NMR spectroscopy for Structural Biology
Prof. Ashutosh Kumar and Prof. Ramkrishna Hosur
Department of Chemistry
Indian Institute of Technology - Bombay

Lecture: 26
Application of NMR in the Area of Structural Biology: Structure of DNA and RNA 3

So, we have been discussing about the various aspects of nucleic acid structure how the whole thing started with fibre diffraction and single crystal x-ray data on shorter oligonucleotides has helped in obtaining great details about the structure of the nucleic acids at atomic resolution. The various aspects of the structure we have discussed and we mentioned about the different types of models with the B-DNA, A-DNA, C-DNA, D-DNA and things like that.

We also indicated the importance of this nucleic acid with regard to the hereditary functions and we also talked about one of the new discoveries which is called as the Z-DNA and here actually this slide is a continuation of that discussion and makes a direct comparison of the most prominent nucleic acid structure which is the B-DNA and then you have the left handed which is the Z-DNA.

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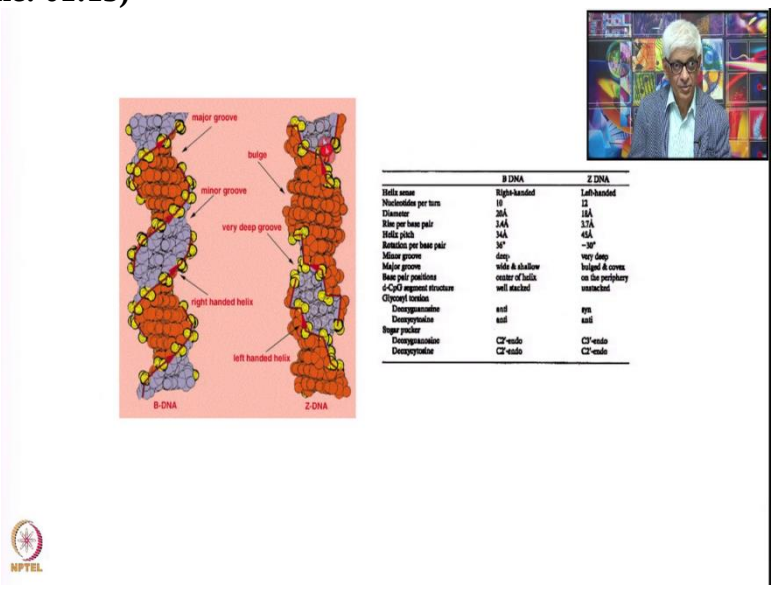

	B DNA	Z DNA
Helix sense	Right-handed	Left-handed
Nucleotides per turn	10	12
Diameter	20Å	18Å
Rise per base pair	3.4Å	3.7Å
Helix pitch	34Å	45Å
Rotation per base pair	36°	−30°
Minor groove	deep	very deep
Major groove	wide & shallow	bulged & covers
Base pair positions	center of helix	on the periphery
d-CpG segment structure	well stacked	unstacked
Glycosyl torsion		
Deoxyguanosine	anti	syn
Deoxycytosine	anti	anti
Sugar pucker		
Deoxyguanosine	C3′-endo	C3′-endo
Deoxycytosine	C2′-endo	C2′-endo

And this is the comparison here of the 2 by and large you can see here this B-DNA which is the one which is the prominent one in all systems it is a right handed helix you can see the helix goes in this manner and there is a duplex. Of course the other strand also goes in this manner here both are right handed helices but they run in opposite directions. So, the 5 prime into 3 prime end sense other one goes from the other end 5 prime into 3 prime end antisense.

And they are held together by the base pairs here and these ways base pairs are called the Watson Crick base pairs. So, these are all the base pairs and it is the overall features of the B-DNA are given here. So, you can see there is a big groove which is indicated by this here this is the big groove it is called the major groove and there is a smaller groove which is called the minor groove here.

And therefore you can see that all the base pairs one end opens in the minor groove the other end opens on the major groove. So, these are the characteristic appearances of the B-DNA. On

the other hand the Z-DNA is actually a left handed helix you see the helix goes like this and it is also zigzag it is not as smooth as it is as the B-DNA is. It also goes in a zigzag manner and you have the left handed helix as indicated by this and there is a deep there is a deep groove here and there is a bulge at this point.

So, therefore this structure is not as smooth and symmetric as this one is and here are the parameters which are given for this 2 structure types this is the firstly right handed DNA B-DNA is right handed versus a left handed DNA here and the number of nucleotides per turn. So, when the system repeats there the cycle repeats itself how many nucleotide base pairs are there the B-DNA has 10 base pairs and therefore we say 3.4 angstroms into 10 there is a 34 angstroms is the rise per that is indicated here.

Next and then whereas the G-DNA has 12 base pairs per turn and the diameter of this helix the entire helix here this is 20 angstroms and here it is 18 angstroms somewhat less. And the rise per base pair is 3.4 angstroms here this is 3.7 angstroms here and the total helix pitch that is 34 angstrom because if you take 30, 10 base pairs per turn 3.4 into 10 that makes it 34 whereas this one goes to 45 angstroms.

One particular turn what is the rise what is the rise per one turn 45 angstroms here and the random per base pair there is a rotation per base where this is 36 degrees and this is minus third what is – 30 degrees because it has to go in the negative sign because it is a left-handed DNA. If I take the right-handed rotation as positive the left-handed rotation will be negative and therefore it is – 30.

So, 36 into 10 will be 360 degrees that makes a complete turn whole way and minus 30 into 12 makes it 360 degrees and therefore that is a 12 into this will be – 30. And there are grooves here wide and shallow through different kinds of goals and these are very well stacked and these the base pairs are not very well stacked in the Z-DNA. So, you see the stacking is not very good whereas here the base pairs are parallel to each other and they stack one over the other and that is there is a quite a good structure symmetrical structure.

And now there is one more the important parameter which is not of course visible from here that is called as the glycosidic torsion angle. What is the glycosidic torsion angle I will show you that soon and then I also mentioned in the last time that the in the case of B-DNA it is a monomer which is a repeating unit monomer is the repeating unit whereas in the Z-DNA it is the dimer which is a repeating unit and that is why these are given separately here.

And for the B-DNA there are 2 kinds of glycosidic torsion for the Z-DNA 2 kinds of torsion angles are indicated here syn and anti, one of the nucleotides the guanine nucleotide has the syn conformation whereas the cytidine nucleotide has the anti-conformation and the sugar geometries whereas in the B-DNA they are all C2 prime endo which is uniform whereas here it alternates. So, C3 prime and gaunine has the C3 prime endo sugar geometry.

And the cytosine has the C2 prime windows or geometry therefore this makes the dinucleotide as the repeating unit.

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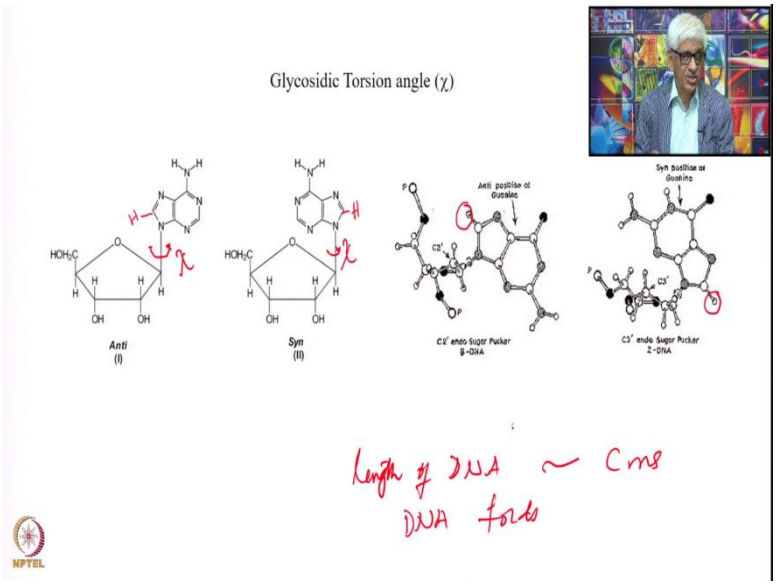

Now what is the glycosidic torsion angle? This is explicitly indicated here. So, you see here this is the sugar ring the sugar ring is a 5 membered ring here this is shown for the RNA but it does not matter it is the same for the DNA as well. So, in the case of DNA this OH group is replaced by the hydrogen same here. Now and the glycosidic torsion angle is this, this is the glycosidic torsion angle rotation around this bond.

This is labelled as chi and proper model of the this is the schematic on the left hand side and the proper model of that is shown on the on the right hand side. So, here it is both the all the things are included in this. So, this torsion angle you notice here what is the difference between these 2 here it is shown for the purine ring this is a purine base and this one is the guanine what is chosen here is a guanine because you have NH 2 group here and adenine also has an NH 2 group here.

So, this is the guanine has a NH2 group here adenine has an NH2 group there. So, if the rotation is around this bond what is the difference between these two. See the 5 member ring this is the 5 membered ring of this purine ring comes on the side of the oxygen here the this torsion angle is defined with respect to this 4 atoms. If it you can either define this way or you can define with respect to these 4 atoms.

So, either way it is the same thing. So, you can choose a convention where you want how I want to choose one particular convention is used. So, the essential point to note is from the structure point of view is that the 5 member ring here comes on side of the oxygen and here there is a proton attached notice the proton is not shown here but there is a proton here. There is a proton here and that proton is called as the H 8 proton and in this case this proton is here.

So, the protons are on two opposite sides in the two cases. Now in this case this is called as the syn conformation whereas this one goes outside relative to this oxygen position and in this case it comes closer and this is called as the anti-conformation. Typically it is shown in terms of the structure when you actually build a model how does it look. So, you have the C2 prime endo geometry here sugaring is in the C2 prime endo geometry and the anti glycostatic torsion angle.

So, this orients rotation around this bond is detected here you see this NH 2 graphs come close and this is the proton this is the; and this is the proton here you see this proton comes closer to

the oxygen of the sugar ring here. So, whereas that proton is far away this far away compared to oxygen that is this one here this is far away as I mentioned this is far away but this one will.

Now be this will be closer to the sugar ring sugar ring protons here the H 1 prime protons that will be close this proton will be close to the sugar ring protons here whereas this proton will be further away from the H1 prime or the H2 double prime protons in the case of the anticonformation C2 prime of the sugar and the anti position of the glycosidic of torsion angle. So, and these will be important why I am mentioning this is.

Because this will be extremely important when we actually use these information for structure calculations with regard to determination of the structures what are the short distances from the NMR point of view which are the important distances one has to see from that point of view this is very important that is why I am pointing out these things a definition of the glycosidic torsion angle.

So, we have C3 prime endo geometry for the sugar ring in A type structures or RNA structures and B type structures it is the C2 prime endo geometry and the glycosidic torsion angle is anticonformation it is both in B-DNA and A-DNA whereas you have possibilities of glycolic torsion angle in the syn and anticonformations in the case of Z-DNA and there are other possibilities as well.

Now is that all about the nucleic acid structure surely this is not why we are saying this because you see you remember the DNA if it were duplex as indicated here for so, long the length of the DNA length of DNA will be of the order of centimetres. Considering one billion base pairs and DNA length in this every cell it will be in the order of centimetres. Because 34 angstroms per rise and 1 billion base pairs if you take it will come to the order of centimetres.

Now this cannot be accommodated how in the cell which is only of 1 micron size and the nucleus is even smaller than that therefore DNA folds DNA folds multiple times. There may be stretches of various other kinds of strands where other kinds of base pairing possibilities there may be single strand possibilities all sorts of things can be present. And in the case of RNA we mentioned already that the mRNA is a single standard RNA.

And in the case of tRNA and ribosomal RNAs there can be different kinds of structures possible with various kinds of folds of the backbone and resulting in various different kinds of base-base interactions. What are the possible base-base interactions?

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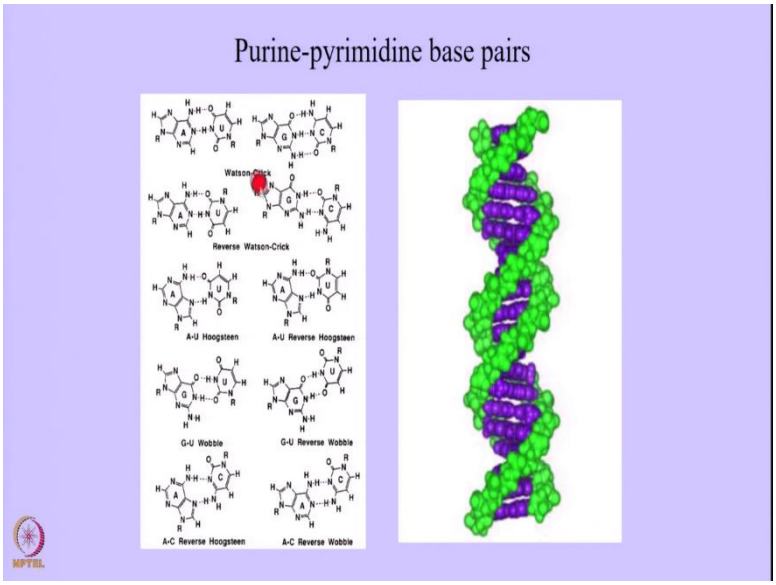

That is what we are going to see here. So, you can have. So, far we talked about the purine pyrimidine base pair that is the one which is indicated here on the top A T base pair. Now this is purine pyrimidine base pair. So, what is this is the pyrimidine ring and this is the purine ring this is AU and GC for the AU how many hydrogen bonds are there 2 hydrogen bonds and for the GC or the for the GC we have 3 hydrogen bonds which are holding them together.

Notice carefully which watch is the nature of the hydrogen bond this particular position is hydrogen bonded to this nitrogen here and what is R? R is a place where the sugar ring is attached here the sugar ring is attached in this position and in this case in the purine sugar ring is attached at this position this position is called as the N9 position this is a N9 position and this is N1 position this is N1 the nomenclature goes in that manner.

Whereas for the pyrimidine this is this position is called as the N3 position N3 the numbering goes in that manner. So, the standard nomenclature with regard to the IUPAC conventions etc you have this is the N9 position this is the N1 position this is the N3 position this is all we have to remember here. So, so far as the purine, pyrimidine, base pair are concerned these are the Watson Crick base pair which are there in this B-DNA.

So, duplex both the backbone is in green and the purple are the base pairs this is the possibility. Now there is another possibility also here see look what is involved here. So, what has happened here this base pair this is different from this a base pair the reverse Watson Crick this portion is the same the A is in the same configuration NH. Now what has changed in this NH, NH and N the R is here.

Whereas the R is here in this case the R is up which means there is a rotation with respect to that with respect to this axis with respect to this axis there is a 180° rotation therefore this R has come on to the top this R is at the same place the sugar ring is at the same place. Here the sugar ring goes on the top. So, therefore this is called as reverse Watson Crick and same happens here as well NR is here and in this case the NR is there.

So, this is both in the AU as well as the GC base pairs it goes in this manner. Now so, this is the other possibility of hydrogen bonding surely these people are toyed around with all these possibilities finally came up with this it turned out that this what they came out was finally the

correct one with regard to the B-DNA. But this kind of things also people have toyed around to see whether these ones fit.

Some experimental data did the building model, model building did not fit into this once they came out with this but this can be there this can be there in other kinds of situations where the DNA folds and various kinds of interactions can happen these ones can be there. And then look at this, this is called as the reverse this is the EU Hookstein. This is the Hookstein base pairing Hookstein base pairing.

What happens here the NH is base pair to this configuration is the same here. Now this is the purine ring and it is this nitrogen it is this nitrogen the 5 member ring nitrogen is involved in hydrogen bonding with this NH here. Whereas in this case it is the NH of the end of the six membered ring whereas here is the end of the 5 member ring. So, that is here this is free here right this N is free and that. Now comes here to take part in the.

So, therefore there is a rotation of the glycosidic torsion angle which brings this nitrogen closer to this hydrogen here this is the N3 of U is base to N7 of the purine and that is called as the Hookstein base pairing. So, Hookstein probably which is the one who proposed this. Similarly there is a reverse Hookstein base pair in this case the NR here NR is here and NR is there on the same side of the duplex or the on the base pair that is.

So, they are both open in the same groove whereas here you see the NR is here and this NR is here and therefore this is the AU reverse Hookstein in base pair. Once again this is the N 7 N 3 but the glycosidic torsion angle is different and therefore this one has gone on to the other side your reverse Hookstein and this one is a wobble base pair. Now then you have the so called Wobble well. So, that was the reverse 16. Now, this is the wobble base pair GU wobble.

See so, far we talked about the AU base pair but here it is a GU. Now the GU, GU is not the thing which is normally supposed to happen we used to we have to have a GC base pair. But here we are now talking about GU base way the G pairs with U conventionally we have AT base pair or AU base pair but here it is the GG pairs with U this also is possible. And now this hydrogen bonding scheme here is like this.

So, this N 1 of G pairs with this oxygen here and the once again this is the normal GU base pair NR here NR here and the reverse is again the NR goes on the other side. So, it depends on which oxygen is involved in the hydrogen bonding whether it is this oxygen or this oxygen that is what determines whether it is in the normal way or it is in the reverse way. So both this is called as the wobble base pair.

Because this is normally not there in the duplex DNA and then similarly you have the AC you see here this is the AC reverse Hookstein. AC reverse hook stream AC reverse meaning was we normally have AC base pair right. So, when the T is replaced by C we call it as a wobble AC is a wobble base pair but this is also possible.

So, such hydrogen bondings are also possible. So, you have this NH N here and H and both are NH N hydrogen bonds in this case. In all of these cases one is and these are NH 2 hydrogen bonds in this case. In these ones you have NH N hydrogen bonds one NH O hydrogen bond in all of these one NH-N one NH-O here also one NH N and one NH O whereas here you see AC in this GU wobble we both hydrogen bonds are NH O and the reverse also both are NH-O hydrogen bonds.

And in this AC reverse they are both NH N hydrogen bonds NH N hydrogen bonds is the amino proton is participating in the hydrogen bonds. Therefore you see how many different possibilities are there for hydrogen bond formation.

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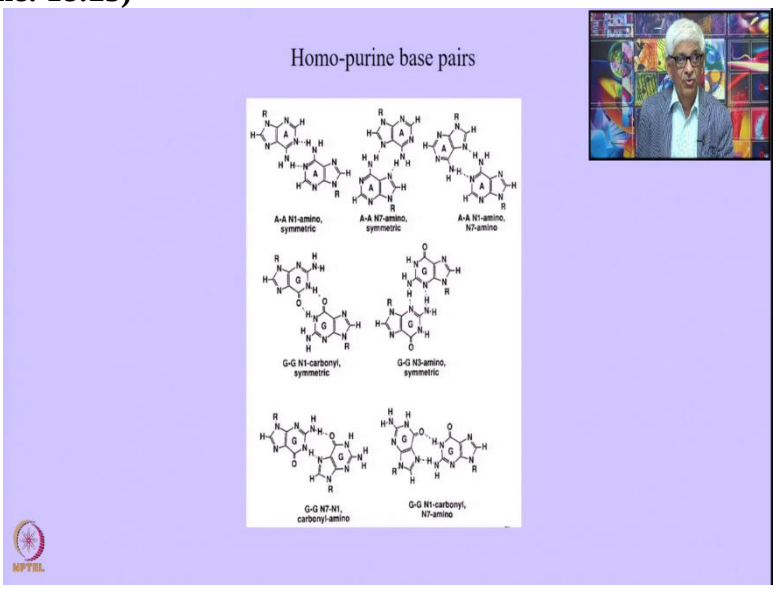

Now then you can also homo your purine base pairs just as we talked about purine pyrimidine base pairs you can also have purine-purine base pairs. So, here it is A and AA base pair and different types. So, AAN1 N1 to amino. So, you have the one of the proton is the amino and the other one is the nitrogen. So, you have here this amino of this is hydrogen bonded to this nitrogen here of the six membered ring and similarly six membered ring of this is paired to this nitrogen here A this is one A N1 amino symmetric base pair.

And then you have a N7 N7 is involved in this case you see it is a N7 which is hydrogen bond to the amino this is the N7, N7 is hydrogen bond to the amino an H proton here and correspondingly for this one N7 is paired to the hydrogen bond here. So, this is we have the amino protons participating in this. And similarly here as well AAN1 amino N7 amino. So, here you use both N7 both places N7 here we use both places see N1 and here we use N1 and N7 one case it is N7 other case it is N1.

So, the enormous possibilities of hydrogen bonding schemes are possible and of course only when of course you cannot remember this when you but certainly when you actually have to build models try and understand the structures which you actually observe theN1 should take into account all of these possibilities. How does one determine all of this? This of course one determines by NMR by looking at which are the ones which are hydrogen bonded which are the protons which are involved in the hydrogen bond.

Whether it is imino protons amino protons which a nitrogen is involved. So, all of this can be determined by from NMR data. So, this is the G1 N1 carbonyl symmetric CG GG. So, you have G1, G1 is this. Now G1 is car hydrogen bonded to the carbonyl here. Earlier you are using NN hydrogen bonds. So, here is NH O. So, NH O hydrogen bond here N1 position N1 position of this goes to the oxygen of this and one position of this one goes to the oxygen of this.

And both here in this case only the six membered ring is involved and what happens here. Now this is GG N3 amino symmetric. Now here it is NH-N hydrogen bonds and this is amino to N3

position this is the N3 position. In this case this was used iN1 position here we are using the N3 position and N3 to this amino proton GG N3 amino symmetric hydrogen bond and the last one is GG N7 N7 N1 carbonyl amino.

So, N7 that is that is this one this is the NH-N hydrogen bond here to the N1 and the amino is hydrogen bonded to the oxygen here. So, you have here one NH-O hydrogen bond and one NH-N hydrogen bond similarly GG N1 carbonyl N seven hydrogen bond. So, N1 is where this is the N1, N1 is bonded to the oxygen here this is N1 is go to the oxygen here and this the N7 is going to the amino.

So, this is the N1 there is the imino proton on the G this G imino is hydrogen bonded with oxygen whereas this nitrogen is hydrogen bonded to the amino of the G. So, these are GG base pairs. So, you can have. So, many different kinds of bases homopurine base pairs we saw AA base pairs and then we have the GG base space different possibilities of hydrogen bonds.

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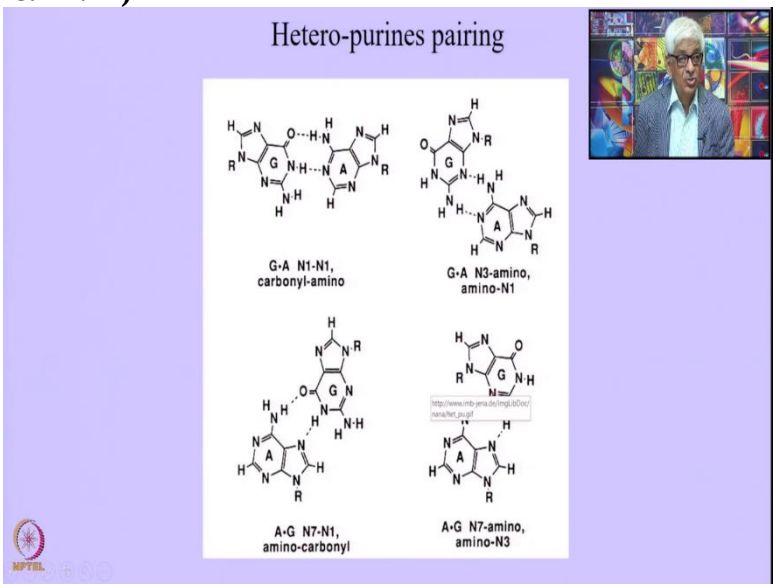

Then heteropurine, base pairing. So, far we looked at AA or GG but you can also have GA base pairing. So, GA base pairing is indicated here different possibilities of GA pairing here. So, the G here you see N1 carbonyl amino. So, it is amino of the A is hydrogen bonded to the carbonyl of the G and the imino of G is hydrogen bonded to the nitrogen of A. So, this is NH N hydrogen bond and this is the NH-O hydrogen bond. So, this was GA N1 N1 carbonyl amino.

So, these are both N1 positions there N1 N1 and these are GA this is a notice here in the case of G there is a proton here I indicated to you earlier and what is present in the case of A there is a proton at in the case of G there is an amino here there is NH 2 group this is position number 2 at 2 position there is the amino group here. In the case of a at position number 2 there is also a proton and you have an amino group at the this position there.

So, this is the proton here is N2 position this is N9 and this is N8. So, there is H8 proton here and the H2 proton here let me write that here this is H8 and this is H2 and this is H8. So, these are the positions according to the labelling and that is what we have there. So, in the same manner you have the GA N3 amino N1 GA N3. So, where is G this is the G and N3 is this and this is going to the amino of the A. So, this is the NH2.

So, this NH-N hydrogen bond is there and this amino this is at the 2 position is hydrogen bonded to the N3 of of this and. So, therefore again NH N these are both NH-N hydrogen bonds here one NH-O and 1 NH-N and involves amino groups and the imino protons. And the next one is AG N7 N1 aminocarbon. So, this is the GA one possibility and this is the next possibility here.

So, this amino is going to the oxygen of the A amino is going to the oxygen of the G, A amino is going to the oxygen of the G and then this NH N and this is the N1 position is going to the N7 here N1 to N7 AG N7 N1 this is A this is N7 this is N1 and AG N7 amino N3 and look at these possibilities. Because there are so, many hydrogen bond acceptors and donors in the base structure all these acceptors and donors can accept a hydrogen bond and give a hydrogen bond give a proton.

And that is why you have this so, many different kinds of possibilities of hydrogen bonds pyrimidine-pyrimidine base pairing as well likewise. So, far we looked at the pyrimidine-pyrimidine base pairs you have possibilities of CC amino CC symmetric base pairing CC carbonyl amino symmetric base pairing and CU there is a CU pairing possibility although N3 and 3 here and then UU pairing carbonyl N3 to symmetric and we will not describe it in detail further.

So, just the main structures are shown here then you have possibility of UC N3 N3 and UU hydrogen bonding possible. So, you have. So, many different possibilities of hydrogen bonding and because all of these nitrogens and the carbonyl oxygens they are all acceptors and you have the donors are the I mean amino protons the NH 2 and the NH protons and these are present on both the all the bases you have such kind of acceptors and donors and that is why you get different kinds of hydrogen bonds.

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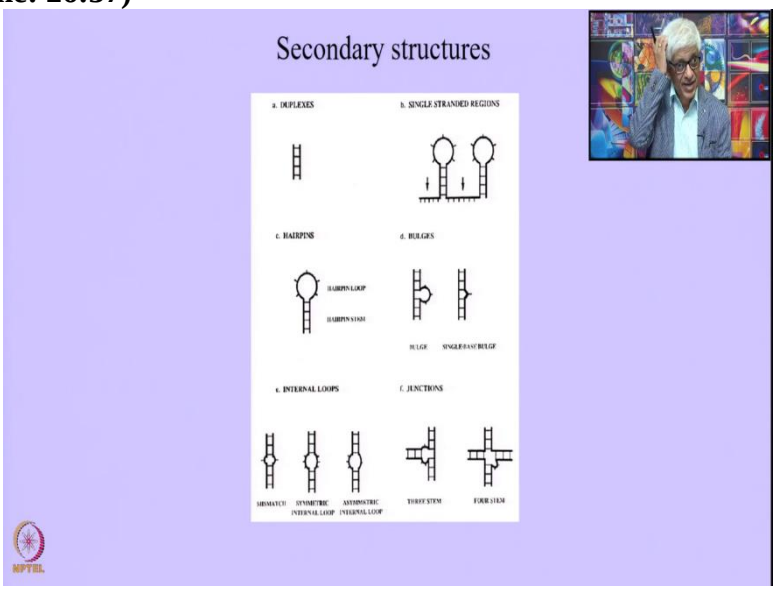

Now as a result of all of these now I indicated here what are the different possibilities of the structures we said. So, far we talked about the various kinds of base pairing schemes and where do they occur where do they occur. Now you have possibilities of a duplex standard duplex then you can have a running chain is going on depending upon the nature of the sequence which is present here it can assume different kinds of secondary structures single standard regions.

It has a single standard regions and you have a loop here there are loops coming out here in this place and these are the. So, single stranded regions you will have in this, this is not paired at all. So, this portion is paid this is not paired. So, all kinds of folding schemes can occur. So, these are and then you can have the hairpins. So, the thing goes like this, this looks like a hairpin right.

So, therefore and then you have these bulges here in a duplex in between the base sequence is such that it is not pairing possibility here this fellow bulges out. So, you will have a bulge here. So, similarly there is a small bulge here there is only one but this is several bases are involved in this therefore it becomes a longer loop and this is only one base which is going out here such kind of possibilities are there.

And now in the internal loops within the within the duplex itself you can have certain regions where there are bulges in the middle. So, because these are not complementary why does it happen because these are not complementary sequences. When there are not complementary sequence the possibility of a base pair does not exist then you will have these kinds of loops symmetric loops in the parallel structures.

And you can have anti-symmetric structures anti-symmetric loops and you have this kinds of possibilities and you can have 4 stranded structures. So, in this place so, you have the 3 stem this structure has 3 stem this structure has 3 stem and we will see that such structures do occur in RNA ribosomal RNA, tRNA and things like that. And there is an actually a region which is bulged out here.

So, the chain has to run like this. So, these are all the possibilities indicating the folds of the nucleic acid structure. And you see here is a 4 stem structure and such kind of structures do occur in the functional aspect whenever there is a kind of a recombinant process going on inside the in the replication process or such kind of this kind of structures do happen in this, this is a 4 stem process.

So, the stable DNA structure RNA structure is one thing but the during the when there are activities going on the DNA has to open up and interact with other systems other DNA segments or other protein segments and such kind of transient structures do happen and these transient structures the for example one of them is called the holiday junction. So, they have here this is the 4 stranded structure.

So, there are many such kind of structures which are possible these are functionally relevant. So, the DNA has to open itself to express itself to form either for producing the proteins or replication process and things like that and in all those processes such kind of transient structures do occur now.

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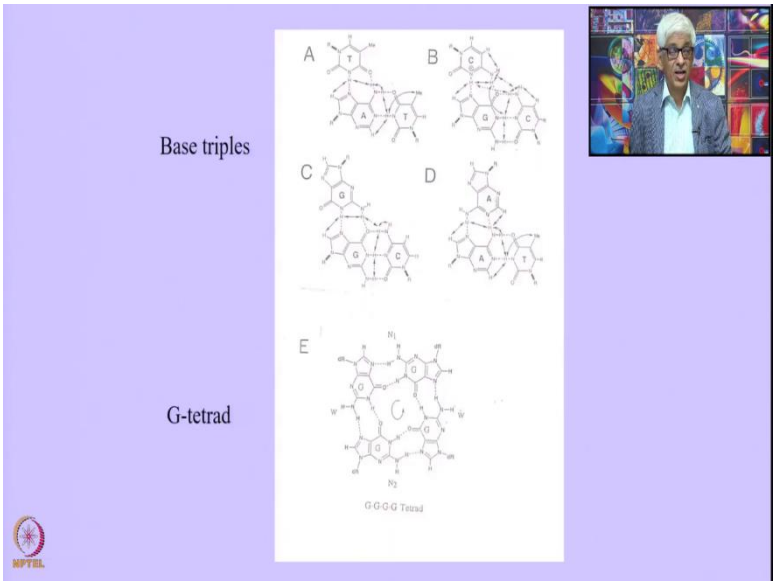

So, far we talked about 2 bases interacting with each other but you can also have base triples base triple means. So, your 3 base pairs 3 bases are interacting with one another. See here you have the normal Watson Crick AT base pair normal Watson Crick base pair and here the normal Watson Crick GC base pair and on the top comes here a third base which is the T. So, you have AT AT triplet this is called as a base triple T AT triple and here it is a CGC triple.

And look here in this base pairing what happens in the free position which is here the N7 position is used up for this base pairing in the for the third base. The oxygen of this uses this amino proton this proton here okay amino proton and the N7 is used up for the T and this place. So, this kind of a this triple base pairing is possible. Similarly for the GC you see also same thing happens the free donors and the acceptors.

In the Watson Crick base pair can accommodate another base in the major group or if it comes on this other side it is a major group. So, on this side it is a minor group. So, you can have this sort of possibilities here. So, you have a GC and the G coming here okay what you had here T AT, T is the pyrimidine AT and then of course the third base is the pyrimidine here there is a third base which is the purine the G is coming.

And similarly in this case you have AT pair and then the A is coming the third base is A and what are these arrows here these arrows are indicating which are the short distances because these are the observables in NMR spectra. See this proton pro order indicated are the proton-proton distances. So, all these proton-proton distances are the ones which are short distances and we use these kinds of short distances to identify or assign the individual bases and the individual protons.

That is why these are indicated here indicated by double headed arrows that we can actually observe these ones by recording spectra in water. Now these are base triples. Now you can also have quadruplexes it is called the G tetrad. So, 4 G's can hydrogen bond with each other and to form what is called as the GGGG tetrad there are 4 G's here very symmetric see and all the all the donor and the acceptor sites are used up here.

So, it uses this nitrogen this oxygen this nitrogen amino proton and this amino proton. So, all of these are involved in hydrogen bonding in a very symmetrical manner. So, this produces a G tetrad which is an extremely stable structure very stable structure. We will see I will show

you examples of this how this 4 stranded structure is possible and how this can be extremely stable.

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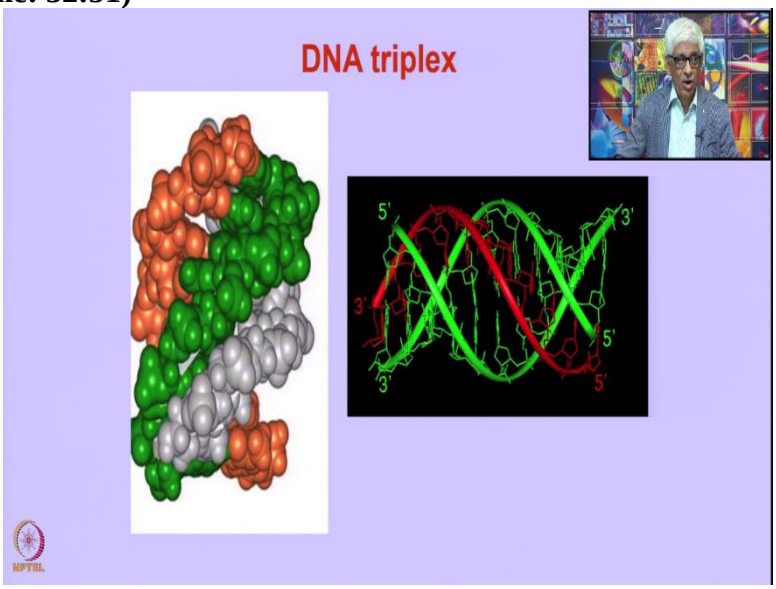

So, typically how does the BS DNA triple helix look like. So, you have the green one is the normal duplex and the triple helix comes the third strand comes in this major groove it comes on this and then you see the third strand is hydrogen bonded to the base pairs in the duplex and this is the space filling model of the same sort of a structure. And these ones are such kind of structures are possible in the quadruplexes.

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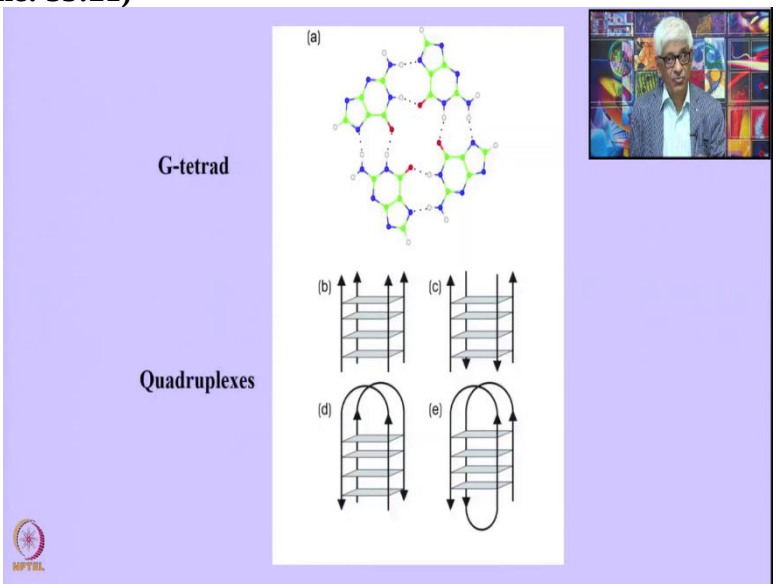

So, the 4 stranded structures are possible here. So, you have the G tetrad and you can have quadruplexes of various types various types of quadruplexes are possible these are called parallel standard quadruplexes. And here you have 2 strands going in one direction 2 strands going in other direction and you can also have loops here the chain runs like this and loops around come here the other chain runs like this and loops around and comes down here.

And these 4 G's which are in the thing they can form hydrogen bonded structures. And in all of these is the glycosidic torsion angles becomes important. So, and depending upon what is the orientation of this you can have different kinds of base pairing schemes.

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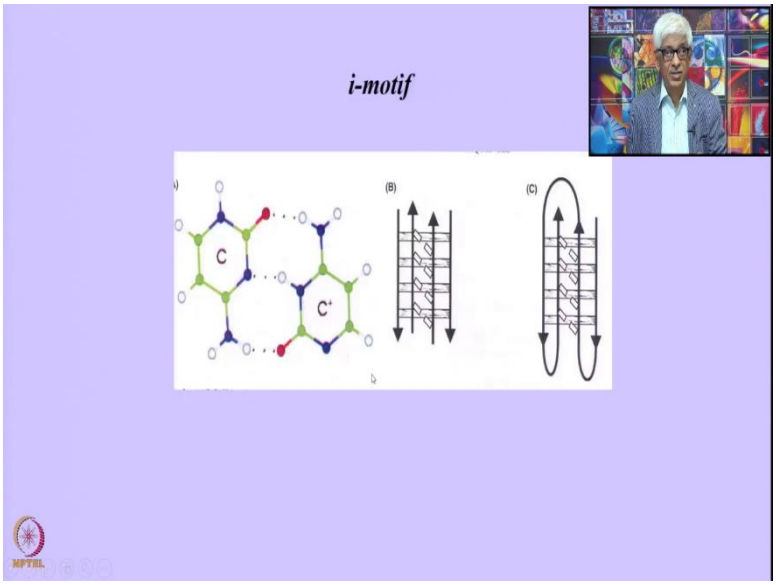

And so, that determines the base percent then the last one structure which has been discovered some time back is called the i-motif. The i-motif is a structure which is between CC plus. So, the CC base pairing is possible but the one of the C gets protonated here and because of that protonation it gets a positive charge therefore it is called as the CC structure. Now here what happens is you have 2 duplexes inter-digitating.

That is why it is called as i-motiff. So, it is it can be different molecules or the same molecule loops around turns around and things like that and comes back and that is shown is in this case the chain starts here let us say goes like this goes like this and then goes like this and then turns around and then so, these are the various possibilities that all these are required because the DNA has to fold in many different ways and all those structures will have to be stabilized this stabilization happens because of the different possibilities of hydrogen bonding pairs.

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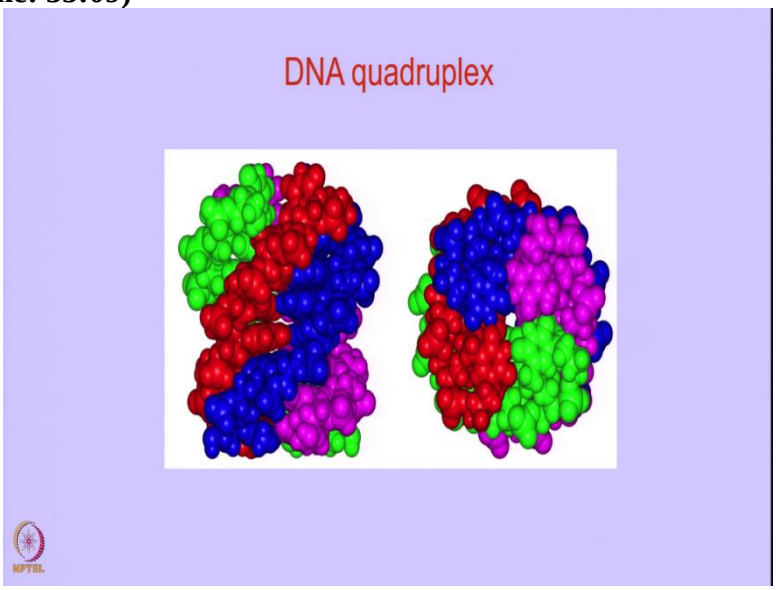

So, this is actually a quadruplex how does the code apply structure look like. So, this shows here the 4 how are the 4 strands accommodated in this. So, that is the quarter play structure you have this 4 colours here these are the individual strands which are going as you can form a structure of this type this is the DNA quardruplex. So, I think we possibly stop here.

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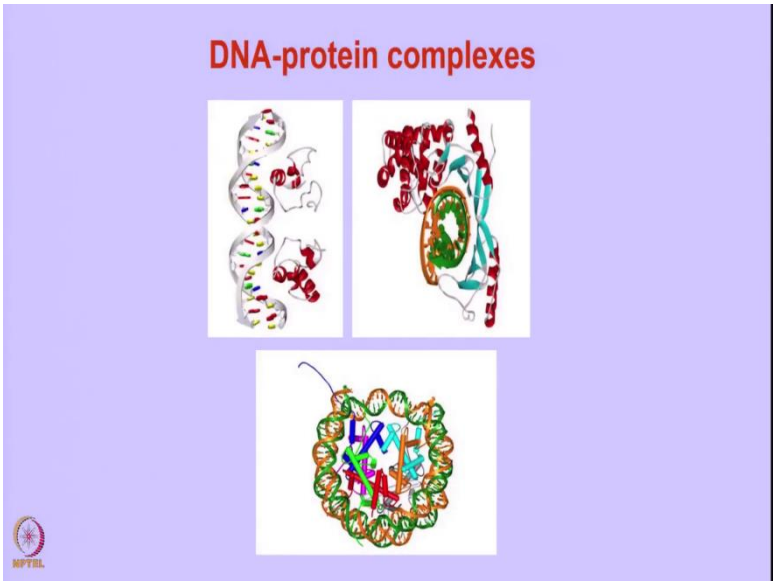

And now of course here the DNA protein complexes can be formed DNA protein complexes are important in various. Now here it shows how a duplex DNA can fold and accommodate the proteins and the proteins can interact with the DNA and proteins will have to express and protein will have to interact at various sites in the DNA duplex or with other various kinds of structure that are possible.

Either with the single standard areas the double standard areas different possibilities of interactions are possible. So, there is a whole variety of structural possibilities enormous complexities in the DNA structure and people thought the only duplex DNA is a simple thing that is the only thing about the DNA but of late we know that there are so, much there is; so, much more about the nucleic acid structure which remains to be explored.

Much more needs to be done with regard to the nucleic acid and especially RNA structures. So, many different varieties of RNA structures are possible. So, I think with that I will stop here.