The Effects of Quantum Entanglement on Chromatin and Gene Expression

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Abstract: Quantum entanglement has recently been demonstrated in macroscopic structures at the scale of microns. The densely-packed chromatin that efficiently stores DNA strands may allow for gene expression through epigenetic modifiers within the close proximity of nearby strands and may also experience gene expression through quantum entanglement of epigenetic modifiers. Such an approach may have an evolutionary advantage in the densely packed realm of chromatin.
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I. Introduction

The quantum world has been traditionally constrained to nanometer scales with very little knowledge of the transition to the macroscopic scale. This is partly due to the incoherence associated with entropy and thermal variation in atomic scale entities at the macroscopic level which breaks the correlation between entangled states. Quantum entanglement has recently been demonstrated at the macroscopic scale at room temperature, however. Lee has demonstrated entanglement through non-classical photon correlation in diamonds at the millimeter scale at room temperature and Klimov has demonstrated entanglement between electron-nuclear spin ensembles separated at the micron scale in a Silicon-Carbide array, with distances that mimic cellular volumes [1][2]. Both experiments demonstrate the potential coherence between electron-nuclei pairs within carbon matrices and therefore open the door to considering coherence and entanglement in other, highly-ordered carbon arrays , such as those that exist in biological molecules. As in the Silicon-Carbide or diamond array, the requirements for coherence and stability in the biological carbon array are necessary considering the high thermal energy, so carbon matrices with interacting mechanisms over a macroscopic scale are preferred to maintain stability. Although many long hydrocarbon chains may seem ideal for this situation, the lack of interlocking thermal stability from the beginning of the chain to its end represents a challenge for coherence of the system. One example of particular significance where there is interlocking stability is through the coiled nature of chromatin, the storage structure of DNA. The basic unit of chromatin is a protein octamer containing histones H2A, H2B, H3 and H4. Coiled around the histone proteins is 147 bp of DNA and extending from the histone proteins are amino-terminal tails that allow for covalent modification from external transcription factors [3]. The supercoiled 30-nm fiber around the histones presents close proximity and electrostatic interaction to the previous windings and affects the larger scale structure of chromatin and associated transcription factors [4]. These closely interacting factors between 30-nm and 100-nm chromatin structures may facilitate the coherence and stability associated with quantum entanglement.

II. Gene Expression Through Coherence of Chromatin

Based on the experimental work of Klimov demonstrating coherence in Silicon-Carbide arrays and the compacted nature of chromatin, there is a reasonable expectation of coherence between some segments of chromatin in the approximately 3 billion base pairs of human DNA. At a very broad level, with the approximate coiling of 147 bp around the histone proteins and based on the millimeter scale coherence results of Klimov, we would expect many potential interactions between base pairs ($n = 3x10^9$, $k = 147$) assuming no limit to range:

$$\binom{n}{k} = \frac{n!}{k!(n-k)!} \quad (1)$$

A more realistic interpretation may be to define k based on the median size of transcriptional factors and interacting locations (*k**) and to modify the level of interaction based on range, such as a Yukawa coupling. There is evidence for the limited range of entanglement in DNA based on modeling of the Coulomb potential dipole in the electron cloud of the DNA base, where phonon interaction models show limited range [5]. Based on this model, we can modify (1) with a Yukawa scale factor based on a Coulomb potential:

$$\binom{n}{k*} = \frac{n!}{k!(n-k)!} e^{-ur} \quad (2)$$

Where *u* is the scale factor and r is the range of interaction between transcriptional factors and gene promoters or inhibitors. It is well known that histone proteins have modification sites for covalent bonding through methylation, phosphorylation, acetylation, ubiquitylation, and sumoylation [3]. These post-translational modifications have effects on gene expression within the compacted chromatin and may also activate the Yukawa coupling that establishes coherence between transcriptional factors and gene promotion or inhibition sites. It is well known that remote activation of eukaryotic genes can be up to many kilobases in distance from the gene locus and due to these limits of how far the remove activation occurs, we propose the Yukawa potential as a way to model the quantum range limit [4]. Although the explanation for these long range activators is currently unknown, a possible explanation is the coherent Yukawa coupling of chromatin due to early interaction in the cellular environment through previous replication and transcription. One way to determine if this coherent interaction is occurring is to measure the Yukawa scale factor *u* based on gene expression outcomes from the same modifiers as a function of distance in coiled chromatin. A scale factor that remains consistent throughout many experiments of several different modifiers would provide evidence for quantum entanglement of these interactions.

Additional modeling by Rieper of nucleotide bases as phonons (due to dipole interactions of the electron cloud associated with the base) over a long range of the helix shows quantum coherence at room temperature [5]. The effects of longer standing waves over the length of the helix results in phonon trapping, which has been demonstrated in silicon structures of a similar size at room temperature. The entanglement from the phonon interaction binds the DNA helix, as it would normally completely collapse from a classical standpoint. These models add additional evidence to theory of gene expression by remote modifiers through quantum entanglement.

III. Conclusions

Coherent, quantum entanglements have been considered as an explanation for the long-range interaction of gene modifiers and their locus targets. Additional experimental evidence that is focused on individual coherent interactions between specific modifiers and their gene locus targets is needed to validate if there are Bell states associated within chromatin. A Yukawa coupling model of electron potential is introduced to describe the entanglement interaction and limitations over distance. Similar models based on the interactions of the electron clouds of the base pairs as phonons show stability of the DNA helix only through quantum entanglement of the photons and instability if a classical model is used. The implications to science and biotechnology if quantum entanglement is shown to be active in gene expression would be substantial. From sequencing to gene therapy, there will likely be many improvements in the way medical care is delivered and the way new genes are discovered.

References

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