Gene Expression Switch Model based on liquid Crystalling like phenomena of Double stranded DNA chain

Yasuo Yonezawa [1)&2)*] and Hidetoshi Kuramochi [2)]
1) Division of system Engineering and Information Science,
Graduate School of Science and Engineering,Ibaraki University,
4-12-1,Nakanarusawa,Hitachi,316-8511,Japan
2) Complex Functional Systems Laboratories,Graduate School
of Science and Engineering,Ibaraki University,
4-12-1,Nakanarusawa,Hitachi,316-8511,Japan

Abstract

Metaphase chromosome as packed DNA in nuclear are dynamically switch in interphase driven on genrative complexity. This research focuses on how these topological structure can be switched, and explores the functional mechanism and significance of these changes. In this paper, We proposed Gene Expression Switch model based on the formation of liquid crystalline like DNA aggregate as our experimental results. In this paper deals with Gene Expression Switch Model, we are presented the possibility of various kind decode in DNA chains.

1. Introduction

In living organisms, Higher multi-cellular are well as known as typical Complex adaptive systems. Many multicellular individuals each start as single cell as fertilized egg. egg. But, we have not enough the generative complexity at decode properties in DNA(chromosome) systems. In order to elucidate the generative mechanism of Comeplex system like multi-cellular living organisms, we proposed the gene expression switch model be able to generate on the complex system as multi-cellular organisms. Primitive genetic system are constructed the DNA sequence described by bases and the genetic information transfer processing call as "Central Dogma (shown in Fig 1). The depend on this genetic system cannot encode the all information due to generating Biotic Complex adaptive system as multicellular organism for missing numerous control mechanism. Therefor, missing mechanism for generation of biotic complex system must be exist due to biotic generating complexity. In previous research, the decode of genetic information are well known based on chromosome structures and the depend on the DNA volume (shown in Fig 2). Also, Decode of Genetic information is regulated at relaxed from tight structure of aggregate of double stranded DNA chain (shown in Fig3).

* To whom correspondence should be address: yonezawa@life01.dse.ibaraki.ac.jp, FAX +81-294-38-5208

These analytical data suggested the decode various information needed generating higher multicellular organisms. Most important contents at the generation of biological complexity are the dynamics created with interaction of the reaction between of genetic products. Namely,Variety of Time-space pattern of the decoded information of DNA are needed.

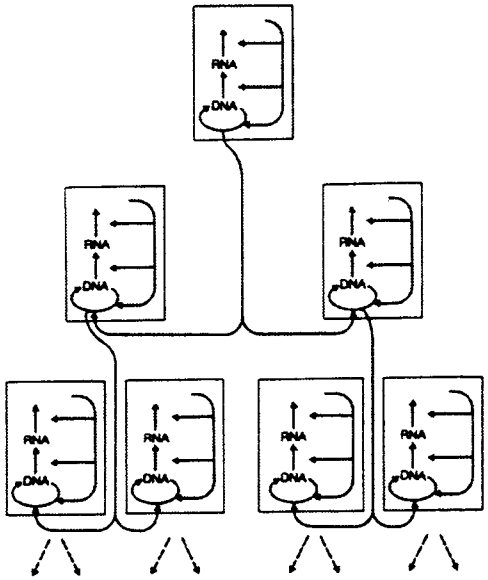

Fig 1. Central Dogma of living Organisms

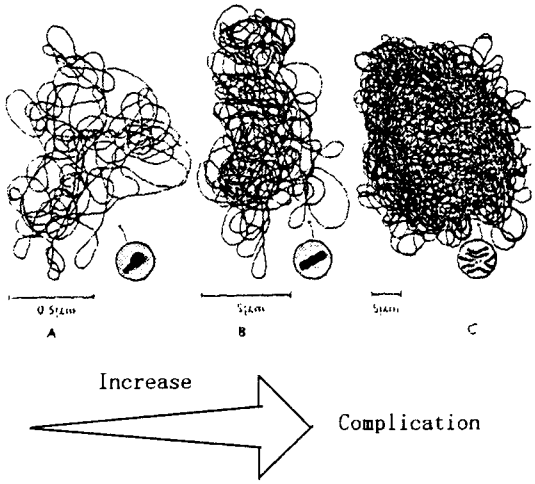

Fig 2. DNA volume of several organisms.
A: Bacteriophage T4, B: E.coli,
C: Drosophila

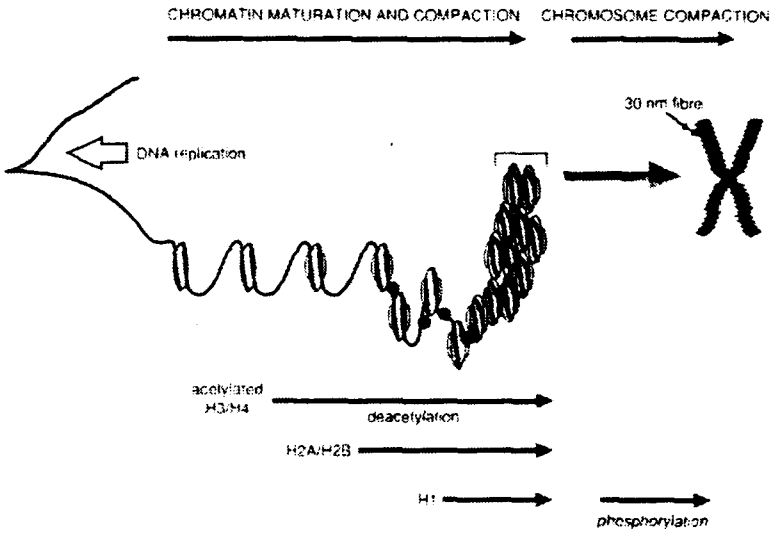

Fig 3. Chromatin assembly on replicating DNA.

2. Experimental Results based of " Gene Expression Switch model "

2.1 Coil-globule transition depend on Sequence Properties

We are obtained that nucleation occurs at the ends of the single T4 phage DNA chain and in region with positions of higher GC contents by fluorescence microcopy analysis. Namely, Nucleation is observed only in the region containing the position with relatively high GC content region along DNA chain. By previous research, As it is highly expected that the manner of packing of long DNA chains is concerned with the mechanism of self-regulation in gene expression, the specific character of nucleation as very beginning of the process of folding in a long DNA chain seems to be very important.[1)]

2.2 Formation of liquid-Crystal-like DNA aggregate under Biological Condition[2)]

We are experimented the spermidine-DNA macro-aggregate in a primitive λ DNA(Bacteriophage DNA of E.Coli)-TE buffer system, and then observed the following multistage process in the macro-aggregation: the formation of anisotropic long fiber, their parallel bundle and spool, and liquid-crystal-like assemble with multilayers(shown in Fig 4).In this experiments, the precipitation data of both DNA aggregates by spermidine in presence of Mg- ion were measured by UV absorption spectrometry to make their phase diagram.

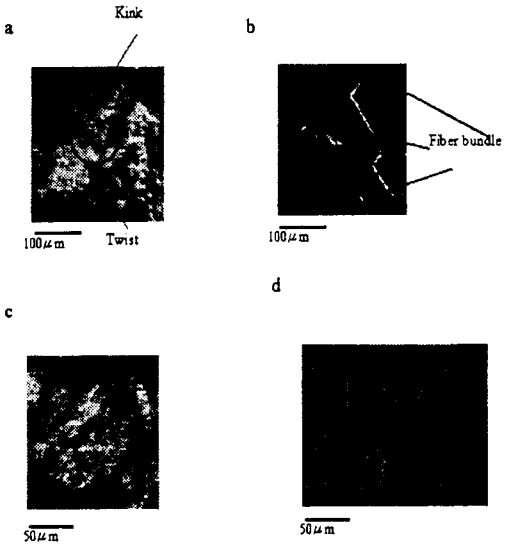

Fig 4. Aspect of DNA macroaggregates in polarizing microscopy
a: anisotropic fibers and their kink and twist
b: parallel bundle and spool of anisotropic fibers
c: cholesteric-like texture at 0.55 mM spermidine
d: cholesteric-like texture at 7.0 mM spermidine

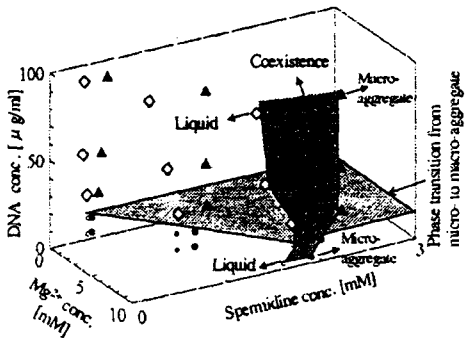

Fig 5. Phase diagram of the spermidine-λ DNA aggregate in the presence of Mg^{2+}

Furthermore, the phase transition from micro-to macro-aggregate was determined by used of the hyperchromic effect due to the micro-aggregate size. The phase diagram is depicted in Fig 5 . Mg-ion play a role of inhibitor for the formation of DNA aggregates: The threshold concentration for the aggregation is shifted into the more concentration of spermidine as increasing Mg^{2+} concentrations in the buffer solution. It is interesting at biological reaction view that the influence of DNA concentration under the macro-aggregation phenomena in absence of Mg^{2+} large differed from that in missing condition of Mg^{2+}. The morphological variation of the macro-aggregate were observed by polarizing microscopy.

3. Gene Expression Switch Model

3.1 Essential contents as back ground of Gene Expression Switch Model

This section is deals with the back ground as "Gene Expression Switch Model". These results from experimental consequence described at section 2, we could obtained on essential contents for Gene Expression Switch Model described as bellows;

1) Coil globule transition depend on the character of base composition in DNA sequence.For example: The creation are occurred with center of high GC contents region in single double stranded DNA chain.
2) Aggregation like liquid crystal structure λ by Multi-stage self-assembly under biochemical condition(Mg^{2+}, polyamine, ATP etc).[2)]

Experimental results newly observed the multi-stage(about 3 stage) aggregation process :1st stage: The creation of Anisotropic fiber form, 2nd stage:Parallel bundles and spools of the several numbers fibers. 3rd stage: Their multi-layered assembly including a cholesteric-like phase.From these essential contents, we are proposed that preparation of model in order to explain of the generation of biotic complex adaptive systems.

3.2 Design of "Gene Expression Switch Model

The system scenario for the generation of biotic complexity are summarized described as bellows contents. :

(1) DNA long chain structure into cell are very complicated as small packed DNA by self-aggregation.
(2) DNA Packing by coil globule transitions are depended the composition properties(ex: AT rich or GC rich region etc of DNA sequence)
(3) In population of Double stranded DNA chain, Long DNA chains could be pack on the liquid crystal like

aggregate by various environments(Mg^{2+}, ATP and Polyamine of several concentrations)[3]

(4) The Information decode from DNA chain are needed the relax state form packed form. In the case of tight topology at aggregate DNA, the information decode could not activation.[4]

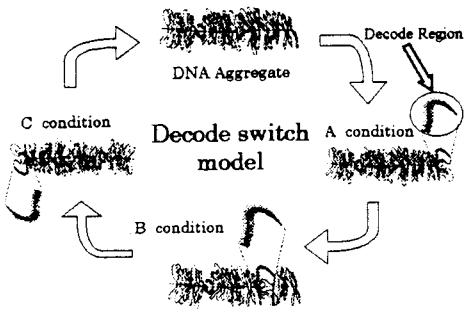

Fig. 6 Outline of Gene Expression Switch model; Condition: Polyamine's, ATP, Mg^{2+} concentration's etc.

"Gene Expression Switch Model " is made from these described system rules. Gene expression switch of our model is the change of relax and tight topological structures by biochemical environments for examples ATP, Mg^{2+}, polyamine depended cell growth each stages.[5,6,7]

The outline scheme of this model is described as Fig 6. Our Gene express switch of DNA sequence are could be generate the various kinds biological information in according to biochemical conditions of cell growth. Also, this model is created various information from same source code by the change of relax and tight region of long DNA chain in according to ATP,Mg^{2+},Polyamines, etc depended on each growth phases. [8,9]

4. Summary and Perspective

In this paper deals with the Gene Expression Switch Model, We are represented the model of gene expression switch of long DNA chains based on the change of aggregate form under several biochemical environments. These biochemical environments are changed in according to Each Cell growth phase[10], ex., concentrations of Mg^{2+}, ATP, Polyamines etc. Furthermore, these biochemical environments components are regulated on the relax and tight form of DNA aggregate in according to sequences composition characters. Namely, the change of biochemical condition in inner-cellular are regulated on DNA aggregate form at each growth phase. These change of biochemical conditions are given the variety of decode Information for the generation complexity.

Therefore, Our model hope that it could be the biotic gene expression like in vivo similar simulation. We are in progress the further works of computer simulation depend on our experimental results(in preparation for publication) .

Acknowledgements

We would like to thank Dr.Hirofumi Doi for useful discussion in this research fields. Also, we would like to thank Mr.Hiroshi Yokohama in our laboratory student for technical supports.This research is supported by SV-BL grant of Ibaraki University.

References

1) Matsuzawa.Y., Yonezawa.Y and Yoshikawa.K, " Formation of Nucleation Center in Single Double stranded DNA chain, Biochemical and Biophysical Research Communication, 225 pp796-800 (1996).

2)Kuramochi.H and Yonezawa.Y., "Formation of liquid -Crystal-like DNA aggregate under Biological Condition: Phase Diagram, Morphology and Biological Implication", Abstract of the 18th International Liquid Crystal Conference(ILCC 2000), p499 (2000).

3)Yonezawa.Y and Kasamizukami.A., " Chromatine chain processing model generated on the self-organized complexity", Proc. IIAS workshops of Order and structure in Complex system, pp 107-116 (1998).

4) Wolffe.A., " Chromatine: Structure and Function" Academic Press (1995).

5)Strzelecka.T.E, Davidson.M.W and Rill.RL., "Multiple liquid crystal phase of DNA at high concentration"., Nature, 4, 331, pp457-460 (1988).

6)Pelto J.Jr., Durand .D., Ducet.J and Livolast.F., "DNA mesophases induced by spermidine; Structure properties and Biological implications", Biophys J, 71(1), pp48-63 (1996).

7) Reich.Z., Levin-Zaidman.S., Gutman.SB and Mensch.A., " Supercoiling-regulated liquid crystalline packing of topologically-Constrained, nucleosome-Free DNA molecules., Biochemistry., 33(47),pp14177-14184(1994)

8) Yonezawa.Y and Horikoshi.K., "Polyamine in Alkalophilic Bacillus Y-25".,Agric.Biol. Chem.,42, pp1955-1961 (1978).

9)Horikoshi.K and Yonezawa.Y., " A Bacteriophage active on Alkalophilic Bacillus sp", Journal of General Virology.,139, pp 183-188 (1978).

10)Yonezawa.Y and Ohtomo.K., " Structure properties of Generative from by hormonal proliferation algoritm," FORMA,15,pp163-167 (2000).