

The Complexity of Interactions in Transcription and Cell Replication: Biochemistry and Physics

Flavin DF*

*Faculty of Health and Life Sciences, Leicester School of Pharmacy, De Montfort University,

UK. Received December 28, 2019; Accepted December 10, 2019; Published August 15, 2020

INTRODUCTION

It appears that the energy required for DNA transcription is from the magnetic fields or waves, generated from the many areas of oscillation in the DNA itself. This oscillation energy in DNA is constantly active. This oscillation changes as the cells prepare to transcribe or replicate with supercoiling potentially giving extra energy. Oscillation varies depending on the complex biochemical interactions be they hydrogen oscillations, enzymatic oscillation such as RNA polymerase starting at a site of transcription or high frequency currents carrying waves along the DNA in forms like “bubbles” for additional EMW/EMF which can also effect ATP. Electrical charge oscillations govern protein DNA recognition. Additionally, non-histone proteins allow for other enzymes coming into play for influencing structural changes in DNA, allowing specific sections of the DNA to be available for transcription in an organized coding of DNA, avoiding non-sense coding errors.

In order to understand the complexity of transcription in DNA, one must consider the interactions in the cell between and among the biochemical constituents and their targets. Beginning with changes in the membrane of the cell in early stages of replication or in tumor promotion, there is an influx of calcium from the membrane binding on calcium calmodulin. This calcium then activates the enzyme ornithine decarboxylase (ODC) [1]. ODC is unique in the fact that its products, spermine and spermidine, block the cyclic GMP phosphodiesterase which raises the ration of cGMP over cAMP, a trigger, for GMP Kinases, as an early step in cell division [2].

DNA is constantly oscillating at various amplifications depending on many factors including cell cycle, circadian rhythm and more [3]. The oscillation or rhythms are complex interactions among genes, proteins and metabolites. They control every aspect of cell physiology from signaling, motility and development to growth division and even death

[4]. DNA of bacteria and viruses has been shown to emit electromagnetic signals carrying the DNA information through water [5]. Further data in yeast; show a genomic oscillation in transcription. The transcription cycle gates synchronous bursts in DNA replication with genes being synthesized at opposite phases of the cycle [6].

Studies in energy patterns in twist-opening models of DNA show that plane waves are inherent to DNA dynamics and describe slight oscillations of strands. Some evidence to their contribution to the initiation of the so called in “DNA breathing” has been obtained, and that they also carry energy. Tabi et al. [7] have shown that the energy that has a strong biological effect on DNA should be localized in specific regions of the DNA lattice as enzymes such as RNA-polymerase contribute to the collection of the vibrational energy in the molecule for a better initiation of the transcription process. In other studies on DNA, high frequency currents are shown to carry waves through trajectory “bubbles” [8] effecting transition gates [9]. This oscillation changes as the cells prepare to transcribe or replicate [10] with supercoiling of the DNA potentially giving the extra energy [11]. Since movement is energy and EMF is known to be generated by DNA oscillation, this might explain the ATP increase noted with some studies from the generated EMF increased from oscillation of the DNA [12].

Corresponding author: Flavin DF, Faculty of Health and Life Sciences, Leicester School of Pharmacy, De Montfort University, UK, Tel: +49-8151-4463970; E-mail: drflavin@collmed.org

Citation: Flavin DF. (2020) The Complexity of Interactions in Transcription and Cell Replication: Biochemistry and Physics. J Genet Cell Biol, 3(2): 154-157.

Copyright: ©2020 Flavin DF. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

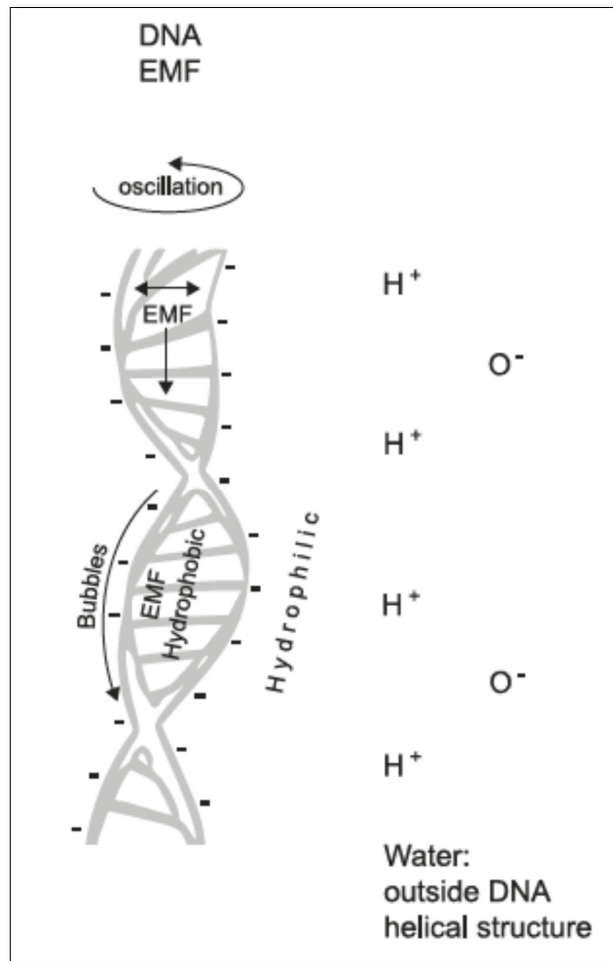


Figure 1. High frequency currents generated from DNA oscillation are carried in trajectory “bubbles” along the DNA. Transcription energy appears to be increased from the increased DNA oscillation before transcription.

Transcription energy appears to be increased from the increase in oscillation and DNA electric charge oscillations govern protein-DNA Recognition. The conformational arrangement of the protein-DNA complex results from a resonance process that involves more efficient energy exchanges between the protein and DNA than with the environment [13]. The structural changes in the chromosomes [14], the DNA bending from non-histone proteins [15] and the phosphorylated histones [16,17] all play a role in energy transmission, messaging to other parts of the DNA for designated areas of DNA that will open up for transcription with specific DNA coding.

In histones, the amino acids have been shown to experience several modifications, of at least twelve types: acetylation (lysine), methylation (lysine and arginine), phosphorylation (serine and threonine), sumoylation (lysine), ubiquitylation (lysine), ADP ribosylation, butyrylation, citrullination, crotonylation, formulation, proline isomerization, propionylation [18]. The acetylation and methylation on

DNA from the structural changes in the histones is not coincidental. Additionally, the non-histone proteins make nucleosome structural changes on the chromosomal proteins HMGN1 and HMGN2 [19]. This was suspected for decades to be affecting the cell activity in relationship to cancer and tumor promotions [20]. Without the NHP’s and the enzymatic influences, which allow only specific portions of the DNA strand to be coded from, we would have nonsense coding. The histones, with their structural modifications are imperative for proper DNA coding, transcription and replication. Without histones, the transcription or coding for proteins is only a non-sense coding without any activity. In other words, the changes in the structure from NHP’s and the enzymes allow a logical specific coding from DNA [21]. An example of this would be if we took AGCT and gave them corresponding numbers 1234, without the structural changes in the histones on the DNA and the enzymatic alterations we would only have 1234, 1234, 1234. This would mean a nonsense coding, which is what we see when coding from DNA without histones, however, with the

changes in the structure caused by biochemical alterations, phosphorylation, methylation and acetylation etc., we can alter the coding of the DNA depending on the structural change of the DNA and the enzymatic change. We could then have coding of 1, 2, 1, 4, skipping the 3 or 1, 2, 1, 3,

skipping the representative nucleotides. This changes the whole coding to practical, logical and very systematically organized transcription and eliminating nonsense coding of DNA.

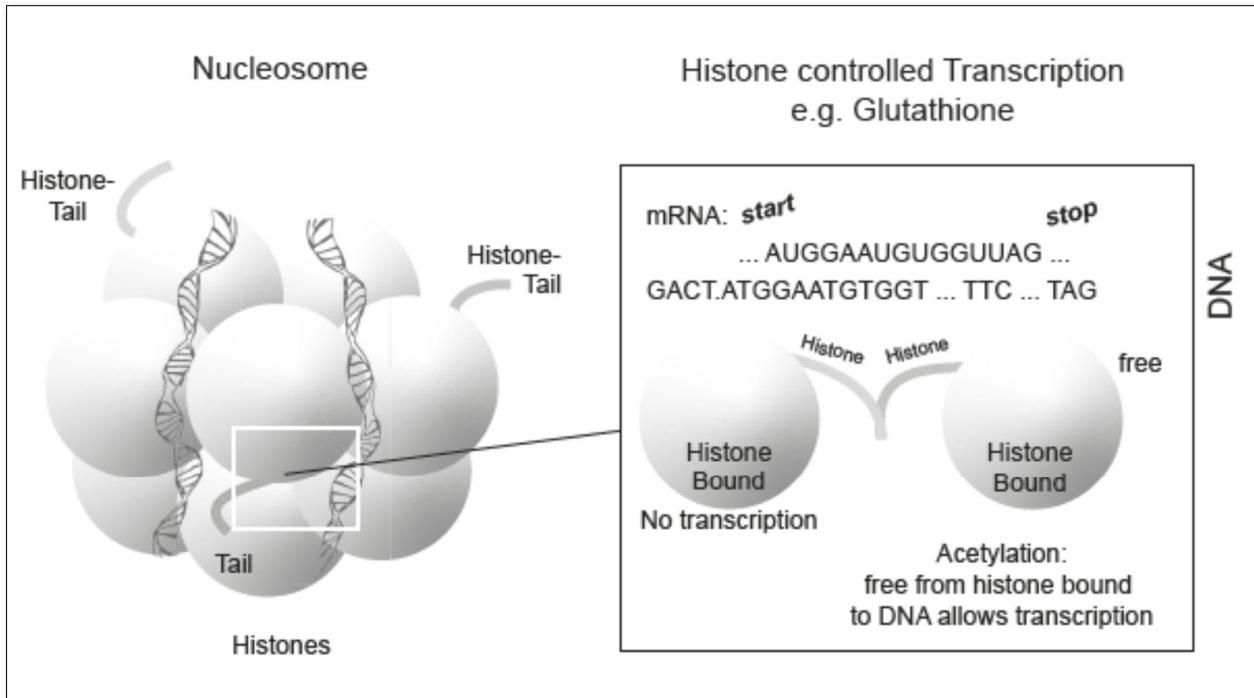


Figure 2. Histones bind on to a specific section of DNA codons not allowing them to be copied. However, when a histone section is acetylated, the histone section no longer binds onto the complete DNA and allows specific DNA transcription. Here seen as the chain of DNA codons starting with GACT. GACT is bound to the histone and therefore not copied, whereas.. ATGGAATGTGGT.. is freed because of acetylation and can then be copied into a codon for mRNA to transcribe for glutathione.

The structural changes in the histones effect the structural changes in the DNA during early transcription, creating a necessary early structure within the single DNA strand that has been exposed for early transcription. This DNA strand structure appears to be a moebius coil and is said to be an effective form of a super conductor for electromagnetic fields [22]. The spermine that has gone into the nucleus from ornithine decarboxylase in the cytoplasm takes this coil that is unstable and in a right handed DNA ring and flips it over to a stable left handed ring form of DNA which amplifies circular movement of magnetic fields with an enhanced energy required for cell replication or transcription. Essentially, it forms a closed super conductor from the structural changes resulting from the biochemical interactions that have allowed it to end in a stable left handed ring or coil. This is a potential constant source of energy needed during transcription or replication.

CONCLUSION

To summarize this complexity of transcription and replication, structure from biochemical interactions and

biochemical oscillators, effect oscillation movement, increase energy-generating magnetic fields and alter the electron or EMF activity. Biochemistry changes the coding from DNA by opening up specific points on the DNA via histone structural changes that would only be nonsense coding were it not for the structural changes. These structural changes allow for enzymatic influences throughout the histones for a perfect coding of DNA for replication, or transcription. Biochemistry directly influences the structural changes necessary for the proper DNA coding and for the amplification and concentrated localization of EMF/energy concentrated in the left-handed ring for a continuous supply of the energy either working with ATP or increasing the ATP when needed for DNA synthesis/transcription or replication. Biochemistry influences the physics involved in DNA transcription and replication via effects on structure and oscillation, which allows for an organized endogenous energy supported efficient transcription and/or replication in DNA.

REFERENCES

1. Ginty DD, Seidel ER (1989) Polyamine-dependent growth and calmodulin-regulated induction of ornithine decarboxylase. *Am J Physiol* 256: G342-348.
2. Zeilig CE, Goldberg ND (1977) Cell-cycle-related changes of 3':5'-cyclic GMP levels in Novikoff hepatoma cells. *Proc Natl Acad Sci U S A* 74: 1052-1056.
3. Oikonomou C, Cross FR (2010) Frequency control of cell cycle oscillators. *Curr Opin Genet Dev* 20: 605-612.
4. Novak B, Tyson JJ (2008) Design principles of biochemical oscillators. *Nat Rev Mol Cell Biol* 9: 981-991.
5. Montagnier L, Del Giudice E, Aïssa J, Lavallee C, Motschwiller et al. (2015) Transduction of DNA information through water and electromagnetic waves. *Electromagn Biol Med* 34: 106-112.
6. Klevecz RR, Bolen J, Forrest G, Murray DB (2004) A genomewide oscillation in transcription gates DNA replication and cell cycle. *Proc Natl Acad Sci U S A* 101: 1200-1205.
7. Tabi CB, Bineli G, Mohamadou A (2015) Energy patterns in twist-opening models of DNA with solvent interactions. *J Biol Phys* 41: 391-408.
8. Grinevich AA, Ryasik AA, Yakushevich LV (2015) Trajectories of DNA bubbles. *Chaos Soliton Fract* 75: 62-75.
9. Dalal Y, Fleury TJ, Cioffi A, Stein A (2005) Long-range oscillation in a periodic DNA sequence motif may influence nucleosome array formation. *Nucleic Acids Res* 33: 934-945.
10. Papagiannakis A, Niebel B, Wit EC, Heinemann M (2017) Autonomous metabolic oscillations robustly gate the early and late cell cycle. *Mol Cell* 65: 285-295.
11. Bruot C, Xiang L, Palma JL, Li Y, Tao N (2015) Tuning the electromechanical properties of single DNA molecular junctions. *J Am Chem Soc* 137: 13933-13937.
12. Zhang S, Michael C, Donghui C, Luquan R (2016) The effects of the bio-inspired pulsed electromagnetic fields on ATP and health. 15th International conference on Bionics Engineering ICBE 2016, Ningbo Campus, University of Nottingham, Ningbo, China.
13. Stepanek J, Kopecky V, Turpin PY, Li Z, Alpert et al. (2015) DNA electric charge oscillations govern protein-DNA recognition. *PLoS One* 10: e0124444.
14. Magnan D, Bates D (2015) Regulation of DNA replication initiation by chromosome structure. *J Bacteriol* 197: 3370-3377.
15. Bajpai G, Jain I, Inamdar MM, Das D, Padinhateeri R (2017) Binding of DNA-bending non-histone proteins destabilizes regular 30 nm chromatin structure. *PLoS Comput Biol* 13: e1005365.
16. Brehove M, Wang T, North J, Luo Y, Dreher et al. (2015) Histone core phosphorylation regulates DNA accessibility. *J Biol Chem* 290: 22612-22621.
17. Rossetto D, Avvakumov N, Cote J (2012) Histone phosphorylation: A chromatin modification involved in diverse nuclear events. *Epigenetics* 7: 1098-1108.
18. Prakash K, Fournier D (2017) Deciphering the histone code to build the genome structure. *bioRxiv* 2017: 217190.
19. Shimahara H, Hirano T, Ohya K, Matsuta S, Seeram et al. (2013) Nucleosome structural changes induced by binding of non-histone chromosomal proteins HMGN1 and HMGN2. *FEBS Open Bio* 3: 184-191.
20. Flavin DF (1986) Cancerous esoterous. *AFRBM* 2: 445-451.
21. Hnilica LS (2017) Structure and biological functions of histones. CRC Press.
22. MacDermott A (1982) Beyond the Double Helix. *New Scientist*, pp: 228-231.