The TGD based view about dark matter at the level of molecular biology

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Abstract

The notion of dark matter as phases of ordinary matter with effective Planck constant $h_{eff} = nh_0$ is the basic prediction of the number theoretic vision about Topological Geometrodynamics (TGD). This article is devoted to the possible role of magnetic body (MB) and dark matter in the TGD sense in chemistry and biology.

The first group of questions relates to the role dark protons and electrons, in ordinary chemistry and organic chemistry. Could the protons donated by acids be dark? What about the protons associated with hydrogen bonds? What about biologically important ions? What about oxidation and reduction: are the electrons involved dark: do valence electrons have $h_{eff} > h$?

Second group of questions relates to the role of the magnetic body (MB) carrying dark matter in biochemistry. Does the transition to biochemistry involve Pollack effect in which the fraction 1/4 of protons becomes dark and is transferred to the magnetic flux tubes? Do

dark protons organize into triplets forming analogs of DNA, RNA, tRNA, and amino-acids, and are their chemical representations only secondary representations, kind of mimicry?

Dark protons could neutralize the phosphates of DNA and RNA. Do they also neutralize the phosphates at the ends of the lipids of the cell membrane: does cell membrane realize genetic code? What about microtubules having GTPs associated with tubulins? ATP molecule has 3 units of charge: is it neutralized by dark proton triplet: could the energies of this triplet and dark valence electrons explain the high energy phosphate bond? Amino-acids should be accompanied by dark proton triplets: could the binding with dark electrons neutralize them?

Could basic biomolecules and their dark analogs interact by exchanging dark photons in energy resonance. Could bio-photons result from dark extremely low frequency (ELF) photons? Could energy resonance conditions select the basic biomolecules?

1 Introduction

This chapter has been written together with Reza Rastmanesh as a kind of appendix to an article representing TGD based model for language [L34, L35]. The basic idea of the TGD based vision about living matter is that dark matter having effective Planck constant $h_{eff} = nh_0$ ($h = 6h_0$) located at the flux tubes of magnetic body controls ordinary matter: MB would be the boss and biological body the slave. This hypothesis can be justified by number theoretic vision about TGD, which unifies ordinary physics as physics of sensory experience described by real number based physics and the physics of cognition based on p-adic number fields: real and various p-adic number fields are fused to adele.

1.1 Physical motivations for the TGD notion of dark matter

The notion of dark matter as control of biomatter emerged before its number theoretic justification.

1. The findings of Blackman *et al* [J1] about the effects of ELF radiation (in EEG frequency range) on vertebrate brain led to the hypothesis that besides protons also ions have dark variants having $h_{eff} = nh_0$ with $h_{eff} = h_{gr}$.

2. Also electrons could have these phases but now the value of h_{eff} would be much smaller and satisfy generalized Nottale hypothesis $h_{eff} = h_{em}$, where h_{em} is the electromagnetic analogue of h_{gr} assignable to flux tubes assigned with valence bonds [L12]. This leads to a model of valence bond [L12] predicting that the value of $h_{eff}/h_0 = n = h_{em}$ increases along the rows of the periodic table. This would explain why the molecules such as proteins containing atoms towards the right end of the rows serve as carriers of metabolic energy and why biologically important ions like C^{++} are towards the left end of the rows.

   The energy scale of dark variants of valence electrons is proportional to $1/heff^2$ so that the orbital radii are scaled up and the identification as a Rydberg atom is the only possibility in the standard physics picture: could dark valence electrons be in question? There is empirical evidence known for decades for the mysterious disappearance of valence electrons of some rare earth metals. The article "*Lifshitz transition from valence fluctuations in YbAl3*" by Chatterjee *et al* published in Nature Communications [D2] discusses the phenomenon for Yb.

   The finding [D3] about misbehaving Ruthenium atoms supports the view that covalent bonds involve dark valence electrons. Pairs of Ru atoms were expected to transform to Ru dimers in thermo-dynamical equilibrium but this did not happen. This suggests that valence electrons associated with the valence bond of Ru dimers are dark in TGD sense and the valence bonded Ru dimer has a higher energy than a pair of free Ru atoms. TGD based explanation [K3] could be justified by a resonant coupling of the dark electron with an ordinary Rydberg state of the valence electron. In the lowest approximation dark valence electron has energies in the spectrum of ordinary valence electrons so that a resonant coupling with Rydberg states can be considered. The evidence found by Randell Mill [D4] for atoms with an abnormally large scale of binding energy suggests the formula $h = 6h_0$. Color vision is a possible application [L17]. Adelic physics [L13] predicts h_{eff} hierarchy and allows to understand the findings.

3. Nottale hypothesis [E1] introduces the notion of gravitational Planck constant $\hbar_{gr} = GMm/v_0$ and is in the TGD framework identified as a particular value of h_{eff} assignable to gravitational flux tubes [K9, **?**, K8, K2] [L15]. One trivial implication reflecting Equivalence Principle is that the cyclotron energy spectrum $E_c = n\hbar_{gr}eB/m = nGMeB/v_0$ does not depend on the mass m of the charged particle and is thus universal. The energies involved are proposed to be in the range of biophoton energies (at least) suitable for control of the transitions of bio-molecule.

The difference between non-organic and in-organic matter would be the presence of dark protons and electrons. The notions of acids and bases would reduce to the presence of dark protons: pH would characterize the fraction of dark protons. The notion of reduction and oxidation (REDOX reaction) would reduce to dark electrons associated with valence bonds [L12].

In biochemistry the density of dark protons would be much stronger and Pollack effect it in which the irradiation of water in presence of gel phases generates exclusion zones (EZs) as negatively charged regions by transferring every 4^{th} proton to dark proton at flux tubes forming dark proton sequences as dark nuclei. Also dark ions become important in biochemistry, at least positively charged ions would have an important control role in TGD based view about biochemistry.

1.2 Realization of the vision about MB as controller of ordinary biomatter

$M^8 - H$ duality [L21, L20] concretizes the general vision. This duality states the representability of space- times as a 4-D surfaces in either complexified M^8 or $H = M^4 \times CP_2$. $n = h_{eff}/h_0$ has interpretation as dimetinsion of extension of rationals and would the degree of a polynomial determining the space-time surface in M^8 as a root of polynomial of degree n. Roots would correspond to different sheets of n-sheeted space-time surface and Galois group of extension would permute the sheets with each other and act as a number theoretic symmetry group. Dark matter states at the flux tubes of B_{end} would be in representations of Galois group and Galois confinement [L24] forcing n-particle states to behave as single unis like hadrons as color confined states.

The model of bio-harmony [L5, L6, L22] based on the icosahedral and tetrahedral geometries in turn predicts that genetic codons correspond to dark photon triplets as 3-chords of lights. The representation of 12-note scale as a sequence of quints reduced by octave equivalence fixes the harmony for a given Hamiltonian cycle and realizes the symmetries of the harmony defined by some subgroup of the icosahedral group.

Combination of 3 icosahedral harmonies with 20 chords and having different symmetries with tetrahedral harmony with 4 chords gives bioharmony 20+20+20+4=64 chords assigned to DNA codons. Amino-acids are identified as orbits of 3-chords under the symmetries of a given harmony, and one obtains 20 amino acids. DNA codons coding for a given amino acid correspond to the chords at the corresponding orbit and the numbers of DNA codons coding for a given amino acid come out correctly.

Bio-harmony assigns the binary aspects of information to the 6 bits of codon and emotional aspects to the bio-harmony characterized by allowed chords fixed by a given Hamiltonian cycle at icosahedron and the unique tetrahedral cycle. The model of bio-harmony requires that the values of B_{end} correspond to those associated with Pythagorean scale and defined by quint cycle.These frequencies would correspond to energies that a molecule must have to serve as a candidate for a basic biomolecule.

In the model of genetic code [L9, L14] identifying codons as dark proton triplets, the numbers of dark proton triplets correspond to numbers of DNA, RNA, tRNA codons and amino acids and one obtains correctly the numbers of DNA and RNA codons assignable to given amino-acid in the vertebrate genetic code. Genes would correspond to sequences of dark proton triplets. Dark proton triplet would be analogous to baryon and Galois confinement [L24] would force it to behave like a single quantum unit. Dark codons would in turn bind to Galois confined states of the Galois group of extension of the extension associated with the codons.

Galois confinement would be realized also for the dark photon triplets as representation of genetic codons and also for the sequences of N dark-photon representing genes as dark 3N-photon states. Genes would serve as addresses in the communications based on dark $3N$-photon resonances. For communications between levels with the same value of h_{eff} there would be both energy and

frequency resonance and for levels with different values of h_{eff} only energy resonance. It is an open question whether for dark-ordinary communications dark photon $3N$-plets transforms to single ordinary biophoton.

The basic hypothesis is that both DNA, RNA, tRNA, and amino acids are paired with their dark analogs, and that energy resonance mediates the interaction between the members of pairs. In this article the goal is to clarify the dark-ordinary pairing and the interaction between the members of the pairs. To achieve this, we first propose some questions below and then synthetize the answers to them.

1.3 Questions

In the sequel we will address the following questions about the roles of MB in the biochemistry of the basic biomolecules.

1. Do dark protons appear already in non-organic chemistry? Does acid/base tend to give/bind with a dark proton? The basic process is $OH \rightarrow O^- + H_+$. Water represents the basic example containing ions H_3O^+ and OH^-: the dark proton from H_2O would bind to the second H_2O acting in the role of base. pH characterizes the fraction of protons equal to 10^{-7} for $pH = 7$.

   Does the transition to biochemistry mean Pollack effect [I14, L4] in which the fraction of dark protons becomes 1/4 corresponding to $pH = log_{10}(4)$. This would be the case for DNA, RNA, amino-acids, and tRNA also? Are the transitions between dark and ordinary states a key element of biochemistry. Could the gravitational flux tubes of MB take an active role in biochemistry?

2. Could the proton in hydrogen bond be dark? Could length of the hydrogen bond vary corresponding to different values of $h_{eff} = h_{gr}$. Could this explain the behavior of water below 100 C, in particular at physiological temperatures, challenging the standard thermodynamical model.

3. Do dark electrons play a role in chemistry as suggested in [L12]? Does oxidation/reduction mean almost giving/receiving a dark valence electron in the valence bond? REDOX reactions are central also in biochemistry. The basic example is combustion in which O==O in presence of hydrocarbon such as sugar C_nH_{2n} gives rise to CO_2 and H_2O and $C_{n-1}H_{2n-2}$. O is reduced so that it almost receives valence electrons from C and H and C and H are in turn oxidized. The notion of electronegativity parametrizes the tendency to receive an electron. Is it possible to state that in inorganic and organic chemistry the electromagnetic part of MB is by far more important than the gravitational part of MB whereas in biochemistry also the gravitational part becomes important.

   Also ions are proposed to appear as dark variants and one can wonder whether the valence electrons of positively charged biologically important dark ions like Ca^{++} are actually dark.

The following question can be asked about the role of MB in biochemistry of basic biomolecules.

1. Does the energy resonance for dark proton triplets and even for their sequences between biomolecules and their dark variants select the basic biomolecules like DNA, RNA, tRNA, and amino-acids having dark proton counterparts? Base pairs in DNA double strand involve also hydrogen bonds. Could these hydrogen bonds have also dark variants?

2. Dark proton triplets would neutralize the negative charges assignable to the phosphates of DNA and RNA nucleotides and could be imaged as coming from $POH \rightarrow PO^- + H^+$ by a transformation of proton to dark proton by the analog of Pollack effect making DNA negatively charged.

   What about the cell membrane, whose lipids have also phosphate ions at their ends? Could this give a higher level representation of the genetic code and genes at cell membrane level making possible dark 3N-photon communications between genome and cell membrae? Or do the dark protons serve at least as an energy storage? In fact, it has been proposed that cell membranes could involve a genetic code [I13].

Microtubules are accompanied by negatively charged GTP molecules possibly associated with tubulins. 6-bit code defined also by DNA codons has been proposed by Hameroff *et al* as a memory code [J2]. Could it be associaed with genetic code represented using dark proton triplets?

3. The amino-acids in proteins should pair with dark variants of amino-acids by energy resonance. Amino-acid backbone does not however carry negative charge. Are the dark protons coming from NH_2 and COOH neutralized by electrons so that one would have dark hydrogens?

4. Also the ATP molecule has a negative charge of 3 units. Is it neutralized by a dark proton triplet serving as a temporary storage of metabolic energy? Could this energy at least partially explain the somewhat questionable notion of the high energy phosphate bond (also dark valence electrons would contribute)? Could ATP$\rightarrow$ ADP liberate metabolic energy by splitting one dark valence bond and transforming one dark proton to ordinary one? Do the dark protons assigned with the proteins serve as metabolic energy storage besides valence electrons, whose reduced Coulombic binding energies also give rise to higher than expected bond energies?

The next sections will be devoted to the possible answers to these questions.

Note: This chapter was prepared in collaboration with Dr Reza Rastmanesh who provided a lot of biological knowhow and made inspiring questions.

2 Some number theoretical aspects of quantum biology

In this section the number theoretical aspects of TGD inspired quantum biology relevant to the recent article are considered. The role of the number number theory in TGD inspired view about cognition relying on adelic physics [L13] is not discussed here.

Fig. 1 summarises the role of number theory in the TGD inspired vision concerning consciousness, cognition, and quantum biology and **Fig. 2** the role of dark matter in TGD inspired quantum biology.

2.1 Dark proton representation of genetic code

Fig. 3 summarizes the TGD based vision about genetic codes.

2.1.1 Codons as dark nucleons?

The model for codons of genetic code emerged from the attempts to understand water memory [**?**] The outcome was a totally unexpected finding [**?**] the states of dark nucleons formed from three quarks connected by color bonds can be naturally grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAs, 20 amino acids, and tRNA and there is natural mapping of DNA and RNA type states to amino acid type states such that the numbers of DNAs/RNAs mapped to given amino acid are same as for the vertebrate genetic code.

The basic idea is simple. The basic difference from the model of free nucleon is that the nucleons in question - maybe also nuclear nucleons - consist of 3 linearly ordered quarks - just as DNA codons consist of three nucleotides. One might therefore ask whether codons could correspond to dark nucleons obtained as open strings with 3 quarks connected by two color flux tubes or as closed triangles connected by 3 color flux tubes. Only the first option works without additional assumptions. The codons in turn would be connected by color flux tubes having quantum numbers of pion or η.

This representation of the genetic would be based on entanglement rather than letter sequences. Could dark nucleons constructed as a string of 3 quarks using color flux tubes realize 64 DNA codons? Could 20 amino acids be identified as equivalence classes of some equivalence relation between 64 fundamental codons in a natural manner? The codons would not be separable to letters but entangled states of 3 quarks anymore.

Genetic code would be defined by projecting DNA codons with the same total quark and color bond spin projections to the amino acid with the same (or opposite) spin projections. The attractive

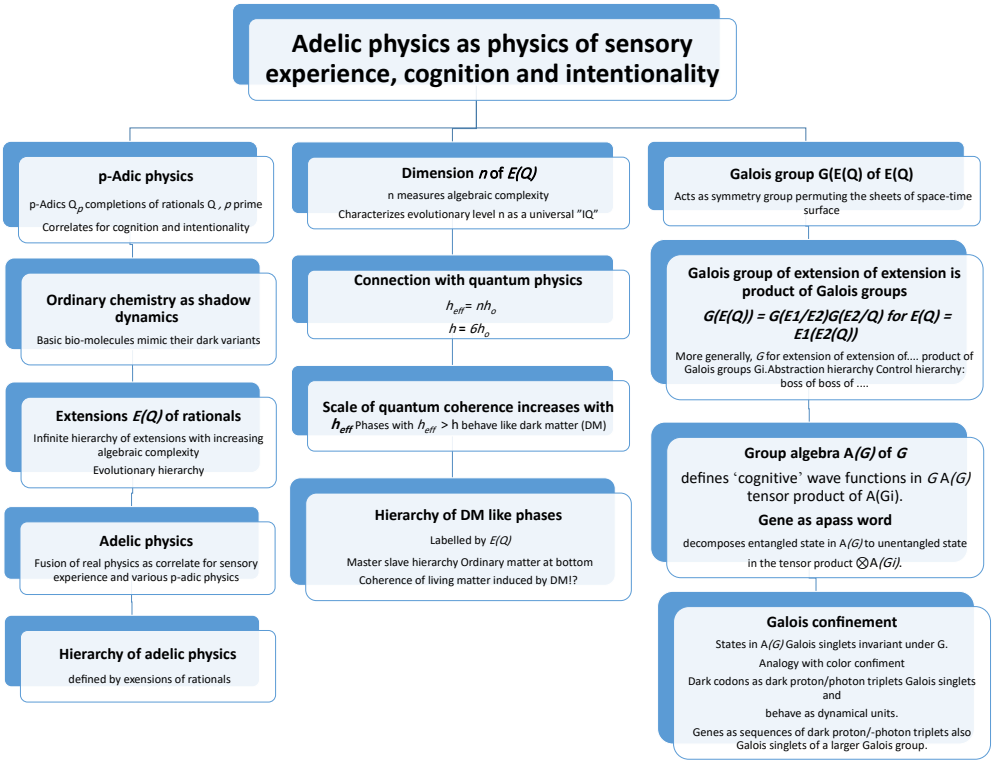

Figure 1: Adelic physics as physics of sensory experience, cognition and intentionality

force between parallel vortices rotating in opposite directions serves as a metaphor for the idea. This hypothesis allows immediately the calculation of the degeneracies of various spin states. The code projects the states in $(4 \oplus 2 \oplus 2) \otimes (5 \oplus 3)$ to the states of 4×5 with the same or opposite spin projection. This would give the degeneracies $D(k)$ as products of numbers $D_B \in \{1, 2, 3, 2\}$ and $D_b \in \{1, 2, 2, 2, 1\}$: $D = D_B \times D_b$. Only the observed degeneracies $D = 1, 2, 3, 4, 6$ are predicted. The numbers $N(k)$ of amino acids coded by D codons would be

$$[N(1), N(2), N(3), N(4), N(6)] = [2, 7, 2, 6, 3] \quad .$$

The correct numbers for vertebrate nuclear code are $(N(1), N(2), N(3), N(4), N(6)) = (2, 9, 1, 5, 3)$. Some kind of symmetry breaking must take place and should relate to the emergence of stopping codons. If one codon in the second 3-plet becomes stopping codon, the 3-plet becomes doublet. If 2 codons in 4-plet become stopping codons it also becomes doublet and one obtains the correct result $(2, 9, 1, 5, 3)$!

2.1.2 Codons as dark proton triplets?

The model of codon as dark nucleon predicts analogs Δ resonances whose masses differ from those of nucleons.

The hint comes from the fact that DNA nucleotides have a negative charge, which is problematic from the point of view of DNA stability. This suggests that dark codons should have a charge of 3 units screenng the charge of the ordinary DNA codon. Pollack effect [**?**]eans formation of negatively charged exclusion zones as protons are transferred to dark protons at magnetic flux tubes. Could DNA be formed by Pollack effect? Could codons be represented as dark proton triplets?

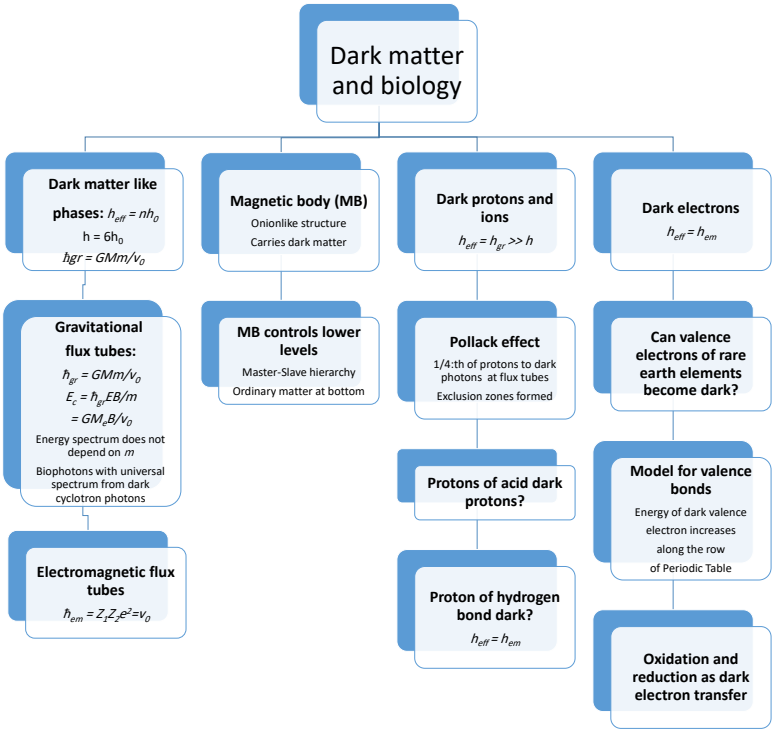

Figure 2: Dark matter in TGD inspired quantum biology

The problem is that protons however have only 2 spin states: 4 states would be needed as in the case of quarks having also color. Where could the counterparts of spin and color come from?

One could consider adding a neural pion-like and/or ρ_0 meson-like bond connecting neighboring protons. Since ρ_0 has spin 1, this would give 1+3=4 states per bond. However, 2 states are enough and one must get rid of 2 states. The string-like structure of the proton triplet suggests that the rotation group reduces to $SO(2) \subset SO(3)$ so that ρ meson states split into singlets with helicities 0,1,-1. The doublet (-1,1) would serve as the analog of the isospin doublet (u,d) for baryons and enough to achieve a correct effective number $N = 4$ of states per single DNA codon. Helicity would replace isospin and the tensor product states could be constructed effectively as tensor products of 3 representations $2 \otimes 2$.

There is also an issue related to the fermionic statistics. Protons are fermions and the total wave function for them must be antisymmetric. For baryons color singlet property allows this. Can one require statistics in the ordinary sense also now? Or could the effective 1-dimensionality of the magnetic flux tube allow braid statistics?

The following variant gives good hopes about the ordinary statistics.

1. Adelic physics [**?**]rings in additional discrete degrees of freedom assignable to the group algebra of Galois group of extension of rationals inducing the extensions of p-adic number fields appearing in the adele [**?**]

2. Galois group acts on the space of space-time surfaces, and one can say that one has wave function at the orbit of the Galois group consisting of space-time sheets. At quantum level quantum states correspond to wave functions in the group algebra of Galois group of extension.

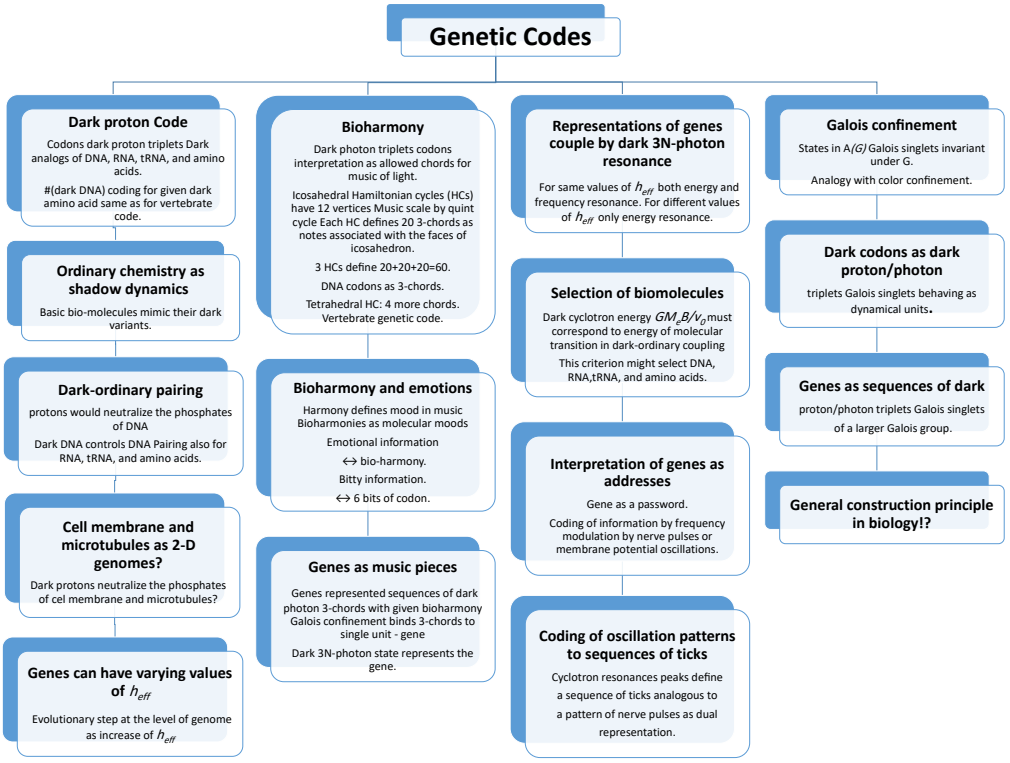

Figure 3: Genetic codes in TGD framework

3. The role of color degrees of freedom in helping to achieve correct statistics in the case of baryon could be taken by Galois degrees of freedom. One can even consider the notion of Galois confinement as a generalization of color confinement [**?**]inding codons as dark proton triplets to dynamical units. Codons should be antisymmetric under exchange of dark protons in Galois degrees of freedom. Also genes as sequences of codons could be bound to dynamical units as Galois singlets. Could this allow ordinary statistics.

One can consider the replacement of u and d quarks with proton and neutron: color degrees of freedom would be missing but also now Galois confinement could come in rescue. Now however the charge screening of DNA by dark DNA would not be complete.

If this picture is correct, genetic code would be realized already at the level of dark nuclear physics or even at the level of ordinary nuclear physics if the nuclei of ordinary nuclear physics are nuclear strings. Chemical realization of genetic code would be induced from the fundamental realization in terms of dark nucleon sequences and vertebrate code would be the most perfect one. Chemistry would be a kind of shadow of the dynamics of positively charged dark nucleon strings accompanying the DNA strands and this could explain the stability of the DNA strand having 2 units of negative charge per nucleotide. Biochemistry might be controlled by the dark matter at flux tubes.

2.1.3 Cell membrane and microtubules as a higher level representation of genetic code?

Also the representation of genetic code at the level of cell membrane can be considered [L18]. This kind of proposal have been made with different motivations by Okecukwu Nwamba [I13].

The motivation for the current proposal is that the lipids have at their ends negatively charged phosphates just as DNA nucleotides have. The generalization of DNA as a 1-D lattice like structure to a 2-D cylindrical lattice containing nucleotide like units - letters - possibly assignable to lipids and realized as dark protons. Single lipid could be in the role of ribose+nucleotide unit and accompanied by a neutralizing and stabilizing dark proton. For axons one would have cylindrical lattice dark DNA lattice. The two lipid layers could correspond to two DNA strands: the analogs of the passive and active strand.

The finding is that membrane affects protein's behavior. This would be understandable in the proposed pictures 2-D analog of 1-D nucleotides sequences with codons replaced with counterparts of genes as basic units. That lipids are accompanied by phosphates with charge -1 gives the hint. Phosphate charge is neutralized by a dark proton as an analog of a nucleotide.

The notion of Galois confinement identifying genes as units consisting of N dark proton triplets representing genetic codons suggests that genes possibly assignable to the lipid layers of the cell membrane could communicate using dark $3N$-photon sequences with the proteins, genome, RNA and DNA. Dark variants of the control genes could initiate a nerve pulse pattern. An interesting possibility is that ganglions, nucleus like structures assignable to sensory organs and appearing as basal ganglia in brain [I7] could communicate with genes.

Also microtubules have GTPs with charge -3 bound to tubulins. In dynamical instability known as treadmilling the transformation of GTP$\rightarrow GDP$ bound to β tubulin by hydrolysis induces the shortening of the microtubule at minus end whereas the addition of tubulins bound to GTP induces the growth at plus end. Also actin molecules bound to ATP show a similar behavior. Could they be accompanied by dark DNA codons? Are all codons allowed or does the absence of XTP, X= T,C,G mean that only codons of type GGG would be present?

For the dark codons for the cell membrane the p-adic length scale $L(151) \simeq 10^{-8}$ m would correspond to the lipid's transversal size scale and would be the distance between the dark protons. The scale of dark nuclear energy would be proportional to $1/L(151)$ and scaled down by factor $\sim 10^{-3}$ from that for DNA. The energy scale should be above the thermal energy at room temperature about .025 eV. If the energy scale is 2.5 eV (energy of visible photon) for DNA, the condition is satisfied. Note that 2.5 eV is in the bio-photon energy range. For p-adic large scales longer than $L(151)$ thermal instability becomes a problem.

It is interesting to compare the number of codons per unit length for ordinary genetic code (and its dark variant) and for various membranes and microtubules.

For the ordinary genetic code there are 10 codons per 10 nm defining p-adic length scale $L(151)$. This gives a codon density $dn/dl = 10^3/\mu m$ in absence of coiling. The total number of codons in human DNA with a total length $L \sim 1$ meter is of order $N \sim 10^9$ codons. The packing fraction of DNA due to coiling is therefore huge: of order 10^6.

If each lipid phosphate is accompanied by a dark proton and if lipid correspond to square at axonal cylinder with side of length $d = L(151)$ and the radius R of axon corresponds to the p-adic length scale $L(167) = 2.5\mu$ m (also of the same order as nucleus size), there are about $dn/dl = 2\pi(R/d)^2 \sim (2\pi/3) \times 10^4 \sim 1.3 \times 10^5/\mu m$. Axon should have length $L \sim 1$ cm to contain the entire genome.

The same rough estimate applies to microtubules except that there would be one codon per GTP so that the estimate would be 3 times higher if GTP corresponds to length scale $L(151)$ of tubulin molecule. It has been proposed that genetic code is realized at the microtubular level.

The nuclear membrane assumed to have a radius about $L(167) = 2.5\mu$m could represent $N \sim (4/3)R^2/d^2 \sim .8 \times 10^5$ codons. This is a fraction 10^{-5} about the total number of codons. For a neuronal membrane with radius $R \sim 10^{-4}$ meters assignable to a large neuron the fraction would be roughly 10^{-1}. The fraction of dark codons associated with membranes could correspond to genes involved with the control and communication with genome and other cell membranes. Note that the non-coding intronic portion dominates in the genome of higher vertebrates. One can ask whether the chromosome structure is somehow visible in the membrane genome and microtubular genome.

2.2 Bio-harmony as a realization of genetic code

TGD leads to a notion of bio-harmony in terms of icosahedral and tetrahedral geometries and 3-chords made of light assigned to the triangular faces of icosahedron and tetrahedron [L5, L6, L22]. The surprise was that vertebrate genetic code emerged as a prediction: the numbers of DNA codons coding for a given amino acid are predicted correctly. DNA codons correspond to triangular faces and the orbit of a given triangle under the symmetries of the bio-harmony in question corresponds to DNA codons coding for the amino acid assigned with the orbit.

Codon corresponds to 6 bits: this is information in the usual computational sense. Bio-harmony codes for mood: emotional information related to emotional intelligence as ability to get to the same mood allowing to receive this information. Bio-harmony would be a fundamental representation of information realized already at molecular level and speech, hearing and other expressions of information would be based on it. For emotional expression at RNA level possibly involved with conditioning at synaptic level see [L16].

Does the generation of nerve pulse patterns by a gene mean at the cell membrane from dark DNA to dark protein map to dark protein (it could be also dark RNA or dark DNA even) associated with the cell membrane. What about communications with RNA and enzymes involved with transcription and translation. Do all basic biocatalytic processes involve them.

What about a generalization of Josephson currents? Dark ions certainly define them but could also dark proton triplets and their sequences associated with proteins give rise to oscillating Josephson currents through cell membrane and therefore to dark Josephson radiation with 3N dark photon units! Proteins themselves need not move much!

The universal language could be restricted to the genetic code which would be realized by dark proton triplets.The 64 codons are formed from 3 20-chord harmonies associated with icosahedron and the unique 4-chord harmony associated with tetrahedron. Bio-harmonies are associated with the so-called Hamiltonian cycles ,which go through every vertex of Platonic solid once. For icosahedron the number of vertices is 12, the number of notes in 12-note scale.

Also tetrahedron, cube, octahedron and dodecahedron are possible and one can consider the possibility that they also define harmonies in terms of Hamiltonian cycles. Dodecahedron would have 5-chords (pentagons as faces) as basic chords and there is only single harmony. Same mood always, very eastern and enlightened as also the fact that scale would have 20 notes.

Also octahedron gives 3-chords (triangular faces) whereas cube gives 4-chords (squares as faces). One can of course speculate with the idea that DNA could also represent this kind of harmonies: sometimes the 3N rule is indeed broken, for instance for introns.

Galois confinement [L25] allows the possibility to interpret dark genes as sequences of N dark proton triplets as higher level structures behaving like a single quantal unit. This would be true also for the corresponding dark photon sequences consisting of 3N dark photons representing the gene in bio-harmony as an analog of a music piece consisting of 3-chords and played by transcribing it to mRNA.

The picture can be viewed even more generally. Any discrete structure, defining graph, in particular cognitive representation providing a unique finite discretization of space-time surface as points with the coordinates of the 8-D embedding space coordinates in the extension of rationals, defines harmonies in terms of Hamiltonian cycles. Could also these harmonies make sense? The restrictions of the cognitive representations to 2-D partonic 2-surfaces would define something analogous to bio-harmony as Hamiltonian cycle of 2-D graph (Platonic surfaces solids can be regarded as 2-D graphs). The interpretation as representations of Galois groups and the notion of Galois confinement is possible although one loses the symmetries of the Platonic solids allowing to identify genetic code.

2.2.1 Brief details of the genetic code based on bio-harmony

TGD suggests several realizations of music harmonies in terms of Hamiltonian cycles representing the notes of music scale, most naturally 12-note scale represented as verticehttps of the graph used. The most plausible realization of the harmony is as icosahedral harmony [L5, L6].

1. Icosahedron (for basic facs see the Wikipedia article) has 12 vertices and Hamiltonian cycle as a representation of 12-note scale would go through all vertices such that two nearest vertices along the cycle would differ by quint (frequency scaling by factor 3/2 modulo octave

equivalence). Icosahedron allows a large number of inequivalent Hamiltonian cycles and thus harmonies characterized by the subgroup of the icosahedral group leaving the cycle invariant. This group can be Z_6, Z_4, or Z_2 which acts either as a reflection group or corresponds to a rotation by π.

2. The fusion of 3 icosahedral harmonies with symmetry groups Z_6, Z_4 and Z_2 gives 20+20+20=60 3-chords and 3+1 + 5 + 10 =19 orbits of these under symmetry group and almost vertebrate genetic code when 3-chords are identified as analogs of DNA codons and their orbits as amino acids. One obtains counterparts of 60 DNA codons and 3+1 + 5 + 10 =19 amino acids so that 4 DNA codons and 1 amino acid are missing.

3. The problem disappears if one adds tetrahedral harmony with 4 codons as faces of tetrahedron and 1 amino acid as the orbit of the face of tetrahedron. One obtains 64 analogs of DNA codons and 20 analogs of amino acids: this harmony was coined as bio-harmony in [L5, L6]. The predicted number of DNA codons coding for given amino acid is the number of triangles at the orbit of a given triangle and the numbers are those for genetic code.

4. How to realize the fusion of harmonies? Perhaps the simplest realization found hitherto is based on the union of a tetrahedron of 3 icosahedrons obtained by gluing tetrahedron to icosahedron along its face which is a triangle. The precise geometric interpretation of this realization has been however missing and some possibilities have been considered. The model could explain the two additional amino acids Pyl and Sec appearing in Nature [L5, L6] as being related to different variant for the chemical counterparts of the bio-harmony.

   There is also a slight breaking of symmetries: ile 4-plet breaks into ile triplet and met singlet and trp double breaks into stop and trp also leu 4-plet can break in leu triplet and ser singlet. This symmetry breaking should be understood.

2.3 Galois group of space-time surface as new discrete degrees of freedom

2.3.1 Galois confinemenent

The problem is to understand how dark photon triplets occur as asymptotic states - one would expect many-photon states with a single photon as a basic unit. The explanation would be completely analogous to that for the appearance of 3-quark states as asymptotic states in hadron physics - the analog of color confinement [L26]. Dark photons would form Z_3 triplets under the Z_3 subgroup of the Galois group associated with corresponding space-time surface, and only Z_3 singlets realized as 3-photon states would be possible.

The invariance under $Gal(F)$ would correspond to a special case of Galois confinement, a notion introduced in [L24] with physical motivations coming partially from the TGD based model of genetic code based on dark photon triplets.

2.3.2 Cognitive measurement cascades

Quantum states form Galois group algebra - wave functions in Galois group of extension E. E has in general decomposition of extension E_1 as extension of E_2 as extension of ... to a series . Galois group of E has decomposition to product of $Gal(E) = Gal(E/E_1)Gal(E_1)$ and same decomposition holds true for $Gal(E_1)$ so that one has hierarchy of normal subgroups corresponding extension of extension of...hierarchy defined by a composite polynomial $P(x) == P_1(P_2(x))$ with P_2 having similar representation. P defines in M^8 picture the space-time surface. This maps a tensor product composition for group algebra and the factors of group algebra entangle. SSFR corresponds to a cognitive quantum measurement cascade: SSFR in $Gal(E/E_1)$, SSFR in $Gal(E_1/E_2)$ etc.. The number theoretic measurement cascades for purely number theoretic Galois degrees of freedom are discussed in [L27].

Could this cascade be analogous to the parsing of a linguistic or mathematical expression as cognitive measurements proceeding from higher to lower abstraction levels? Could the cascade correspond to a sentence S_1 about a sentence S_2 about ... such that one substitutes a concrete

sentence for S_1 first, then to S_2, etc...? This is indeed suggested by the cascade of SSFRs since $h_{eff}/h_0 = n$ is the dimension of E_n.

Could cascade of flux tubes decaying to smaller flux tubes with smaller value of h_{eff} should correspond to this hierarchy. Certainly this is linguistics but the sentence as argument could correspond to several sub-sentences - different flux tubes. Could a neural pathway defined by the branching axon correspond to a concretization of this kind statement about statement (or multistatement, perhaps nerve pulse pattern generated by nerve pulse patterns arriving to a given neuron) about...

2.4 Energy and frequency resonance as basic elements of dark photon communications

Dark photon realization of genetic code leads to a view about fundamental linguistic communication based on resonance and we will write a separate paper connecting TGD with language soon. Two systems can be in communication when there is resonance. $E = h_{eff}f$ and energy conservation implies

$$h_{eff,1}f_1 = h_{eff,2}f_2 \quad . \tag{2.1}$$

For $h_{eff,1} = h_{eff,2}$, energy conservation implies that both energies and frequencies are identical: $E_1 = E_2$ and $f_2 = f_2$. Both energy and frequency resonances in question.

In the general case one has $f_1/f_2 = h_{eff,2}/h_{eff,1}$ and frequency scaling takes place. The studies of water memory lead to the observation that this kind of phenomenon indeed occurs [I3]. The communications of dark matter with ordinary matter and those between different values of h_{eff} involve only energy resonance. Frequency and wavelength scaling makes it possible for long scales to control short scales. Dark photons with EEG frequencies associated with the big part of MB transform to bio photons with a wavelength of say cell size scale and control dynamics in these short scales: for instance, induce molecular transitions. This is impossible in standard physics.

The resonance condition becomes even stronger if it is required there is a large number of biomolecules in resonance with dark matter realized as dark variants of biomolecules and dark ions. Cyclotron resonance energies are proportional to $\hbar_{eff}$ characterizing magnetic flux tubes and to the valued of the magnetic field strength dictated by the quantization of the monopole flux quantization by the thickness of the flux tube which can be do some degree varied by varying the thickness of the flux tube giving rise to frequency modulation.

The findings of Blackman *et al* [J1] suggest that $B_{end} = 0.2$ Gauss defines an important value in the spectrum of B_{end} values. It could correspond to the field strength for the predicted monopole flux part of the Earth's magnetic field $B_E \simeq .5$ Gauss not allowed by Maxwell's theory. Besides B_{end} there would also be a non-monopole flux part allowed also in Maxwell's theory. Monopole flux part requires no currents as sources: this allows the understanding of the presence of magnetic fields in cosmological scales and also why B_E has not dissipated away long time ago [L8].

There are however indications that the value B_{end} is quantized and is proportional to the inverse of a biologically important p-adic length scale and thus would be quantized in octaves. This could relate directly to the octave equivalence phenomenon in music experience. The model of bio-harmony [L5, L6, L22] suggests a further quantization of the octave to Pythagorean 12-note scale of music. This would not be only essential for the music experience but communications of emotions and molecular level using the music of light.

2.4.1 Selection of basic biomolecules by energy resonance

The dark particles must have energy resonance with bio-molecules in order to induce their transitions. This seems to pose extremely strong conditions possibly selecting the bio-molecules able to form interacting networks with dark matter and with each other. One expects that only some amino acids and DNA type molecules survive.

Nottale's hypothesis provides a partial solution to these conditions. Nottale proposed the notion of gravitational Planck constant

$$\hbar_{gr} = \frac{GMm}{v_0} \tag{2.2}$$

assignable in TGD to gravitational flux tubes connecting large mass M and small mass m and v_0 is velocity parameter. The gravitational flux tube presumably carries no monopole flux. The TGD based additional hypothesis that one has equals to

$$\hbar_{gr} = h_{eff} = nh_0 \ . \tag{2.3}$$

This implies that the cyclotron energy spectrum

$$E_c = n\hbar_{gr}\frac{eB}{m} = n\frac{GM}{v_0}eB \tag{2.4}$$

of the charged particle does not depend at all on its m. Therefore in a given magnetic field, say B_{end}, the cyclotron resonance spectrum is independent of the particle.

The energy resonance condition reduces to the condition that the charged ion or molecule has some cyclotron energy coming as a multiple of fundamental in its spectrum in the spectrum of its transition energies. Even this condition is very strong since the energy scale for cyclotron energy in B_{end} is in the bio-photon energy range containing energies in visible and UV. The fact that bio-photons have a quasi-continuous spectrum strongly suggests that B_{end} has a spectrum. The model of bio-harmony [L3, L19] suggests that the values of B_{end} correspond to Pythagorean scale constructible by quint cycle familiar for jazz musicians that is by taking $(3/2)^k$ scalings of the fundamental frequency and by projecting to the basic octave by octave equivalence.

The above simplified picture is formulated for single dark photon communications. The dark proton and dark photon realizations of the genetic code requires 3-resonance that is a simultaneous energy resonance for the 3 members of dark photon triplet. In dark-dark pairing also frequency resonance is possible. In dark-ordinary pairing frequency increases and couples long scales with short scales. Also resonant communications between genes with N codons involving $3N$ dark photon frequencies must be possible. This requires new physics provided by number theoretical vision.

2.4.2 What happens in the cyclotron resonance?

3 cyclotron energies for flux tubes characterize dark 3-proton triplet and Nottale's hypothesis predicts that they depend on the values of B_{end} for the flux tubes only. Bio-harmony suggests that the spectrum of frequencies and thus B_{end} corresponds to Pythagorean 12-note scale for a given octave. The allowed chords of bioharmy would characterize the emotional state at the molecular level and correspond to the holistic emotional aspects of the communication beside the binary information.

The resonance would require that the dark cyclotron energy changes are equal to corresponding energies in molecular transitions. Galois confinement [L24] makes possible also 3-N resonance. The resonance condition would select basic biomolecules and the ability of dark analogs of biomolecules to simultaneously resonate with several biomolecules would give additional conditions. In particular this would select DNAs and amino acids.

An open question is whether the coupling to ordinary biomolecules involves a transformation of a dark photon triplet or an N-plet to a single ordinary photon. For instance, does the sum of the 3 cyclotron excitation energies appear in the coupling of dark 3-proton state to amino acid in protein? This would have an analog as 4-wave coupling [D1] in laser physics allowing in biology the transformation of dark photon triplet to single biophoton/or 3 bio-photons or *vice versa*. 6-wave coupling of laser physics would be analogous to the coupling of ordinary 3-photon state to dark 3-photon and back to ordinary 3-photon state.

The resonance itself would mean a process in which dark 3-proton cyclotron excitation returns to the ground state and generates dark 3-photon transforming transforming to ordinary photon (or 3-photon) and absorbed by the ordinary codon or amino acid excitation to hither energy state. This state would in turn emit an ordinary photon transforming to dark 3-photon absorbed by dark codon. This mechanism generalizes to 3N-proton states representing genes or dark proteins.

3 Some applications

3.1 How to understand the pairing between basic biomolecules and their dark variants?

There are interesting questions concerning the analogs of transcription and translation. Could dark DNA send signals also to dark RNA and amino acids and dark RNA to dark amino acids and dark tRNA? Could 3-photon resonance make it possible for biomolecules to find each other in the molecular crowd as proposed. This would be possible when the moods (bio-harmonies are the same - only an unhappy person can really understand an unhappy person!). For genes the 3-flux tube would be replaced with 3N-flux tube made possible by Galois confinement [L24] .

3.1.1 Where do the dark proton sequences associated with proteins come from?

In the formation of protein 3 dark protons drop to a larger space-time sheet. The charges of amino acid residues vary in sign, vanish, or they are neutral, polar, or non-polar. Therefore the dark proton triplets must somehow be associated with the protein backbone as they do in the case of DNA and RNA. This implies that it is ionization of acidic groups OH (as in case of phosphates in DNA) or NH_2. The pairing with the residues would come from 3-photon cyclotron resonance.

Where do the dark protons come from? The backbone of protein is in the same role as sugar phosphate backbone in DNA and RNA. Amino acid residues are in the same roles as DNA nucleotides.

1. Amino acids are acids: NH_2 and COOH groups make them acidic. They tend to release protons and become negatively charged. They could give dark protons. In the formation of protein $NH_2 \to NH$: one proton and electron lost. Does the proton come dark?

   Where does the electron go? Is it also dark and bound with a dark proton to form a dark atom? This kind of option in the case of the TGD based model for cold fusion [L7, L11] involving dark dark proton sequences in a smaller scale.

2. C-OH loses H as C-O-N is formed. Both electron and proton are lost. Also this proton could become dark and bind with the dark electron to form dark hydrogen atom.

3. Where does the third dark proton come from? Is also NH in C-NH of the peptide acidic? Can it lose a proton, which becomes dark? Just as in the case of DNA codon, electrons would neutralize the dark proton. One would have instead of a dark proton sequence a dark H sequence. The additional charge of amino acid can be positive or negative and its possible polarity relates to the residues and to chemistry. The backbone would serve as the interface between dark matter and chemistry. The resonant interaction between the dark amino acid and residue would give the pairing between amino acid and its dark counterpart.

3.1.2 Denaturation of proteins and DNA

One can wonder how the denaturation of proteins and DNA could relate to dark protons.

1. Do the dark hydrogens become ordinary in the case of protein? h_{eff} would be reduced and the protein would decay. The energy liberated from dark protons and be used to store metabolic energy in the catabolism of proteins.

2. In the denaturation of DNA double strand hydrogen bonds between strands are lost. This also happens in DNA strand opening during transcription and translation. This cannot relate to a loss of dark proton sequences, which would lead to depolymerization.

   Why does the loss of hydrogen bonds lead to the denaturation? Is there binding between dark codon sequences inducing the formation of hydrogen bonding? Is Galois singletness for Z_3 replaced with Z_6 singletness so that a bound state of 2 dark proton triplets corresponding to codon and conjugate would be formed: this would be codon pairing at the level of the dark genome. This is considered in [L24].

3.1.3 Hydrogen bonds and energy resonance

If also hydrogen bonds involve dark proton, there should be an energy resonance in which the dark proton returns from an excited cyclotron state and gives energy to the molecule to which it is bound and excites it. This would then decay to ground state and give the energy back to the dark proton. This would be kind of quantum tennis.

Hydrogen bonds would be also present between the paired bases: depending on the base pair their number would be 2 or 3. These dark protons would not correspond to those associated with dark DNA strands. An interesting question is how important the pairing of dark DNA strands and analog of hydrogen bonds of base pairs is and whether it relates to the energetics assigned with hydrogen bonds.

For instance, one can ask why A-T pairing by hydrogen bonds rather than A-C pairing is good.

1. Suppose that the dark codons DA and DT have the same 3-frequency giving rise to frequency resonance between them so that they can pair. DA and DC do not have the same 3-frequency and cannot pair. Pairing is therefore unique at the dark level.

2. The energy resonance condition assigns to a dark codon a unique codon so that one obtains only A-T pairing induced by dark pairing.

3.2 Does high energy phosphate bond involve 3 dark protons?

High energy phosphate bond plays a key role in the modelling of ATP hydrolysis [I1] in the framework of standard chemistry. The official view is that everything is well-understood but for instance Ling has criticised both the notion of the high energy phosphate bond and the reduction to the molecular level [I11, I12, I5, I8, I9] and also emphasised the importanec of a network like structures assignable to the cellular water: in TGD these networks would relate to MB. The work of Ling is discussed from TGD point of view in [L1, L2] [K4, K5].

From the TGD point of view the notion of high energy phosphate bond would be a mistake at the level of fundamental physics: dark matter and MB would be neglected. Thermo-dynamical chemistry can cope with this phenomenologically by introducing the notion of chemical potentials effectively describing the presence of dark matter. What is lost is quantum coherence in longer than atomic scales needed to really understand life.

The energy carried by 3 dark protons should replace the notion of high energy phosphate bond. Pollack effect indeed requires energy feed and this energy would go to dark protons taken from water.

Remark: Pollack effect would be an extreme example of adicity. Every fourth proton would become dark proton at flux tubes. pH would be $log_{10}(4)$! Also ordinary acidity could mean presence of dark protons but their number would be extremely small: one has fraction 10^{-7} for $pH = 7$.

This view would hold also more generally. The dark protons associated with proteins would also serve as a metabolic energy storage. In the denaturation this energy would be liberated. This happens in composts in which the organic material decays and causes heating of the compost. Of course, also the valence bonds which are dark carry energy as energy of dark electrons: by $h_{eff} > h$ the Coulombic bindin energy would be reduced and the energy of the valence bond would increase.

ATP→ADP and also ADP→ AMP [I4] are possible. Dark electrons associated with the valence bonds could contribute to bond energy since large $\hbar$ reduces the negative Coulomb interaction energy assignable to the bond.

Also the dark protons associated with the phosphates could contribute the energy assigned usually with high energy phosphate bond. Pollack's finding [I14] about the formation of exclusion zones (EZs) in presence of irradiation, most effectively IR radiation, led to the TGD based model. A considerable fraction of protons (fraction of 1/4) would be transferred to dark protons at the dark flux tubes. This requires (metabolic) energy and IR radiation would provide it and the energy is stored as energy of dark protons. Hence the pure chemistry based view about high energy phosphate bond would be wrong.

ATP has three phosphates and negative charge of -3 units. It would be screened by charges of 3 dark protons at the flux tube associated with ATP defining possibly a dark DNA codon (adenine triplet?). Dark RNA is not allowed since RNA does not allow A but U instead of it. In ATP → ADP the energy is given as a photon to the enzyme catalyzing the reaction allowing to overcome

activation energy barrier. In microtubules one has GTPs binding stably to α tubulins but not β tubulins.

Microtubules (MTs) define an interesting candidate for the realization of genetic code. One can also try to understand MTs and their dynamics in terms of Galois confinement.

1. The model of 6-bit memory code [J2] discussed by Hameroff *et al* relies on the hexagonal lattice formed by tubulin dimers consting of a pair of α and β tubulins, the 6-foot structure of CaMKII kinase domains, and the fact that the hexagon and CaMKII fit nicely together. The dynamical tubulins must be β tubulins for which the phosphorylation is not stable. The phosphorylation state of a given foot of the CamKII kinase domain represents a single bit so that CaMKII stores 6 bits. Its attachment at the hexagon of 6 tubulin dimers containing one tubulin dimer at is center could transfer the GTPs and thus 6 bits of information to the center tubulin. The proposed interpretation is as a transfer of information from neuronal to microtubular level involved with the synaptic learning.

2. The TGD inspired question is whether the CaMKII kinase domains are accompanied by dark proton triplets transferred to the tubulin dimer at the center of the hexagon so that microtubules would provide a 2-D representation of genetic code. If CamKII affects only the dark codon at the center of the hexagon, the center hexagon can behave as indepent 6-bit units making possible 2-D lattice representation of the genetic code. This framework does not allow charge neutrality, and microtubules are indeed negatively charged having positively charged and negatively charged ends. Second option would be that the stable GTPs associated with α tubulins define an analog of genome with single codon per GTP.

3. GTPs at the minus end of MT stabilize it, and GTP $\rightarrow$ GDP transition liberating energy occurring for β tubulins causes the thread mill instability illustrated by a video of the Wikipedia article about MTs. The 13 linear strands of tubulin dimers separate and bend radially outward. Are the 13 tubulin strands Galois confined states of tubulin dimers? Do also the 13 strands form a Galois confined state? Does the liberated energy overcome the activation energy barrier against the decay to 13 separate tubulin strands?

   The video of the Wikipedia article illustrates the formation of the structure. Could the decay correspond to a cascade of cognitive measurements leading from a state in Galois group algebra to an entangled product state in the tensor product of states assignable to the group algebras of normal Galois subgroups associated with an extension of extensions of ... of rationals [L27].

3.2.1 The energetics at the dark proton flux tube

The energetics of the flux tube containing 3 dark protons must be considered.

1. Consider first the Coulombic interaction energy between dark protons. The interaction energy includes Coulombic interaction energy of nearest neighbor dark protons with distance R and those with distance of 2R.

   (a) If the flux tube is open, then we have

   $$E_c = \frac{2e^2}{R} + \frac{e^2}{2R} = \frac{5}{2}\frac{e^2}{R} \equiv \frac{5}{2}E_0. \tag{3.1}$$

   (b) If the flux tube is closed one has

   $$E_c = 3E_0 \ . \tag{3.2}$$

2. There is also strong interaction energy (one has a dark nucleus) . Strong interaction is short ranged.

(a) If the flux tube is open one has strong interaction energy $2E_s$ and total energy is

$$E_{open} = \frac{5}{2}E_0 + 2E_s \ . \tag{3.3}$$

(b) If the flux tube is closed one has

$$E_s = 3E_0 + 3E_s \ . \tag{3.4}$$

3. There is also the total negative Coulomb interaction energy of dark protons with the total charge of phosphates.

$$E(c,N) = K(N)E_P \ , \tag{3.5}$$

where E_P is interaction energy between dark proton and phosphate. $N = 3, 2, 1$ for ATP, ADP, AMP If the dark protons interact as independent entities with 3 different phosphates one has $K = N$. If both ATP and protons act as single charged entities this energy one has $K = N^2$

4. The total energies for ATP, ADP, AMP are given by

$$\begin{array}{ll} E_{open,3} = \frac{5}{2}E_0 + 2E_s + K(3)E_P \ , & E_{closed,3}(ATP) = 3E_0 + 3E_s + K(3)E_P \ . \\ E_{open,2} = E_0 + E_s + K(2)E_P \ , & E_{closed,3}(ATP) = E_0 + E_s + K(2)E_P \ . \\ E_{open,2} = K(1)E_P \ , & E_{closed,3}(ATP) = K(1)E_P \ . \end{array} \tag{3.6}$$

where $K = N$ or $K = N^2$. Note that for $N = 1$ there is no difference between open and closed cases.

5. What happens in ATP→ADP and ADP→AMP? One organic phosphate (P) transforms to inorganic phosphate ion P_i without dark proton and one dark proton is lost. There are two left. Energy is liberated. There are also other contributions but let us forget them for a moment. The energy liberated is $E \simeq .5$ eV, metabolic energy quantum, energy of an IR photon.

   The liberated energy is in various cases

$$\begin{array}{l} \Delta E_{open}(ATP) \to ADP) = \frac{3}{2}E_0 + E_s + [K(3) - K(2)]E_P \ , \\ \Delta E_{closed}(ATP \to ADP) = 2E_0 + 2E_s + [K(3) - K(2)]E_P \ , \\ \Delta E(ADP \to AMP) = E_0 + E_s + [K(2) - K(1)]E_P \ . \end{array} \tag{3.7}$$

3.2.2 Empirical input

The reconstruction of ATP requires 1 dark proton and free energy about $\Delta G = -.5$ eV is needed. Actually 3 or 4 protons arriving through the cell membrane and getting kinetic energy in the membrane potential are used. Where does the surplus energy go? Or is there any surplus energy at all?

1. Mitochondrial membrane potential for proton which is determined by Coulomb potential and chemical potential due to the proton concentration difference at two sides of the membrane is about .15 eV [I6]. Multiplying this by the number of protons 3 (4) gives .45 eV (0.5 eV) so that 3 dark protons are needed and 1 goes to ADP to give ADP. This gives a nice fit in both cases.

2. It is claimed that the free energy ΔG liberated in ATP→ ADP is the same as in ADP→ AMP. If ΔS matters, one has for the liberated free energy - metabolic energy currency -

$$\Delta G = \Delta E + T\Delta S \ . \tag{3.8}$$

$\Delta G = -.5eV < 0$, the nominal value of metabolic energy currency, holds true approximately.

3.2.3 Can the free energies liberated in ATP→ ADP and ADP → AMP be the same?

The condition that the metabolic energies as free energy changes are same for various options gives the following conditions.

1. For open and closet flux tube option one would obtain the condition:

$$\begin{array}{ll} Open & \frac{3}{2}E_0 + E_s + [K(3) - K(2)]E_P + T\Delta S(ATP) \rightarrow ADP) = \\ & E_0 + E_s + [K(2) - K(1)]E_P + T\Delta S(ADP \rightarrow AMP) \\ Closed & 2E_0 + 2E_s + [K(3) - K(2)]E_P + T\Delta S(ATP \rightarrow ADP) = \\ & E_0 + E_s + [K(2) - K(1)]E_P + T\Delta S(ADP \rightarrow AMP) \ . \end{array} \tag{3.9}$$

   We obtain the following results form $K = N^2$ and $K = N$ options respectively:

$$\begin{array}{ll} (Open, K = N^2): & E_0 = -10E_P - 2X \ , \\ (Open, K = N): & E_0 = -2X \ , \\ (Closed, K = N^2): & E_0 + E_s = -2E_P - X \ , \\ (Closed, K = N): & E_0 + E_s = -X \ , \\ & X = (\Delta S(ATP \rightarrow ADP) - \Delta S(ADP \rightarrow AMP)) \ . \end{array} \tag{3.10}$$

   For $K = N^2$ option E_0 is positive even when $X = 0$ is true. For $K = N$ $E_0 = 0$ holds true for $X = 0$ and one must have $X < 0$ meaning that the entropy increase in ADP→ AMP is larger than in ATP→ ADP.

2. One obtains the following values for E_0 in various cases. All terms are manifestly positive in the expressions as they should be.

$$\begin{array}{ll} (Open, K = N^2): & E_0 = -10E_P - 2X \ , \\ (Open, K = N): & E_0 = -2X \ , \\ (Closed, K = N^2): & E_0 = -2E_P - X - E_s \ , \\ (Closed, K = N): & E_0 = -X - E_s \ , \\ X = (\Delta S(ATP \rightarrow ADP) - \Delta S(ADP \rightarrow AMP)) \ . & \end{array} \tag{3.11}$$

3. Liberated free energy can be positive in all cases unless $E_P < 0$ has too large a magnitude.

$$\begin{array}{ll} (Open, K = N^2): & \Delta G = -7E_P - 2X + Y \ , \\ (Open, K = N): & \Delta G = E_P - 2X + Y \ , \\ (Closed, K = N^2): & \Delta G = -E_P - X + Y \ , \\ (Closed, K = N): & \Delta G = E_P - X + Y \ , \\ & X = -T(\Delta S(ATP \rightarrow ADP) - \Delta S(ADP \rightarrow AMP)) > 0 \ , \\ & Y = T\Delta S(ADP \rightarrow AMP) > 0 \ . \end{array} \tag{3.12}$$

   One can argue that $\Delta S > 0$ in both reactions since the number of $h_{eff}/h_0 > 0$ protons decreases and the "IQ" of the system decreases. Hence one has $Y > 0$. The term E_P in $K = N$ case is negative. The term proportional to X is positive for all cases if $X < 0$ is true. This would mean that $\Delta S(ATP \rightarrow ADP) < \Delta S(ADP \rightarrow AMP)$. Entropy would increase more in the latter reaction. $K = N^2$ options are favored and the most favored is (Open, $K = N^2$) option: open flux tube with 3 dark protons interacting with phosphate charges like single charge of 3 units as the identification as a Galois confined state suggests.

4 Some TGD inspired comments about biocatalysis

It seems that the Pollack effect [I10, L4, I15, I14] could play a fundamental role in living matter. In the TGD framework, Pollack effect has several applications generalizations (see [L4, L10, L29, L23, L30, L28]). OH-bonds, typically associated with acids, are fundamental and they could be dynamical so that Pollack effect and its reversal, that is the transformation $OH \leftrightarrow O^- + p$, where p is dark proton at the monopole flux tube, could be central in quantum biology [L31]. Pollack effect would generate exclusion zones (EZs) with negative charge and also the electrons could be dark. What follows is an attempt to test this proposal.

There are good reasons to believe that this qubit is topological and TGD analog of condensed matter Majorana fermion requiring respecting fermion number superselection rule [L33]. This topological qubit would make possible fully topological quantum computations based on braidings of monopole flux tubes [K1, K10, K7].

Catalyst action by a gel phase bounding water is necessary for the Pollack effect. It could be needed to kick the OH bond near to the criticality against the splitting to $O^- + p$ induced by the Pollack photon. One should also understand catalyst action in the TGD framework. I have proposed that here magnetic monopole flux tubes and large value of h_{eff} behaving like dark matter could play a central role: the latest discussion can be found in [L32]. Magnetic body could serve in the role of midwife or energy investor in bio-catalysis which together with the Pollack effect would make it possible to overcome the potential barrier making the reaction very slow.

In the sequel biocatalysis, Pollack effect, and catabolism and anabolism as aspects of metabolism are considered from the TGD point of view. In particular, the mysterious notions of high energy phosphate bond and the existence of two different phosphates, the organic and inorganic phosphate are discussed.

4.1 Basic facts about biomolecules

It is good to start with some basic biochemical notions relevant for what follows.

1. Acids (see this) is a molecule able to donate a proton (Brönsted-Lowry acid) or to form a covalent bond with an electron pair (Lewis acid). The hydronium ion H_3O^+ is an example of Arrhenius acid. Base (see this) is a substance which dissociates in aqueous solution to form hydroxide ions OH^-. Base is typically metal hydroxide such as NaOH, which dissociates to $Na^+ + OH^-$.

   According to TGD, in Pollack effect the -OH associated with a water molecule can dissociate and give rise to a water ion OH^- and dark proton at monopole flux tube. In the case of base like NaOH one would obtain Na^+ and HO^-. The strange effects of ELF em fields observed by Blackman [J1] and others suggest that Na^+ is a dark ion [K6]. These dark ions would play a key role in the TGD inspired biology. Could acids and bases differ in that the acids can donate ordinary proton and bases can donate dark proton or dark metal ion? Or are dark ions

   Note that besides ions, also radicals involving one unpaired electron, making them highly reactive, are important. H-O radical is a basic example.

2. Reduction means that the reactant gains electrons and oxidation that the reactant loses electrons (see this). One speaks of redox reactions.

3. Catalysts play a central role in biology by increasing the reaction rates dramatically. Enzymes (see this) are proteins acting as catalysts and ribozymes (see this) are RNA sequences serving for the same purpose. Also metal ions such as Mg++ can serve as catalysts. Co-factors NAD, NAD^+, NADP, NADP, $NADP^+$, NADPH, FAP involving phosphates (see this), FAP (this) act as catalysts.

   Within the enzyme, generally catalysis occurs at a localized site, called the active site.

4.1.1 Some facts about the binding energies of bonds appearing in bio-molecules

It is useful to have some basic understanding about the binding energies of various bonds appearing in biomolecules. There are tables about bond energies: usually the bond energies are given using

kJoule/mol as a unit. With particle physics background, eV is a more conventient unit and the energies can be translated to eV:s by using the equation eV= 96.45 kJ/mol. The chemical bonds can be classified to ionic-, valence- and hydrogen bonds.

1. Ionic bonds (see this) typically between ions with opposite valences at opposite ends of the row of periodic table (such as NaCl ionic bond) have energies in the range 1.8-15.6 eV and therefore rather high.

2. Covalent bonds (see this) involving sharing of electrons between bonded atoms. Single -, double -, and even triple bonds can appear. Often the rule that in stable states the total number of bonds is the number of states at the shell, is satisfied. Covalent bonds also have also rather high bonding energies in few eV range (see for instance this). The bond energies are usually given by using kJoule/mol as a unit. eV is a more convenient unit and the energies can be translated to eV:s by using ev= 96.45 kJ/mol.

   The following list gives biologically interesting examples of bond energies. The energies are given in eVs and the subscript $_3$ refers to a triple bond.

$$
\begin{array}{l}
H-H=4.5 \\
\\
C-H=4.3 \quad C-C=3.6 \quad C=C=6.2 \quad C-_3C=8.7 \\
\\
O-H=4.8 \quad O-C=3.7 \quad O=C=8.3 \quad O-_3C=11.1 \\
O-O=1.5 \quad O=O=5.1 \\
\\
N-H=4.0 \quad N-C=3.2 \quad N=C=6.4 \quad N-_3C=9.2 \quad N-O=2.1 \\
N=O=6.3 \quad N-N=1.7 \quad N=N=4.3 \quad N-_3N=9.8 \\
\\
P-H=3.3 \quad P-C=2.7 \quad P-O=6.0 \quad P=O=5.6 \quad P-P=2.1
\end{array}
\tag{4.1}
$$

   In the list the so-called high energy phosphate bond, assumed to appear between organic phosphates, is not mentioned. This notion is poorly understood and in the sequel a TGD based model for it will be discussed.

   ADP (see this) and ATP (see this) molecules would possess high energy phosphate bonds. The metabolic energy currency associated with single ATP molecule is about .22 eV carried by an ATP molecule (see this). ATP synthase (see this)is a molecular machine analogous to a power plant producing about 3 ATP molecules per single rotation and therefore giving energy .66 eV. The glycolysis portion of cell respirations produces two 2 ATP molecules making .44 eV. This energy is often called metabolic energy currency.

   On must be very careful with the meanings of the words when one talks about energies in order to avoid a total confusion. The bond energy associated with P-O bond is about 6.0 eV so that its splitting requires energy. On the other hand hydrolysis of ATP under standard conditions in presence of water by a cleavage of a single phosphate by water (creating ADP + Pi, where Pi is inorganic phosphate) yields -.32 eV change of Gibbs free energy (see this). The cleavage of pyrophosphate by water (creating AMP + PPi) yields .47 eV so that in both cases one can talk about high energy phosphate bond. Other triphosphates, such as UTP, CTP, TTP, and GTP yield equivalent amounts of energy, indicating that the energy source is the triphosphate, not the base in the nucleotide.

   The binding energy of C-N bond or peptide bond (see this, appearing between amino-acids in proteins and between phosphate group and ribosome in DNA, RNA and tRNA, is 3.1 eV. The bond is very stable and split by catalytic action. Peptide bond is formed by dehydration in which O=C-OH of the first amino acid and H^2N of the second amino acid fuse to O=C-N-H. This means that the O-H group disappears and only the second end of the peptide has OH group proposed to act as OH-O^- qubit besides OH groups in the side chains of amino-acids. There are 5 amino-acids which contain an OH group in the side chain implying that they

also have OH group also when in proteins and these correspond to charged amino-acids Thr, Tyr, Ser, Glu, Asp. An interesting question is whether they are somehow special from the point of view of catalysis. For instance, could these amino acids correspond to active sites of enzymes?

3. Hydrogen bonds (see this) appear as H...O bonds between hydrogens and oxygens in water molecules. They appear also as N...HN and NH_2...O bonds between the bases of DNA strands. Their bond energy varies between .01 eV and 1.67 eV.

The rule is that the basic building bricks of biomolecules have large bond energies whereas the dynamical structures have much smaller binding energies. Catalyst are necessary in the ste structural changes.

4.1.2 Some important organic molecules

Also a list of some organic molecules important for what follows is in order.

1. DNA, that is deoxyribonucleic acid, as building bricks DNA nucleotides (see this). The nucleotides have a common building block phosphate making them acids and deoxyribose (sugar). The varying part of the DNA nucleotide is a base. There are 4 different bases: pyrimidines A,T and purines C,G. In DNA double strand the bases form pairs (see this) A-T resp. G-C, with A and T connected by 2 and C and G connected by 3 hydrogen bonds DNA. DNA codon consists of 3 nucleotides forming its letters. RNA codons are pyrimidines U,T and purines C-G.

   DNA codons code for 21 amino-acids having constant part O=C-OH part responsible for the acid property. Proteins are formed as sequences of amino acids in which peptide bonds -O=C-N are formed by dehydration (splicing of a water molecule) so that -O=C-OH and H_2N- is replaced with -O=C-(NH)-.

2. Carbohydrates are decomposed into monosaccharides (sugars). Glucose $C_6H_{12}O_6$ is basic example of monosaccharide. Carbohydrates, lipids and metabolic energy storage

3. Lipids or fats have carbohydrate sequences having O=C-OH carboxyle group at their ends (see this).

4. Alcohols (see this) are organic compound that carry at least one hydroxyl (OH) functional group bound to a saturated carbon atom.

5. Esters are building bricks of fatty acids which in turn are building bricks of lipids composing cell membranes. Ester is obtained from acid by replacing one H in at least OH group by organyl group R with at least one free valence electron in carbon atom so that there is C=O present (see this). Glyceride fatty acid is an ester of glycerol, in which H in at least one OH group is replaced with R. Glycerol is an alcohol.

Phosphate is an enigmatic molecule and deserves a separate discussion.

1. There are two kinds of phosphates (see this). High energy phosphate bond distinguishes between inorganic and organic phosphates. Is the organic phosphate excitation of inorganic phosphate which is near the splitting of OH bond to produce dark proton. Plants load the phosphate bonds with energy. Also animals can do this. Bacteria in soil use the energy of organic phosphates and produce inorganic phosphate.

   The metabolic energy of proteins can transform inorganic phosphate to organic phosphate. This requires energy to generate high energy phosphate bond. Is the energy already present in NAD and ANDP or is it liberated in the catabolism of nutrients and used to excite the inorganic phosphate? Does the formation of organic compound containing phosphorus liberate this energy as a binding energy? PO^4 binds to the molecule by valence bond (see this.

   Phosphorus cycle (see this) is a key cycle in biology. Plants provide the phosphorus needed by metabolism and the formation of bones and teeth. Soil microbes recycle organic phosphate

to inorganic form for plant uptake. Plants transform the inorganic P (in soil and water) to organic phosphate.

2. Cofactors (see this) are metallic ions (such as Mg^{2+}) or complex organic molecules in which case they are called coenzymes. Coenzymes NAD(P)H and NAD(P)$^+$ (see this) contain nicotinamide and diphosphate thought to have what is called higher energy phosphate bond. These coenzymes are needed in catabolism and metabolism and are necessary to produce ATP from ADP. The transformation ADP $\rightarrow$ ATP requires as a coenzyme NAD, NAD$^+$ containing 2 phosphates.

4.2 Metabolism, catabolism and anabolism

Catabolism and anabolism are the destructive and creative aspects of metabolism.

4.2.1 Catabolism

The basic goal of catabolism (see this) as a way to release metabolic energy stored temporarily to ATP molecules and break the molecules involved to basic building bricks so that they can be rebuilt in anabolism.

Catabolism decomposes polysaccharides, lipids, nucleic acids, and proteins to smaller molecules containing large numbers of OH bonds associated with carbons. In particular, molecules such as carbohydrates and fats serving as metabolic energy sources are decomposed to smaller units such as monosaccharides and fatty acids.

Monosaccharides, fatty acids, and proteins can be decomposed further to produce energy. OH groups are transformed to O-phosphate groups used to transform ADP to ATP. This requires phosphate which is basically obtained as inorganic phosphate from soil and water and transformed to organic phosphate characterized by high energy phosphate bond.

1. Glycolysis (see this) is a set of reactions that converts glucose to pyruvate or lactate. This metabolic pathway can be considered as a paradigm of metabolic pathways. Glycolysis is also called the Embden-Meyerhoff pathway. Glycolysis involves two phases: the investment phase during which energy provided by ATP molecules is used and the phase in which energy is stored to ATP molecules. Glycolysis adds phosphates from NAD:s and NADPs to ADPs to build ATP which carries the energy to the molecule using it.

2. In lipid catabolism (see this) the triglycerides produced in glycolysis are decomposed to fatty acids (see this), which are main components of lipids appearing as building bricks of cell membranes.

   Fatty acids exist as three main classes of esters: triglycerides, phospholipids, and cholesteryl esters and serve as dietary sources of fuels and structural components for the lipid layers of cells.fats are decomposed into fatty acids and glycerol which is a simple alcohol, with 3 carbons with OH in each carbon (see this). Lipids or fatty acids are used to store metabolic energy.

   Ketone bodies (see this) serve as energy storages. Ketone bodies are water-soluble molecules or compounds that contain the ketone groups produced from fatty acids by the liver (ketogenesis). Ketone bodies are transported into tissues outside the liver, where they are converted into acetyl-CoA (acetyl-Coenzyme A) which then enters the citric acid cycle (Krebs cycle) and is oxidized for energy. Krebs cycle releases the energy stored in nutrients through the oxidation of acetyl-CoA derived from carbohydrates, fats, proteins, and alcohol.

3. Also proteins can be used as a metabolic fuel when glucose is not available. Also extra proteins are converted to glucose and triglycerides. Catabolism and anabolism are competing processes and a kind of self-amplifying loop in which too much anabolism induces catabolism and vice versa might emerge and must be avoided.

Coenzyme A or briefly CoA (see this) has a key role in Krebs cycle releasing metabolic energy in catabolism.

1. CoA contains a phosphate associated with adenine (A) and monophosphate associated with Acetyl (see this). CoA has a role similar to that of NAD(P). CoA is involved with fat metabolism and attaches to the fatty acyl group (see this), which involves a double-bonded oxygen atom and an organyl group (R C=O) or hydrogen in the case of formyl group (H C=O). CoA serves as an Acyl carrier protein.

2. CoA-acyl group bond to the sulspher of =O-S has a negative bond energy: -0.33 eV slightly below the metabolic energy currency and thus serves as a temporary energy storage and could have a role similar to that of phosphate bond. Note that the metabolic energy carried by a single ATP molecule is .22 eV. Also NAD(P) has a high energy bond so that it can serve for catalytic purposes by providing this energy temporarily.

3. The energy of the high energy phosphate bond is 489.7 kJ/mol= 5.1 eV and therefore much higher than metabolic energy currency. This energy scale is the same as that of valence bonds. A natural guess is that in biocatalysis this energy is used to kick the reactants over the potential barrier making the reaction very slow. The reactants would receive this energy temporarily and give it back after the reaction has occurred.

4.2.2 Anabolism

In anabolism these building brick molecules obtained in catalysis used to rebuild polysaccharides, lipids, nucleic acids, and proteins. From nucleic acids and aminoacids DNA, RNA and proteins are constructed in cells. Also bones are constructed in anabolism. Carbohydrates are constructed in plants and some bacteria by photosynthesis. Photosynthetic carbohydrate synthesis in plants and certain bacteria is an anabolic process that produces glucose, cellulose, starch, lipids, and proteins from CO_2. Lipids are constructed in both plant and animal cells and some lipids animal cells are obtained only in diet.

4.3 The TGD perspective

In the following TGD perspect of metabolism, in particular the role of phosphate and mechanism of catalysis is discussed. The new elements are the new view of space-time, in particular the notions of field body and magnetic monopole flux tubes; the predicted hierarchy of effective Planck constants h_{eff} meaning the existence of hierarchy of dark matter-like phases of the ordinary matter with arbitrarily long quantum coherence scales; Pollack effect interpreted as a transfer of ordinary protons to dark protons of field body; and the topological reactions of monopole flux tubes proposed to play a key role in biocatalysis.

4.3.1 The phosphate mysteries

Phosphate is the black sheet of the standard bio-chemistry. It involves two mysteries. The existence of two kinds of phosphates, the inorganic and organic phosphate, is the first mystery. The high energy phosphate bond is the second mystery.

1. There are two kinds of phosphates: inorganic phosphate $PO_4{}^{3-}$ and organic phosphate R-O-(O=P(OH)$_2$ appearing in di- and triphosphates and plants. The -OHs in the organic phosphate can become negatively charged. The organic phosphates in ATP would provide the metabolic energy to the inorganic phosphate.

   Phosphate cycle is fundamental for living matter. After the biological death, organic phosphate of the body transforms in the soil to inorganic phosphate by bacterial activity, which would use the organic phosphate as a metabolic energy source.Plants would in turn use the inorganic phosphate and transform it to organic phosphate by using the energy provided by photosynthesis. Animal cells would in turn use plants as nourishment and get the organic phosphate in this way. Animals can also use the inorganic phosphate and presumably transform them to organic phosphate by providing the needed energy. This cycle is known as the phosphate cycle.

   What distinguishes between these two kinds of phosphates?

2. There is also the mystery of high energy phosphate bonds. ATP and ADP and various compounds appearing in biology involving more than one phosphate are assumed to have what is called high energy phosphate bonds. The notion of high energy phosphate bond plays a central role in catabolism providing metabolic energy, which is assumed to be temporarily stored to the ATP serving. ATP would provide the metabolic energy currency of about .22 eV to the receptor molecule by forming a connection consisting of a flux tube pair. The bonding energy of the O-P bond in ATP is however 5 eV and has the wrong sign: the splitting of the bond requires this energy. Something goes wrong.

These mysteries inspired two TGD inspired questions.

1. Does the high energy phosphate bond exist at all? Could the TGD counterpart of a high energy phosphate bond be identifiable as a monopole flux loop carrying a dark proton created in the splitting of OH to O^-+p by Pollack effect, where p is dark proton at monopole flux tube [L31]. Could the dropping of the dark proton in the transition $O^-+p \to OH$ provide the metabolic energy currency and lead to the disappearance of the illusory high energy phosphate bond.

2. Could the difference between organic and inorganic phosphate be that the negative charge in the case of organic phosphate is due to the transfer of the proton of -OH to a dark proton at magnetic flux tube producing $-O^-$ ion + dark proton. Also the electron of the O^- in the organic phosphate could be dark? In the case of inorganic phosphate there would be no dark proton and the electron would be ordinary?

If the answers to these questions are affirmative then the notion of a field body (magnetic/electric) could solve the mysteries related to the phosphates.

4.3.2 Catalyst action in the TGD framework

Catalysts make possible biochemical reactions by providing temporarily the energy needed to drive the system near the top of the potential barrier making the reactions slow. How biocatalysts that are enzymes (proteins), ribozymes (RNA) and also metal ions, can provide this energy. Catalyst must provide the energy needed to almost overcome the energy barrier preventing the reaction and measured in few eVs. It would seem that the metabolic energy currency .22 eV provided by ATP$\to$ ADP is much smaller than this energy and can only give the additional energy allowing to overcome the energy barrier. After the reaction has occurred the catalyst would get back the energy.

In the general TGD based picture, the reaction might look as follows.

1. Catalyst, reactants, and ATP possess U-shaped monopole flux tubes acting as tentacles. In the first step a reconnection between the tentacles of the catalyst molecule and those reactants and ATP takes place and connects them by flux tube pairs. The same could occur also for tentacles of reactants. The U-shaped monopole flux tube pairs connecting catalyst to reactants and in the case of enzymes (and perhaps also ribozymes, which however have phosphates) also to ATP molecules would carry energy making it possible to overcome the energy barrier(s) associated with the reaction.

2. This makes it possible for the flux tube pairs to find each other. The reduction of the value of h_{eff} for the flux tube pair would reduce the value of the dark cyclotron energy (proportional to h_{eff}) and possibly also the value of classical magnetic energy. The energy ΔE liberated in this way would help the reactants to get near the top of the potential wall. In the case of cyclotron energy, this would require a large value of h_{eff} and of gravitational Planck constant for the Earth would provide it. ATP could provide the remaining energy of order .22 eV making it possible to get over the potential barrier so that the reaction would take place.

3. After the reaction the reaction products would have additional energy and would have a recoil momentum. They would be associated with the ends of the flux loops connecting the catalyst to the reactants. These would get longer as a consequence and split by a reconnection, a

phase transition increasing the value of h_{eff} back to its original value would occur and the the energy ΔE borrowed from the catalyst would be returned to it. This suggest that the catalyst acts like a shell surrounding the reactants and explodes and takes back the energy ΔE.

This view can be compared with the following proposal that I found in the web (see this).

1. Each reaction in a cell has a specific enzyme. Each enzyme has binding sites for, say, two molecular species *and* for an ATP molecule. When a reaction takes place, the two species bind to the enzyme, and a little later, an ATP molecule binds.

   Comment: The contraction of the flux tube pairs would provide the system consisting of catalyst and reactants with an energy ΔE measured in eVs taking it near to criticality for the reaction to occur. .

2. For some reason (why ?), the ATP$\rightarrow$ ADP reaction is now energetically favourable, so the high-energy bond breaks.

   Comment: The ATP$\rightarrow$ ADP +Pi reaction would be essentially the reversal of a Pollack effect and involve a dropping of a dark proton from the field body liberating the metabolic energy currency .22 eV. This reaction can occur if the sign of the energy difference of -OH and -O^-+ dark proton states changes sign. This could be due to the presence of an electric field modifying the energy difference. I have proposed that this mechanism is central in bio-control [L31].

3. This releases electromagnetic energy as a photon at some characteristic frequency.

   Comment: The photon would be the counterpart of the Pollack photon allowing the reaction to occur if the system is near the criticality that is already near the top of the potential barrier.

4. Certain bonds in the enzyme have a resonant frequency that allow them to absorb this electromagnetic energy (the EM energy disturbs molecular dipoles?).

   Comment: The first step involving the contraction of the flux tube pairs would have driven the system, near criticality for the reaction. The absorption of the Pollack photon would break the camel's back and initiate the reaction.

5. The 3D structure of the enzyme is disturbed (i.e. it bends) in such a way that the 2 molecular species are mechanically forced together, providing sufficient activation energy for the reaction in question.

   Comment: The geometry and charge distribution would change this and the reaction to occur.

6. The newly formed species no longer binds nicely to the enzyme (why ?) so it detaches, as does the ADP, which also doesn't bind as nicely as ATP.

   Comment: TGD would suggest that catalyst molecule should surround the reactants and that catalyst receives recoil momentum forcing the lengthening of the flux tubes and increase of h_{eff} made possible by the energy ΔE that it invested to the reaction.

These considerations raise some questions about the energetics of the field bodies serving as controllers.

1. Field bodies (magnetic or electric), actually flux tube loops, serve as kinds of energy investors in biocatalysis. While reactants and ATP are affected in the reaction, the catalyst leaves the reaction without essential change and gets its energy investment back. The temporary energy gain ΔE needed to overcome energy barriers would come from the shortened flux tube pairs connecting the catalyst to the reactants rather than from the catalyst as is assumed in textbooks. ATP would provide the Pollack photon making it possible to overcome the potential barrier which is already made very low by the energy provided by the field body of the catalyst.

   Catalyst would serve as a kind of midwife. What distinguishes it from the reactants? The active site of a heterogeneous catalyst (heterogeneous catalyst is in a different phase than

reactants) is identified as an ensemble of atoms which directly catalyzes the reaction. Biocatalysts can be regarded as a special case of heterogeneous catalysts. Does the active site distinguish heterogeneous catalysts from the reactants? Does the active site correspond to a higher level of the h_{eff} hierarchy as compared to the reactants?

2. Does the energy provided in biocatalysis correspond to the classical magnetic energy of the flux tubes, the dark cyclotron energy associated with the dark particles at the magnetic body, or to both? The first option would conform with the temporary reduction of h_{eff} shortening the flux tubes and liberating classical magnetic energy proportional to the length of the flux tube. The reduction of h_{eff} would in turn liberate cyclotron energy.

4.3.3 Catabolism and Pollack effect

In the TGD framework, the Pollack effect is proposed to be the basic mechanism of metabolism and lead to the formation of ATP with ionized phosphate and dark protons taking care of the distribution of the metabolic energy as a standard metabolic currency. Essentially a generation of dark protons would be in question. The OH bonds are potential providers of dark protons and monosaccharides (see this) as end products of catabolism of carbohydrates, in particular glucose, are optimal in this respect. For (H-C-OH)$_n$-CHO the number of OHs is maximed so that also the number of potential dark protons is maximized. The process involves oxidation and oxygen obtained in breathing is therefore needed. Carbon dioxide and water is the final outcome of the process.

Consider next the proposed role of Pollack effect.

1. Acid capable of donating H^+. Is the donated proton ordinary proton or is donated proton in biological systems a dark proton, which then drops to the acceptor? DNA is acidic because of phosphate groups, which are usually represented as ionized. The Pollack effect or its reversal could occur when an external electric field changes the sign of the energy difference of the states -OH and -O^- + dark proton. Note that also the electron of -O^- could be dark in organic phosphate.

   The transformation of proton to dark proton or its reversal would in the TGD framework correspond to a process analogous to the change of a value of bit. This leads to the proposal that OH-O^- qubit and more generally, the generalization of this qubit could play a fundamental role in biology and even in systems involving cold plasma [L31]. In fact, OH-O^- could give rise to a topological qubit analogous to Majorana qubit [L33].

   Amino-acids in proteins lose their OH as the peptide bond (C-N bond) between two subsequent amino acids is formed by dehydration so that only the second end of the protein contains O=C-OH group. The 5 amino-acids Thr, Tyr, Ser, Glu, and Asp contain the -OH group in their residue so that Pollack effect could be possible for them. Note that the amino acid Cys (see this)) contains an -SH residue at least chemically analogous to -OH residue. It is frequently observed in functionally important (catalytic, regulatory, cofactor binding, etc.) sites of protein. Among the unique properties of Cys are its ability (i) to react with another Cys forming a disulfide bond, and (ii) to functionally interchange with another amino acid, selenocysteine (Sec).

   Also fatty acids (see this) contain O=C-OH groups at their ends and are potential providers of dark protons.

2. For phosphates the -OH is assumed to split spontaneously to O^- + dark proton, at least in the illustrations. The formation of ATP would generate dark protons. The use of metabolic energy reduces the number of dark protons as they drop back from the magnetic body in the transformation ATP$\rightarrow$ ADP+Pi. The essence of catabolism would be generation of dark protons assignable to the phosphates of ATP and ADP. As proposed, there is no need for a high energy phosphate bond since the dark proton would carry the metabolic energy currency.

3. Pollack effect generates exclusion zones which behave strangely: in particular the arrow of time seems to be reversed. This is possible in the zero energy ontology of TGD. If the electrons in EZs are dark, the duration of the period with the reversed arrow of time would

be scaled up. It would not be surprising if both dark electrons and dark protons at field bodies would distinguish between biochemistry and non-organic chemistry.

How does the Pollack effect relate to bases? Bases are able to donate electrons. Is this electron ordinary electron or could it be a dark electron, possibly formed in Pollack effect.

O=C-OH groups are potential providers of protons eventually transformed to dark protons by Pollack effect. The feed of metabolic energy makes possible Pollack effect and phosphate ions and dark protons are formed. The final outcome is APT containing phosphates (see this, this). Each amino acid contains O =C-OH group but proteins contain this group only at its second end.

1. The oxidation of sugars produces water and carbon oxide. Monosaccharides or simple sugars (see this) are optimal in this respect and are the final outcome of the catabolic process. For $(\text{H-C-OH})_n$-CHO the number of OHs is maximized so that also the number of potentially dark protons is maximized.

   Glycolysis could essentially mean the transformation of protons to dark protons and the transformation ADP→ATP in which inorganic phosphate would receive this dark proton carrying metabolic energy currency of about .22 eV. ATPAse machinery would pump 3 ordinary protons per rotation and transform them to dark protons of the phosphate added to ADP.

2. Alcohols contain OH-group bound to a saturated C atom.which therefore has valence bonds to 3 residues this. Also alcohol burning liberates energy. The psychological effects of sugars and alcohols would relate to the heightening of the level of consciousness as dark protons are created.

3. Dehydration means loss of OH groups because water is formed (see this). The ability for the Pollack effect is reduced in dehydration.

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