PART 1

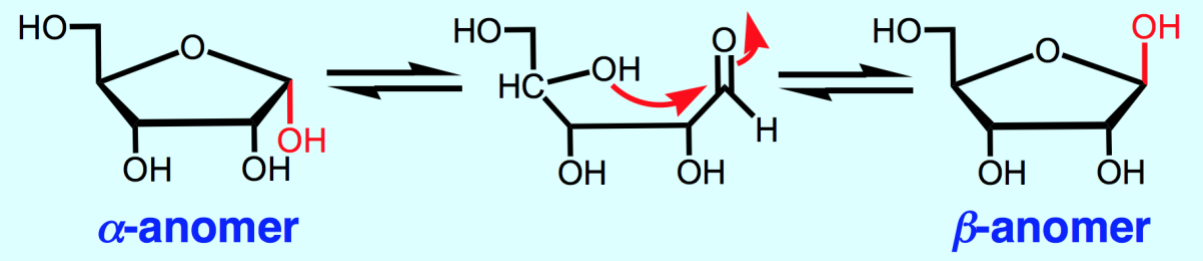
Introduction

- Used self-assembly property of DNA to form lattices, cubes, pyramids and DNA origami structures.
- Formation of m-DNA by placing a metal atom between adjacent base pairs. Allows electrons to be transferred through helix. However, some metals are known to degrade DNA.

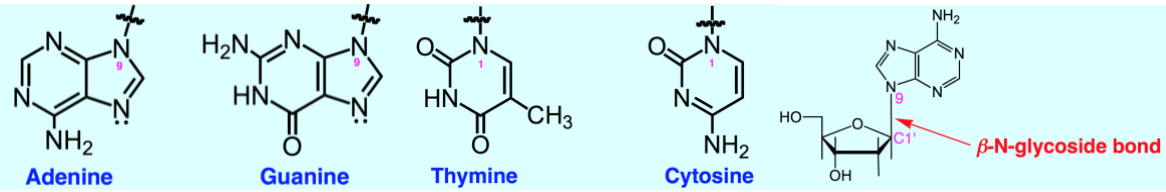
Section 1

Nucleobases: Four bases based on the purine (Adenine, Guanine) or pyrimidine (Cytosine, Thymine) ring structure. Both ring structures are planar and aromatic.

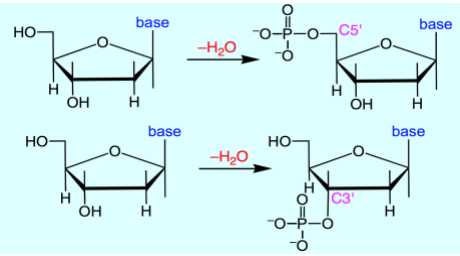
2-deoxy-D-ribose sugar: Formed by an internal attack causing cyclisation. Two possible anomers can be formed and both exist at equilibrium.



Nucleosides: Base attached to sugar. In purines N-9 atoms are covalently linked to a 2-deoxy-D-ribose sugar, while those of pyrimidines are linked by N-1 atoms. The link between the base and the sugar is known as a β-N-glycoside bond.



Nucleotide: Base, attached to sugar and phosphate (esterified H_3PO_4). This phosphate group can either be attached to the C5' or C3' carbon on the sugar.

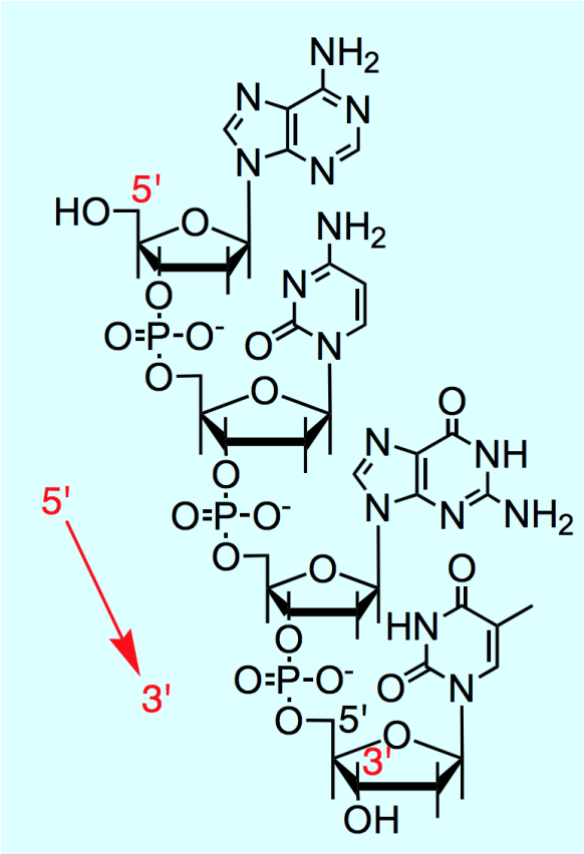


Phosphoryl transfer reactions: Phosphate esters may be further phosphorylated to form di- and tri-phosphates. Example: ATP → ADP → AMP. This hydrolysis is favored because: large negative free energy (entropy); reduction of the electrostatic repulsion between the O^- atoms; better solvation of ATP hydrolysis products in water than ATP itself; products of ATP hydrolysis are more resonance stabilized than ATP itself.

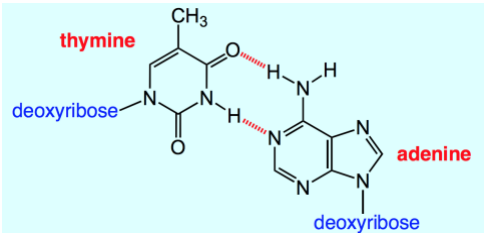
PART 1

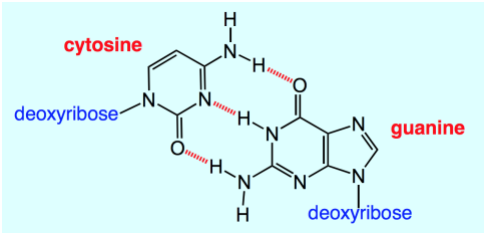
Section 2

Structure of DNA: Each nucleotide is covalently linked by a phosphodiester backbone, forming a 5' end and 3' end. In double helical DNA, two strands are wound antiparallel with H-bonding occurring between purines and pyrimidine bases (A two H bonds to T; G three H bonds to C). However, there are such alternatives to H-bonding between these pairs, known as Hoogsteen base pairing.



Hoogsteen base pairing and Watson-Crick base pairing are energetically similar, however only Watson-Crick base pairing is observed in DNA. This is because Hoogsteen base pairing of G and C is only stable at low pH and has less H-bonding present than in Watson-Crick base pairing.





Stabilisation of DNA: Besides H-bonding of bases, the helix is stabilised through pi-pi stacking between aromatics and is stiffened by electrostatic repulsions between anionic phosphate backbones. Cations lie along the backbone to stabilise the helix further, by neutralizing anionic phosphate charges. This is furthered by a well ordered H_2O molecule network found in the major groove of the A-T region, known as the 'spine of hydration'.

Semi-conservative DNA replication: In replication each DNA stand serves as a template, producing two new DNA molecules (each with 1 new and 1 old strand). This requires DNA denaturation and DNA renaturation. Denaturation is achieved by the disruption of interactions that stabilise the DNA (i.e. H-bonding and pi-pi stacking). This process can be followed by observing the change in UV band absorbance. The single stranded DNA has a higher absorbance than that of the stacked bases due to hyperchromatism.

Double stranded structure: H-bonding, hydrophobic and pi-pi stacking interactions between bases allows the hydrophilic phosphate groups to exist on the outside of the macromolecule. These

phosphate groups are hydrophilic, whereas the bases are hydrophobic so this benefits the entire DNA structure. Pi-pi stacking is a combination of VDW and electrostatic forces. The maximum pi-pi stacking is enabled by the twisting of bases, also reducing the space between base pairs and the amount of water inside the DNA structure.

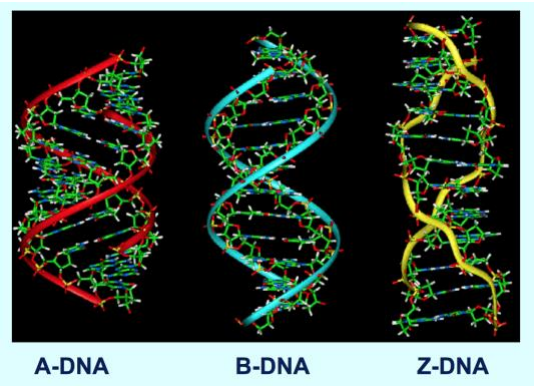
DNA melting: Proceeds via "bubbles" at the A-T rich regions, then opens up the strand at the G-C regions. $T_{melting}$ is the inflection point, being 50% ssDNA and 50% dsDNA. Temperature below $T_{melting}$ will allow annealing to occur.

- Increasing the G-C content of the DNA increases the $T_{melting}$.
- Low and high pH (away from 7.4) gives depurination reactions, lowering the $T_{melting}$.
- The greater the ionic strength of solution, the greater the $T_{melting}$ as the DNA is happier with high ionic interactions.
- The greater the length of DNA, the greater the $T_{melting}$.
- DNA likes to be in water, thus reducing the polarity of the solvent lowers the $T_{melting}$.

B-form of DNA: Right handed helix with distinct major and minor grooves. The helical pitch is approximately 10 b.p (33.8 Å).

A-form of DNA: Right handed helix, shorter and fatter than the B-form. Very shallow minor groove surface. Phosphate groups are much closer together, leading to puckering and a hole in the middle of the helix.

Z-form of DNA: Left handed helix which zig-zags. Long and slender, shallow and wide major groove, narrow and deep minor groove.



DNA sugar conformations: The sugar ring is not flat, rather it is puckered. This relieves steric crowding. In B-form DNA the C2' carbon is puckered, however in A-form DNA the C3' carbon is puckered. The C2' and C3' carbon puckers can rapidly interconvert in solution. In Z-form DNA, purines and pyrimidines are C3' and C2' puckered, respectively. It is this sugar puckering that governs the different structural forms of DNA.

RNA structure: Single stranded containing sugar base and phosphate ester. The sugar is in the D-ribose state as there is an -OH present at C2' carbon and this C3' carbon pucker minimizes steric clashes. Pyrimidine bases are cytosine and uracil as there is no thymine in RNA. RNA has a short half-life and is quickly degraded when not needed. However, double stranded RNA does exist when RNA loops back on itself. When this double stranded structure forms, it exists within the A-form structure, as the -OH group leads to steric clashes in the B-form structure. Common motifs in RNA