Essentials of Biomolecules:
Nucleic Acids, Peptides and Carbohydrates
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Lecture 03
DNA and Proteins

Hello everybody welcome to the lecture again today is the third lecture and we are discussing the structure of DNA and to see how chemistry plays role in determining the specific structure of DNA which in this case is the B form of the DNA.

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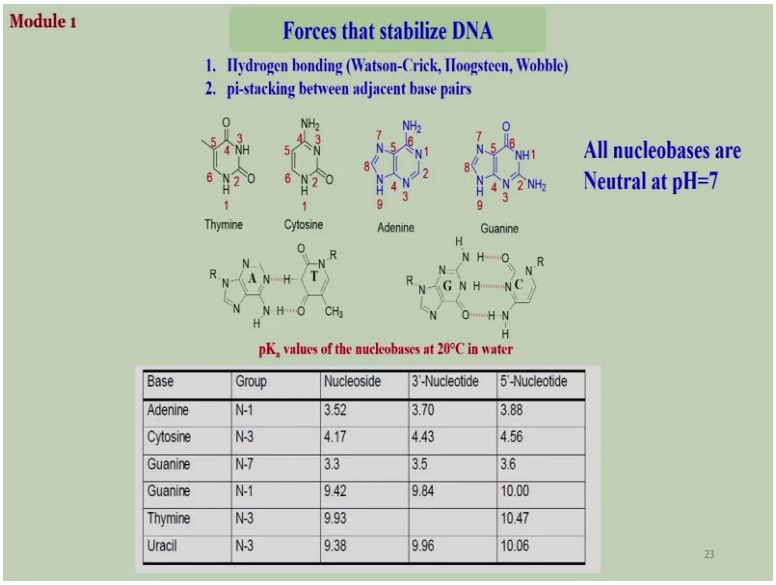

Base	Group	Nucleoside	3'-Nucleotide	5'-Nucleotide
Adenine	N-1	3.52	3.70	3.88
Cytosine	N-3	4.17	4.43	4.56
Guanine	N-7	3.3	3.5	3.6
Guanine	N-1	9.42	9.84	10.00
Thymine	N-3	9.93		10.47
Uracil	N-3	9.38	9.96	10.06

So, earlier what we have seen is that the nucleus is the orientation of the nucleus bases when we have the pyrimidine nucleus as thymine and cytosine and the purine nucleus is adenine and guanine which conformation they exist which form they exist. And we have seen from the I have given the full chart of the pk values of the individual nucleus bases for their individual hetero atom positions nitrogen positions.

And from here you can understand that for all these nucleus bases the keto form which is given in this fashion keto form keto form keto form and keto and amine form here also is the keto form and the amine form here is the amine form. These are the actual forms that will exist under the physiological condition that is at pH 7.4 and that you can explain from their experimental pk values. If you take the enolate forms or their amine forms for the amine groups you will see that those forms are not stable at the physiological pH at pH 7.4 and the keto form and amine forms are the stable form.

So in DNA the nucleus bases will exist in this form the structure of the nucleus bases will be this so which is a kind of locked structure. And that is of course responsible for the Watson-Crick base pairings for these AT base pairs with 2 hydrogen bonds and DC base pairs with 3 hydrogen bonds. If you look at if you take the in all it forms the hydrogen bonding pattern will be entirely different and that does not happen usually.

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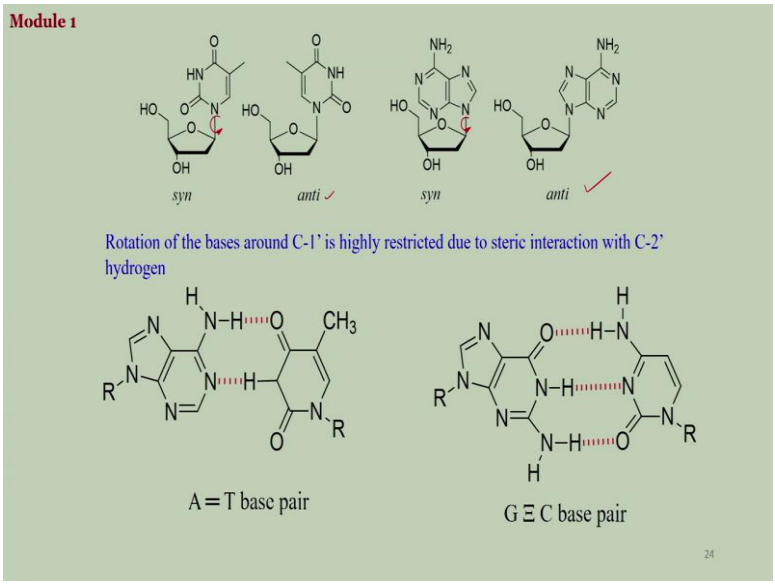

And similarly we have seen the other type of rotation the locked rotation of the nucleus base when it is attached with the sugar deoxyribose sugar. So, this is the Syn form where I have explained that with the double bond oxygen here it is closer to the oxygen of the sugar and similarly for the purine basis for adenine the 6 membered ring is just right on top of the sugar moiety and both of these forms are called the syn forms and they are not stable because they have huge steric crowding and the electron repulsion factor.

So, therefore the tabular form is they will flip they will rotate around the CN single bond because the rotation around a single bond is favourable at room temperature so it will rotate and give you the anti form which is the better form or the more stable conformation for the DNA. So, again so this conformation and this conformation here will be the favourable confirmations that we see also this conformation is present in DNA.

And this is the explanation of why? Of course this has also done that plays a vital role in forming the base pairs. So, if you see that a 6 membered ring here is out is a little bit away from the sugar moiety R is the sugar and that is why it is available for hydrogen bonding.

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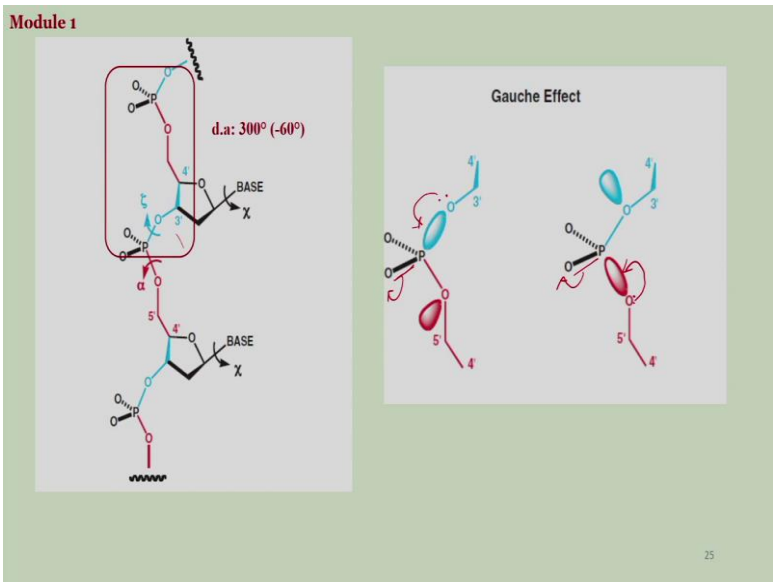

So, next comes today I will talk about the other two factors that are responsible for the helical structures of the B form of the DNA. One is the phosphate the orientation of the phosphate and how the skeleton basic skeleton of the DNA looks like which orientation it will assume. So, if you look at this structure here is the sugar and the base and here is the 5 prime end and this is the 3 prime end of it. So, here if you see it starts from the phosphate P this is one is double bond O one is O minus so O P O and this is the 5 prime end of this sugar.

And then there is a 3 prime end of the sugar with an oxygen that forms a bond with the next phosphate and it goes on like this. So, there are two planes in this case one is this other one is this so that is called so two planes and when there are two there is angle between the two plants and in this case the favourable orientation will have a dihedral angle d a means dihedral angle favourable dihedral angle would be -60 degree that comes from the gauche effect as can be seen here.

So, if you see if you consider this bond P and O so P and O has a single bond with a electron cloud here and then here in the next one you have the oxygen free oxygen with a lone pair of electrons. This is the favourable orientation for this case with the lone pair of electrons away from the Sigma bond because otherwise if it is closer then there will be a bond pair lone pair repulsion and that is not favourable so, this is the favourable structure.

Similarly if you look at this bond take this bond as a sigma bond and then lone pair of electrons on this oxygen they will be away from the sigma bond to avoid bond pair lone pair repulsion.

And that is how the structure or the angles in the backbone or the phosphate skeleton comes from in DNA. Another aspect is that when you see PO bond this PO bond or this PO bond of course they are single bonds but these are not entirely single bonds they can undergo resonance.

If you consider this a double bond then there will be resonating structures possible for the phosphate and that makes partial double bond character of this pure as or less the same thing will happen in this case also resonating structures. So, although these are single bonds free rotation around the single bonds should have been really possible and should have happened but there are somewhat restrictions is there.

And the overall the Gauss effect as well as the resonating structures they actually lock the confirmation of the local conformation of the skeleton in this fashion.

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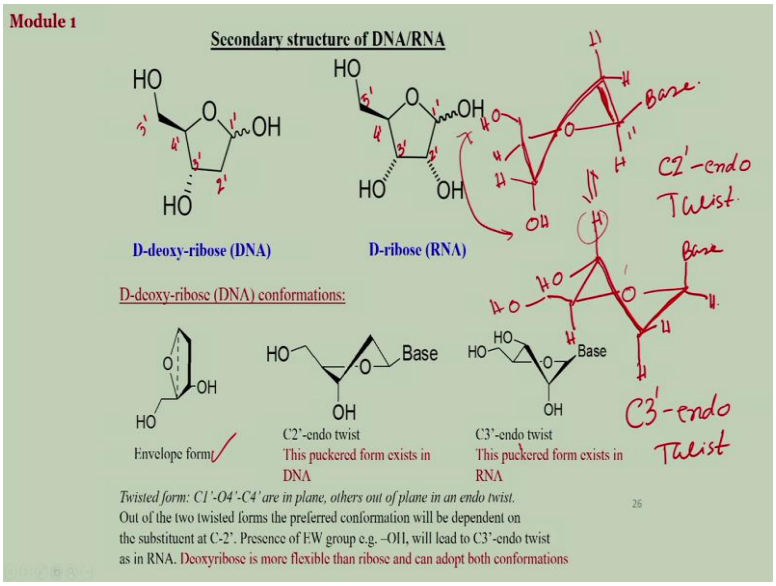

And now coming to another important aspect which is the conformation of the sugar what orientation? The sugar moiety in DNA or in RNA will have. So, to start with that now just consider without that whole DNA structure consider the deoxyribose sugar this is a pure deoxyribose sugar D deoxyribose sugar which is present in DNA with the OH below the down the plane and the 5 prime which up the plane.

If you consider RNA, RNA is d ribose sugar where a 2 prime position you have another hydroxyl group down the plane. So, if you do the numbering it is like this 1 prime 2 prime 3 prime 4 prime 5 prime 1 prime 2 prime 3 prime 4 prime and 5 prime. Now if I go back to the

DNA structure the paper mode you have seen the sugar is oriented in these directions. So, now if you look here in this part it is not actually on the plane of it.

I have a rough draw of the 5 membered ring or 5 membered sugar with the oxygen here. So, if you see the sugar actually exists in this fashion with the oxygen folded up the plane if you consider this is the plane of the sugar then the oxygen would be off the plane. So, it looks like an envelope which you can fold this so this is the closing part of the envelope and this is the plane. So, that is what the 3d structure of this sugar part is that it will be out of the plane and it will be in this direction.

So, here also the same thing it has a envelope form the ribose sugar moieties. And now if you consider the DNA this is this is oxygen so this is 1 prime this is 2 prime 3 prime 4 prime and if you look at the deoxyribose so there is nothing here there is just 2 hydrogen's. In the 3 prime positions you have one hydroxyl group and that is down the plane at for prime position you have the CH2 OH that is up the plane okay.

One prime position I am not defining it because the nucleus base comes and nucleus base comes usually from the up the plane actually here it should be half the plane here also this would be up the plane when the nucleus comes it is after plane. So, now coming to the orientation so if this is the structure then what kind of orientation it can have. So, since this is a sugar and 5 membered ring it can have the puckered conformation.

So here I have written the two sugar puckered confirmations I will come in details there so, if you consider the deoxyribose and if you draw the sugar puckered confirmations with this then it will look like this. So, you know when you draw these other fucker confirmations you can twist the around that the 2 prime and 3 prime position you can keep the plane 1 prime oxygen 4 prime 5 prime ready in one segment and then twist that 2 prime and 3 prime bond and that twisting will give you different confirmations.

So one is that if I twist it at the 2 prime end it will look like this so this would be half the plane this is in front of you this is in front of you and this is on the plane and of course now I am considering with the nucleus bases. Nucleus base is in is up the plane so up the plane here in this case I am writing base for nucleus base up the plane in this case is equatorial position because the axial position is H.

This is the 2 prime this is 1 prime 2 prime position there is no hydroxyl both are H equal axial is H equatorial. 3 prime position you have one hydroxyl group here and that is down the plane so down the plane has to be this, this is down the plane which is axial, equatorial is H. Now CH2 OH is of course up the plane so up the plane is kind of axial, equatorial is H. so, this would be the confirmation the purkered confirmation of the deoxyribose.

If you consider the if you twist it at the two prime end and this is known as two prime end O twist. The same thing if you twist it back if you twist it at the 3 prime end then it will look like this. This is bold because it is in front of you it is towards you and here is the base and this is the 3 prime so you have twisted it in the 3 prime position. Now the base is up the plane and up the plane in this case is axial.

Here to prime nothing 3 prime you have weights down the plane so this is down the plane which is equatorial is down the plane axial is H and this is the 5 prime up the plane is your hydroxyl CH2 OH down the plane is H. So, this is called C3 Prime end O twist. Now out of these two structures which one is more favourable that we have to find out? So if you look here the base is in equatorial position.

Here you have the hydroxyl group in the axial position axial position substitutions are usually not favourable and here also axial position but here the hydroxyl group is little bit away from the carbon so that does not have much interactions much steric interactions with the sugar. This hydroxyl however will have 1-3, 1-3 gosh interactions. So, out of this which one is more favourable? So, if you look at the DNA then and there is another factor that I will talk about.

So, C 2 prime end O twist which is this form will be the predominating or the favourable form for DNA because although you have this is axial position the nucleus base present here is better off because it does not have; in this case if you consider the axial base that has lot of lone pair repulsion and the steady crowding within the other group within this and within this region also. So, that is the display variable part of it.

And in this case nucleus base is in the equatorial position which suffers less interactions or less crowding and less repulsion. So, another thing is that if you look at the phosphate here will be a phosphate here will be phosphate and then the distance between the two phosphate groups in

this case is around 7 angstrom that is if you have a phosphate instead of H if you have P instead of H if you have P then this distance is 7 angstrom.

On the other hand this distance if you have P here and if you have P there this distance is around 6 angstrom close to 6 angstrom. So, this is closer and closer means they will have to face more steric interactions or repulsions. So, for the DNA confirmation this the C2 prime end O twist is the favoured conformation.

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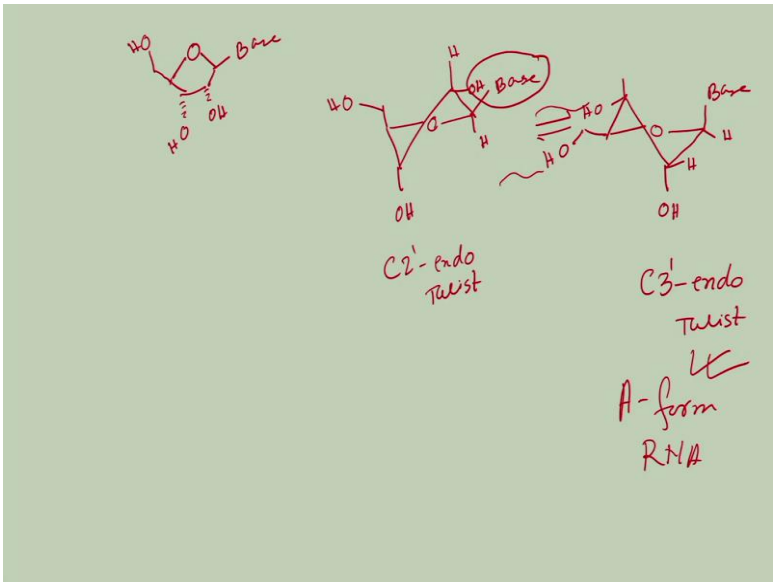

Now if you look at the RNA that is the ribose sugar ribose sugar was this here comes the base of the plinth and here you have the hydroxyl OH down the plane OH down the plane up the plane and then CH 2 this is up the plane. Now the same thing if you draw the C2 Prime and C3 prime end O twist this is the oxygen this is towards you so base is here equatorial and here you have the 2 prime position you have a hydroxyl group and that is down the plane.

So down the plane has to be equatorial rest are all the same and this is kind of axial so that is your C2 prime end O this is up here which is down the plane so axial this is down the plane equatorial and this is up the plane equatorial. So, that is your C3 prime end O twist. Now if you compare for the ribose sugar RNA then you will find that here you have a strong repulsion between the base and the hydroxyl group here.

And in this case although the bases in axial position that actually reduces or that decreases the huge repulsion that comes in this case between the hydroxyl group and the base so in this case for the RNA C3 Prime in the twist will be the favourable structure and that overall changes the

conformation the of the total RNA. So, DNA as I have said has the B form with proper double helical structures and that is that is coming from here.

Because if you have seen C2 Prime in the twist for DNA you can have the x this is the 3 prime end you can have the extension in this way and the 5 prime end will go that way. So, we will have a proper skeleton that is known as the B form. In A form your extension has to be in this part and from the 5 prime end this part and that will give you the A form of RNA. So, RNA mostly has a conformation and DNA has B conformation and that is one of the reason of course it is coming from because of the different sugar puckered confirmation of the DNA and RNA.

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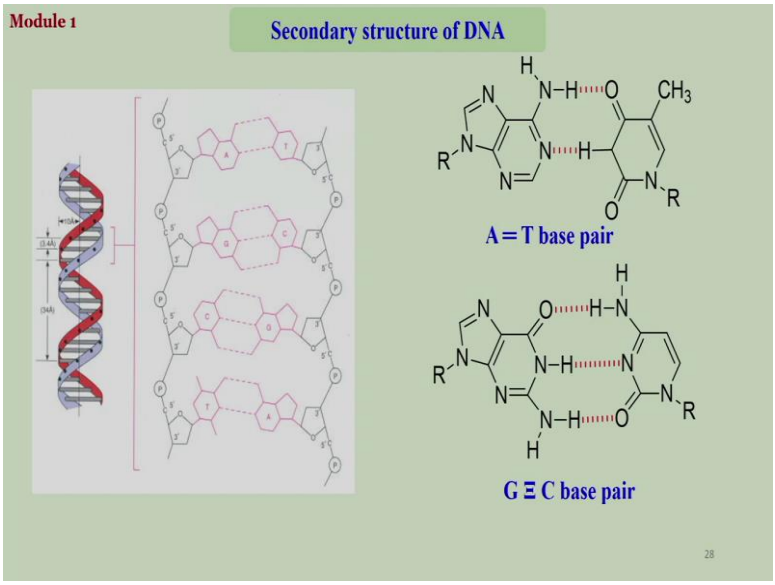

So, these are the factors that play important roles in determining the specific structure of the DNA as I have talked about again and again that is the B form of the DNA with the double helix structures and that is responsible for the proper hydrogen bonding which we usually write in these fashions AT base pairs and the end the GC base pairs. So, this is the most double helical structures.

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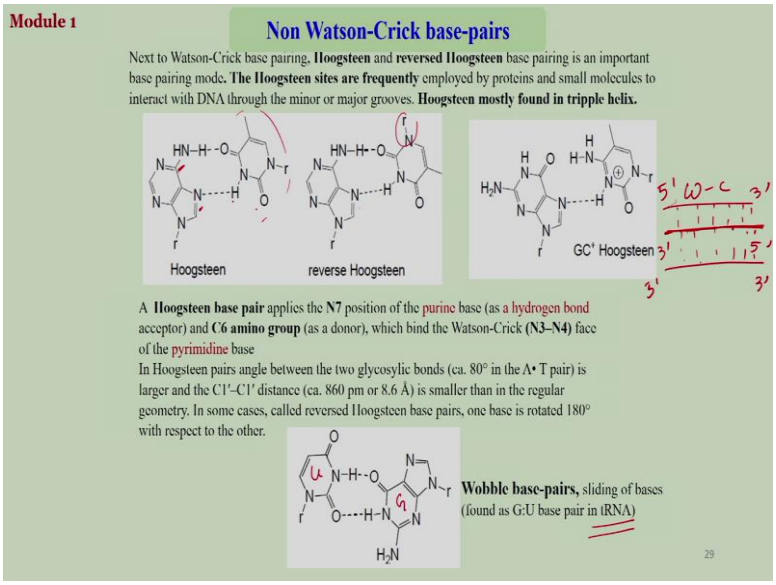

Apart from these so AT base pairs and GC base pairs are usually called Watson-Creek base pairs so apart from those there are some non Watson-Creek base pairs also they are sometimes naturally available at the same time when we make new molecules. So, when we make modifications of the nucleic acids. Then the non Watson-Creek base pairs play a vital role in making the new kind of substitutions or new kind of molecules.

So, naturally also apart from Watson-Creek there are other types of base pairs that are found one is called the Hoogsteen. So, if you look back at the AT base pairs you see that for adenine I have missed the nitrogen again here AT base pairs you see the 6 membered ring of the thymine so this carbon and this NH proton are involved in hydrogen bonding. On the other hand if you look at the adenine inside it is all the 6 membered ring that is involved in the hydrogen bonding NH this NH and this NH 2 both are coming from the 6 membered ring.

The 5-member ring is not involved in hydrogen bonding. Similarly if you see in the GC base pairs of course cytosine has only warning and all 3 of them are involved in the hydrogen bonding but if you look at the guanine it is only the 6 membered ring the substitutions on the 6 membered ring are involved in the hydrogen bonding not the 5 membered. Now if you look at the Hoogsteen hydrogen bonding this is R is sugar again both the 5 membered and the 6 membered are involved in hydrogen bonding.

And as you this is for the thymine part. So, here this will totally change the orientation of the whole DNA because it has to I mean it will; minor group major group minor groups everything will be changed also the structure of the DNA would be changed. So, this is a non unnatural it

is also found sometimes in nature as well this is the non Watson-Crick base pairs one kind other is the reverse Hoogsteen.

In reverse Hoogsteen is if you turn the 6 membered ring thymine a little bit make the sugar here then basically is this and this are present are involved in hydrogen bonding with the Hoogsteen mode taking the 5 membered ring as well as the 6 membered ring. So, this is called the reverse Hoogsteen it is basically if you think is this and this atom or this. So, these two are involved in the hydrogen bonding both are two hydrogen bonds AT base pairs.

GC Hoogsteen and GC plus Hoogsteen cytosine sometimes exists as C plus and then it can undergo hydrogen bonding in a Hoogsteen mode. Hoogsteen mode means again and the 5 membered ring is involved so this is called the GC plus Hoogsteen and the details of this kind of hydrogen bonding are actually written here so you can go through it. And there is third type which is called the Wobble base pairs.

Wobble base pairs are kind of sliding and whatever the normal base pairs you have seen AT if you just slide them a little bit this one if you slide it a little bit then what the orientation the orientation you get and the hydrogen bonding you get is known as the Wobble base pairs. So, in this case the thymine has been slide it down a little bit so that you have now this amine is not coming into the base pairs you have only two. So, this is guanine and this is for uracil.

So GU base pair that is actually present in nature in tRNA this kind of Wobble base pairs are formed. Now Hoogsteen base pairs are mostly they mostly occur in DNA triple helix. Now usually DNA we know and there are the double helix structures. But sometimes DNA can undergo triple helix formation with 3 strands that we will see later also that when we do the modifications we can see how the triple helices are formed.

So, if you have 5 prime to 3 prime DNA and then 3 prime 2 - 5 prime then they take one of this strand, one strand as the key strand and forms and other base pairs. So, here you have one set of base pairs and with this you have the other base pairs with a third strand that is 5 prime to 3 prime end. So, this is Watson-Crick base pairs 6 membered ring versus 6 membered ring and this but the other part is the Hoogsteen base pairs where the 5 membered and the 6th member both are involved this is Hoogsteen. So that is how the DNA triple helices are formed.

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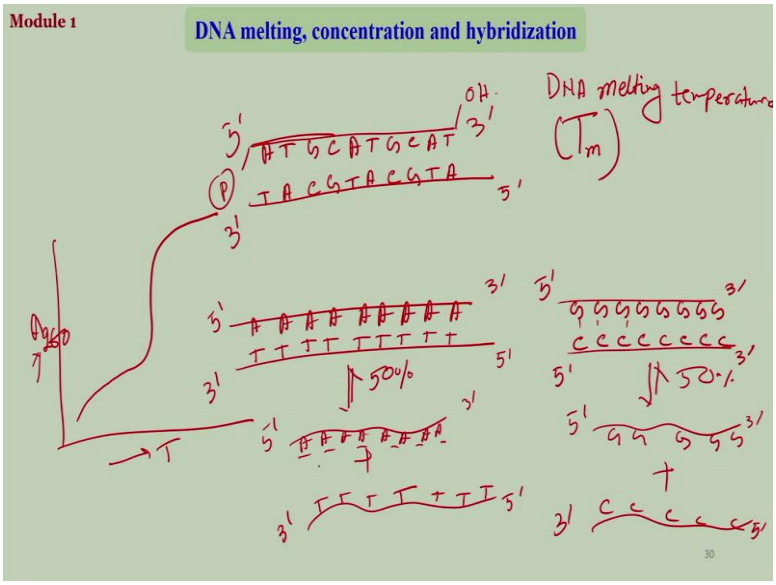

So, we have seen how the structure of DNA looks like. Now usually when you draw when you write a DNA then as i have mentioned before we write it in 5 prime to 3 prime orientation 5 prime is phosphate and 3 prime is hydroxyl. When you write a DNA double strand the convention is you write it in this fashion 3 prime and 5 prime and then you write the sequence of the DNA. I am just writing an arbitrary sequence A T G C and then of course the sequence of the other strand will be the complementary of it so T A C G T A C G T A that is how our DNA double strand is usually been written.

Now in paper when you write and then you do not have to write the whole double helix sequence double strand sequence if you write only one sequence 5 prime to 3 prime strand then it is understandable what will be the other strand. So, you can write either of this sequence that is fine that is what is being usually used to represent the DNA. Now depending upon the sequence of the DNA, DNA has different strengths.

For example if I just take a DNA which is all AT A A A A A A A 5 prime 3 prime T-T-T-T-T-T-T-T-T-T 3 prime 5 prime and so we are talking about two properties of DNA that is called a DNA melting and DNA hybridization 5 prime 3 prime now if you consider all GC obviously they will have different strengths because a AT base pairs have two hydrogen bonds the GC base pairs has 3 hydrogen bonds.

So, GC is stronger this double strand would be much stronger compared to this double strand. So, there is a way to determine the strength of the DNA and that is known as DNA melting temperature in short this is written as TM. Now this is like any other melting point that you

know if you have a compound melting point means the 50% of the compound should melt away.

So for DNA case it is the melting temperature is the temperature at which the 50% of the double strand is melted away into the individual single strand. So, here will be all A here all T that is called the denaturation.

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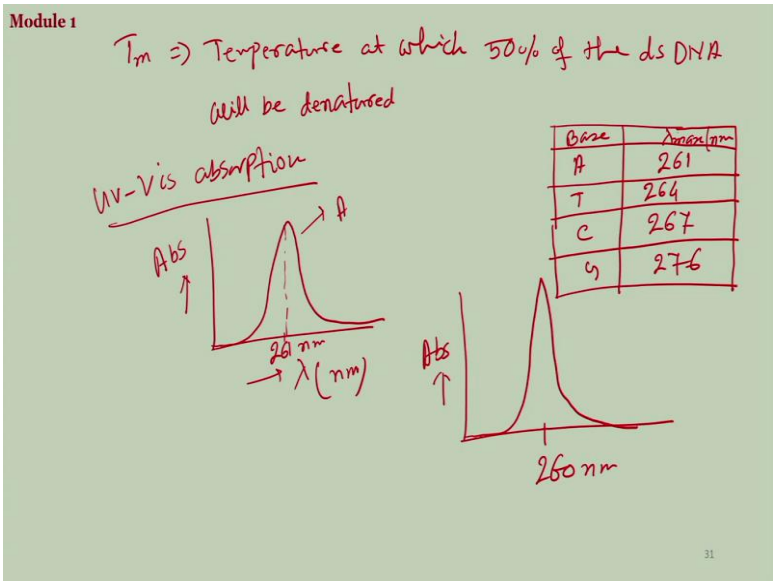

So, is that melt melting temperature is the temperature if I define Tm. Tm is the temperature at which 50% of the double-stranded DNA ds means double strand double-stranded DNA will be denatured. Denatured means melting away the breaking of the double strand because it is against the nature so, doubles will be denature temperature at which 50% of the double-stranded DNA would be denatured. So, that is the definition of the melting point and it is kind of a characteristics of a DNA not really but it gives you an idea how strong is the DNA or what can be the length also of the DNA.

So, obviously now if you look at the AT rich sequence and GC-rich sequence that melting temperature of the GC rich sequence will be higher because you need more heat or more energy to break the GC sequence and this is rich hydrogen bonds. So, 50% here and here you will have 5 prime to 3 prime or G Plus all C. So, this is important actually because when you synthesize sometimes we can nowadays manufacture short sequences of DNA or if you isolate a DNA sample from somewhere else you need to know what is the strength of the DNA sometimes if you break them into pieces.

Now the second question is the how to determine how to know what will be the melting temperature how do you know at what at which temperature the DNA is getting denatured. The point is that DNA like you measure the melting temperature of the compounds because they have visible quantity and you can you can see them and you can take them in a capillary measure. And you can see them getting melted away that is not possible for DNA.

Because the sample of DNA when you isolate a sample of DNA from somewhere else the concentration is so low that sometimes you do not even see them they are less than milligram quantity sometimes to them level of micro gram also. So, with those small quantity you cannot obviously weigh them and you cannot see them transforming from the double standard DNA to the single-stranded DNA. So, how do you determine the melting temperature of a DNA.

We usually do it by UV spectroscopy so the DNA contains the nucleus bases adenine, thymine guanine, cytosine and as I have mentioned all of them are aromatic and all of them are heterocycles so they absorb hugely in the UV visible region ultraviolet region. So, if you do a absorption UV absorption study UV visible absorption UV visible absorption because this is one of the technique which is very sensitive which requires very very small amount of sample and to give you a very good signal.

So that means it is a spectroscopic technique where you can measure how much the light is absorbed by the at which wavelength. So, then you will see that if this is your absorbance and this is the lambda value the wavelength then you will see the nucleus bases they absorb at certain wavelength for example I will just give you one example this one is so it is kind of 260 so this maximum lambda max this value is 261 nanometer.

So lambda is in nanometer at 261 nanometer you have a maximum absorption if you have adenine. So, I will give you a chart where the individual nucleus bases absorb. So, this is base for nucleus and this is your lambda max where you have the maximum absorption in terms of nanometer. If you have adenine it absorbs maximum 261 nanometer. If you have thymine that has a maximum of 264 nanometer. if you have cytosine it is around 267 nanometer and guanine has 276 nanometer.

So, they are more or less close and on average we consider that if you take the absorption of DNA you will see a sharp peak or lambda max at around 260, nanometer. So, 260 nanometer is

kind of a characteristic peak of DNA and that has the absorption maximum for the whole DNA that is an taking average of all the sequences. So, if you can measure the concentration of a DNA by measuring the absorption value. And therefore if you know now if you go on come back here now.

When you have the double-stranded DNA the two strands are intact and it will show you the certain absorption value at 260, nanometer. Now if you if you increase the temperature this is in solution water or buffer. If you increase the temperature and reaches the melting temperature where the two strands will be separated away then what happens is you break all the hydrogen bonding interactions and you break also the all the PI stacking interactions.

So all interactions are broken and as a result the absorption of this individual nucleus bases gets increased because when you had the double strand when there was the hydrogen bonds then the electrons were moving towards the hydrogen bond also or they were involved in the hydrogen bonding and that decreases the absorption or absorbance. Now once the nucleus bases here gets free becomes free then they can behave as the original single-molecule entity and their absorbance gets a higher.

So you will see a increase in absorption on increasing the temperature and there will be this kind of curve that you have slowly increasing the absorption then there will be sharp rise. So, here is the temperature and here is the absorbance at 260 nanometer. So, at the beginning when the temperature is low because the hydrogen bonding were still intact so the amount of increase was low and when you break all the hydrogen bonds when it becomes free to single strands then suddenly the absorption gets increased jumps up and then becomes saturated because now they are all single molecules.

So half 50% of it the half point here this will be your melting temperature. So, that is how you determine the melting temperature of a DNA. Another aspect I should talk about in the DNA is the solubility that I forgot to mention so when you look at the DNA structures of course this is the phosphate means and this double bond O and this O- so, DNA overall is negatively charged because you have the phosphates inorganic compound and the phosphates and in ionic form OH minus form.

So, it is basically the ionized version of phosphoric acid. Now if you look at the nucleus base this is neutral sugar is neutral only phosphate. Phosphate is ionized and it is negatively just so over all DNA is negatively charged and that also make it soluble in water this is the positions where a water molecules bind or when you have salt, salt molecules will stabilize the counter anion. So, you have one acidic component this is the acidic component and nucleus base is the basic component that makes DNA soluble in water pH 7.4 or water either water 7 or in buffer physiological condition that is ph 7.4.

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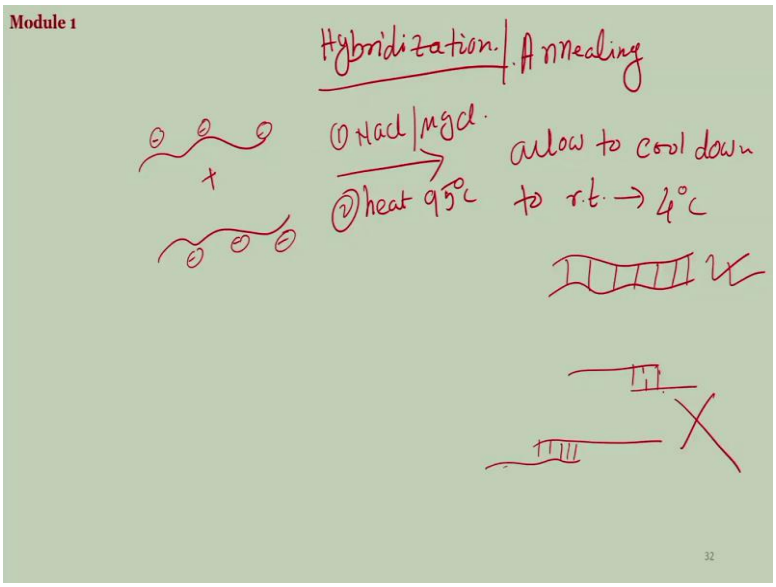

Now coming with DNA hybridization or you can call it annealing. So, we have seen how DNA gets denatured from double-stranded DNA to single-stranded DNA. Now the reverse one if you have two, single standard DNA how do you make a double-stranded DNA that is called the DNA hybridization. So, if you have two single-stranded DNA in water or in buffer solution at pH 7.4 let us say you mix them together and then they always do not form the perfect double helix that you would anticipate.

So, you have to do certain changes to the solution and that will give you the proper hybridization of a DNA. So, that the reason is if you have one single-stranded DNA plus the other single-stranded DNA so at room temperature if you just mix them together without doing anything then what happens is there are already within the same DNA strand there are small interactions certain interactions are present for example it can have the self hybridization partial.

Partial self hybridization some part of the DNA may be complementary to the other part and they can hybridized making a folding structure of DNA not much stable but still stable at room temperature sufficient. The melting temperature is higher than room temperature so at room temperature they will have the self hybridizations similarly for this strand. Second is that of course DNA as I mentioned as negatively charged phosphate phosphate phosphate.

So, if you want to bring the two strands together they will simply repel. So, the hybridization strength or the strength of the double strand if you just bring two single strands together will not be high because the phosphate negative charge repulsions will be there as well as the self hybrid a self hybridisation will be there. So, in order to avoid that what to; what you have to do is? If when you take the two single strands usually you have to use a salt either we use sodium chloride or magnesium chloride to stabilize the counter anions.

Now once you use the salt then they are stabilized and if you mix them together the two single stands then they can perform perfect hybridizations. And second you have to heat it up at higher temperature. We usually do at 95 degree Celsius temperature that is the usual practice to break all the shorter interactions or all kinds of interactions that were present within the same molecule. So, once you heat it up at 95 degree Celsius then all interactions are broken.

Now you mix them together and allow it to cool down at room temperature to room temperature or if your DNA is shorter in strength you can still move to lower temperature just like the fridge aerations 4 degree Celsius. Now if you do that then your thermodynamics is playing role this is a cooling down is a slow process so that will now your thermodynamics will dictate the strength of the DNA.

So, whichever is the best strength in this case of course the double strand that will have the best strength will be the most favourable process. So, therefore all the shorter hybridizations or partial hybridizations like this so partial hybridizations will be thermodynamically unfavourable the full hybridization if you have the complementary strengths will be thermodynamically favourable process. So, this is some aspects of DNA regarding the synthesis of nucleus bases and the synthesis of the whole DNA that we will discuss in the next module.

So, now so much so for the DNA and I will start a brief introduction on the amino acids peptides and proteins so details of the synthesis of the nucleus bases sugars and the phosphate

backbones will talk later in the next module. So, amino acids are part of protein, protein is constituted of amino acids or the peptides are constituted from the amino acids.

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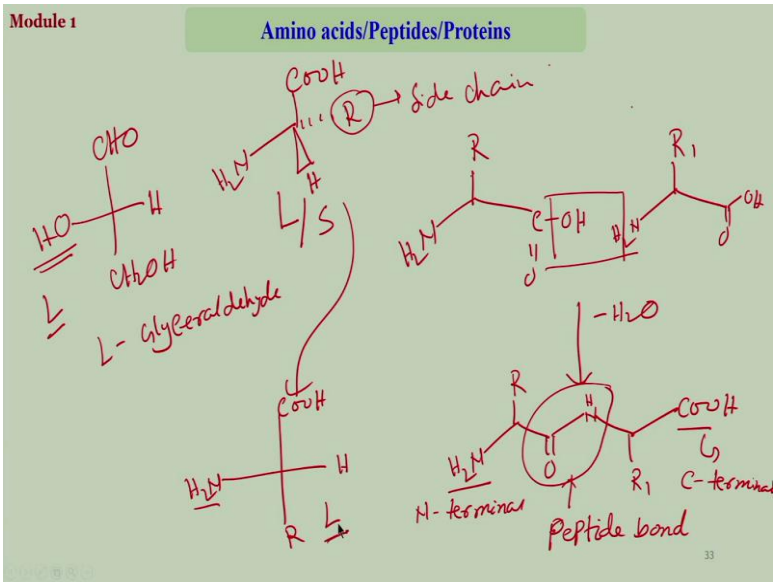

Amino acids has a general structure as they have our carboxylic acid group they have one amine group and they have R group which is called the side-chain and that actually varies mostly from amino acid into amino acid. And here there is an H so this is the primary constitutions of amino acids that make up the structure of the proteins or peptides. So, when you have two amino acids I am just writing flat R NH 2 R 1 NH 2 CO OH and you fuse them together condense basically remove a water molecule then you get a different bond an amide bond.

This is the new bond that has informed that is basically an amide bond but since this is present in the ammonia acid environment we call it we have given a specific name we call it a peptide bond and that is how came the name peptide. So, when you increase this process further you have a a chain of the peptide or chain of the protein composed of peptide bonds. And just like we have seen for DNA we have named it from 5 prime end to the 3 prime end minus are the peptides or the proteins are usually terminated as N terminal and C terminal.

So if you increase the length you will see the left-hand side will always have amine free this is called the N terminal the right hand side you have a carboxylic acid free this is known as C terminal. The stereochemistry of the amino acid is in this fashion which is usually has the L configuration or this is equivalent to a S configuration.

If you see the priority sequence so left-handed and ace configurations this comes obviously from the D and L comes obviously from the tri glyceraldehyde where you have a CHO H CH 2 OH and OH, OH is in the left side and the hetero atom is in the left hand side that has the L confirmations this is called L glyceraldehydes. If you draw this into the Fisher's projections you will see that this has a structure this is the projection of and this is the length the longest chain I mean in the left hand side so this is called L. Amino acids are of L configurations and L means S in this case, so, R varies.

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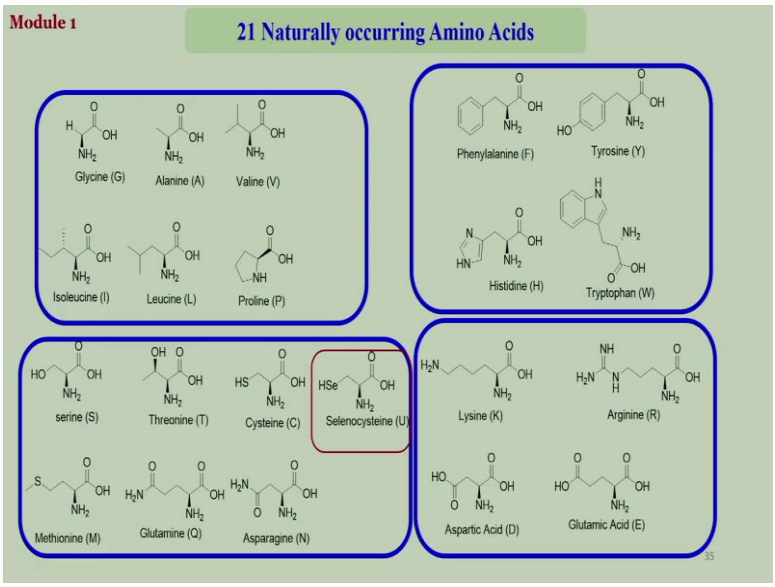

As I said there are around 21 naturally occurring amino acids it is really 20 abundant in nature and one is a Solana system which has this structure which is sometimes available in cells but it does not code for a protein, thank you.