Evolution in Many-Sheeted Space-Time

M. Pitkänen
Email: matpitka@mappi.helsinki.fi.
http://www.helsinki.fi/∼matpitka/.

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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.

Keywords: Topological Geometrodynamics, unified theories, quantum theories of consciousness, evolution.

1 Introduction

This article is about evolution in TGD Universe. Of course, a collection of ideas rather than detailed history of life is in question. If was already early clear that the notion of many-sheeted space-time could allow to understand many puzzles related to the pre-biotic evolution [61, 66]. There are many constraints on the models for pre-biotic evolution. The models have also many difficulties [44, 58].

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 amino-acid 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-amino-acid 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 amino-acid sequences were formed. After a period of symbiosis involving all these three tRNAs a transition to DNA-RNA-amino-acid world took place as an amino-acid 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 [53] 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 [72].

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 [70] 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 article

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 the 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 developed. The symmetries of the genetic code, the observation that tRNA can be regarded as a fusion of two hairpin like DNA molecules, and the finding that the first two nucleotides of 3-codon code for the reaction path leading from a precursor of the amino-acid to amino-acids and for hydrophobic/hydrohilic dichotomy, serve as motivations of the model. In 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. On one hand, amino-acids would have served as

catalysts for the copying of RNA. On the other hand, RNA molecules would have catalyzed the formation of amino-acids from their precursors so that a positive feedback loop would have been present. In the transition to DNA-amino-acid era RNA began to be translated to amino-acid sequences.

3. 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 so 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 during a relatively short geological period of time. 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.

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 environement 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 [61] representing updated view about facts and theories about pre-biotic evolution as well as articles criticing the existing theories [44, 58].

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 where 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 coacervatives were precessors of the cell. Haldade 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 aund 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 [80]. 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 [44] 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 [68] and others to be discussed below would not been satisfied.

2.4 Urey-Miller experiment

Urey-Miller experiment [68] meant a dramatic step of progress on the experimental side, and for a along 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 glyseralhehyde phosphate in presence of COOH [48]. Glyseraldehyde phosphate was generated also in Miller's experiments. In case of deoxiribose 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 [46] thin ice at temperature of 10 K containing H_2O, ammonia, CO, CO_2 methanol was located in vacuum and bombarded by UV radiation to mimick the situation prevaling 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 [53, 57] 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 [61] is recommended warmly).

1. Ribose can be synthetized 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 feeded 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 [42]. Second crucial finding was that these RNAs could act as catalysts in transesterifications crucial for the protein synthesis [57]. Even high fidelity complementary replication of arbitrary short RNA sequences has been demonstrated [59]. 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 [56] and

modified ribozymes are able to act as amino-acyl esterases [74]. Thus RNA seems able to serve synthetizing, 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 posses 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 [61] 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 environement 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 [40]. 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 an plausible candidate for protocell is the gel phase resulting in sol-gel transition inside cell [76, 61]. 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 micro-spheres formed from protenoids in geolocically active sites like hots springs and volcanic rims. He also demonstrated that this really occurs. Protedoids 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 inpermeable cell wall or spore coat rather than a cell membrane [44, 58].

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 [58].

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 [44].

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[28, 25] as well as biological nuclear transmutations for which there is considerable empirical support [26]. 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 [27]. 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 [65]. 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 $p = 2^{127} - 1$, $k = 0, 1, 2, ...$ [M3]. Each p-adic length scale would correspond to this kind of hierarchy. The unit of magnetic flux scales up as $h_0 \to h = rh_0$ in the transition increasing Planck constant: this is achieved by scalings $L(k) \to rL(k)$ and $B \to B/r$.

$B = .2$ 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 $r = 18$ μm, 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 $B_n = 4cos^2(\pi/n)$ 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 biopolymers 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. $ATP \to ADP$ 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 [76] 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, 60] 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. Supergenes 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" [61] 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→ ADP process

AMP, ADP, ATP are phosphorylated RNA nucleosides [96] and the hydrolysis of ATP to ADP [97] 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↔ ADP corresponds to the hydrolysis

$$ATP^{4-} + H_2O \leftrightarrow ADP^{2-} + P_i$$

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 $(1 - 1/4) \times \times E_0(137) = .375$ 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 [73].

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

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

Step 4: ADP is released from the catalyst site: $F_1 \cdot ADP + P_i \to F_1 + ADP + P_i$. $\Delta G \sim 0$ 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 [64, 75, 52]. 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 $ATP \to ADP$ 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 $ATP \to ADP + P_i$. 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 is 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^+ [98] 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 $NADH \to NAD^+$ 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. Alfwen 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 $PO_4H_2^{2-}$ phosphate molecule with ribose. In this process the stub ...-O-H of the phosphate ion combines with H-O-C-... stub of ribose (here C is the carbon atom not belonging to the ribose cycle). This gives rise to ..-O-(H-O)$^-$-C-... 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 $OH^- + H^+$ 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 consists 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 [19] 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 [19]. 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 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.

4 Physical model for genetic code and its evolution

The original number theoretic models for genetic realied 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 [24]. 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 [53] 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 $RNA_2 \to RNA_1$ 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 [103], provides the mechanism transforming RNA sequences to DNA sequences inside pre-nucleus so that DNA→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 to $tRNA_3$, the recent tRNA, made $RNA_2 \to RNA_1$ and $RNA_2 \to RNA_2$ 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→ 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 te 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 [61]. 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 [61] 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 [81] (for an article about RNA genes and RNA world see [47]). 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 genes. There is also evidence that centrosomes possess their own genome based on RNA rather than DNA [88].

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

The beautiful results (for a popular summary see [38]) 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 [84]. 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 [55] such that B

forms a loop and C is a palindrome [90]. 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 [84] 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 dublex 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.

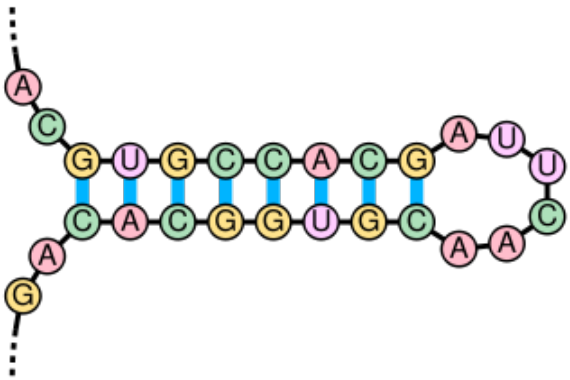

Figure 1: The structure of DNA hairpin (stem loop)

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 loose 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 [99] 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.

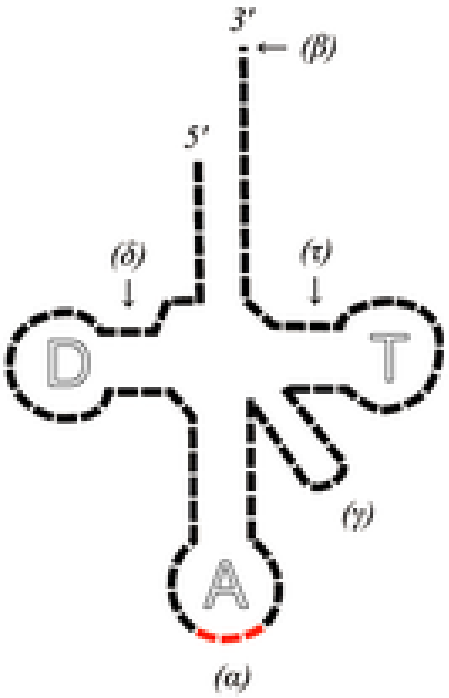

Figure 2: The structure of tRNA

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) [91]. 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 ($(T,C,A,G) \to X$, whether 4-column decomposes into two doublets: $[(T,C),(A,G)] \to [X,Y]$, or whether it decomposes to triplet and singlet ($[(T,C,A),G] \to [ile,met]$). There are also the 4-columns containing stop codon: $[(U,C),(A,G)] \to [(tyr,tyr),(stop,stop)]$ and $[(U,C),A,G] \to [(cys,sys),stop,trp]$. 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.

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 tRNA_1 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 amimno-acids Pro and Leu). The study of concrete examples [102] 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 [92], 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: $Q_a(amino) = -Q_a(codon)$.

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 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 [101] 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. tRNA_1 and tRNA_2 correspond naturally to the horizontal and vertical segment in the recent tRNA formed as a fusion of tRNA_1 and tRNA_2 to form a cross like structure (see figure above). Hence tRNA_1 and trNA_2 should represent in their structures the respective genetic codes.

1. tRNA_2 should contain both the conjugate of the coding RNA nucleotide attaching to RNA_2 plus the conjugate of the coded nucleotide to which RNA nucleotide was attached and then transferred to RNA_2 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 TψC arm. This is possible since all loops are physically near to each other. The structure of D and Tψ 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 RNA_1 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.* disphosphate 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 polymeraze 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 [63]. 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 tRNA_1 and tRNA_2 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 deoxiribose 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. RNA_2 consists of exotic RNA doublets with nucleotides connected by $2', 5'$ monophosphate bonds. tRNA_2 brings $2', 5'$ doublet $\mathrm{XMP}_2 \circ \mathrm{YTP}_2$ to the growing strand and glues it to the $5'$ position of the ribose in the already existing polymer. The YTP suffers the cleavage $\mathrm{YTP}_2 \to \mathrm{YMP}_2$ as in the case of DNA polymerization and the amount of metabolic energy provided by the cleavage is the same. The formation of $\mathrm{XMP}_2 \circ \mathrm{YTP}_2$ 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 $\mathrm{XTP}_2 \to \mathrm{XDP}_2$ 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$\to$ ADP cleavage, which usually occurs in the ordinary metabolism instead of ATP$\to$ AMP cleavage: only during a very intense metabolism ATP$\to$ AMP cleavage occurs. Since ATP metabolism is a functional fossil from a very early period of evolution, one might expect that ATP$\to$ 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 [53] 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 [24].

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 tRNA_3, gives valuable information about the course of events leading to the translation of mRNA to amino-acids. The cross like structure of tRNA_3 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 tRNA_1 and tRNA_2. tRNA_2 brought pairs of nucleotides forming the 2-codon part of RNA triplet to the growing RNA_2 sequence during replication and 2-code was simply RNA conjugation. tRNA_1 was involved with transcription of RNA_2 to RNA_1 bringing RNA_1 nucleotides one-by own to the growing sequence. In tRNA_3 the third nucleotide does not quite correspond to ordinary RNA but to to A, G, U or I(nositol) and is believed to differ geometrically from ordinary nucleotide, and one can assume that these nucleotides were the building blocks of RNA_1 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 not 1-to-1 nor deterministic but given by the correspondence $\{U \to A, C \to G, \{A, G\} \to U, \{U, A, C\} \to I\}$ 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 RNA_2 sequence coding for tRNA_1, 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 RNA_2 sequences.

3. From the fact that amino-acids are attached to the ACC stem of tRNA_2, 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 coded 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 tRNA_1 and tRNA_2 to tRNA_3 along their ends containing RNA_1 nucleotide and RNA_2 doublet which thus combined to RNA triplet. Presumably tRNA_3 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 $tRNA_3$ 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 $tRNA_3$ corresponding to single amino-acid was stable. Isospin symmetry was broken only weakly or not at all (human mitocondrial 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 $tRNA_3$ 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 $tRNA_3$ 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 stabile 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 suggest that the counterpart of the cell membrane was present already at that time. Quite recently it was reported [70] 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 [103] 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 RNA→ 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 → 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 [43] 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 [100]. 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 [65], 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 [85] 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 [87] are fundamental repeating units in eukaryotic chromatin [86] 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 [87] 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 Plasmoid like life forms in laboratory

It seems that one of the most craziest predictions of TGD inspired theory of consciousness has been realized at laboratory. Quite recent report tells about plasmoids generated in a simple diode involving plasma generator creating plasma column between itself and the positively charged anode [65]. The plasmoids are self-organizing structures able to evolve in a period of few microseconds. They possess many properties that life forms are expected to have. Plasmoids
i) grow from micrometer size up to cm size,
ii) replicate by simply dividing into two pieces,
iii) have an outer negatively charged surface separating the positively charged interior from the environment and obviously analogous to the cell membrane. Hence the plasmoid is analogous to a capacitor, and the exchange of matter with the environment could correspond to a di-electric breakdown essential for qualia in TGD based model of the sensory receptor,
iv) possess a metabolic cycle involving the transfer of matter between the interior of the plasmoid and environment. This cycle is seen as a periodic generation of visible light at specific frequencies: the light balls are typically found to be red or yellow. The frequency of metabolic oscillations is at 25-45 kHz frequency range,
v) are able to communicate by generating electromagnetic radiation by inducing vibrations in the receiving plasmoid at the same frequency.

These findings give valuable hints concerning the more detailed modelling the "biology" of plasmoids. For instance, one can ask whether the preferred colors might be interpreted in terms of quantized increments of zero point kinetic energies liberated when atoms or ions (such as C, N, and O) drop from the hot $k = 131$ space-time sheets (temperature being of the order of the zero point kinetic energy) to larger space-time sheets.

5 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 [29] 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 [30] 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 The claims of Adams

The basic claims of Adams were following.

1. The radius of Earth has increased during last 185 million years (dinosaurs [94] 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 [33]. 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.

5.2 The critic of Adams of the subduction mechanism

The prevailing tectonic plate theory [31] 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 litosphere 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 [32] 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 [34] (orogeny), earth quake zones, and associated zones of volcanic activity [36].

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.

5.3 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 [33], 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 time 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.

5.4 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 [54] 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 ($\omega R^2 = constant$) 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 [39], 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 [45] conforms with this picture.

5.5 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 multicellular 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 [67] 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 the 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.

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