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Informatics and Physics Models of Recognitions of DNA Replication and Their Biological Applications

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Abstract: We initially propose concepts of Informative Intensity, Informative Response Intensity and Informative Flux, with different expressions. In a special expression of electrostatics, we describe Informative Intensity, Informative Response Intensity and Informative Flux in terms of electric field intensity, electric field force and electric field flux respectively. In a special expression of quantum mechanics, we originally propose a concept of Probability Flux. Then we present Informative Intensity in terms of a wave function of Schrödinger equation and Informative Response Intensity in terms of an interactive force between or among objects, Informative Flux in terms of a probability flux. Based on these concepts, we develop our Informatics and physics models of recognitions between a DNA polymerase and an initiation site and of pairing deoxyribonucleotides, for a natural DNA replication, beyond lengths of chemical bounds and half quantitatively explain a probability of the wrong paring. We originally hypothesize the information is, stored in structured charges or masses, transmitted with Informative Intensity in a media and recognized with an Informative Response Intensity by other structured charges or masses. We further generalize, Informative Intensity as multiple layers of fields, potentials or waves, Informative Response Intensity as multiple layers of forces and Informative Flux as an integration of Informative Intensity. We also initially define Transverse Information: Informative Intensity is perpendicular to the direction of information propagation, e.g. electromagnetic wave or magnetic field; and Longitudinal Information: Informative Intensity is parallel or antiparalell to the direction of information propagation, e.g. electric field or gravitational field.

Key words: Electromagnetic, quantum, gravity, field, wave, potential, force, flux

INTRODUCTION

It is well known that scientists have investigated recognitions between a DNA polymerase and an initiation site[1-6] and of pairing deoxyribonucleotides[6-11] for DNA replication for many decades. But, those studies have been performed in a perspective of molecular biology or biochemistry and the recognition distance is limited to lengths of chemical bounds.

In electrostatics, to understand mechanism how a cell inherits its parents' information, we have modeled mitosis and cytokinesis for eukaryocytes[12], at a cellular level; separation of nucleotide sequences and DNA unwinding[13] at a bio-molecular level. In our previous modeling papers, we have proposed several concepts: Life Objects are biological units that exchange information, mass and energy, from each other and with their environments to preserve or to proliferate their (inherited) information by themselves, such as cells; Informative Objects are objects that carry information, such as chromosomes; Virtual Objects are objects without rest masses and sizes, such as electric fields. However, our modeling results also raise questions: How is the bio-information stored, sent, transmitted and recognized? To our knowledge, there is not any theory, model, or hypothesis to answer the questions in a view of informatics and physics.

In quantum mechanics, we obtained wave functions of Schrödinger equations of a deoxyribonucleotide and a complex of a DNA template strand and a DNA polymerase during DNA replication in our previous study and half quantitatively explained why and how there could be an empty position in a DNA strand[14]. But, to our knowledge, the question how deoxyribonucleotides are recognized or paired has not been answered in a perspective of informatics and physics; the meaning of the wave function was poor because it was known only a state function related to a probability.

To answer the questions, in this investigation, we propose informatics and physics models of recognitions between a DNA polymerase and an initiation site and of pairing deoxyribonucleotides, for a natural DNA replication, beyond lengths of chemical bounds.

Models

Informative recognition between a DNA polymerase and an initiation site for a DNA replication: We initially propose concepts of Informative Intensity, Informative Response Intensity and Informative Flux, with different expressions. In a special expression of electrostatics, we describe Informative Intensity, Informative Response Intensity and Informative Flux in

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terms of electric field intensity, electric field force and electric field flux respectively. Furthermore, we present the Informative Intensity and the Informative Response Intensity with two layers and three layers respectively in this investigation.

The protoplasm has been considered as an electrolyte with an uneven charge distribution and the natural cellular electric field has been considered as quasi static[12-16]. We use the same consideration to propose our new models of an informative recognition between an initiation site (a sender of information) for a natural DNA replication and a DNA polymerase (a receiver of information) beyond lengths of chemical bounds (Fig. 1). The molecular biological data in Fig. 1 are referenced to a published experimental research[17]. We estimate a low layer of Informative Intensity (II), at point P(x,y,z), with a Coulomb's electric field intensity (EFI) that is a multiplication of charge unit dq_s (r_s), at a point $P_s(x_s,y_s,z_s)$, of a sender, a medium function M_{EF}(r-r_s) and a transmitting function T_{EF}(r- r_s), where, r is a position vector from the origin to P, r_s is a position vector from the origin to P_s in or on the sender. $|r-r_s|$ is a distance between P and P_s.

$$II_{dq}(r) = EFI_{dq}(r) = M_{EF}(r-r_s)T_{EF}(r-r_s)dq_s(r_s) \quad (1)$$

$$M_{EF}(r-r_s) = \frac{1}{\varepsilon(r-r_s)} \quad (2)$$

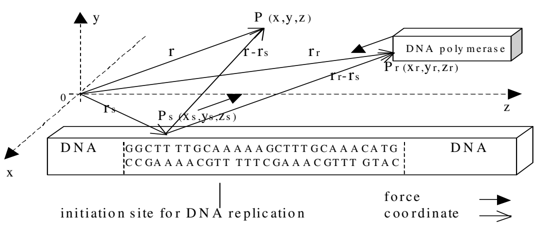

Fig. 1: An informative recognition between a DNA polymerase and an initiation site for a natural DNA replication in a Cartesian coordinate system. The initiation site is considered as a sender with an assumed net charge Q_{sn} (<0) and an assumed DNA polymerase is considered as a receiver with an assumed net charge Q_{rn} (>0), respectively. The draw is not in scale

$$T_{EF}(r-r_s) = \frac{r-r_s}{4\pi|r-r_s|^3} \quad (3)$$

Then, we estimate a high layer of Informative Intensity (II) with a convolution of a production of a medium and a transmitting functions and a total charge distribution $Q_s(r_s)$,

$$II(r) = EFI(r) = [M_{EF}(r)T_{EF}(r)] * Q_s(r) = \int_{Q_s(r_s)} \frac{(r-r_s)dq_s(r_s)}{4\pi\varepsilon(r-r_s)|r-r_s|^3} \quad (4)$$

Where * means a convolution mathematically.

We estimate a middle layer of Informative Response Intensity (IRI) with an electric field force $F_{dq}(r_r)$, based on Coulomb's law,

$$F_{dq}(r_r) = EFI(r_r)dq_r(r_r) \quad (5)$$

Where, $dq_r(r_r)$ is a integral unit of a receiver's total charge distribution $Q_r(r_r)$. r_r is a position vector from the origin to a point $P_r(x_r,y_r,z_r)$.

Finally, we estimate a high layer of Informative Response Intensity (IRI) in terms of a total electric field force F_t,

$$F_t = \int_{Q_r(r_r)} EFI(r_r)dq_r(r_r) = \int_{Q_r(r_r)} [\int_{Q_s(r_s)} \frac{(r_r-r_s)dq_s(r_s)}{4\pi\varepsilon(r_r-r_s)|r_r-r_s|^3}]dq_r(r_r) \quad (6)$$

where, $|r_r-r_s|$ is a distance between P_s and P_r, the distance is greater than a distance of any chemical bound. Other parameters have the same meanings as those in equations (1) - (5). We initially define a positive, negative or zero informative recognition when the interactive force is repulsive, attractive, or zero respectively. We believe, a DNA polymerase and an initiation site for a natural DNA replication have a negative informative recognition, equations (5) and (6) control or adjust their relative movement and the spatial positions, equation (6) makes a final decision, for a DNA polymerase, to hug, to leave or to ignore an initiation site for a natural DNA replication.

Informative recognition of deoxyribonucleosides during DNA replication: In a special expression of quantum mechanics, we propose a new concept of a Probability Flux (PF), where Φ is a quantum wave function of Schrödinger equation, A and dA are area and unit area of the integration respectively. We respectively describe Informative Intensity in terms of a quantum wave function Φ or a potential function of an object, Informative Response Intensity in terms of an interactive force between or among objects and Informative Flux in terms of Probability Flux. Based on the concepts, we propose our models to understand recognition mechanism of pairing deoxyribonucleotides during DNA replication.

Figure 2 illustrates our quantum mechanics model of informative recognition when an incoming deoxyribonucleoside (C) triphosphate (+x direction) pairs with a deoxyribonucleoside (G) in a DNA polymerase that moves along an assumed DNA template strand in the elongation (+y direction) of a DNA replication. We assume the incoming deoxyribonucleoside triphosphate has a quantum wave function Φ with a free state, the complex of a deoxyribonucleoside (G) and DNA polymerase forms a potential function to attract a complementary deoxyribonucleoside (C) and to repulse other deoxyribonucleosides (G, A or T) triphosphates. V and L were defined respectively, for a convenient

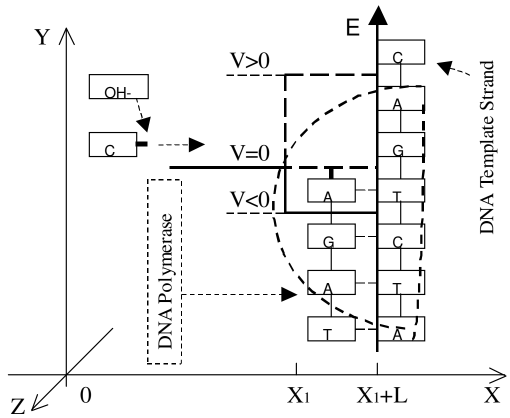

Fig. 2: During a natural DNA replication, an incoming deoxyribonucleotide (C) triphosphate, with a free state quantum wave function Φ, is being trapped into a potential well with an effective constant height (V < 0). The potential well is made by a complex of deoxyribonucleotide (G) and a DNA polymerase bound on an assumed DNA template strand. The potential function is respect to x axis. A barrier (V > 0) and a plain (V = 0) of an effective constant heights are also plotted for a comparison. The draw is not in scale

calculation, as an effective constant height and length of the potential function in our previous studies[18,19]. We assume L is about a size of a DNA polymerase in x direction (greater than a distance of any chemical bound). When the height is a barrier (V > 0), well (V < 0) or plain (V = 0), the interactive force F between the incoming deoxyribonucleoside and the complex is repulsive, attractive or zero respectively and its absolute value is proportional to the height, based on Ehrenfest law in quantum mechanics:

$$F = -\frac{dV(x)}{dx} \tag{8}$$

Where, V(x) is a potential function of energy. According to our model, a normal pairing of C and G or A and T, have a negative informative recognition because their interactive force is attractive; an abnormal pairing of others (not shown in the figure) have a positive informative recognition because their interactive force is repulsive. If the probability of wrong paring is from 10^{-6} to 10^{-9}[11], the barrier height at a temperature of 37 C°, using our published method[18,19], is from 0.3 to 0.5 eV. Therefore, we half quantitatively explain a probability of the wrong paring.

Applications: The principle of our electrostatic models in this study could be also applicable to the following biological researches: binding of an antigenic determinant on a macromolecule to the antigen-binding site of an antibody molecule in immunology; recognition at an initiation site of RNA transcription; recognition and excision of palindrome sites of restriction endonucleases; recognition of pronuclear movements; recognition of centriole replication and signal recognition in nerve system.

The principle of our quantum mechanical models in this study could be also applicable to selectivity of biological ion channel currents, informative recognition of an incoming aminoacyl tRNA and a complex of a ribosome and a mRNA template during protein presentation and informative recognition of an incoming rebonucleoside and a complex of a RNA polymerase and a DNA template strand during RNA transcription.

Generalization: Roles of a sender (producer) and a receiver (responder) of information can be mutualy exchanged. A sender can be a second sender that reflect Informative Intensity from the first sender. In gravity, we originally propose a new concept of Gravitational Field Flux (GFF),

$$GFF = \int GFI \bullet dA$$

where, GFI is a wellknown gravitational field intensity in physics and A and dA are area and unit area of the integration respectively. We respectively describe Informative Intensity in terms of gravitational field intensity and Informative Flux in terms of Gravitational Field Flux. A typical biomedical application of gravitational field is a study of bone rehabilitation.

We originally hypothesize the information is, stored in structured charges or masses, transmitted with Informative Intensity in a media and recognized with Informative Response Intensity by other structured charges or masses. We further originally generalize, Informative Intensity as multiple layers of fields, potentials or waves, Informative Response Intensity as multiple layers of forces and Informative Flux as an integration of Informative Intensity. Informative Intensity is, produced or reflected by a sender, transmitted in a media following a transmitting function and recognized (responded) by a receiver. A media is a transmitter and a receiver is a responder. Informative Response Intensity (a force) represents a positive, negative or zero informative recognition when it is repulsive, attractive or zero respectively, between a sender and a receiver. We also initially define Transverse Information : Informative Intensity is perpendicular to the direction of information propagation, e.g. electromagnetic wave or magnetic field; and Longitudinal Information: Informative

Intensity is parallel or antiparallel to the direction of information propagation, e.g. electric field or gravitational field.

DISCUSSION

Our models in this study could be tested in future by using dynamic images and measuring the accurate electric field with high resolution. The limitation of the model is to obtain the distributions of electric charges and permittivities in real world environments today.

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REFERENCES

1. Lee, S.J. and C.C. Richardson, 2005. Acidic residues in the nucleotide-binding site of the bacteriophage T7 DNA primase. J. Biol. Chem., 280: 26984-91.
2. Hwang, G.T. and F.E. Romesberg, 2006. Substituent effects on the pairing and polymerase recognition of simple unnatural base pairs. Nucleic Acids Res., 34: 2037-45.
3. Landthaler, M., B.W. Shen, B.L. Stoddard and D.A. Shub, 2006. BasI and I-HmuI: two phage intron-encoded endonucleases with homologous DNA recognition sequences but distinct DNA specificities. 1: J Mol Biol., 358: 1137-51.
4. Henry, A.A., C. Yu and F.E. Romesberg, 2003. Determinants of unnatural nucleobase stability and polymerase recognition. J. Am. Chem. Soc., 125: 9638-46.
5. Jezewska, M.J., R. Galletto, W. Bujalowski, 2002. Dynamics of gapped DNA recognition by human polymerase beta. J. Biol. Chem., 277: 20316-27.
6. Alberts, B., A. Johnson, J. Lewis, M. Raff, K. Roberts and P. Walter, 2002. Molecular Biology of The Cell. 4th Edn. Garland Science, New York, NY, pp: 191-298.
7. Hogg, M., W. Cooper, L. Reha-Krantz and S.S. Wallace, 2006. Kinetics of error generation in homologous B-family DNA polymerases. Nucleic Acids Res., 34: 2528-35.
8. Wang, L. and S. Broyde, 2006. A new anti conformation for N-(deoxyguanosin-8-yl)-2-acetylaminofluorene (AAF-dG) allows Watson-Crick pairing in the Sulfolobus solfataricus P2 DNA polymerase IV (Dpo4). Nucleic Acids Res., 34: 785-95.
9. Nair, D.T., R.E. Johnson, L. Prakash, S. Prakash and A.K. Aggarwal, 2005. Human DNA polymerase iota incorporates dCTP opposite template G via a G.C + Hoogsteen base pair. Structure, 13: 1569-77.
10. Sismour, A.M. and S.A. Benner, 2005. The use of thymidine analogs to improve the replication of an extra DNA base pair: a synthetic biological system. Nucleic Acids Res., 33: 5640-6.
11. Hwang, H. and J.S. Taylor, 2005. Evidence for Watson-Crick and not Hoogsteen or wobble base pairing in the selection of nucleotides for insertion opposite pyrimidines and a thymine dimer by yeast DNA pol eta. Biochemistry, 44: 4850-60.
12. Cheng, K. and C.H. Zou, 2006. Theoretical models of cytokinesis and mitosis (without asters). Am. J. Plant Physiol., 1: 21-27.
13. Cheng, K. and C.H. Zou, 2006. Electromagnetic field effect on separation of nucleotide sequences and unwinding of a double helix during DNA replication. Med Hypotheses, 66: 148-153.
14. Cheng, K. and C.H. Zou, 2003. A three dimensional (3-D) physical model of DNA polymerase movement in DNA replication. Biomed. Sci. Instrument., 39: 83-88.
15. Cheng, K. and C.H. Zou, 2005. Physics models of pronuclear movements in eggs. A. J. Biochem. Biotechnol., 1: 13-16.
16. Meggs, W.J., 1988. Electric fields determine the spatial organization of microtubules and actin filaments. Med. Hypoth., 26: 165-170.
17. Jay, E., R. Roychoudhury and R. Wu, 1976. Nucleotide sequence with elements of an unusual two fold rotational symmetry in the region of origin of replication of SV40 DNA+. Biochem. Biophys. Res. Commun., 69: 678-86.
18. Cheng, K., P.P. Tarjan and C.H. Zou, 1993. Schrodinger equation, Maxwell-Bolzmann distribution and single channel current. Biomed. Sci. Instrument., 29: 361-367.
19. Cheng, K., 1997. Improved 3-D quantum mechanical models of ion movements in a cylindrical ion-channel. Proc. 16th Southern Biomed. Engg. Conf., IEEE Press, Piscataway, NJ, USA, pp: 220-223.