Molecular Level Epigenetics with DNA structure

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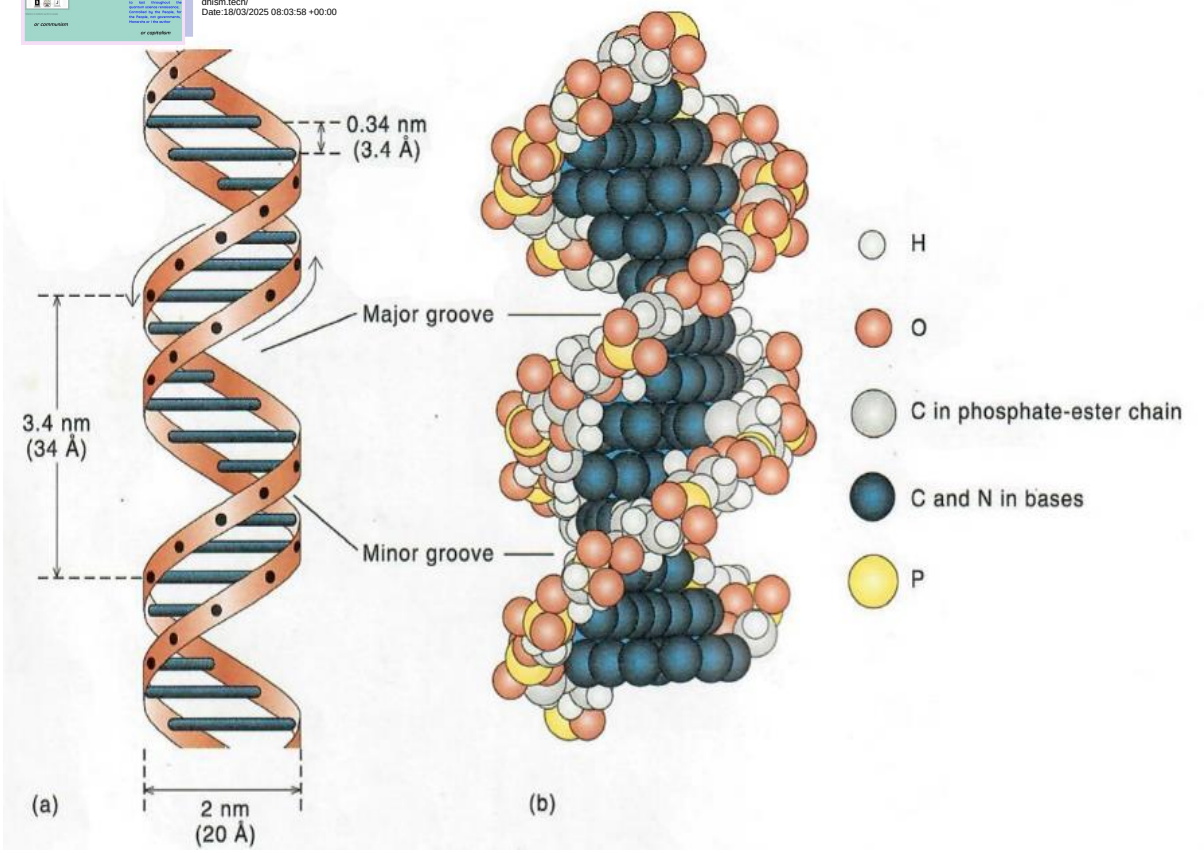


Figure 1a shows the α-helix structure of DNA and four base pairs with a + b. Adapted graphics from W.Parson, G.L.Zubay, D.E.Vance (1995)

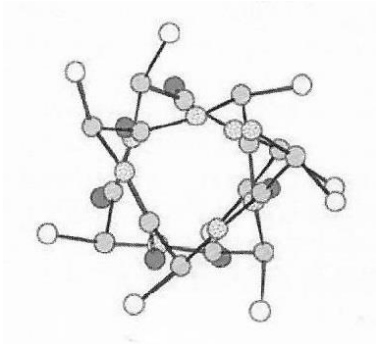


Figure 1c shows a top view of a DNA α-helix *(see figure 1a)*.

Adapted graphics from Y.Marechal (2007)

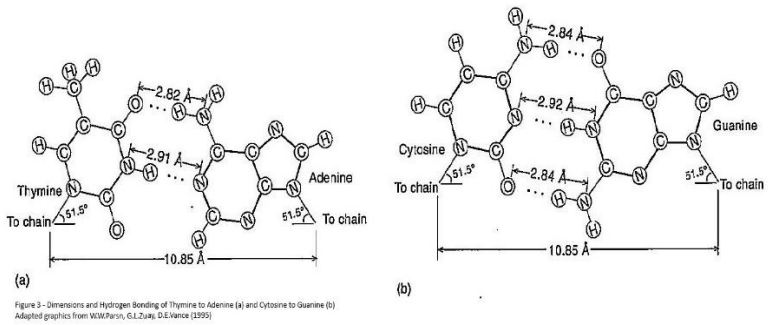


Figure 1d shows the four base pairs of DNA (Thymine to Adenine and Cytosine to Guanine scaffolding structure of the α-helix with a + b base pairs *(see figure 1a and 1b)*.

Adapted graphics from W.Parson, G.L.Zubay, D.E.Vance (1995)

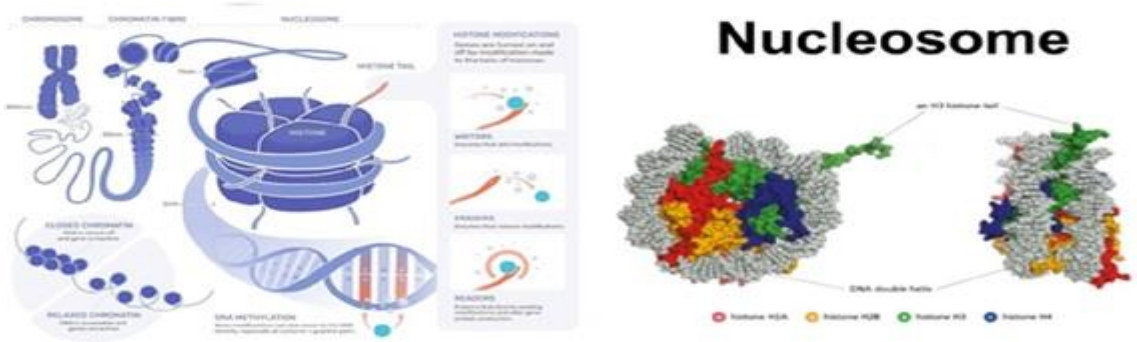
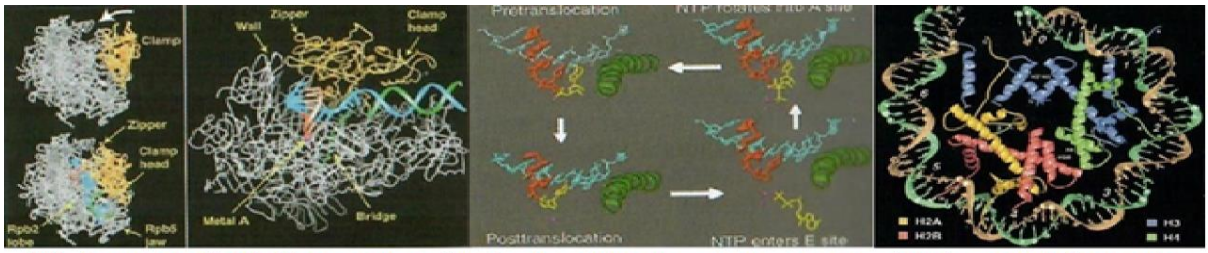


Figure 1b shows graphical representation and x-ray diffraction analysis (front and side orientation) of the nucleosome and histone tails providing access for transcription, mostly controlled by histone proteins. the nucleosome consists of an octamer made of **two subunits** contain four histone proteins: **H2A**, **H2B**, **H3**, and **H4**. (With tails) that is a total of eight histone proteins, 2 tetramers (H2-H4) and 2 (H2A-H2B) dimers in the histone/octamer core complex. The ammo acid linker proteins – H1 etc.... functions to bind and stabilize inter-nucleosol DNA, the linker DNA joins octamer together to make the nucleosome; the histone proteins undergo post-translational (PTM) and post transcriptional modifications in different ways (some are salt dependent). Some histone modifications disrupt nucleosol DNA interactions, thereby the nucleosomes **unwind** or relax for gene expression **Adapted graphics from J.L.King (2021)**



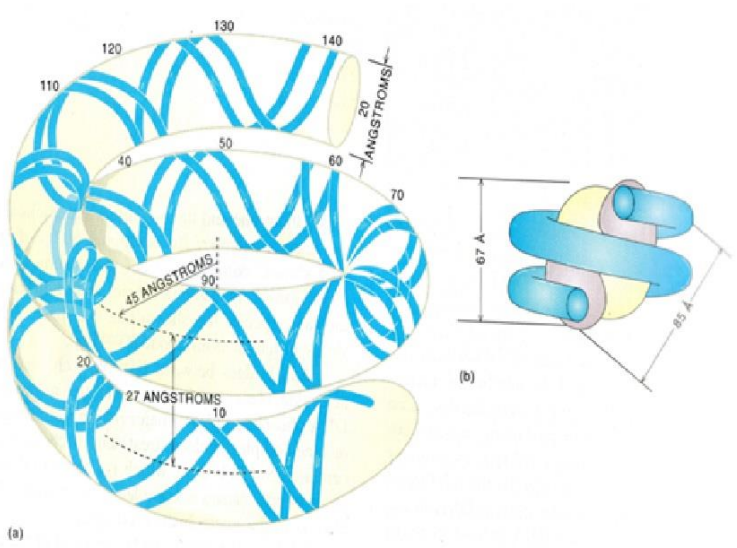
Histone methylation can activate or suppress gene expression in accordance to different lysine dependent states (i.e. Mono-methyl, Di-methyl, or Tri-methyl states; the demethylated function is in reverse (relaxes the DNA coils) on the histone-tails during transcription. There are **seven** transcriptional regulatory core histone modifications on the H3 histone-tail that is:– 2 active promoters (**H3K9ac**, **H3K4me3**), 2 enhancer promoters (**H3K4me1** (stem cell line), **H3K27ac**), 1 transcribed gene bodies (**H3K36me3**), 1 polycomb promoters (**H3K27me3**), 1 heterochromatin (**H3K9me3**) it is possible to define chromatin profile status (biomarkers) of the genome via the histone-tail modification epigenetic biomarker status (see figure, 1d & Appendix, I, II).

Other than **Acetylation(Ac) and methylation(Me)** there are other types of histone modifications have been discovered:- **phosphorylation(P), sumoylation, ubiquitylation(Ub), GlcNAcylation, citrullination, krotonilation, and isomerization** the later three are more recent discoveries, all the above modifications **add or remove from histone protein's amino acid residues** via a set of enzymatic reactions (see figure 1c & 1d, and Appendix, I, II).

Histone proteins are (H1-linker protein, H3, H4, H2A, H2B) which are dependent on Post-Translational Modification (PTMs); PTMs normally are reversible and effect all chromatin remodelling and centromere formation. PMTs are classified as reader, writer and eraser and are either: Effectors(enhancers) or Presenters(promoters). Histone PTMs may alter the chromatin state making it active, inactive or poised state. PTM associations may occur with cis or trans events on same or nearby histone tails, within the same or neighbouring nucleosome (Zang T et al – 2015, graphics adapted from J.Darnell 2010).

Electron Level Epigenetics

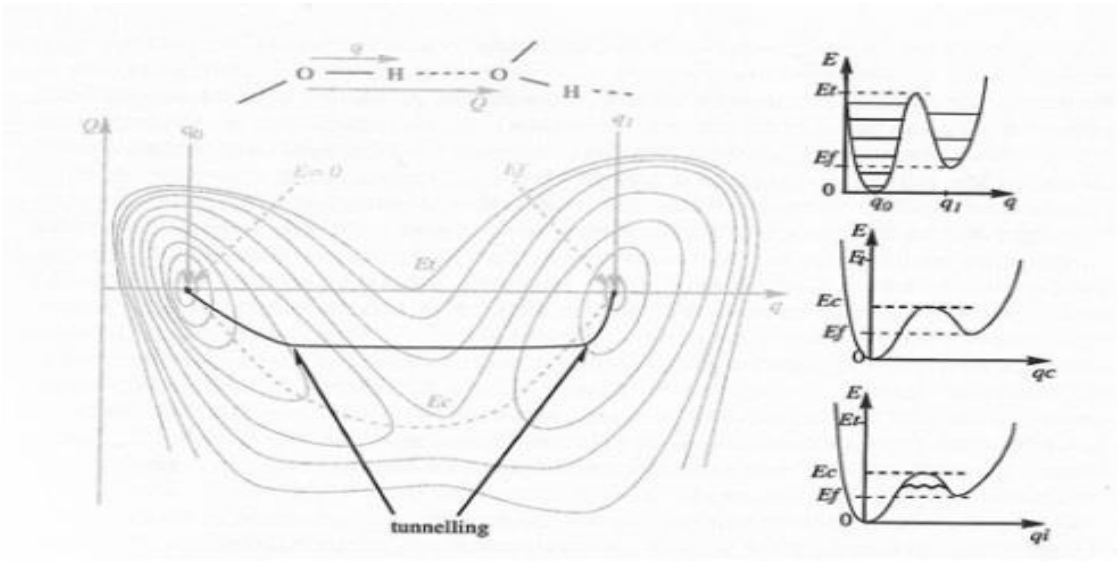
The Structure of nucleosome is significant with reference to dynamic functionality of coiling and uncoiling around the histone proteins, as figure a and b shows the angstroms of the chromatin fibre that coil around the histone proteins *(H2A, H2B, H3 and H4) has* a mechanical functionality: -



Adapted graphics from W.W.Parson, G.L.Zubay, D.E.Vance (1995)

The magnetism of the changing polarities govern the coiling and uncoiling of the chromatin fibre *(also see figure (1b);* although the polarity_charge is significant with reference to the rate that the chromatin fibre coils and uncoiled in according to the histone modifications and strength of polarity change; it is postulated to be + or – polarity charge of varying charge(s) and thus accelerating or decelerating the dynamics of epigenetics during normal electron associated epigenetic reactions that are resultant of quantum interactions.

Quantum Level Epigenetics focusing on quantum tunnelling of 0-H-0 bonds in water

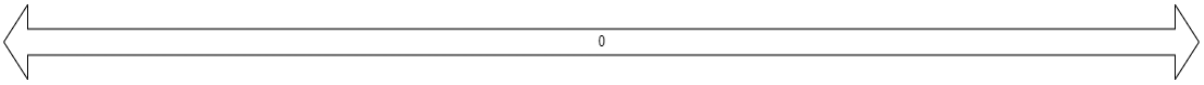


Adapted graphics from Y.Marechal (2007)

An example is with the quantum tunnelled H-bonds within the water molecule as shown above together with induced entanglement; the concept is also applicable for the base pairs of the structure of DNA as entanglement, tunnelling and some additional quantum phenomena has functionality during the dynamic coiling and uncoiling of meiotic and miotic cellar division; though the principles are based on the pattens of science evolution: -

O = Neutral is the Quantum Equilibrium of the quantum polarities is the pattens of science evolution
by J. L .king (2021)

O = + 10 or - 10 according to corresponding quantum polarity charges affecting the rate of dynamic quantum and electron interactions; the quantum entanglement initiates the polarity change of varying charges; initiating the differentiation of quantum flavours induced via quantum entanglement, tunnelling and additional phenomena not yet known; thus, the politized voltage/charge that an memory cell is set within the neurological dendrite is fixed, until electron leakages degradation occurs (see Nutrition functional foods and epigenetics book - J L king (2021)); Also it would be resemble to postulate that dynamic quantum interactions occur governing meiotic and mitotic mechanical systems (also see quantum planetary interactions and space whether associated to hydrogen flares from the sun and magnetic interactions of the moon). See:- https://bio-functional-foods.com/media/other/1144/Towardstheevolutionofastrology_9jlk5.2_WithDigitalSignature.pdf



+ 10 ---------- 0 ---------- - 10

Also see: https://bio-functional-foods.com/media/other/1144/Towardstheevolutionofastrology_9jlk5.2_WithDigitalSignature.pdf

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