Biochemistry - I

Prof. S. Dasgupta

Department of Chemistry

Indian Institute of Technology, Kharagpur

Lecture # 20
Nucleic Acids-I

We start our discussion on nucleic acids and their components before we understand what are nucleic acids. So far we have studied all the other molecules. Basically for life molecule life meaning the carbohydrates, the lipids that form the cell membranes and other components such as amino acids and then proteins. When we go on to nucleic acid, we will see how important they are in their manifestation in the formation of the proteins that we have studies so long. When we look at the central dogma of biology which goes as follows: It is DNA to RNA to protein.

This is known as the central dogma of biology going from DNA to RNA. The process known as transcription, RNA to the protein is process known as the translation and we know that all the information is stored in the DNA. That is the storage medium. It is then formed or rather transferred to RNA forming the transmission medium that then forms the proteins, expressing a protein what we mean by the protein formation that ultimately is required in all the activities that go on in the body in terms of enzymes so and so forth.

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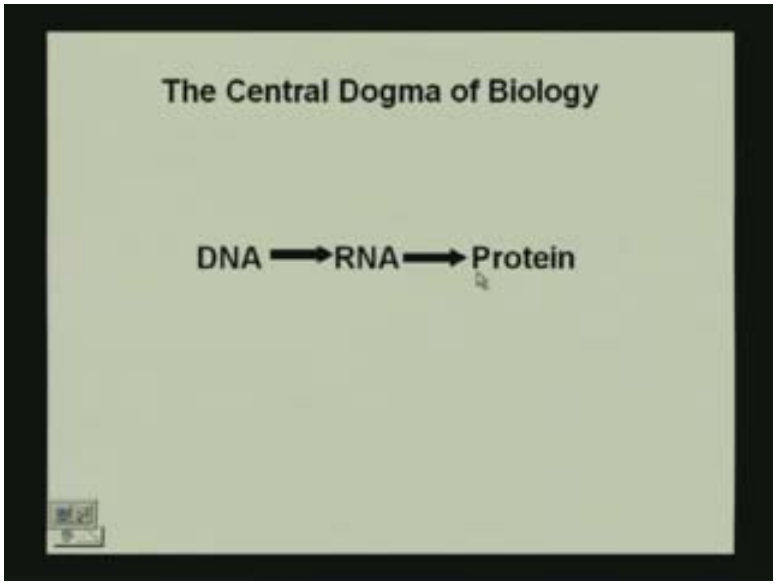

What we are going to do in nucleic acid? We looked at some of the components but we will see how the structures are related and how actually some of these processes are going through. If we look at just some idea of the biological length scale, we looked at

chemical bond something that you looked at for a long time now. They are in the order of Angstroms.

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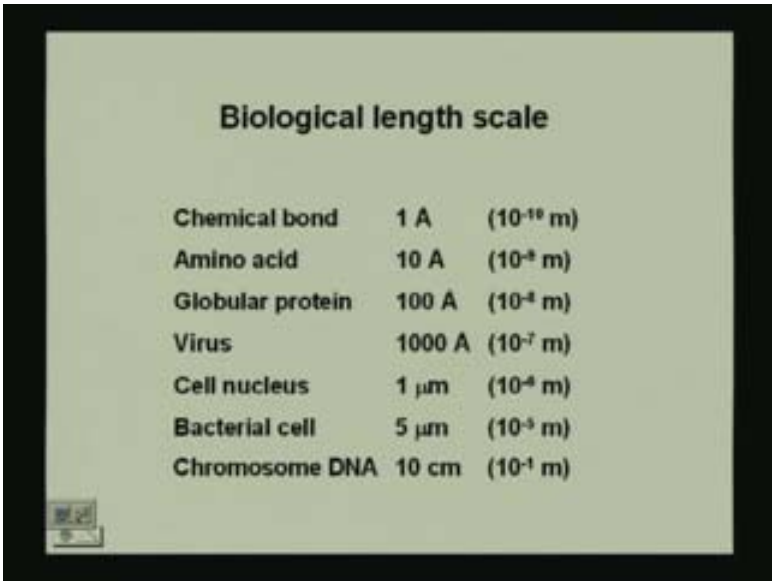

If we look at the amino acids, they are in the order of 10 Å. When we look at proteins they are in the order of 100 Å. As we go higher and higher, you see how this lengths scale actually goes on and ends at DNA which is actually 10 cm which is pretty long, if you look it from protein point of view considering that you have a globular protein that is still in the Å realm where you have it in the order of 100 Å. We have chromosome DNA that is around 10 cm.

Now the fact that you have DNA replication and DNA processing going on extremely fast in the body. It is extremely important to understand how structurally it is place in the body, how it is located and what holds the two as will study later on the 2 trans of the double helix together? This is something we have looked at before when we are doing vitamins and coenzymes. We consider what are called nucleotides. DNA is deoxyribonucleic acid and RNA is ribonucleic acid. Now in the formation of these RNA, this nucleic acid DNA and RNA, there are certain terminologies that we have to go through once more to understand their structure their bonding.

In nucleotides, we have what is called nitrogenous base, a sugar and a phosphate. We now know what is sugar and phosphate. We will just go through what are nitrogenous base. When we consider the nitrogenous bases, there are 2 types of bases that we consider purines and pyrimidines. This is something that we consider when we did vitamins and coenzyme just to revise what we were studied there. When we consider this nucleic acid, we have the sugar and phosphate which is actually called a sugar phosphate backbone. The primary structures of both DNA and RNA are similar. They have a sugar phosphate backbone.

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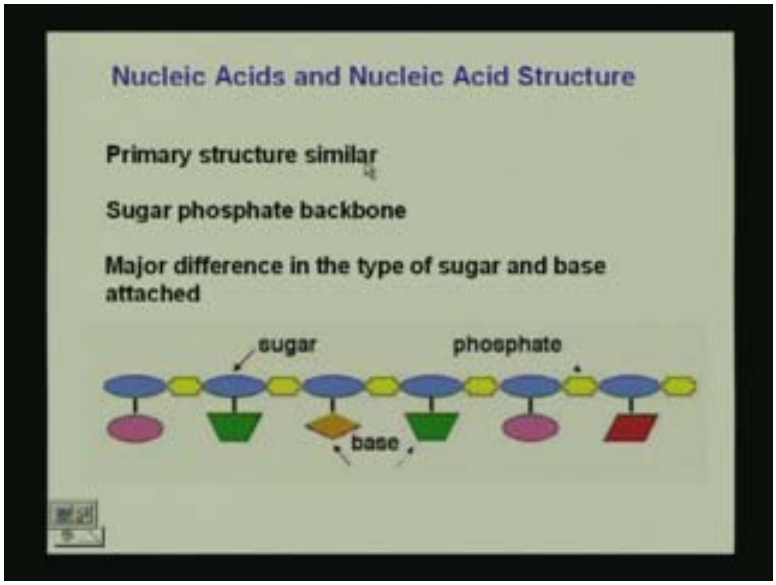

The difference is in the type of sugar because one is ribose sugar and another one is deoxyribose sugar. The difference again also lies in the type of base that is attached to the ribose or the deoxyribose ring. So what we have is, we have a phosphate that is shown in yellow color here and sugar shown in blue. We have different kinds of bases depending on nucleic acids that is attached to the sugar. What we have basically is the sugar phosphate backbone and we have the bases attached to the sugars in the backbones. The sugars that are used in these two types of nucleic acids are ribose. Ribose is used in RNA and the essential difference between ribose and deoxyribose is the missing OH at the 2 prime position of the sugar ring in DNA.

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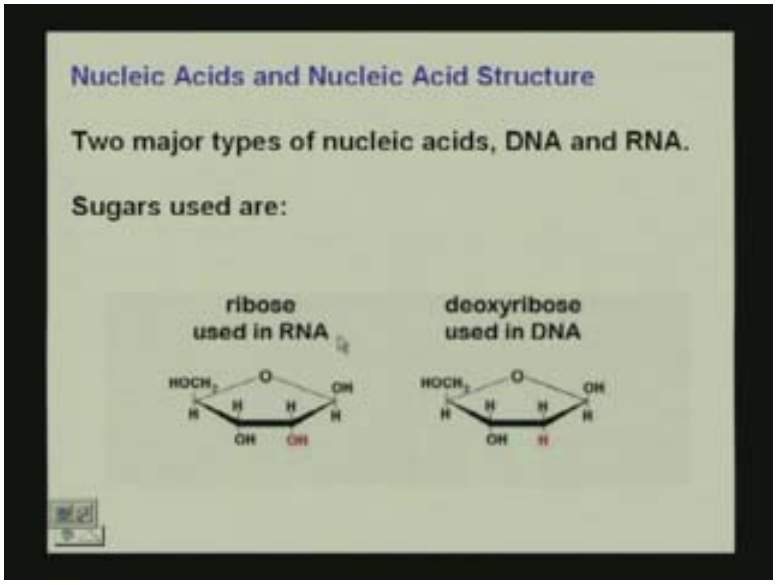

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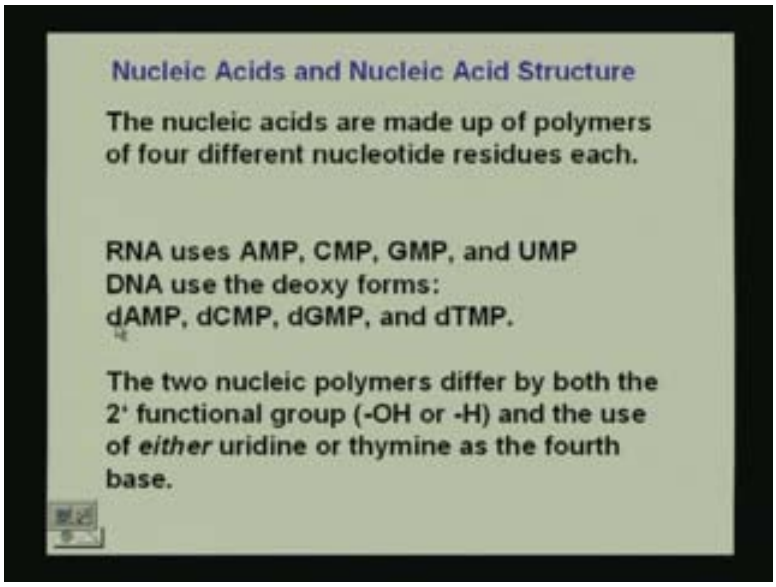

When we have this linkage, this fine end will attach to a phosphate, this end will attach to a base and the bases will be different. The sugar is essentially different when we link these together as will see RNA. If we link these together we will have DNA and there is basic difference between structure, this is also going to be reflected in the stability of RNA and DNA. We have a nucleic acid that is made up of polymers of four different nucleotide residues. We will see what these are in a moment. We have A C G U that makes of the alphabets of RNA. A C G T that make up the alphabets of DNA because the ribose sugar in a deoxyform, we have d prefixed to the AMP, CMP, GMP and TMP.

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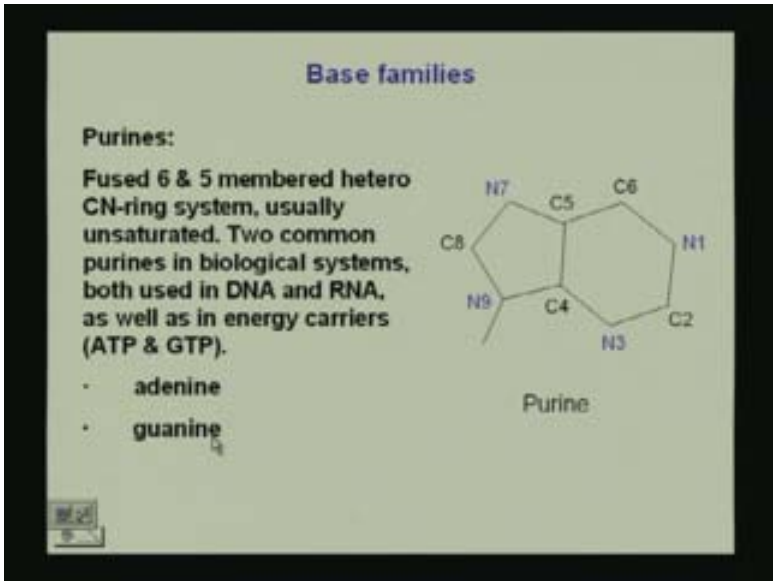

If you write AMP it is a ribose sugar, you have to specify the deoxy type of the sugar by writing d, which means that are the two prime functional groups and you do not have the OH attached to it. What are these base families? We have the nitrogen base purines. What are these purines? They are fused 6 and 5 membered rings a hetro carbon nitrogen ring system and two commonly used ones in DNA and RNA are adenine and guanine, these are the purines.

The pyrimidines are 6 membered carbon nitrogen rings that are usually unsaturated. There are three common purines that are formed in biological systems, C and T are used in DNA that is cytosine and thymine. Cytosine and uracil are used in RNA. We have the purines and pyrimidine that are going to form the nitrogenous bases of the nucleotides that are going to be attached to the sugars in the nucleotide structure to form nucleic acid. These are our purines and pyrimidines and they are in definite structures. This is the numbering system that you have the purines and pyrimidines. And as we mentioned before that when we are looking at DNA we have A G C and T.

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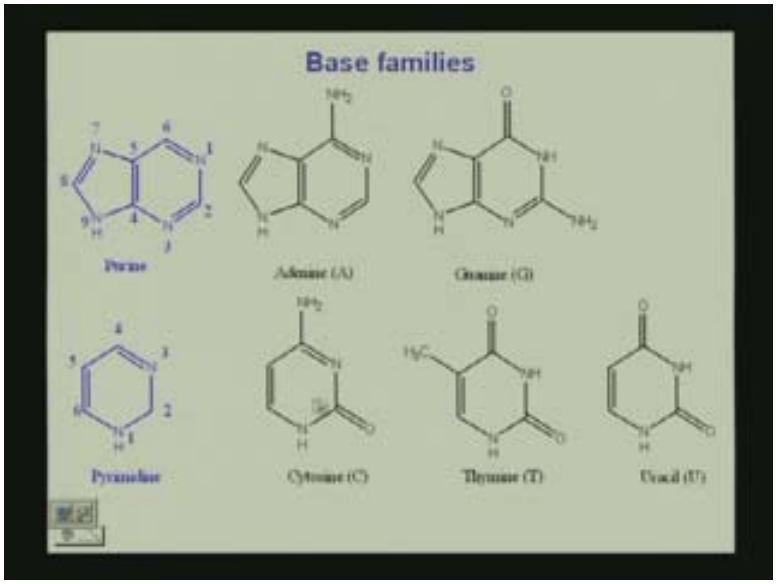

When we have RNA, we have A G C and U instead of T. These are our different base families. This is something that we looked at before when we are forming the nucleotide, we have a sugar. The sugar in this case is a ribose sugar because the OH at the $2'$ position is present. We have a β-N glycosidic bond. We know why it is β, why it is glycosidic and why it is N. Why is it β because, it is cis to the CH_2OH. Why is it N because it is linking with the N of the purine or the pyrimidine base? Why is it glycosidic because you are linking a sugar? Any time you link a sugar it becomes the glycosidic linkage. This is the β-N glycosidic linkage i.e. linking the sugar ring to the purine or the pyrimidine base at the $1'$ position.

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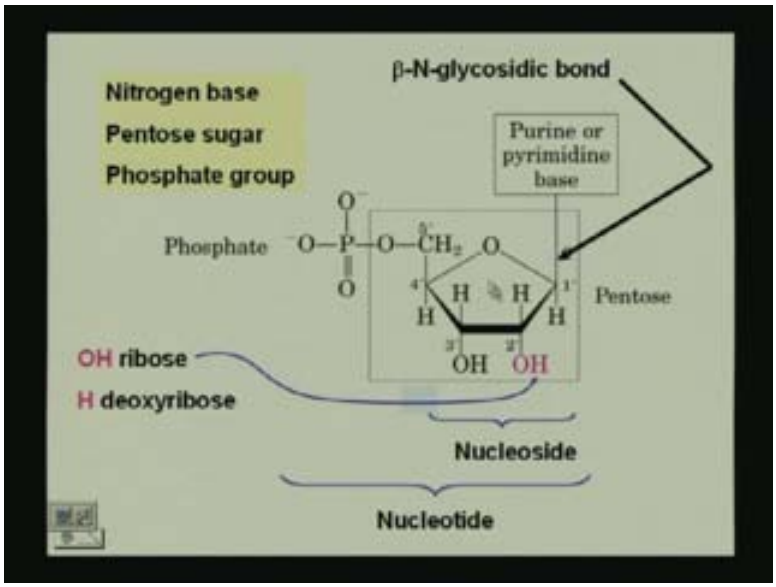

At the $2'$ position, you have either OH or H being the ribose sugar or a deoxyribose sugar. Then you have the phosphate attached to the $5'$ position where you have either this 1 phosphate or you can have 3 phosphates as we looked at the structure of ATP. So when we have the OH we have the ribose, when we have just the H we have deoxyribose. We know how to designate these by writing either a d or without the d when we want to specify a ribose sugar. When we have the base attached to the sugar we have the nucleoside, as soon as the phosphate is attached to the $5'$ position we have a nucleotide. We have a nucleobase and adenine. We have nucleoside which is the base attached to the sugar. The sugar in this case is $2'$ deoxy which means there is the H and there is no O.

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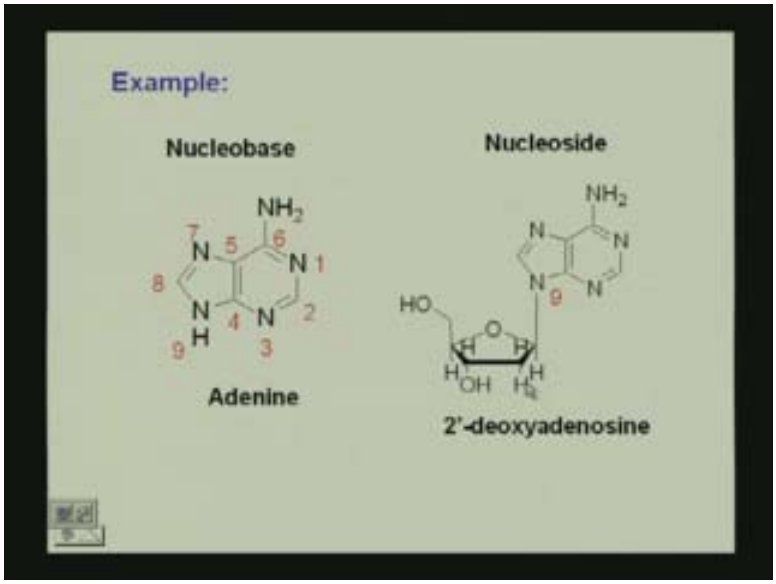

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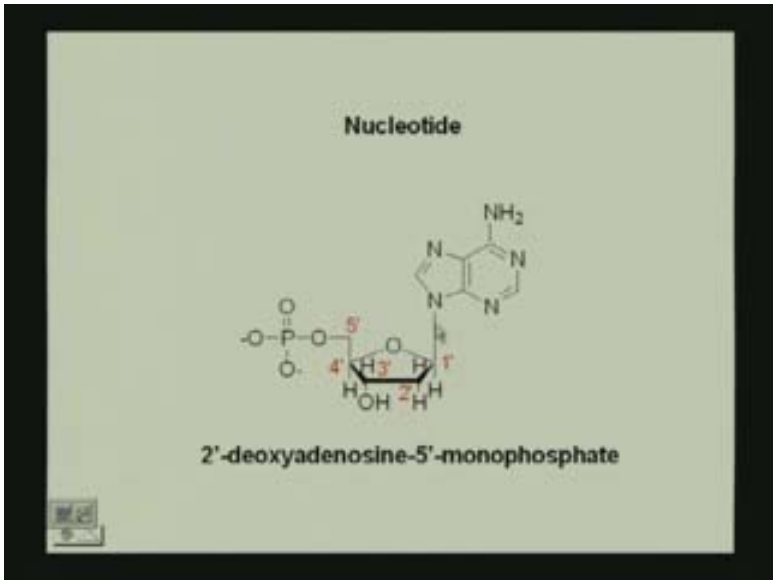

Then we have our nucleotide which is 2' deoxyadenosine 5' mono phosphate but I could have just written is this as DAMP. Just writing it as DAMP you know that this is the structure. The D is signifying no OH, the A signifying this (Refer Slide Time: 11:42) and MP signifying the mono phosphate. Each of these, so the DAMP you know exactly how you have to write it even for the DCMP or the AMP, ATP. Considering that we have the sugar of the phosphate attached to one another and we have this bases basically sticking out that is what I showed in the first picture. It means that we have to look at conformational configurations. Conformational considerations in terms of the backbone just like we had in the protein.

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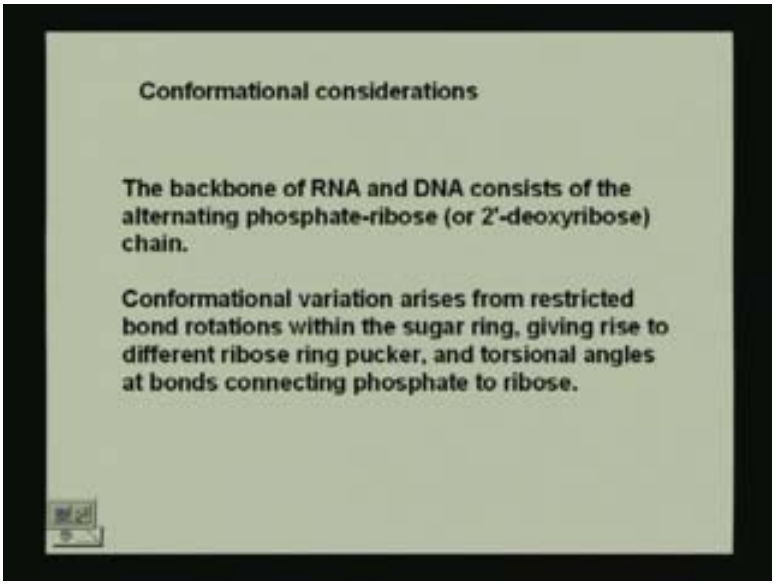

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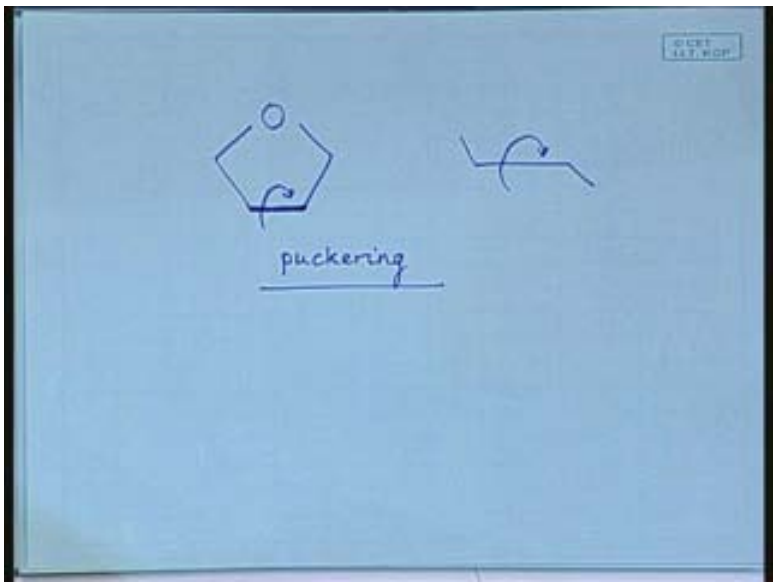

What did you have in the protein? You had certain $\phi\ \chi$ angles that mention how the backbone would be oriented. What did we have sticking out the backbone; the side chains the different R groups sticking out from the amino acids. See α groups of the backbone and we had different orientation possible. We can have the same here. What is that? This backbone of RNA and DNA consists of the alternating phosphate ribose or deoxyribose $2^{'}$ deoxyribose chain. We have alternating phosphate and ribose. You see how that is formed, once we understand the torsional angles. When we have conformational variation this arises from restricted bond rotation. Where are we going to get restricted bond

rotation? We have a sugar ring. We have single ring, what do we have? We have something like this. This is our sugar ring.

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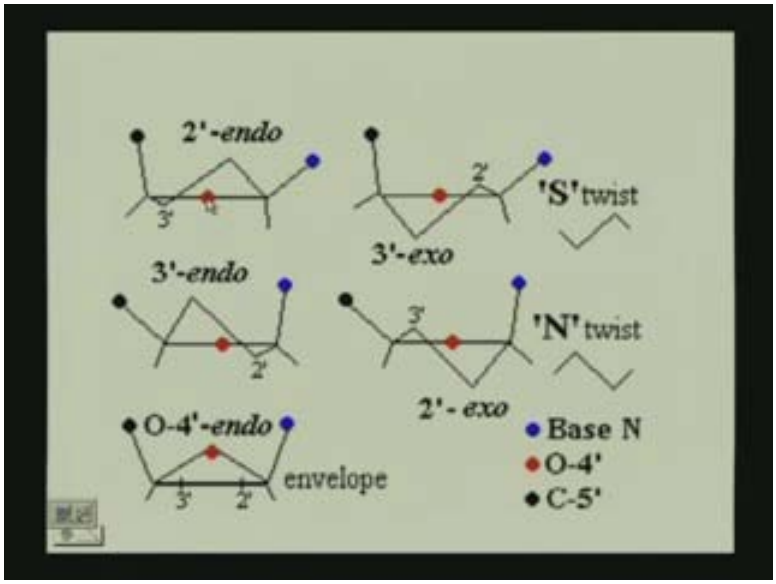

You have to remember all of these are single bonds. What is possible puckering? You do not call rotation because it is restricted in its rotation. If we have just single bond we know that we can rotate all the way through. We have something like this. You cannot have all the way gone through, because it is going to twist the molecule. This twisting is what is known as puckering. What kind of observation can we have? We can have the oxygen go up, go down with respect to this bond here. So we can have restricted bond rotations within the sugar ring because of ring system. We are not free to rotate all through. This give rise to different ribose ring pucker and torsional angle, that bonds connect the phosphate to the ribose. Let us see what we mean by that.

We have here, just look at one of these figure. First this red sphere is the oxygen of the sugar ring. We have 5 membered sugar ring so if you just look at the different, so this is 1, 2, 3, 4 and 5 atoms that we have to connected to form the 5 membered ring. This is $5'$ carbon atom that is usually attached to the phosphate. See this is what we are looking at, you have something like this. This is attached to the phosphate and where is this attached? This is attached to the base so this is $2'$. This is the $3'$ prime position. This is the $1'$, this is our $4'$, this is our $5'$. When we go back to this we recognize what is happening here. We have 1, what is attached to the base. So the blue circle represents the base nitrogen that is attached to it.

We remember that this is the N glycosidic bond, so the sugar is attached to the base by the nitrogen. It is β because these are cis to one another. We have the phosphate or let us look at the $5'$ carbon, so we have basically the $5'$ carbon here which is essentially attached to the phosphate and we have the base. Now we are looking at what can happen

to the sugar ring? The sugar ring can bend in such a way that we can have some thing that is called $2'$ endo, $3'$ endo and O-$4'$ endo. If I look at each of these structures, you will see that the bond or rather the atom that is forming the endo conformation is getting close or rather in the same direction as the phosphate and the base.

When you have the $2'$ endo, pucker up to be cis to the phosphate and the nitrogen. You have an $2'$ endo, if the $3'$ takes up towards in the same direction as the base and the phosphate, you have the $3'$ endo. If the oxygen picks up in the same direction, you have an O$4'$ endo. The endo configuration is, when you have some carbon atom or the oxygen atom pushed to a position or pucker to a position that is in the same direction as the base attachment and the phosphate attachment. Only if these are in the same positions would you have, what is called endo conformations so you would have the opposite if you have the exo, you can a have $3'$ exo which would mean that the $3'$ carbon is away from the phosphate and the nitrogen.

The $2'$ exo means that you would have $2'$ carbons away from the phosphate and the base. If you look at just away and trace the numbers here or we just trace the carbon here, if you go down this way then up this way and down this way. You are basically tracing S in this way.

So you are going down this way because you are $3'$ endo going up $3'$ coming down again. What you are looking? You are looking at what is called then S twist. The twist is such you can just imagine the twisting of the wire. If you just connect wires, where you have one as oxygen then you connect these wires by twisting it in such a way that you have the S twist. You can twist in the opposite direction that is going to give you what is called N twist. If you just trace the atoms here we will have in this case $3'$ endo. You follow the direction from this carbon up we have this and this. What it is tracing? Something like the N.

If you go in this way, the $2'$ exo we would have this up down again, up again tracing some thing look like a N. This is why just two name given to this called S twist and N twist. This is how we represent the sugars. This is important because now if you look at the orientation of the phosphate and the nitrogen there is a slide change in how the bases are connected. How we are going to see? How this is going to help later on in the overall structure? Basically we are going to have a polymerization. A polymer formation based on the orientations of the sugar rings and their conformational considerations you can position the base.

The reason why we need to position the base is to form favorable interactions. So this is what we have here a dinucleotide. Why do I call this as a dinucleotide because I have 2 nucleotides? You recognize here that this red, we know the oxygen of the sugar. This is the nitrogen of the base. This is the other sugar and what do we have here? We have this again this $5'$ that is linked to the phosphate. This is the phosphate. Try and recognize this, so $2'$ does have the oxygen.

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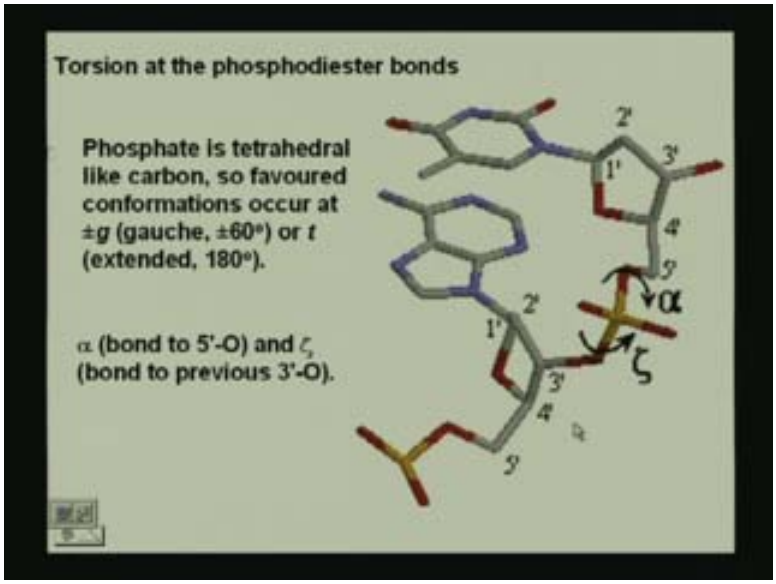

Does it have the oxygen? It does not have the oxygen, so what is this? It is a deoxyribose. We are just going to look at this for torsional configurations because now we know that when we have a single unit.

Let us consider a single unit, when we have. This is one unit here, the top this is one unit and this is another unit. We have linked these units together we will see how they linked together later on. First we have to understand how actually the conformational considerations are going to play an important role? What we have learnt from the previous slide is we can have puckering in this sugar ring and also in this sugar ring. Due to the puckering, what is going to happen? The positions of this phosphate and position of the base are going to change. This is the overall backbone and we can have positional changes due to the ring puckering.

We can also have positional changes due to rotations about this bond and this bond. Remember the ϕ ψ angles of proteins, if we just consider that we have the sugar the phosphate, we have here single bonds. What do single bonds allow? They allow free rotation. Because of this rotation we can have again changes in the position of the bases and the position of the phosphate. What happens if I rotate about this χ angle, the base is going to come up all the way on the other side.

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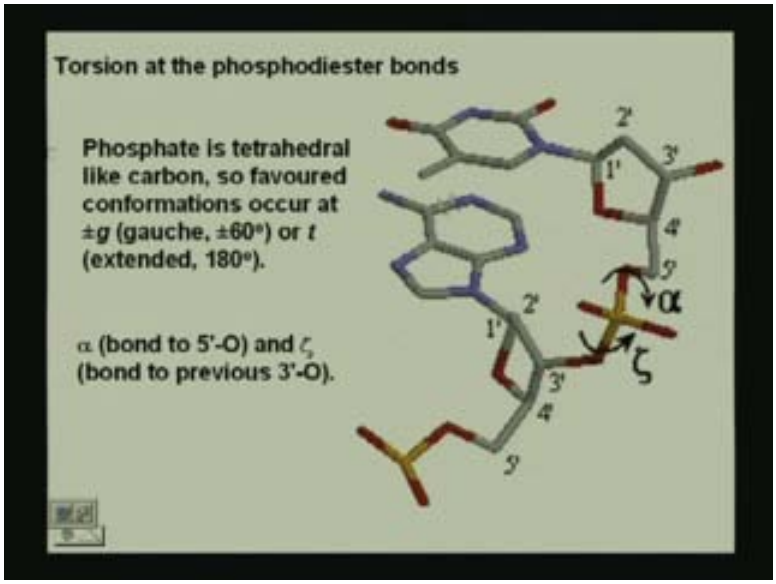

What is going to happen if I rotate about this? This base can shift, so we have a α rotation and we have a χ rotation or η rotation. We have to give another reason why we are looking at this is? If we look at the previous slide, what happened here is? You had changes in the orientation of the bases. Why, because of the puckering due to the sugar. What is that doing? That is changing the position or the orientation of the base and also the phosphate. But you can also have rotations about these two angles. What is that going to lead? That is also going to lead to changes in the positioning of the bases. The changing in the positioning of the bases is going to help in the bond formation that we are going to see later on.

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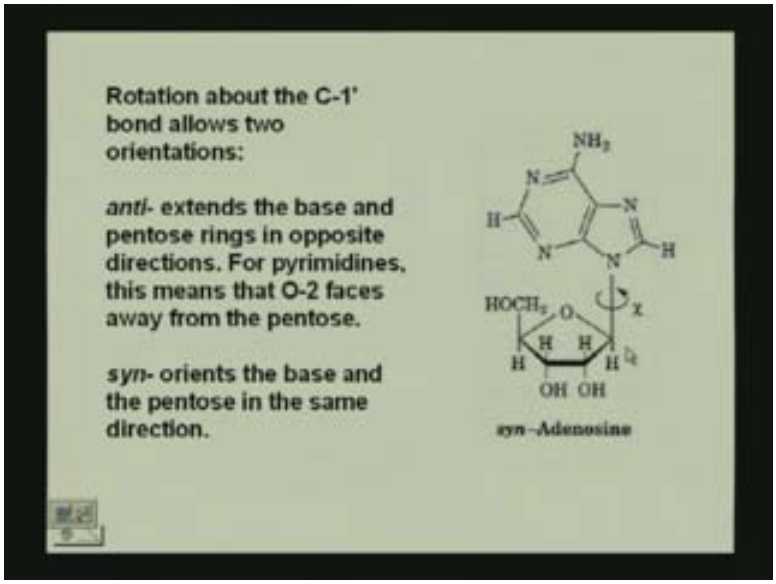

We have to look at another χ angle. What we are looking at here? What is this? Is this a nucleoside or nucleotide? It is a nucleoside why because it does not have the phosphate attached to it. It has the base attached to the sugar. You have to remember again we have the single bond here so what is possible? Rotation about the bond is possible. This is a syn orientation, because in the purine case we have the 6 membered and 5 membered ring fused to one another. When you have the syn orientation, you have the base and the pentose that is this part of the sugar on the same side. It is anti when it goes on the other side. This rotation is also possible. What are you getting? Since we have to study nucleic acid structure and its components we are looking at all the different structural aspects are possible because you have the single bond. These single bonds allow a rotation and sugar ring for puckering.

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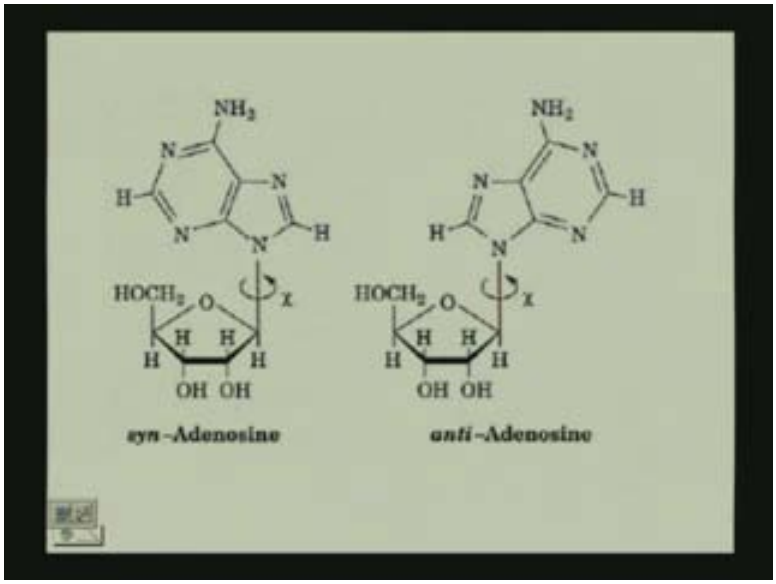

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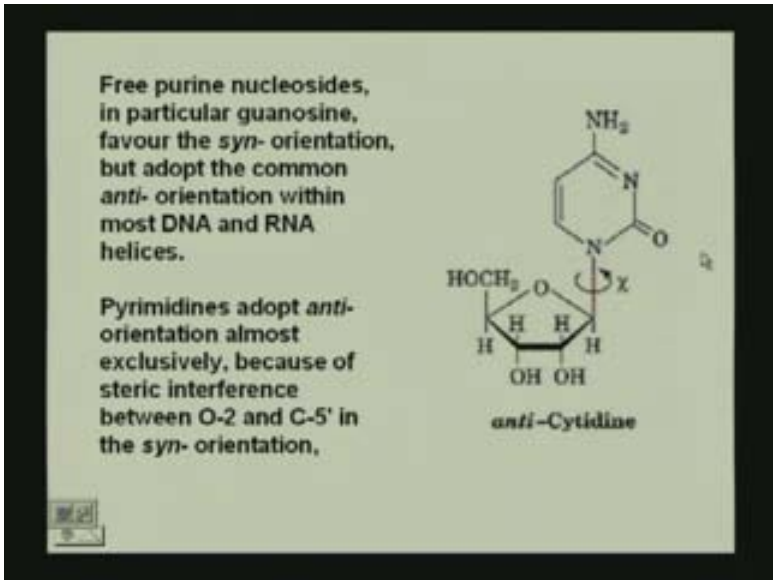

All these put together is going to get this into very-very flexible structure but the structure in the sense is not flexible. We will see later on. What we have? We can have syn-adenosine and anti-adonsine where we have the sugar ring and base away from the pentose sugar. When we have the purine nucleosides we have an anti-configuration. When this oxygen is away from this part, we can have the syn orientation. When there is rotation about this and this oxygen comes about this part. Usually the pyrimidine adopts this anti-configuration because we obviously going to result in some steric clash if the oxygen comes here. Again we have phosphate attached to it so on and so forth. We rather have an anti orientation but since this allows rotation, it may be possible that in some cases you might have a syn orientation also.

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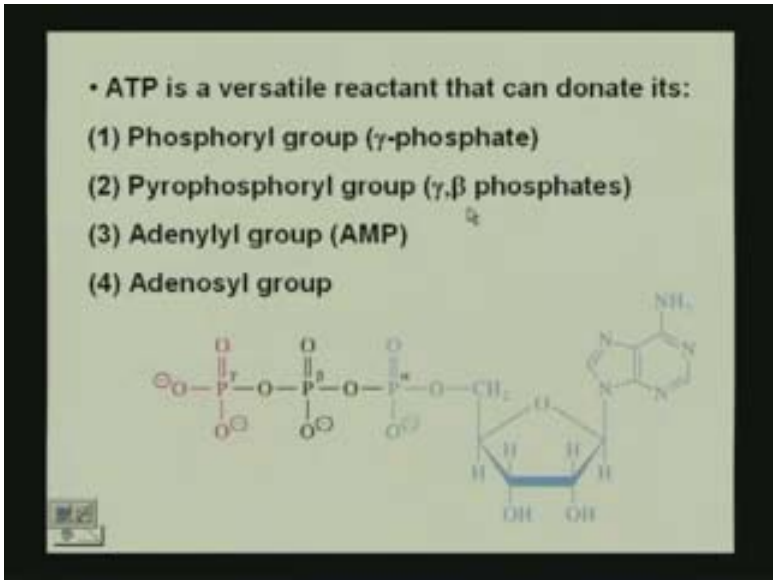

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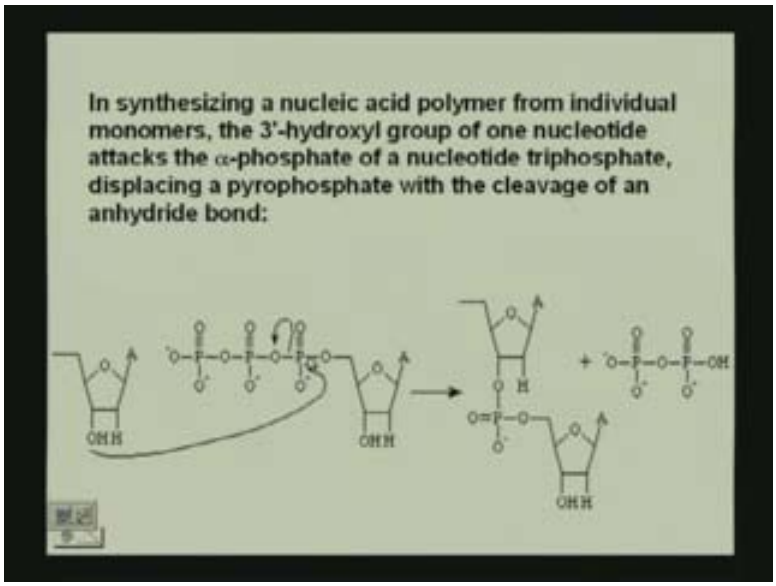

Before we get into how these are formed, we need to look at the structure of ATP once more. What we look at, what is this now? As soon as attached to the phosphate it becomes nucleotide. Now that we have the nucleotide, a α, β and γ position. This is the α phosphate that forms AMP. When we have the phosphorylation here, it is ADP but when we have at the γ position as well, it is ATP. So we have AMP, ADP and ATP. We are going to see how we can actually form these? We are synthesizing a nucleic acid polymer. Essentially what we have is something like this. This is our sugar. What do we have attached to this position? A base. What do we have? We have something else

attached here. If we have the phosphate then we have the nucleotide, OH and this here. What is this? Deoxy, now we have ATP.

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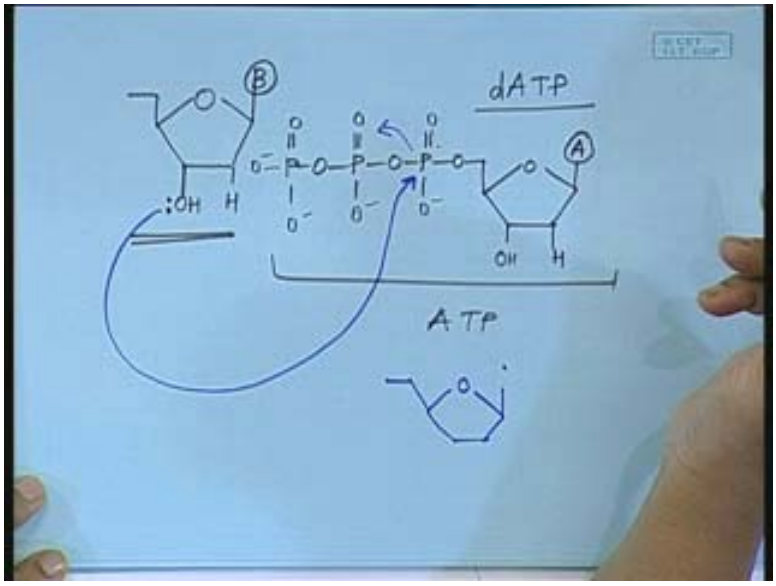

ATP means, I have O here. What do I have here? I have A basically here and OH. This is then what? dATP, then I have O P O P O P. What do I have? dATP, O O^- so I have one part here and ATP here. What is happening now? Is this lone pair attacks this phosphate. What we are going to form then? What is going to happen? What I am going to have here? If we have this A here, this oxygen is now linked to this phosphate. This oxygen is now linked here and we have this part released (Refer Slide Time: 31:53). So what are all essentially done? I have linked this with this. Where I have linked it at this position?

What is this position? The $5'$ position. The 3 is going to 5. What can this do? This has now its $3'$ position open. What can it do? It can now attack another one with another base. You can have GTP. What I am going to have here? Then my base is going to be different. I am actually linking or polymerizing into forming a linear chain of the sugar phosphate backbone. You recognize why this is now a sugar phosphate backbone? Let us back to the slides here.

What we are looking at?

We have the $3'$ hydroxyl group here. What it is doing? Attacks this phosphate of the triphosphate, releasing the pyrophosphate with the cleavage of anhydride bond. What do you have? What is this? It is dinucleotide. This $3'$ OH can do what? It can go and attack another triphosphate that has another base attached to it. It is going to then form a linear chain of the nucleic acid polymer. What do we have? We have a sugar, phosphate, a sugar if we have another linkage and another phosphate and so on and so forth.

We have the polymer made by linking nucleotides by phosphodiester bonds. How are these formed? Synthesized by the attack of the alcohol residue from the ribose on the α phosphate to release diphosphate residue. What is the diphosphate? We are talking about the pyrophosphate that comes up after, this attack takes place. Then what do we have? We have this linkage.

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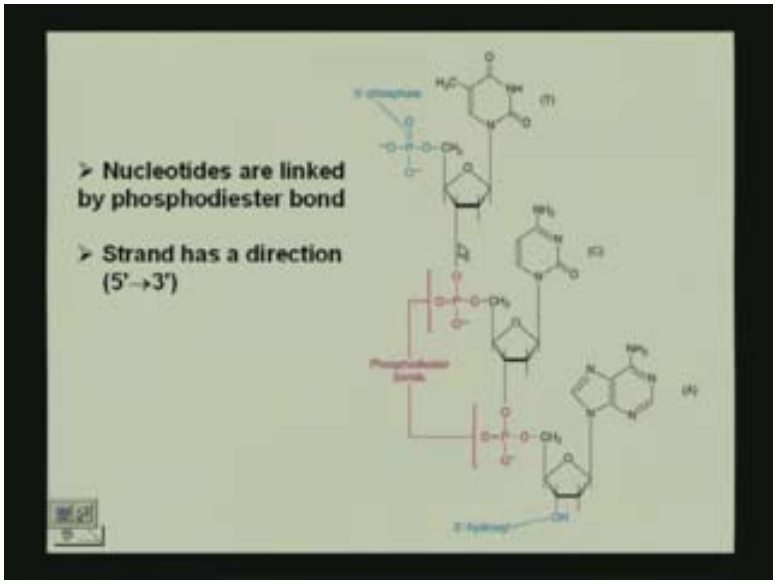

What are we looking? We are looking at a $5'$ phosphate. It was this OH that attack to CTP and you linked T and C together. What you are essentially doing? You have a $5'$ phosphate. You have the base attached by this glycosidic linkage to the sugar. What is happening? This OH is free to attack the triphosphate. What happens then the formation of dinucleotide. This OH is again free. What can that do? It goes and attacks other triphosphate. In this case now has attacked ATP. This is adenine. It has attacked ATP. We have now a trinucleotide which has the sequence T C A. Just like, we did in proteins. What do we need to know? We just need to the bases that are attached because we need to know the type of sugar that's all the information. If we looked at I am sure you have seen books or just the DNA sequence.

When you look at the DNA sequence, what do you see A C T G and so on and so forth. What does it mean? It means that, the structure is like this because you have the specific sugar. You have it linked by phosphodiester bond in the sugar phosphate back bone. The difference lies in the types of bases that are attacked or attached to the sugar. Just like in the protein. Do we like the peptide bond? We don't, we just write V A G T what ever. What does it mean? We have valine, alanine, glycine and threonine but we know that they are linked by peptide bonds. Is the same thing here, we have the sugar phosphates. All the information I need to know is just what are the bases, because I know that. I need to know the deoxyribose or ribose. The strand has a direction that is referred to as $5'$ to $3'$. This $3'$ then can attach another one and so on so forth.

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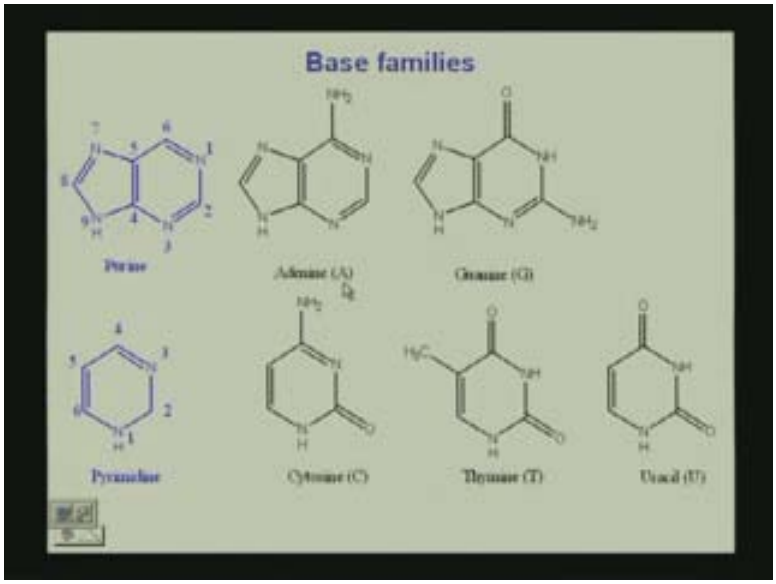

You can have the increasing length of the nucleic acid based on this. So if you look at this base families, all the information you need to know is, what is attached to what. If I say A G C T, you know what it means. I have a linear polymer that is A T G C. What do we know? First of all you know its DNA, why do you know it is DNA because I have included T instead of U. You know what sugar you have to draw, you know what bases you have to draw and you know that they are linked by the phosphate backbone. Let me just go back to one structure, last picture now. We know how does it looks like (Refer Slide Time: 38:20)? You understand that you have the phosphodiester linkage so with the phosphodiester linkage what can happen apart from the sugar puckering which is going to change the orientation of the base. We can also have rotation about this, which is also going to change the directionality of the bases. How does that help? What can that do?

Once we have these bases we can have base pairing. What is base pairing? Base pairing is when we have say now that we have a sugar phosphate backbone. What is that sugar phosphate backbone mean? It means you have this and you have your P. You have your base attached here. Again what you are going to have? One strand here and another strand here. You are going to look at how does this happen later on.

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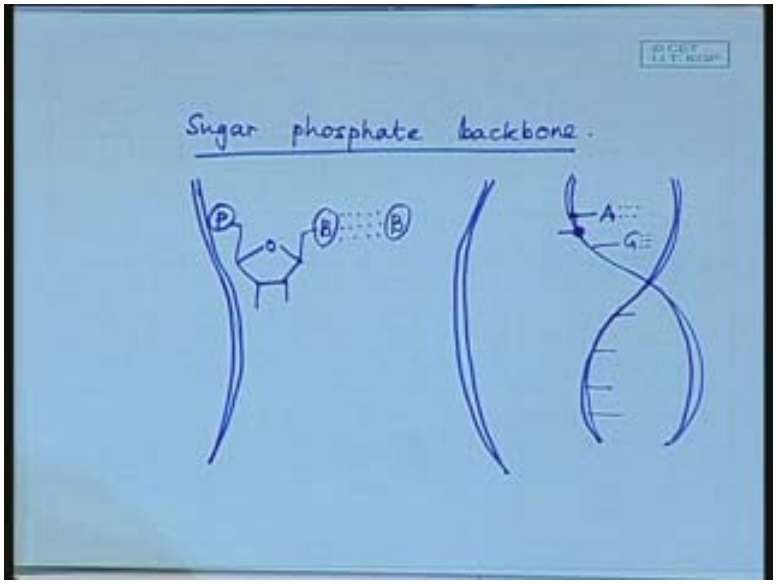

In base pairing, what you have is you have specific hydrogen bonds interactions between bases, between the two transfers. What is this strand made up? This is just the sugar phosphate backbone. This is the sugar phosphate back bone and we have basically the bases sticking out. When you see DNA is actually drawn, it is just drawn with A G and so on and so forth. Where, this is coming from? This linked to the sugar that forms part of the sugar phosphate backbone. What do we have here in between? We have phosphodiester linkages, sugar, the base attached to the sugar. This is the strands of DNA. This is another strand of DNA. What do we have? We have linkages between the bases, these linkages and these pairings is extremely important in the structure of DNA. We have here what is called Watson Crick base pairing.

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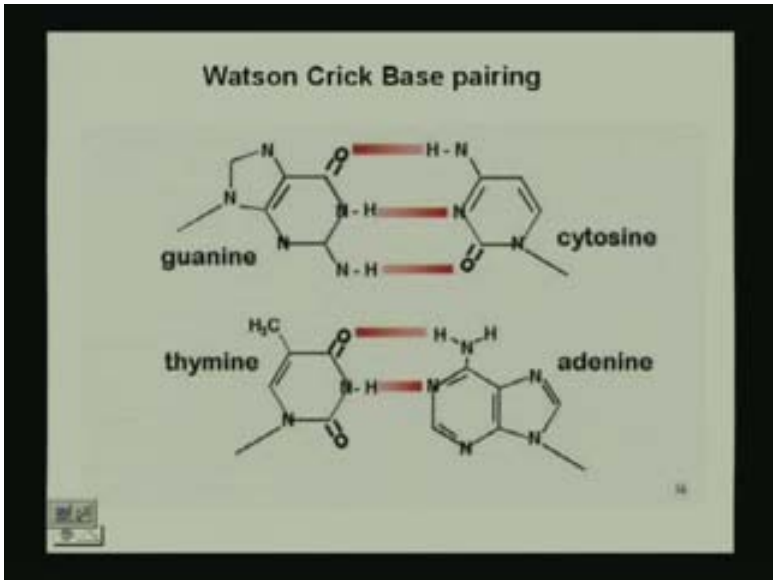

Now if you notice, you have here guanine and cytosine. What is guanine? Guanine is a purine, cytosine is a pyrimidine. You have a link between a purine and the pyrimidine. If we look at the other base pairing, we have adenine. What is adenine? It is a purine. What is thymine? It is a pyrimidine. We have purine pyrimidine pairing. In the paring you will notice which is extremely important for the structure of DNA. We have hydrogen bond formation. These red thick lines are actually representation of the hydrogen bonds. What we are talking about? We are talking about an oxygen, hydrogen and nitrogen, here is one hydrogen bond here we have another hydrogen bond. We have three hydrogen bonds in the pairing of G and C. We have two hydrogen bonds in the pairing of T and A.

If we look at the structure what is going to happen when we have T at this position. We are going to have linking of the T with an A of the other strand. If we are looking at C, we are going to have this link with G of the other strand. If we have a on this strand it is going to link with the T on the other strand. If you look very carefully the pairing as I mentioned is between the purine and pyrimidine, there is one member of the pair that has a fused 6 and 5 membered rings, being part of the purine family. And we have just 6 CN ring that is part of the pyrimidine family. This is extremely important if we look at the distance between these two. What kind of pairing we are going to have?? We can have A T. That is represented like that or we can have G C. What is that means? It means you have two hydrogen bonds here and three hydrogen bonds here.

We have purine and pyrimidine base pairing. We have another type of base pairing, the one that I mentioned before is Watson Crick base pairing. There is another type of base pairing that is called Hoogsteen Base pairing. What do you notice here? What is this? What is that? This is it purine or a pyrimidine purine. What is this? It is also purine. In this case you not only have purine pyrimidine base pairing but you can have purine purine base pairing also.

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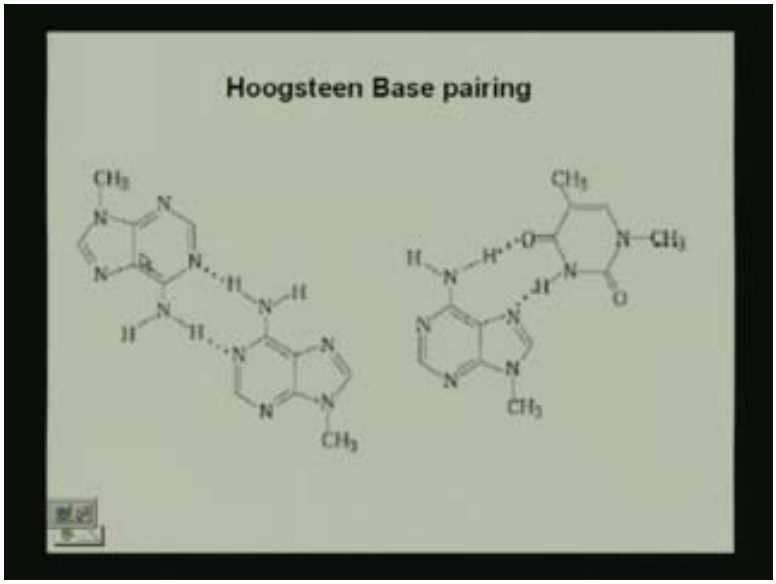

We will see how this is not seen in the double stranded DNA, because double stranded has to form a uniform distance between the helices. You have to have purine pyrimidine fit in every case. When we have the two strands of the DNA come together so we have one strand this way and one strand this way. Then the length between has to be the same. We have one purine that is the 6 and 5 membered fused together. We have the one pyrimidine that is the 6 membered. Both of them coming together gives the exact distance that is the distance between the strands but in the Hoogsten base pairing what happens you can have the base between 2 purine. You also have pruine pyrimidine base pairing.

Since this is also possible you do not see in the double stranded DNA. There are some cases this is observed. So far what we need to know is the basic pairing between the purines and the pyrimidines, that form the bases of double stranded DNA, where we have three hydrogens between G and C and two hydrogen between A and T. If we look at basically adenine here, we have this face. How many hydrogen bonds are in the adenine 2 A T in the Watson Crick face, here also in the Hoogsteen face that is part of the 5 membered rings and the NH of the NH_2. If we go back and look at where this is formed, you see this is a Hoogsteen pairing.

This is between the 6 membered ring here and the 6 membered ring here. In this case when we look at the A, this is between what? 2 is 2 purines, when we look at normal Hoogsteen base pairing the difference between the Watson crick pairing is, let us look at the Watson crick pairing, we have where is the hydrogen bonding? It is all from the 6 membered ring. In the Watson Crick base pairing, the base paring that adenine forms with thymine is from the 6 membered ring. But you have a fused 5 membered ring in Hoogsteen base pairing so what did we have? We had this face that was forming the hydrogen bonds in the Watson Crick base pairing.

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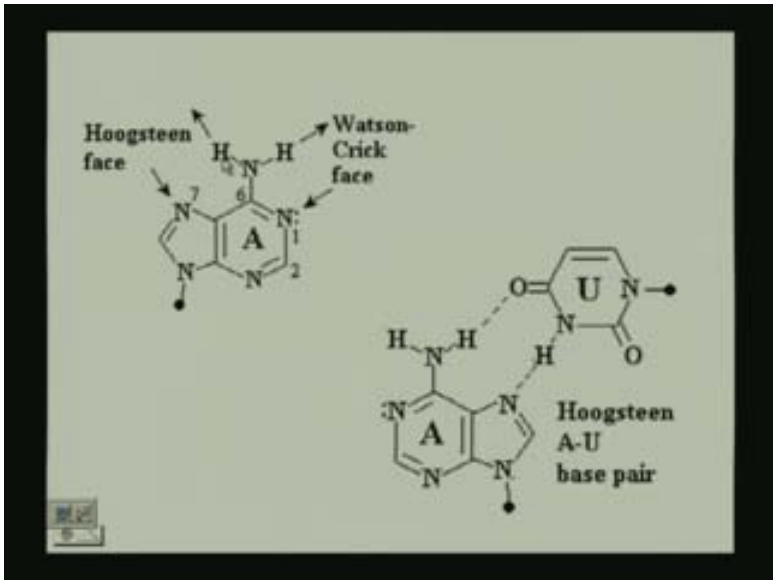

In the Hoogsteen base pairing we have 1 hydrogen from the 6 membered rings and the nitrogen taking part in the hydrogen bonding from the 5 membered ring. What we essentially have is we have what is called Hoogsteen face where it is the 5 membered ring nitrogen and the NH of the 6 membered ring taking part in, what it is taking part in? The hydrogen bonding. The Watson Crick face it is only the 6 membered rings that is taking part, this is the essential difference in the pairing that occurs so when we have a Hoogsteen. This is the normal purine pyrimidine linkage A and U. U is found where in RNA? So when we have an A and U linkage, and you see that the linkage is between obviously, we are going to have it between 2 electronegative atoms but you see it between, What or what is taking part that is what you have to look at. What do you see taking part here? We see the 6 membered and 5 membered ring taking part.

What kind of base pairing is this? Hoogsteen base pairing that is essentially what we have to recognize. When we see Watson base pairing in this case what would happen? The linkage would be on this side because it would be the 6 membered ring that would be involved in the base pairing. So we have a Watson Crick face, we have Hoogsteen face. By far it is the Watson crick base pairing that is the most important. Essentially what we have done is we have looked at how we have the linkages of the 2 base pairs. We have A T G C, two hydrogen bonds and three hydrogen bonds. These are coming from where? They are coming from our sugar phosphate backbone that is essentially what is happening. We have essential rotations about the backbone. Where are these rotations possible? We have the phosphodiester. If we have the phosphate atom here, we have rotations about this. We have the sugar ring somewhere here. We have puckering about the sugar ring now. What is going to happen? This puckering is going to orient this G in a specific position; this rotation is going to orient the overall backbone in the specific position. What is that is going to assistance that is going to assist in orienting the bases in such a manner that you can have the specific hydrogen bonding possible.

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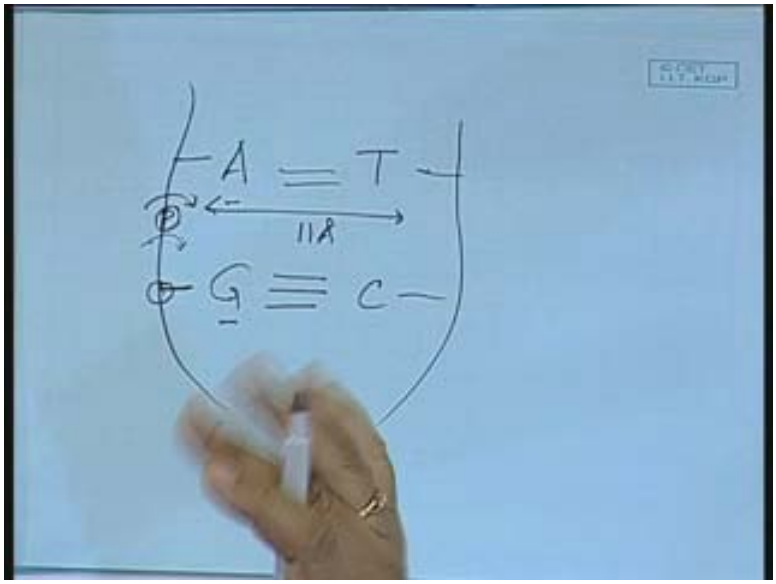

Without this slide flexibility it would not be possible to have the hydrogen bonding. You understand that because you have to have the nitrogen and oxygen in the specific orientation, specific distance requirements for this to occur. If you look at this result, we have A and T. What is this base pairing? What base pairing are we looking at here? Only the 6 membered ring involved, so it is Watson Crick, if we look at the A and T pairing and the G and C pair, you see the distance from the C1' here. What is the C1'? It is where it is attached to the sugar the β N glycosidic linkage that is what C1' is. What is the distance 11 Å? When you have A, T, G and C it is also the 11 Å, so you see how nature has sort of designed it in such a manner that you would have a purine and pyrimidine link together. You would have a constant distance here that would give you actually 11 Å that holds the bases together. You have base pairing in such a way that not only the distances but also the hydrogen bonding is complementary and also you have the flexibility possible that makes it feasible for the hydrogen bonding.