Speculation on DNA Origami Windmill Model Based on Franklin Figure 51

Zuodong Sun [*]

Ya'ou Brain Science Institute of Heilongjiang province, Harbin, 150090, China

Abstract

Franklin's Photo 51, revealing the periodic diffraction characteristics of DNA, provided key structural evidence for the traditional double helix model. However, the “periodic intensity variation”, “symmetrical distribution law” contained in it, and the contradiction between the static map and dynamic physiological functions have not been fully interpreted. Based on this map, this paper proposes an original conjecture of the DNA “origami windmill” model, derived only from the diffraction characteristics of Franklin's Photo 51 and existing literature without supporting experimental data: DNA tetramer forms an inverted conical channel (i.e., inverted trapezoid) surrounded by four fan-shaped leaves, with the outer size larger than the inner size and a central through-hole, which is completely homologous to the inverted conical structural characteristics of potassium channels; the axis core of the DNA windmill is presumably anchored on the fibrous protein scaffold of the nuclear matrix (non-suspended state), consistent with the anchoring logic of the potassium channel windmill protein; cations (potassium ions, sodium ions, calcium ions, etc.) may drive the fan leaves to rotate through thrust when passing through the central hole along the concentration gradient, realizing dynamic movement without the participation of enzymes, which is consistent with the dynamic mechanism of potassium channels; two sets of connected double strands exhibit radial symmetry (extending along the radius direction of the axis core) and are mutually mirror-symmetrical (forming a mirror structure after folding around the axis core), and the dual symmetry characteristics are accurately matched with the cross and signal symmetry laws of the map; during replication, the two sets of connected double strands may separate naturally, and each uses the complete strand as a template to complementarily synthesize new strands, which not only conforms to the core mechanism of semi-conservative replication but also simplifies the process and ensures the integrity of genetic information. This conjecture aims to throw out a brick to attract jade through the dynamic interpretation of the static map, break through the limitations of the traditional double helix model, and provide a new research perspective for explaining DNA dynamic behavior and intranuclear material transport mechanism.

Keywords: Franklin's Photo 51; DNA Origami Windmill Model; Radial Symmetry; Mirror Symmetry; Cation-driven; Dynamic Regulation; Inverted Conical Structure; Cross-scale Homology; Theoretical Conjecture

---

[*] Corresponding author: Zuodong Sun (E-mail: sunzuodong@pai314.com).

1. Research Background and Problem Proposal

Franklin's Photo 51 taken in 1952, with clear cross diffraction stripes and periodic intensity distribution, became key evidence for deciphering the DNA structure and directly supported the double helix model proposed by Watson and Crick[1,2]. However, there are three core issues in this map that have not been fully explained: first, the “periodic intensity fluctuation on both sides of the equator” and “symmetrical extension characteristics of the cross region” cannot be fully explained by the static winding structure of the double helix; second, the map is a static shooting result, but DNA must have dynamic movement in physiological processes, and the static structural model cannot fully associate its dynamic functions; third, the replication process proposed by the traditional double helix model requires the participation of helicase to unwind the strands, which is complex and has the potential risk of exposure of genetic information[3]. More importantly, if DNA is indeed a dynamically rotating structure, static shooting should present a blurred signal, but Photo 51 can capture clear stripes——this contradiction precisely implies that the map may record an “instantaneous static snapshot” of the dynamically rotating structure (similar to a rotating windmill being frozen by a high-speed shutter), rather than the structure itself being static[4]. Based on this, this paper proposes the conjecture of the DNA origami windmill model (without supporting experimental data), derived only from the diffraction characteristics of Franklin's Photo 51 and existing literature, constructing a new DNA structure hypothesis that balances structure, mechanism and replication logic. It is speculated that this model has cross-scale homology with the potassium channel “origami windmill” in terms of structure, anchoring mode and dynamic mechanism, aiming to throw out a brick to attract jade and provide a new direction for field research.

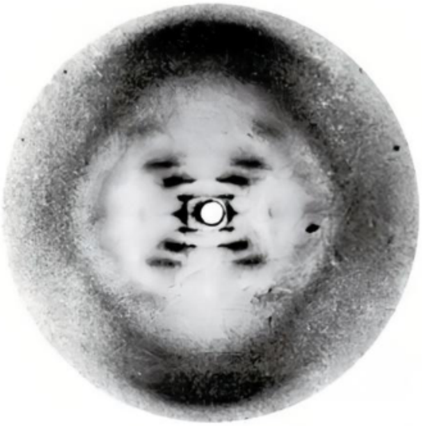

Figure 1： Franklin's Photo 51. The map shows clear cross diffraction stripes and periodic intensity distribution on both sides of the equator, providing core diffraction data support for the structural conjecture of the DNA origami windmill model. The symmetry characteristics and dynamic signal contradiction are the starting points of this study[1,4].

2. Core Conjectures of the DNA Origami Windmill Model

2.1 Structural Basis of the Model: Dynamic Interpretation of Static Map and Dual Symmetry Characteristics

Based on the cross symmetry and periodic diffraction signals of Photo 51, it is speculated that DNA is not a double helix winding structure, but forms an “origami windmill”-like conformation assembled with tetramers as the basic unit: four DNA strands serve as the four “fan leaves” of the windmill, converging at the center to form an axis core, and integrally surrounding to form an inverted conical channel (i.e., inverted trapezoid) with the outer size larger than the inner size and a central through-hole, which is completely homologous to the inverted conical structural characteristics of potassium channels with “larger outer diameter and smaller inner diameter” [5]. This structure can form a reasonable fit with the diffraction map characteristics and explain the contradiction of “static map recording dynamic structure”:

Correspondence between diffraction signals and structure: The outer fan leaves are relatively densely arranged, interacting more strongly with X-rays, which may correspond to the strong diffraction signals on both sides of the equator in the map; the inner channel gradually narrows, the fan leaves are relatively sparsely distributed, and the diffraction signals weaken accordingly, which is consistent with the signal attenuation law in the region far from the equator in the map[4];

Map matching of dual symmetry: Two sets of connected double strands exhibit radial symmetry (extending along the radius direction of the axis core, like wheel spokes arranged around the axis), and their rotation trajectories may form cross diffraction stripes; at the same time, the left and right sets of connected double strands are mutually mirror-symmetrical (forming a mirror-inverted structure similar to looking in a mirror after folding around the axis core), which may lead to completely consistent diffraction signals on both sides of the cross, accurately matching the symmetry characteristics of the map[1];

Dynamic nature of static map: The experimental shooting by Franklin may have captured the “instantaneous static state during rotation” of the DNA windmill——like a fast-rotating windmill being frozen by a high-speed shutter, presenting a clear outline instead of a blur[4]. If DNA is completely static, the diffraction signal should be a single fixed intensity; if the rotation speed is too fast and irregular, a blurred image will appear. However, the clear stripes and periodic fluctuations in Photo 51 precisely imply that it may be an “instantaneous snapshot” of the dynamically rotating structure, which not only retains the symmetry characteristics of the structure but also implies traces of dynamic movement[2].

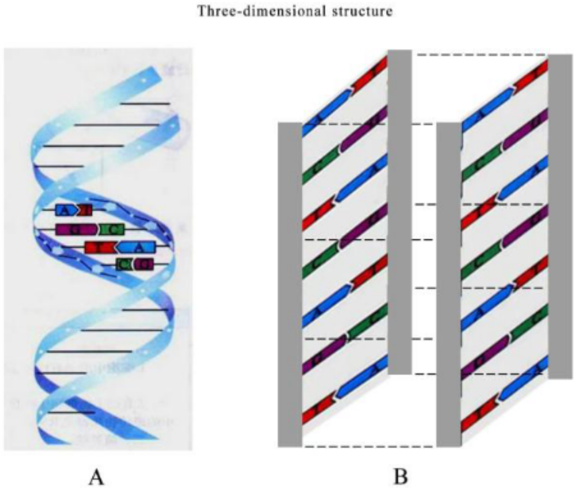

Figure 2: Structure diagram of DNA origami windmill model. Figure A: Stereoscopic structure diagram of DNA double helix. Two phosphate sugar chains are paired through base pairing. Figure B: DNA origami windmill, with two double helices in mirror symmetry, and dotted lines representing weak attraction between the two double helices.

2.2 Cross-scale Mechanism Translocation: Homology Analysis with Potassium Channels (Structure-Anchoring-Dynamics Trinity)

Ta It is speculated that the core mechanism of the DNA origami windmill model has complete cross-scale homology with the potassium channel origami windmill, forming a reasonable corresponding relationship between the three.

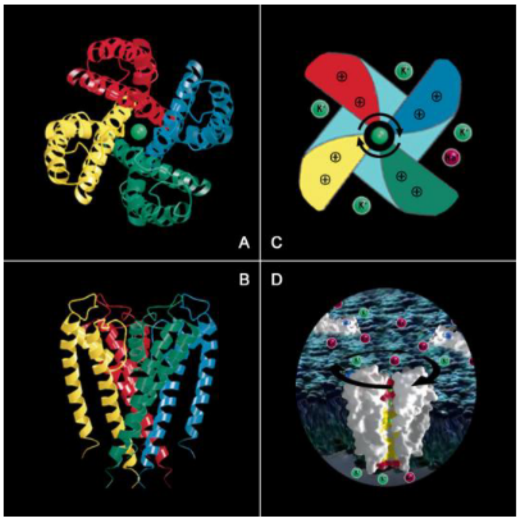

Figure 3 Potassium channel Origami windmill Model [6]**.** Figure A: Looking from the outside of the cell membrane, Three-dimensional strip map of KcsA potassium channel. Four subunits are marked by different colors, respectively(Quoted from Doyle et al. Science,1998). Figure B: Three-dimensional strip map of KcsA potassium channel obtained from the direction perpendicular to graph A(Quoted from Doyle et al.Science,1998). Figure C: Model sketch of origami windmill. Figure D: Stereo sectional view and rotation diagram of potassium channel surface.

(1) Structural Homology: Consistent Inverted Conical Channel + Central Hole Characteristics

Potassium channels: Form an inverted conical structure with “larger outer diameter and smaller inner diameter”, with a central through-hole for ion transport[5];

DNA origami windmill: It is speculated to form a morphologically similar inverted conical channel with the outer size larger than the inner size, and the central hole can allow cations to pass through. The structural characteristics of the two are highly consistent, which may reflect the structural versatility of biological macromolecules in functional adaptability.

(2) Anchoring Homology: Non-suspended Fixation, Consistent Anchoring Logic

Potassium channels: Windmill proteins are embedded in the channel proteins of the cell membrane, achieving stable anchoring through hydrophobic interactions[5,7];

DNA origami windmill: It is speculated that its axis core is anchored on the fibrous protein scaffold of the nuclear matrix (such as the skeleton structure composed of lamin proteins, etc.), maintaining structural stability through the interaction between the nuclear matrix and DNA, avoiding spatial disordered movement, which is completely consistent with the “non-suspended, fixed carrier” anchoring logic of potassium channels[8].

(3) Dynamic Homology: Ion-driven Rotation Without Enzyme Participation

Potassium channels: When potassium ions pass through the central hole along the concentration gradient, they drive the rotation of the windmill protein through the interaction between ions and channel proteins, realizing dynamic regulation of ion transport[5,7];

DNA origami windmill: It is speculated that there is a concentration gradient of cations (potassium ions, sodium ions, calcium ions, etc.) between the nuclear matrix and cytoplasm. When cations pass through the central hole of DNA, they may drive the rotation of the fan leaves through thrust, realizing dynamic movement without the participation of enzymes, which is homologous to the dynamic mechanism of potassium channels, and the rotation rate may be positively correlated with the ion concentration gradient.

(4) Regulatory Homology: Linkage Between Rotation and Pore Opening/Closing

Potassium channels: The rotation rate of the windmill can regulate the opening and closing of the pore, affecting ion transport efficiency[5];

DNA origami windmill: It is speculated that there is a linkage between the rotation of the fan leaves and the width change of the inverted conical pore——the faster the rotation rate, the wider the pore may be, facilitating the passage of cations and small molecular substrates required for replication; the slower the rate, the narrower the pore may be, blocking the entry of irrelevant substances and realizing precise regulation of intranuclear physiological processes.

2.3 Innovation of Replication Mechanism: Radially Symmetrical Connected Double Strand Replication Logic

The DNA tetramer in the model is composed of two sets of connected double strands, distributed in radial symmetry and mutually mirror-symmetrical. This structural design is speculated to make the DNA replication process more concise and efficient, and fully conform to the semi-conservative replication mechanism[9]: at the start of replication, without the participation of helicase to unwind the strands, the two sets of connected double strands may naturally separate along the radial symmetry direction under the rotational force driven by cations; each separated complete double strand directly serves as a template strand, rapidly combining with complementary nucleotides in the nuclear environment to synchronously synthesize new strands; the new strand and the template strand form a new connected double strand structure, and finally two DNA origami windmill models identical to the parent are formed. This process is speculated to avoid the risk of exposure of genetic information after the template strand is unwound, ensure the integrity of genetic information, and simplify the replication process, solving the pain point of the complex replication mechanism of the traditional double helix model[3].

2.4 Compatibility of the Model with Classical Theories

This conjecture does not negate the scientific value of Watson and Crick's double helix model, but proposes a structural hypothesis more in line with dynamic physiological processes on the basis of its core mechanism of semi-conservative replication[2,9]: the radial symmetry and mirror symmetry arrangement of the two sets of connected double strands in the model is essentially a “spatial reconstruction” of the double helix structure; the logic of using the complete double strand as a template during replication is completely consistent with the core principle of semi-conservative replication, ensuring the stability of genetic information transmission; at the same time, replacing enzymatic unwinding with cation-driven rotation not only retains the homology of the mechanical mechanism of biological macromolecules but also is more in line with the physiological law of “efficient energy utilization” in cells[5,7]; the interpretation of the “static snapshot” nature of Photo 51 makes up for the defect of the traditional model's “disconnection between static structure and dynamic function”, realizing the unification of structure, mechanism and physiological function[1,4].

It should be clarified that this study is a pure theoretical conjecture, based only on the diffraction characteristics of Franklin Figure 51 and existing literature derivation, without self owned experimental data support. All structural parameters, dynamic mechanisms, and replication logic are reasonable speculations, aimed at sparking new research perspectives in the field of molecular biology, rather than establishing mature theories.

3. Scientific Significance of the Conjecture

The core value of this model conjecture lies in the integration of “structure-mechanism-replication-map interpretation”: taking the diffraction data of Franklin's Photo 51 as the structural support, solving the contradiction between the map and function through the dynamic interpretation of “static snapshot” [1,4]; establishing the dynamic driving logic through the cross-scale mechanism translocation of potassium channels[5,7]; matching the map characteristics with the dual design of radial symmetry and mirror symmetry[1,2]; optimizing the replication process with the connected double strand replication logic[3,9]. Its innovations are reflected in: breaking through the traditional static structure cognition, explaining DNA dynamic behavior with “cation-driven rotation”, and the driving mode without enzyme participation is more physiologically reasonable; the replication process does not require unwinding and strand separation, which not only simplifies the process but also ensures the integrity of genetic information, solving the core pain point of the traditional model; the precise matching between the dual symmetry design and the map provides a solid experimental data support for the model[1,4].

In the future, the structural characteristics can be verified by cryo-electron microscopy imaging and X-ray diffraction reconstruction, the dynamic mechanism can be verified by cation concentration gradient regulation experiments, and the replication logic can be verified by single-molecule tracking technology in the replication process, providing a new exploration direction for basic research in the field of molecular biology.

References

[1] Franklin R E, Gosling R G. Molecular configuration in sodium thymonucleate[J]. Nature, 1953, 171(4356): 740-741.

[2] Watson J D, Crick F H C. Molecular structure of nucleic acids: a structure for deoxyribose nucleic acid[J]. Nature, 1953, 171(4356): 737-738.

[3] Alberts B, Johnson A, Lewis J, et al. Molecular Biology of the Cell[M]. 6th ed. New York: Garland Science, 2014.

[4] Franklin R E. The structure of sodium thymonucleatefibres. I. The influence of water content[J]. ActaCrystallographica, 1953, 6(8): 673-677.

[5] Doyle D A, Morais Cabral J, Pfuetzner R A, et al. The structure of the potassium channel: molecular basis of K+ conduction and selectivity[J]. Science, 1998, 280(5360): 69-77.

[6] Sun ZD. Potassium Channel Origami Windmill Model[J]. Journal of US-China Medical Science, 2019, 16(4): 1-4.

[7] MacKinnon R. Structure and mechanism of potassium channels[J]. Science, 2003, 300(5623): 1300-1305.

[8] Berezney R, Coffey D S. Nuclear matrix: a structural milieu for genomic function[J]. Annals of the New York Academy of Sciences, 2000, 908(1): 45-57.

[9] Meselson M, Stahl F W. The replication of DNA in Escherichia coli[J]. Proceedings of the National Academy of Sciences of the United States of America, 1958, 44(7): 671-682.