

Construction and Biological Significance of Four stranded DNA Inverted Cone Windmill Model

Zuodong Sun *

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

Abstract

Inspired by the structure of the potassium channel “origami windmill” model, and combining the multi-strand folding characteristics of DNA molecules, ion regulation mechanisms, and genetic information transmission rules, a four-strand DNA inverted cone windmill model is proposed, breaking through the linear structural limitations of the traditional double helix model. The model utilizes a four-stranded DNA core scaffold, forming a windmill-like radial spatial conformation through a “double ladder inverted” mechanism. The strands are stabilized by hydrogen bonding, base stacking, and ionic regulation, while relying on the “single ladder inheritance” mechanism to achieve precise transmission of genetic information. This article elaborates on the construction lineage, structural characteristics, genetic mechanism, and potential biological significance of the model, providing a new perspective for the study of DNA multi-strand structure and genetic regulation.

Keywords: potassium channel; origami windmill model; quad-stranded DNA; inverted cone windmill model; double ladder inverted; single-strand inheritance

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

1. Introduction

Since the proposal of the DNA double helix model, its linear structure as a genetic information carrier has been widely recognized. However, with the discovery of tetrahelical DNA (e.g., G-quadruplexes) in telomeres and promoter regions of the genome, the traditional double helix model can hardly fully explain its special spatial conformation and biological functions ^[1]. Studies have shown that the formation of tetrahelical DNA is closely related to DNA replication and gene expression regulation, and the diversity of its spatial structure determines the specificity of its functions ^[2].

In previous studies on the structure and function of potassium channels, the author proposed the potassium channel “origami windmill” model: taking channel protein subunits as “blades”, a windmill-like spatial structure is formed through radial folding, allowing cations to be selectively transported along the central axis. Its core features lie in “radial arrangement” and “dynamically adjustable spatial conformation”^[3]. This model provides a new idea for the structural analysis of ion channels. As a core substance of life activities, DNA molecules share significant structural similarities with potassium ion channels in terms of multi-strand folding characteristics and ion regulation mechanisms. Inspired by this, the author further extends the structural concept of “origami windmill” to DNA research, innovatively integrating the structural feature of “double ladder inversion” and the genetic mechanism of “single ladder inheritance” to construct the tetrahelical DNA inverted cone windmill model. By analyzing its structural stability and genetic adaptability, this study aims to provide new structural model support for deciphering the biological functions and genetic information transmission mechanisms of tetrahelical DNA.

2. Construction Origin and Core Characteristics of the Tetrahelical DNA Inverted Cone Windmill Model

2.1 Construction Origin: Structural Inspiration from the Potassium Channel “Origami Windmill” Model

The core design of the potassium channel “origami windmill” model lies in: four channel protein subunits fold radially along the central axis to form a symmetric windmill-like structure, stabilized by hydrophobic interactions and ionic bonds between subunits, and cations can achieve selective transport through the central channel ^[3]. The key innovations of this model—“radial arrangement of four chain-like structures” and “dynamically adjustable spatial conformation”—provide direct inspiration for the structural modeling of tetrahelical DNA:

Structural similarity: Both the four nucleotide chains of tetrahelical DNA and the four protein subunits of potassium channels are arranged in a multi-strand parallel manner, laying the foundation for the formation of radial structures;

Functional relevance: Both need to realize core functions through dynamic changes in spatial conformation (transport function of ion channels, replication and expression functions of DNA);

Regulatory consistency: Both are regulated by cations (e.g., potassium ions), which can stabilize multi-strand structures through charge neutralization and adjust the opening and closing degree of spatial conformation.

Based on the above structural and functional relevance, the author combines the radial arrangement concept of “origami windmill” with the multi-strand folding characteristics of DNA, introduces the “double ladder inverted” design, and finally forms the tetrahelical DNA inverted cone windmill model.

2.2 Core Skeleton Structure: Windmill-like Arrangement of Double Ladder Inverted

Taking four homologous or heterologous nucleotide chains as the basis, the model first forms two groups of parallel “single ladder structures” (each single ladder is connected by two nucleotide chains through base pairing, with the phosphate backbone as the ladder beam and base pairs as the rungs). The two groups of single ladders are inverted oppositely with the central axis as the symmetry point, forming an “upper narrow and lower wide” inverted cone spatial conformation—namely the “double ladder inverted” structure.

This conformation perfectly reproduces the radial characteristics of the origami windmill: the two groups of single ladders correspond to two sets of symmetric “blades” of the windmill, evenly distributed along the central axis. It not only avoids face-to-face parallel stacking of chains to reduce steric hindrance but also enhances structural stability through cross-support of the double ladders; the inverted cone gradient space is similar to the central hub area of the windmill, providing an adaptive space for molecular interactions and ion transport.

2.3 Stabilization Mechanism

Base interactions: The interior of each group of single ladders forms stable rungs through Watson-Crick base pairing, and the single ladders are connected by G-G pairing and Hoogsteen hydrogen bonds to form base quadruplexes, which constitute the connection hub of “double ladder inverted”, similar to the fixed structure between windmill blades and the central axis;

Ion regulation: Cations (e.g., potassium ions) bind to the interior of base quadruplexes and the junction of double ladders, stabilizing the tetrahelical structure through charge neutralization. This mechanism is consistent with the ion regulation logic of the potassium channel “origami windmill” model, realizing dynamic opening and closing regulation of the inverted cone space;

Hydrophobic interactions and van der Waals forces: The phosphate backbone and base side chains of nucleotide chains further stabilize the conformation of double ladder inversion through hydrophobic interactions and van der Waals forces, ensuring the structural integrity of the model in the physiological environment.

2.4 Genetic Mechanism: Information Transmission Model of Single Ladder Inheritance

The model realizes accurate transmission of genetic information relying on the “single ladder inheritance” mechanism: during DNA replication, the “double ladder inverted” structure unwinds, and the two groups of single ladders serve as template strands respectively, synthesizing new complementary strands through base complementary pairing to form two new single ladders; the newly synthesized single ladders maintain structural consistency with the parent single ladders, and then form new “double ladder inverted” inverted cone windmill structures through re-pairing, completing the transmission of genetic information and the intergenerational continuation of the structure.

The advantages of this mechanism are: as the basic unit of genetic information, the single ladder has a simple structure and high stability, which can avoid replication errors caused by multi-strand entanglement; at the same time, the conformation of double ladder inversion can protect the single ladder template strand from nuclease degradation, ensuring the integrity of genetic information. Compared with the semi-conservative replication of the double helix model, "single ladder inheritance" is more suitable for the multi-strand structural characteristics of tetrahelical DNA, providing a reasonable molecular mechanism explanation for the genetic regulation of multi-strand DNA.

3. Discussion on the Biological Significance of the Model

3.1 Gene Expression Regulation

The inverted cone space formed by double ladder inversion can expose more base recognition sites, facilitating the binding of regulatory proteins such as transcription factors, thereby affecting the initiation of gene transcription; at the same time, the dynamic folding of the single ladder can regulate the spatial conformation of the gene promoter region, participating in the positive and negative regulation of gene expression.

3.2 Telomere Function Maintenance

When the G-quadruplex DNA in the telomere region adopts the inverted cone windmill conformation, the tip of the double ladder inversion can protect the telomere end from nuclease degradation, and the open structure at the bottom facilitates the binding and extension of telomerase; the single ladder inheritance mechanism ensures the length stability of telomere DNA during replication, avoiding cell senescence caused by telomere shortening.

3.3 Molecular Recognition and Transport

The gradient space formed by double ladder inversion can serve as a molecular channel to realize the selective transport of cations and small molecule substrates, whose functional logic echoes the ion transport mechanism of the potassium channel “origami windmill”¹ model; the base sequence specificity of the single ladder endows the model with high molecular recognition ability, providing a new target for targeted drug design.

4. Conclusion and Prospects

The tetrahelical DNA inverted cone windmill model is inspired by the potassium channel “origami windmill” model, integrating the spatial feature of “double ladder inverted” and the genetic mechanism of “single ladder inheritance”, constructed based on the multi-strand folding characteristics and ion regulation mechanism of DNA. It breaks the structural and genetic mechanism limitations of the traditional double helix model. The proposal of this model not only establishes an intermolecular association between ion channels and DNA structures, enriches the cognitive diversity of DNA spatial structures, but also provides new ideas for the research on gene regulation mechanisms and targeted drug development.

In the future, it is necessary to verify the structural authenticity of the model through techniques such as X-ray crystallography and nuclear magnetic resonance, and verify the feasibility of the “single ladder inheritance” mechanism through in vitro replication experiments. At the same time, further explore the structural evolutionary correlation between this model and the potassium channel “origami windmill” model, providing more systematic theoretical support for the structural design and functional regulation research of biomolecules.

References

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