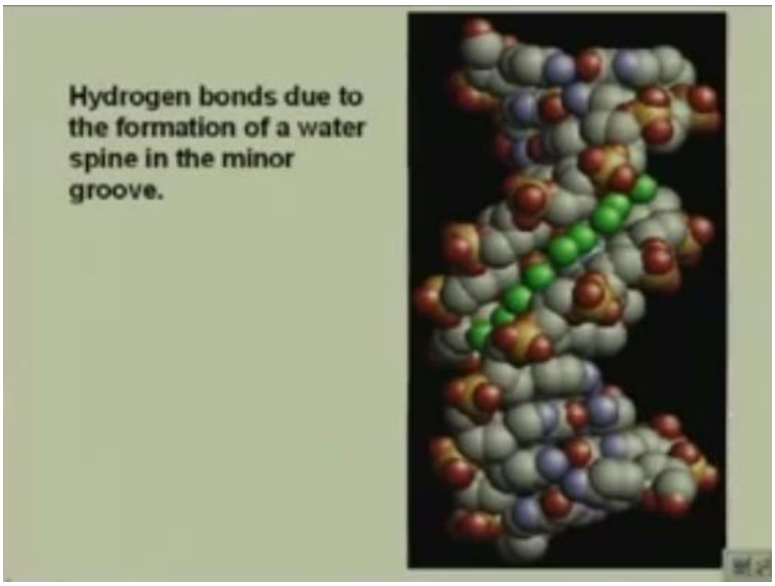

Now let me just show you where we can have intercalation okay. If we have the bases like, this you see how they are stacked on one another okay. So we have like a stacking part here okay. So when we have the stack of the DNA base pairs, we have them like this stack one another. You can have intercalation, what is intercalation mean something that is going to set itself in between.

Now this is very important if you design any say drug that is going to cleave the DNA okay. Any drug you want, now 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 right. That is a lot of research activities going on here, going on even in this department.

What we have here is you have intercalating agents. When we speak of intercalating agents we are talking of agents that are going to disrupt certain interactions. What happen 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 is 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 it will then prevent the proper protein expression okay.

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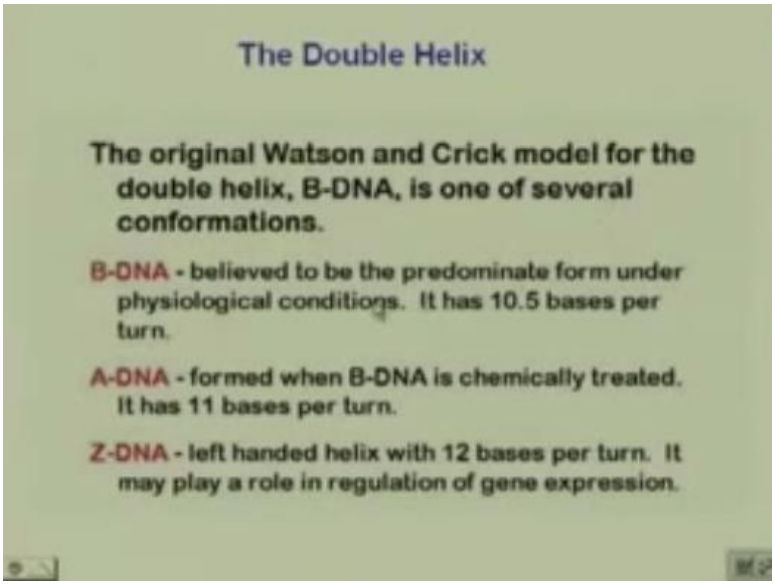

Now there are three types of DNA, the original Watson and Crick model, we just completed 50 years. It was first discovered in 1953 and the paper is available on the net where you can look at the original paper of Watson and Crick that came out in nature.

You have B-DNA that is actually the most prominent form of DNA. It has 10.5 bases per turn. What are we talking about here, we are talking about a 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 alpha helix, it is similar to something like that.

When we have the A-DNA, this is formed when B-DNA is chemically treated. It basically does not have those water molecules in the water spine that 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. So these are the three forms of DNA and the most common by far is the B-DNA okay.

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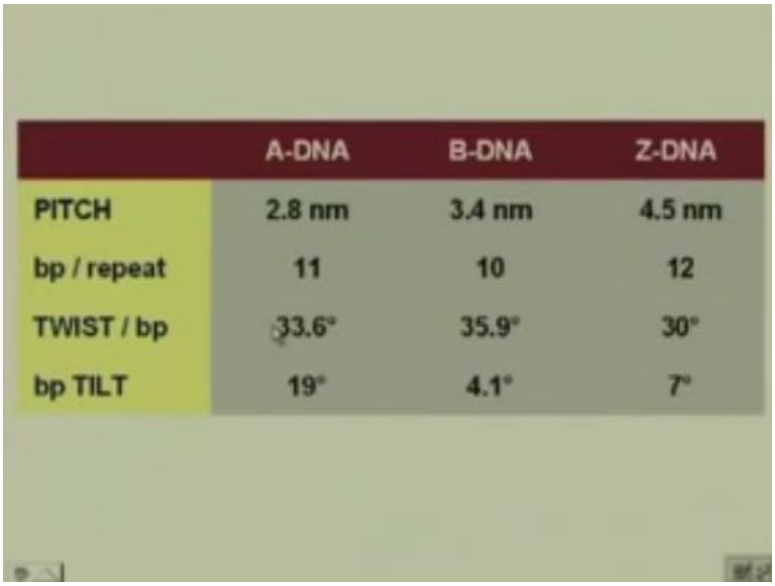

	A-DNA	B-DNA	Z-DNA
PITCH	2.8 nm	3.4 nm	4.5 nm
bp / repeat	11	10	12
TWIST / bp	33.6°	35.9°	30°
bp TILT	19°	4.1°	7°

These are some of the features of the A-DNA, B-DNA and Z-DNA. We have a PITCH, what is a PITCH, the distance covered by one rotation. So the A-DNA PITCH is 2.8 nanometres. The B-DNA is 3.4 nanometres and the 4.5 nanometres for Z-DNA. The base pair repeats our 11 bases per turn, 10 bases per turn and 12 bases per turn.

The twist per base pair, you realise that there is a slight twist has you have the base pair like you would also have angle disposition for the alpha helix. These are the twists per base pair and we have a slight base pair TILT, which is not very much in the B-DNA just 4 degrees okay that is a slight base pair TILT.

So the three DNAs, we have the B-DNA, the A-DNA and the Z-DNA and the most structure that we will be considering is just a B-DNA okay. That has about 10 base pairs per turn, 3.4 nanometres and a base pair TILT of 4 degrees.

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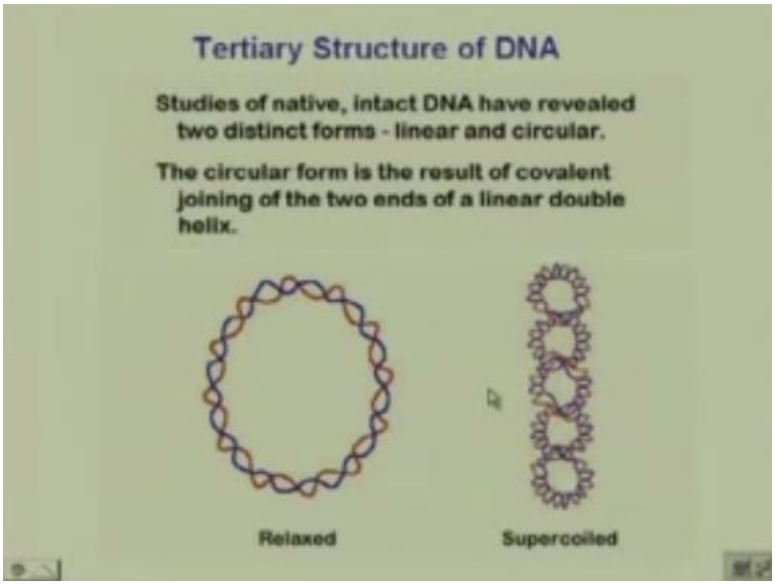

So that the double helix of DNA is actually well, it would not be a secondary structure that is the structure of DNA, but there are other forms of DNA also. Studies have shown that the native intact form of DNA can be linear and circular. If you look at the double helix here, if it goes straight up and straight down, we would have a linear structure. Now what happens is if the two ends are covalently joined together okay. If we chop this up, we are going to get a linear form right.

So when we have a covalent joining of the two ends of a linear double helix, we obviously will get a circular helix okay. Now the circular helix remains actually in these two forms. This is the tertiary structure of DNA. We have a relaxed form and we have a super coiled form. Now in the super coiled form, there are certain terminologies that are used.

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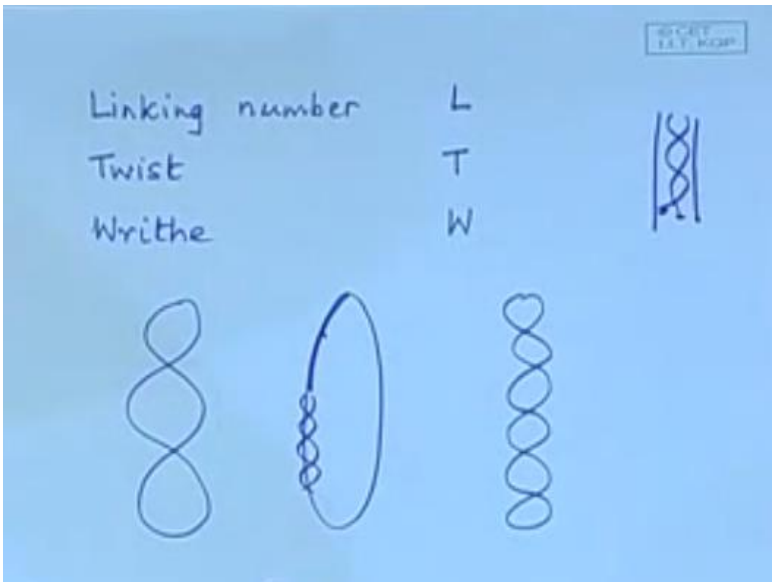

Something that you just probably need to know, so that we have a Linking number, we have a Twist and we have a, what is called a Writhe okay. This is referred to as L, T and W. What happens here is you have something like that okay. That is formed from this. You can even have this go even further okay. So you are basically going to have, now you have to remember that each of these is also a double stranded part. This that I have drawn here is actually this right.

It is the linear part of the DNA that has covalently linked the ends to form this. So this is actually something like that right, which you have joined together to form this circular DNA, that has then further twisted itself right this like a ringing motion that you have when you suppose you are squeezing your clothes or something okay.

So you would have a Link, Twist and a Writhe, but the reason why I am telling you this is when we consider the tertiary structure of DNA, see as you combine this, you can get smaller and smaller parts, I mean structural aspects of DNA. So what you have is this is useful for the storage of DNA. You cannot have the linear strands all around right.

So what happens is you have this super coiled DNA that is actually the way you would have the DNA being stored okay because the DNA has to be stored, there has to be, this DNA get to add in a transfer its information to RNA and this information has to be stored in the DNA okay and because this linear strand does not remain as such, we have what is called super coiled DNA okay.

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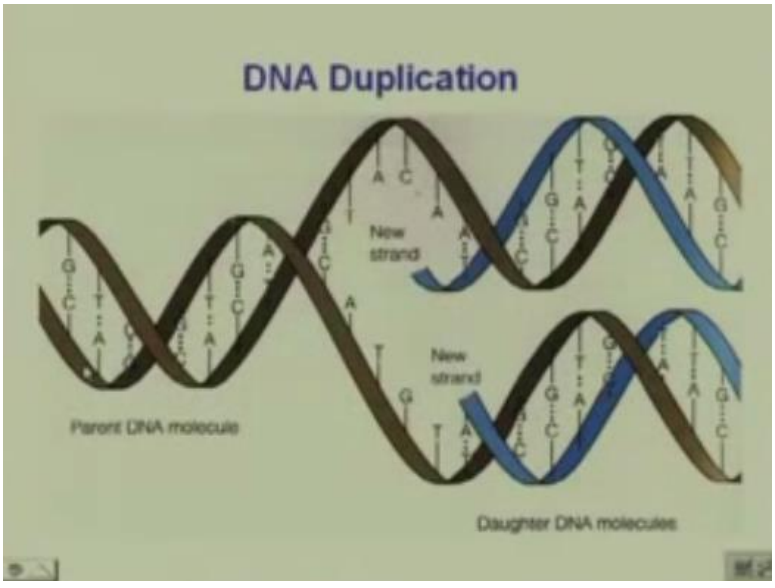

This is when you have DNA duplication. You have these two strands what is this, what is this region, this is the major groove of DNA, this is the minor groove of DNA right. When we have DNA duplication, parts of the strands unwind okay and we have the ones in blue here are the dotted DNA molecules okay. So what is happening here, you again have a similar strand form here, if this is A, what was it originally linked to in the DNA double helix, a 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, do not I have a replication, it is I am just doubling up the DNA that I has, so it is a duplication okay while duplication was probably the correct terminology that should be used. So we have a duplication of the DNA, so where I had one strand now, I have new strands right. So I have my daughter DNA molecules also formed from the parent DNA molecules okay.

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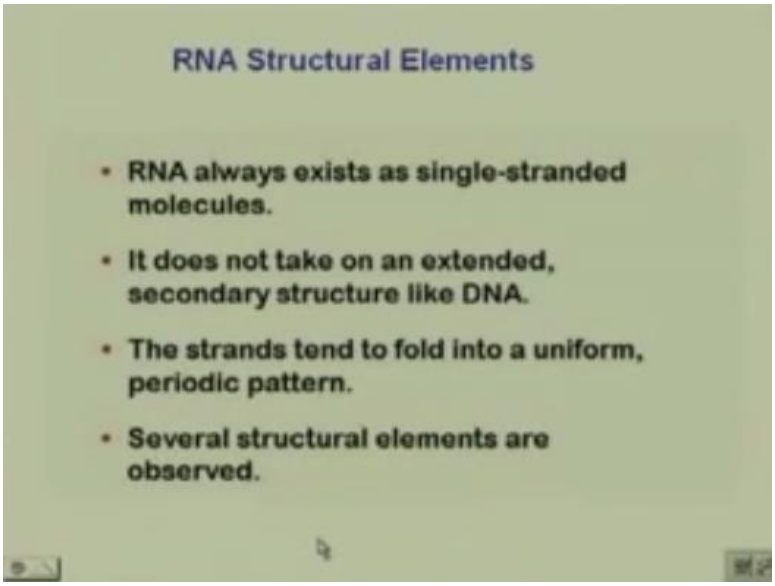

Now RNA now considering that the DNA structural aspects, we always have as a double helix. In RNA, it exists as single stranded molecules. These single stranded molecules usually do not take on an extended secondary like DNA in the form of a double helix. So you understand that in this case, there is no necessity for a complementary base pairing right. 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 all observed. We have what are called bulges and helices so on and so forth, which we will see in a moment. But the basic difference is here are that we do

not have an extended linear double helical structure like DNA has. It usually is single stranded and it falls and while it falls, it forms different type of structural elements. What are these, these are Hairpin turns.

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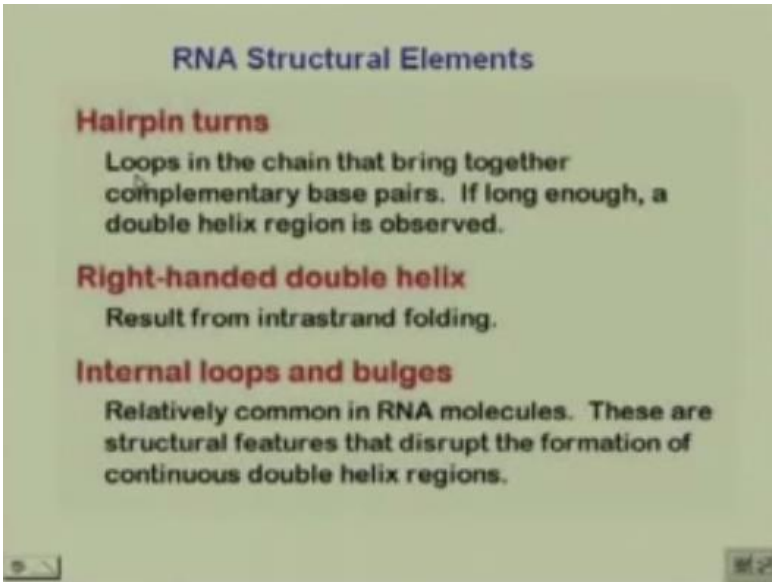

Hairpin turns are loops in the chain that bring together complementary base pairs.

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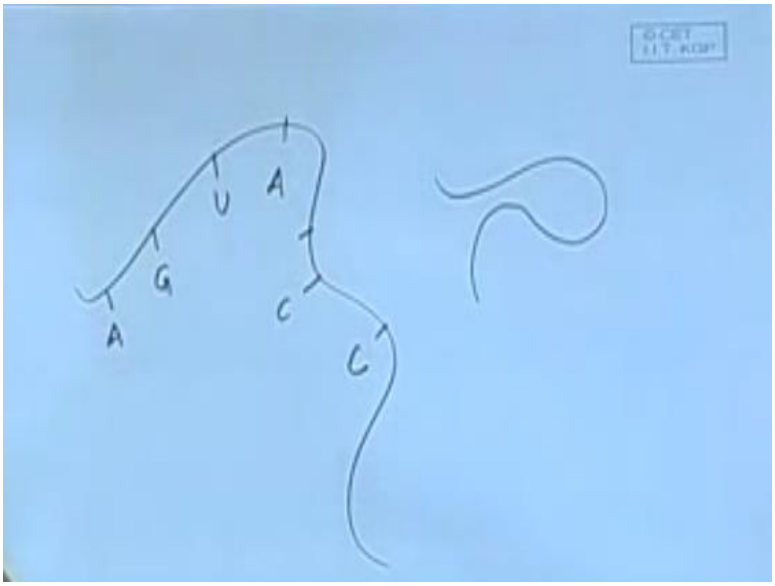

So when we are talking about RNA actually, we have a strand, a single strand oaky. I may have A here, a G, a C here, a U here, and another A here and so on and so forth, a C here. So may happen in certain cases is we know that this G forms hydrogen bonding with C okay. So in some cases, we may have complementary base pairing. What is that going to result in, it is going to bring part of these two structures close to one another.

So you are going to have probably something shape like that okay. So it is not as regulars what you see DNA at all okay. It just parts with some pieces of the structure coming together into forming different types of structural elements that either what are called Hairpin terms, Hairpin terms, 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 and this is because you do not have any complementary base pairing there okay. So if you look at the structure, it something like this.

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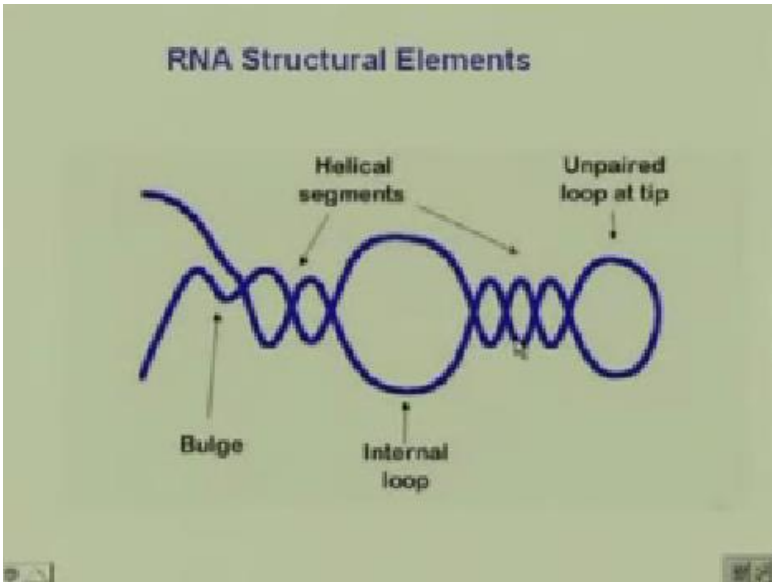

We have a bulge, we have an internal loop and why do we have this internal loop because we do not have any complementary base pairing possible here. We cannot helical segments here, we can have an unpaired loop at the tip right. So we have partial helicity here and we have bulges, it is probably such so. Now you understand in these cases, there is a possibility for Hoogsteen pair to occur right, which is unlikely in the Watson Click 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. For the DNA double helix to form, there has to be this constant distant of 11 angstroms between the C1 prime, atoms in the double helix, but there is no such restrictions here in the RNA right. So we have these single stranded RNA, but just have all this helical segments and loops in the bulges and so on and so forth okay.

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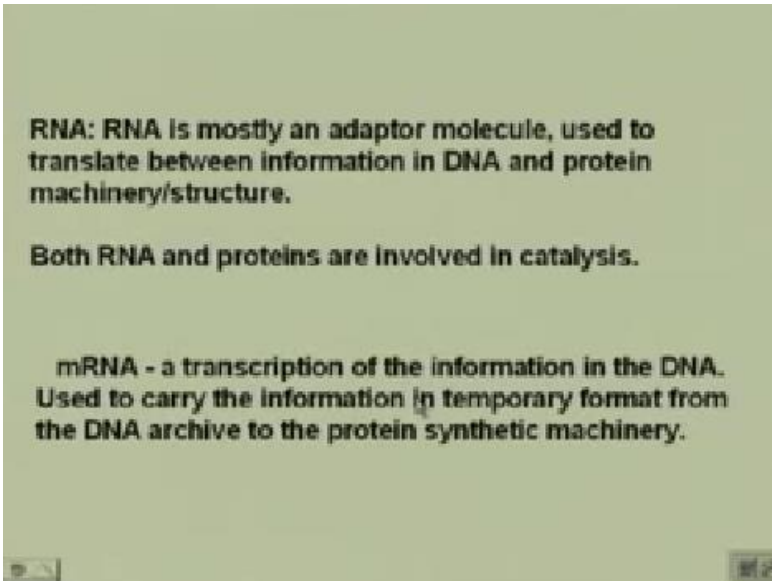

So RNA is basically an adaptor molecule, it translates from information in DNA and the protein right. So when we go from DNA or RNA, it is called transcription, RNA to protein is translation. Now we have three types of RNA. This is something probably that we studied in school. You have messenger RNA. Messenger RNA is a transcription, the process of DNA going to RNA is called transcription and this transcription of the information of DNA and it carries the information in a temporary format from the DNA.

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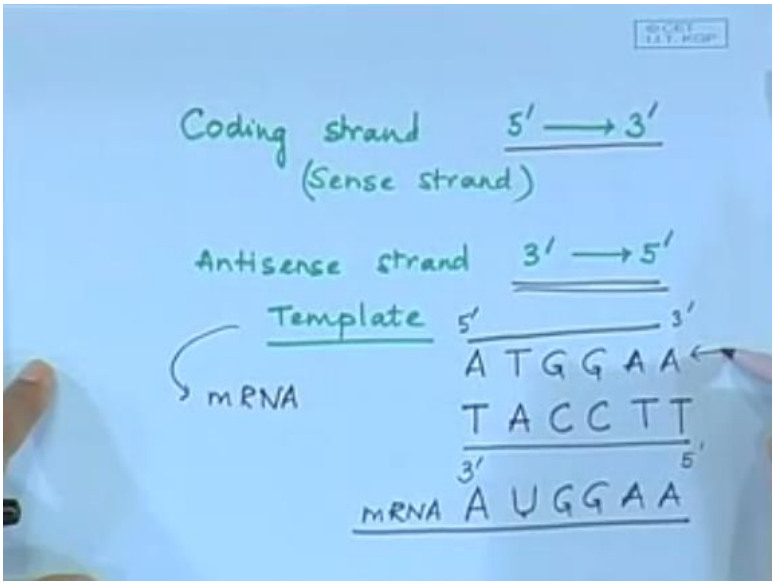

Now how this occur, if we look at the previous thing I was showing you here, this coding strand, suppose we have this from 5 prime to 3 prime, the antisense strand which is the template strand, which is used by MRNA is the 3 prime to 5 prime strand. What happens in this case, say our coding strand is A T G G A A something like, then what is the antisense strand going to be, what I am going to have here, T A C C T T right.

So this is my sense strand that goes from 5 prime to 3 prime. This is my antisense strand that 3 prime to 5 prime, then I have my MRNA, which actually is linked to the antisense strand. So what is the code for the MRNA going to be, what is that going to be it because it is going to be complementary to this now. So what I am going to get A then U G G A A right. Why U because now I am speaking of MRNA.

So now when this is going to form the next, so per this information it has taken from this right, you understand that. This is the sense strand, the coding one, this is the template, this is the MRNA okay. That is what is it does in transcripting the information from the DNA. So it has taken the information from the DNA now okay.

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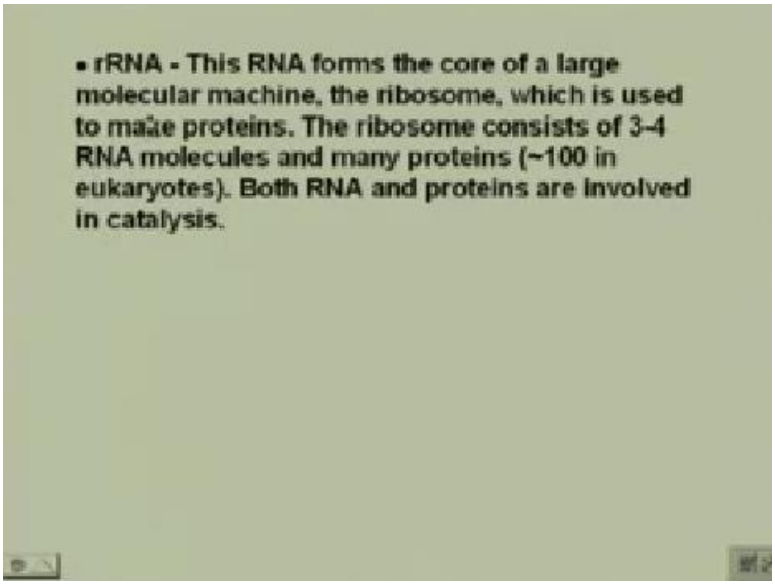

So we have ribosomal RNA. This actually forms the core of a large molecular machine, which makes the proteins okay. It has a huge number of proteins, not all of the structures of this have been solved yet okay.

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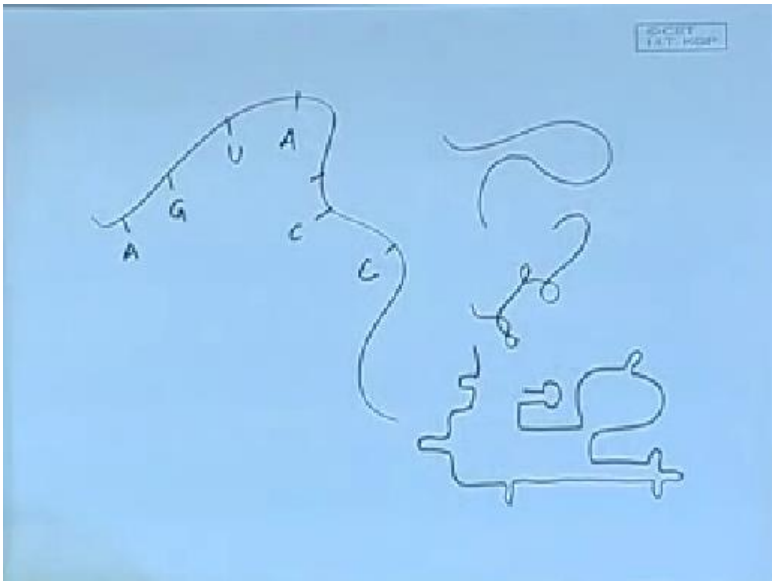

Remember you at the RNA structure right now, where you had part on, what did you have, you had part helices, part bulges and so on and so forth, well this looks a lot more complicated when we look at the ribosomal RNA. You will have some bits and pieces like this and then you have loops like this, if you look at a picture of, I could not get a proper picture, so it will like this something and they huge, huge okay.

They have associated with them proteins and these are ribosomal RNAs are actually formed in the ribosomes, where they are used to make the proteins oaky. We would not see actually the process of making the protein, but it is extremely interesting and if you go to the internet and type in protein animation okay, animation of the synthesis of proteins, you can see how the MRNA and the RRNA and the TRNA, which is speak about in the women and all work in a tandem to get you the polypeptide chain.

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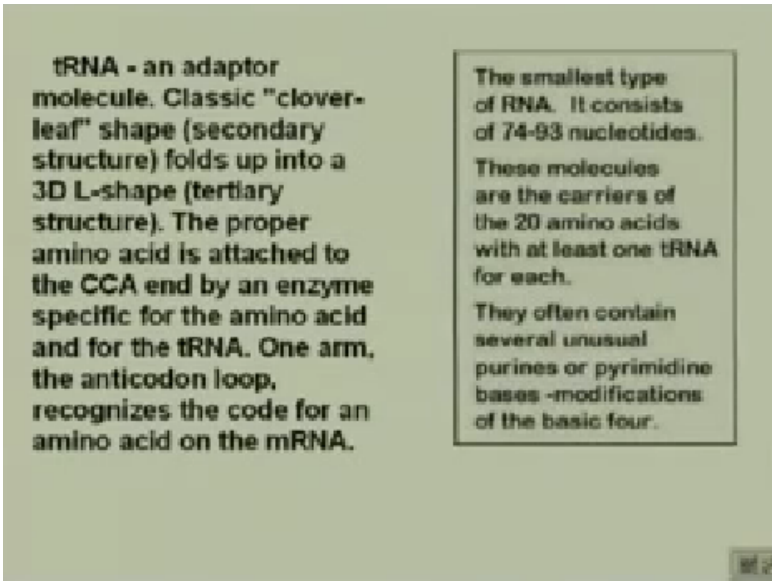

The transfer RNA is the smallest type of RNA that has just 64 to 93 nucleotides okay. It has what is called a cloverleaf structure, which I will show in a moment and it is folded up into an L-shape tertiary structure. We have attached to each TRNA, a specific amino acid okay and this amino acid is required for the protein chain to grow okay. The information present in the TRNA will tell us from the genetic code, which amino acid it is suppose to bring to attach to the polypeptide chain. I will show you that in a moment.

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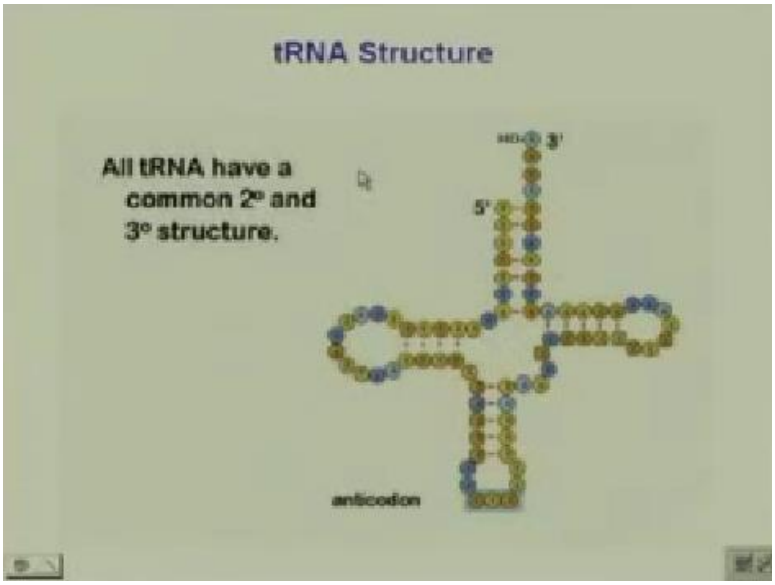

So what we have here is we have the smallest type RNA, the TRNA, it has it is classic cloverleaf structure okay. So this is what is called a classic cloverleaf structure okay, this cloverleaf has 1, 2, 3 looks like that. Now what do we see here, specific complementary base pairing okay, but we have these bulges at the two ends, this is what is called the anticodon.

Now what happens here in the anticodon is this is the part that links on with the RNA to get the information as to which polypeptide chain or which amino acid as to be brought okay.

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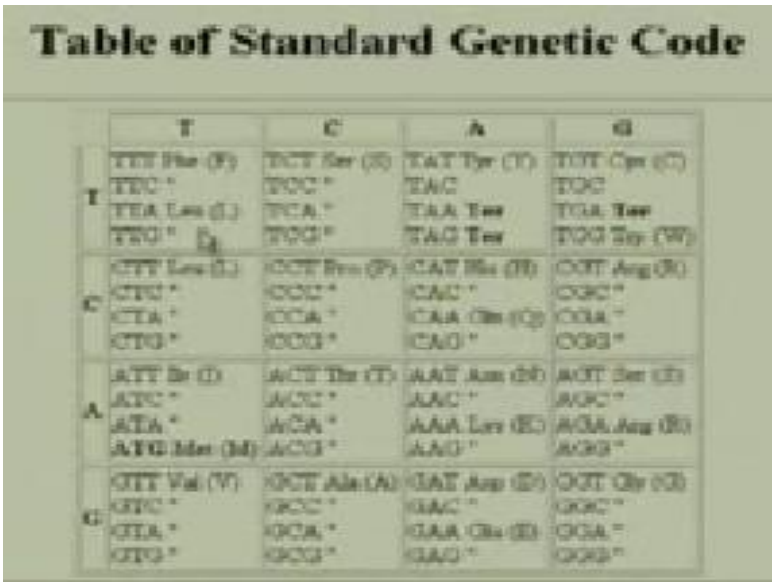

Now what I want to show you, this is what is called a genetic code okay. Now in the genetic code, I am going to show you it means.

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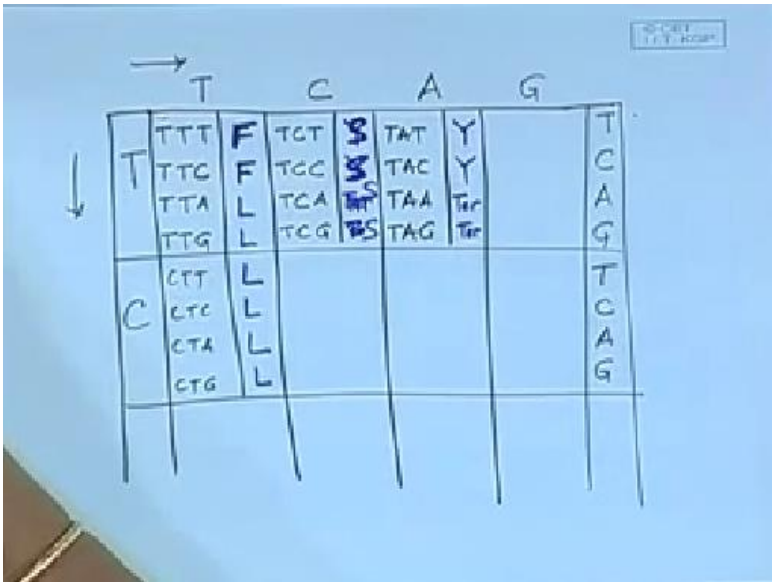

We have something like this. This is the first base pair, we have T C A and G. Here we have T, here we have again T C A G. Here we have C, again T C A G. This is something that was found by Har Gobind Khorana okay. Now what we have here is this the first, second and third okay. So what is the first T T T, the second one will be T T C, third one is going to T T A, T T G okay.

In this case, we have T C T, because first one 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 okay. So this is what your genetic code is. So this is C T T, C T C, C T A, C T G. Now each of this code for an amino acid, we have triplet codons. These are triplet codons okay.

The triplet codons will code for an amino acid. These two code for phenylalanine. These code for leucine. These codes for tyrosine. This is actually a terminal codon, this is also a terminal codon, sorry, all these are serine. The A ones are (()) (49:40) terminal codons. So you have T A T, T A C, T A A, T A G and this is where we have tyrosine, tyrosine, terminal, terminal. So you understand how many codes I am going to get like this 64, they will code for 20 amino acids right.

We have an initiation codon and we have terminal codon okay. So this is how if you go back to what we have here, this is what we have and if you can see this, then we have you get his as I just got this from the internet. You have coding for phenylalanine, this for leucine and so on and so forth. Now the interesting thing here is that you see for this case, the third base actually does not matter.

Why it is the third base not matter, if you look at the leucine codes just look at them, the C T T, C T C, T C A, T CG all give you leucine right. So it means that this base may be something else and where this is base, this base is in our part here. This is the triplet codon; it is the anticodon for that triplet that is for the specific amino acid. What did we seen in the genetic code? we had a triplet that corresponds to an amino acid. That amino acid is what is used for your polypeptide or rather your protein synthesis okay.

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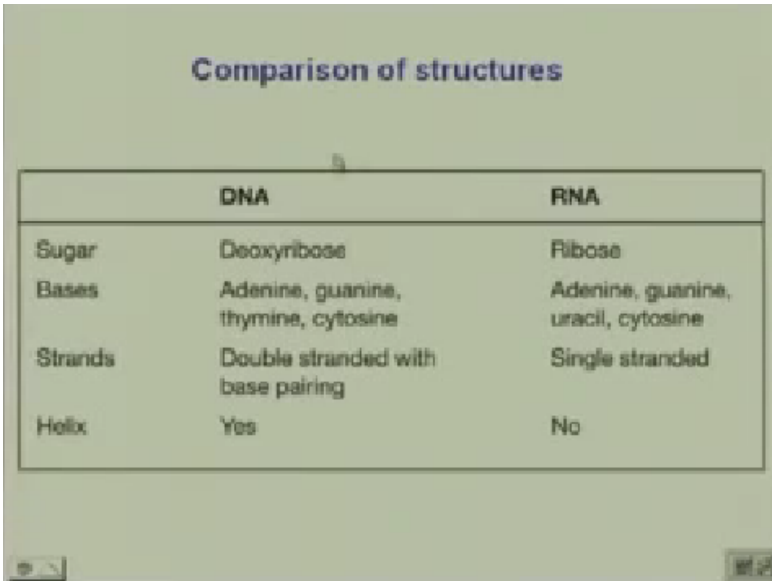

So if you just summarise here in a comparison of the structures, we have the sugar, for DNA we have deoxyribose and we have ribose for RNA. The bases are A G T C and here A G U C. The strands are double stranded with base pairing, here RNA single stranded. This forms the helix, this does not okay. We will stop here for this class. Thank you.