BIOL1009: FROM MOLECULES TO CELLS AND ORGANISMS

MODULE 1: MOLECULES AND INFORMATION TRANSFER

1.0 MOLECULES

Properties of life: adaptation, regulation/homeostasis, order, energy processes, sensitivity/response to stimuli, evolution,reproduction, growth and development

Essential elements of life: CARBON, H, N, O, small amounts of P, S, Cl, Na, Mg, K, Ca and trace amounts of F, I and other transition metals

Primary molecules of life: water, carbohydrates, sugar, *saccharides (building units of carbohydrates)*, lipids, amino acids, nucleotides.

- Water: polar compound with extensive hydrogen bonds to stabilise internal temperature (evaporative cooling, freezing/melting of habitats to buffer changes, floating habitat platforms, water tension, capillaries)
- Carbohydrates/Sugar/Saccharides: composed of C, H and O
    - *Monosaccharides:* the simplest forms of sugar and the most basic units (monomers) from which all carbohydrates are built (e.g. glucose (dextrose), fructose (levulose) and galactose)
        - Cn(H20)n where n = the number of carbon
    - *Disaccharides:* two monosaccharides joined together (sucrose, lactose, maltose)
    - *Sugar Polymer:* long chain of monosaccharides such as ribose, cellulose and starch
- Lipids: diverse set of fats (energy stores), oils, waxes, steroids, sterols - insoluble in water
    - Phospholipids: form cell membranes, hydrophobic with polar end that interacts with aqueous environment. Lipid bilayer is formed to separate inside and outside.
- Amino Acids: building blocks of proteins, containing amino and carbonyl groups. 20 common amino acids coded by basic alpha structure, in aqueous solution (normal state) amino acid groups are charged (pH < 6)
    - Nucleic acid: phosphate, sugar (ribose and deoxyribose) and nitrogenous base (purine and pyrimidine)
        - dAMP: mononucleotide (1 phosphate)
        - dADP: dinucleotide (2 phosphate)
        - dATP: trinucleotide (3 phosphate)

2.0 GENETIC CODE - DNA AND RNA

Biopolymers: contained in DNA, RNA and proteins - the sequence of subunits/monomers are essential to the function. Definitive beginning and end, synthesised in one direction, increasing the backbone from left to right.

Residues: part of the monomer lost in polymerisation which is incorporated into the growing chain, biopolymer synthesis relies on dehydration reactions and are *anabolic*.

Proteins: amino acid building blocks from N-terminus (amino terminus) to C-terminus (carboxy terminus). NB peptides if short (<50 amino acids) and protein if long (>50 amino acids)

Nucleic Acid Polymers (DNA/RNA): sugar phosphate backbone (negative charge on phosphate, hydrophilic, acidic, 5' to 3' from numbering sugar)

- Electrophoresis: nucleic acids migrate in an electric field due to charge, distance migrated depends on size
- Ethanol precipitation: nucleic acids become insoluble when mixed with salt - to neutralise charge and ethanol

Peptide bond formation: condensation reaction - two amino acids form to form a dipeptide through energy (water produced as side product)

- **Peptide bond resonance:** partial double bond makes peptide bond flat and rigid, charges encourages hydrogen bonds

DNA (b-DNA): source of genetic information identical in all cell types but expressed a different gene subset. Strands run in opposite directions, flat bases stack, phosphate ions repel each other, right handed with grooves

- Griffith 1928: bacterial transformation
- AMC 1944: purified DNA
- Chargaff's rule: A+G (purine) and C+T (pyrimidine)
- Franklin, Watson and Crick: discovery of the double helix structure and complementary base pairing (C and G triple hydrogen bonds, A T U double hydrogen bonds - bond strength can be tested using spectrometer 260 nm)

THE GENETIC CODE (degenerate/redundant and universal) - things to consider are possible redundant code and some amino acids have one more than one code.

- Singlet: 4 different bases and use only one position (4 combos of A, G, C and U)
- Doublet: 16 possible pairs
- Triplet: 64 possible pairs

Codon: combination of 3 bases which code for an amino acid (5' to 3' of mRNA). Find start codon (AUG) and read frames until stop codon (e.g. UAA).

3.0 PROTEIN SYNTHESIS

DNA REPLICATION: To make a complementary copy of DNA from template, it is copied from the new strand 5' - 3'

- Nucleotide triphosphates are used as a substrate, and nucleotide monophosphate to the 3'OH end of the growing chain (dNTPs: dATP, dGTP, dTTP, dCTP)
- DNA polymerase enzyme and primer (short piece of DNA/RNA) are used to start the process
- Form a high energy phosphodiester bond, release pyrophosphate (PPi)
- Pyrophosphate is released and breaks down to 2 phosphates and provides energy for the reaction

BIOPOLYMER SYNTHESIS

1. *Initiation:* origin (ORI) is an AT rich site of initiation that pulls strands apart and unwinds part of the DNA. Single stranded binding proteins coat single stranded DNA to keep it separated and stop small segments of base pairing (hairpins).
2. *Chain elongation:* Both strands are copied at the same time, joining to become two circular chromosome strands.
3. *Termination:* Four stands join to form two, terminated roughly opposite of the origin. Chromosome ends are joined up by DNA polymerase. At each replication fork there will be one leading and one lagging strand.

TRANSCRIPTION

RNA polymerase: make an RNA copy from DNA template by using ribonucleotide triphosphates as substrate.

note: this differs from DNA replication as there is no primer to start and there is limiting proofreading (no 3' to 5' exonuclease activity - more mistakes in genetic code)

1. *Initiation:* RNA polymerase binds to a region of DNA known as the promoter (-10 to -35), which sits just upstream (past to the 5' end) and starts transcribing down strand (only one strand). In the promoter region, the consensus sequence, transcription factors facilitated the binding of RNA polymerase.
2. *Elongation:* Two strands of DNA reanneal once the RNA polymerase passes and the transcription bubble unwinds.
3. *Termination:* G/C rich signal causes the T/A sequence to form a hairpin structure, pausing the polymerase.

   TRANSCRIPTION REGULATIONS

   1. *Repression:* protein repressors bind to strand to block the binding of the sigma factor. If there is no polymerase binding → no transcription → no gene expression