

On the Representations of Genetic Code by Dark Nuclear Strings in TGD Framework

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Abstract

The mainstream view of evolution as a random process suggests that genetic code is pure accident. The author is of the view that something so fundamental as life cannot be based on pure randomness. TGD has led to several proposals for genetic code, its emergence and various realizations based on purely mathematical considerations or inspired by physical ideas. One can argue that genetic code is realized in several manners just like bits can be represented in very many manners. Two especially interesting proposals have recently emerged. The first proposal is based on geometric model of music harmony involving icosahedral and tetrahedral geometries. The second proposal has two variants based on the concept of dark nuclear strings: The original version maps codons to dark nucleons and the latest version maps codons to dark 3-nucleon states. Both models predict correctly the numbers of DNA codons coding for a given amino-acid but the latter model is favoured by some recent findings which suggest pairing between DNA nucleotides and dark nucleons. Further, the counterparts of RNA, tRNA, and amino-acids are predicted.

Keywords: DNA, genetic code, dark, nuclear string, TGD framework.

1 Introduction

The view about evolution as a random process suggests that genetic code is pure accident. My own view is that something so fundamental as life cannot be based on pure randomness. TGD has led to several proposals for genetic code, its emergence, and various realizations based on purely mathematical considerations or inspired by physical ideas (see chapters of [10] and [14, 13]). One can argue that genetic code is realized in several manners just like bits can be represented in very many manners.

Two especially interesting proposals have emerged. The first one is based on geometric model of music harmony [19] involving icosahedral and tetrahedral geometries. Second one having two variants is based on dark nuclear strings. Both models predict correctly the numbers of DNA codons coding for a given amino-acid. In the sequel the nuclear string variant and also its connection with the model of harmony is discussed in detail.

It is good to start with an overall view about physical realization of genetic code that I have discussed during last twenty years.

1.1 Genetic code and Combinatorial Hierarchy

The first proposal [11] was purely mathematics inspired and in terms of so called Combinatorial Hierarchy consisting of certain Mersenne primes $M_k = 2^k - 1$ via the formula $M(n+1) = M_{M(n)}$ having interpretation in terms of abstraction. The list beginning from $M(1) = 2$ is $2, M_2 = 3, M_3 = 7, M_7 = 127, M_{127} = 2^{127} - 1$: it is not known whether subsequent integers are Mersenne primes. The idea is that the $2^k - 1$ points define almost full Boolean algebra spanned by k bits- one visualization is as a polygon. The algebra defined $k - 1$ bits is maximal full Boolean sub-algebra having interpretation as maximal number of mutually independent statements, which can hold true simultaneously. For M_7 ($k = 3$) one

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would have 2 bits and 4 codons. For M_7 one would have $k = 7$ and 6 bits and genetic code. For M_{127} one would have 126 bits and one would have "memetic" code realizable in terms of sequences of 21 DNA codons.

1.2 Geometric theory of harmony and genetic code

The idea that the 12-note scale could allow mapping to a closed path going through all vertices of icosahedron having 12 vertices and not intersecting itself is attractive. Also the idea that the triangles defining the faces of the icosahedron could have interpretation as 3-chords defining the notion of harmony for a given chord deserves study. The paths in question are known as Hamiltonian cycles and there are 1024 of them [1]. There paths can be classified topologically by the numbers of triangles containing 0, 1, or 2 edges belonging to the cycle representing the scale. Each topology corresponds to particular notion of harmony and there are several topological equivalence classes.

In the article [20] I introduced the notion of Hamiltonian cycle as a mathematical model for musical harmony and also proposed a connection with biology: motivations came from two observations. The number of icosahedral vertices is 12 and corresponds to the number of notes in 12-note system and the number of triangular faces of icosahedron is 20, the number of amino-acids. This led to a group theoretical model of genetic code and replacement of icosahedron with tetra-icosahedron to explain also the 21st and 22nd amino-acid and solve the problem of simplest model due to the fact that the required Hamilton's cycle does not exist. The outcome was the notion of bioharmony.

All icosahedral Hamilton cycles with symmetries (Z_6, Z_4, Z_2^{rot} and Z_2^{refl}) turned out to define harmonies consistent with the genetic code. In particular, it turned out that the symmetries of the Hamiltonian cycles allow to predict the basic numbers of the genetic code and its extension to include also 21st and 22nd amino-acids Pyl and Sec: there are actually two alternative codes - maybe DNA and its conjugate are talking different dialects! One also ends up with a proposal for what harmony is leading to non-trivial predictions both at DNA and amino-acid level.

The conjecture is that DNA codons correspond to 3-chords perhaps realized in terms of dark photons or even ordinary sound. There are 256 different bio-harmonies and these harmonies would give additional degrees of freedom not reducing to biochemistry. Music expresses and creates emotions and a natural conjecture is that these bio-harmonies are correlates of emotions/moods at bio-molecular level serving as building bricks of more complex moods. Representations of codons as chords with frequencies realized as those of dark photons and also sound is what suggests itself naturally. This together with adelic physics involving hierarchy of algebraic extensions of rationals would explain the mysterious looking connection between rational numbers defined by ratios of frequencies with emotions.

1.3 Letter-wise representations of genetic code in terms of single particle states

The model for DNA-cell membrane system as topological quantum computer with lipids and DNA nucleotide or codons connected by flux tubes led to a proposal for the correspondence of letters of genetic code with particle states.

1. The original proposal was that the 4 letters A,T,C,G correspond to dark u and d quark and their antiparticles \bar{u} and \bar{d} . Quarks and their antiparticles would reside at the ends of the flux tube. Spin would not matter in this model. The obvious criticism is that introducing dark antiquarks is too far fetched.
2. One can also consider a variant for which one has u and d quarks and spin matters.
3. TGD based model of bio-superconductivity assumes that flux tubes appear as pairs with members of Cooper pair at parallel flux tubes [15, 16]. This suggests that electron pairs at in spin 1 and

spin 0 states could realize the code. The spin of the electrons would matter and one would obtain 4 states - two qubits in correspondence with A,T,C,G.

Also the model of dark nuclear strings allows to imagine letter-wise representations of the genetic code. The model for cold fusion based on the findings of Prof. Holmlid and his group [2, 4] leads to the idea that Pollack's EZs [21] are accompanied by dark nuclear strings consisting of dark protons connected by color flux tubes analogous to mesons [22, 25]. Color bonds would have quark and antiquark at their ends [14]. This leads to non-trivial predictions and nuclear anomalies giving support for the notion of nuclear string have emerged, the latest anomaly is so called X boson with mass of 17 MeV [5, 3] having identification as p-adically scaled analog of pion.

Dark protons could also decay to neutrons by dark weak decays rapidly since dark weak bosons are effectively massless below dark Compton length. Furthermore, proton plus negatively charged color bond could behave like neutron as far as chemistry is considered. The X boson anomaly of nuclear physics [5] suggests that the flux tubes in the ground state correspond to pion-like states which can be colored: this could bind the nucleons to form a nucleus. The evidence for the occurrence of cold fusion in living matter gives support for the role of dark nuclear strings [18] [25]. One can consider several representations of the genetic code in this framework.

Consider first models for which letters are represented separately.

1. Dark protons and neutrons have 4 spin states and could correspond to letter A,T,C,G. In this case dark color bonds would not matter. A rather convincing proposal for a pathway leading to a selection purines as DNA nucleotides has been proposed [6]. TGD based model [23] suggests that acidic solutions contain dark protons and purine results when the precursor amine combines with dark proton such that the proton remains dark. Could DNA nucleotide pair with dark protons and neutrons (resulting in dark beta decay from dark proton strings yielded by Pollack's mechanism)?
2. Also the 4 states of dark color bonds between dark nucleons (3 pion-like states and one eta meson like state: spin 1 bonds would be analogous to ρ and ω mesons and have higher mass) correspond to letters A,T,C,G. Now the dark protons and neutrons would not matter. This option would require that the character of the nucleotide correlates with the color flux tube attached to the dark proton. They would have at their ends charge conjugate color bonds. The states would be of form $u\bar{u}, d\bar{d}, u\bar{d}, d\bar{u}$ with the ordering of q and \bar{q} correlating with the direction in which transcription and replication take place being thus same or opposite). For conjugate strand the direction of strand would be opposite in the sense that one would have $\bar{u}u, \bar{d}d, \bar{d}u, \bar{u}d$.

For this option one could consider the strands of dark DNA double strand being connected by flux tube pairs resulting when U-shaped color flux tube have reconnected. If color flux tubes are colored, color confinement could bind the dark protons to dark nucleus. Similar mechanism could be at work for the ordinary nuclei.

The basic problem of all the proposals based on letter-wise correspondence is that they do not even try to explain the numbers of DNA codons coding for a given amino-acid and are also silent about tRNA.

1.4 Codon-wise representations of genetic code realized in terms of dark nuclear strings

For this option entire codons rather than letters would be represented. The difference between two representations is analogous to that between spoken and written languages. In spoken languages words are not analyzed further to letters. These models are able to predict also the numbers of codons coding for a given amino-acid successfully.

1. The geometric theory of harmony represents codons as 3-chords without assigning fixed notes to A,T,C,G and explains also DNA-amino-acid correspondence.

2. The map of codons to the dark nucleon states of dark nucleon consisting of dark u and d type quarks does the same and also predicts the degeneracies successfully.
3. This model can be modified by replacing u and d by dark nucleon states p and n without any change in predictions related to genetic code. The evidence that DNA codons indeed couple to dark nucleon states [23] supports this option.

In the sequel I consider the models mapping DNA codons to dark nucleons and then generalize the model so that it applies to triplets of dark nucleons.

2 Models of genetic code based on dark nuclear strings

Water memory is one of the ugly words in the vocabulary of the main stream scientist. The work of pioneers is however now carrying fruit. The group led by Jean-Luc Montagnier, who received Nobel prize for discovering HIV virus, has found strong evidence for water memory and detailed information about the mechanism involved [13, 17], [7]. The work leading to the discovery was motivated by the following mysterious finding. When the water solution containing human cells infected by bacteria was filtered in purpose of sterilizing it, it indeed satisfied the criteria for the absence of infected cells immediately after the procedure. When one however adds human cells to the filtrate, infected cells appear within few weeks. If this is really the case and if the filter does what it is believed to do, this raises the question whether there might be a representation of genetic code based on nano-structures able to leak through the filter with pores size below 200 nm.

The question is whether dark nuclear strings might provide a representation of the genetic code. In fact, I posed this question year before the results of the experiment came with motivation coming from the attempts to understand water memory. The outcome was a totally unexpected finding: the states of dark nucleons formed from three quarks can be grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAs, and 20 amino-acids 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.

2.1 Mapping DNA and amino-acids to dark nucleon states

The dark model emerged from the attempts to understand water memory [13]. The outcome was a totally unexpected finding [14, 13]: 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 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 be not be anymore separable to letters but entangled states of 3 quarks.

If this picture is correct, genetic code would be realized already at the level of dark nuclear physics and maybe even in ordinary nuclear physics if the nucleons of ordinary nuclear physics are linear nucleons.

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 kind of shadow of the dynamics of positively charged dark nucleon strings accompanying the DNA strands and this could explain the stability of DNA double strand having 2 units of negative charge per nucleotide. Biochemistry might be controlled by the dark matter at flux tubes.

The ability of the model to explain genetic code in terms of spin pairing is an impressive achievement, which I still find difficult to take seriously.

1. The original model mapping codons to dark nucleon states assumed the overall charge neutrality of the dark proton strings: the idea was that the charges of color bonds cancel the total charge of dark nucleon so that all states uuu, uud, udd, ddd can be considered. The charge itself would not affect the representation of codons. Neutrality assumption is however not necessary. The interpretation as dark nucleus resulting from dark proton string could quite well lead to the formation the analog of ordinary nucleus via dark beta decays [25] so that the dark nucleus could have charge. Isospin symmetry breaking is assumed so that neither quarks nor flux tubes are assigned to representations of strong $SU(2)$.

There is a possible objection. For ordinary baryon the mass of Δ is much larger than that of proton. The mass splitting could be however much smaller for linear baryons if the mass scale of excitations scales as $1/h_{eff}$ as indeed assumed in the model of dark nuclear strings [22, 25].

2. The model assumes that the states of DNA can be described as tensor products of the four 3-quark states with spin content $2 \otimes 2 \otimes 2 = 4 \oplus 2_1 \oplus 2_2$ with the states formed with the 3 spin triplet states $3 \otimes 3 = 5 \oplus 3 \oplus 1$ with *singlet state dropped*. This means that flux tubes are spin 1 objects and only spin 2 and spin 1 objects are accepted in the tensor product. One could consider interpretation in terms of ρ meson type bonding or gluon type bonding. With these assumptions the tensor product $(2 \otimes 2 \otimes 2) \otimes (5 \oplus 3)$ contains $8 \times 8 = 64$ states identified as analogs of DNA codons.

The rejection of spin 0 pionic bonds looks strange. These would however occur as bonds connecting dark codons and could correspond to different p-adic length scale as suggested by the successful model of X boson [26].

One can also ask why not identify dark nucleon as a closed triangle so that there would be 3 color bonds. In this case $3 \otimes 3 \otimes 3$ would give 27 states instead of 8 ($\oplus 1$). This option does not look promising.

3. The model assumes that amino-acids correspond to the states 4×5 with $4 \in \{4 \oplus 2 \oplus 2\}$ and $5 \in \{5 \oplus 3\}$. One could tensor product of spin 3/2 quark states and spin 2 flux tube states giving 20 states, the number of amino-acids!
4. 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 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 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

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

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 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 $(2, 9, 1, 5, 3)!$

It is difficult to exaggerate the importance of this simple observation suggesting that genetic code is realized already at the level of dark or even ordinary nuclear physics and bio-chemistry is only a kind of shadow of dark matter physics.

2.2 Objections based on group theory and statistics

The model and its generalization replacing u, d with nucleon states p, n works amazingly nicely but is better to try to invent objections against the proposal and try to find inconsistencies. Fermi and Bose statistics are the most obvious providers of killer arguments.

1. The basic objection is that if the quarks are organized in linear structures, one cannot talk about representation of 3-D rotation group since symmetry breaking to $SO(2)$ acting along common axis which could be either the local axis along dark DNA helix or the axis of the entire helix. The linear ordering of the quarks is not consistent with the full harmonics. Rather, harmonics restricted to half space $0 \leq \theta \leq \pi/2$ ($\pi \geq \theta \geq \pi/2$) should characterize the "upper" ("lower") flux tube direction at the position of quark in the middle.

If reflection along quantization axis and $SO(2)$ generate the symmetries one still has labelling of the states by angular momentum projection and states form doublets $(m, -m)$. The representations of $SO(3)$ split into these representations and the numbers of states with given spin projection remain the same. Therefore the predictions for the numbers of DNA codons coding given amino acid are not changed. It is quite possible that braid statistics made possible by 1-dimensionality is needed to realize the idea about ordering and this would allow to have full DNA multiplets.

2. In quark model one forms tensor product of tensor products of 3 quark spin states and 3 quark isospin states and by color singletness requires that the state is completely antisymmetric in quark degrees of freedom. The state is completely symmetric in the non-colored degrees of freedom. One obtains only two representations $\Delta \leftrightarrow (3/2, 3/2)$ and $N = (1/2, 1/2)$ with positive parity. In quark model context the presence of other tensor products in $(4 \oplus 2_1 \oplus 2_2)_S \otimes (4 \oplus 2_1 \oplus 2_2)_I$ is forbidden. One reason is that spatial wave function is assumed to be symmetric in ground state. This forbids 2_2 in spin degrees of freedom. Symmetrization leaves only the Δ and N (Note that the total number of these states is 20!). Now strong isospin is broken and it is natural to not include it to the tensor product.
3. The presence of 2_2 would be forbidden in quark model since it would require antisymmetric spatial wave function to compensate for the antisymmetry of 2_2 . In the recent case the situation is 1-dimensional and the ordering along nuclear string forces localization of quarks and one cannot have identical wave functions for quarks.

1-D situation also suggests strongly braid statistics. Perhaps the situation could be understood in terms of fermionic oscillator operators along nuclear string having anti-commutation relations corresponding to non-trivial braid statistics - maybe making the statistics commutative. This could naturally allow anti-symmetrization along nuclear string for 2_2 states.

4. If one assumes ordinary statistics, one could take care of the statistics of the 16 states in $2_2 \otimes (5 \oplus 3)$ by assuming that for 2_2 the color state is symmetric and thus 10-D representation of $SU(3)$. The state associated with color flux tubes cannot compensate this color (triality is 1) since it must correspond to triality zero representation. If the colors of DNA strand and conjugate correspond to 10 and $\overline{10}$ and color entanglement could guarantee color singletness for the codon pairs. This would however require anti-quarks for the conjugate strand.

3 10:s associated with 3 codons contains in their tensor product a singlet (see <http://tinyurl.com/zjxxqhj>). Minimal color singlet dark DNA sequence would require 3 color codons. One can of course wonder whether the presence of 3 decouplet codons - 2 at the beginning and 2 at end and one in the middle could define genes as basic units.

5. The statistics problem is encountered also for the flux tubes. 5 (and 1) as symmetric representation is allowed by statistics but triplet is antisymmetric and thus not allowed. Again braid statistics might help. If one assumes that the flux tubes are colored - say color octets - and color wave function for flux tube pairs is antisymmetric, one can achieve Bose statistics for 3. Flux tube pair would correspond to $8 \in \{8 \times 8\}$ and minimum of two flux codons would be needed for color singletness in flux tube degrees of freedom.
6. For the counterparts of amino-acids one has only $4 \otimes 5$ allowed also by statistics considerations assuming color singlets. Could distinction between DNA/RNA and amino-acids related to statistics, perhaps braid statistics. The suggested role of braid strands possibly connecting DNA double strands and DNA double strands and lipid layers of cell membrane encourages the question whether the DNA strand and its conjugate entangle via via the reconnection of the color flux tubes defining U-shaped "tentacles" to a flux tube pair connecting the strands. For amino-acids they would not be needed. Same could happen in the transcription process of DNA to mRNA and in the translation process for mRNA tentacles and those associated with tRNA.

2.3 Also the mapping of DNA and amino-acids to dark 3-nucleon states is possible

The assumption that entire codon rather than letter corresponds to a state of dark proton does not conform with the model for the origin of purines as DNA nucleotides [23] assuming that purines and in fact all nucleotides are combined with dark proton unless one assumes that 3 nucleotides combine with the same dark proton. This looks somewhat artificial but cannot be excluded.

Amazingly, the arguments of the model involve only the representations of rotation group and since p and n have same spin as u and d , the arguments generalize to 3- nucleon states (ppp, ppn, pnn, nnn) connected by two color bonds and organized to linear structures. Concerning genetic code, exactly the same predictions follow in the recent formulation of the model. In this case quark color is not present. One could however use the 1-dimensionality and the ordering of dark nucleons as already described.

This variant has several nice features. The model is consistent with the model for dark nucleon strings consisting of nucleons and color bonds between them. There is no need to introduce Δ type nucleon states and colored states are not needed in fermionic sector. Color bonds must be colored if one wants ordinary bosonic statistics for flux tubes but here braid statistics might help. Colored bonds could of course have some important function.

2.4 Ordinary or braid statistics?

There are four options to consider: ordinary/braid statistics (1/2) and dark nucleon/dark nucleon triplet as representation of DNA codon (a/b). One has options 1a,1b,2a,2b.

1. Option 1a. For the ordinary statistics amino-acid like dark nucleons are color singlets. Part of DNA codons represented as dark nucleons and would be colored and 10-D representation of $SU(3)$. Dark amino-acids need not have color bonds with dark parts of other colored biomolecules like DNA, RNA, with exception possible formed by dark tRNA. DNA double strand could realize color confinement via the reconnection of color flux tubes.
2. Option 1b. Option 1b requires in ordinary statistics for antisymmetric doublet an antisymmetric wave function for the 3 nucleons not allowing constant valued wave function also disfavored by the linear ordering. This condition might have the same implications as braid statistics.

3. Options 1a and 1b. DNA is the only molecule that appears as double strands. A possible explanation is that codons and anticodons are paired by U-shaped flux tubes associated with the color bonds of dark DNA to form color singlets. Nucleonic colors would sum up to zero along the strand.
4. Option 2a. For braid statistics it could be possible to avoid colored states of nucleon and flux tubes altogether.
5. Option 2b. The codons would have no color and amino-acids could obey braid statistics reducing to ordinary statistics. This would not be the case for DNA/RNA.

2.5 Objections against the identification of codons as dark nucleon states

Consider next some particle physicist's objections against the option mapping codons to dark nucleon states.

1. The realization of the model requires the dark scaled variants of spin $3/2$ baryons known as Δ resonance and the analogs (and only the analogs) of spin 1 mesons known as ρ mesons. The lifetime of these states is very short in ordinary hadron physics. Now one has a scaled up variant of hadron physics: possibly in both dark and p-adic senses with latter allowing arbitrarily small overall mass scales. Hence the lifetimes of states could be scaled up.
2. Both the absolute and relative mass differences between Δ and N resp. ρ and π are large in ordinary hadron physics and this makes the decays of Δ and ρ possible kinematically. This is due to color magnetic spin-spin splitting proportional to the color coupling strength $\alpha_s \sim .1$, which is large. In the recent case α_s could be considerably smaller - say of the same order of magnitude as fine structure constant $1/137$ - so that the mass splittings could be so small as to make decays impossible.

The color magnetic spin interaction energy give rise to hyperfine splitting of quark in perturbative QCD is of form $E_c \propto \hbar g B/m$, where m is mass parameter which is of the order of baryon mass. Magnetic flux scales as \hbar by flux quantization and if flux tube thickness scales as \hbar^2 , one has $B \propto 1/\hbar$. Mass splittings would not depend on \hbar , which does not make sense. Mass splitting becomes small for large \hbar if the area of flux quantum scales as \hbar^{2+n} , $n > 0$ so that color magnetic hyper-fine splitting scales as $1/\hbar^n$ from flux conservation. The magnetic energy for a flux tube of length L scaling as \hbar and thickness $S \propto \hbar^{2+n}$ has order of magnitude $g^2 B^2 L S$ and does not depend on \hbar for $n = 1$. Maybe this could provide first principle explanation for the desired scaling.

The size scale of DNA would suggest that single DNA triplet corresponds to 3 Angstrom length scale. Suppose this corresponds to the size of dark nucleon. If this size scales as $\sqrt{\hbar}$ as p-adic mass calculations suggest, one obtains a rough estimate $\hbar/\hbar_{0} = 2^{38}$. The proton- Δ mass difference due to hyper-fine splitting would be scaled down to about $2^{-38} \times 300 \text{ MeV} \sim 10^{-9} \text{ eV}$, which is completely negligible in the metabolic energy scale .5 eV. If the size of dark nucleon scales as \hbar the mass difference is about 12 eV which corresponds to the energy scale for the ionization energy of hydrogen. Even this might be acceptable.

For these reasons the option mapping codons to dark nucleon triplets is clearly favored and will be discussed in the following.

3 More detailed view about the model mapping codons to dark 3-nucleon states

The model based on dark 3-nucleon states is discussed seems more realistic and will be discussed in more detail in the sequel.

3.1 Could Dark DNA, RNA, tRNA and amino-acids correspond to different charge states of codons?

If dark codons correspond to dark nucleon triplets as assumed in the following considerations there are 4 basic types of dark nucleon triplets: ppp, ppn, pnn, nnn . Also dark nucleons could represent codons as uuu, uud, udd, ddd : the following discussion generalizes as such also to this case. If strong isospin/em charge decouples from spin the spin content is same independently of the nucleon content. One can consider the possibility of charge neutralization by the charges assignable to color flux tubes but this is not necessarily. In any case, one would have 4 types of nucleon triplets depending on the values of total charges.

Could different dark nucleon total charges correspond to DNA, RNA, tRNA and amino-acids? Already the group representation content - perhaps correlating with quark charges - could allow to distinguish between DNA, RNA, tRNA, and amino-acids. For amino-acids one would have only 4×5 and ordinary statistics and color singlets. For DNA and RNA one would have full multiplet also color non-singlets and for tRNA one could consider $(4 \oplus 2_1 \oplus 2_2) \times 5$ containing 40 states. 31 is the minimum number of tRNAs for the realization of the genetic code. The number of tRNA molecules is known to be between 30-40 in bacterial cells. The number is larger in animal cells but this could be due to different chemical representations of dark tRNA codons.

If the net charge of dark codon distinguishes between DNA, RNA, tRNA, and amino-acid sequences, the natural hypothesis to be tested is that dark ppp, ppn, pnn , and nnn sequences are accompanied by DNA, RNA, tRNA, and amino-acid sequences. The dark beta decays of dark protons proposed to play essential role in the model of cold fusion [22, 25] could transform dark protons to dark neutrons. Peptide backbones are neutral so that dark nnn sequence could be also absent but the dark nnn option is more natural if the general vision is accepted. There is also the chemically equivalent possibility that only dark protons are involved: dark proton + neutral color bond would represent proton and dark proton + negatively charged color bond would represent neutron. At this moment it is not possible to distinguish between these two options.

Is this picture consistent with what is known about charges of amino-acids DNA, RNA, tRNA, and amino-acids? Consider first the charges of these molecules.

1. DNA strand has one negative charge per nucleotide. Also RNA molecule has high negative charge. This conforms with the idea that dark nucleons accompany both DNA and RNA. DNA codons could be accompanied by dark ppp implying charge neutralization in some scale and RNA codons by dark ppn . The density of negative charge for RNA would be $2/3$ for that for DNA.
2. Arg, His, and Lys have positively charged side chains and Asp, Glu negative side chains (see https://en.wikipedia.org/wiki/Amino_acid). The charge state of amino-acid is sensitive to the pH value of solution and its conformation is sensitive to the counter ions present. Total charge for amino-acid in peptide however vanishes unless it is associated with the side chain: as in the case of DNA and RNA it is the backbone whose charge is expected to matter.
3. Amino-acid has central C atom to which side chain, NH_2 , H and $COOH$ are attached. For free amino-acids in solution water solution $NH_2 \rightarrow NH_3^+$ tends to occur $pH=2.2$ by receiving possibly dark proton whereas $COOH$ tends to become negatively charged above $pH=9.4$ by donating proton, which could become dark. In peptide OH attach to C and one H attached to N are replaced with peptide bond. In the pH range 2.2-9.4 amino-acid is zwitterion for which both $COOH$ is negatively charged and NH_2 is replaced with NH_3^+ so that the net charge vanishes. The simplest interpretation is that the ordinary proton from negatively ionized $COOH$ attaches to NH_2 - maybe via intermediate dark proton state.
4. The backbones of peptide chains are neutral. This conforms with the idea that dark amino-acid sequence consists of dark neutron triplets. Also free amino-acids would be accompanied by dark

neutron triplets. If the statistics is ordinary only 4 dark nnn states are possible as also 5 dark color flux tube states.

5. tRNA could involve dark pnn triplet associated with the codon. An attractive idea is secondary genetic code assigning RNA codons to tRNA-amino-acid complex and projecting $8 \otimes (5 \oplus 3)$ containing 64 dark RNA spin states to $8 \otimes 5$ containing 40 dark tRNA spin states with same total nucleon and flux tube spins. Dark tRNA codons would in turn be attached to dark amino-acids by a tertiary genetic code projecting spin states $8 \otimes 5$ to $4 \otimes 5$ by spin projection. In the transcription dark tRNA would attach to dark mRNA inducing attachment of dark amino-acid to the growing amino-acid sequence and tRNA having only dark tRNA codon would be left. The free amino-acids in the water solution would be mostly charged zwitterions in the pH range 2.2-9.4 and the negative charge of COO^- would be help in the attachment of the free amino-acid to the dark proton of tRNA codon. Therefore also the chemistry of free amino-acids would be important.

An interesting question is why pnn triplets for tRNA would only 5 in flux tube degrees of freedom entire 8 in nucleon degrees of freedom. For RNA consisting of ppn triplets also 3 would be possible. What distinguishes between ppn and pnn?

The model should explain the widely different properties of DNA, RNA, tRNA, and amino-acids. There are two options.

1. DNA/RNA/amino-acid codons could correspond to ppp/ppn/nnn and tRNA would correspond to pnn (order is not necessarily this). Different charge or dark codons explain why DNA (RNA) has H (OH) in 2' position. The repulsive Coulomb energy between dark codons would be stronger for DNA and the compensation of this forces by the magnetic tension associated with the flux tube pair connecting codon and anticodon this might have something to do with the stability of DNA double strand.
 - (a) The instability of RNA as compared to DNA would result from the instability of the ribose in RNA (deoxyribose in DNA) as indeed believed. The absence of RNA double strands could be due to the instability of the flux tube pair assignable to n-n. This trivially implies absence of replication and transcription if it is based on same mechanism as in the case of DNA.
 - (b) pnn structure could explain why tRNA does not form sequences and allow to understand wobble pairing, which states that the third mRNA codon does not correspond to unique tRNA anticodon but one has $\text{C,A,U} \rightarrow \text{I}$ and $\text{U} \rightarrow \text{I}$. Due to the symmetries of the third letter of the codon, this is consistent with the genetic code. The physical explanation for wobble base pairing could relate to pnn structure of tRNA. If the charge ordering is random one would have nnp, npn, pnn and $\text{C,A,U} \rightarrow \text{I}$ could correspond to these 3 situations whereas for $\text{U} \rightarrow \text{I}$ the correspondence would not depend on the ordering. Also for RNA one would have ppn, pnp, npp degeneracy but in this case one would have charge independence.

A possible charge pairing between RNA and tRNA would be $\text{p} \leftrightarrow \text{n}$. The charge pairing between DNA and RNA could be $\text{p} \rightarrow \text{n}$ for the third least significant letter of DNA. This would minimize the coding errors possibly induced this pairing.
 - (c) One can criticize the charge assignment ppn (possibly allowing permutations) for RNA codons. Could dark weak beta decays give rise to 1-D lattice like structure? Could the repetitive structure be due to energy minimization.
2. Could the correspondence be letterwise? For DNA A,T,C,G would correspond to p, and for RNA A,C,G to p and U to n. Codons not containing U would be ppp type codons and one can wonder why the oxiribose for them is not replaced with de-oxiribose. The possible presence of n in dark codons could explain why RNA sequences are highly unstable and why they do not replicate and transcribe.

An interesting question is how the RNA world vision relates to this general picture.

3.2 Replication, transcription, translation

The formation of flux tube pairs between molecules would be central in replication and transcription and in all bio-catalysis. Dark DNA would replicate first to dark DNA or mRNA. This requires that the building bricks of dark DNA and mRNA emerge from environment perhaps by mechanism involving reconnection for the magnetic tentacles and reduction of h_{eff} bringing the molecules near each other. Flux tube pairs between dark DNA codons and their conjugates (individual dark RNA codons) would be formed during replication (transcription). The formation of flux tube pair between mRNA and dark tRNA part of tRNA would bring tRNA to mRNA, where amino-acid would associate with the growing amino-acid sequence.

For options 1a and 1b based on ordinary statistics color singletness condition could play an important role in the replication and transcription.

1. If the value of h_{eff} before reconnection and contraction of flux tube dictating the scale of color confinement is large enough, colored dark nucleons could float as free - possibly colored states - in the environment for option 1a). For option 1b dark nucleons could be present in environment - this could relate directly to the ionization in electrolyte. For options 1a and 1b dark codons representing dark tRNA molecules would accompany them.
2. For options 1a) and 1b) color confinement in flux tube degrees of freedom by forming dark color flux tube pairs between dark DNA and its conjugate in codon-wise manner could give rise to DNA double strands as chemical shadows of dark double strands. The coupling between codon and anticodon would be defined by the condition that the total color bond spins of paired codons are opposite. Quark color could be compensated for option 1a along DNA strand: 3 10:s give singlet. One can of course ask whether dark DNA RNA sequences exist rather than being built during replication and transcription.

3.3 Are sound-like bubbles whizzing around in DNA essential to life?

I got a link to a very interesting article [I2] about sound waves in DNA (see <http://tinyurl.com/z7hod9b>). The article tells about THz de-localized modes claimed to propagate forth and back along DNA double strand somewhat like bullets. These modes involve collective motion of many atoms. These modes are interpreted as a change in the stiffness of the DNA double strand leading to the splitting of hydrogen bonds in turn leading to a splitting into single strands. The resulting gap is known as transcriptional bubble propagating along double strand is the outcome. I do not know how sound the interpretation as sound wave is.

It has been proposed that sound waves along DNA give rise to the bubble. The local physical properties of DNA double strand such as helical structure and elasticity affect the propagation of the waves. Specific local sequences are proposed to favor a resonance with low frequency vibrational modes, promoting the temporary splitting of the DNA double strand. Inside the bubble the bases are exposed to the surrounding solvent, which has two effects.

Bubbles expose the nucleic acid to reactions of the bases with mutagens in the environment whereas so called molecular intercalators may insert themselves between the strands of DNA. On the other hand, bubbles allow proteins known as helicases to attach to DNA to stabilize the bubble, followed by the splitting the strands to start the transcription and replication process. The splitting would occur at certain portions of DNA double strand. For this reason, it is believed that DNA directs its own transcription.

The problem is that the strong interactions with the surrounding water are expected to damp the sound wave very rapidly. Authors study experimentally the situation and report that propagating bubbles indeed exist for frequencies in few THz region. Therefore the damping does not seem to be effective. How this is possible? As an innocent layman I also wonder how this kind of mechanism can be selective: it would seem that the bullet like sound wave initiates transcription at many positions along DNA. The transcription should be localized to a region assignable to single gene. What could guarantee this?

Can TGD say anything interesting about the mechanism behind transcription and replication?

1. In TGD magnetic body controls and coordinates the dynamics. The strongest hypothesis is that basic biochemical processes are induced by those for dark variants of basic bio-molecules (dark variants of DNA, enzymes,...). The belief that DNA directs its own transcription translates to the statement that the dark DNA consisting most plausibly from sequences of dark proton triplets ppp at dark magnetic flux tubes controls the transcription: the transcription/replication at the level of dark DNA induces that at the level of ordinary DNA.
2. If the dark DNA codons represented as dark proton triplets (ppp) are connected by 3 flux tube pairs, the reverse of the reconnection should occur and transform flux tube pairs to two U-shaped flux tubes assignable to the two dark DNA strands. Dark proton sequences have positive charge $+3e$ per dark codon giving rise to a repulsive Coulomb force between them. There would be also an attractive force due to magnetic tension of the flux tubes. These two forces would compensate each other in equilibrium (there also the classical forces due to the negatively charged phosphates associated with nucleotides but these would not be so important).

If the flux tube pairs are split, the stabilizing magnetic force however vanishes and the dark flux tubes repel each other and force the negatively charged DNA strands to follow so that also ordinary DNA strand splits and bubble is formed. The primary wave could therefore be the splitting of the flux tube pairs: whether one can call it as a sound wave is not clear to me. Perhaps the induced propagating splitting of ordinary DNA double strand could be regarded as an analog of sound wave.

The splitting of flux tube pairs for a segment of DNA would induce a further splitting of flux tubes since repulsive Coulomb force tends to drive the flux tubes further away. The process could be restricted to DNA if the "upper" end of the split DNA region has some dark DNA codons which are not connected by flux tube pairs. This model reasons why for dark proton sequences.

3. This model does not yet explain how the propagating splitting wave is initiated. Could a quantum phase transition increasing the value of h_{eff} associated with the flux tube pairs occur for some minimal portion of dark DNA "below" the region associated with gene and lead to the propagating wave induced by the above classical mechanism? That the wave propagates in one direction only could be due to chirality of DNA double helix.

An interesting question is how the RNA world vision (see https://en.wikipedia.org/wiki/RNA_world) relates to this general picture.

1. There are strong conditions on the predecessor of DNA and RNA satisfies many of them: reverse transcription to DNA making possible transition to DNA dominated era is possible. Double stranded RNA exists https://en.wikipedia.org/wiki/RNA#Double-stranded_RNA in cells and makes possible RNA genome: this would however suggest that cell membrane came first. RNA is a catalyst. RNA has ability to conjugate an amino-acid to the 3' end of RNA and RNA catalyzes peptide bond formation essential for translation. RNA can self-replicate but only relatively short sequences are produced.
2. TGD picture allows to understand why only short sequences of RNA are obtained in replication. If the replication occurs at the level of dark ppn sequences as it would occur for DNA in TGD framework, long RNA sequences might be difficult to produce because of the stopping of the propagation of the primary wave splitting the flux tube pairs. This could be due to the neuron pairs to which there is associated no Coulomb repulsion essential for splitting.
3. In TGD framework RNA need not be the predecessor of DNA since the evolution would occur at the level of dark nucleon strings and DNA as the dark proton string is the simplest dark nucleon string and might have emerged first. Dark nuclear strings would have served as templates and biomolecules would have emerged naturally via the transcription of their dark counterparts to corresponding biopolymers.

3.4 Is bio-catalysis a shadow of dark bio-catalysis based on generalization of genetic code?

Protein catalysis and reaction pathways look extremely complex (see <http://tinyurl.com/kp3sdlm>) as compared to replication, transcription, translation, and DNA repair. Could simplicity emerge if biomolecules are identified as chemical shadows of objects formed from dark nuclear strings consisting of dark nucleon triplets and their dynamics is shadow of dark stringy dynamics very much analogous to text processing?

What if bio-catalysis is induced by dark catalysis based on reconnection as recognition mechanism? What if contractions and expansions of U-shaped flux tubes by h_{eff} increasing phase transitions take that reactants find each other and change conformations as in the case of opening of DNA double strand? What if codes allowing only the dark nucleons with same dark nuclear spin and flux tubes spin to be connected by a pair of flux tubes?

This speculation might make sense! The recognition of reactants is one part of catalytic action. It has been found in vitro RNA selection experiments that RNA sequences are produced having high frequency for the codons which code for the amino-acid that these RNA molecules recognize (<http://tinyurl.com/kp3sdlm>). This is just what the proposal predicts!

Genetic codes DNA to RNA as $64 \rightarrow 64$ map, RNA to tRNA as $64 \rightarrow 40$, tRNA to amino-acids with $40 \rightarrow 20$ map are certainly not enough. One can however consider also additional codes allowed by projections of $(4 \oplus 2_1 \oplus 2_2) \otimes (5 \oplus 3(\oplus 1))$ to lower-dimensional sub-spaces defined by projections preserving spins. One could also visualize bio-molecules as collections of pieces of text attaching to each other along conjugate texts. The properties of catalysts and reactants would also depend by what texts are "visible" to the catalysts. Could the most important biomolecules participating biochemical reactions (proteins, nucleic acids, carbohydrates, lipids, primary and secondary metabolites, and natural products, see <https://en.wikipedia.org/wiki/Biomolecule>) have dark counterparts in these sub-spaces.

The selection of bio-active molecules is one of the big mysteries of biology. The model for the chemical pathway leading to the selection of purines as nucleotides [23] assumes that the predecessor of purine molecule can bind to dark proton without transforming it to ordinary proton. A possible explanation is that the binding energy of the resulting bound state is higher for dark proton than the ordinary one. Minimization of the bound state energy could be a completely general criterion dictating which bio-active molecules can pair with dark protons. The selection of bio-active molecules would not be random after all although it looks so. The proposal for DNA-nuclear/cell membrane as topological quantum computer with quantum computations coded by the braiding of magnetic flux tubes connecting nucleotides to the lipids wlead to the idea that flux tubes being at O=-bonds [9].

3.5 Comparing TGD view about quantum biology with McFadden's views

McFadden [8] has very original view about quantum biology: I have written about his work for the first time for years ago, much before the emergence of ZEO, of the recent view about self as generalized Zeno effect, and of the understanding the role of magnetic body containing dark matter [12]. The pleasant surprise was that I now understand McFadden's views much better from TGD viewpoint.

1. McFadden sees decoherence as crucial in biological evolution: here TGD view is diametric opposite although decoherence is a basic phenomenon also in TGD.
2. McFadden assumes quantum superpositions of different DNAs. To me this looks an unrealistic assumption in the framework of PEO. In ZEO it is quite possible option.
3. McFadden emphasizes the importance of Zeno effect (in PEO). In TGD the ZEO variant of Zeno effect is central for TGD inspired theory of consciousness and quantum biology. Mc Fadden suggests that quantum effects and Zeno effect are central in bio-catalysis: the repeated measurement keeping reactants in the same position can lead to an increase of reaction rate by factors of order billion.

McFadden describe enzymes as quantum mousetraps catching the reactants and forcing them to stay in same position. The above description for how catalysis catches the reactants using U-shaped flux tube conforms with mousetrap picture.

McFadden discusses the action of enzymes in a nice manner and his view conforms with TGD view. In ZEO the system formed by catalyst plus reactants could be described as a negentropically entangled sub-self, and self indeed corresponds to a generalized Zeno effect. The reactions can proceed in shorter scales although the situation is fixed in longer scales (hierarchy of CDs): this would increase the length of the period of time during which reactions can proceed and lead to catalytic effect. Zeno effect in ZEO plus hierarchies of selves and CDs would be essentially for the local aspects of enzyme action.

4. Protons associated with hydrogen bonds and electronic Cooper pairs play a universal role in McFadden's view and the localization of proton in quantum measurement of its position to hydrogen bond is the key step of enzyme catalysis. Also TGD dark protons at magnetic flux tubes giving rise to dark nuclear strings play a key role. For instance, McFadden models enzyme catalysis as injection of proton to a very special hydrogen bond of substrate. In TGD one has dark protons at magnetic flux tubes and their injection to a properly chosen hydrogen bond and transformation to ordinary proton is crucial for the catalysis. Typical places for reactions to occur are C=O type bonds, where the transition to C-OH can occur and would involve transformation of dark proton to ordinary proton. The transformation of dark proton to ordinary one or vice versa in hydrogen bonds would serve as a biological quantum switch allowing magnetic body to control biochemistry very effectively.

What about electronic Cooper pairs assumed also by McFadden. They would flow along the flux tube pairs. Can Cooper pairs of electrons and dark protons reside at same flux tubes? In principle this is possible although I have considered the possibility that particles with different masses (cyclotron frequencies) reside at different flux tubes.

McFadden [8] has proposed quantum superposition for ordinary codons: This does not seem to make sense in PEO (since the chemistries of codons are different) but could make sense in ZEO. In TGD one could indeed imagine quantum entanglement (necessary negentropic in p-adic degrees of freedom) between dark codons. This NE could be either between additional degrees of freedom or between spin degrees of freedom determining the dark codons. In the latter case complete correlation between dark and ordinary DNA codons would imply also the superposition of their tensor products with ordinary codons.

The NE between dark codons could also have a useful function: it could determine physically gene as a union of disjoint mutually entangled portions of DNA. Genes are known to be highly dynamical units, and after pre-transcription splicing selects the portions of the transcript translated to protein. The codons in the complement of the real transcript are called introns and are spliced out from mRNA after the pre-transcription (see https://en.wikipedia.org/wiki/RNA_splicing).

What could be the physical criterion telling whether a given codon belongs to exonic or intronic portion of DNA? A possible criterion distinguish between exons and introns is that exons have NE between themselves and introns have no entanglement with exons (also exons could have NE between themselves). Introns would not be useless trash since the division into exonic and intronic region would be dynamical. The interpretation in terms of TGD inspired theory of consciousness is that exons correspond to single self.

3.6 Is there a connection between geometric model of harmony and nuclear string model of genetic code?

There should exist a connection between the geometric model of harmony and genetic code and the model of genetic code discussed.

1. Dark DNA strands could be connected by color flux tubes to form a double strand by reconnections of U-shaped color flux tubes. What would induce a codon-wise or letter-wise pairing of DNA codons and their conjugates represented as dark quark triplets to form double DNA strand? Cyclotron resonance could accompany reconnection (magnetic field strength would be identical and reconnection could occur).
2. One has the correspondence codon \leftrightarrow state of dark nucleon or codon \leftrightarrow state of dark nucleon triplet. The geometric model of harmony and genetic code [19] represents the codons as 3-chords. The 3-chord would be represented in terms of cyclotron frequencies of dark photons assignable to the 3 dark quarks (nucleons) in the state. Each quark-color bond pair (including the pion-like bond) could be in 12 states with corresponding cyclotron frequency mappable to the basic octave. The cyclotron frequency triplets would be same for codons and conjugates. The only manner to understand the scale is in terms of spectrum of magnetic field strengths for U-shaped flux tube pairs.

This would require 3 pairs of flux tubes between the dark codons of DNA strands. If the quarks inside linear dark proton are connected by color flux tubes (like protons in the model of dark nucleus). Reconnection for U-shaped flux tube connecting quarks would give rise to the double strand formed by dark proton strings. The magnetic field strength of the 3-flux tubes would be determined by the state of dark proton and would be same for DNA and RNA codons and also for RNA codons and corresponding tRNA-amino-acid complexes. The cyclotron frequencies would define a scaled up variant of Pythagorean scale projected to the basic octave [19]. This option does not favor the idea about separator 4-letter code.

3. The geometric model for harmony is formulated in terms of orbits of the subgroups of the isometry groups of tetrahedral and icosahedral geometries. The DNAs coding particular amino-acid correspond to the orbit of the triangle of icosahedron corresponding to the amino-acid. The decomposition $60 \rightarrow 20 + 20 + 20$ suggests strongly decomposition of I to 20 Z_3 cosets containing 3 elements each other and in correspondences with the triangular faces of icosahedron.
4. The model of the genetic code just discussed relies on the model of dark nucleon based on group theory. The symmetric groups of Platonic solids are in turn associated with inclusion of hyper-finite factors and appear in Mc Kay correspondence, whose proof involves decompositions of $SU(2)$ representations to the representations of the discrete subgroups of Platonic solids. A further observation is that the numbers of elements for isometries of icosahedron and tetrahedron are 60 and 4 respectively: the sum is 64. Could the action of Z_3 leaving face invariant could be posed as an additional condition on amino-acids and reduce the amino-acid representation to $4 \otimes 5$.
5. In the geometric model of harmony genetic icosahedral $20+20+20$ part of the code involves a combination of three different Hamilton's cycles mapping 60 DNAs to 20 amino-acids: in terms of icosahedral group I and its coset space I/Z_3 these maps correspond to coset projections. Could the decomposition $(4 \oplus 2_1 \oplus 2_2) \otimes (5 \otimes 3)$ be understood in terms of a reduction to icosahedral and tetrahedral subgroups of rotation group or of their spin coverings.

In this process finite-dimensional representation of $SO(3)$ decomposes to a direct sum of representations of the discrete subgroup if its dimension is larger than any of the dimensions of representations of the finite sub-group (for basic facts about these see <http://tinyurl.com/ho4onbs>). One might hope that the decomposition of the representations of $SO(3)$ appearing in the above formula under icosahedral group and or tetrahedral group could allow to understand the emergence of DNA, RNA, tRNA, and amino-acids as kind of symmetry breaking.

6. In the geometric model of harmony 64-codon code [19] is obtained as a fusion 60-codon code assignable to icosahedron + 4 codon code assignable to tetrahedron. There are actually two codes corresponding to tetrahedron and icosahedron as disjoint entities and tetrahedron glued to icosahedron along one face. The model explains the two additional amino-acids Pyl and Sec coded for a variant of the genetic code.

How could these two successful models relate to each other? In p-adic physics of cognition Platonic solids and polygons can be seen as discrete approximation for sphere [24] and biomolecules could be understood as cognitive representation in the intersection of real and p-adic space-time surface consisting of algebraic points. Could one assign icosahedron and tetrahedron to a codon in some concrete manner? Could the attachment of tetrahedron to icosahedron along one face have concrete meaning? The answer seems to be negative.

1. One can about the interpretation of the 12 vertices of the icosahedron - how number 12 could be assigned with the genetic code? The vertices correspond to notes perhaps represented as magnetic field strength at the flux tubes assignable to color bonds. This field strength should be determined by the spin state of dark 3-nucleon. No concrete nuclear string counterpart seems to exist for the closed Hamiltonian cycle consisting of 12 notes and in case of tetrahedral extension of 13 notes. 12 vertices of icosahedron correspond to 12 notes and 20 faces to 3-chords so that there is not need for more concrete correspondence.
2. The attachment of tetrahedron to icosahedron would bring in further note very near to one of the notes of Pythagorean scale and corresponding 3-chords. This has concrete interpretation and there is no need to make this more concrete at the level of geometry of DNA. If icosahedron and tetrahedron are disjoint one obtains four additional codons. It seems that all these 4 3-chords be assigned with the 3 color bonds, one note for each of them. What distinguishes at the level of dark nucleon string the situations in which tetrahedron is attached and non-attached to the color bond? In presence of attachment there would be 1 shared 3-chord corresponding to stop codon assignable with the shared face. The 13:th note appearing in 4 3-chords differs very little from one of the notes of the icosahedral scale: this corresponds to the fact that 12 perfect fifths do not quite give 7 octaves as already Pythagoras realized. Crazy question: Could this small difference relate to the small relative mass difference $(m_p - m_n)/m_p \simeq .0014$ making itself possible visible in cyclotron frequency scale? The idea does not seem plausible: $[(3/2)^{12} - 2^7]/2^7 \simeq .014$ is 10 times larger than $(m_p - m_n)/m_p \simeq .0014$.

The conclusion is that genetic code can be understood as a map of stringy nucleon states induced by the projection of all states with same spin projections to a representative state with the same spin projections (total quark spin and total flux tube spin). Genetic code would be realized at the level of dark nuclear physics and biochemical representation would be only one particular higher level representation of the code. A hierarchy of dark baryon realizations corresponding to p-adic and dark matter hierarchies can be considered. Translation and transcription machinery would be realized by flux tubes connecting only states with same quark spin and flux tube spin.

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