

Evolution in Many-Sheeted Space-Time

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Abstract

The topics of the chapter has been restricted to those, which seem to represent the most well-established ideas. There are many other, more speculative, ideas such as the strong form of the hypothesis that plasmoid like life forms molecular life forms has evolved in "Mother Gaia's womb", maybe even in the hot environment defined by the boundary of mantle and core.

1. Basic facts about and TGD based model for pre-biotic evolution are discussed.
2. A model for the ATP-ADP process based on DNA as topological quantum computer vision, the identification of universal metabolic energy quanta in terms of zero point kinetic energies, and the notion of remote metabolism is discussed.
3. A model for the evolution of the recent genetic code (3-codons) as a fusion of codes for which codons are nucleotides (1-codons) and di-nucleotides (2-codons) is discussed. The symmetries of the genetic code, the observation that tRNA can be seen as a fusion of two hairpin like DNA molecules, and the finding that the first nucleotides of 3-codon code for the reaction path leading from a precursors of the aminoacid to aminoacids for hydrophobic/hydrohilic dichotomy, serve as motivations of the model. 1- and 2-codes corresponding to the two forms of RNA (the exotic 2' – 5' RNA and the usual 3' – 5' RNA) would have prevailed in RNA world. Aminoacids would have served as catalysts for the copying of RNA on one hand, and RNA molecules would have catalyzed the formation of aminoacids from their precursors on one hand, meaning the presence of a positive feedback loop. In the transition to DNA-aminoacid era RNA began to be translated to aminoacid sequences.
4. Cambrian explosion represents a rather mysterious period in biology: new highly developed phylas emerged out of nowhere. A second strange finding is that continents would fit together to form single super-continent covering entire Earth's surface at time of Cambrian explosion if the radius of Earth would have been one half of its recent value. This finding has inspired Expanding Earth theories but it has not been possible to identify the mechanism causing the expansion. The success of the standard tectonic plate theory requires that possible expansion must have occurred in relatively short geological time scale. The hierarchy of Planck constants implies that cosmic expansion has occurred in quantum leaps increasing the value of \hbar and thus of quantum scales by factors which tend to be powers of 2. Cosmic expansion would have occurred as jerks even in the case of planets. In the proposed model Cambrian explosion would have accompanied the expansion of the Earth's radius by a factor of 2: during this period an outburst of highly developed life forms from underground seas to the surface of Earth would have taken place.
5. The last section of the chapter compares TGD based view about the evolution of genetic code to the views of McFadden. This section is a little bit out of date. For instance, the hypothesis that magnetic body of DNA could induce mutations purposefully is not

discussed. This hypothesis is natural if one believes that magnetic flux tubes connecting bio-molecules play a key role in bio-catalysis. This idea is discussed in the chapter devoted to protein folding.

Keywords: Topological Geometro-dynamics, unified theories, quantum theories of consciousness, evolution.

1 Introduction

This chapter was originally about prebiotic evolution but gradually extended so that it became natural to drop the attribute "prebiotic" away. Of course, a collection of ideas rather than detailed history of life is in question.

It was already early that the notion of many-sheeted space-time could allow to understand many puzzles related to the pre-biotic evolution [58, 61]. There are many constraints on the models for pre-biotic evolution. The models have also many difficulties [46, 55].

TGD replaces materialistic view about universe with a continual re-creation in which classical universe in 4-dimensional sense is replaced by a new one in each quantum jump. p-Adic length scale hypothesis allows to formulate the notion of evolution precisely as a generation of increasingly larger space-time sheets characterized by preferred p-adic primes. A second aspect is the emergence of new levels in dark matter hierarchy making possible macroscopic quantum coherence and inducing great leaps in evolution. Also a hierarchy of dark weak bosons and gluons becomes an essential part of the physics of living matter. The notion of field/magnetic body carrying dark matter is a further key element in the model and has become increasingly important during years, and the vision about DNA-cell membrane system as a topological quantum computer utilizing braids defined by magnetic flux tubes connecting nucleotides to lipids meant a breakthrough in the understanding of the real function of DNA in information processing.

1.1 Questions and answers about evolution

A good manner to introduce the essentials of the TGD inspired model for the prebiotic evolution is by a sequence of questions and answers relating to evolution.

Q: Is life as we know it result of an accident?.

A: Quantum TGD predicts a genuine cosmic evolution occurring by quantum jumps for which dynamics is characterized by Negentropy Maximization Principle [H2]. The generalization of the notion of space-time implies dark matter hierarchy with levels characterized by arbitrarily large values of Planck constant so that macroscopic quantum coherence is possible even in astrophysical length scales. Even astrophysical systems are analogous to atomic systems which implies a strong standardization of planetary system so that Earth like planets are abundant. There are also other good reasons for why the evolution of life would not have been accident in TGD Universe and life should appear everywhere in TGD Universe.

Q: What were the most primitive living systems?

A: The notion of magnetic body brings to biology several completely new elements. Magnetic flux quanta containing dark charged matter and quantum controlling ordinary matter in plasma phase is perhaps the simplest system which can develop characteristics of a living system. The braiding of magnetic flux tubes makes possible topological quantum computation and a fundamental representation of memories and its presence could be even taken as a definition for what it is to be living. Tqc programs correspond to asymptotic self organization patterns for liquid flows inducing braidings and are non-trivial in presence of external energy feed.

Q: How metabolic machinery emerged?

A: Many-sheeted space-time concept predicts a hierarchy of universal metabolic energy quanta as differences of zero point kinetic energies for space-time sheets characterized by different p-adic length scales. What remains is to understand how chemical energy storage and utilization mechanisms developed.

Q: What is behind biocatalytic machinery?

A: The magnetic flux tubes connecting bio-molecules imply long range correlations between molecules. The reduction of Planck constant for magnetic flux tubes implying their shortening provides a mechanism making possible for bio-molecules to "find" each other in a very selective manner, and explains also why molecules end up to precisely defined conformations necessary for a selective bio-catalysis.

Q: How symbolic dynamics emerged?

A: The notion of N -atom suggested by the fractionization of electron quantum numbers for dark matter hierarchy brings in a candidate for a symbolic dynamics assigning to molecules "names" which need not correlate very strongly with the chemical properties of the molecule but would dictate to a high degree its biochemical behavior. Molecular "sex" emerges in the sense that molecules labeled with "names" and "co-names" tend to pair. The model of DNA as tqc assumes a 4-coloring of braid strands realized by an assignment of DNA nucleotides to quarks and anti-quarks. Also this means symbolic dynamics since only molecules connected by colored braids have high probability to participate in same biochemical reaction and do it in a very specific manner. Since the quarks involved with braid strands can have fractional charges, molecular sex can be realized also in this manner.

Q: What selected the bio-molecules during chemical evolution?

A: The proposed symbolic dynamics based on the notions of colored braids and N -atom poses very strong constraints on the subsets of bio-molecules that can react with considerable rates.

Q: How biochemical pathways emerged?

A: It is now possible to realize in practice sequences of arbitrarily complex self-catalyzing biochemical reactions utilizing DNA hairpins. The mechanism generalizes to more complex molecules. At a given step of the reaction sequence the structure formed during the previous steps acts as a key fitting to a lock represented by some hairpin in the solution, and opens it to a linear molecule and in this manner makes it a key. The braids between reactants make it possible for the key and lock to find each other.

Q: How genetic code evolved?

A: The symmetries of the third codon of the genetic code allow in DNA as tqc model an interpretation as isospin and matter antimatter symmetries for quarks and antiquarks assigned with DNA nucleotides and representing 4-color of braid strands. These symmetries together with the study of the detailed structure of tRNA lead to a model for the evolution of the genetic code as a fusion of a non-deterministic 1-code and one-to-one 2-code corresponding to the conjugation of mRNA molecules. During RNA era two kinds of RNAs, call them RNA_1 and RNA_2 , were present and played the roles of mRNA and aminoacid sequences. 2-code *resp.* 1-code mediated the analog of replication *resp.* translation using hairpin like molecules $tRNA_1$ and $tRNA_2$ to bring in RNA nucleotides and RNA doublets to the growing RNA_i sequence. Amino-acids attached to the stem of $tRNA_2$ acted as catalysts. The transition to RNA-aminoacid era took place via a fusion of the $tRNA_1$ and $tRNA_2$ to the ordinary tRNA and instead of sequences of two kinds of RNAs were replaced by aminoacid sequences were formed. After a period of symbiosis involving all these three tRNAs a transition to DNA-RNA-aminoacid world took place as an aminoacid sequence acting like reverse transcriptase emerged.

Q: Did RNA world precede the life as we know it?

A: The model for the evolution of the genetic code forces to conclude tha RNA world [52] preceded the recent biology and allows also to deduce that the nucleotides involved with second form of RNA where A,T,U,I(nositol). The exotic RNA in question could have been 2', 5' form of

RNA rather than 3', 5' RNA produced also in the classical experiments of Leslie Orgel [100].

Q: Does the notion of protocell make sense?

A: The model of DNA as tqc involves essentially the magnetic flux tubes connecting DNA nucleotides and cell membrane. Since topological quantum computation should have taken place also during the RNA era, some kind of cell membrane consisting of exotic RNA should have been present. It has been found that DNA indeed forms membrane like structures which are liquid crystals consisting of sequences of DNA nucleotides with length up to 20 nucleotides [96] and same might be true in the case of exotic RNA.

Q: How life could evolve in the harsh primordial environment? Does the notion of primordial ocean make sense?

A: Evolving life had to cope with the grave difficulties due to the irradiation by UV light and meteoric bombardment. A simple solution of these problems is to evolve in the interior of Earth, say in underground lakes. This idea conforms nicely with the observation that continents would have formed a single super continent at time of Cambrian explosion provided the radius of Earth at that time was by a factor 1/2 smaller than now. TGD predicts that cosmic evolution does not occur continuously but by quantum jumps in which the Planck constant of appropriate space-time sheet increases. A phase transition of this kind increasing the radius of Earth during a relatively short time interval would have led to a burst of life from underground lakes to the surface of Earth. This would also explain the sudden emergence of a huge variety of highly developed life forms during Cambrian explosion.

1.2 Topics of the chapter

The topics of the chapter has been restricted to those, which seem to represent the most well-established ideas. The topics of the article have been restricted to those, which seem to represent the most well-established ideas about evolution in TGD Universe. There are many other, more speculative, ideas such as the notion of N-atom based on fractalization of electron charge and strong form of the hypothesis that some life forms has evolved in "Mother Gaia's womb", maybe even in the hot environment defined by the boundary of mantle and core.

1. Basic facts about and TGD based model for pre-biotic evolution are discussed.
2. A model for the evolution of the recent genetic code (3-codons) as a fusion of codes for which codons are nucleotides (1-codons) and di-nucleotides (2-codons) is discussed. The symmetries of the genetic code, the observation that tRNA can be seen as a fusion of two hairpin like DNA molecules, and the finding that the first nucleotides of 3-codon code for the reaction path leading from a precursors of the aminoacid to aminoacids for hydrophobic/hydrophilic dichotomy, serve as motivations of the model. 1- and 2-codes corresponding to the two forms of RNA (the exotic 2' – 5' RNA and the usual 3' – 5' RNA) would have prevailed in RNA world. Aminoacids would have served as catalysts for the copying of RNA on one hand, and RNA molecules would have catalyzed the formation of aminoacids from their precursors on one hand, meaning the presence of a positive feedback loop. In the transition to DNA-aminoacid era RNA began to be translated to aminoacid sequences.
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the value of \hbar and thus of quantum scales by factors which tend to be powers of 2. Cosmic expansion would have occurred as jerks even in the case of planets. In the proposed model Cambrian explosion would have accompanied the expansion of the Earth's radius by a factor of 2: during this period an outburst of highly developed life forms from underground seas to the surface of Earth would have taken place.

4. The last section of the chapter compares TGD based view about the evolution of genetic code to the views of McFadden [62]. This section is a little bit out of date. For instance, the hypothesis that magnetic body of DNA could induce mutations purposefully is not discussed. This hypothesis is natural if one believes that magnetic flux tubes connecting bio-molecules play a key role in bio-catalysis. This idea is discussed in the chapter devoted to protein folding [L8].

2 What is known about pre-biotic evolution?

In the following the basic facts and ideas about pre-biotic are summarized.

2.1 Some believed-to-be facts about the early history of life

The following basic facts allow to get rough view about the time scales of the pre-biotic evolution.

1. The origin of Earth occurs roughly 4.5 Ga (Ga=billion years ago). Bombardment phase, that is the period of large scale impacts, ended roughly 4-3.8 Ga.
2. ^{12}C enrichment is seen as a signature of photosynthesis. By this criterion the oldest known micro-fossils date back to 3.5 Ga and are found in volcanoes. There is a hot debate going on about whether these micro-fossils are really genuine micro-fossils. For instance, they are accompanied by complex quartz structures and this does not conform with what one might expect.
3. Levels of atmospheric oxygen began to increase during second half of precambrian era (2 Ga) and reached 10 per cent level at the eon's end at 1 Ga.
4. There are not many fossils or fossil bearing rocks from the precambrian eon. The simplest explanation is that the precambrian fossils have been soft bodied. Abundant fossils appear at Cambrian period which started .55 Ga. Cambrian explosion meant emergence of extremely rich spectrum of various life-forms.
5. The time interval between bombardment phase and the emergence of the first micro-fossils is only .3 billion years. This means that the time window for the life to develop on the surface of Earth is surprisingly narrow, and one can ask whether the primordial life could really have developed spontaneously in the environment provide by the surface of young Earth.

2.2 Standard approaches are mechanistic

Various hard science approaches to the pre-biotic evolution share a common philosophy dating to the beginning of the previous century. This philosophy is reductionistic materialism according to which life can be explained as a purely mechanistic phenomenon which just happened to occur by change ("change and necessity" using the phrase in the title of the classic of Monod). This view is highly questionable and certainly in dramatic conflict with more modern views relying on macroscopic and even astrophysical quantum coherence as basic elements.

At the experimental level the failure of mechanistic approach is easy to see. The components of cell inside test tube do not form a living system. The numerical simulations using computer models have demonstrated convincingly that spontaneous emergence of life is not possible. Empirical facts support completely different conclusion: the emergence of life is unavoidable and occurs everywhere in the universe, and there are good reasons that it has some universal characteristics. The challenge is to develop the conceptual framework so that it can explain this naturally.

2.3 The notion of primordial ocean

The following discussion uses basic facts which I have learned from articles of Chris King [58] representing updated view about facts and theories about pre-biotic evolution as well as articles criticizing the existing theories [46, 55].

The generation of biomonomers requires the presence of C, H and O. During 1920's Oparin and Haldane independently proposed that life, or its chemical precursors including amino-acids, formed spontaneously under the conditions associated with primordial atmosphere. Genetic code was not yet known, and both Oparin and Haldane believed that life evolved from proteins, and that life's precursors including amino-acids were formed spontaneously in a reducing atmosphere whose principal components were CH_4 and/or CO_2 , NH_3 , and H_2O .

Oparin suggested that methane served as the source of carbon whereas Haldane believed that the source was CO_2 . Oparin also suggested that what he called coacervates were precursors of the cell. Haldane thought that the gradual increase in the complexity of pre-biotic molecules in the presence of UV radiation led automatically to the generation of a protocell.

The assumption that the atmosphere is reducing is essential: the presence of oxygen would be fatal for the biomonomers. This assumption can be however questioned. The primordial atmosphere was due to the outgassing associated with volcanic eruptions but and volcanic fumes the atmosphere is oxidizing which means that biomonomers would have been rapidly destroyed by oxidation. Interestingly, the photographs of Earth taken during the Apollo 16 mission allow to conclude that a gigantic cloud of hydrogen, extending 40,000 miles into space surrounds the Earth. The only source of hydrogen can be water vapour, bombarded by high energy UV light rays above ozone layer [71]. If this water has been there during the primordial period, the atmosphere must have contained oxygen so that the basic assumption would be wrong.

Even if the atmosphere was reducing, one encounters a problem. There would have been no shield against UV radiation which according to [46] would have dissociated COOH whereas CH_4 and heavier hydrocarbons would have polymerized forming an oil slick 1-10 deep over the surface of the Earth. Ammonium would have photo-dissociated into nitrogen and hydrogen so that the conditions of the experiments of Miller [63] and others to be discussed below would not been satisfied.

2.4 Urey-Miller experiment

Urey-Miller experiment [63] meant a dramatic step of progress on the experimental side, and for a long time it was believed to be conform the vision of Oparin and Haldane. The experiment involved a reducing atmosphere and electric sparks simulating the effect of lightnings. In the later experiments 19 of 20 amino-acids were identified. Also nucleosides A, G were produced. Cyanoacetaldehyde together with urea believed to be accumulated to primordial ponds, allowed to generate U and C as was discovered by Miller 40 years after his classical experiment. These impressive results were interpreted as a support for the view about primordial ocean as a "dilute soup" of organic molecules which precipitated out of the atmosphere.

For a long time it was believed that the synthesis of ribose necessary for the generation of RNA was impossible in these circumstances. It turn out that ribose was generated from glyseraldehyde phosphate in presence of COOH [48]. Glyseraldehyde phosphate was generated also in Miller's

experiments. In case of deoxyribose necessary for DNA no plausible synthesis mechanism has been identified.

Organic compounds (in particular A, U, C, G) and even membrane forming products are present in carbonaceous chondrites (meteorites). Chondrites are essentially what the Earth is made of. Galactic gas clouds contain sugars, amino-acids, nucleic acids. In an experiment of Dworkin and his colleagues [47] thin ice at temperature of 10 K containing H₂O, ammonia, CO, CO₂ methanol was located in vacuum and bombarded by UV radiation to mimick the situation prevailing in the interstellar space. Contrary to expectations, hundreds of different complex organic molecules appearing also in meteorites were generated. Thus it seems that the molecules generated by pre-biotic evolution appear everywhere in cosmos but ironically, the environment provided by the surface of young Earth's does not seem to favor the pre-biotic evolution.

2.5 RNA world

One of the basic questions in theorizing about pre-biotic evolution is which came first: proteins, nucleic acids or both or possibly something else. The vision known as RNA world [52, 54] is dominating the stage at this moment. It is assumed that RNA polymers serve all the basic functions associated with DNA, RNA and amino-acids. These functions are based on genetic and catalytic capacity of RNA. Later a genetic takeover occurred involving the emergence of DNA and genetic code in which amino-acids replaced RNA somehow.

One can represent good experimental justifications for the RNA world vision (for the summary and for references the article of Chris King [58] is recommended warmly).

1. Ribose can be synthesized in the same circumstances as amino-acids and nucleosides. The presence of kaolinite clays and volcanic magmas stabilizes RNA polymerization. When montmorillonite, a positively charged clay believed to exist copiously in young Earth, was added to a solution of negatively charged amino-acids, a solution of RNA nucleotides gave rise to RNA 10-15 nucleotides long [49]. These chains attached to the surface of the clay, and when more nucleotides were fed by washing them with the solution, they grew up to 55 nucleotides long. It seems that reversible dehydration in a medium containing phosphates, bases and sugars provides the routes to polynucleotide formations. Besides water, Mg₊₊ plays a key role in stabilizing mono- and oligonucleotides by compensating the negative charges of the phosphates.
2. RNA can form double helices and has 3-dimensional tertiary structures analogous to that of proteins so that one might expect the ability to act as catalyst. The discovery of spontaneous splicing of RNAs in living systems is possible meant a breakthrough in this respect [106]. Second crucial finding was that these RNAs could act as catalysts in transesterifications crucial for the protein synthesis [54]. Even high fidelity complementary replication of arbitrary short RNA sequences has been demonstrated [56]. Simple biological RNAs have shown to have autocatalytic self-assembling capacity. The catalytic activity hinges on various forms of proton transfer (perhaps the leakage of protons between space-time sheets is involved). RNA appears to be the agent of peptide-bond synthesis in the modern ribosome [53] and modified ribozymes are able to act as amino-acyl esterases [66]. Thus RNA seems able to serve synthesizing, transfer, messenger and ribosomal functions so that it can guide both its own replication and ordered polymerization of proteins.
3. Support for the RNA world pictures comes also from the fact that the ancient fossil nucleotide coenzymes including ATP, NAD, coenzyme A and vitamin B12 are all ribonucleotides. Eucariote organisms continue to possess massive RNA processing within the nucleus. Reverse transcriptase, whose function contradicts the Central Dogma, and encountered in retroviruses (such as HIV), might have ancient origin. Reverse transcriptase is indeed crucial for

the transition from RNA→RNA predecessor of genetic code to DNA→amino-acid genetic code in TGD framework.

2.6 How biochemical pathways and DNA-amino-acid code emerged?

The traditional viewpoint is that biochemical pathways have developed from some simple basic systems. This approach encounters difficulties when one tries to understand how integrated systems such as electron transport and metabolic machinery could have worked in primitive systems. TGD based solution to the problem is the universality of metabolism and other basic functions relying on super-conductivity and its breakdown by the leakage of various supra currents between space-time sheets.

Furthermore, one can also decompose the evolution to two parts corresponding to the development of genetically controlled structures and self-organizing structures not controlled genetically [L2]. Chris King has formulated the same idea in a more concrete manner in his article [58] from the point of view of complex systems. According to King, the basic mechanisms developed without genetic control and were finally taken under control as the genetic takeover occurred. These kind of generic structures include proteins and nuclei acids, nucleotide coenzymes, bilayered membrane structures, ion transport and membrane excitability, membrane bound electron transport, glycolysis and the citric acide cycle. In TGD framework one can add to this list topologically quantized classical fields as universal structures.

A second open question is how DNA and amino-acids took the command. Here many-sheeted space-time provides a possible answer. DNA nucleotides are stable only inside regions containing ordered or liquid crystal water forming a macroscopic quantum phase. The transformation of DNA to RNA nucleotide requires water molecule which is not available in this kind of environment. The transition from RNA-RNA predecessor of genetic code to DNA-amino-acid genetic code is also a deep problem and here the trick might be very simple: reverse RNA transcriptase used by retro-viruses (also HIV) could have transformed RNA genes to DNA genes.

The model for the evolution of genetic code as a fusion of singlet and doublet codes in turn allows to understand the emergence of amino-acids as being due to a change in tRNA structure implying that amino-acids acting as catalyzers of the attachment of RNA to tRNA molecule began to stick to tRNA, and were loosened only when tRNA was attached to RNA so that the used amino-acids began to form amino-acid sequences replacing RNA sequences as coded sequences.

2.7 Problems with the polymerization in primordial ocean

Polymerization occurs universally by dehydration in case of polynucleotides, polypeptides, polysaccharides and lipids serving as basic building blocks of living structures. The basic difficulty is that polymers are not stable in an aqueous environment. Several cures to this problem have been proposed.

1. Various mineral interfaces could serve as templates for the formation of polymers and the evaporation of water from these structures could give rise to polymers. For instance, mud flats might have made possible polymerization.
2. Fox has proposed that the heat flow from geoactive sites like hot springs, volcanic rims and submarine vents could have caused the dehydration [51]. Fox has indeed managed to show how to generate protenoids consisting of up to several hundred amino-acids possessing weak catalytic activities. The temperatures needed are typically above 100 C and somewhat too high. Archea as well as nanno-bacteria are indeed found in this kind of environments, and they utilize heat and sulphur compounds as a source of metabolic energy. The first objection is that the high temperature destroys the biological molecules in this kind of environment.

Furthermore, the atmosphere around volcanoes contains CO_2 and water and only minor amounts of nitrogen, hydrogen sulfide and sulfur dioxide so that this kind of atmosphere does not give rise to the biomonomers in analogs of Urey-Miller experiments.

3. The un-stability of polymers against hydration is so serious a shortcoming for the primordial soup approach that it has inspired quite radical alternative proposals. For instance, Crick has concluded that pre-biotic life might have extraterrestrial origin. The panspermia hypothesis however only shifts the problem to the outer space. The evolution of life in intra-terrestrial environment is much less radical variant of this approach if one is ready to accept the notion of many-sheeted space-time.
4. Dr. Cairns-Smith has proposed that so called clay genes appeared as predecessors of genes [45]. For instance, Al atoms in the lattice containing Si and O can have three states at each site so that enormous information storage capacities become available. These structures would have acted as scaffolding for present day bio-molecules of RNA and DNA. This idea might create more problems than it solves. One could however turn the idea around and ask whether primitive life-forms such as nanno-bacteria could express their genetic code with the help of kaolinite clays.

To my personal opinion, an invention of a clever mechanism is probably not enough to solve the basic problem. Polymerization in modern cells is basically a process involving metabolic control, and it seems that the metabolic control must have been present from the beginning in some primitive form. TGD predicts that magnetosphere can perform quantum control in astrophysical length scales from the magnetic flux tubes of the Earth's magnetic field B_E or, rather, from the flux quanta of dark magnetic field accompanying it and having strength $B_E = 2B_E/5$. A further prediction is that metabolism is completely universal and existed in primitive form already during the primordial period. This in turn makes possible the option that the pre-biotic life need not have developed through stages differing dramatically from the recent life forms. One could even assume that a generalization of ontogeny recapitulates phylogeny principle holds true for the intracellular dynamics so that it would give precise information about pre-biotic evolution.

One must also clarify what one really means when one speaks of aqueous environment. Water allows an extremely rich variety of structures. Liquid crystal water/ordered water encountered inside cells might automatically stabilize polymers, and provide also a solution to how DNA and polymers were stabilized. Sol-gel transition giving rise to macroscopic quantum coherence would generate this liquid crystal phase.

2.8 The notion of protocell

The emergence of membrane bounded structures has certainly been decisive for the evolution of life. Cell membrane made possible differentiation forced by the competition for metabolic resources. Cell membrane imports metabolics, exports waste products, and acts as a signalling system. In TGD universe the receptors at cell membrane also serve as cellular sensory receptors.

A variety of answers to the question about the predecessor of the cell has been proposed. The natural constraint is that the membrane in question results via self-organization. If one requires consistency with the generalization of ontogeny recapitulates phylogeny principle (ORP), the number of options is reduced dramatically.

1. Lipid bi-layers are certainly a natural guess since they formed spontaneously in solutions on biological conditions. There is thus a consistency with the generalized ontogeny recapitulates phylogeny principle requiring that all primordial structures appear also in modern cells.
2. An elegant and plausible candidate for protocell is the gel phase resulting in sol-gel transition inside cell [67, 58]. Gel phase has indeed many properties of cell membrane bound region and

is routinely generated also inside modern cells. A compact ordered liquid crystal type phase is in question. Negatively charged proteins are generated inside the gel phase and gel phase rejects Na_+ ions and attracts K_+ ions just as cell interior. Also negatively charged proteins are stable inside gel phase. In TGD framework gel phase is a macroscopic quantum phase so that new physics is necessary involved. In particular, the evolution by quantum jumps is expected to lead to this kind of self-organized structures automatically. In TGD framework one expects that the liquid crystal/ordered water phase leads to the stabilization of RNA and that even DNA nucleotides become stable.

3. The proposal of Sidney Fox [51] is that protocells could correspond to the called microspheres formed from protenoids in geologically active sites like hot springs and volcanic rims. He also demonstrated that this really occurs. Protodoids are amino-acid sequences differing from ordinary peptides in that peptide bonds are different: hence this option is not consistent with the generalization of ORP. When proteneids are washed into a warm water allowed to cool, micro-spheres are formed. Micro-spheres are bilayered structures able to divide. A concentration roughly 10 million times higher than believed to appear in primordial soup is required so that either the idea of protenoid or of primordial soup is wrong. Further objections are that micro-spheres do not perform any functions of cell, and that the structure is like an impermeable cell wall or spore coat rather than a cell membrane [46, 55].

The common problem of all these options is that the required concentrations of biomonomers are much higher than those expected in the primordial soup. This forces to question the notion of primordial soup and even the assumption about the occurrence of the pre-biotic evolution at the surface of Earth.

3 TGD based scenario about pre-biotic evolution

TGD framework leads to a radical view about life. Magnetosphere can be seen as a living system controlling the evolution of life and chicken-egg question can be seen in a totally new perspective. Super-conducting magnetosphere can be seen as a higher level life-form which controls and guides the biological evolution from the very beginning. Second key element is dark matter hierarchy.

3.1 Basic prerequisites

A short summary of basic requirements and problems is in order.

1. A stable star and planet providing appropriate conditions such as temperature for liquid water is needed.
2. Atoms like C, N, and O and smaller amounts of P and S giving rise to bio-monomers, and metals like Al, Fe, and Zn are the basic building blocks. The formation of various chemical bonds like hydrogen bonds, covalent bonds, and peptide bonds is necessary.
3. The formation of biological monomers (amino acids, nucleotides, fatty acids, sugars) is an essential element of life. Except for DNA nucleotides, basic monomers evolve in the circumstances simulating to what have been believed to be the primordial atmosphere. These bio-monomers are found even in the interstellar space and in galactic clouds so that the question is not whether the pre-biotic life can develop but whether our recent day materialistic science allows to understand how it develops. The standard wisdom about primordial

atmosphere as a reducing environment (containing no oxygen) indeed leads to grave difficulties. Also the concentrations in the primordial ocean seem to be quite too low for the bio-monomers to be synthesized [55].

4. The formation of the biological polymers such as proteins, nucleic acids, lipids, and carbohydrates occurs universally by dehydration. The problem is that in water environment polymers are un-stable against decay by hydration: it would seem that a metabolic energy feed is required already at this stage to guarantee non-equilibrium situation. The assembly of these macro-molecules into organized aggregates like chromosomes, micro-tubules and cell organelles suggests the emergence of symbolic representations and only a weak independence of hard facts of chemistry which makes the problem even more difficult from the point of view of standard physics.
5. The emergence of catalysts and metabolism, should be understood. Here one encounters an egg-hen problem. Standardized metabolic currency seems to be necessary for effective catalysis but metabolism according to the standard view involves extremely complex web of reaction pathways needing refined catalytic actions.
6. Membrane bound structures are essential for life and one should understand how they emerge and even predict correctly basic facts about them.
7. The emergence of the genetic code has remained a mystery in various scenarios of pre-biotic evolution.
8. How the incredible ability of the components of bio-systems to co-operate pops up from primordial soup is not always included to the list of mysteries since everything smelling "holism" is regarded as pseudo science in reductionistic circles.

3.2 TGD based vision about pre-biotic evolution

The prevailing mechanistic world view forces to conclude that life emerged accidentally in young Earth during a relatively short time period of about .3 billion years. On basis of extensive computer simulations, one can fairly say that a spontaneous generation of life in primordial ocean seems extremely implausible [46].

TGD replaces materialistic view with a continual re-creation in which classical universe in 4-dimensional sense is replaced by a new one in each quantum jump. p-Adic length scale hypothesis allows to formulate the notion of evolution precisely as a generation of increasingly larger space-time sheets characterized by preferred p-adic primes meaning also a sequence of symmetry breakings. A second aspect is the emergence of new levels in dark matter hierarchy meaning great leaps in evolution. A crucially new element is the predicted fractal hierarchy of copies of electro-weak and color physics. Dark weak bosons and gluons thus become an essential part of the physics of living matter.

Macroscopic and even astrophysical quantum coherence becomes a key feature of living matter. Theory is partially non-deterministic also in classical sense but the variational principle for Kähler action implying that space-time surfaces are analogous to Bohr orbits and self-organization lead to Darwinian selection of selected patterns.

3.2.1 Is life really a result of accident?

Life is often regarded as an extremely improbable accident. The estimates for the probability of the formation of amino-acids, DNA, and of emergence of genetic code from random soup of molecules are indeed found to be extremely small. In TGD Universe the situation is different.

1. Intentional action is basic aspect of TGD Universe. Negentropy Maximization Principle [H2] states that the dynamics of quantum jumps maximizes the information content of the conscious experience and implies evolution as a continual recreation of the Universe eventually leading unavoidably to the emergence of information rich systems and explaining also why the values of "fundamental constants" seem to be tailored for the emergence of life as we are used to identify it. p-Adic dynamics for cognitive space-time sheets implies local randomness but long range fractal correlations for the real dynamics.
2. The hierarchy of Planck constants implies macroscopic and macro-temporal quantum coherence in all length scales. Universe becomes single conscious organism in this framework. This has many implications. For instance, low frequency photon can have arbitrarily high energy. This makes it possible control of short length and time scales by the dynamics in long scales, say by EEG. The enormous values of gravitational Planck constant for dark matter and the assumption that visible matter condenses around dark matter imply that planetary orbits correspond to Bohr orbits [D7, D8]. Only very few orbital radii are possible and for a star with mass around solar mass planets at distance of Earth are possible and probable irrespective of the mass of the planet. Hence solar systems are standardized to high degree. Also the quantization of masses of stars is highly suggestive and the number of stars with mass not far from solar mass is large. Obviously this raises the probability for having Earth like environments dramatically.
3. TGD based nuclear physics [F9] explains cold fusion[22, 23] as well as biological nuclear transmutations for which there is considerable empirical support [24]. The direct empirical evidence comes from the observation that the abundances of heavier elements in an astrophysical object at distance of order 10 billion light years are essentially the same as in solar system [25]. If elements are created only in the stellar interiors, the abundances should be much smaller. This suggests that the heavier elements result by cold fusion in the interstellar space. The implication is that environments allowing life have existed much earlier than believed hitherto.
4. The hierarchy of Planck constants and the notion of magnetic body allow a mechanism of topological quantum computation [L7] based on the representation of braids represented as flux tubes of wormhole magnetic field whose presence might provide a definition for what it is to be living. The first implication is an explanation for the miraculous ability of biomolecules to find each other in terms of the reduction of Planck constant inducing a shortening of the flux tubes connecting reactants and catalysts. The structure of flux tube patterns connecting various molecules allows to program complex series of biochemical reactions to the structure of braids connecting the molecules since given spots of molecules can be forced to meet each other in reaction. Conserved braid color allowing to identify whether the braid strand comes from A,T,C or G implies even stronger selection rules. One can assign also to amino-acid a 3-braid corresponding to one of the DNA codons coding for it. These extremely selective interactions between living bio-molecules give good hopes of understanding why DNA and amino-acids were selected as molecules able to co-operate.
5. Many-sheeted space-time concept implies the existence of fundamental metabolic energy currencies [J7] defined by the differences of zero point kinetic energies of particles for space-time sheets labeled by different value of p-adic prime p . The existence of standardized metabolic currencies simplifies the situation dramatically and living matter must face only the problem of storing metabolic energy. Plasmoid like life forms suggest themselves as predecessors of biological life. p-Adic length scale hypothesis $p \simeq 2^k$ is what implies standardization of zero point kinetic energies and follows from zero energy ontology which also assigns to a particle labeled by prime p a time scale $T_p = \sqrt{p}L_p/c = L_p(2)/c$ characterizing the temporal size

of the space-time sheet having particle and its negative energy counterpart at its time-like boundaries. The fact that the fundamental 10 Hz biorhythm corresponds to the time scale assignable to electron suggests that fundamental biological time scales are hidden in the space-time structure of fundamental particles.

3.2.2 The notions of magnetic body and plasmoid

The model of high T_c super-conductivity and the general vision about dark matter hierarchy have led to a rather precise model for magnetic body as an intentional agent utilizing biological body or its part as motor instrument and sensory receptor [M3]. Dark matter plasmoids and plasma oscillation patterns as representations of control commands are one important aspect of the model. The prediction is that plasmoids should have been predecessors of ordinary life forms. There is laboratory evidence that plasmoids behave like life forms [72]. Very high temperatures catastrophic for ordinary life forms could prevail at magnetic flux quanta associated with plasmoids. This forces a radical reconsideration of the question how pre-biotic life have evolved and forces to ask whether even the hot interior of Earth could have served or still serve as a seat of life.

3.2.3 Does the Earth's magnetic field have a dark counterpart?

The notion of dark matter as a hierarchy of phases characterized by arbitrarily large values of Planck constant has established itself as a part of TGD [A9, M3]. This raises several questions. For instance: does the magnetic body of Earth have a dark counterpart and its the dark magnetic body relevant for functioning of living matter?

A partial answer to this question came from a frustrating realization that I had for years erratically believed that the magnitude of the magnetic field assignable to the biological body is $B_E = .5$ Gauss, the nominal value of the Earth's magnetic field. Probably I had made the calculational error at very early stage when taking Ca^{++} cyclotron frequency as a standard. I am grateful for Bulgarian physicist Rossen Kolarov for pointing to me that the precise magnitude of the magnetic field implying the observed 15 Hz cyclotron frequency for Ca^{++} is .2 Gauss and thus slightly smaller than the minimum value .3 Gauss of B_E . This value must be assigned to the magnetic body carrying dark matter rather than to the flux quanta of the Earth's magnetic field. This field value corresponds roughly to the magnitude of B_E at distance $1.4R$, R the radius of Earth.

Dark matter hierarchy leads to a detailed quantitative view about quantum biology with several testable predictions [M3]. In principle all integer and even rational values of Planck constant are allowed. Number theoretical arguments suggest a general formula for the favored values of $r \equiv \hbar/\hbar_0$ [A9] as $r = n_1^{\pm 1} n_2^{\pm 1}$, where n_i characterizes the quantum phase $q = exp(i\pi/n_i)$ characterizing Jones inclusion [A8]. The values of n_i for which quantum phase is expressible in terms of squared roots are number theoretically preferred and correspond to integers n expressible as $n_i = 2^k \prod_n F_{s_n}$, where $F_s = 2^{2^s} + 1$ is Fermat prime and each of them can appear only once. $n = 2^{11}$ obviously satisfies this condition. The lowest Fermat primes are $F_0 = 3, F_1 = 5, F_2 = 17$. The prediction is that also r -multiples of p-adic length scales are possible as preferred length scales.

The applications to living matter suggests that one hierarchy corresponds to a hierarchy of Planck constants coming as $r = 2^{11k}$ for $p = 2^{127} - 1$, $k = 0, 1, 2, \dots$ [M3]. Each p-adic length scale would correspond to this kind of hierarchy. The unit of magnetic flux scales up as $h_0 \rightarrow h = rh_0$ in the transition increasing Planck constant: this is achieved by scalings $L(k) \rightarrow rL(k)$ and $B \rightarrow B/r$.

$B = .2$ Gauss would corresponds to a flux tube radius $L = \sqrt{5/2} \times L(169) \simeq 1.58L(169)$, which does not correspond to any p-adic length scale as such. $k = 168 = 2^3 \times 3 \times 7$ with $n = 5$ would predict the field strength correctly as $B_{end} = 2B_E/5$ and predict the radius of the flux tube to be $r = 18 \mu\text{m}$, size of a large neuron. However, $k = 169$ with flux $2h_5$ would be must more attractive option since it would give a direct connection with Earth's magnetic field. Furthermore, the model

for EEG forces to assume that also a field $B_{end}/2$ must be assumed and this gives the minimal flux h_5 . Note that $n = 5$ is the minimal value of n making possible universal topological quantum computation with Beraha number $B_n = 4\cos^2(\pi/n)$ equal to Golden Mean [E9].

Concerning the interpretation of B_{end} there are two options. It could correspond to a personal magnetic body or a to dark copy of the Earth's magnetic field. At this moment it is impossible to say which if any hypothesis is right. However the fact that the ELF fields have no direct effect on conscious experience mildly supports the identification as the dark variant of B_E .

3.2.4 Emergence of symbols at molecular level and new view about hydrogen bond, water, and bio-catalysts

The hierarchy of dark matter leads to novel ideas about what distinguishes living matter from ordinary matter. The emergence of symbols and symbolic dynamics and what might be called "molecular sex" could be a fundamental step in the process and I have considered two visions for how this would take place.

1. First vision

First vision is relies on the model of DNA as tqc based on braids and has quite close contact with empirical reality [L7, L5, J7]. In this case DNA nucleotides are analogous to colors of braid strands and base pairing corresponds to molecular sex for DNA molecules. The color of braid strand implies long ranged highly selective interactions between DNA and distant molecules, such as lipids of the lipid layer of cell membrane or amino-acids. Free amino-acids inherit the colors of the first two nucleotides in the codon XYZ whereas the color of the third nucleotide corresponds to a quantum superposition of colors for codons coding for the amino-acid: this defines the quantum counterpart of wobble base pairing. Amino-acids can be divided into amino-acids and their conjugates analogous to opposite sexes and generalized base pairing determines the interactions of the amino-acids to a high degree. Hydrogen bond can be identified as a special case of flux tube. There are also flux tubes connecting acceptors of hydrogen bonds acting as plugs in the connection lines formed by the magnetic flux tubes and Y corresponds to this kind of plug at the level of amino-acids.

2. Second vision

The mathematical realization for the hierarchy of Planck constants leads to a generalization of the notion of imbedding space and this leads to four kinds of phases resulting as combinations of phases with increased or reduced unit of spin and quantum numbers associated with CP_2 degrees of freedom. Each phase corresponds to its own Planck constant and is characterized by a discrete symmetry group.

Especially interesting are phases with large value of Planck constant involving charge fractionization and increase of spin unit. The electrons of free electron pairs of aromatic cycle are reasonable candidates for dark electrons of this kind. One can consider variants of hydrogen atom containing $n \leq N$ fractionally charged electrons with with lepton number and electronic charge equal to n/N . The values n/N and $(N - n)/N$ for the fractional charge would correspond "name" and "conjugate name" since their combination would give a maximal charge and a state analogous to a full electron shell. Thermal stability poses strong constraints since atomic and molecular energy scales are reduced as Planck constant increases.

The notion of fractional electron inspires the notion of "half" hydrogen bond for which electron has a fractionized fermion number. The full hydrogen bond would be formed in the fusion of half hydrogen bonds and give rise to a structure analogous to a full electron shell expected to be especially stable. Catalyst sites might correspond to half hydrogen bonds and the basic recognition mechanism could be the fusion of half bond and its conjugate to form a full hydrogen bond. One could speak about "molecular sex". The sequences of half bonds would represent words so that

molecules would have names. Also interpretation as quantum computer codes might make sense. The problem of this vision is the lack of direct contact with experimental facts and for this reason it will not be discussed in the sequel.

3.2.5 Universal metabolic currencies

In TGD framework a primitive many-sheeted metabolism is present from the beginning and becomes only refined during evolution. Most importantly, metabolic currencies identified as zero point kinetic energies liberated as particles drop to larger space-time sheets are constants of nature by the p-adic length scale hypothesis.

Phosphate-sugar polymers form the backbone of nucleic acids and metabolism is based on ADP and ATP formed from adenine and phosphate ions. It has been already earlier found that the generation of ATP and its metabolic utilization involve the flow of protons between the atomic space-time sheets and some larger space-time sheets, say magnetic flux tube of Earth [K6]). It will be found that this mechanism is involved also with the dehydration leading to polymerization and phosphorylation. The reversal of this process also implies the in-stability of DNA in an ordinary aqueous environment.

The interpretation of the role of phosphate ions as metabolic energy batteries seems to be wrong in TGD framework: the main function of negatively charge phosphates would be to make bio-polymers critical against local modifications making them thus ideal for catalytic manipulations. Even deeper function would be the role as standard plugs to which magnetic flux tube can attach and which second flux tube can begin. $ATP \rightarrow ADP$ would in this framework mean reconnection process for a magnetic flux tubes modifying the hardware of tqc.

3.2.6 Time mirror mechanism, intentional action, memory, and remote metabolism

Time mirror mechanism having negative energy MEs as space-time correlate has phase conjugate laser waves as standard physics counterparts. Essentially negative energy signals propagating to the geometric past and reflecting back is in question. Intentional action realized in terms of negative energy signals to the geometric past and appearing already at the level of molecular magnetic bodies, is expected to become an increasingly important when the complexity of the structures increases. The charge entanglement by negative energy W MEs is especially interesting control mechanism and makes also possible sharing of mental images. Time mirror mechanism allows also remote metabolism by inducing the dropping of population inverted system to the ground state liberating in this manner positive energy photons received by the sender of negative energy signal. What makes this mechanism so elegant is its enormous flexibility (credit card is the counterpart in economy). Time mirror mechanism provides also a mechanism of memory as communications with the geometric past.

3.2.7 Emergence of membrane bounded structures

Self-organization in many-sheeted space-time is expected to automatically lead to the generation of the ordered water phases which would have evolved to the gel phase defining in turn a natural predecessor of the membrane bounded structures. Self-organization would have also led to the emergence of membrane structures containing liquid crystal water stabilizing also DNA nucleotides.

In fact, the TGD inspired model for high T_c super-conductivity as quantum critical super-conductivity involving simultaneously two kinds of super-conductivities in a narrow range of temperatures around critical temperature (presumably $T \simeq 37$ °C) predicts correctly the double-layered structure of cell membrane and the length scales involved [J1, J2]. A fractal hierarchy of super-conductivities and cell membrane like structures is predicted corresponding to the dark

matter hierarchy and p-adic length scale hierarchy [M3]. Josephson junctions and corresponding Josephson currents are in a crucial role in the model for the hierarchy of generalized EEGs responsible for the communication to and control by magnetic body.

According to unexpected findings about behavior of the cell membrane [67] discussed from TGD viewpoint in [M2], the usual picture based on pumps and channels for ions is not correct. Rather, cell interior is in gel phase in which water is in structured phase around charged bio-polymers intermediate between ice and water. One implication of this is stabilization of RNA and DNA polymers since hydrolysis is impossible due to the lack of free water molecules. Cell membrane would have guaranteed the long term stability of gel phase.

Second function of the membrane like structure consisting of lipids or perhaps even DNA or RNA molecules could relate to the topological quantum computation and memory in the manner discussed in [L7]. The phase transitions changing the length of the wormhole magnetic flux tubes defining the braid strands and making possible tqc would also make possible biocatalysis via reconnection of flux tubes and via \hbar changing phase transitions changing the length of flux tube.

In this framework water and lipids molecules playing the role of lipids could have been present in very early stage since they emerge as a result of self-organization process and are not genetically determined.

3.2.8 Did life evolve in Mother Gaia's womb?

The proposed framework poses strong conditions on pre-biotic environment and one ends up to to interpretations for the notion of Mother Gaia's womb, which are by no means mutually exclusive.

1. *Mother Gaia's womb as underground seas?*

Braiding in the proposed sense requires the presence negatively charged polymers and membranes consisting of lipids or their analogs. Water seems to be necessary but also gel phase is needed since free water induces depolymerization. The coherent structure of gel would be due to the braiding of distant molecules. The phase transitions of gel phase are good candidates for a basic mechanism of bio-control and would stabilize these polymers via the formation of structured water around them preventing hydrolysis. The developing life forms should be shielded from UV radiation and meteor bombardment.

The combination of these constraints leads to the idea that life as we define it could have evolved in the womb of Mother Gaia in underground seas with the Earth's crust shielding from UV and meteors. The necessary ingredients of biomolecules, in particular phosphates making possible phosphorylation making DNA and RNA charged and appearing also in hydrophilic ends of phospholipids, would have dissolved to the water from the ground. Cambrian revolution would have meant the burst of these highly developed life-forms to the Earth surface and resulting as a phase transition increasing the value of Planck constant for Earth's space-time sheet by a factor of two would have occurred. This would also provide a justification of Expanding Earth theory explaining the strange finding that the continents fits nicely together to form a single super continent covering entire Earth's surface if the radius of Earth is one half of its recent value and actually the same as the recent radius of Mars, which is now known to contain reservoirs of underground water.

2. *Mother Gaia's womb as mantle-core boundary?*

What about the period before the life in underground seas?

1. The plasma like aspects of cytoplasm suggests that some kind of plasma phase must have been present. Also the postulated Bose-Einstein condensates of bosonic ions at dark magnetic flux quanta represent kind of quantum plasma.
2. Plasmoids involving magnetic flux tubes and charged particles could have been predecessors of more complex molecular life forms and could have developed in the interstellar space.

Their metabolism could have been based on universal metabolic energy quanta. Simple metabolic cycles and short term chemical storage of energy based on fusion and decay of simple molecules induced by say UV radiation from the nearby stars might have developed during this era. Quite high temperatures can be considered so that after the interstellar period this kind of life forms could have survived and developed in the hot interior of planets receiving their metabolic energy from radiation by high temperature plasma. A possible candidate for the womb of Mother Gaia is the mantle-core boundary, where intensive self-organization processes are expected to take place.

3. Ultimately the charged molecules must have come in contact with ordinary water in underground seas. One can imagine that the polymerization of the charged molecules and the formation of structured water around them stabilizing them and giving rise to a gel phase took place simultaneously in presence of metabolic energy feed.

The primordial womb containing plasmoid like life forms could have been located somewhere below the boundary at which $k = 137$ atomic space-time sheets transform to very hot $k = 131$ space-time sheets: this should occur when the thermal de Broglie wave length becomes equal to the p-adic length scale $L(131)$. The transition occurs above the crust-mantle boundary (1300 K). Mantle-core boundary (4000 K) is a good candidate for a seat of high- T life forms.

The dropping of O, C, N ions from the hot $k = 131$ space-time sheets to larger space-time sheets generates light at visible frequencies replacing solar light so that even intra-terrestrial counterpart of photosynthesis could develop. The dropping of oxygen atoms could make also possible development of oxygen based metabolism.

Magnetic flux quantum structure of the magnetosphere acting as a nervous system and a metabolic circuitry of the magnetic Mother Gaia could make possible controlled metabolism already during the pre-biotic period and allow to circumvent these difficulties.

3.2.9 Model for the genetic code

The emergence of genetic code is one of the basic mysteries of models for pre-biotic life. The exact A-G symmetry and slightly broken T-C symmetry of the genetic code strongly suggest that the evolution of the triplet code occurred as a fusion of singlet and doublet codes. One ends up with a detailed model for how this happened by studying the structure of tRNA molecule carrying in its fossilized parts detailed information about the evolution of the code.

Nanno-bacteria [50, 57] might correspond to some predecessor of the recent genetic code. Nanno-bacteria accompany mineral structures and actively manipulate them: this conforms with the view that mineral interfaces have been indeed important for the evolution of polymers.

Introns are the basic mystery of DNA. TGD predicts that language is a universal phenomenon appearing at level of eukaryotes. Memes represented as sequences of 21 DNA triplets and expressing themselves as field patterns associated with MEs would realized this universal language.

3.2.10 What makes possible the coherence of bio-chemical activities?

In TGD Universe the control of genome by magnetic body relies on magnetic flux sheets traversing through DNA strands [M3, L2]. The model implies a generalization of the notion of gene. Super-genes correspond to sequences of genes inside single organism belonging to single magnetic flux sheet and organize like text lines at a page of a book. The expression of super-genes as an intentional action of magnetic body occurs therefore coherently at the level of entire organs. This explains to the miraculous coherence of bio-chemical activities at the level of single organism. Also hyper-genes involving genomes of several organisms, not necessary belonging to even same species, become possible. Collective gene expression at this level makes possible the development of co-operation and social structures and are predicted to be present already at the bacterial level.

Braiding defined by magnetic flux tubes of their wormhole counterparts carrying dark variants of charged particles seem to represent especially important part of the magnetic body and this leads to models of topological quantum computation and bio-catalysis.

3.3 Pre-biotic chemistry and new physics

The emergence of symbolic representations at dark matter level is certainly the most fascinating possibility suggested by dark matter hierarchy.

3.3.1 Overall view

The most important implications can be deduced readily.

1. The dropping of ions and atoms between space-time sheets involves a liberation of zero point kinetic energy. By p-adic length scale hypothesis these energies define a fractal hierarchy of universal metabolic currencies which have not changed at all during evolution and are the same in the entire universe. The presence of the metabolic machinery from the beginning helps enormously in the attempts to understand how life has evolved.
2. Chiral selection resulting in bio-polymers having a definite handedness is a deep mystery in standard physics framework. TGD predicts entire hierarchy of standard model physics meaning scaled up variants of electro-weak and color physics and dark variants of these. The hierarchy of dark weak gauge bosons predicted by TGD imply strong parity breaking effects in arbitrarily long length scales above atomic length scales, and the presence of the chiral selection supports the view that also dark weak bosons play key role in bio-control. Indeed, charge entanglement generated by W MEs would be in central position in TGD based model for how magnetic bodies control biological bodies.
3. The emergence of life means emergence of symbolic representations (including names), and also what might be called "molecular sex". Formation of wormhole magnetic flux tubes between biomolecules having quark pair and its conjugate is an attractive candidate for this process and means coding of DNA nucleotides to quarks and antiquarks appearing as dark matter at the flux tubes. This leads to a new view about bio-catalysis based on the temporary dropping of the liberated proton to a larger space-time sheets and ensuing liberation of metabolic energy quantum kicking the complex formed by reactants over the potential wall separating it from the final state. A new view about water and its role in bio-catalysis emerges. Stability considerations allow a general model for how first bio-polymers able to replicate emerged.

3.3.2 Dark matter and the emergence of symbolic representations at molecular level

The most important new physics element of pre-biotic chemistry has been already discussed and corresponds to the presence of dark matter hierarchy suggesting new views about hydrogen bond, water, and catalytic action. A highly attractive hypothesis is that symbolic representations at molecular level in the sense that quarks and antiquarks code for DNA nucleotides [L7] and also for amino-acids [L5, L8].

3.3.3 Evolution of pre-biotic chemistry as a sequence of bifurcations

In his article "Biocosmology" [58] Chris King discusses biochemistry from the point of view of mathematician using the notions of symmetry breaking and bifurcation. This discussion allows for a physicists to get a wider perspective to the complexities of biochemistry. In the following I

modify the arguments of King to TGD framework. The first basic new element is that generation of new space-time sheets corresponds to a sequence of symmetry breakings.

Besides hydrogen C, N, and O atoms with charges 6, 7, and 8 are the most important elements appearing in basic bio-monomers. The bonds with hydrogen are formed between $1s$ and $2p^3$ orbitals. The covalent bonds between C, N, and O atoms are the bonds appearing in various bio-monomers like ribose. Also peptide bonds between C and N in amino-acid sequence are covalent bonds. In standard chemistry one can characterize the atom in given molecule by its electronegativity telling how effectively it attracts electrons.

Electronegativity increases in the sequence C, N, O so that the bonds are more and more polar. Also Si, P, and S in the next row of the periodic table form covalent bonds but the bond energy tends to be lower which reflects itself as lower boiling points. For instance, the boiling point of H_2S is below the freezing point of water). Consider now the bifurcations.

1. Polar-non-polar bifurcation is fundamental in biology. Non-polar molecules are hydrophobic and are not water-soluble whereas polar molecules are hydrophilic and water-soluble. For instance, the formation of biological membranes is based on hydrophobic character of the second ends of lipids. A rough characterization of amino-acids is by polar-non-polar dichotomy. Also DNA base stacking is based on polarity.
2. Second bifurcation corresponds to acid-base dichotomy. Acids are able to act as donors of positive and bases donors of negative charge. For instance, this allows to classify polar amino-acids to acidic and basic ones. A working hypothesis worth of studying is that many-sheeted physics is involved in the sense that the protons in acid and electrons in base have dropped to some larger space-time sheet from the atomic space-time sheet.
3. The third bifurcation corresponds to that between second and third row of the periodic table that is Na^+-K^+ and $Mg^{++}-Ca^{++}$ bifurcations. The covalent bonds involving K and Ca are in general weaker. Na^+ concentration is higher outside cell whereas K^+ concentration is higher inside cell. Same applies to gel phase, a possible predecessor of cell membrane bound regions. Mg^{++} acts as stabilizer of polymers and Ca^{++} ions are key players in cellular and intracellular control. In particular, Ca^{++} waves appear in extremely wide range of frequencies and conduction velocities.
4. The fourth bifurcation corresponds to the d-orbital elements forming a catalytic group. Almost all transition elements Mn, Fe, Co, Cu, Zn are essential biological trace elements, promote pre-biotic synthesis and are optimal in their catalytic ligand-forming capacity and valency transitions. For instance, Zn^{2+} catalyzes RNA polymerization in pre-biotic synthesis and occurs in both polymerases and DNA binding proteins.
5. The fifth bifurcation corresponds to chiral symmetry breaking not easy to understand in standard model predicting extremely small parity breaking. There is empirical evidence such as circular polarization of light from the region of star formation in the constellation of Orion suggests that parity breaking occurs also in interstellar space. Also the amino-acids in Murchison meteorite were found to be dominantly left handed.

In TGD Universe the interpretation of bifurcations is not quite the same as in the world obeying standard chemistry.

1. The polar-non-polar bifurcation corresponds to hydrophilic-hydrophobic dichotomy. The model for protein folding and bio-catalysis relies on the hypothesis that wormhole flux tubes connect conjugate amino-acids. This process is analogous to base pairing. Stating it roughly, amino-acid and its conjugate correspond hydrophilic and hydrophobic amino-acid. This bifurcation is thus important from the point of view of molecular symbolism and bio-catalysis

if is based on the coding of DNA are nucleotides and amino-acids by quarks and antiquarks at the ends of wormhole magnetic flux tubes connecting them to other molecules. The emergence of wormhole magnetic flux tubes could be seen almost as a definition of emergence of life. This might have happened already during prebiotic molecular evolution if water molecules have been present from the beginning.

2. Acid-non-acid bifurcation brings in protons and there is obviously a connection with the role of protons in the basic mechanisms of metabolism and catalysis. What is also essential is the role of negative charge of bio-polymers making bio-polymers critical against local deformations so that a wide repertoire of catalytic actions using \hbar changing phase transitions of wormhole magnetic flux tubes and their reconnections becomes possible. Phosphate ions would not serve as batteries of metabolic energy but make bio-polymers sensitive to catalytic actions.
3. Fifth bifurcation is difficult to understand in standard physics framework but is consistent with the presence long ranged weak fields predicted by TGD and possibly associated with dark matter. This bifurcation is not the last one in TGD Universe since already plasmoids identified as rotating magnetic systems break parity because the sign of the charge density generated by the induced radial ohmic current depends on the orientation of rotation and only the second orientation is favored energetically. W MEs induce charge entanglement giving rise to plasma oscillation patterns in turn inducing various physiological waves. This mechanism can be used as a control tool by magnetic bodies at various levels of hierarchy. Long range weak forces due to the exotic ionization of atomic nuclei could provide a tool for controlling conformations of nucleic acid polymers. Same applies to kaolinite clays consisting of Al, Si, O suggested to be of biological importance (Al can have three different states at a given lattice site): in this case the state of Al atoms in the lattice might be manipulated using weak forces.
4. The hierarchy of bifurcations defines also a hierarchy of decreasing cyclotron frequencies. The cyclotron frequencies would be associated with both with Bose-Einstein condensates of ordinary and exotic bosonic ions at magnetic flux sheets. For the bosonic ions cyclotron frequencies in the $B_{end} = 2B_E/5$ are in alpha band and in TGD Universe they play a fundamental role in communications to and control by magnetic body using hierarchy of generalized EEGs. Ca^{++} and other waves associated with bosonic ions are of special importance in the bio-control by magneticbody using plasmoids and plasma oscillation patterns.

3.3.4 What selected the bio-molecules?

The extremely low probabilities for the selection of bio-molecules from a super-astrophysical number of alternatives represents one of the bottleneck problems of biology relying on the prevailing view about biochemistry. The notion of braid could resolve this problem.

Suppose that the presence of braids distinguishes between living and dead matter, that the four nucleotides are mapped to colored braid strands (that is to 2 quarks + 2 anti-quarks), and that a given amino-acid is mapped in a non-deterministic manner to one of the 3-braids associated with the DNA triplets coding for it. Braids could be associated besides DNA, amino-acids, and lipids also to other bio-molecules and define more general analogs of genetic codes as correspondences between bio-molecules able to react.

The implication would be that the step of catalytic reactions bringing together the catalyst and reactants would occur by a temporary reduction of Planck constant only for subsets of bio-molecules connected by braid strands and the pattern of braid strands involved would define the geometro-dynamical pattern of the reaction. The outcome would be a selection of very restricted subsets of bio-molecules able to form reaction networks and of reaction pathways. This would

imply Darwinian selection of subsets of bio-molecules able to co-exist and dramatically enhance the probability for the emergence of life as we know it.

One challenge is to predict what kind of braids can begin from a given bio-molecule, say nucleotide or amino-acid. The physicist's guess would be that the (electromagnetic only?) interaction energy between bio-molecule and given pattern of wormhole contacts having quark and anti-quark at its throats should select the preferred braids as minima of the interaction energy. How closely the presence of hydrogen bond relates to this is also an interesting question.

3.3.5 Polymerization, dehydration, phosphorylation, and new physics

The generation of phosphate polymers and polymers in general occurs by dehydration which quite generally seems to involve dropping of a proton to larger space-time sheet and liberation of metabolic energy quantum. It is interesting to find how one could understand these processes in TGD framework. Since the notion of wormhole magnetic flux tube playing a central role in the model of DNA as topological quantum computer and in the model of bio-catalysis, it is natural to look whether the basic steps of these processes could be understood in this conceptual framework.

1. $ATP \rightarrow ADP$ process

AMP, ADP, ATP are phosphorylated RNA nucleosides [115] and the hydrolysis of ATP to ADP [116] plays a key role in the metabolism. Obviously also the molecules XMP, X=U,C,G are important biologically. Each PO_3 in ATP corresponds to one unit of negative charge except for the last one which carries two units of negative charge. According to the standard chemistry $ATP \leftrightarrow ADP$ corresponds to the hydrolysis



where P_i denotes orthophosphate HPO_4^{-2} . In ADP the last phosphate group is $HO - PO_2^{-2}$ rather than $O = PO_2^{-2}$ as in the case of ATP.

The actual process is however much more complex than this.

1. The process involves several steps such that energy is liberated in two steps in which the change of Gibbs free energy is $\Delta G = .42$ eV and $\Delta G = .31$ eV making altogether $.73$ eV, which should closely relate to the liberated metabolic energy.
2. Three protons are accelerated in electric field during the generation of ATP. The interpretation would be in terms of driving of electrons from larger space-time sheet to $k = 137$ atomic space-time sheet. If the larger space-time sheet corresponds to $k = 139$, the increment of the zero point kinetic energy of proton is $(1 - 1/4) \times E_0(137) = .375$ eV for $E_0(137) = .5$ eV of metabolic energy quantum. Three protons would give net zero point kinetic energy increment of 1.125 eV which is higher than $\Delta G_{tot} = .73$ eV. The explanation of the discrepancy should relate to Coulombic binding energy of protons with ATP and F_1 . This interpretation conforms with the observation that the liberated energy is higher for the third proton.

Consider now a more detailed model for the process. The binding of ATP to the catalytic site involves several steps.

Step 1: The binding $ATP + F_1 \rightarrow ATP \cdot F_1$ to the catalyst site is a complex process involving the break-up of the hydrogen bonds between cellular water and ATP molecule and cell water and catalyst site and generation of hydrogen bonds between catalyst site and ATP molecule. In TGD framework this means that protons can be kicked to and dropped back from atomic space-time sheets. Only the net number of protons dropped however matters.

This process involves liberation of Gibbs free energy about $\Delta G_{ATP} = .42$ eV. It was earlier believed that this energy is liberated instantaneously but the findings about the behavior of the

F_1 motor coupled to dissipative load, lead Oster and Wang to suggest that the process is more complex and starts from a loose binding and ending up to a strong binding [77].

Step 2 Hydrolysis: $F_1 \cdot ATP \rightarrow F_1 \cdot ADP \cdot P_i$. The change of free energy is small during this step: $\Delta G \sim 0$.

Step 3: Orthophosphate is released from the catalyst site: $F_1 \cdot ADP \cdot P_i \rightarrow F_1 \cdot ADP + P_i$. Free energy $\Delta G \sim .31$ eV is liberated at this step.

Step 4: ADP is released from the catalyst site: $F_1 \cdot ADP + P_i \rightarrow F_1 + ADP + P_i$. $\Delta G \sim 0$ holds true also for this process.

This picture suggests that the notion of the high energy phosphate bond is not quite correct as suggested also by some empirical findings [78, 79, 80]. The metabolic energy would be stored as the zero point kinetic energy of protons rather than in phosphate bonds. Perhaps the fundamental function of phosphates would be to make DNA and RNA polymers charged in turn making possible the formation of wormhole magnetic flux tubes and braiding making possible a wide repertoire of catalytic actions.

2. Model of $ATP \rightarrow ADP$ based on wormhole magnetic flux tubes

Consider first the basic philosophy behind model.

1. In the model of DNA as topological quantum computer *XMPs*, $X = A, T, C, G$ can be connected to oxygen atoms by wormhole magnetic flux tubes having quark and antiquark at opposite throats of wormhole contact and charge conjugated quark-anti-quark pairs at the ends of the flux tubes. Dark u quark and its charge conjugate code for A, T and d quark and its conjugate for G, C so that the conjugation for nucleotides corresponds to charge conjugation for quarks and $A - G$ and $T - C$ symmetries of the third nucleotide of the codon to isospin symmetry.
2. Basic bio-catalytic processes are identified as a reconnection of the wormhole magnetic flux tubes and change of the length of the flux tube induced by the change of the value of Planck constant associated with it. It would not be too surprising if this kind of mechanism were involved also in $ATP \rightarrow ADP + P_i$. The reason for the special role of ATP among XTP might be that the positive charge $q(u) = 2/3$ of u -quark maximizes the attractive interaction between u quark and phosphate.
3. Flux tubes connect to oxygen atoms in the proposed model of bio-catalysis and protein folding [L8]. The model relies on ideas inspired by the model of DNA as topological quantum computer [L7]. In this model hydrogen bonds are assumed to correspond or to be accompanied by (wormhole) magnetic flux tubes. Also flux tubes connecting acceptor atoms or molecules of hydrogen bonds are assumed to be connected long flux tubes and represent genuinely new physics. Examples of acceptors are $O =$ atoms in phosphates and amino-acids and aromatic rings in DNA and also in some amino-acids. The model for protein folding has tight connections with existing chemistry and leads to a very simple and successful criterion for the formation of hydrogen bond between $N - H$ and $O =$ in the constant part of amino-acid and to a successful proposal for the folding code.
4. DNA as tqc model gives further constraints. The structure of the phospholipids suggest that in the case DNA nucleotides long flux tubes connect the aromatic ring of the nucleotide to the $O =$ atom at the hydrophilic end of the lipid acting as a standard plug which in turn can be connected to another acceptor and eventually terminates to a donor of hydrogen bond. The detailed charge structure of the aromatic ring(s) should determine the quark-nucleotide correspondence. The connection line to the lipid could involve several intermediate $O =$ plugs and the first plug in the series would be the $O =$ atom of the monophosphate of the nucleotide. Not surprisingly, phosphorylation would be absolutely essential for the operation of DNA as

topological quantum computer. $O = -O =$ flux tubes could also act as switches inducing a shortcut of the flux tube connection by reconnecting with a hydrogen bond connecting two water molecules. This is an essential step in the model for how DNA acts as topological quantum computer.

A possible model (perhaps the simplest one found hitherto) for the reaction $ATP \rightarrow ADP + P_i$ is based on the assumption that it splits a flux tube connection defining strand of a braid defining topological quantum computation. A change of the hardware of topological quantum computer would be therefore in question.

1. Suppose that ATP defines a standard plug in flux tube connections. This would mean that aromatic ring and the oxygen atoms $O =_1$, $O =_2$, and $O =_3$ of the phosphates are connected by magnetic flux tubes to a string and $O =_3$ in turn is connected to some (hydrogen bond) acceptor elsewhere, say $O =$ or aromatic ring. These flux tubes represent genuinely new physics in accordance with the fact that "high energy phosphate bonds" are not really understood in the standard chemistry.
2. The reconnection of $(O =_2) - (O =_3)$ flux tube with the hydrogen bond connecting two water molecules leads to the splitting of the flux tube so that the incoming and outgoing the flux tubes are shortcut by $(O =_2) - -H - (OH)$ resp. $(O =_3) - -H - (OH)$ hydrogen bonds (connection to ground is the analog in circuit theory). This corresponds in the usual terminology the liberation of the third phosphate: $ATP \rightarrow ADP + P_i$. P_i however remains at the end of flux tube to be attached later to another ADP.
3. The process involves also hydration. $(OH)^-$ ion joins to the third P to give P_i^{-3} and H^+ to $O - P$ in second P to give $H^+ - O$ in ADP^{-1} . The exchange of electron would lead to the final state $ADP^{-2} + P_i^{-2}$.

A possible model for the dropping of protons would be following.

1. It is absolutely essential to realize that F_1 is an open system and that naive thermodynamic considerations can lead to misunderstandings. In particular, the notion of high energy phosphate bond does not make sense. The source of the metabolic energy is the chemical energy used to drive protons to the atomic space-time sheets of F_1 . The function of the large negative charge of ATP is to increase the rate for the binding of ATP^{-4} to F_1 . In the classical picture the binding to F_1 is followed by the dropping of two protons to larger space-time sheet. The value of the metabolic quantum could be reduced from .5 eV to about .21 eV by the Coulombic interaction energy of proton with PO^{4-} . The Coulombic binding energy of the remaining protons at F_1 with $ADP + P_i$ is smaller and the dropped proton liberates larger energy about .31 eV. In quantum picture the division of the process to this kind of sequence might not be a good approximation.
2. One function of the $ATP \rightarrow ADP$ would be to induce the dropping of the third proton from F_1 space-time sheet. Second function would relate to the topological quantum computation like process since the decay would correspond to a splitting of a braid strand coming to the aromatic ring of A and proceeding along string defined by the ring and three $O =$ s of phosphates and continuing further. This would make possible tqc as a braiding for both halves of the split flux tubes. After the reconnection the total braid structure would be different. Quite generally, reconnection process would make possible to modify the hardware of topological quantum computer.
3. The reason for why P_i leaves the catalyst site and proton is dropped (step 2) should be the in-stabilization of the bound state of positively charged proton with $ADP^{-2} + P_i^{-2}$ which

does not have so strong Coulomb interaction energy with proton as ATP^{-4} . As a consequence, proton can drop to the larger space-time sheet.

4. What remains open are the details of the transformation of the chemical energy to zero point kinetic energy of protons. Remote metabolism suggests that protons send negative energy phase conjugate photons to the geometric past inducing a transition of an energy carrying molecule to a lower energy state (zero energy ontology gives justification for this picture). This would mean the failure of the standard description in terms of reaction kinetics. The catabolism of nutrients is the eventual provider of the metabolic energy and the coenzyme nicotinamid adenic dinucleotide NAD^+ [117] receives electron and the energy liberated in the catabolic reaction. In the proposed framework it is not an surprising that NAD^+ is analogous to RNA dinucleotide (perhaps as remnant from RNA era when dinucleotides defined the 2-codon code) and consists of two phosphates and adenine and nicotinamide nucleosides. The oxidation reaction $NADH \rightarrow NAD^+$ in turn liberates this energy. Protons could gain their energy by sending negative energy photons to $NADH$. Negative energy photons would propagate along "topological light rays" parallel to the flux tubes connecting the system in a precisely targeted manner to $NADH$ aromatic rings. Alfvén waves propagating along magnetic field lines would be the standard electrodynamics counterpart for these topological light rays.

Many details of the process remain open but it would seem that the key ideas of TGD based quantum vision about living matter are fused together in rather detailed manner in this picture.

3. Polymerization of DNA and RNA

The polymerization of RNA and DNA by dehydration involves the fusion of $PO_4H_2^-$ phosphate molecule with ribose. In this process the stub $\dots-O-H$ of the phosphate ion combines with $H-O-C-\dots$ stub of ribose (here C is the carbon atom not belonging to the ribose cycle). This gives rise to $\dots-O-(H-O)^-C-\dots$ plus proton dropping to a larger space-time sheet and liberating metabolic energy quantum. Too large negative charge of three units makes the complex unstable and $(H-O)^-$ ion splits out. Metabolic energy quantum might be also used in the process.

A possible interpretation is in terms of recombination process in which the flux tubes connecting both phosphate ion and $H-O-C$ stub of ribose with water molecule are reconnected to flux tubes connecting phosphate ion and ribose and second water molecule and resulting OH^- by flux tube which then contracts in \hbar changing phase transition and splits OH^- out..

Hydration destabilizes long polymers unless there is a continual feed of protons to the atomic space-time sheets. This could be achieved by irradiation with photons with energy equal to the metabolic energy currency. Situation changes also if water is ordered/structured water, in liquid crystal form, or as ice, and therefore unable to provide the water molecules needed for the hydration. Stabilization of RNA and DNA polymers could be achieved in this manner in gel phase.

Clay structures are known to act as catalyzers of RNA polymerization. The general model of catalysis based on the recombination and \hbar changing transition for magnetic flux tubes should explain also this.

3.3.6 Why DNA is stable inside cell nucleus?

Inside membrane bound surface both DNA and RNA nucleotides and polymers are stable. The un-stability of the DNA nucleotides and polymers outside membrane bound surfaces could involve many-sheeted physics.

1. What one expects that DNA transforms to RNA unless it is inside a membrane bound region. A possible reason is that water molecule is needed to transform DNA to RNA but not available inside membrane bound structure where water is structure water in gel phase.

2. In the case of A, G, and C nucleotides DNA \rightarrow RNA transformation means simply an addition of one oxygen atom to the de-oxyribose ring, that is replacement of one C-H with C-O-H. If ordinary water is present this could be achieved by the dissociation of the water molecule to $\text{OH}^- + \text{H}^+$ followed by the replacement of C-H in the de-oxyribose cycle with C-OH $^-$ so that a negatively charged ribose results. The outcome is free hydrogen atom. If H^+ drops to a larger space-time sheet, the liberated zero point kinetic energy is of order .5 eV. This process is basically the same which should occur when single ATP molecule is utilized in metabolism.
3. In the case of T nucleotide also CH_3 group differentiating T from U must be de-attached. This is achieved if the hydrogen atom from the water molecule is taken by the de-attached CH_3 group to give CH_4 molecule. As a result a negatively charged U results. Inside cell nucleus or in gel phase this process is not favored because the water is in liquid crystal form and it costs energy to take the needed H_2O molecule from it.

3.4 DNA as a topological quantum computer

For years ago I developed a model of topological quantum computation combining TGD based view about space-time with basic ideas about topological quantum computation and ended up with the proposal that DNA might act as a topological quantum computer. One can imagine several manners in which DNA or RNA could act as a topological quantum computer and it good to try to state clearly what one wants.

1. Natural requirements are that the topological quantum computer programs can be naturally combined to larger programs and evolution means this kind of process; that the programs have a natural modular structure inherited from the previous stages of evolution; and that the computation is not restricted inside single nucleus.
2. DNA and/or RNA defines the hardware of topological computation and at least for more advanced topological quantum computers this hardware should be static so that only programs would be dynamical. This leaves only DNA in consideration and the entangled initial and quantum states at the ends of braids quantum states would be assignable to static DNA structures.
3. The program would be determined by different braidings connecting the states of DNA in time direction or in spatial direction. Since the genomes are identical in different nuclei, the strands could connect different nuclei or conjugate strands of double DNA strand. Reconnection process would allow to modify the hardware for tqc.

3.4.1 The recent progress in quantum TGD and TGD inspired quantum biology

After the advent of the first model for topological quantum computation in TGD Universe [E9], the mathematical and physical understanding of TGD has developed dramatically and the earlier quite speculative picture can be replaced with a framework which leads to a rather unique view about topological quantum computations by DNA.

1. Universe as a topological quantum computer

One can say that the recent formulation of quantum TGD states that the entire Universe behaves like a topological quantum computer. This notion of topological quantum computer differs however from the standard one in many respects.

1. The emergence of hierarchy of Planck constants realized as a generalization of the notion of imbedding space is now a basic piece of TGD allowing an elegant formulation of quantum TGD [A8, A9]. The phases of matter with large Planck constant are interpreted as dark matter. Large values of Planck constant make possible topological quantum computations in arbitrary long time scales so that the most fundamental objection against quantum computation can be circumvented.
2. Zero energy ontology forces to unify S-matrix and density matrix to M-matrix - the product of the square root of density matrix and S-matrix- defined as time-like (or rather light-like) entanglement coefficients between positive and negative energy parts of zero energy state [C2, C3]. Connes tensor product emerging naturally from the notion of finite measurement resolution described in terms of inclusions of hyperfinite factors of type II_1 defines highly uniquely the M-matrix. M-matrix would be natural candidate for defining topological quantum computation in light-like direction. Connes tensor product makes sense also in space-like direction and would define quantum storage of functions represented as entanglement coefficients.
3. The notion of number theoretic braid [B4, C2] is now well-understood and has become a basic element of the formulation of quantum TGD based on the requirement of number theoretical universality. As a matter fact, the notion of braid is generalized in the sense that braid strands can fuse and decay. The physical interpretation is as motion of minima of the generalization eigenvalue of the modified Dirac operator which is function of transversal coordinates of light-like partonic 3-surface and has interpretation as vacuum expectation of Higgs field. Fusion of braid strands corresponds to fusion of minima.

For generalized Feynman diagrams partonic light-like 3-surfaces meet at 2-dimensional vertices defined by partonic 2-surfaces [C3]. This implies that braids replicate at vertices: the interpretation is as a copying of classical information. Quantum information is not copied faithfully. The exchange of partonic 2-surfaces in turn corresponds to quantum communications. Hence quantum communication and quantum copying emerge naturally as additional elements. Space-like Connes tensor product in turn defines quantum memory storage.

4. Computation time is a fundamental restriction in both ordinary and quantum computation. Zero energy ontology makes possible communications in both directions of geometric time, which suggests the possibility of geometric time loops in topological quantum computations. Could this mean that computation time ceases to be a restriction and ordinary computations lasting for infinite amount of geometric time could be performed in a finite time interval of observer's time? This is perhaps too much to hope. The subjective time taken by the computation would be infinite if each step in the iteration corresponds to single quantum jump. If this is the case and if each quantum jump of observer corresponds to a finite increment of geometric time perceived by the observer, time loops would not allow miracles.

2. The notion of magnetic body and the generalization of the notion of genome

The evolution of ideas related to quantum biology provides also new valuable insights. In particular, the notion of magnetic body leads to a model of living system in which dark matter at magnetic flux quanta of the field body of biological system uses biological body as a motor instrument and sensory receptor [M3]. Quantum control would be naturally via the genome and sensory input would be from cell membrane containing all kinds of receptors. This would suggest that magnetic flux sheets traverse through DNA strands and cell membranes.

The quantization of magnetic flux with unit defined by Planck constant having arbitrarily large values leads naturally to the notions of super-genome and hyper-genome [L2]. Super-genome would consist of DNA strands of separate nuclei belonging to single magnetic flux sheet and these

sequences of genomes would be like lines of text at the page of book. Super-genomes in turn can combine to form text lines at the pages of a bigger book, I have used the term hyper-genome. This hierarchy of genomes would give rise to a collective gene expression at the level of organs, individuals of a species, and at the collective level consisting of populations containing several species. Even biosphere could express itself coherently via all the genomes of the bio-sphere. The model of topological quantum computation performed by DNA should be consistent with this general picture.

3.4.2 Model for DNA based topological quantum computation

The most promising model of DNA as topological quantum computer relies on the hierarchy of genomes. The flux sheets or collections of parallel flux tubes assignable to a magnetic body would traverse the DNA strands of several nuclei so that strands would be analogous to lines of text on the page of a book.

DNA strands would define the intersections of magnetic or number theoretic braids with plane and braiding would be associated with with the magnetic field lines or flux tubes transversal to DNA. The M-matrix defining topological quantum computation would act on quantum states assignable to nucleotides.

1. *The interpretation of nucleotides*

The interpretation of the A,T,C,G degree of freedom is not obvious and one can consider several options.

1. The quantum numbers entangled by braids having nothing to do with (A,T,C,G) assignable to nucleotides and the braiding does not affect nucleotides.
2. The nucleotides (A,T,C,G) correspond to four different colors (a,t,c,g) for braid strands with conjugate nucleotides defining conjugate colors. The subgroup of allowed braidings would preserve the color patterns. The minimal assumption consistent with the mapping of nucleotides to quarks and antiquarks [L7] is that braid strands connect only nucleotides and conjugate nucleotides.
3. The model requires that the genomes in different nuclei are identical: otherwise it is not possible to realize braidings as symmetry transformations mapping portions of DNA to their conjugates (as noticed, this map would not occur at the chemical level). An interesting question is whether also the permutations of nucleotides of different codons are allowed or whether only codons are permuted so that they would define fundamental sub-programs.
4. One can understand why the minimum number of nucleotides in a codon is three. The point is that braid group is non-commutative only when the number of strands is larger than 2. The braidings acting as symmetries would correspond to a subgroup of ordinary braidings leaving the color pattern of braid invariant. Obviously the group is generated by some minimal number of combinations of ordinary braid generators. For instance, for two braid strands with different colors the generator is e_1^2 rather than e_1 (two exchange operations/full 2π twist). For codons one would have four different subgroups of full braid group corresponding to codons of type XXX, XYY, XXY, and XYZ. Each gene would be characterized by its own subgroup of braid group and thus by an M-matrix defining topological quantum computation.
5. It might be possible to understand the "junk DNA" character of introns. Introns are the most natural candidates for the portions of genome participating topological quantum computations. The transcription process would disturb topological quantum computation so that introns should be chemically passive. Since the portion of "junk DNA" increases with

the evolutionary level of the species evolution would indeed correspond to an increase the amount of topological quantum computations performed.

2. Two realizations of topological quantum computation and their combination

One can imagine two basic realizations of topological quantum computation like processes- or to be more precise - entanglement by braiding. In TGD framework this entanglement could be interpreted in terms of Connes tensor product.

2.1 Space-like entanglement

The first realization would rely space-like braids. Braid strands would connect identical lines of text at the page of book defined by sequences of genomes of different nuclei. Inside nucleus the strands would connect DNA and its conjugate. The braiding operation would take place between lines.

In this case it would be perhaps more appropriate to speak about quantum memory storage of a function realized as entanglement. These functions could represent various rules about the behavior of and survival in the physical world. For this option A,T,C,G cannot correspond to entangled quantum numbers and the interpretation as braid colors is natural. Braiding cannot correspond to a physical braiding of nucleotides so that (A,T,C,G) could correspond to braid color (strands would connect only identical nucleotides).

Strands would not connect strand and its conjugate like hydrogen bonds do but would be like long flux lines of dipole field starting from nucleotide and ending to its conjugate so that braiding would emerge naturally. Color magnetic flux tube structures of almost atom size appear in the TGD based model of nucleus and have light quarks and anti-quarks at their ends [F9]. This could be the case also now since quarks and anti-quarks appear also in the model of high T_c superconductivity which should be present also in living matter [M3].

2.2. Light-like entanglement

Second realization would rely on light-like braids at the boundaries of light-like 3-surfaces connecting 2-surfaces assignable to single genome at different moments of time. Braiding would be dynamical and dance metaphor would apply. The light-like surface could intersect genomes only at initial and final moments and strands would connect only identical nucleotides. Light-likeness in the induced metric of course allows the partonic 3-surface to look static at the level of imbedding space. The fundamental number theoretic braids defined by the minima of the Higgs like field associated with the modified Dirac operator would be very natural in this case.

Genes would define only the hardware unless they code for the magnetic body of DNA too, which looks implausible. The presence of quantum memory and quantum programs would mean a breakdown of genetic determinism since the braidings representing memories and programs would develop quantum jump by quantum jump and distinguish between individuals with the same genome. Also the personal development of individual would take place at this level. It would be these programs (that is magnetic bodies) which would differentiate between us and our cousins with almost identical genome.

2.3 Combination of the two realizations

These two variants of tqc accompany each other automatically if DNA nucleotides are connected to the lipids by magnetic flux tubes [L7]. In this case the 2-D flow of lipids induced by the self organization pattern of the metabolically induced flow of cellular water would induce the tqc as dance and this in turn would generate braiding of flux tubes connecting lipids to the nucleotides. Presumably a gel-sol transition of cytoplasm accompanies tqc in this kind of situation.

3.4.3 Biological evolution as an evolution of topological quantum computation

This framework allows to understand biological evolution as an evolution of topological quantum computation like processes in which already existing programs become building blocks of more complex programs.

1. The transition from RNA era to DNA era involving also the emergence of cell membrane bounded structures would mean the emergence of the topological quantum computation using a static hardware.
2. For mono-cellulars double DNA strands define space-like topological quantum computations involving only single step if the braids connect the nucleotides of the two DNA strands: obviously a reason why for double DNA strands.
3. For multicellular organisms more complex space-like topological quantum computations would emerge and could code rules about environment and multicellular survival in it. At this step also introns specialized to topological quantum computation would emerge.
4. A further evolution as a generation of super-genomes in turn forming hyper-genomes and even higher structures would have a concrete counterpart as the organization of braids of lower level to form braids at higher level so that topological quantum computations would become increasingly complex and program module structure would emerge very naturally.

subsection Water memory and braids

There are several grand visions about TGD Universe. One of them is as a topological quantum computer in a very general sense. This kind of visions are always oversimplifications but the extreme generality of the braiding mechanism suggest that also simpler systems than DNA might be applying tqc.

3.4.4 Water memory: general considerations

With few exceptions so called "serious" scientists remain silent about the experiments of Benveniste and others relating to water memory [120, 121, 118, 119] in order to avoid association with the very ugly word "homeopathy".

The Benveniste's discovery of water memory initiated quite dramatic sequence of events. The original experiment involved the homeopathic treatment of water by human antigene. This meant dilution of the water solution of antigene so that the concentration of antigene became extremely low. In accordance with homeopathic teachings human basophils reacted on this solution.

The discovery was published in Nature and due to the strong polemic raised by the publication of the article, it was decided to test the experimental arrangement. The experimental results were reproduced under the original conditions. Then it was discovered that experimenters knew which bottles contained the treated water. The modified experiment in which experimenters did not possess this information failed to reproduce the results and the conclusion was regarded as obvious and Benveniste lost his laboratory among other things. Obviously any model of the effect taking it as a real effect rather than an astonishingly simplistic attempt of top scientists to cheat should explain also this finding.

The model based on the notion of field body and general mechanism of long term memory allows to explain both the memory of water and why it failed under the conditions described.

1. Also molecules have magnetic field bodies acting as intentional agents controlling the molecules. Nano-motors do not only look co-operating living creatures but are such. The field body of molecule contains besides the static magnetic and electric parts also dynamical parts characterized by frequencies and temporal patterns of fields. To be precise, one must speak both

field and relative field bodies characterizing interactions of molecules. Right brain sings-left brain talks metaphor might generalize to all scales meaning that representations based on both frequencies and temporal pulse with single frequency could be utilized.

The effects of complex bio-molecule to other bio-molecules (say antigene on basofil) in water could be characterized to some degree by the temporal patterns associated with the dynamical part of its field body and bio-molecules could recognize each other via these patterns. This would mean that symbolic level in interactions would be present already in the interactions of bio-molecules.

If water is to mimic the field bodies of molecules using water molecule clusters, at least vibrational and rotational spectra, then water can produce fake copies of say antigenes recognized by basofils and reacting accordingly.

Also the magnetic body of the molecule could mimic the vibrational and rotational spectra using harmonics of cyclotron frequencies. Cyclotron transitions could produce dark photons, whose ordinary counterparts resulting in de-coherence would have large energies due to the large value of \hbar and could thus induce vibrational and rotational transitions. This would provide a mechanism by which molecular magnetic body could control the molecule. Note that also the antigenes possibly dropped to the larger space-time sheets could produce the effect on basofils.

2. There is a considerable experimental support for the Benveniste's discovery that bio-molecules in water environment are represented by frequency patterns, and several laboratories are replicating the experiments of Benveniste as I learned from the lecture of Yolene Thomas in the 7:th European SSE Meeting held in Rörös [122]. The scale of the frequencies involved is around 10 kHz and as such does not correspond to any natural molecular frequencies. Cyclotron frequencies associated with electrons or dark ions accompanying these macro-molecules would be a natural identification if one accepts the notion of molecular magnetic body. For ions the magnetic fields involved would have a magnitude of order .03 Tesla if 10 kHz corresponds to scaled up alpha band. Also Josephson frequencies would be involved if one believes that EEG has fractally scaled up variants in molecular length scales.
3. Suppose that the representations of bio-molecules in water memory rely on pulse patterns representing bit sequences. The simplest realization of bit would be as a laser like system with bit 1 represented by population inverted state and bit 0 by the ground state. Bits could be arranged in sequences spatially or by variation of zero point energy defining the frequency: for instance increase of frequency with time would define temporal bit sequence. Many-sheeted lasers are the natural candidates for laser like systems are in question since they rely on universal metabolic energy quanta. Memory recall would involve sending of negative energy phase conjugate photons inducing a partial transition to the ground state. The presence of metabolic energy feed would be necessary in order to preserve the memory representations.

3.4.5 Water memory in terms of molecular braidings

It is interesting to look water memory from the point of view of tqc. Suppose that the molecules and water particles (space-time sheet of size of say cell length scale) are indeed connected by color flux tubes defining the braid strands and that splitting of the braid strands can take place so that water flow can give rise to a braiding pattern and tqc like process.

The shaking of the bottle containing the diluted homeopathic remedy is an essential element in the buildup of water memories also in the experiments of Benveniste [120]. Just like the vigorous flow of sol near the inner monolayer, this process would create a water flow and this flow creates a

braiding pattern which could provide a representation for the presence of the molecules in question. Note that the hardware of braiding could carry information about molecules (cyclotron frequencies for ions for instance).

The model for the formation of scaled down variants of memories in hippocampus discussed above suggests that each half period of theta rhythm corresponds to tqc followed by a non-computational period during which the outcome of tqc is expressed as 4-D nerve pulse patterns involving cyclotron frequencies and Josephson frequency. Josephson currents at the second half period would generate dark Josephson radiation communicating the outcome of the calculation to the magnetic body. Entire hierarchy of EEGs with varying frequency scale would be present corresponding to the onion like structure of magnetic body. This pattern would provide an electromagnetic representation for the presence of the antigene and could be mimicked artificially [121, 122].

This picture might apply be the case also in the case of water memory.

1. The shaking might drop some fraction of antigene molecules to dark space-time sheets where they generate a dark color magnetic field. Because of the large value of Planck constant super-conductivity along color flux tubes running from molecular space-time sheets could still be present.
2. TGD based model of super conductivity involves double layered structures with same p-adic length scale as cell membrane [J1]. The universality of p-adic length scale hierarchy this kind of structures but with a much lower voltage over the bilayer could be present also in water. Interestingly, Josephson frequency ZeV/\hbar would be much lower than for cell membrane so that the time scale of memory could be much longer than for cell membrane for given value of \hbar meaning longer time scale of memory recall.
3. Also in the case of homeopathic remedy the communication of the result of tqc to the magnetic body would take place via Josephson radiation. From the point of view of magnetic body Josephson radiation resulting in shaking induced tqc induced would replace the homeopathic remedy with a field pattern. The magnetic bodies of basophils could be cheated to produce allergic reaction by mimicking the signal representing the outcome of this tqc. This kind of cheating was indeed done in the later experiments of Benveniste involving very low frequency electromagnetic fields in kHz region allowing no identification in terms of molecular transitions (magnetic body and cyclotron frequencies) [121].

3.4.6 Why experimenter had to know which bottle contained the treated water?

Why experimenter had to know which bottle contained the treated water? The role of experimenter eliminates the possibility that the (magnetic bodies of) clusters of water molecules able to mimic the (magnetic bodies of) antigene molecules electromagnetically are present in the solution at geometric now and produce the effect. The earlier explanation for experimenter's role was based on the idea that memory storage requires metabolic energy and that experimenter provides it. Tqc picture suggests a variant of this model in which experimenter makes possible the recall of memories of water represented as braiding patterns and realized via tqc.

1. Does experimenter provide the metabolic energy needed to store the memories of water?

What could be then the explanation for the failure of the modified experiment? Each memory recall reduces the occupation of the states representing bit 1 and a continual metabolic energy feed is needed to preserve the bit sequence representations of antibodies using laser light systems as bit. This metabolic energy feed must come from some source.

By the universality of metabolic energy currencies population inverted many-sheeted lasers in living organisms define the most natural source of the metabolic energy. Living matter is however

fighting for metabolic energy so that there must be some system willing to provide it. The biological bodies of experimenters are the best candidates in this respect. In this case experimenters had even excellent motivations to provide the metabolic energy. If this interpretation is correct then Benveniste's experiment would demonstrate besides water memory also psychokinesis and direct action of desires of experimenters on physics at microscopic level. Furthermore, the mere fact that we know something about some object or direct attention to it would mean a concrete interaction of our magnetic with the object.

2. *Does experimenter make possible long term memory recall?*

The alternative explanation is that experimenter makes possible long term memory recall which also requires metabolic energy.

1. If braiding pattern represents, the water memory the situation changes since the robustness of the braiding pattern suggests that this representation is still in the geometric past (which is replaced with a new one many times). If the dark variants of molecules created in the process are still in the water, the braid representation of water memories could be available even in the geometric now but it is better to not make this assumption. The challenge is to understand how this information can be made conscious.
2. What is certainly needed is that the system makes the tqc again. This would mean a fractal quantum jump involving unitary U process and state function reduction leading to the generation of generalized EEG pattern. Only the sums and differences of cyclotron frequency and Josephson frequency would matter so that the details of the flow inducing braiding do not matter. The shaking process might be continuing all the subjective time in the geometric past so that the problem is how to receive information about its occurrence. Experimenter might actually help in this respect since the mechanism of intentional action initiates the action in the geometric past by a negative energy signal.
3. If the magnetic body of the water in the geometric now can entangle with the geometric past, tqc would regenerate the experience about the presence of antigene by sharing and fusion of mental images. One can however argue that water cannot have memory recall in this time scale since water is quite simple creature and levels with large enough \hbar might not be present. It would seem that here the experimenter must come in rescue.
4. The function of experimenter's knowledge about which bottle contains the homeopathic solution could be simply to generate time-like entanglement in the required long time scale by serving as a relay station. The entanglement sequence would be *water now - experimenter now - water in the past* with "now" and "past" understood in the geometric sense. The crucial entanglement bridge between the magnetic body of water and experimenter would be created in the manufacturing of the homeopathic remedy.

Note that this explanation does not exclude the first one. It is quite possible that experimenter provides also the metabolic energy to the bit representation of water memories possibly induced by the long term memory recall.

This picture is of course just one possible model and cannot be taken literally. The model however suggest that magnetic bodies of molecules indeed define the braiding; that the generalized EEG provides a very general representation for the outcome of tqc; that liquid flow provides the manner to build tqc programs - and also that shaking and sudden pulses is the concrete manner to induce visible-dark phase transitions. All this might be very valuable information if one some day in the distant future tries to build topological quantum computers in laboratory.

4 Physical model for genetic code and its evolution

The original number theoretic models for genetic code relied on the idea that genetic code has deeper number theoretical significance. The neglect of some obvious physical inputs however generated some pseudo problems. These models however led to what I believe is the correct track concerning the understanding of the prebiotic evolution. The original model for the evolution of genetic code as a fusion of singlet and doublet codes to triplet code has been discussed in [?]. The model to be discussed here is obtained from this model by some dramatic simplifications.

The basic questions are following.

1. What were the physical counterparts of the pre-amino-acids and pre-tRNAs for singlet and doublet codes?
2. How the triplet code emerged from the singlet and doublet codes? How the tRNA molecules evolved and how the amino-acids replaced pre-amino-acids?
3. Can one identify singlet and doublet life-forms or at least some predecessors of triplet life forms as existing life-forms?

In an attempt to answer these questions p-adic length scale hypothesis and the vision about the molecular evolution as a sequence of spontaneous symmetry breakings induced by the generation of new space-time sheets serve as valuable guide lines. The following biological input is needed.

1. RNA world [52] as a model for pre-biotic evolution allows to identify pre-amino-acids as RNA sequences (RNA_1 for short) differing somehow from the ordinary RNA sequences (RNA_2 for short). 1-code was associated with the transformation of $RNA_2 \rightarrow RNA_1$ and 2-code in the simplest case with the transcription of RNA_2 to its conjugate.
2. The cross like structure of tRNA molecule identifiable as a composite of its singlet and doublet predecessors allows to read directly the main steps in the evolution of the triplet code as a fusion of singlet and doublet codes and also gives detailed and highly non-trivial information about RNA_1 .
3. The reverse transcriptase, appearing in retro-viruses like HIV and acting also as a transcriptase [70], provides the mechanism transforming RNA sequences to DNA sequences inside pre-nucleus so that DNA \rightarrow RNA code emerged and also evolved rapidly since reverse transcriptase makes a lot of errors.
4. The basic idea is that the fusion of $tRNA_1$ and $tRNA_2$ to $tRNA_3$, the recent tRNA, made $RNA_2 \rightarrow RNA_1$ and $RNA_2 \rightarrow RNA_2$ transformations impossible and the amino-acids originally catalyzing the attachment of RNA_2 doublet in RNA_2 transcription began to be attached to a growing amino-acid sequence and mRNA \rightarrow amino-acid part of genetic machinery was established. The emergence of reverse transcriptase brought in DNA. DNA as topological quantum computer idea generalized to RNA context provides tight additional conditions on the course of events: in particular, membrane like structures, most naturally consisting of RNA_1 should have been present already at RNA era.
5. Nanno-bacteria claimed to be even the dark bio-matter are excellent candidates for singlet and doublet life-forms or at least, predecessors of the recent life-forms. There are reasons to believe that RNA era is still continuing inside cell nucleus.

Second group of questions relates to the quantum control of the translation process. There are many questions also now.

1. What makes a codon stopping codon?
2. What is behind the symmetries of the code with respect to the third codon.
3. What is the origin of breaking of the canonical A-T, C-G rules for mRNA-tRNA association?

The model for the transition from RNA era to RNA-amino-acid era allows to answer these questions and the DNA as tqc picture leads to a physical interpretation of these symmetries and their breaking.

4.1 RNA world

The hypothesis that pre-biotic life before the emergence of the cell membrane structures was RNA dominated (the notion of RNA world) is based on a strong empirical evidence summarized in detail in [58]. For instance, only RNA can be generated spontaneously in the absence of cell membrane bounded structures. There is also a lot of support for the ability of RNA to take care of functions like replication, translation, and transfer (see the [58] and references therein). Ribozymes could even replace enzymes as RNA based catalyzing agents so that even amino-acids might be unnecessary in RNA world and the system could consist of RNA only. This of course does not mean that this system could yet realize genetic code and evolve.

An important implication is that pre-amino-acids might be identifiable as 2',5' RNA, which was produced in the classical experiments of Leslie Orgel at 1980s mimicking primordial ocean. There are however also other candidates and the structure of tRNA more or less fixes identification to a high degree.

Ontogeny recapitulates phylogeny principle suggests that if RNA coded RNA during primordial period, the remnants of these RNAs could still exist and be coded by specific genes. This is indeed the case [75] (for an article about RNA genes and RNA world see [76]). RNA genes were discovered already 1990 in the genome of *Caenorhabditis elegans*, the small nematode worm but it took years to realize that they do not code proteins but small RNA molecules that somehow turn off other genes that play a role in worm development. Later these small RNA coding genes were found in flies, mollusks, fish, and even humans. As many as 200 microRNA genes in *C. elegans* were known at time of the writing of the article, which would represent about 1 percent of the genes of its genome. There is also evidence that centrosomes possess their own genome based on RNA rather than DNA [127].

4.2 Programming of bio-molecular self assembly pathways from TGD point of view

The beautiful results (for a popular summary see [87]) about programming of bio-molecular self assembly - described above - when combined with the earlier model for the pre-biotic evolution - inspire interesting insights about the role of braiding in translation. The basic observation is that the structure of tRNA- although more complex than that of hairpin- has much common with that of hairpins. Therefore it is interesting to look this structure from the point of view of TGD. For instance, one can find whether the notions of braiding, anomalous em charge and quark color could provide additional insights about the structure and function of tRNA.

The brief summary of the resulting picture is as follows. According to the TGD based model of pre-biotic evolution [L5], 3-code should have resulted as a fusion of 1- and 2- codes to 3-codes involving fusion of $tRNA_1$ and $tRNA_2$ to $tRNA_3 \equiv tRNA$. Second hypothesis is that during RNA era the function of $tRNA_2$ was to generate RNA_2 double helix from single RNA strand and that amino-acids catalyzed this process. The considerations that follow strongly suggest that $tRNA_1$ was involved with a non-deterministic generation of new RNA sequences essential for the evolution.

After the establishment of 3-code these two process fused to a deterministic process generating amino-acid sequences. RNA era could still continue inside cell and play an important role in evolution.

There is an interesting work about programming bio-molecular self assembly pathways [88]. The catalytic self assembly of complexes of nuclei acids is carried out automatically by a program represented implicitly as a mixture of linear DNA strand acting as catalyst and so called hairpin DNA:s containing three nucleation sites a_t, b_t, c_t - so called toeholds.

4.2.1 Key ideas

The basic idea is that a set of bio-molecular reactions can be programmed to occur in a desired order by using a generalization of lock and key mechanism. The simplest self assembly pathway can be specified by a collection of keys and locks. In the beginning there is only one key and the this key fits to only one door, which leads into a room with several doors. The lock eats the key but gives one or more keys. If the room contains several doors to which the keys fits, the reaction corresponds to addition of several branches to the already existing reaction product. By continuing in this manner one eventually ends up to the last room and at the last step the lock gives back the original key so that it can act as a catalyst.

The translation of this idea to a program defining self assembly pathway is following.

1. DNA hairpin define key structural element of the self-assembly program. Hairpin is a single-stranded DNA strand in meta-stable configuration having form $A+B+C$ [89] such that B forms a loop and C is a palindrome [91]. The formal expression for palindromy is $C = A_t^*$: this means that C read backwards (C_t) is conjugate A^* of A implying that A and C running in opposite direction can form a double helix (duplex) by hydrogen bonding. As catalytic a^* acting as key forms a double helix with a , the hairpin molecule opens to a linear DNA molecule and energy is liberated. In this process original key is lost but the two other toeholds b_t and c_t contained by the hairpin become available as keys. Each hairpin in the mixture of catalyst and hairpin molecules has its own lock and two keys.
2. The process of opening new doors continues until all hairpin molecules are used. The key given by the last lock must be catalyst strand a^* . The outcome is a molecule consisting of pieces of DNA strands and can possess a very complex topology. For instance, the formation trees and star like structures can be easily programmed.
3. To run this program one needs only an optimal mixture of catalyst molecule and hairpin DNA molecules. In the applications discussed in [88] hairpins have length of order 10 nm which corresponds to p-adic length scale $L(151)$ defining also cell membrane thickness. That $L(151)$ corresponds also to the length of 30-nucleotide sequence defining the codon of the code associated with Mersenne prime $M_{61} = 2^{61} - 1$ might not be an accident. The simplest applications are autocatalytic formation of DNA duplex molecules and of branched junctions, nucleated dendritic growth, and autonomous locomotion of a bipedal walker.

The basic idea in the realization of the autonomous motion of bipedal walker is to cheat the walker to follow a track marked by food. The walker literally eats the food and receives in this manner the metabolic energy needed to make the step to the next piece of food. The menu contains two kinds of hairpins as foods: hairpins A attached regularly along the desired path of the walker (second DNA strand) and hairpins B but not attached to the strand. The front leg l of the walker attaches to A and this catalyzes the formation of the duplex $A \cdot B$ as a waste and the liberated metabolic energy allows to make a step in which hind leg becomes the front leg.

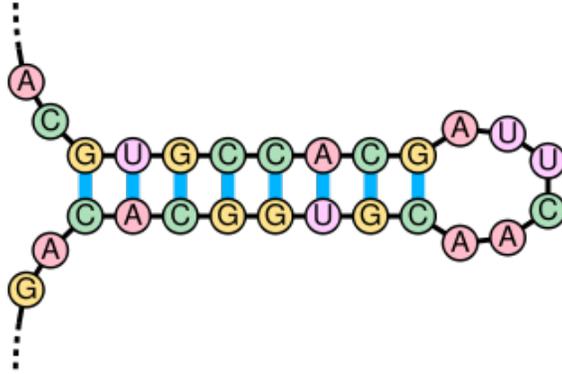


Figure 1: The structure of DNA hairpin (stem loop)

4.2.2 TGD view about the situation

The possibility to program the self-assembly relies on the almost deterministic realization of the lock and key mechanism. The presence of braid strands could make this possible.

1. Consider first the hypothesis about the cancelation of anomalous DNA charge. The palindromic character of A means that the neck of the hairpin has vanishing anomalous em charge and also vanishing color charge is possible. Hence palindromes are favored in TGD Universe. The circular piece B is not in general color singlet. It could have braid strands connecting it to it to some other DNA or nuclear membrane but this is not necessary. Same applies to the toehold a_t at the end of the other strand of neck.
2. The attachment of the lock to key could be seen as a process in which a braid consisting of magnetic flux tubes connecting lock and key strands (DNA and its conjugate) is formed spontaneously and followed by a phase transition reducing \hbar contracting the flux tubes and in this manner guiding the key to the lock.

If one assumes that only paired nucleotides of single DNA strand possess braid strands, one must assume the same for mRNA. As a consequence one would lose the nice interpretation for the formation of AAA... tail of mRNA as a manner to guarantee integer valuedness and small value (or even vanishing) of the anomalous em charge. If there is braid strands associated with entire mRNA, it could end at the nuclear membrane. In this case the transfer of tRNA to mRNA during translation by a phase transition reducing \hbar of braid strands could be initiated by the fusion of the braid strand ends coming from mRNA codon and from its conjugate codon at tRNA at nuclear membrane.

4.3 The archeology of tRNA molecules as a guideline

The study of the structure of the ordinary tRNA molecule is of considerable help in the attempts to guess what might have been its predecessor.

4.3.1 The structure of the tRNA molecule

The shape of the tRNA molecule [73] in 2-D representation is that of cruciform.

1. tRNA molecule has a cross like appearance, and decomposes into a body coded by tRNA gene and an acceptor stem which is same for all amino-acids and added separately and can be replaced during the lifetime of the tRNA molecule. Acceptor stem, to which the amino-acid is attached with the mediation of amino-acyl-tRNA synthase, can be said to be a passive component and is same for all tRNAs so that its structure does not determine which amino-acid is attached to it. The stem is not coded by genes and contains 4 nucleotides.
2. tRNA molecule can be seen as single RNA strand just as hairpin. The five stems are double helices analogous to the necks of the hairpin. Strand begins at 5' end of the acceptor stem directed upwards. The second strand of acceptor stem continues as a toehold ending to 3' end of tRNA. The toehold has at its end ACC to which the amino-acid (rather than conjugate DNA) attaches.
3. tRNA molecule contains three arms with hairpin structure. *A* arm containing the anticodon is directed downwards. *D* and *T* arms are horizontal and directed to left and right. Between *T* arm and *A* arm there is additional variable hairpin like structure but with highly degenerate loop is degenerate. It has emerged during evolution.
4. The structure of tRNA minus anticodon depends on anti-codon which conforms with the fact *T* and *D* arms are related to the binding of amino-acid so that their nucleotide composition correlates with that of anticodon.
5. Anticodon arm contains the anticodon of mRNA codon and thus corresponds to RNA. For doublet part of the mRNA codon the correspondence is 1-1 but for the third nucleotide the correspondence is more complex due to wobble base pairing to be discussed below. Wobble base pairing indeed leads to the recent simplified model for the evolution of the triplet code as a fusion of 1-code and 2-code.

4.3.2 Wobble base pairing

The phenomenon of wobble base pairing [93] is very important. There are only about 40 tRNA molecules instead of 61 which means that one-to-one map between mRNA nucleotides and tRNA conjugate nucleotides is not possible. Crick suggests that so called wobble base pairing resolves the problem. What happens that the first nucleotide of anticodon is either *A*, *G*, *U*, or *I* (nosine) [92]. The base-pairings for third nucleotide are $\{A - U, G - C, U - \{A, G\}, I - \{U, A, C\}\}$. The explanation for the non unique base pairing in the case of *U* is that its geometric configuration is quite not the same as in ordinary RNA strand. *I* is known to have 3-fold base pairing.

Minimization of the number of tRNAs requiring that only three mRNA codons act as stopping signs predicts that the number of tRNAs is 40.

1. It is convenient to classify the 4-columns of code table according to whether all four codons code for the same amino-acid ($(T, C, A, G) \rightarrow X$, whether 4-column decomposes into two doublets: $[(T, C), (A, G)] \rightarrow [X, Y]$, or whether it decomposes to triplet and singlet ($[(T, C, A), G] \rightarrow [ile, met]$). There are also the 4-columns containing stop codon: $[(U, C), (A, G)] \rightarrow [(tyr, tyr), (stop, stop)]$ and $[(U, C), A, G] \rightarrow [(cys, sys), stop, trp]$. Mitochondrial code has full A-G and T-C symmetries whereas for vertebrate nuclear code 3 4-columns break this symmetry.
2. Consider first 4-columns for which the doublet symmetry is broken. $[tyr, tyr, top, stop]$ column must correspond to first tRNA nucleotide which is *A* or *G* (tyr). The absence of anti-codons containing *U* implies stop codon property. For $[cys, sys, stop, trp]$ one must have *A, G* and *C* but *U* is not allowed. ile-met column can correspond to tRNAs with *I* and *C* as the first nucleotide.

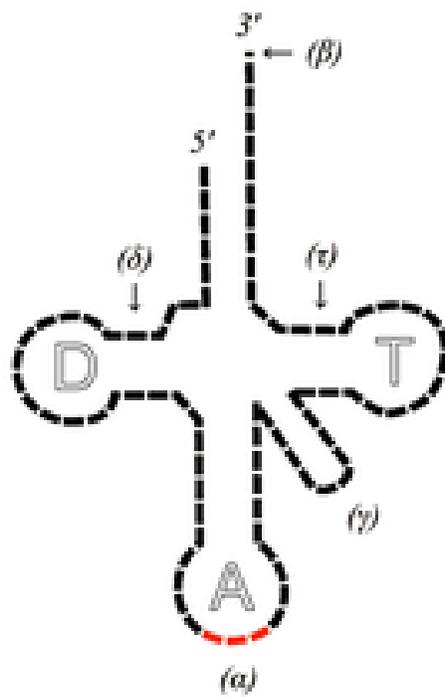


Figure 2: The structure of tRNA

3. For 4-columns coding for two doublet amino-acids the minimal set of first tRNA codons is $\{A, G, U\}$. For completely symmetric 4-columns the minimal set of tRNA codons is $\{I, U\}$. Thus $\{A, G, U, I\}$ would replace $\{A, G, U, C\}$.
4. There are 9 completely symmetric 4-columns making 18 tRNAs, 5 doublet pairs making 15 tRNAs, ile-met giving 2 tRNAs, and the columns containing stopping codons giving 5 tRNAs. Altogether this gives $18+15+2+5=40$. Also the deviations from the standard code can be understood in terms of the properties of tRNA.

Consider the interpretation of wobble base pairing in TGD framework assuming the braiding picture and the mapping of nucleotides to quarks. The completely symmetric 4-columns correspond to unbroken isospin and matter-antimatter asymmetries. 4-columns decomposing into doublets result from the breaking of matter-antimatter asymmetry at quark level. ile-met column corresponds to the breaking of both symmetries. The base pairings of I obviously break both symmetries.

The non-unique based pairing of U and I means that they cannot correspond to a unique quark or anti-quark in braiding U pairs with both A and G so that the braid strands starting from these RNA nucleotides must both be able to end to tRNA U . Hence tRNA U is not sensitive to the isospin of the quark. This non-uniqueness could relate to the assumed anomalous geometric character of the binding of U codon to tRNA sequence. The braid strands beginning from U , A , and C must be able to end up to I so that I can discriminate only between $\{U, C, A\}$ and G .

4.3.3 Anomalous em charge and color singletness hypothesis for tRNA

One can test also whether the vanishing of anomalous em charge of tRNA leads to testable predictions. One can also try understand translation process in terms of the braiding dynamics. One must distinguish between the states of tRNA alone and tRNA + amino-acid for which braidings are expected to be different.

Before continuing it must be made clear that braiding hypothesis is far from being precisely formulated. One question is whether the presence of the braiding could distinguish between matter in vivo and vitro. For instance, the condition that anomalous em charge is integer valued or vanishing for DNA hairpins in vivo gives strong condition on the loop of the hairpin but or hairpins in vitro there would be no such conditions. Second point is that amino-acids and I and U in tRNA₁ could carry variable anomalous em charge allowing rather general compensation mechanism.

1. tRNA without amino-acid

1. The minimal assumption is that braiding hypothesis applies only to the stem regions of tRNA in this case. In this case the strands can indeed begin from strand and end up to conjugate strand. The possibility of color singletness and vanishing of total anomalous em charge are automatically satisfied for the stem regions as a whole in absence of non-standard base pairings. In general the acceptor stem contains however $G*U$ base pair which is matter-antimatter asymmetric but breaks isospin symmetry and gives unit anomalous charge for the acceptor stem. Also other stems can contain $G*U$, $U*G$ pairings as also $P*G$ and $L*U$ pairings (P and L denote amino-acids Pro and Leu). The study of concrete examples [95] shows that single $G*U$ bond is possible so that anomalous em charge can be non-vanishing but integer valued for double strand part of tRNA. Suppose that a given amino-acid can have anomalous of any codon coding for it. If P in $G*P$ pair has the anomalous em charge of the codon CCG, $G*P$ pair has vanishing anomalous em charge. If L corresponds to CUA the value of anomalous em charge is integer.
2. The anomalous em charge in general fails to vanish for the loops of hairpins. For the braids possibly associated with the loops of tRNA the strands can only end up to tRNA itself or

nuclear membrane. If there are no braid strands associated with these regions, there is no color or anomalous em charge to be canceled so that the situation trivializes. On the other hand, in the case of tRNA I and U associated with the first nucleotide of the anticodon of tRNA can have a varying value of anomalous em charge. Therefore integer valued em charge and color singletness become possible for tRNA. tRNA can also contain amino-acids. If the amino-acids can carry a varying anomalous em charge with a spectrum corresponding to its values for DNA codons coding it, also they could help to stabilize tRNA by canceling the anomalous em charge.

2. tRNA plus amino-acid

1. Amino-acyl tRNA synthetase, which is the catalyst inducing the fusion of amino-acid with ACC stem [?], could have braid strands to both amino-acid and tRNA and have regions with opposite anomalous em charges compensating separately that of amino-acid and of the active part of tRNA. The required correlation of amino-acid with anticodon would suggest that both D and T loops and A -loop are included. The simplest option is however that the anticodon is connected by braid to amino-acid so that braiding would define the genetic code at the fundamental level and the many-to-one character of genetic code would reflect the 1-to-many character of amino-acid-quark triplet correspondence. This hypothesis is easy to kill: for the portion of catalyst attaching to a given portion of DNA strand amino-acids and codons should have opposite anomalous em charges: $Q_a(\text{amino}) = -Q_a(\text{codon})$.
2. After the catalysis involving reduction of \hbar amino-acid and tRNA would form a system with a vanishing net anomalous em charge but with a braiding structure more complex than that before the fusion.
3. In the translation process the braiding structure of tRNA- amino-acid system should re-organize: the braid strands connecting anticodon with amino-acid are transformed to braid strands connecting it to mRNA codon with a subsequent reduction of \hbar of braid strands bringing tRNA into the vicinity of mRNA. In the transcription the anticodon-codon braiding would be replaced with amino-acid-mRNA braiding forcing formation of the amino-acid sequence. It will be later found that the simpler option without this step corresponds to the earlier hypothesis according to which amino-acids acted originally as catalysts for the formation of RNA double helix.
4. tRNA is basically coded by genes which suggests that the general symmetries of the genetic code apply to the variants of tRNA associated with same anticodon. Hence the variants should result from each other by isospin splits and modifications such as permutations of subsequent nucleotides and addition of AT and CG pairs not changing overall color and isospin properties. Also anomalous base pairs $X*Y$ can be added provide their net anomalous em charge vanishes.
5. tRNA has a complex tertiary (3-D) structure [94] involving base pairing of distant nucleotides associated with the roots of the stem regions where tRNA twists sharply. This pairing could involve formation of braid strands connecting the nucleotides involved. The reduction of Planck constant for these strands could be an essential element of the formation of the tertiary structure.

4.3.4 The fossilized components of tRNA as record about the evolution of the recent form of the genetic code

The ordinary tRNA indeed seems to contain in its structure fossilized components providing a record about how the molecular evolution proceeded. tRNA₁ and tRNA₂ correspond naturally to

the horizontal and vertical segment in the recent tRNA formed as a fusion of tRNA₁ and tRNA₂ to form a cross like structure (see figure above). Hence tRNA₁ and tRNA₂ should represent in their structures the respective genetic codes.

1. tRNA₂ should contain both the conjugate of the coding RNA nucleotide attaching to RNA₂ plus the conjugate of the coded nucleotide to which RNA nucleotide was attached and then transferred to RNA₂ and added to the growing RNA sequence. This means that the structure of tRNA should help to deduce the doublet code experimentally. The pairs formed by the RNA triplet XYZ at the end of the anticodon arm of the ordinary tRNA and the pair formed by the triplet $X'Y'Z'$ and its conjugate on right and left sides of XYZ should provide detailed information about the doublet code. The pairs $XY - X'Y'$ should represent the doublet code apart from possible symmetry breaking effects. These effects might be induced at the level of $X'Y'Z'$ -amino-acid correspondence level and thus not visible in the structure of tRNA.
2. The transition to the triplet code added one RNA nucleotide to both the exotic doublet $(XY)_2$ and the doublet $X'Y'$ and its conjugate coded by it. The exotic $2', 5'$ doublet plus the added singlet transformed to ordinary triplet. The simplest assumption is that these RNAs came from D arm and T ψ C arm. This is possible since all loops are physically near to each other. The structure of D and T ψ loops conforms with the assumption that the predecessor of the first *resp.* second loop has lost the coding *resp.* coded RNA. The structure of these loops forces also to conclude that all tRNA loops have been stem like structures before their deactivation just as the acceptor stem is. Deactivation of RNA₁ translation process must have meant the completion of these stems to loops by addition of a conjugate of the conjugate of the coded RNA.

4.3.5 The components of tRNA as ribozymes which have acted originally as RNA polymerases

The mechanism of ribozyme catalyzed polymerization for both the exotic RNA with mono- *resp.* diphosphate backbones, and their their double strand can be guessed from the fact that the process can be seen as an unfaithful replication. Hence the tRNAs involved would play a role analogous to DNA polymerase in the polymerization of DNA. The only difference is that, instead of the conjugate of the template strand, a copy of strand is reproduced and the copy can be un-faithful.

DNA replication utilizes the conjugate strand as a template and occurs with the mediation of DNA polymerase enzyme, which brings dXTP, $X = A, T, C, G$ rather than dXMP, to the vicinity of the DNA conjugate strand [60]. The di-phosphate is cleaved out from dXTP and the liberated energy makes it possible to add the resulting dXMP to the growing DNA strand.

The prediction is that tRNA₁ and tRNA₂ have originally been ribozymes acting as exotic RNA polymerases. In the case of DNA strand dXMP pairs with its conjugate in the template strand by hydrogen bonds and $3', 5'$ bond is formed between monophosphate deoxyribose of previous nucleoside. In the case of exotic RNA strand the XMP associated with the tRNA pairs with its conjugate in the template RNA strand, $2', 5'$ bond with the ribose of the previous RNA unit is formed. tRNA is not so selective as a polymerase as DNA polymerase and this ultimately gives rise to the many-to-one correspondence crucial for the non-triviality of the genetic code.

1. RNA₂ consists of exotic RNA doublets with nucleotides connected by $2', 5'$ monophosphate bonds. tRNA₂ brings $2', 5'$ doublet $XMP_2 \circ YTP_2$ to the growing strand and glues it to the $5'$ position of the ribose in the already existing polymer. The YTP suffers the cleavage $YTP_2 \rightarrow YMP_2$ as in the case of DNA polymerization and the amount of metabolic energy provided by the cleavage is the same. The formation of $XMP_2 \circ YTP_2$ proceeds by gluing of XTP_2 to YTP_2 by a similar process so that the net metabolic energy used per nucleotide is essentially the same as in the ordinary DNA polymerization.

2. RNA_1 consists of exotic RNA singlets connected by 2',5' diphosphate bonds. $tRNA_1$ brings XTP_2 near the growing strand, the cleavage $XTP_2 \rightarrow XDP_2$ occurs, and XDP_2 is glued to the 5' position of the ribose of the previous RNA nucleotide. The amount of metabolic energy provided by the cleavage is roughly one half of that in the case of RNA_2 polymerization, and this might partially explain why diphosphate exotic RNA strands are rare whereas monophosphate exotic DNA strands can be found inside cells. On the other hand, it is $ATP \rightarrow ADP$ cleavage, which usually occurs in the ordinary metabolism instead of $ATP \rightarrow AMP$ cleavage: only during a very intense metabolism $ATP \rightarrow AMP$ cleavage occurs. Since ATP metabolism is a functional fossil from a very early period of evolution, one might expect that $ATP \rightarrow ADP$ cleavage has in fact occurred naturally, if not even more naturally, also in the polymerization of 2',5' RNA during (exotic) RNA era.
3. In the case of double exotic RNA strand of ordinary and exotic RNA the predecessor of the recent tRNA formed by $tRNA_1+tRNA_2$ would be a ribozyme bringing energized singlet and doublet RNAs to the double strand acting as a template with $tRNA_1$ component catalyzing the cleavage of the monophosphate and $tRNA_2$ component catalyzing the cleavage of the diphosphate.

The crucial and testable prediction is that the ribozymes responsible for the exotic mono- and diphosphate 2',5' RNA polymerization should have a strong resemblance with the two structural components of the recent tRNA. Furthermore, the replication catalyzed by these ribozymes should be unfaithful, perhaps in a manner consistent with the genetic code before the breaking of its symmetries. Ribozymes responsible for the ordinary RNA polymerization are known but I am not aware about how much is known about the corresponding ribozymes in the case of 2',5' RNA. The building blocks of recent tRNA would however provide a good starting point for innovative RNA engineers. In any case, the very fact that this form of RNA does not even allow DNA, makes it a more natural candidate for the basic building block of RNA life than 3',5' RNA.

4.4 Recent genetic code as a fusion of singlet and doublet codes?

There are several guidelines helping to answer the question how DNA-amino-acid translation might have emerged from singlet and doublet codes producing only RNA from RNA.

The following vision about evolution leading from RNA era to the recent DNA-RNA-amino-acid era inspired by a combination of RNA world vision [52] with the detailed study of the structure of tRNA suggesting the presence of 1- and 2-codes during RNA era with the DNA as tqc vision suggesting the presence of cell membrane like structures as a necessary ingredient making possible topological quantum computation like processes already during RNA era. The recent model is considerably simpler than the earlier models [?].

4.4.1 RNA era and the transition to RNA-amino-acid era

1. Translation of mRNA to amino-acid sequences separates from the transcription of DNA to mRNA. One expects that during RNA two different kinds of RNAs, call them RNA_2 and RNA_1 , analogous to mRNA and proteins existed. RNA_2 can be identified as the ordinary 3',5' RNA acting in the role of mRNA. A natural candidate for RNA_1 playing the role of proteins is 2',5' RNA since it is generated in the experiments of Orgel and appears also in genomes. Of course, also other candidates can be considered and the structure of tRNA gives valuable information about the character of this RNA. The copying of RNA_2 to its conjugate was the counterpart of RNA replication. The transcription of RNA_2 to RNA_1 was the counterpart of translation.

2. The structure of tRNA, call it tRNA₃, gives valuable information about the course of events leading to the translation of mRNA to amino-acids. The cross like structure of tRNA₃ and the decomposition of RNA triplet appearing in it to 2-codon and 1-codon suggests that it resulted as a fusion of two hairpin like molecules tRNA₁ and tRNA₂. tRNA₂ brought pairs of nucleotides forming the 2-codon part of RNA triplet to the growing RNA₂ sequence during replication and 2-code was simply RNA conjugation. tRNA₁ was involved with transcription of RNA₂ to RNA₁ bringing RNA₁ nucleotides one-by one to the growing sequence. In tRNA₃ the third nucleotide does not quite correspond to ordinary RNA but to *A, G, U* or *I*(inositol) and is believed to differ geometrically from ordinary nucleotide, and one can assume that these nucleotides were the building blocks of RNA₁ possibly appearing in 2', 5' form. The phenomenon of the wobble pairing can be assumed to have been present already during RNA era so that correspondence 1-code was not 1-to-1 nor deterministic but given by the correspondence $\{U \rightarrow A, C \rightarrow G, \{A, G\} \rightarrow U, \{U, A, C\} \rightarrow I\}$ deduced from the number 40 of tRNAs and assigning unique 1-codon to only *G* could be interpreted as a many-to-one and non-deterministic correspondence generating new RNA sequences from existing ones. If there was RNA₂ sequence coding for tRNA₁, this sequence appearing in hairpin structure could have coded the inverse of the translation. As a consequence, the occurrence of transcription and its reversal generated a rapid evolution by creating new kinds of RNA₂ sequences.
3. From the fact that amino-acids are attached to the ACC stem of tRNA₂, one can guess that the role of amino-acids during RNA era was to catalyze the replication. If single amino-acid would have catalyzed the attachment of given RNA doublet to the growing sequence, there would be at most 16 amino-acids and genetic code would not depend at all on the third nucleotide. This is indeed the case for roughly half of the code table (both matter antimatter symmetry and isospin symmetry with respect to third codon). For those mRNA codons for which A,G and T,C correspond to different amino-acids (breaking of matter antimatter asymmetry but isospin symmetry) two amino-acids catalyzed the attachment. Same amino-acid could also catalyzed two different attachments (ser, arg, leu for standard genetic code).
4. The crucial step was the fusion of the 1-code and 2-code to 3-code took place via fusion of tRNA₁ and tRNA₂ to tRNA₃ along their ends containing RNA₁ nucleotide and RNA₂ doublet which thus combined to RNA triplet. Presumably tRNA₃ in its original form was translated from a linear mRNA molecule and transformed spontaneously to the cross like shape because of the presence of palindrome structures in both. The original functions of tRNAs were not possible anymore since the triplet was not at the end of the molecule. The catalyzing amino-acid however was at the ACC end of and the function of tRNA₃ became to assist the translation of mRNA to amino-acid sequence. For those 3-codons for which single amino-acid catalyzed the fusion of 2-codon, a full matter antimatter and isospin symmetry resulted. For those 3-codons for which two amino-acids catalyzed the fusion, a breaking of matter antimatter symmetry took place in the sense that for given mRNA codon only the tRNA₃ corresponding to single amino-acid was stable. Isospin symmetry was broken only weakly or not at all (human mitochondrial code). Thus codons with A,G as third nucleotide almost always coded the first amino-acid and those with T,C as the third nucleotide the second one. Stopping codons resulted when all tRNA₃ corresponding to mRNA triplet were unstable. That same RNA can code for both amino-acid and act as a stop codon in certain situations, can be understood if the stability of corresponding tRNA₃ depends on the chemical environment.

4.4.2 Symbiosis with membrane bounded structures

In DNA as tqc picture nuclear and cell membranes make possible topological quantum computation. The magnetic flux tubes connecting DNA nucleotides to lipids of the cell membrane could also explain why DNA is stable inside cell. The emergence of cell membranes consisting of lipids and generated via self-organization rather being coded by genes would have stabilized DNA generated in this manner during DNA-RNA-amino-acid era. Membrane bounded structures emerged when the space-time sheets corresponding to the p-adic length scale $k = 151$ emerged in the condensate.

Topological quantum computation should have taken place already during RNA era. This suggests that the counterpart of the cell membrane was present already at that time. Quite recently it was reported [96] that DNA duplexes of length 6 to 20 base pairs can join to longer cylinders which in turn form liquid crystals and that the liquid crystal phase separates from the phase formed by single DNA strands. Long strands had been already earlier known to form liquid crystals. This encourages to think that also RNA duplexes are able to self-organize in this manner so that the analog of cell nucleus containing RNA double helices as genetic material could have existed already during RNA era.

The latter option would allow to distinguish between RNA_2 and RNA_1 used as building block of various structures. This suggests that RNA_1 , which disappeared in the transition to RNA-amino-acid era, might have formed liquid membranes containing inside then RNA_2 such that RNA_2 nucleotides were connected by magnetic flux tubes to RNA_1 nucleotides. The minimal function of RNA_1 would have been to make possible the buildup of cell membrane. In this case the lengths of RNA_1 needed to be only of order $L(151) = 10$ nm. The sequences consisting of 30 RNA_1 base pairs would correspond roughly to the thickness of cell membrane and to the codon of M_{61} code. Lipid layer of thickness 5 nm would correspond to roughly 16 base pairs and to the codon assignable to M_{17} . If magnetic flux tubes indeed stabilize DNA, the presence of RNA_1 membrane might have been enough to stabilize also DNA so that RNA era could have been followed by DNA-RNA era and eventually by DNA-RNA-amino-acid era with RNA_1 membrane being replaced by double lipid layer membrane.

4.4.3 Reverse transcription of RNA to DNA

The basic problem was how to build DNA sequences which would later take the command. If one, in conflict with the Central Dogma, assumes the presence of the predecessor of the so called reverse RNA transcriptase [70] associated with retro-viruses (in particular HIV virus), one can understand how this step occurred. Reverse RNA transcriptase allowed to transform ordinary RNA sequences to DNA sequences inside newly emerged pre-nuclei. The reverse transcriptase catalyzes also the transcription of DNA back to RNA so that DNA began to produce new RNA.

Reverse transcriptase requires amino-acids sequences. Amino-acids appeared as catalysts in tRNA_2 already during RNA era but the spontaneous emergence of reverse transcriptase before $\text{RNA} \rightarrow$ amino-acids translation look improbable. After the fusion of tRNA_1 and tRNA_2 RNA_2 could replicate only if tRNA_1 , tRNA_2 and tRNA_3 continued to live in symbiosis for some time. This could have led naturally to the generation of reverse transcriptase and DNA. After that DNA could have taken care of the production of RNA and tRNA_1 and tRNA_2 might have lost in the fight for molecular survival or at least their importance could have diminished. The emergence of DNA could have been associated with the replacement of RNA_1 membrane with ordinary cell membrane. For instance, it might be that DNA was able to form only magnetic flux tubes only with lipid bilayer membrane.

The reverse transcription is not reliable (one error per about 1000 nucleotides), and this led to a rapid evolution of DNA analogous to that of HIV virus. This meant an escape from the fixed point situation, and a genuine DNA \rightarrow RNA predecessor of the genetic code emerged. Together with the emergence of membrane bounded structures this meant genuine evolution at DNA level.

Reverse transcription is possible only for the ordinary RNA and explains why exotic doublet RNA has disappeared from cell.

4.4.4 What were the first self replicators?

The TGD inspired model of pre-biotic evolution suggests a reasonable guess for the first self-replicating molecular entities. Both $tRNA_1$ and $tRNA_2$ molecules must have resulted as more or less copies of corresponding RNA_2 sequences (amino-acid was added after transcription to $tRNA_2$) and the minimal self-reproducing system could have consisted of $tRNA_1$, $tRNA_2$ and corresponding RNA_2 molecules. Since $tRNA_1$ and $tRNA_2$ are hairpins in the usual configuration and the mechanism making possible biochemical reaction series suggests that these hairpin molecules catalyzed the opening of the corresponding RNA_2 pieces and their coding to $tRNA_1$ or $tRNA_2$.

Note that double strands in the sense they occur for DNA are not necessary since the double strand part of hairpin is analogous to DNA double strand and the opening of hairpin structure is analogous to the opening of DNA double strand during transcription and replication. The non-determinism of 1-code could have rapidly led to a genuine evolution and one can also imagine a spontaneous generation of RNA_2 sequences as oligonucleotides consisting of copies of pieces of RNA_2 coding for $tRNA_2$.

Also more general hairpin might be used to construct a self-catalyzing system. Since exotic and normal RNA do not differ too much, a reasonable amount of guess work might allow to identify $tRNA_1$ and $tRNA_2$, and perhaps even create simple pre-biotic life-forms in the laboratory.

4.5 Is RNA era continuing inside cell nuclei?

The last issue of [81] contains an article about the discovery that only roughly one half of DNA expresses itself as amino-acid sequences. A detailed summary of the results has been published in Nature [82]. The Encyclopedia of DNA Elements (ENCODE) project has quantified RNA transcription patterns and found that while the "standard" RNA copy of a gene gets translated into a protein as expected, for each copy of a gene cells also make RNA copies of many other sections of DNA. In particular, intron portions ("junk DNA", the portion of which increases as one climbs up in evolutionary hierarchy) are transcribed to RNA in large amounts. What is also interesting that the RNA fragments correspond to pieces from several genes which raises the question whether there is some fundamental unit smaller than gene.

None of the extra RNA fragments gets translated into proteins, so the race is on to discover just what their function is. TGD proposal is that the RNA gets braided and performs a lot of topological quantum computation [E9]. Topologically quantum computing RNA fits nicely with replicating number theoretic braids associated with light-like orbits of partonic 2-surfaces and with their spatial "printed text" representations as linked and knotted partonic 2-surfaces giving braids as a special case [C4]. An interesting question is how printing and reading could take place. Is it something comparable to what occurs when we read consciously? Is the biological portion of our conscious life identifiable with this reading process accompanied by copying by cell replication and as secondary printing using amino-acid sequences?

This picture conforms with TGD view about pre-biotic evolution. Plasmoids [72], which are known to share many basic characteristics assigned with life, came first: high temperatures are not a problem in TGD Universe since given frequency corresponds to energy above thermal energy for large enough value of \hbar [A9]. Plasmoids were followed by RNA, and DNA and amino-acid sequences emerged only after the fusion of 1- and 2-letter codes fusing to the recent 3-letter code. The cross like structure of tRNA molecules carries clear signatures supporting this vision. RNA would be still responsible for roughly half of intracellular life and perhaps for the core of "intelligent life".

I have also proposed that this expression uses memetic code which would correspond to Mersenne $M_{127} = 2^{127} - 1$ with 2^{126} codons whereas ordinary genetic code would correspond to $M_7 = 2^7 - 1$ with 2^6 codons. Memetic codons in DNA representations would consist of sequences of 21 ordinary codons. Also representations in terms of field patterns with duration of .1 seconds (secondary p-adic time scale associated with M_{127} defining a fundamental bio-rhythm) can be considered.

A hypothesis worth of killing would be that the DNA coding for RNA has memetic codons scattered around genome as basic units. It is interesting to see whether the structure of DNA could give any hints that memetic codon appears as a basic unit.

1. In a "relaxed" double-helical segment of DNA, the two strands twist [83] around the helical axis once every 10.4 base pairs of sequence. 21 genetic codons correspond 63 base pairs whereas 6 full twists would correspond to 62.4 base pairs.
2. Nucleosomes [86] are fundamental repeating units in eukaryotic chromatin [85] possessing what is known as 10 nm beads-on-string structure. They repeat roughly every 200 base pairs: integer number of genetic codons would suggest 201 base pairs. 3 memetic codons makes 189 base pairs. Could this mean that only a fraction $p \sim 12/201$, which happens to be of the same order of magnitude as the portion of introns in human genome, consists of ordinary codons? Inside nucleosomes the distance between neighboring contacts between histone and DNA is about 10 nm, the p-adic length scale $L(151)$ associated with the Gaussian Mersenne $(1+i)^{151} - 1$ characterizing also cell membrane thickness and the size of nucleosomes. This length corresponds to 10 codons so that there would be two contacts per single memetic codon in a reasonable approximation. In the example of Wikipedia [86] nucleosome corresponds to about $146=126+20$ base pairs: 147 base pairs would make 2 memetic codons and 7 genetic codons. The remaining 54 base pairs between histone units + 3 ordinary codons from histone unit would make single memetic codon. That only single memetic codon is between histone units and part of the memetic codon overlaps with histone containing unit conforms with the finding that chromatin accessibility and histone modification patterns are highly predictive of both the presence and activity of transcription start sites. This would leave 4 genetic codons and 201 base pairs could decompose as memetic codon+2 genetic codons+memetic codon+2 genetic codons. The simplest possibility is however that memetic codons are between histone units and histone units consist of genetic codons. Note that memetic codons could be transcribed without the straightening of histone unit occurring during the transcription leading to protein coding.

4.6 Could nanno-bacteria correspond to predecessors of the triplet life-forms?

The experiments of Leslie Orgel (at 1980) imitating the primordial ocean demonstrate the emergence of the exotic RNA for which doublet effectively replaces the triplet. The so called nanno-bacteria represent a mystery at the borderline between living and non-living matter. The web article of Robert L. Folk [50], who is one of the pioneers in the field besides Y. Morita [65] and E. O. Kajander [57], provides a brief summary about nanno-bacteria and contains also references. A priori one cannot exclude the possibility that nanno-bacteria might represent a predecessor of the triplet code, perhaps even singlet or doublet life-form or their symbiosis.

4.6.1 Basic facts about nanno-bacteria

Nanno-bacteria (often called also nanobacteria) are considerably smaller than ordinary bacteria. The sizes of the nanno-bacteria vary from about 20 nm to .2 micro-meters. Thus the smallest nanno-bacteria have size scale not much above $L(151)$ so that optical microscope does not allow to study them. Indeed, geologists discovered nanno-bacteria by using scanning electron microscope.

Nanno-bacteria can originate a precipitation in calcite and argonite crystals by providing the seed of the crystal. Nanno-bacteria act also as catalysts by attracting cations to their negatively charged cell walls. They appear as dense clumps in various minerals and rocks such as limestones, dolomites, native sulphur crystals, and metallic sulfide minerals [50]. Nanno-bacteria produce complex silicates such as clays, where their sizes can be as small as 30 nanometers. They are involved even with the construction of birds' eggs! Nanno-bacteria of size about .1 micro-meters were found in the Martian meteorite ALH84001 [64], and there is evidence that carbonaceous chondrite meteorite Allende [50] contains them. According to Folk, the nanno-bacteria might be the biological counterpart of the dark matter perhaps dominating over the ordinary bio-matter in the entire universe. An interesting question is how deep in the rock nanno-bacteria based life forms can survive. The hypothesis about intra-terrestrial life suggests that there is no limit here!

Although nanno-bacteria have been demonstrated to replicate [50], the prevailing belief has been that nanno-bacteria cannot be real life forms since by their small size they cannot contain the usual genetic apparatus. A Finnish biologist Kajander and his collaborators have done a lot of self-funded pioneering work in the study of the nanno-bacteria [57]. It has not been demonstrated that nanno-bacteria possess DNA-mRNA-amino-acid translation machinery, the existence of which is often taken almost as a definition for what it is to be a living system (a size larger than .2 micro-meters has been the second prevailing definition of a living system!). This failure could be understood if nanno-bacteria contain only replicating DNA or if only the RNA-to-RNA translation machinery exists possibly accompanied by RNA-DNA transcriptase transforming the code to DNA-RNA code. Due to the hard cell wall of nanno-bacteria, the study of DNA/RNA is very difficult but according to the Kajander's private communication to Folk [50], the nanno-bacterial DNA exists and consists of very short strands.

4.6.2 Nanno-bacteria as RNA life?

Nanno-bacteria could correspond to some predecessor of the recent genetic code. One can consider several options.

1. Nanno-bacteria represent an RNA life form involving two kinds of RNA sequences and closed inside RNA_1 membrane. This does not require DNA.
2. If the claim of Kajander about nanno-bacterial DNA is correct, then two options remain.
 - i) Nanno-bacteria are able to just replicate DNA and do not possess genetic code. Thus nanno-bacteria would be at a higher level than viruses.
 - ii) RNA-DNA reverse transcription is utilized so that nanno-bacteria could realize DNA-RNA code and would probably be at a higher developmental level than RNA life-forms but had not yet realized DNA-amino-acid code. The objection against this is that the reverse transcriptase enzyme probably requires RNA-aminoacid translational machinery.

One can ask what what RNA life-forms (option 1) would look if they still exist.

1. Singlet RNA would express itself as RNA sequences containing only U (or C) and A (or G) nucleotides. The tRNAs used by these life-forms should appear as fossil remnants in the ordinary tRNA.
2. In the case of a singlet life-form the layer could correspond to the length scale $L(2, 73) = L(146)$ and be formed by doublet atomic layer corresponding to the twin pair of p-adic length scales formed by $L(16, 9) = L(144)$ and $L(2, 73) = L(146)$.

3. In the case of doublet life-forms the length scale $L(2, 29) = L(145)$ and the tertiary p-adic length scale $L(3, 7^2) = L(147)$ form a twin pair and could define a double-layered structure. The reported hard cell wall could correspond to this double layered structure. A cell wall consisting of minerals (also nanno-bacteria induce also the precipitation of mineral crystals) might however be most appropriate for life-forms living in the pores of rock, and possibly utilizing tectonic energy in some form to satisfy their metabolic needs.

The generation of the triplet code would have been accompanied by the generation of double lipid layers and possibly a transition to water environment. The most natural location for the primitive RNA-RNA translation machinery is at the inner surface of a lipid membrane if present inside nanno-bacteria.

The singlet or doublet RNA life-forms and their fusions could correspond to what I have christened plasmoids. Intelligent looking plasma balls occur repeatedly in UFO reports and they are also reported to occur around crop formations. There is even a report about a plasma ball in the act of constructing the crop formation. The plasmoid like life forms serving as couriers of ITs could be also seen as multicellulars consisting of nanno-bacterial cells or, more probably, of their predecessors. The immune response against nanno-bacteria and their predecessors generated during very early evolution would make possible encounters with crops and even humans (abduction experiences) without fatal consequences. The reported immune response against exotic doublet RNA suggests that plasmoids contain exotic doublet RNA. The visible light from plasmoids suggests that the metabolism indeed involves also the hot $k = 131$ space-time sheet so that ITs or IPs might be in question.

4.6.3 Was the encounter of nanno-bacteria and plasmoids the moment of Gaian fertilization?

Earth consists mostly of ancient meteorites known as chondrites. Carbonaceous chondrites are shown to contain not only basic bio-monomers but even nanno-bacteria. The meteoritic material can end up to the interior of Earth along magnetic flux tubes even today. Recall that this mechanism actually explains the magnetized iron from meteors found in crop circles [N2]).

Thus IT life might have developed nanno-bacteria contained by meteorites in the womb of Mother Gaia. The bio-molecules/nanno-bacteria contained by the meteorites from outer space would thus take the role of the sperm as in panspermia theory.

There is a temptation to develop the fertilization metaphor to a more concrete level in order to understand what happened when the symbiosis of pre-nucleus containing DNA and and pre-cell containing RNA was established and led to the development of the genetic code and established a genuine evolution.

1. The simple nanno-bacteria in the meteorites having only replicating DNA or perhaps only the ability to produce DNA nucleotides would have been the sperm. Cell nucleus is much smaller than cell and might itself be regarded as having originated from ancient nanno-bacteria. The much more complex pre-cells containing RNA, amino-acids, and reverse transcriptase as well as the potentiality for the realization of the genetic code plus the needed metabolic machinery, were located in the interior of Earth and played the role of the egg. Since the hot $k = 131$ space-time sheets essential for the metabolic machinery were also involved, primitive plasmoid is an excellent candidate for the egg.
2. The encounter of nanno-bacteria and plasmoids led to the fertilization of Mother Gaia. What is fascinating that balls of light reported to appear near the crop circles and reported to even fabricate them might be there in order to get fertilized by nanno-bacteria contained by meteors! Alternatively, the simultaneous appearance of pre-biotic egg and sperm might

be interpreted as a symbolic hint about what happened in the key event of the pre-biotic evolution.

5 Did life evolve in the womb of Mother Gaia?

The idea that Earth interior, even the hot regions at the boundary of core and mantle, could serve as a seat for life, sounds totally outlandish in the standard physics framework. The many-sheeted space-time and hierarchy of Planck constants however allow to consider at least half seriously this idea although I hasten to admit that during these years I have very often had the feeling that this is one of those painfully stubborn fix ideas that like to tease imaginative theoretician. This idea has variants characterized by a varying degree of craziness. It is a fact that rocks contain simple life forms down to surprising depths. A crazier idea is that underground lakes could have served as seats for evolving life. The really crazy variant of the idea is that the boundary between mantle and Earth's core as a regions containing strong gradients has been a seat of self organization leading to the emergence of life in some form.

Recently however completely unexpected support for this idea came as I learned that the geological evolution of Earth involves an anomaly. The continents would fit nicely to form a single super continent (Wegener's theory does not predict complete fit) if the radius of Earth would have been at the time of Cambrian explosion by factor of 1/2 smaller than now. The fact that Cambrian explosion is one of the biggies mysteries of biology puts bells ringing. For long time ago this anomaly has inspired what have been called Expanding Earth Theory but the physical mechanism giving rise to expansion has been lacking.

Quantum TGD provides this mechanism. TGD predicts that cosmic expansion does not take place smoothly but via quantum jumps induces by the growth of the Planck constant by a factor of 2 for space-time sheet considered. This holds true also in planetary scales and TGD variant of Expanding Earth theory predicts relatively fast expansion of Earth's radius with a factor 2. The sudden appearance of completely new life forms in Cambrian explosion could be understood as a burst of various multicellular life forms which have developed in the womb of Mother Gaia sheltered from UV light and meteoric bombardment. What remains open is how deep in Earth's interior life is possible. This of course depends also on the definition of life: probably biological life would not be possible at core mantle boundary but one can consider much more general forms of molecular life.

In the following I will proceed in stepwise manner from not totally crazy (I hope so) to really crazy and discuss first the quantum version of Expanding Earth theory and its possible connection with Cambrian explosion and only after consider the really crazy possibilities.

5.1 Quantum version of Expanding Earth theory and Cambrian explosion

TGD predicts that cosmic expansion at the level of individual astrophysical systems does not take place continuously as in classical gravitation but through discrete quantum phase transitions increasing gravitational Planck constant and thus various quantum length and time scales. The reason would be that stationary quantum states for dark matter in astrophysical length scales cannot expand. One would have the analog of atomic physics in cosmic scales. Increases of \hbar by a power of two are favored in these transitions but also other scalings are possible.

This has quite far reaching implications.

1. These periods have a highly unique description in terms of a critical cosmology for the expanding space-time sheet. The expansion is accelerating. The accelerating cosmic expansion

can be assigned to this kind of phase transition in some length scale (TGD Universe is fractal). There is no need to introduce cosmological constant and dark energy would be actually dark matter.

2. The recently observed void which has same size of about 10^8 light years as large voids having galaxies near their boundaries but having an age which is much higher than that of the large voids, would represent one example of jerk-wise expansion.
3. This picture applies also to solar system and planets might be perhaps seen as having once been parts of a more or less connected system, the primordial Sun. The Bohr orbits for inner and outer planets correspond to gravitational Planck constant which is 5 times larger for outer planets. This suggests that the space-time sheet of outer planets has suffered a phase transition increasing the size scale by a factor of 5. Earth can be regarded either as $n=1$ orbit for Planck constant associated with outer planets or $n=5$ orbit for inner planetary system. This might have something to do with the very special position of Earth in planetary system. One could even consider the possibility that both orbits are present as dark matter structures. The phase transition would also explain why $n=1$ and $n=2$ Bohr orbits are absent and one only $n=3,4$, and 5 are present.
4. Also planets should have experienced this kind of phase transitions increasing the radius: the increase by a factor two would be the simplest situation.

The obvious question - that I did not ask - is whether this kind of phase transition might have occurred for Earth and led from a completely granite covered Earth - Pangeia without seas - to the recent Earth. Neither it did not occur to me to check whether there is any support for a rapid expansion of Earth during some period of its history.

Situation changed when my son visited me last Saturday and told me about a Youtube video [31] by Neal Adams, an American comic book and commercial artist who has also produced animations for geologists. We looked the amazing video a couple of times and I looked it again yesterday. The video is very impressive artwork but in the lack of references skeptic probably cannot avoid the feeling that Neal Adams might use his highly developed animation skills to cheat you. I found also a polemic article [32] of Adams but again the references were lacking. Perhaps the reason of polemic tone was that the concrete animation models make the expanding Earth hypothesis very convincing but geologists refuse to consider seriously arguments by a layman without a formal academic background.

5.1.1 The claims of Adams

The basic claims of Adams were following.

1. The radius of Earth has increased during last 185 million years (dinosaurs [112] appeared for about 230 million years ago) by about factor 2. If this is assumed all continents have formed at that time a single super-continent, Pangeia, filling the entire Earth surface rather than only 1/4 of it since the total area would have grown by a factor of 4. The basic argument was that it is very difficult to imagine Earth with 1/4 of surface containing granite and 3/4 covered by basalt. If the initial situation was covering by mere granite -as would look natural- it is very difficult for a believer in thermodynamics to imagine how the granite would have gathered to a single connected continent.
2. Adams claims that Earth has grown by keeping its density constant, rather than expanded, so that the mass of Earth has grown linearly with radius. Gravitational acceleration would have thus doubled and could provide a partial explanation for the disappearance of dinosaurs: it is difficult to cope in evolving environment when you get slower all the time.

3. Most of the sea floor is very young and the areas covered by the youngest basalt are the largest ones. This Adams interprets this by saying that the expansion of Earth is accelerating. The alternative interpretation is that the flow rate of the magma slows down as it recedes from the ridge where it erupts. The upper bound of 185 million years for the age of sea floor requires that the expansion period - if it is already over - lasted about 185 million years after which the flow increasing the area of the sea floor transformed to a convective flow with subduction so that the area is not increasing anymore.
4. The fact that the continents fit together - not only at the Atlantic side - but also at the Pacific side gives strong support for the idea that the entire planet was once covered by the super-continent. After the emergence of subduction theory this evidence as been dismissed.
5. I am not sure whether Adams mentions the following objections [35]. Subduction only occurs on the other side of the subduction zone so that the other side should show evidence of being much older in the case that oceanic subduction zones are in question. This is definitely not the case. This is explained in plate tectonics as a change of the subduction direction. My explanation would be that by the symmetry of the situation both oceanic plates bend down so that this would represent new type of boundary not assumed in the tectonic plate theory.
6. As a master visualizer Adams notices that Africa and South-America do not actually fit together in absence of expansion unless one assumes that these continents have suffered a deformation. Continents are not easily deformable stuff. The assumption of expansion implies a perfect fit of *all* continents without deformation.

Knowing that the devil is in the details, I must admit that these arguments look rather convincing to me and what I learned from Wikipedia articles supports this picture.

5.1.2 The critic of Adams of the subduction mechanism

The prevailing tectonic plate theory [33] has been compared to the Copernican revolution in geology. The theory explains the young age of the seafloor in terms of the decomposition of the lithosphere to tectonic plates and the convective flow of magma to which oceanic tectonic plates participate. The magma emerges from the crests of the mid ocean ridges representing a boundary of two plates and leads to the expansion of sea floor. The variations of the polarity of Earth's magnetic field coded in sea floor provide a strong support for the hypothesis that magma emerges from the crests.

The flow back to would take place at so called oceanic trenches [34] near continents which represent the deepest parts of ocean. This process is known as subduction. In subduction oceanic tectonic plate bends and penetrates below the continental tectonic plate, the material in the oceanic plate gets denser and sinks into the magma. In this manner the oceanic tectonic plate suffers a metamorphosis returning back to the magma: everything which comes from Earth's interior returns back. Subduction mechanism explains elegantly formation of mountains [36] (orogeny), earth quake zones, and associated zones of volcanic activity [38].

Adams is very polemic about the notion of subduction, in particular about the assumption that it generates steady convective cycle. The basic objections of Adams against subduction are following.

1. There are not enough subduction zones to allow a steady situation. According to Adams, the situation resembles that for a flow in a tube which becomes narrower. In a steady situation the flow should accelerate as it approaches subduction zones rather than slow down. Subduction zones should be surrounded by large areas of sea floor with constant age. Just the opposite is suggested by the fact that the youngest portion of sea-floor near the ridges is largest. The

presence of zones at which both ocean plates bend down could improve the situation. Also jamming of the flow could occur so that the thickness of oceanic plate increases with the distance from the eruption ridge. Jamming could increase also the density of the oceanic plate and thus the effectiveness of subduction.

2. There is no clear evidence that subduction has occurred at other planets. The usual defense is that the presence of sea is essential for the subduction mechanism.
3. One can also wonder what is the mechanism that led to the formation of single super continent Pangeia covering 1/4 of Earth's surface. How probable the gathering of all separate continents to form single cluster is? The later events would suggest that just the opposite should have occurred from the beginning.

5.1.3 Expanding Earth theories are not new

After I had decided to check the claims of Adams, the first thing that I learned is that Expanding Earth theory [35], whose existence Adams actually mentions, is by no means new. There are actually many of them.

The general reason why these theories were rejected by the main stream community was the absence of a convincing physical mechanism of expansion or of growth in which the density of Earth remains constant.

1. 1888 Yarkovski postulated some sort of aether absorbed by Earth and transforming to chemical elements (TGD version of aether could be dark matter). 1909 Mantovani postulated thermal expansion but no growth of the Earth's mass.
2. Paul Dirac's idea about changing Planck constant led Pascual Jordan in 1964 to a modification of general relativity predicting slow expansion of planets. The recent measurement of the gravitational constant imply that the upper bound for the relative change of gravitational constant is 10 times too small to produce large enough rate of expansion. Also many other theories have been proposed but they are in general conflict with modern physics.
3. The most modern version of Expanding Earth theory is by Australian geologist Samuel W. Carey. He calculated that in Cambrian period (about 500 million years ago) all continents were stuck together and covered the entire Earth. Deep seas began to evolve then.

5.1.4 Summary of TGD based theory of Expanding Earth

TGD based model differs from the tectonic plate model but allows subduction which cannot imply considerable back-flow of magma. Let us sum up the basic assumptions and implications.

1. The expansion is or was due to a quantum phase transition increasing the value of gravitational Planck constant and forced by the cosmic expansion in the average sense.
2. Tectonic plates do not participate to the expansion and therefore new plate must be formed and the flow of magma from the crests of mid ocean ridges is needed. The decomposition of a single plate covering the entire planet to plates to create the mid ocean ridges is necessary for the generation of new tectonic plate. The decomposition into tectonic plates is thus prediction rather than assumption.
3. The expansion forced the decomposition of Pangeia super-continent covering entire Earth for about 530 million years ago to split into tectonic plates which began to recede as new non-expanding tectonic plate was generated at the ridges creating expanding sea floor. The initiation of the phase transition generated formation of deep seas.

4. The eruption of plasma from the crests of ocean ridges generated oceanic tectonic plates which did not participate to the expansion by density reduction but by growing in size. This led to a reduction of density in the interior of the Earth roughly by a factor 1/8. From the upper bound for the age of the seafloor one can conclude that the period lasted for about 185 million years after which it transformed to convective flow in which the material returned back to the Earth interior. Subduction at continent-ocean floor boundaries and downwards double bending of tectonic plates at the boundaries between two ocean floors were the mechanisms. Thus tectonic plate theory would be more or less the correct description for the recent situation.
5. One can consider the possibility that the subducted tectonic plate does not transform to magma but is fused to the tectonic layer below continent so that it grows to an iceberg like structure. This need not lead to a loss of the successful predictions of plate tectonics explaining the generation of mountains, earthquake zones, zones of volcanic activity, etc...
6. From the video of Adams it becomes clear that the tectonic flow is East-West asymmetric in the sense that the western side is more irregular at large distances from the ocean ridge at the western side. If the magma rotates with slightly lower velocity than the surface of Earth (like liquid in a rotating vessel), the erupting magma would rotate slightly slower than the tectonic plate and asymmetry would be generated.
7. If the planet has not experienced a phase transition increasing the value of Planck constant, there is no need for the decomposition to tectonic plates and one can understand why there is no clear evidence for tectonic plates and subduction in other planets. The conductive flow of magma could occur below this plate and remain invisible.

The biological implications might provide a possibility to test the hypothesis.

1. Great steps of progress in biological evolution are associated with catastrophic geological events generating new evolutionary pressures forcing new solutions to cope in the new situation. Cambrian explosion indeed occurred about 530 years ago (the book "Wonderful Life" of Stephen Gould [114] explains this revolution in detail) and led to the emergence of multicellular creatures, and generated huge number of new life forms living in seas. Later most of them suffered extinction: large number of phylae and groups emerged which are not present nowadays.

Thus Cambrian explosion is completely exceptional as compared to all other dramatic events in the evolution in the sense that it created something totally new rather than only making more complex something which already existed. Gould also emphasizes the failure to identify any great change in the environment as a fundamental puzzle of Cambrian explosion. Cambrian explosion is also regarded in many quantum theories of consciousness (including TGD) as a revolution in the evolution of consciousness: for instance, micro-tubuli emerged at this time. The periods of expansion might be necessary for the emergence of multicellular life forms on planets and the fact that they unavoidably occur sooner or later suggests that also life develops unavoidably.

2. TGD predicts a decrease of the surface gravity by a factor 1/4 during this period. The reduction of the surface gravity would have naturally led to the emergence of dinosaurs 230 million years ago as a response coming 45 million years after the accelerated expansion ceased. Other reasons led then to the decline and eventual catastrophic disappearance of the dinosaurs. The reduction of gravity might have had some gradually increasing effects on the shape of organisms also at microscopic level and manifest itself in the evolution of genome during expansion period.

3. A possibly testable prediction following from angular momentum conservation ($\omega R^2 = \text{constant}$) is that the duration of day has increased gradually and was four times shorter during the Cambrian era. For instance, genetically coded bio-clocks of simple organisms during the expansion period could have followed the increase of the length of day with certain lag or failed to follow it completely. The simplest known circadian clock is that of the prokaryotic cyanobacteria. Recent research has demonstrated that the circadian clock of *Synechococcus elongatus* can be reconstituted in vitro with just the three proteins of their central oscillator. This clock has been shown to sustain a 22 hour rhythm over several days upon the addition of ATP: the rhythm is indeed faster than the circadian rhythm. For humans the average innate circadian rhythm is however 24 hours 11 minutes and thus conforms with the fact that human genome has evolved much later than the expansion ceased.
4. Scientists have found a fossil of a sea scorpion with size of 2.5 meters [125], which has lived for about 10 million years for 400 million years ago in Germany. The gigantic size would conform nicely with the much smaller value of surface gravity at that time. The finding would conform nicely with the much smaller value of surface gravity at that time. Also the emergence of trees could be understood in terms of a gradual growth of the maximum plant size as the surface gravity was reduced. The fact that the oldest known tree fossil is 385 million years old [126] conforms with this picture.

5.1.5 Did intra-terrestrial life burst to the surface of Earth during Cambrian expansion?

Intra-terrestrial hypothesis is one of the craziest TGD inspired ideas about the evolution of life and it is quite possible that in its strongest form the hypothesis is unrealistic. One can however try to find what one obtains from the combination of the IT hypothesis with the idea of pre-Cambrian granite Earth. Could the harsh pre-Cambrian conditions have allowed only intra-terrestrial multi-cellular life? Could the Cambrian explosion correspond to the moment of birth for this life in the very concrete sense that the magma flow brought it into the day-light?

1. Gould emphasizes the mysterious fact that very many life forms of Cambrian explosion looked like final products of a long evolutionary process. Could the eruption of magma from the Earth interior have induced a burst of intra-terrestrial life forms to the Earth's surface? This might make sense: the life forms living at the bottom of sea do not need direct solar light so that they could have had intra-terrestrial origin. It is quite possible that Earth's mantle contained low temperature water pockets, where the complex life forms might have evolved in an environment shielded from meteoric bombardment and UV radiation.
2. Sea water is salty. It is often claimed that the average salt concentration inside cell is that of the primordial sea: I do not know whether this claim can be really justified. If the claim is true, the cellular salt concentration should reflect the salt concentration of the water inside the pockets. The water inside water pockets could have been salty due to the diffusion of the salt from ground but need not have been same as that for the ocean water (higher than for cell interior and for obvious reasons). Indeed, the water in the underground reservoirs in arid regions such as Sahara is salty, which is the reason for why agriculture is absent in these regions. Note also that the cells of marine invertebrates are osmoconformers able to cope with the changing salinity of the environment so that the Cambrian revolutionaries could have survived the change in the salt concentration of environment.
3. What applies to Earth should apply also to other similar planets and Mars [39] is very similar to Earth. The radius is .533 times that for Earth so that after quantum leap doubling the radius and thus Schumann frequency scale (7.8 Hz would be the lowest Schumann frequency)

would be essentially same as for Earth now. Mass is .131 times that for Earth so that surface gravity would be .532 of that for Earth now and would be reduced to .131 meaning quite big dinosaurs! have learned that Mars probably contains large water reservoirs in it's interior and that there is an un-identified source of methane gas usually assigned with the presence of life. Could it be that Mother Mars is pregnant and just waiting for the great quantum leap when it starts to expand and gives rise to a birth of multicellular life forms. Or expressing freely how Bible describes the moment of birth: in the beginning there was only darkness and water and then God said: Let the light come!

To sum up, TGD would provide only the long sought mechanism of expansion and a possible connection with the biological evolution. It would be indeed fascinating if Planck constant changing quantum phase transitions in planetary scale would have profoundly affected the biosphere.

5.2 Did pre-biotic life evolve in mantle-core boundary?

In the sequel this question is taken to mean simple prebiotic life forms preceding the life that possibly developed in underground seas near to the surface of Earth. One can imagine that pre-biotic life moved from high temperature environment in the Earth's interior to the underground seas and charged molecules polymerized in this process and generated gel like phase around them.

5.2.1 Some arguments supporting IT life

The following arguments favor IT hypothesis.

1. Life would have originated already in interstellar space via evolution of primitive metabolic cycles involving temporary chemical storage of metabolic energy. The decay of molecules would have been induced by incoming radiation in UV and visible range and fusion would have occurred spontaneously liberating energy quantum. As stars and planetary systems formed these primordial predecessors of life would have naturally ended into the planetary and even interiors and received their metabolic energy from the hot environment. The dropping of particles, in particular protons and electrons, to large space-time sheets would have provided fundamental metabolic energy quanta, and the anomalies lines in the IR, visible, and UV radiation from interstellar space indeed contains this kind of lines with energies which can be understood in terms of the spectrum of these quanta [J7].
2. Boundary layers are ideal places for self-organization since they contain gradients which give rise to energy currents feeding self-organization. Liquid state is certainly crucial for life since this makes it possible quantum control the atomic space-time sheets very effectively. Ordinary life relies actually on the liquid crystal property of water which suggests that the same is the case quite generally. Thus those parts of the planetary core which correspond to boundary regions between solid and liquid phases and thus analogous to ordered water, could be ideal places for IT life forms to flourish, and it is actually difficult to imagine any other state of matter making possible life able to control the surrounding world effectively.
3. This picture is consistent with and would realize concretely the general vision about magnetosphere as a living system. In Earth's interior the mantle-core and core-inner core boundaries are especially interesting in this respect since these boundaries represent solid liquid boundaries.
4. Mg, Fe, Al, Si, and O are the dominant elements in mantle. Also Ca is present. These are the basic minerals involved with life. Also the minerals believed to be important for the evolution of polymer structures (like kaolinites consisting of Al, Si, and O) could form both

at the hot space-time sheets and atomic space-time sheets. Below mantle-core boundary Fe and S are the prevailing elements. Fe-S centers play a key role in high temperature and pressure models for photosynthesis pathways [58]. The establishment of the photosynthesis has been proposed to occur first in a sulphur containing environment with S replacing O. Inner core contains mainly Fe at hot space-time sheets.

5. A further possibly important aspect is the transparency of the liquid glass state at mantle-core boundary implying that visible light propagates over long distances without absorption. This might be absolutely essential for the possibility of visible photons to propagate through sufficiently long distances. For dark photons situation changes, and the transparency of liquid glass might be due the fact that some fraction of photons propagate as dark photons through it. Hence quartz is transparent in liquid state, and thus an optimal candidate for a medium whose behavior is quantum controlled from larger space-time sheets.
6. Magnetic body means the presence of both magnetic nervous system and the analog of blood circulation which could bring in sufficient amounts of elements needed for the synthesis of bio-polymers. The low concentrations of the elements needed to build up bio-monomers need not be a problem anymore since magnetic Mother Gaia could control them.

5.2.2 Structure of the Earth's interior and IT life

Combining the above described general ideas with the knowledge about Earth interior, one ends up with a more detailed picture.

1. Earth's interior decomposes into a relatively thin crust of thickness 30-60 km; a plastic mantle consisting mainly of Si, O, Mg, Fe, and Al mostly in form of silicates FeO-SiO₂ and MgO-SiO₂; a liquid core containing mainly Fe and S; and the inner core consisting mainly of solid Fe. There are thus two solid-liquid boundary regions. The upper boundary region could contain at least glass in liquid crystal form and the lower boundary region Fe in liquid crystal form.
2. Theoretically, the thickness for the mantle-core layer is expected to be of order few meters. The reflection of tectonic waves from mantle-core boundary has given evidence for a rich structure at this boundary and suggests that this expectation is not quite correct [69]. Structures of thickness about 150 meters and with of several kilometers and between liquid and solid state have been identified at the top of the liquid core. One explanation is that lighter elements in the core-inner core boundary saturate and condense to solid form and being lighter than iron, raise up and form kind of puddles at the highest points of core.

A more radical explanation is that these structures relate to a highly developed self-organization patterns which have given rise to some kind of life-forms. In the mantle-core layer the velocity of tectonic waves gets ultra-low. The velocity of sound in solid phase is quite generally higher than in liquid phase: this reflects directly the fact that the approximately harmonic forces between atoms are stronger. If liquid crystal phase is present the velocity in transversal liquid directions should be low. What is fascinating that sooner or later the analysis of reflected tectonic waves could give detailed information about mantle-core boundary.

3. Earth contains a previously unidentified core region with size of 300 km [26]. Assuming that the magnetic field behaves like a dipole field down to the distances of order 300 km, the electronic cyclotron frequency at this distance is 5 GHz which corresponds to the wave length of about 6 cm, the size scale of BOLs for the dark companion $B_{end} = 2B_E/5$ of B_E . If the magnetization density below this distance is constant (so that the core would be like ordinary magnet), the magnetic field would be constant below this length scale.

Also some other experimental findings support this picture. It has been found that the times for of the compressional waves to travel through Earth in magnetic north-south direction and equatorial direction differ by 2-3 seconds [27]. This suggests a gigantic crystal structure with symmetry axis parallel to magnetic field. If the join along boundaries condensate associated with atomic space-time sheets is hollow with a hole of radius 300 km, and if only $k = 151$ space-time sheet consisting of cold and magnetized iron is at this space-time sheet one can understand the crystal structure and how Earth's magnetic field results by magnetization. The estimated velocity of propagation for compressional waves in the crystal is about 3 km/s which is rather near to the 5 km/s for steel at room temperature. The appearance of a relatively small hole at the atomic space-time sheet is not so surprising since typically the field equations of TGD imply hole like singularities at given space-time sheet, and the hole could be analogous to black hole like singularity carrying inertial and gravitational masses at its boundary.

The simplest hypothesis is that the magnetic field associated with the plasmoids is the Earth's magnetic field in the core region of Earth. This would mean that some kind of plasmoid like life forms could reside also at the boundary layer associated with the new core. If the $k = 151$ space-time sheet is not ferromagnet above the radius $r = 300$ km, the boundary region could be in spin glass type magnetic phase and the bio-control from magnetic flux tubes would operate on the local direction of magnetization of the magnetized regions in the boundary region.

5.3 What conditions can one pose on life at mantle-core boundary?

In the following some conditions on life at high temperatures at pressures are discussed as a mere intellectual exercise certainly not to meant taken deadly seriously. The speculations rely on the ideas which should be already familiar such as presence of strong gradients driving self-organization as indeed found in mantle-core boundary, magnetic bodies as controllers of biological bodies, dark matter as phases with large value of Planck constant able to form macroscopic quantum phases even at high temperatures, and the notion of universal metabolic currencies. Gel-sol phase transitions are also key element in the model of life. The condition that topological quantum computation like information processing based on braids requires existence of some kind of polymers defining braids and consisting of some basic building blocks stable under the conditions in question. The presence of analogs of lipids and cell membranes might be argued to be also necessary.

5.3.1 Plasmoid life as minimum option

The least non-realistic assumption is that IT life corresponds to plasmoid like life forms having magnetic body containing dark matter with large Planck constant controlling visible matter at high temperatures and in plasma phase. Fractality suggests that the high frequency analog of EEG is present and allows magnetic body to use the visible body as a sensory receptor and motor instrument. Frequencies and the values of Planck constant should be such that the energies of dark photons are above thermal energy. General vision about evolution suggests that the values of Planck constant are not very high so that frequency scale should be rather high.

1. Only biologically important ions and relatively simple molecules are expected to be present. Primitive metabolic cycles based on the fusion and decay of molecules induced by the radiation coming from environment can be considered. Cyclotron Bose-Einstein condensates of ions at magnetic flux tubes correspond to energies above thermal threshold only if the magnetic field is strong enough.
2. At temperature of about 4000 K at mantle core interior hydrogen bonds are still stable and metabolic energy quantum of $E_0 = .5$ eV is near thermal energy. There exists of course other metabolic quanta coming as power of two multiples of this quantum. Hence one can

assumes that the dropping of protons and possibly of electrons from larger space-time sheets is responsible for metabolic energy quanta also now. One might argue that the typical p-adic length scale associated with the space-time sheets corresponds to the de-Broglie wavelength $\lambda_{dB} = \sqrt{3\hbar}/\sqrt{2mT}$ associated with electron. For electron this wavelength is around 35 slightly below $L(149) = 50$ A defining the thickness of the lipid layer of ordinary cell membrane. This scale increases with increasing \hbar .

3. Dark micro-waves amplified by quartz crystals might be crucial for the metabolism of plasmod life-forms and replace visible light serving as the "food" of the terrestrial life forms. Tectonic activity might be as important for these life-forms as solar radiation is for us. The crust and mantle could serve as amplifiers of em waves in a wide wave length range and make possible communications between IT and us.

5.3.2 Could topological quantum computation like activities be considered?

Could even more advanced life forms have evolved in the environment provided by mantle-core boundary? The presence of magnetic body makes possible braidings and simple versions for the mechanisms of memory, of topological quantum computation like information processing, and of catalysis. The presence of braids could be taken almost as a basic prerequisite of life. The presence of polymers of some basic molecules seems necessary if one wants something resembling DNA as tqc.

1. The presence of polymers consisting of some thermally stable basic units is the basic requirement. Hydrocarbons, lipids, aminoacids, and nucleotide polymers are not chemically stable at temperatures considered and mantle contains carbon only in trace amounts. The dominating elements in mantle are *O*, *Si*, and *Mg* whereas *C* is present only in trace amounts. *S* is present in core and thus also in mantle-core boundary. *P* is so called siderophilic element meaning that it tends to avoid *Si*. It is theorized that during the formation of Earth from magma ocean siderophilic elements including *P* separated from the mantle and went to core. In [42] ratio of concentrations of *P* in core and mantle was estimated to be $D(P) = 30$ but the article does not report the concentration of *P* on mantle. In [43] the phosphorus content of upper mantle is reported to be in the range 130-220 ppm which would give 3-7 percent in core. One can also imagine a formation of phosphate deposits in mantle core boundary: in absence of oxygen these kind of deposits are formed at sea floor. This kind of deposits might have formed at the top of the solid structures reported to exist at mantle core boundary [69]. These structures could themselves have formed as light elements from inner core has gradually diffused to the mantle core boundary and could include phosphate deposits. If so then mantle-core boundary could contain considerable amounts of *P* and the replacement *C, N, O* with *Si, P, O* or *Si, P, S* might make sense.
2. Water flow is not the only flow which could generate the self-organization patterns defining braidings as the analogs of tqc programs. Since *O* dominates in mantle water is however the first guess. It is known that lower mantle can contain water at least up to .2 weight per cent [41]. Water molecules are stable at the temperatures considered. The phase diagram of water [21] shows that water is in overcritical phase in the temperatures and pressures considered: 4000 K and 1.4 million atm and at the bottom of the mantle.
3. The replacement of *O* with *S* might be considered in the mantle-core boundary since *S* is present in liquid core. Water would be replaced with hydrogen sulfide H_2S (responsible for the smell of rotten eggs!) if it appears in liquid form H_2S at temperatures and pressures considered. H_2S could be also used as food. H_2S is used by some bacteria living in deep ocean volcanic vents as a nutrient and also in our own gut: chemically this means that H_2S

acts as electron donor in primitive photosynthesis like process to give ATP. That sulphur is essential for growth and physical functioning of plants might be due to the fact that it preceded oxygen based life [44]. For instance, Cys and met containing sulphur are very important amino-acids.

4. The polymers should contain atoms acting as plugs for flux tubes acceptors flux tubes ($O =$ or $S =$) and terminal points of flux tubes identifiable as donors of hydrogen bonds. $S - H$ shows only very weak tendency for hydrogen bonding so that Si, P, O option looks more promising and is of course especially natural if IT life forms are considered. For instance, silicic acids [40] satisfying the formula $[SiO_x(OH)_{4-2x}]_n$ are candidates for polymers containing both $O =:s$ and $OH:s$. The presence of PO_4 could have made possible the formation simple analogs of nucleotides and AMP, ADP, and ATP molecules. It might be possible to abstract nucleotides with a polymer consisting of four different simple molecules which are phosphorylated and attached to the backbone made of sugars.
5. One can continue the analogy with carbon life even further. The backbone could consist of the variants of riboses with carbon cycles replaced with Si cycles, the variants of aromatic rings with C and N replaced with P , and base pairing between $N - H$ and $O =$ replaced with $P - H$ and $O =$. In the case of amino-acids one can also consider the replacement of $C, N \rightarrow Si, P$. It is of course far from obvious that the possibly existing silicon analogs of organic polymers are stable enough against rapid burning to SiO_2 and water. One might hope that the higher mass of Si stabilizes them chemically at temperatures involved. Professional chemist could probably kill this kind of ideas without big effort.

Could one consider analogs of cell membrane and gel phase crucial for cellular life?

1. The first guess would be that gel like phase might have emerged only after these plasmoid like life-forms came in contact with water and induced the generation of structure water in presence of metabolic energy feed. On the other hand, it could well be that structured dater might form around charged polymers also at high temperatures and pressures as in the case of ordinary cell. Also silica (SiO_2) is known to form a gel. Also glass consists of SiO_2 : the transparency of glass to visible light might be also relevant. A group of algae polymerize silicic acid to so called biogenic silica used to construct their cell walls.
2. Lipids forming cell membrane would be replaced with structures consisting of hydrosilicons with the silicon analog of carbon residue as its hydrophilic head and silicon analog of the hydrophobic fat forming the tail of the lipid. The formation of these double layers would be an outcome of self-organization. The analogs of phospholipids having PO_4 at their hydrophilic tail would be needed for tqc.
3. Super-conductivity plays an essential role in the TGD based model for cell membrane. Large enough values of Planck constant in principle allow to have super-conductivity at magnetic flux tubes.
4. The requirement that the energy $E = ZeV$ associated with Josephson junctions over the cell membrane like structure is above thermal energy requires very strong electric field over the membrane unless the membrane is thick. In the case of ordinary cell membrane the energy is rather near to thermal energy at room temperature. Now the energy would be roughly ten times higher and correspond to about .5 eV. Whether this kind of strong electric field is realizable is not clear. One might hope that the densities of ions could be high enough in the dense environment.

5.3.3 Do metabolism and photosynthesis possess signatures telling about intra-terrestrial evolution?

Also the intra-terrestrial metabolism should rely on atomic/molecular "Karma's cycles". Assume that the protons and electrons can be modeled as free particles in box. This assumption might not be correct as the model for ATP-ADP involving Coulomb binding energy of proton with negatively charge ATP molecule reducing the size of metabolic energy quantum already demonstrated. In this case the wavelength would be roughly by a factor 1/2 longer than predicted meaning Coulombic binding energy of order .25 eV.

In any case, with this assumption the quanta saturating to $E_{max}(k) = [.5, 1, 2, 4, 8, 16]$ eV and wavelengths $\lambda_{min} = [1240, 620, 310, 155]$ nm could have been important. The maximal quanta $E_0(k)$ correspond to the dropping from space-time sheet labeled by $k = 137 - \Delta k$ (in the case of proton) to a very large space-time sheet. The size of the space-time sheets would be given by $L(k) = r \times 2^{(k-151)/2} \times L(151)$, $L(151) = 10$ nm and $r = \hbar/\hbar_0$ the ratio of the Planck constant in question to its standard value. Actually and entire spectrum of quanta given by the formula $E_n = (1 - 2^{-n})E_0(k)$ saturating to $E_0(k)$ for large values of n . In [J7] the presence of unidentified lines in the spectrum of UV, visible, and IR radiation from interstellar space has been shown to have a satisfactory explanation in terms of universal metabolic energy quanta.

The spectrum of diffuse interstellar medium exhibits three poorly understood structures [28]: Unidentified Infrared Bands (UIBs), Diffuse Interstellar Bands (DIBs) [29], and Extended Red Emission (ERE) [30] allowing an interpretation in terms of dropping of protons or electrons (or their Cooper pairs) to larger space-time sheets. The model also suggests the interpretation of bio-photons in terms of generalizes EREs.

1. Unidentified infrared bands (UIBs) contain strong bands at $\lambda = 3300, 6200, 11, 300$ nm. Th
2. There are diffuse interstellar bands (DIBs) at wavelengths 578.0 and 579.7 nanometers and also at 628.4, 661.4 and 443.0 nm. The 443.0 nm DIB is particularly broad at about 1.2 nm across - typical intrinsic stellar absorption features are 0.1 nm [28].
3. The Extended Red Emission (ERE) [28, 30] is a broad unstructured emission band with width about 80 nm and located between 540 and 900 nm. The large variety of peak wavelength of the band is its characteristic feature. In majority of cases the peak is observed in the range 650-750 nm but also the range 610-750 nm appears. This general vision can be compared with experimental facts.

The generalization ontogeny recapitulates phylogeny principle would suggest that the recent metabolism should have some features serving as telltale signatures of the IT past. The IT past could in turn reflect the primordial evolution in interstellar dust. The signatures of this period would be maxima of the action spectrum for wavelengths which correspond to both the universal metabolic energy quanta and transition energies for transitions of simple molecules present in the molecular dust. Visible and UV range are the most promising regions to consider.

1. There are two wave lengths of maximal effectiveness in the photosynthesis of plants and these correspond to what are called photo-system I and II (see p. 287 of [60]). Photo-system I is maximally activated at $\lambda = 680$ nm, corresponds to the chlorophyll a, and is not involved with the oxygen evolution. $k = 136$ corresponds to wavelength saturating to $\lambda_{min} = 620$ nm (1 eV). The model of ATP-ADP process suggests that Coulombic binding energy is increases the wavelength.
2. Photo-system II is activated by shorter wave lengths and maximum effectiveness is between 500-600 nm. Photo-system II utilizes second type of chlorophyll (b, c or d) plus some accessory pigments. All photosynthetic cells producing oxygen possess both photo-systems

whereas bacteria which do not produce oxygen have only the photo-system I. Hence at least the photo-system I might derive from a very early intra-terrestrial period. The spectrum of metabolic energy quanta for $k = 135$ corresponds to the wave length range [620,413,354,...,310] nm. Coulombic binding energy could increase the wavelength from the 413 nm for $k = 135$ and $n = 2$.

3. The action and absorption spectra of green alga *Ulva Taeniata*, see p. 284 of [60], have besides 680 nm maximum also a broad maximum in the range 400-500 nm peaked around 430 nm. The action spectrum has also a shoulder like structure around 600 nm. For $k = 135$ the first peak could correspond to $n = 1$ (620 nm) and second peak $n = 2$ (412 nm).
4. For some bacteria encountered in hot springs [74] the effective wave length range is in the near infrared range 700-1000 nm rather than in the range of visible frequencies dominating the sunlight. This looks strange since in general the evolution favors maximal metabolic economy. This leads to ask whether these bacteria might be kind of living fossils evolved in an intra-terrestrial environment. This range of wavelength corresponds in a reasonable approximation to that obtained by scaling the wave length range 400-500 nm in previous case and thus to $k = 136$.
5. DNA bases (A, G, T, C) strongly absorb UV light at around 260 nm. For $k = 16$ the nearest metabolic energy quanta correspond to $n = 2$ and $n = 3$ giving wavelengths 310 nm and 207 nm. For proton the p-adic length scale is below atomic size for $\hbar/\hbar_0 \geq 16$.

5.4 What about analogs of EEG?

It looks strange to mention EEG if one speaks about primordial life forms. These analogs of EEG have of course nothing to do with brains. The prediction is that the fractally scaled counterparts of EEG (in loose sense of course) provide the fundamental communication and control tool for the magnetic body. This analog of EEG is determined by the cyclotron energy spectrum nE_c of biologically important ions scaling like \hbar and by the characteristic energy $E_J = ZeV$ associated with Josephson junctions assignable to membrane like structures and having no dependence on \hbar . The energies nE_c and the differences $nE_c \pm E_J$ define the harmonics of bands and their satellites. Alpha band corresponds to E_c and beta and theta bands to differences in the case of ordinary EEG.

5.4.1 Conditions from the thermal stability of the analog of EEG

The analogs of EEG and its scaled up variants are in a fundamental role in the control of biological body by magnetic body and this should hold true also for ITs. According to the model of EEG resulting as a special case of the model for the fractal hierarchy of EEGs and its generalizations [M3], the analog of EEG involves two components.

1. Cyclotron component

The first component corresponds to the harmonics of cyclotron frequencies of biologically important ions: many of them belong to the alpha band in the case of ordinary ions.

Since 10 Hz corresponds to a secondary p-adic time scale assignable to electron defining an inherent time scale of elementary particle in zero energy ontology, one can ask whether this frequency means breakdown of the fractality hypothesis and raises the frequency scale of ordinary EEG in special role. One can also wonder whether 10 Hz frequency could define a universal biorhythm.

Dark ions reside at magnetic flux sheets traversing DNA and cyclotron radiation affects directly DNA. Cyclotron frequencies are associated with motor control affecting directly DNA and inducing

gene expression among other things. The models leads naturally to the introduction of the notions of super DNA and hyper DNA [M3].

2. Josephson junction component

Josephson junctions associated with cell membrane define second contribution to EEG as frequencies associated with coherent state of photons emitted by Josephson current. This component is present only if Josephson junctions, naturally assignable with a membrane like structure separating the plasmoid from environment, are present.

The frequencies are expressible as $f_{n,\pm} = nf_c \pm f_J$ and in the case of ordinary EEG alpha band and its harmonics split into counterparts of beta and theta band. Alpha band has scaled variant also in more general case and corresponds to ions which define alpha band for ordinary ions.

1. The essential condition is that cyclotron energy scale is above the thermal energy. This fixes the minimal value of the integer k_{em} characterizing the level of dark matter hierarchy involved. For ordinary EEG frequencies the minimal value of k_{em} is $k_{em} = 4$. DNA cyclotron frequencies assuming that the charge of DNA is solely due to the phosphate groups PO_4^{2-} is around 1 Hz and just above the thermal threshold. The thermal stability of DNA cyclotron frequencies is satisfied if the ratio of the cyclotron energy to thermal energy is not smaller than one. Hence the ratio B/T cannot be smaller than at the surface of Earth unless $k_{em} = 5$ is assumed.
2. Second condition is that Josephson energy determined by the membrane voltage is above thermal energy. The minimum condition is that membrane voltage scales up as $V/V_{room} = T/T_{room}$.

Josephson frequency f_J would scale as

$$f_J = \frac{T}{T_{room}} \times f_{J,room} ,$$

where $f_{J,room} \simeq 5$ Hz holds true. Alpha band and its harmonics and also the widths of theta and beta bands would scale like B . The positions of theta and beta bands would scale like temperature, and one would have the formula

$$f_{n,\pm} = \frac{B}{B_E} nf_c \pm \frac{T}{T_{room}} f_J$$

for the frequencies in the generalized beta and theta bands, when $k_{em} = 4$ holds true also in the high- T environment.

It is illustrative to consider some examples.

1. Mantle-core boundary

The temperature is $T = 4000$ K $\sim 13T_{room}$ at the mantle-core boundary. This temperature allows simple ordinary molecules like carbon monoxide and water (due to the high pressure).

2. Sunspots

The average temperature of the solar photosphere is about 5800 K whereas the minimum temperature is $T_{min} = 4000$ K and same as the temperature at mantle-core boundary. Inside sunspots the temperature varies in the range 3000-4800 K and sunspots, which are analogous to tornadoes, would be good candidates for the seats of solar life forms. Spectral analysis demonstrates the presence of water inside sunspots [123]. There is also evidence for a solid calcium ferrite surface at photosphere [124].

The value of the sunspot magnetic field is between 1600-2500 Gauss and thus cyclotron frequency is about 3200 – 5000 times higher than at the surface of Earth. Also in this case

$k_{em} = 4$ level would correspond to thermally stable "EEG" photons with frequencies in the range of ordinary EEG.

5.4.2 What could the analog of EEG for IT look like?

In the following estimates for cyclotron frequencies are for the possibly existing dark companion $B_{end} = 2B_E/5$ of the Earth's magnetic field for which the effects of ELF fields on vertebrate brain provide a direct support.

If the sensory representations of IT life-forms are realized at the personal magnetic canvas and at magnetosphere in the same manner as ours, the cyclotron frequency of the representing ion at distance r_1 is must be same as the cyclotron frequency of the represented ion at distance r_0 . Assuming that magnetic field strength scales like $1/r^3$, this gives cyclotron transitions at the distance of about

$$r_1(A) = (A/A_1)^{1/3} \times r_0 \ ,$$

giving

$$y(A, A_1) = (A/A_1)^{1/3} \times x \ .$$

Here $r_0 = xR$ is the radius associated with the life-form, and $r_1 = yR$ is the distance at which the sensory representation is realized. R denotes the radius of Earth and A the mass of the ion at r_0 associated with IT cyclotron transition and A_1 the mass of the ion at r_1 defining the cyclotron transitions associated with the sensory representation.

If the most important frequencies of generalized EEG correspond to cyclotron frequencies, if prebiotic live resides at the mantle-core and core-inner core boundaries, and if the magnetic field inside Earth behaves as dipole field in a reasonable approximation, one can deduce the EEG frequency range of aliens by scaling the human frequency range by the ratio

$$x^{-3} = \left(\frac{R}{r}\right)^3 = \left[\frac{f_S(r)}{f_S(R)}\right]^3 \ ,$$

where r is the distance of the boundary region from the center of the Earth. The constraint that representation is realized in inner magnetosphere gives the bound $y \leq 6$ and the constraint that it is realized in ionosphere gives $y \simeq 1$.

1. Biosphere

In this case the basic equation is obtained by putting $x = 1$ in the general equation so that one has

$$y = \left(\frac{A}{A_1}\right)^{1/3} \ .$$

For protonic representations with $A_1 = 1$ possible in entire inner magnetosphere the constraint $y \leq 6$ allows all possible values of A .

2. Mantle-core boundary

For mantle-core boundary the ratio is roughly $x^{-3} = 7.1$ so that the EEG frequency range 1.5 – 90 Hz scales up to 107 – 639 Hz. Sensory representations can in this case be realized as ionic transitions in atmosphere. The basic equation is

$$y = \left(\frac{A}{A_1}\right)^{1/3} x \ ,$$

where A is the mass number of the ion in mantle-core boundary and A_1 is the mass number of representative ion. For protonic representation one has

$$y = 1.92A^{1/3} .$$

The condition $y \leq 6$ guarantees that representation is realized in the inner magnetosphere and gives $A \leq 27$. This corresponds in ordinary EEG to frequencies $f \geq 11$ Hz. For $A_1 > 1$ also scaled up variants of alpha and theta frequencies are representable: note however that the densities of these ions are probably much smaller than in ionosphere.

One can consider also ionospheric ion representations satisfying $y \simeq 1$ for mantle-core boundary. Now the mass numbers of the ions involved are related by

$$\frac{A}{A_1} \simeq x^{-3} \simeq 7.1 .$$

The biologically most interesting ions have $A > 7$ and are representable. One manner to realize this sensory representation is using cells or brains of various organisms and one might consider the possibility that we actually are life-forms which have developed as magnetospheric sensory representations of the life-forms at the mantle-core boundary.

3. Core-inner core boundary

For core-inner core boundary the ratio is roughly $x^{-3} = 263$ for $f_S(r) = 50$ Hz and $x^{-3} = 135$ for $f_S(r) = 40$ Hz. In this case only electronic sensory representations are possible and one has

$$y = \left(\frac{Am_p}{m_e}\right)^{1/3} x ,$$

1. For $x^{-3} = 263$ this gives

$$y \simeq 1.98 \times A^{1/3} .$$

The range $[1, 6]$ for y corresponds to the inner magnetosphere and the upper bound $A \leq 27$ and to scaled up variants of cyclotron frequencies above 11 Hz in ordinary EEG. Only beta and gamma bands would be represented.

2. For $x^{-3} = 135$

$$y \simeq 2.48 \times A^{1/3}$$

The upper bound for A is $A \leq 14$ and to the scaled up variants of cyclotron frequencies above ~ 20 Hz in ordinary EEG.

4. Inner core-most inner core boundary

The boundary of the most inner core of radius 300 km could also be carrier of life-forms, perhaps plasmoid like life-forms. The simplest hypothesis is that the magnetic field associated with the plasmoids is the Earth's magnetic field in the core region of Earth, which would be constant and of order .2 Tesla below this distance if dipole approximation makes sense.

If important "EEG" frequencies correspond to cyclotron frequencies, part of the "EEG" would be scaled up by a factor $2^{169-157} = 2^{12} \simeq 4000$ so that EEG frequency range .25 – 90 Hz would be mapped to 1 – 360 kHz. Ionic cyclotron frequencies would be in the MHz range with proton cyclotron frequency equal to 1.2 MHz. The cavity resonance frequency analogous to the lowest Schumann frequency for a structure with radius 300 km is 159 Hz.

If the sensory representations of IT life-forms possibly existing at $r_0 = 300$ kilometers are realized as electronic cyclotron transitions one has

$$y \simeq .59 \times A^{1/3} .$$

Ions with $A \geq 6$ would be represented above Earth's surface. All ionic representations would be realized in Earth's interior.

6 Comparison of McFadden's views with TGD

In his book Quantum Evolution [62] Johnjoe McFadden discusses the deep problems of molecular biology from quantum point of view and develops very interesting ideas about evolution and consciousness. Because of deep insights about what is not understood in biology, this discussion should provide new insights for any quantum consciousness theorist attempting to build a bridge between theory and biological reality. In the sequel McFadden's vision is compared with TGD view and some new ideas inspired by it in TGD framework are proposed.

6.1 General ideas

Before dwelling into concrete examples, it is good to compare McFadden's general starting points with those of TGD.

1. In accordance with most interpretations of quantum mechanics, McFadden assumes that the initial situation involved no de-coherence and that the biological evolution means basically the emergence of de-coherence, essentially the appearance of conscious observers performing quantum measurements.

In TGD framework the situation is just the opposite: evolution means the emergence of effective macro-temporal quantum coherence meaning that the duration of sharp mental images (sub-selves) increased. During the primordial stage typical lifetime of self was of order 10^4 Planck times and defined minimal de-coherence time. Dark matter hierarchy provides a hierarchy of Planck constants a concrete realization for a hierarchy of moments of consciousness with increasing geometric duration and quantum parallel dissipation which is second new element of TGD picture.

The number theoretic generalization of Shannon entropy having negative values for rational and even algebraic entanglement is a further mathematical concept. Quantum computers are basic examples of systems possessing positive number theoretic negentropy, and this certainly conforms with the genuine information content of multi-verse states. It is not clear whether Negentropy Maximization is really consistent with the Second Law of thermodynamics and one must keep mind open for the possibility that Second Law is illusion created by the neglect of dark matter hierarchy meaning at the same time neglect of living life forms.

2. McFadden does not fix his views about quantum measurement theory but assumes that de-coherence is an outcome of quantum measurements performed by environment or some subsystem of it. McFadden sees enzymatic action as a basic example of quantum measurement in which an amplification to a macroscopic phenomenon occurs.

In TGD framework one can imagine two basic elements.

- i) The emergence of symbolic representations as names of molecules made possible lock and key mechanism and "molecular sex". Once it is possible to name molecules, it becomes possible to regard bio-chemical pathways as analogs of computer programs proceeding rather

deterministically. As already found, this idea has very concrete implications for understanding of bio-catalysis.

ii) The most important bio-molecules could be seen as selves with especially long wake-up periods in a highly negentropic state of macro-temporal quantum coherence, and able to perform intentional actions applying the time mirror mechanism. The magnetic bodies of bio-structures are at the top of the intentional hierarchy.

3. McFadden sees quantum Zeno effect and its inverse as basic quantum control tools used by enzymes to increase reaction rates or induce mutations. Although the Zeno effect has also TGD counterpart, the intentional action of molecular magnetic bodies based on time mirror mechanism seems a more plausible option. Long ranged dark weak forces, in particular charge entanglement by W MEs, exotic ionization, and the control of the strength of the screening of the classical Z^0 force provides an additional mechanisms of enzyme control explaining chiral selection. Sol-gel transition inducing polymerization and its reverse allows to control the stability of bio-polymers. The leakage of particles between space-time sheets is a further control mechanism and involved with the time mirror mechanism.
4. McFadden assumes that the superpositions of peptide-environment product states involving different peptides with different neutron and proton numbers are possible so that the measurement involves also measurement of proton and neutron numbers. This option looks implausible because it is very difficult to think that states with different fermion numbers, masses, and charges would quantum superpose.

In fact, it has become clear quite recently that TGD could in well-defined sense allow also quantum superpositions of different DNA molecules. This kind of superpositions are routinely assumed for coherent states of Cooper pairs in super-conductivity although they break conservation of charge, fermion number, and energy. The point is that in zero energy ontology [C3] the total quantum numbers of physical states always vanish and the states decompose into positive energy part such that negative energy part located in its geometry future. Therefore it is possible to have quantum superpositions which in positive energy ontology, which is excellent approximation, would look like quantum superpositions of different DNA molecules. This possibility is not discussed in this chapter but it is needless to say that it could mean a revolution in the understanding of living matter. Even thermodynamics could be interpreted in a completely new manner since thermodynamical states which are "superpositions" of states with different values of conserved charged could have genuine quantal counterparts.

6.1.1 McFadden's view about biochemistry

McFadden represents a very general view about the essentials of bio-chemistry.

1. Protons associated with hydrogen bonds and electronic Cooper pairs serve as basic tools of quantum bio-control.
2. The localization of proton induces what McFadden interprets as a quantum measurement of proton's position.

In TGD framework the mechanism of catalytic action based on the temporary dropping of proton from the H_N -atom associated with catalyst or reactant, replaces this mechanism. Catalytic action could be seen as a short lasting period of "group sex" between catalyst and reacting molecules. Liberation of standard metabolic energy quantum is automatically involved with the process.

6.1.2 Important problems of quantum biology

The following list provides examples of problems that McFadden wants to understand in terms of quantum physics.

1. The extreme effectiveness of enzyme action.
2. The mechanism of mutations, in particular that of adaptive mutations and multiple mutations.
3. Evolution.
 - i) The loss of complexity in computational models of evolution contra the increase of complexity in real evolution.
 - ii) The emergence of the first self replicators.
 - iii) The evolution of extremely complex reaction pathways, such as the one leading to the buildup of the ATPase enzyme.

6.2 Enzyme action

Enzymes as quantum mouse traps is the metaphor introduced by McFadden. Typically enzyme catches the reactant molecules to a fixed conformation and fires a proton to the substrate molecule inducing in this manner a re-organization of some chemical bonds. The enzyme gains the lost proton later from a water molecule.

Mouse trap metaphor conforms completely with the TGD described view about catalytic action and also with the idea about enzyme as a quantum critical system.

1. *Production of lactic acid from pyruvate*

McFadden represents the production of the lactic acid from pyruvate, which is one of the last steps of catabolism, as a typical example of enzyme action. The process involves LDH, lactate dehydrogenase, catalyzing the transformation of the pyruvate to lactic acid, and NADH providing a proton and an electron pair. LDH donates the proton involved with the transformation of C=O to C-O-H. NADH in turn provides proton and electron pair so that C=O is replaced with H-C-OH. NAD⁺ receives proton and a compensating electron pair from water and LDH₋ receives a proton from a water molecule.

2. *Catabolism of lactose*

Second example used by McFadden relates to the catabolism of lactose induced by the enzyme beta galactose. The rate of the process is trillion times higher than one might expect. McFadden proposes that the process involves a localization of proton in certain amino-acid of the beta galactose to a particular hydrogen bond. If the localization occurs to a correct hydrogen bond, the proton is injected to the lactose molecule and induces hydration. The suggestion is that a repeated quantum measurement of proton's position in beta galactose keeps the proton in the correct position so that the decay occurs with a much higher rate than it would occur otherwise.

It is not necessary to repeat how the catalysis could be understood in TGD framework. The decay of the lactose involves hydrolysis in which lactose molecule receives water H_N-O-H molecule from the environment and the loss of proton destabilizes the negatively charged molecule.

Hydrolysis could involve local gel-sol type transition transforming ordered water to ordinary water, which is able to provide the needed water molecule. The gel-sol transition could closely correlate with the non-standard localization of the proton inside enzyme. The process could involve an intentional action of a magnetic body of some system involved and thus negative energy topological light rays and charge entanglement by *W* MEs.

6.3 Quantum evolution

McFadden considers evolution from a quantum point of view. After the criticism of the RNA world paradigm McFadden poses several questions. How complexity could have emerged during the evolution? What was the first self-replicator? How the complex metabolic pathways could have evolved? What might be the quantum mechanisms of adapted and multiple mutations?

6.3.1 How evolution can create complexity?

McFadden pays attention to the fact that in the computational models of evolution final states tend to be less complex than the initial ones. This can be seen as a consequence of dissipation which leads to asymptotic self-organization patterns which are very simple. This is just the opposite of what is observed in Nature (note however the fact that the rapid extinction of new species after Cambrian explosion might be interpreted in terms of a loss of complexity).

In TGD framework the ability of living systems to circumvent the loss of complexity is due the facts that TGD Universe is quantum critical and p-adic cognition implies p-adic evolution predicting the emergence of systems characterized by increasing values of the p-adic prime and the integer characterizing the levels of dark matter hierarchy serving as their "intelligence quotients".

At the molecular level TGD allows to resolve this puzzle elegantly. During the pre-biotic exotic RNA period the predecessor of the genetic code is realized as many-to-one replication of exotic RNAs meaning a loss of information. This occurred for both singlet and doublet exotic RNA and for their composite forming a double helix with the size of the singlet helix being scaled up by a factor two. This however led to a dead alley involving only the RNAs representing the maximal invariant set of the RNA→RNA mapping as an asymptotic state. Final state was indeed simpler than the initial state.

At some stage the product code transformed to a code coding for RNA triplets, and amino-acids which originally catalyzed the mapping of RNA to RNA, took the role of the coded molecules. RNAs were mapped to DNAs by reverse transcriptase and the high error rate of the reverse transcription implied a rapid mutational rate. The many-to-one character of RNA→RNA replication implying the dead alley thus transformed from a curse to a blessing since it represented implicitly the protein-DNA genetic code.

6.3.2 Criticism of RNA world

McFadden represents severe critics against RNA world paradigm which is the dominating vision about pre-biotic evolution [54]. The basic objections are following.

1. In water environment bio-polymers become un-stable against depolymerization by hydration. This makes the idea of primordial sea implausible. The presence of the ordered water could resolve this problem even in the standard physics based models. In many-sheeted space-time the hypothesis that pre-biotic evolution occurred intra-terrestrially in the womb of the magnetic Mother Gaia makes sense and could resolve basic objections against the notion primordial sea.
2. Enzymatic action requires chiral selection. In TGD framework this can be interpreted as a strong indication for the necessity of the classical long ranged weak forces in the enzymatic control (say charge entanglement by W MEs).
3. McFadden lists several reasons for why RNA is implausible as a pre-biotic chemical. RNA consists of three components: RNA base, ribose, and phosphate. RNA bases and phosphate have been generated in the experiments trying to simulate pre-biotic evolution but the spontaneous emergence of ribose looks implausible. The problem is that a plethora of other sugars are produced.

Some property of ribose should distinguish it from the other sugars. In TGD framework one might argue that for the ribose self "wake-up" periods or even periods of macro-temporal quantum coherence meaning sharp and non-entropic mental images are longer than for the other sugars. Quite generally, important bio-molecules could be identified as maximally autonomous systems able to "stay awake" and realize intentions.

A more concrete explanation is based on stability.

- i) Both RNA, DNA and aminoacids are negatively charged and thus inherently unstable. The assignment of "names" to generalized hydrogen bonds represented by quark and antiquark at the ends of the magnetic flux tube to the basic building bricks of these polymers could make them stable and lead automatically to highly selective catalytic actions.
 - ii) Suppose that the OH groups associated with the sugars have tendency to form a hydrogen bond with water molecules leading to ionization of the water molecule and liberation of proton dropping to a larger space-time sheet so that the polymer generates negative charge. If the number of O-H groups is too large the resulting negative charge can destabilize polymers formed by ribose, phosphate, and RNA nucleotides. Note that also the formation of double strand a liberates one proton per hydrogen bond which has a further de-stabilizing effect. This could explain why RNA with 4 O-H groups forms only short double strands whereas DNA having only 3 O-H groups forms very long double strands.
4. One can also wonder why just phosphate, ribose and RNA bases find each other and why the large number of other combinations are not realized. The naming based on flux tubes would restrict dramatically the possible combinations able to form spatially and temporally coherent systems bound together by flux tubes and automatically lead to a final state in which molecules having no braids with environment disappear from the system. Phosphate, ribose and RNA base could also find each other by tuning to common wave length by sending negative energy MEs entangling them with each other.
 5. The presence of RNA bases, phosphate and ribose is not enough. McFadden finds it difficult to understand why only RNA molecules amongst many other reaction products of its three basic components are selected. In laboratory the activation of the RNA base allows to select RNA as a dominant reaction product. One possibility is that the liberation of activation energy helps to overcome the potential wall hindering the formation of RNA. This is could also due to the fact that the bound states of the activated RNA base with other two components are short-lived or decay to RNA in accordance with the idea RNA selves have especially long wake-up periods and is winner in the fight for survival. Magnetic body could be able to intentionally activate the RNA bases using universal metabolism present even without ATPase machinery.
 6. In the laboratory isolation, purification, and channeling of the reactants to the reaction volume are crucial parts of the process producing RNA and ribozymes, and almost-self-replicators. In the conventional chemistry framework it is very difficult to imagine how these processes could have occurred during pre-biotic evolution.

The notion of magnetic body might come in rescue. Magnetic flux quanta could make possible highly controlled reaction network. A possible concrete toy model goes as follows. Suppose that quantum-classical correspondence holds true in the sense that the shape of the magnetic flux tube containing charged particles reacts to the presence of the charged particles so that it can be regarded as a classical orbit of a charged particle in the average magnetic field inducing Lorentz force. This makes sense only if a given magnetic flux tube contains particles with a fixed charge-to-mass ratio, and means that magnetic body indeed isolates and purifies the reactants to the magnetic flux tubes and allows them to react at the nodes of the magnetic web.

6.3.3 Evolution of metabolism

McFadden describes basic aspects of catabolism in an enjoyable manner. Catabolism can be seen as a process in which electrons from the orbitals of complex bio-molecules (in particular glucose) are gradually transferred to the orbitals of oxygen atoms. This process releases energy used as a metabolic energy in the form of ATP molecules.

In the standard chemistry framework the mechanisms behind $\text{ADP} \rightarrow \text{ATP}$ transformation seem miracle like. It is not easy to understand how an evolution based on mere chance and necessity could have led to the recent form of this machinery: intermediate steps seem to be simply absent. For instance, according to McFadden the reaction pathways generating the ATPase enzyme catalyzing the generation of ATP involves 13 steps and all these steps are necessary. The probability that this pathway could have been generated by a random change is infinitesimally small and comparable to that for a monkey playing with a typewriter to compose Shakespeare's sonnets by accident.

1. *Universal metabolic currencies*

In TGD framework the predicted universal metabolic currencies remove partially the veil of mysteries surrounding the evolution of metabolism.

The dropping of a proton from atomic space-time sheet to a larger one generates a universal metabolic energy quantum. Thus metabolism would have been present already before the chemical storage of the metabolic energy. At the pre-biotic period the generation of negative energy topological light rays with photon energy $\sim .5$ eV could have induced the dropping of protons and remote utilization of the liberated energy. Indeed, the model for intra-terrestrial life led to the hypothesis that the infrared radiation corresponding to a temperature of about 4000 K near the mantle-core boundary could have provided the energy quanta of about .4 eV driving protons back to the atomic space-time sheets. The evolution of photosynthesis led later to the chemical storage of the metabolic energy.

The mitochondrial battery is kept at the potential of .15 eV by the metabolic energy feed. This process involves oxidation process in which electrons from the orbitals of molecules like glucose end down to the orbitals of oxygen atoms. The electron pairs are provided by NADH molecules in mitochondrial metabolism occurring in the water filled space between mitochondrial membranes. The energy liberated in this manner drives protons from the interior of the mitochondria to the space between the membranes. NAD^+ ion then receives the compensating electronic Cooper pair from water later.

The molecular battery provides the energy to generate ATP molecules serving as universal energy currencies. Three protons leaking back along the channel inside ATPase molecule, which is analogous to the wire connecting the plus and minus poles of a battery, gain a net energy of $3 \times .15 = .45$ eV. This energy they donate to a proton, which uses it to get back to the atomic space-time sheet of the ATP molecule.

2. *Does metabolism generate cell level qualia?*

In a philosophical mood one could wonder the purpose of the endless ATP Karma's cycle: why not just the primitive metabolism involving only .5 eV photons? A partial explanation is the possibility to store metabolic energy chemically so that system becomes less dependent on environment. A connection with the TGD based model of sensory receptor as a quantum capacitor suggests a deeper interpretation. The dielectric breakdown of the quantum capacitor gives rise to qualia which correspond to the increments of the total quantum numbers at either electrode when the dielectric breakdown occurs. ATPase could be seen as generating local di-electrical breakdown inducing primitive protonic qualia as a side product.

3. *Molecular intentionality*

The basic challenge of the bio-chemistry based approach to evolution is to understand how

simple reaction steps coherently integrate to long multi-step reaction pathways. The assumption of molecular intentionality simplifies dramatically this task. Indeed, the best manner to understand and plan a complex electronic instrument is to know its purpose. The manual provides explanation of the purpose and magnetic body serves as the manual of the bio-logical body. For instance, it is much easier to understand how the reaction pathway leading to ATPase has developed if one knows that the function of this pathway is to liberate universal metabolic energy quanta from mitochondrial battery besides possibly producing protonic qualia.

The fact the number of steps is 13 suggests 13-adicity and it would be interesting to see whether various reaction pathways tend to have a prime number of steps. It deserves to be noticed that $k = 169 = 13^2$ defines the p-adic prime associated with the magnetic flux tubes of the Earth's magnetic field and its possible dark companion $B_{end} = 2B_E/5$, and that the micro-tubular surface defines naturally cognitive code with $k = 13^2$ bits consisting of 13 13-bit sequences defined by tubuline conformations for a full 2π twist around micro-tubule.

Biological evolution could be seen as being induced by the evolution of cognition and of intentional actions. By the properties of the p-adic topology it proceeds from long time and length scales to shorter ones (p-adically short corresponds to something long in the real sense since rational space-time points are common to real and p-adic sectors of the imbedding space). This would suggest that the evolution of bio-logical functions is induced by the evolution of the intentional actions of the magnetic bodies, which were initially like rough sketches and gradually became more and more refined. Also motor skills develop in the same manner.

4. *The emergence of molecular pathways*

The emergence of names attached to molecules makes possible generation of computer program like dynamics in which programs call corresponds to association of molecules with names conjugate to some name of catalyst molecule to clusters so that catalytic action leading to a particular final state becomes possible.

The names of molecules could dictate the dynamics to a high degree. Situation could be like in the human society: knowing that person carries the label "physics teacher" allows to make amazingly precise long term predictions about the daily behavior of the person whereas the knowledge of all imaginable chemical and physical data about the person would not allow to predict anything interesting about the activities of the person in time scales longer than few seconds.

6.3.4 Quantum mechanism of mutations

McFadden suggests the reduction of the superposition of normal and enol configurations of T nucleotide to a tautomeric enol configuration as a quantum mechanism of mutation. The position measurement of the proton can locate it to the second nitrogenic hydrogen bond and thus transform T nucleotide to the isomeric but short-lived enol configuration having only two hydrogen bonds connecting it to the complementary base. In the enol state DNA replication assigns G instead of A with T.

Zeno effect could allow to effectively freeze T to this configuration and thus increase the rate of mutations. The same mechanism could work also at the level DNA → mRNA transcription and protein translation and assign lys instead of glu to the enol configuration.

The mechanism poses an additional condition to the proposal that DNA nucleotides correspond to quarks and antiquarks. The question is what determines which quark or antiquark corresponds to a given nucleotide and the mechanism of mutation based on disappearance of hydrogen bond suggests that the number of hydrogen bonds (2 or 3) determines this so that one would have correlation with with the weak isospin of quark (u or d) and number of hydrogen bonds (3 or 2).

1. *Adaptive mutations of E. coli*

In adaptive mutations the bacterium E. coli unable to catabolize lactose to get metabolic energy

develops a mutation allowing it to generate beta galactose inducing the decay of the lactose. This mutation occurs with a probability which is higher than predicted by randomness. McFadden poses the question how the information about the presence of the lactose is communicated from the environment to the DNA level.

If life would be mere quantum chemistry, the only possibility would be that the information transfer sequence $\text{DNA} \rightarrow \text{mRNA} \rightarrow \text{proteins}$ of Central Dogma is somehow reversed. What McFadden suggests is DNA-mRNA-beta-galactose-lactose entanglement such that DNA appears as a superposition of ordinary and enol configurations. Lactose would take the role of quantum measurer of the proton's position inside T nucleotide, and Zeno effect would increase the rate of the mutation.

In TGD Universe the bacterial magnetic body receives information about the presence of lactose and its intention to "eat" lactose is transformed to a desire represented by a negative energy ME entangling directly with DNA. The intention of the magnetic body of *E. coli* would be to push the DNA to enol configuration by kicking the proton to the abnormal position. Negative W ME could induce long lasting entanglement with normal and enol configurations of T nucleotide so that the enol configuration would appear with a higher probability than in the absence of quantum entanglement and mutated DNA results more often in the replication. The alternative option is that magnetic body induces the gel-sol transition inducing mutation in the manner already described.

Quite generally, feeding of dark protons to atomic space-time sheets and gel-sol transition would serve as switches used by the cellular magnetic body to realize its desires. This mechanism could be seen as a refined form of remote metabolism providing metabolic energy for the starving bacterium.

2. Multiple mutations of TB bacteria

TB (tubercle bacillus) bacteria are able to develop a simultaneous resistance against several drugs [62]. This occurs for bacteria which have only brief growth periods followed by long dormant periods. McFadden interprets dormant periods in terms of entanglement with the environment. When this period ends even multiple mutations could result in the quantum measurement at DNA level.

In the TGD framework the magnetic body of TB population would receive information about the fates of various members of the population in the multi-drug environment and would have a strong desire to develop multi-drug resistance. The long dormant periods of bacteria allowing them to survive bring in mind the sleeping periods of higher life forms, and suggests the entanglement of the bacteria with the other members of the population, also those living in the geometric past and already deceased as victims of the drugs. This kind of entanglement would allow the magnetic body to manipulate the genomes of the still-living bacteria so that they have better changes to survive in the multi-drug environment. McFadden does not discuss whether the simple mechanism of mutations working in the case of *E. coli* might be enough in the case of TB bacteria.

Note that the notion of hyper-genome allows to understand bacterial colonies as systems analogous to multi-cellulars controlled by genes expressed collectively.

3. Mutations and intronic DNA

The TGD based view about pre-biotic evolution allows to imagine more effective mechanisms of mutations replacing the simple mechanism utilized by *E. coli* and working in case of eukaryotes.

In the TGD Universe reverse transcriptase plays a key role in the pre-biotic evolution as a generator of the genetic variation. The variation is due to the high error rate of the reverse transcription. For instance, the amazing ability of the HIV virus (retro-virus) to adapt is based on the reverse transcription of HIV RNA to DNA. It would be strange if this ability would have been lost during the sub-sequent evolution. Perhaps fragments of DNA are transformed to mRNA

also during dormant, "inwards directed" periods. mRNA fragments are however not translated to proteins now but transformed back to DNA fragments by reverse transcriptase replacing the previous DNA fragment in DNA with a new one. This mechanism might work at least in case of eukaryotes having cell nucleus and mean that mRNA is not transferred outside the nucleus. The replacement of DNA fragment need not occur immediately. mRNA fragments would thus act like retro-viruses to produce the needed genetic variation. In this framework ordinary retro-viruses such as HIV might be seen as kind of fallen angels.

This kind of activity in which collective selves of populations modify the genomes of their members might be present in all eukaryotes during sleeping (or more generally, dormant) periods. The generation of mutations might be one of the fundamental purposes of sleep and explain why sleep is so important for healing.

This mechanism of mutations might be still too primitive for eukaryotes. In TGD framework the intronic portion of DNA expresses itself as temporal field patterns using p-adic cognitive codes, in particular memetic code. Introns play the role of the computer software whereas genes take the role of the hardware. In this picture introns would be naturally involved with the control of the adaptive mutations of higher organisms. In the modern home computers hardware is becoming more and more dynamical, and computer metaphor suggest that the passive DNA could contain segments representing kind of computer store containing variants of various genes taken in use if required. Transposons might represent these new pieces of the hardware.

This replacement need not involve the removal of the old gene fragment and could be only functional. Computer metaphor inspires the idea that the intronic portion of DNA represents a given gene as a dynamical list of addresses, kind of links or program calls, specifying which portions of DNA contribute to the gene, and that this list characterizes how the splicing of mRNA occurs. Therefore the mutation could occur at the intronic software level as a mere updating of the list representing the gene.

The challenge is to understand how this addressing might be realized physically. For instance, addressing might involve simply common fragments of DNA in meme and corresponding portions of gene serving as addresses making possible a "tuning to a common wave length". Alternatively, magnetic flux tubes might serve as space-time correlates of the links. They could be generated intentionally as wormhole magnetic fields consisting of pairs of positive and negative energy magnetic flux tubes parallel to DNA strand. The generation of wormhole magnetic fields identified as the basic motor activity of the magnetic body could also explain the appearance and disappearance of EEG bands. By the p-adic fractality similar mechanism could be at work also in DNA length scale.

4. Could zero energy ontology be relevant for living matter?

Zero energy ontology [C3, A2] emerged originally from the observation that Robertson-Walker cosmologies correspond in TGD framework to vacuum extremals for which all conserved classical charges vanish (the non-conserved gravitational mass density does is non-vanishing). The construction of S-matrix led to a precise formulation of zero energy ontology.

Zero energy ontology states that physical states have vanishing net quantum numbers and consist of positive energy states at boundaries of future directed light-cones in the geometric past ("not so big bang") and negative energy states at the boundaries of past directed light cones in the geometric future ("not so big crunch") assignable to arguments of N-point function.

Due to the fact that conformal weights are complex it is possible to distinguish between positive energy particles propagating to the geometric future and negative energy particle propagating to geometric past. Phase conjugate laser photons contra ordinary laser photons represent basic empirical example about this distinction.

In the construction of S-matrix identified as unitary entanglement coefficients between these two kinds of states (this notion makes sense for hyper-finite factors of type II_1) these states represent incoming and outgoing states of particle reaction so that measurement of reaction rates

is basically quantum measurement in which time-like entanglement is reduced instead of space-like entanglement [C3].

A rather strong argument in favor of zero energy ontology comes from superconductivity [J1]. The models super-conductivity utilize formally the notion of coherent state of Cooper pairs involving quantum superposition of arbitrary numbers of Cooper pairs. This is in conflict with various conservation laws in standard ontology but in zero ontology it is quite possible to consider quantum superposition of zero energy states with various values of quantum numbers for positive energy states.

This opens the gates for rather fascinating speculations. Time-like charge entanglement would allow to imagine a time-like variant of the capacitor model of sensory receptor. For instance, sensory qualia could result in the reduction of coherent state of Cooper pairs to a state with a well defined charge.

Also different DNA sequences with different masses and charges might appear in quantum superpositions for time like entanglement and this might be relevant for evolution of genetic code. In particular, the model of McFadden for mutations might generalize dramatically. As a matter fact, the proposed identification of S-matrix (or rather its generalization M-matrix which need not be unitary) as time-like entanglement coefficients assumes the presence of all pairs of initial and final states appearing in the S-matrix in the superposition so that this possibility could be seen as a prediction.

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