A model and genomic evidence of imprinting DNA sequence on water structure around nucleosomes

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Abstract

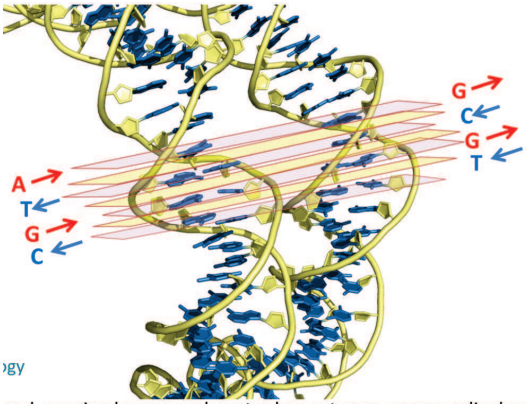
This paper presents a model where DNA imprints its structure on water, proposing a continuous and dynamic self-reorganization process of water clusters, called snowflake signaling. The model's hypothesis is that DNA structure affects water structure in the cell nucleus. Genomic evidence supports the model, revealing evolutionary genomic imprinting of DNA-DNA interactions through structured water.

Introduction

The concept of DNA imprinting on water structure is introduced with reference to previous work on the bioholographic theory based on DNA hologram (*1*–*3*), An interface electromagnetic interaction between DNA inside the nucleus and external microtubules was proposed (*4*). Quantum models of aromaticity collapse in DNA base stack were presented, suggesting that the collapse of uncertainty in DNA bases is the basis for consciousness and the illusion of time (*5*). Here we focused on the continuous self-reorganization of chromatin a DNA-based dynamic gel that reorganizes in a sequence-specific manner. We used molecular modeling of water structures surrounding DNA to predict DNA-DNA interactions in folded chromatin and their evolutionary imprinting on the genome. This imprinting was then computationally tested.

Methods

DNA sequence imprinting on water



A molecular model was built of DNA and water layers. The model demonstrated that DNA may imprint its structure on water through honeycomb hexagonal structures, with the DNA sequence of the base stack would serve as a crystallization seed for honeycomb water layers perpendicular to the DNA axis. The model predicted that the purine sequence of the DNA would define relative shifts of water layers in 3 directions perpendicular to the DNA axis. This would explain how two double helices of similar purine sequences would align in a parallel alignment via water layers. This was applied to two loops of double-helical DNA a nucleosome.

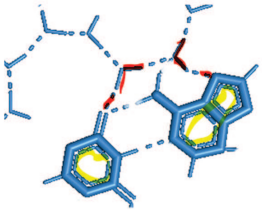
Genomic Evidence

Two observations were produced supporting the model:

1. **Purine Jumps**: Analyzing the whole human genome, a peak of purine homology jumps around 76 bases was observed in three independent subsets of the genome, indicating evolutionary imprinting on the genomic sequence of the proposed water layer structure in nucleosomes. A purine homology jump predicted by our nucleosome model was defined as a direct tandem repeat (such as 123xx123) of two 40 bp fragments in the purine DNA sequence where repeated fragments were shifted relative to each other by 76±5 nucleotides. Partial purine homology was allowed.

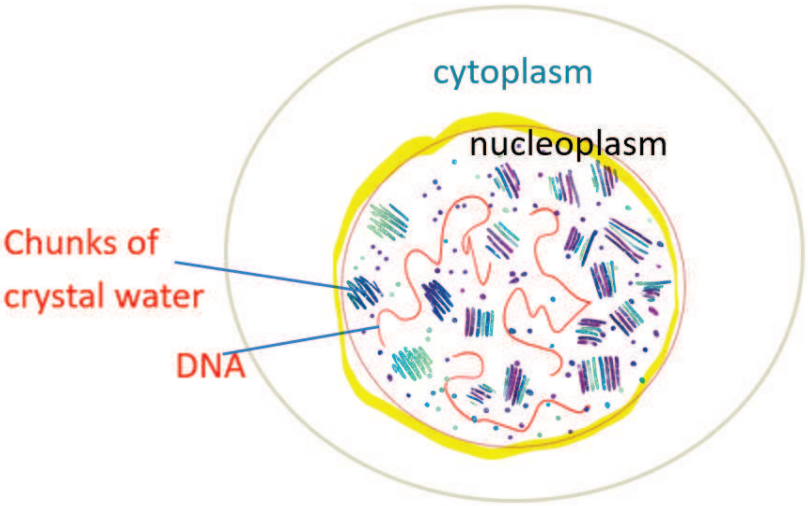
2. **Even and odd nucleotide homology**: The model predicted more homology in even nucleotides and less in odd ones in nucleosome size homology jumps. The genomic data confirmed this, supporting the model of parallel layers of water perpendicular to the DNA axis.

Results



Previous research on DNA oscillations uncovered the hydrogen bond connection of DNA bases to the surrounding water. This led us to the theory that DNA might initiate water's micro-crystallization and imprint its sequence on the water structure, a phenomenon we called crystal pattern propagation or snowflake signaling. It suggests that nucleoplasm (the dense fluid inside the cell nucleus) might contain continuously self-organizing segments of structured water.

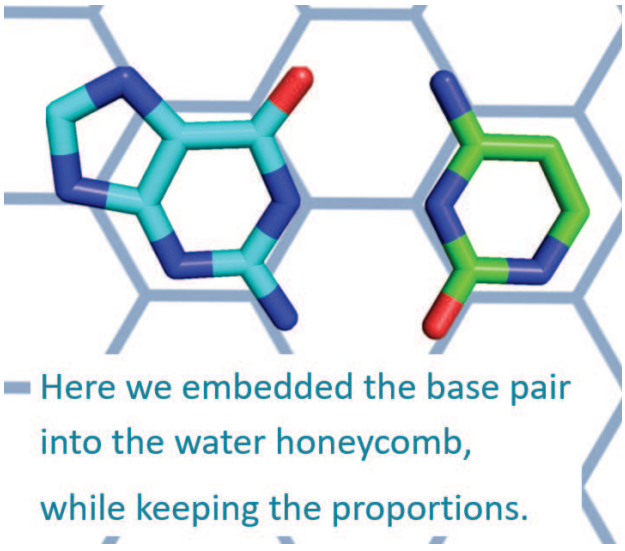
Two intertwined mechanisms form the core of this system. First is the continuous self-restructuring where the DNA sequence acts as a structural template extending into the nucleoplasm. Second, the nucleoplasm operates as a biocomputer, continuously restructuring itself. This forms a biofield guided by DNA that directs specific structures during the continuous self-organization of the nucleoplasm, with bidirectional information flow from DNA to the biofield and vice versa.



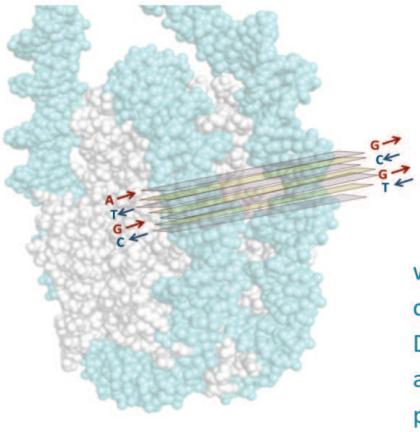
In exploring this concept, we observed the well-known honeycomb structure of Ice IV in atomic force microscopy photographs, as reported in the literature. We also identified hexagonal shapes in DNA base pairs, recognizing a honeycomb pattern in them. Classical ice models did not suit our needs as they didn't allow for shifting layers relative to each other; they are strictly parallel and strongly bound. Therefore, we considered polywater from Lippincott's 1969 work (*6*). These models allow for shifts between layers and are suitable for imprinting DNA structure, being electrically neutral honeycombs with gaps (termed canyons), and accommodating continuous dynamic self-reorganization.

We embedded the base pair into the water honeycomb while maintaining proportions, implying that DNA acts as a crystallization seed with water layers growing perpendicular to the double helix. Importantly, we noticed that the planes of water would shift relative to each other based on the purine sequence of DNA. Purines, being double-ring bases, cause water layers to shift slightly depending on their position. Each subsequent water layer shifts in one of three directions, enabling identical DNA sequences to align with each other due to these shifts in water layers.

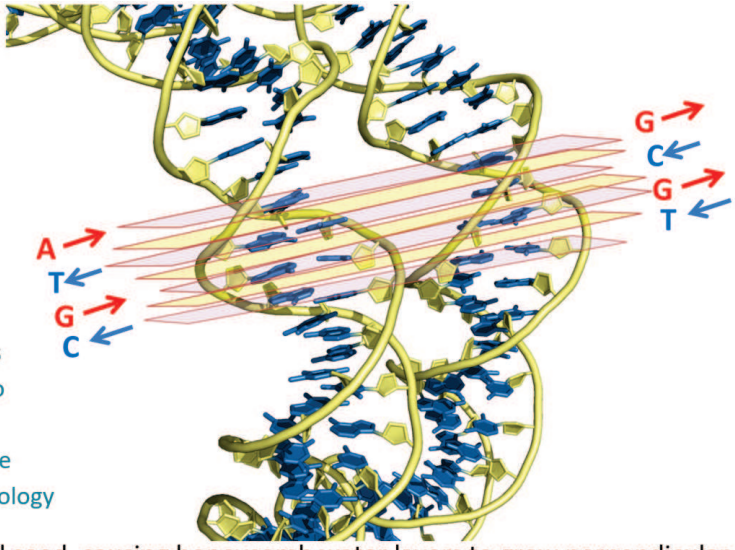
In eukaryotes, DNA is wrapped around nucleosomes, akin to a videotape around a magnetic recording head, with two loops of double helix being parallel in the nucleosome. This led to a hypothesis that these parallel DNA loops might have evolved to possess identical purine sequences, allowing for better alignment through parallel water sheets. In search of evidence for these patterns in the human genome, we analyzed purine jumps. Across the entire human genome, a peak of purine homology jumps at intervals of around 76 bases was observed in three independent genome subsets. This suggests evolutionary imprinting on the genomic sequence of the proposed water layer structure within nucleosomes. A purine homology jump, as predicted by our nucleosome model, is characterized as a direct tandem repeat (e.g., 123xx123) of two 40 bp fragments in the purine DNA sequence, where repeated fragments are shifted relative to each other by 76±5 nucleotides. Partial purine homology was permitted in our analysis.



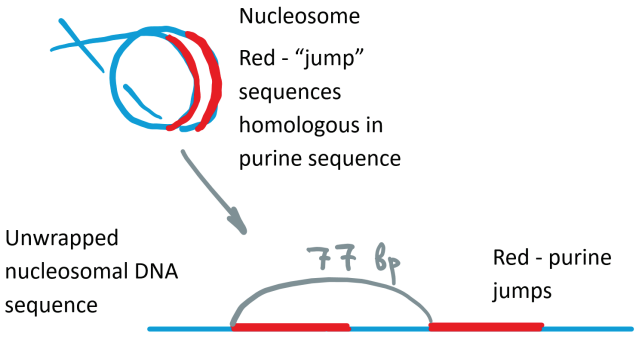
Two DNA loops in nucleosome



water layers connect two DNA loops and promote purine homology



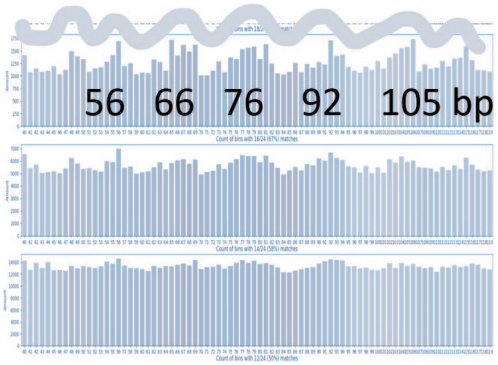
It is postulated that DNA functions as a structural seed, causing honeycomb water layers to grow perpendicular to the DNA axis. The purine structure within the DNA influences shifts in the water layers relative to each other, allowing the shifted water structure to connect two double-helical loops of DNA within a nucleosome. Over the course of evolution, this phenomenon has led to a slight preference for identical purine sequences in the DNA loops of nucleosomes, resulting in the occurrence of approx. 76 bp purine jumps in the genomic sequence.



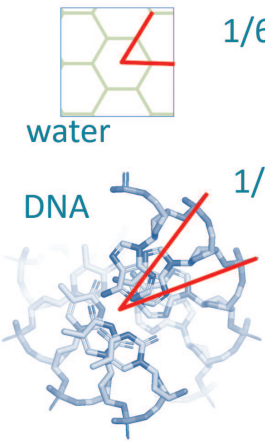
Due to the dimensions and orientation of nucleosome structure, we predicted that there will be prevalence of tandem jumps near 76 bp jump size.

In the purine sequence of the human genome, specifically within conserved nucleosome-bound intergenic areas, we detected a significant peak centered around a 76 bp jump. This observation was consistent and reproduced in three non-overlapping subsets of sequences. Additional peaks were also found around 56, 66, 76, 92, and 104 bp jumps, potentially correlating to varying sizes of DNA loops. Thus, the data reveal an evolutionary imprinting of the water structure on the genome, supporting our theory.

The second piece of evidence for a genomic imprint of water structure arises from the difference in rotational symmetry between DNA and water. Water layers are parallel, and the honeycomb pattern in water repeats itself every 1/6 of a turn. In contrast, DNA steps repeat every 1/10.5 of a turn. Considering that DNA can be slightly untwisted to fit 12 nucleotides per turn, every two nucleotides will match the symmetry of water, which is 1/6 per turn. Consequently, even nucleotides align with water layers, while odd nucleotides are poorly aligned with water. This led to the prediction that DNA sequence homology jumps would be more pronounced for even nucleotides within nucleosomes. Supporting this prediction, odd nucleotides jumps exhibited 35% less homology than even nucleotides, with high statistical significance ($p < .001$).



We observed the evolutionary imprinting of nucleosomal water structure on the genome



The rotational symmetry of honeycomb water layer and DNA in

Discussion

The findings of this study provide significant support for a model in which continuous self-reorganization of chromatin's water gel-like structures plays a critical role in the dynamic interaction between DNA and water. The concept of DNA imprinting its structure on water, with hexagonal honeycomb water layers growing perpendicular to the DNA axis, offers a profound insight into the mechanism underlying this intricate relationship. Our work focused on two main aspects of this relationship, leading to the observations of purine jumps and even and odd nucleotide homology. Both findings are instrumental in providing robust evidence for the model.

1. **Purine Jumps**: By analyzing the human genome, we identified a distinctive pattern of purine homology jumps centered around 76 bases. This was consistently observed across three independent genome subsets, indicating evolutionary imprinting of the proposed water layer structure in nucleosomes. The observed additional peaks at intervals of 56, 66, 76, 92, and 104 base pairs hint at the varying sizes of DNA loops, enhancing our understanding of the DNA-water interface.

2. **Even and Odd Nucleotide Homology**: The rotational symmetry between DNA and water led to our prediction that even nucleotides in purine jumps would align with water layers, while odd ones would not. This pattern was not only confirmed but quantified in our genomic data, showing a 35% less homology among odd nucleotides in purine jumps compared to even ones with high statistical significance ($p < .001$).

The concept of snowflake signaling, or the continuous and dynamic self-reorganization process of water clusters around DNA, represents a novel approach to comprehending the structure and function of the nucleoplasm. This new understanding is likely to have implications for various biological processes, opening doors to potential applications and research directions. Furthermore, our findings resonate with the idea of bidirectional communication between living matter and the bio-field, potentially connecting to universal consciousness. The DNA-based dynamic gel-like chromatin structure, capable of continuous self-organization, may function as a complex interface bridging the biological and metaphysical realms.

By presenting these observations, this work not only enhances the existing understanding of DNA's relationship with water but also initiates a dialogue about the deeper, perhaps even metaphysical, implications of these interactions. Our insights into the dynamic relationship between DNA and water structure provide a foundation for future investigations, which may unravel further complexities of life's blueprint and its profound connections to the universe.

Conclusion

This paper's introduction of a novel model of DNA imprinting on water, supported by substantial genomic evidence, marks a significant step in exploring the genomic self-organizing process. The connections drawn between DNA and water, and potentially even to human consciousness, represent an exciting frontier in scientific research, extending our comprehension of life's fundamental building blocks. The discovery of these water-DNA structures, their formation, and their role in biological processes may lead to new avenues for understanding, diagnosis, and treatment in various fields of biology and medicine, thereby advancing our ability to interact with and harness the power of life's most elemental components.

Acknowledgments

We thank Paul LeMay, and Klaus Oehr for the discussions of water-DNA structures.

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