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DNA as classical and quantum information system: Implication to gene expression in normal and cancer cells

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ABSTRACT

Usually, we think about DNA as a molecular machinery system responsible to make proteins. Protein looks like a second side of DNA code because mapping function is based on a classical information system (chemical/physical) by code $4^3 = 64$. However, in organisms like paramecium DNA works 95% as molecular machinery for proteins synthesis, while in humans it is only about 10%. Is 90% of human genetic structure "junk"? What does other 90% DNA work in human organism? What type of information system, different than classical, does DNA possess? To give answer to this question we are rethinking well-known facts of biomolecules from both classical and quantum information point of view. Basic element in our consideration is hydrogen bond, which possess both classical and quantum properties. Based on new vision of old data we develop synergetic (classical/quantum) model of DNA information processing, which may help for better understanding the functions of "junk" sequence in genetic code. We believe that "junk" sequences may be active regulatory factor of system complexity trough microtubules (centrioles) and water in living systems. Synergetic approach (classical/quantum) of information channels may open a new vision and understanding of the genomic programming and molecular interconnection on distance based on matching classical and quantum properties of hydrogen bonds and entanglement.

KEY WORDS: *DNA; Hydrogen Bonding; Genetic Code; Neoplasms; Gene Expression; Melanoma; Quantum Theory*

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INTRODUCTION

In scientific fields, it is crucially important to understand how internal structure relates to external form. The internal molecular structure of DNA is the key to understand how it works, but it is too far to be fully understood. Biomolecules are complex nanosystems, in which structure, energy, and information are coupled in nonconventional way. Standard model of DNA is based on classical (biochemical) signaling approach. According to nowadays knowledge the main function of DNA is protein coding. However, it is not complete function of this system because there are nonprotein-coding sequences, which have been considered as "junk" (Figure 1).

Traditional view of gene activity in eukaryotes is based on individual genes comprise exon sequences that code for segments of protein separated by noncoding intron sequences. When a gene is active, it is entirely transcribed as RNA, but than the intronic RNA is spliced out and the exotic RNA is assembled as messenger RNA. In other words, the cell translates the messenger RNA into protein while breaking down and recycling the intronic RNA, which serves to no purpose. However, a new view of gene activity in eukaryotes is modification of previuos one, where some of the intronic RNA and even some of the assembled exonic RNA may play a direct regulatory role by interacting with the DNA, RNA, and proteins (Mattick, 2003).

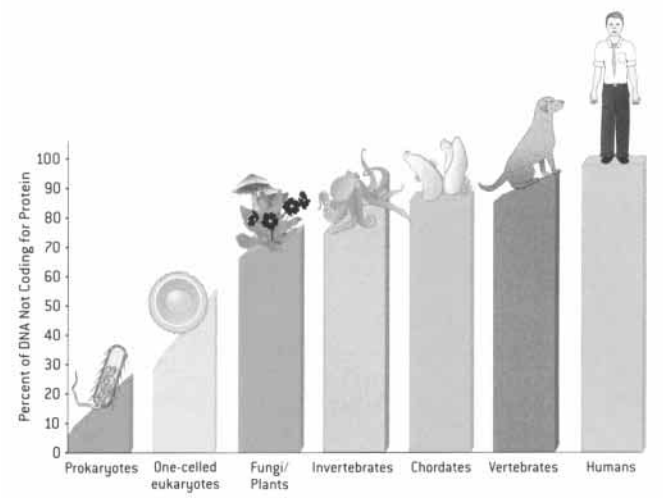

Figure 1. Nonprotein-coding sequences and organisms' complexity (Mattick, 2003)

PROBLEM IDENTIFICATION

Schrodingor's book "What is Life?" has had a enormous influence on the development of molecular biology, stimulating scientists such as Crick and Watson to explore double helix of DNA as the basis of life (Schrodinger, 1943; Watson and Crick, 1953). One of the central points in his book is statement "that the most essential part of a living cell-the chromosome fiber - may suitably be called *an aperiodic crystal*. In physics we have dealt hitherto

only with *periodic crystal*". Crick was crystallographer and he very well understood Schrodinger's words. This lead to idea how DNA works as a classical information system based on ternary coding system with $4^3=64$ coding words (Crick, 1963). Many years later it was recognized that that genetic ternary code, which coding amino acids in proteins, also, may be represent as a classical binary code $2^6=64$ (BOX 1) (Rakočević 1988, Rakočević, 1998).

$\log_2 8 = 3$	Genetic code		Amino acid	2^3	$\log_2 8 = 3$	Genetic code		Amino acid	2^3
	2^6	4^3				2^6	4^3		
(0)	000000	UUU	F		(0)	011000	ACU		
(1)	000001	UUC			(1)	011001	ACC	T	
					(2)	011010	ACA		
(2)	000010	UUA	L		(3)	011011	ACG		
(3)	000011	UUG		I					IV
					(4)	011100	GCU		
(4)	000100	CUU			(5)	011101	GCC	A	
(5)	000101	CUC	L		(6)	011110	GCA		
(6)	000110	CUA			(7)	011111	GCG		
(7)	000111	CUG							
					(0)	001000	UCU		
(0)	010000	AUU			(1)	001001	UCC	S	
(1)	010001	AUC	I		(2)	001010	UCA		
(2)	010010	AUA			(3)	001011	UCG		
									II
(3)	010011	AUG	M	III	(4)	001100	CCU		
					(5)	001101	CCC	P	
(4)	010100	GUU			(6)	001110	CCA		
(5)	010101	GUC	V		(7)	001111	CCG		
(6)	010110	GUA							
(7)	010111	GUG			(0)	110000	AAU	N	
					(1)	110001	AAC		
(0)	111000	AGU	S						
(1)	111001	AGC			(2)	110010	AAA	K	
				VIII	(3)	110011	AAG		VII
(2)	111010	AGA	R						
(3)	111011	AGG			(4)	110100	GAU	D	
					(5)	110101	GAC		
(4)	101100	CGU							
(5)	101101	CGC	R		(6)	110110	GAA	E	
(6)	101110	GCA			(7)	110111	GAG		
(7)	101111	CGG							
				VI	(0)	100000	UAU	Y	
(0)	101000	UGU	C		(1)	100001	UAC		
(1)	101001	UGC							
					(2)	100010	UAA	□	
(2)	101010	UGA	*		(3)	100011	UAG		
(3)	101011	UGG	W						V
					(4)	100100	CAU	H	
(4)	111100	GGU			(5)	100101	CAC		
(5)	111101	GGC	G	VIII					
(6)	111110	GGA			(6)	100110	CAA	Q	
(7)	111111	GGG			(7)	100111	CAG		

Box 1

Since 1943 scientists have been only looking at one segment of Schrodinger's idea and developed classical approach to understanding how DNA works. It is one side of "coin", or truth. In spite that other side of "coin" was also indicated in Schrodinger's book, scientists have not recognized DNA as a quantum mechanical system in property way. In Chapter 4, of his book, "The quantum-mechanical evidence", Schrodinger clearly indicates that DNA is "unexplainable by classical physics" and recommends to do research from quantum mechanics. But, from some reason, no one scientist yet pays serious attention to consider DNA as a quantum system. There were many tries to calculate energetic state of DNA from both classical and quantum mechanical point of views but without satisfactory results. According to our consideration, the main reason for this situation is the absence of synergetic classical/quantum (unity of structure-energy-information) approach.

NEW CONSIDERATION HOW DNA WORKS

There are many things to learn about DNA, but we tried to select the most important and general points. DNA is structure made of three things: phosphates, sugars, bases, and these compounds are linked together making double helix structure. Key points for our consideration are connection between outside hydrogen bonds (phosphor interaction with outside water) and inner hydrogen bonds (base-pairs connection trough gaps).

The phosphate group is essentially a rigid tetrahedron, having a phosphorus atom at its center and one oxygen atom at each vertex. Freedom of rotation for adjacent links of the chain is given via sugar carbon atoms. The calculation tells us something that agrees closely with experiment: almost all DNA double helices have 10 ("B" form), 11 ("A" form), and 12 ("Z" form) phosphates per turn of helix, within each stand. Flexibility of sugar-phosphate chains, trough freedom of rotation of adjacent links, gives these three possibilities of DNA form. However, in all cases the bases fill compactly the surface of "DNA cylinder" and successfully protect the centers of the double helices from the surrounding water. Polarized water molecules fully interact with phosphorous groups via hydrogen bonds. However, the center of the double helix, as quasi 1D dimensional space is consist from discrete units of two and three hydrogen bonds, which bases A=T and G≡C are formed by genetic code law.

Why "A" form of DNA is dominant in nature? From structural and energetic point of view, all three forms look similar. However, careful consideration shows that "B" and "Z" forms have some jagged features in its sugar-phosphate chain as irregularities in the packing of bases on the inside of the helix. Law of bases packing is second key point in new consideration how DNA works. If DNA is primary information device in living systems than its structure has to be organized by optimal information coding law. Coding systems may be defined in different ways but sphere packing approach is basic one (Sloane, 1984). If structure of DNA is designed by sphere packing law than form "A" (number 11) is optimal from digital transmission of information. Packing of spheres gives that the optimal coding number could be 11,13, 35, and 37, with specific state of 10 and 12 (Figure 2).

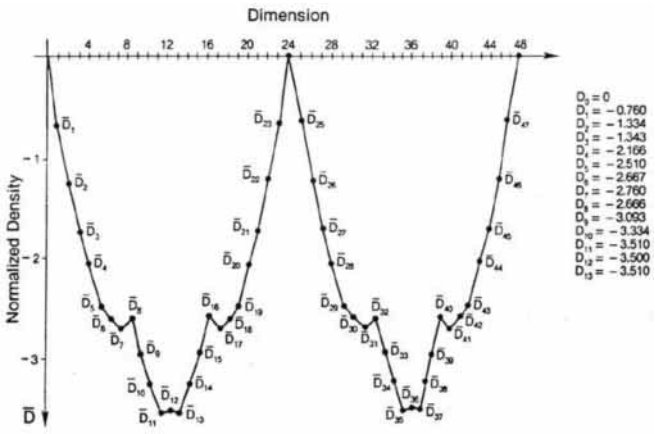

Figure 2. Design of a code for the efficient transmission of information is equivalent to the sphere-packing problem. There are two optimal sets (11,12*,13 and 35,36*,37), with sphere packing in helix (11,13,35 and 37) and with sphere packing on sphere surface (12* and 36*). In biological systems DNA follow role 11, microtubules 13, while water should follow 12* (adapt from Sloane, 1984, Koruga, 1986)

There is equivalence of spheres packing in helix (coding number 11 and 13) and the packing on sphere surface (coding number 12). Bearing in mind that DNA is primary information device, coding number 11 is the first optimal number from the set of optimal numbers. Coding number 13 is next optimal number and should be important for protein structure design, because it represents the second side of DNA code. It is known that microtubule (MT) is coding structure with 13 subunits and possess $K_1[13,2^6,5]$ code, capable to transmit digital information (Koruga, 1986). Cell structure is organized from a central focal region near the nucleus called the microtubule organizing center (MTOC).

The principle component of this center is the centriole, an organelle that consists of two perpendicular microtubule cylinders. Each of these cylinders is made up of 27 microtubules organized in nine MT triplets. The centriole has three main movements (1) rotation, (2) twisting, and (3) duplication during cell division. Centrioles and MTOC play key roles in dynamic coordination of cell cytoplasm and activities. Many scientists call MTOC and cytoskeleton as "cortex" and "cell-brain", respectively. Experiment showed an unexpected effect, when cell is separated into two parts; one with nucleus and cytoplasm, the other with centriole with some cytoplasm. The "new" cell with the nucleus cannot produce a new cen-

triole, in spite that DNA is responsible to make protein tubulin, which is basic component of MT. In other words, microsurgical removal of centriole blocks the cell reproduction and a new centriole generation (Moniotis and Schliwa,1991). Since coding systems 11 (DNA) and 13 (MT) are functionally closely interconnected and arise from same sphere packing law, those two systems are entanglement. This means that only cells, which have both nucleus and centriole have normal biological properties of mitosis (cell division) and general functionality.

The first potential importance of hydrogen bonding in the structure and function of biological macromolecules was predicted by the earliest investigators (Pauling, Corey, and Branson, 1951). According to Linus Pauling, the concept of the hydrogen bond is to be attributed to M. L. Huggins and independently to W. M. Latimir and W. H. Rodebush, whose are proposed it in 1919 and 1920, respectively. Bearing in mind that most biological systems contain water from 60% to 80%, importance of hydrogen bonds has become most relevant for understanding how biomolecular machinery, as a complex system, works. In water, there are two types of bonds that are related to hydrogen: *hydrogen bonds* between water molecules and *sigma bonds* within a single water molecule, between oxygen and hydrogen atoms. It is well known that covalent bond may only be described by quantum mechanics, because each electron does not really belong to a single atom - it belongs to both simultaneously. For a long period scientists believed that hydrogen bond could be perfectly understood by principle of electrostatic interaction by Coulomb's law (pre-20th century classical physics), based on the attraction and repulsion between charged particles separated from each other by a distance. However, recent experimental data indicate that hydrogen bonds has double identity: classical and quantum (Isaacs, 1999, Barbiellini, and Shukla, 2003).

This is the key point for understanding a new approach how DNA and proteins are working in water. However, water itself may be a coding structure, via its hydrogen bonds, if it is organized in spherical clusters. Same local areas of water, under the influence of DNA and microtubules, may be generators to organize water molecules in spherical clusters as complementary coding forms. In human organism of all water, 60% is free water, while 40% is captured by biomolecules. Estimation gives that only 5% of free water may be in cluster form by sphere packing law of coding number 12. Other 95% of free water is in form of "chaos" with local polymerized islands. In other words, we indeed do not know how water is organized in living systems.

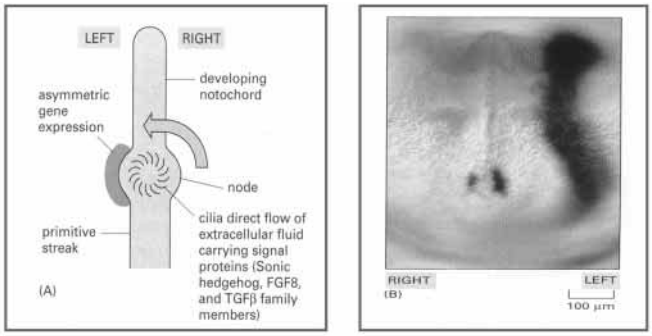

Figure 3. Asymetric gene expression as a rsult of cilia (microtubule) influence on direct flow of water (extracellular fluid) (Kierszenbaum, 2002)

According to coding approach based on sphere packing optimal water organization should be as a hydrogen-bonded $(H_2O)_n$ polyhedra $5^{12}6^n$ (n=0,2,4.....), where 5^{12} represents 12 pentagons and *n* different number of hexagons (Jeffrey,1997). Through hydrogen bonds dynamics, this water clathrate possess spherical coding system $2^5=32$. Bearing in mind that arrangement of water, based on number 12, may represents coding system which is part of optimal information peak (11,12 and 13) of sphere packing, than water hydrogen-bonded polyhedra is both compatible and complementary coding system with genetic code (DNA and proteins).

This means that "junk" sequence in genetic code may be active regulatory factor of system complexity, like asymmetry, trough microtubules (cilia and centrioles) and water in living systems (Figure 3). However, water organization could be main problem of satisfactory functionality of "junk" sequence via hydrogen bonds.

SYNERGY OF THE CLASSICAL AND QUANTUM INFORMATION

We found from both classical and quantum calculation that A=T, C≡G in DNA, and peptide plain in protein possess two major oscillations; acoustical (phonon) and optical, (electrical) (Koruga, Tomic, Ratkaj, Matija, 2003). This indicates that both classical and quantum mechanical approach give same phenomenological results for those structures. Reason for similar result is simple one: for stationary quantum state Hamilton is a sum of kinetic (T) and potential (V) energy, while Lagrangion is a difference between them when system is in equilibrium with external forces (BOX 2).

Lagrangian

$$d/dt\ (\partial T/\partial x'_j) - \partial T/\partial x_j = Q_j$$

Hamiltonian

$$ih/2\pi(\partial\psi/\partial t) = -H\psi$$

Planck constant h is the first value for estimation which type system is: classical or quantum

F_{orce}=? (N) $d_{istance}$=? (m) t_{ime}=? (s)

$$h = F\ d\ t\ (Js) = 6.626\ 10^{-34}$$

Example:

F= 10^{-10} (N) d=10^{-8} (m) t=10^{-8} (s) Classical (10^{-26})

F= 10^{-12} (N) d=10^{-10} (m) t=10^{-12} (s) Quantum (10^{-34})

F= 10^{-12} (N) d=10^{-9} (m) t=10^{-9} (s) Quantum/Classical(10^{-30})

Box 2

We have two similar pictures, one classical (type A) another quantum (type B), of same object. Planck constant (*h*) is the first criteria to estimate whether an object is classical or quantum. If the product of force (*F*), distance (*d*) and time of action (*t*) in some process has value: (1) close to h (between 10^{-34} and 10^{-32} *Js*) than it is quantum system; (2) between 10^{-32} and 10^{-29}*Js* it is quantum/classical system; (3) between 10^{-29} and 10^{-26} *Js* it is classical/quantum; and (4) less than 10^{-26} *Js* it is classical system.

The classical channel, type A, is based on binary code system, like $2^6=64$, while the second is quantum one, because its divisor function $\sigma(n)=2n$ is $\sigma(q)=q+1$ (for $n=q$, where q is prime number). For communication channel in form 2^n this gives solution, $\sigma(2^n)=2^{n+1}$-1, what is exactly the number of quantum states in communication channel (Ustinov, 2003). From synergy point of view $[2^n(2^{n+1}-1)]$ we can say that type A contains communication part 2^n (*classical*) and type B 2^{n+1}-1 (*quantum*).

The most important entity of classical information theory is the *bit*, which can have either the value "0" or "1" with both values separated by a large energy gap so that the unwanted spontaneous transition from one to the other value is impossible or extremely unlikely (for example the bit error rate in standard channels of telecommunication is 10^{-9}-10^{-12}).

The quantum mechanical analogy of the bit is the quantum bit or *qubit* (Nielson and Chang, 2000). It is a quantum system with two states $|o\rangle$ and $|1\rangle$ forming Hilbert space as an orthogonal basis in the qubit space. In contrast to the classical bit, it is possible to crate qubits (Figure 4, down-left) in a coherent superposition of $|o\rangle$ and $|1\rangle$, with the general state being $|\psi\rangle_{qubit}$, where $\alpha^2+\beta^2=1$. Since some biological molecules DNA (Rakocevic, 1998), microtubules and clathrin (Koruga, 1993) are composed by golden mean law than values α and β should be; $\alpha=\sqrt{\phi}$ and $\beta=\phi$, where ϕ = 0.61803 is value of the golden mean. One of the key differences between the familiar classical world we inhabit, and exotic quantum world, is the wire of superposition. It is ability of quantum things to exist simultaneously in two different states.

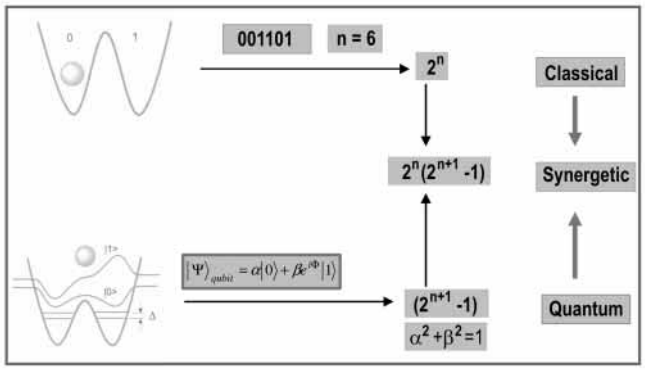

Figure 4. In classical chanel, basic unit of information is defined as 'bit' (0 or 1, north-south pole) state (picture up-left); in quantum physics, basic information state is presented as 'qubit' of wave function states $|0\rangle$ and $|1\rangle$ (picture down-left). Superposition on qubit sphere gives coherent superposition of $|0\rangle$ and $|1\rangle$ which lie on the shell inside of the sphere (for DNA n=6 there are 127 states), while 'bit' states (there are 64) lie on the shell ouside of the sphere

Key point to understand biological communication system is synergy of classical and quantum process based on perfect numbers and the golden mean laws. Perfect numbers are positive integers n such that $n=s(n)$ where $s(n)$ is restricted divisor function $\sigma(n) = 2n$, where $\sigma(n)$ is the divisor function. The first four perfect numbers are 6,28,496 and 8128. For the first two perfect numbers their divisors are 1+2+3=6, and 1+2+4+7+14=28. Sum of reciprocate value of perfect number divisors is $H_d=(1/d_i=2$ (1/1+1/2+1/3+1/6=2). Perfect numbers were deemed to have important numerological properties by the ancients, and were extensively studied by the ancient Greeks, including Euclid and Plato. Now, perfect numbers arise again as an important class of numbers in information and control theories. From system organization point of view, relationship *part-whole* is crucial one. In modeling, combination of perfect numbers and harmonic numbers gives the best results for control theory. Perfect numbers are connected with a class of Mersenne primes numbers in the form $M_p = 2^p-1$.

In our synergetic approach to processing free water - DNA interaction, and *vice versa*, we used three channels to carry signals in molecular system (Figure 5).

The first one is a classical channel (cC^M, as binary system 2^n) based on classical signal behavior. The second is hybrid one, which is based on *phonon-photon* coupling phenomena of phosphor-sugar-base group. This system also works as binary 2^n system. The third one is inner side of the DNA bases and may activate at the same time left and right side of their hydrogen bonds (2^n x 2), or only left or right side of them (2^n x1/2) may be active. In the first case communication system is type A (left-right side is synchronized):

2^n x 2 x 2^n = 2^n, or $2^{n-1}(2^n-1)$,

where: 2^n represents classical channel, while $2^{n+1}-1$ represents quantum channel (Figure 4). In the second case, system is type B (there is not photon-phonon coupling during DNA or peptide plane oscillation). Left and right sides of DNA or peptide plane works separately, including the extreme case like splitting): $2^n/2$ x $2^n=2^n/2$, or $2^{n-1}(2^n-1)$

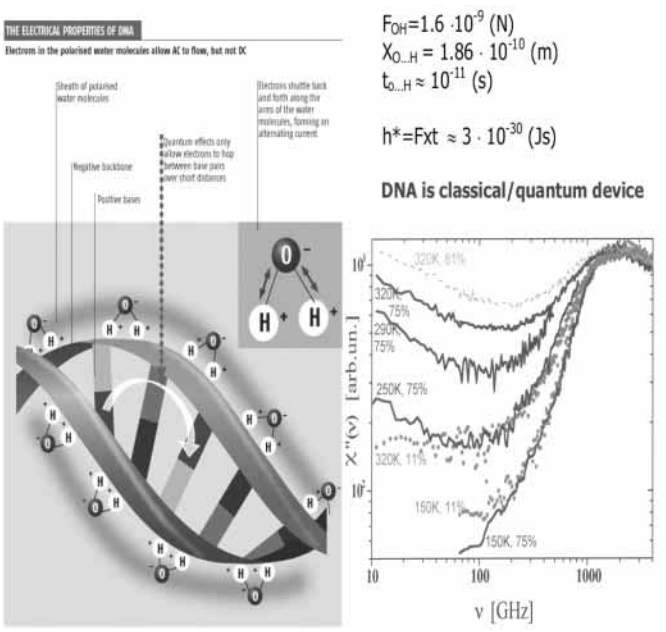

Figure 5. In classical comunnication channel DNA has $4^3=2^6$ code words, while its quantum channel has $2^{6+1}-1=127$ statets based on hydrogen bonds. Total number of DNA coding words is 8128 (adapt from Biever, 2003)

For $n=6$, type A will give DNA working process by forth perfect number 8128, while type B will give solution by "non-perfect" number 2016. Type A has enough elements for right coding, both classical and quantum states, while the second one has not enough coding worlds for quantum channel. Number 2016 is symmetry breaking element between the third (496) and the forth (8128) perfect numbers, because according to $2^{n-1}(2^n-1)$ formula, for n=5 value will be 496. Since water naturally works by 2^5 code (n=5), than when DNA code in same sequence of gene collapse from n=6 to n=5, then this event, as DNA disharmony, will transmit trough water very quickly in given region ("good news travel fast, bed even faster").

SYNERGY CHANNEL VIOLATION AND CANCER

Cancer is one of the leading causes of death in the last century. Knowledge improvement in this field is crucial one. However, our current knowledge about cancer is very limit. According to synergy of DNA-microtubule-water coding system based on hydrogen bonds (perfect numbers and golden mean) we will consider skin cancer and melanoma, as symmetry braking phenomena of hydrogen bonds.

The epidermis is a dynamic renewing structure that provides life-sustaining protection from

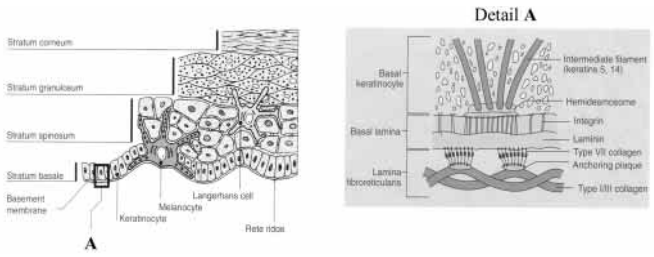

Figure 6. Cross-sectional anatomy of the epiderms (left), and detailed view of the basement membrane zone at the dermo-epidermal junction. Colapse of collagen 'woof' of stratum basale is responsible for cancer penetration into dermes (Gawkrodger, 2002)

the environment. Keratinocytes and melanocytes are the major cells types responsible for the structure of the epidermis (Figure 6).

They begin as stem cells in the basal epidermal layer. As keratinocytes move to the epidermal surface, the cells cease cell division and undergo morphological changes to form the spinous, granular, transition, and cornifield layers. One melanocyte cell may overlap a few keratinocytes giving them melanin, which is responsible for protection of the environmental electromagnetic radiation (UV radiation) and neutralization of free radicals (Varni et al, 2004).

Also, collagen distortion below basement membrane (lamina fibroreticularis) occurs when cancer penetrates from epidermis into dermis, and "opens the door" for metastases. From classical communication channels point of view, gene expression is responsible for it: normal collagen, type I [$\alpha1(I)_2\alpha2(I)$], consists from two procollagen chains $\alpha1(I)$, which gene location is on chromosome 17 (q21-q22), and one procollagen chain $\alpha2(I)$, which location is on chromosome 7(q21-q22). According to quantum theory, quantum communication channel (entanglement) based on DNA hydrogen bonds, between keratinocyte or melanocyte and fibroblast cells, exists. When symmetry-braking of hydrogen bonds happens in DNA, than automatically, trough DNA-microtubule-water coding entanglement, classical and quantum communication is broken (Figure 7).

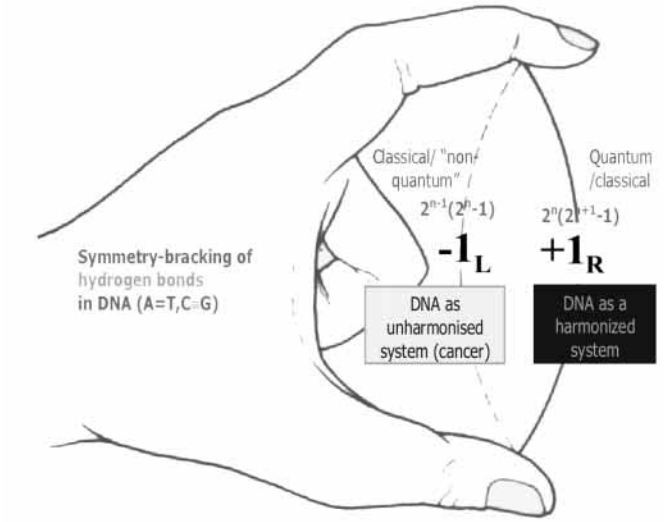

Figure 7. Symetry bracking of DNA funcionality: when exists non adequate matching of hydrogen bonds between water-phosphate and hydrogen bonds of DNA pairs (A=T, C=G) than funcionality of DNA is violet (-1_L state). When hydrogen bonds matching is correct than classical and quantum chennels make synergy state ($+1_R$ state)

There is experimental evidence that fibroblast cells and human melanoma cells interact with tumor cell growth as a function of tumor progression (Cornil, et al.1991). If UV radiation damages DNA on chromosome 7, in keratinocyte or melanocyte cells, then trough non-classical quantum channel this information will transfer to both centriole (damaged cell) and fibroblast cells in region. Centriole will become "wild" and will start to divide chromosomes irregularly. Nucleus of initial cancer cell will become bigger than in normal cell. The "wild" cell will be duplicated and number of them will rapidly increase because positive feedback control mechanism water-centriole will change perpendicularity of centriole pairs (Koruga, et.al.1992). From other side, fibroblast cells will stop to produce collagen $\alpha2(I)$. In absence of $\alpha2(I)$, procollagen chains during assembly into procollagen molecule will incorporate one more $\alpha1(I)$ procollagen chain. This will give collagen type I-trimer with structure $[\alpha1(I)_3]$. In I-trimer links between procollagen chains do not fit well, and OH groups will be removed from collagen to make free water molecules. Volume of free water will increase for 20% in tissue (Foster and Schwan, 1986). Similar situation happens skin aging and that is why people in age frequently have cancer (Richard, 2004). When this type of collagen becomes dominant in given tissue then lamina fibroreticularis (as "a woof" of basal lamina) becomes week, because interconnection between procollagen chains into procollagen molecule, based on hydrogen bonds, is not adequate. Then, mass of skin cancer or melanoma, penetrate basal lamina and touch superficial arteriovenous plexus (Brinkley, 2001).

Bearing in mind that entanglement in biological tissue can produce effects in classical channel (initial remove collagen's OH group), then quantum entanglement of hydrogen bonds might be the key to understanding not only carcinoma but also life itself. If so, the proverb, "every cloud has a silver lining" may have sense.

SUMMARY

Hydrogen bonds look like a "soul" of biomolecule network as well as their complex intermolecular connections. It is a link between classical and quantum behaviors of matter on molecular level, and it is basic element for synergy of mass-energy and information in living matter.

Understanding DNA as synergetic classical/quantum device, based on golden mean and the forth prefect number, may help us not only for better understanding of the origin of life, but also for finding methods for prevention and healing the most illnesses. Bearing in mind that proteins are the second side of DNA code, interaction and communication DNA-protein may be both through separate classical and quantum communications channels, and through synergetic one. Applicability of current genetic knowledge is limited because it is based only on classical information approach. However, synergetic approach may open new possibilities for diagnosis and therapy of many illnesses including cancer. Based on molecular genetics of skin and synergetic approach we proposed a possible mechanism how skin cancer and melanoma generate and penetrate basal lamina. Symmetry braking of synergetic channel, based on hydrogen bonds, is a key point for understanding how normal cell and tissue are transformed into cancer.

DNA and water are in very delicate relationship. In normal situation, the first entity works by the forth perfect number law, while second entity by the third one. In normal situation, DNA-water system works harmonically. However, when from some reason DNA function collapses (from the forth to the third perfect number law) then information about disharmonic state of system travels more smoothly trough water than harmonic one.

DNA is more than just molecule of the biological form of life - it is also "Ariadne's magic ball of thread" for understanding point of departure of information physics. If we do not use DNA as a classical/quantum object of investigation, we will not be able to escape from labyrinth of complexity and to understand basic principle of natural information. Also, without fully understanding how DNA works we could not be able to make nanoscopic structures and devices relevant for engineering and nanomedicine. Health, together with ecology, should be the first criteria in future human development. Since prevention, early detection and effective therapy are the foundation of our fight against cancer, then a new type of quantum nanodevices are needed in future. We have to keep in mind that engineering without medicine is blind, while medicine without engineering is feeble.

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