Article

An Overall View about Models of Genetic Code & Bio-harmony

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Abstract

During last years kind of brain storming period has occurred in the TGD inspired models of bio-harmony and genetic code. A lot of ideas, some of them doomed to be short lived, have emerged, and it seems that now it its time for a thorough cleanup and integration with the general ideas of TGD inspired quantum biology. TGD leads to 3 basic realizations of the genetic code. One can also consider 3 realization also for bio-harmony. The question is which of them is the realistic one or whether several options can be considered. In this article these ideas are discussed critically and open problems are summarized. The three genetic codes correspond to a fundamental realization in terms of dark proton sequences (dark nuclei) with 3-proton representing codon. Second realization is the chemical realization and the third realization is in terms of dark photon 3-chords mediating the interaction between various realizations. Frequency resonance is very natural interaction between dark levels and energy resonance between dark level and chemical level. The possibility to modify the value of h_{eff} for flux tube makes possible to have for given codon single resonance energy.

The homonymy of the genetic codes at various levels is discussed. At the dark level the fact that icosahedral harmonies can have common 3-chords implies the first homonymy. The basic difficulty of Pythagorean scale realized in terms of quint cycle realized already by Pythagoras becomes the solution of this problem. The well-known homonymies in RNA-tRNA correspondence and even in RNA-AA correspondence can be understood in the model in which dark photon 3-chords mediate the interactions. Also questions related to the relationship of bio-harmony with ordinary genetic code are considered. Why 3 copies of icosahedral harmony and only one copy of tetrahedral harmony? A special triangle assignable to the 3 copies of icosahedron and tetrahdron is analogous to a singular point of covering: do these 4 triangles correspond to exceptional codons breaking symmetries? How do the dissonant 3-chords present in some icosahedral harmonies relate to stop codons? How do the codons of bio-harmony and ordinary codons relate and is this relation consistent with what is known about transcription and translation?

1 Introduction

During last years kind of brain storming period has occurred in the model of bio-harmony [13]. A lot of ideas, some of them doomed to be short lived, have emerged, and it seems that now it its time for a thorough cleanup and integration with the general ideas of TGD inspired quantum biology.

TGD leads to 3 basic realizations of genetic code: this is now relatively well established part of TGD inspired quantum biology. One can also consider 3 realization also for bio-harmony. The question is which of them is the realistic one or whether several options can be considered.

1.1 3 basic realizations of the genetic code

In TGD Universe there are at least 3 realizations of the genetic code.

Besides biochemical realization one has a realization in terms of dark nuclei realized as dark proton sequences and possibly in terms of more general sequences involving effective dark neutrons. The states of 3 dark protons defining the dark codon have multiplet decomposition 64 + 64+ 40 + 20 corresponding to dark variants of DNA, RNA, tRNA, and amino-acids (AA). I will denote these dark variants by DDNA, DRNA, DtRNA, and DAA.

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If one allows also dark analogs of neutrons by allowing negatively charged color bonds between protons, the number of code letters doubles: this could relate to the recently constructed Hachimoji DNA [3] (see `http://tinyurl.com/y2mcjb4r`) discussed from TGD viewpoint in [21].

Dark photon 3-chords assignable to the realization of bio-harmony with the note scale identified as Hamilton cycle on a polytope with triangular faces gives a third realization coupling dark and ordinary representations together. I have proposed 3 realizations in terms of icosahedral and tetrahedral [13], icosahedral and toric [16], and icosahedral and dodecahedral [21] geometries (for the latter 5-chords would effectively reduce to 3-chords).

If there is DDNA-DNA, DRNA-RNA, DAA-AA pairing, the negative charges of DNA, RNA, and tRNA nucleotides finds explanation in terms of positive charge of dark proton sequence. For AAs the situation is not clear since the charge per unit length for amino-acids varies and depends on pH. DAA-AA pairing would require that dark analogs of neutrons are present in the dark proton sequence.

1.2 3 models of bioharmony

There are now 3 models of bioharmony [13, 16, 21] making very similar pedictions. Harmony for given graph is defined as a Hamiltonian cycle connecting neighboring points and going through all points of the graph without self-intersections. Scale is identified by assigning notes to the vertices and faces correspond to the chords of the harmony obtained in this manner. Bio-harmonies are fusions of 3 or 4 sub-harmonies.

1. The original proposal - icosa-tetrahedral bio-harmony - is based on the fusion of 3 icosahedral harmonies with symmetry groups Z_6, Z_4 and Z_2 permuting the triangles of given orbit of Z_n. Given icosahedral harmony corresponds to an imbedding of 12-note scale as a Hamilton cycle at icosahedron. The 12 vertices of icosahedron are identified as the notes of 12-note scale and 20 triangular faces define the 3-chords of the harmony.

   The distance between nearest vertices is assumed to correspond to quint that is scaling of the frequency by 3/2. Each cycle defines a collection of 20 3-chords defining an icosahedral harmony. Octave equivalence is used to map the 12 frequencies obtained to single octave. There is however a slight inconsistency since 12 quints corresponds to slightly more than 7 octaves as already Pythagoras realized. The addition of tetrahedron to icosahedral harmony is interpreted as an addition of one vertex adding one note which should be very near to one of the 12 notes.

   Icosahedral harmonies are characterized by a symmetry group Z_n, $n = 6, 4, 2, 1$, $n = 1$ corresponds to chaotic cycles, which might serve as correlate for dis-harmony and might relate to the correlates of emotions: at the level of genetic code is AA would be coded by single DNA codon.

   Icosahedron decomposes to orbits of Z_n consisting of triangles or equivalently chords. The chords can be classified further by the frequency ratios correlating with the emotional effect. One has the orbits $3 \times 6 + 2 = 20$ for Z_6, $5 \times 4 = 20$ for Z_4 and 10×2 for Z_2. Z_6 harmony is unique but there are 3 Z_4 and even more Z_2 harmonies for which Z_2 can correspond to rotation by π or reflection. This can be understood as breaking of symmetry splitting the Z_6 orbits to pieces. This gives $60 = 2 + 20 + 20$ 3-chords. The numbers of chords at give orbit rather neatly correspond the numbers of DNA codons coding for given AA.

   4 chords and DNAs and AAs are however missing. Tetrahedral harmony would add $3 + 1 = 4$ chords: Z_3 would the symmetry group instead of Z_4. This would be due to the symmetry breaking due to gluing of one-tetrahedral face with icosahedral face, which is however counted as separate face and corresponds to 1-triangle orbit under Z_3 permuting its vertices. This gives 64 3-chords corresponding to codons of genetic code.

   $3 + 1$ decomposition would naturally correspond to (ile, ile, ile, met) 4-plet coded by codons AUX. The numbers of codons coding given AA identified as orbit of Z_n come out almost correctly. The only exception is trp-stop doublet for which doublet decomposes to stop and singlet. One must

understand the reason for this symmetry breaking - it might just the need to have stop codon and this could be arranged if there is no tRNA coupling to this codon. Note that for some code variants stop codon UAG corresponds to Pyl and UGA to Sec.

Since music generates and expresses emotions, the interpretation would be in terms of moods. Even molecules would have moods.

2. Also icosa-dodecahedral and icosahedral-toric harmonies contain the Z_6 and Z_4 icosahedral harmonies (20_1 and 20_2) so that one must only add the missing 10 doublets and 3+1 codons assigned to tetrahedron in icosa-tetrahedral case.

   The dodecahedral harmony with 6 chords arranged in doublets is unique from the uniqueness of the Hamiltonian cycle [21]. The icosa-dodecahedral harmony would give $20_1 + 20_2 + 12_1 + 12_2 = 64$. 12 decomposes into 6 Z_2 doublets so that one has 12 doublets. The realization of scale for dodecahedral harmony would in 20 powers of rational scaling x such that x^{20} is as near to a power of two as possible [21]. $x = 2^{1/20}$ would correspond to the Eastern variant of well-tempered scale.

   There are objections against icosa-dodecahedral harmony. Chords are 5-chords rather than 3-chords. The 5-chords of dodecahedral harmony however turn out to be equivalent to 3-chords as far as information content is considered [21]. The number of vertices for dodecahedron is 20, not 12, but one could argue that dodecahedron corresponds to Eastern harmony having micro-intervals. Two copies of the dodecahedral harmony are needed. What could distinguish between these copies will be discussed later. Also 3+1 is missing.

3. The icosahedral-toric harmony [16] decomposes as $20_1 + 20_2 + 24 = 64$ involving torus with 24 triangles and 12 vertices. Toric harmony has Z_{24} as isometries and gives 12 doublets. One could argue that the fusion of icosahedral and toric harmonies is geometrically un-natural. One must be however cautious if the geometric realization is in extension of rationals. Also now 3+1 is missing.

The considerations in the sequel suggests that the icosa-tetrahedral option is the most realistic if not unique.

1.3 About the geometric interpretation of icosahedral and other symmetries

The geometric interpretation of icosahedral and possible other geometries is a challenge. The 60-element group A_5 of rotations - alternating group of 5-letters - acts as orientation preserving isometries of icosahedron.

1. Since Galois group is central in adelic physics, and all finite groups can appear as Galois groups, one can ask whether icosahedral group and tetrahedral groups could act as Galois group for some extension of rationals relevant for biology. Going to web gives an affirmative answer [1] (see `http://tinyurl.com/y4qsea6h`)! Icosahedral symmetry appears as Galois group of the general quintic equation! The lowest order polynomial equation not allowing closed expressions for the roots.

   Galois theory (see `http://tinyurl.com/y6e955ke`) allows to understand the situation in terms of the discriminant defined as product $D = \prod_{i<j}(r_i - r_j)^2$, where r_i are the roots of the irreducible polynomial considered. S_n is the symmetry group in the generic case and odd permutations of S_n change the sign of D. If D is square of rational number in the field K considered (which can be also extension of rationals now), Galois group reduces to alternating group A_5.

   Remark: For octahedron and its dual cube the group is S_4 and can be realized as Galois group of 4^{th} order polynomials. For tetrahedron the group is A_4 and can be also realized as Galois group of 4^{th} order polynomials for which discriminant is square in K.

2. Icosahedral and dodecahedral geometries having the same isometry group are common in biology, and one can wonder whether there could be a gometric realization - perhaps at the level of magnetic

body. This might somehow relate also to the frequent appearance of Golden mean involving $\sqrt{5}$ in biology and Golden angle rated to the fifth root of unity.

3. $M^8 - H$ duality provides besides the usual formulation of TGD also a formulation in complexified M^8 identified as complexified octonions [15]. The associativity of the tangent or normal space of space-time surface is assumed as a dynamical principle and implies quaternionicity. Quaternions have $SO(3)$ as automorphism group analogous to Galois group and have the finite isometry groups of Platonic solids as finite subgroups.

   Could quaternionicity give a connection with the geometric picture? In adelic physics discretizations of space-time points as points with coordinates in the extension of rationals are in central role. Could discretizations contain orbits of the Platonic isometries as quaternionic Galois groups? This could also give to the geometric picture although icosahedral symmetries are not obvious in the geometry of say DNA.

4. Is the genetic code really unique as its dark nucleus realization and the fact that the isometry groups of Platonic solids are finite subgroups of quaternionic isomorphisms suggests? Could any Galois group give rise to an analog of bioharmony and of genetic code? Could the recent genetic code correspond to a first step in the process going beyond the solvable polynomial equations?

   What about toric code? The group of toric isometries is Z_{24} and 24 is one of the magic number of mathematics, and dimension 24 is crucial in bosonic string model. Could Z_{24} correspond to the Galois group for 24:th roots of unity defining 24-D algebraic extension of rationals. We cannot sensorily imagine higher dimensions but can do this cognitively. I have proposed that the ability to imagine higher dimensions could be due to the possibility of higher-dimensional extensions of rationals and p-adics.

   Could one realize the icosahedron and 24-torus as imagined object in the algebraic extension of rationals? Could the n-dimensional discrete geometric objects assignable to n-dimensional extensions of rationals have quite generally this kind of representations as a generalized Platonic solid in algebraic extension. Could they define cognitive harmonies as Hamiltonian cycles? Could one imagine also cognitive variant of genetic code whereas as sensory/biological variant of genetic code would be forced by dark proton physics?

1.4 Mistracks

In the attempts to understand the connection with standard realization of the genetic code I have also considered the possibility that the frequencies of 3-chord might be mapped to their sum in the interactions. This possibility was considered in the model of homonymy [18]. In the light of afterwisdom this proposal looks ad hoc.

Also a proposal for how 12-note scale could quite concretely correspond DNA codons was discussed [19]. The idea was to assign notes with individual letters of the codon such that the note depends on the position of the letter whereas the model of harmony assignment the chord to the entire codon represented as entangled state of 3 dark protons. It is now clear this proposal very probably cannot realize all possible harmonies and is in conflict with the general model which as such fixes the correspondence between chords and codons without any additional assumptions.

2 Interactions between various levels

One challenge is to understand how the various realizations of the genetic code interact with each other. There are DX-DY interactions, DX-Y interactions and X-Y interactions and in living matter they should occur in long length scales so that they should be mediated by dark photons.

1. How dark photon triplets assumed to be generated by dark nucleon sequences interact with ordinary DNA? Here one can bring in rather stable ideas of TGD inspired view about quantum biology. Dark matter in TGD sense represents long length scale quantum coherence and bio-chemistry short scale coherence. The interaction is therefore between long and short scales.

2. There are two manners to interact: frequency resonance and energy resonance. Frequency resonance mediates long length scale interactions and if DX-X pairing exists, the exchange of dark photon triplets - 3-chords - allows long range DX-DY interactions. DX-X interaction by energy resonance is short range interaction so that X-(DX-DY)-Y interaction would give rise to long range interaction between X-Y as interaction induced by dark level (MB).

3. DX-X interaction involves energy resonance and transformation of dark photons to ordinary photons with the same energy. Bio-photons would be an outcome of the transition $h_{eff} \to h$. Also the reversal of this transition and more general transitions $h_{eff,1} \to h_{eff,2}$ are of course possible.

   Bio-photons have a universal energy spectrum corresponding to molecular and atomic transition energies. This is possible if they result from dark cyclotron photons if the condition $h_{eff} = h_{gr} = GMm/v_0$ introduced originally by Nottale and implying that the cyclotron energy does not depend on the mass of the charged particle producing the dark cyclotron photons.

2.1 The independence of the interaction energy on frequency

Dark matter as a hierarchy phases labelled by $h_{eff}/h_0 = n$ identifiable as a dimension of extension of rationals implies evolutionary hierarchy: n serves as a kind of IQ. This strongly suggests that ordinary matter is controlled by dark matter at MB and mimics its behavior.

Evolution would not proceed by change and necessity but would be a process controlled and guided by MB. MB would be an active intentional agent guiding the evolution. Situation in biology would be much like that in modern technological society where intentional technical progress leads to more and more refined products. How could this be realized at the level of basic bio-molecules? One should also understand how genetic code evolves gradually to a more refined form.

1. The selection of basic bio-molecules having energy resonance with their dark variants mediated by dark photon 3-chords by change would be extremely in-effective process. MB should have mechanisms of tuning the energies of dark photons to achieve energy resonance.

   This is achieved if the value of h_{eff} at the flux tubes mediating the interaction can be controlled. Since the length of flux tube is proportional to the h_{eff} by Uncertainty Principle, the variation of h_{eff} would mean variation of the length L of the flux tube: a kind of motor action of MB. Cyclotron frequencies are proportional to the value of monopole magnetic field B at flux tube and by flux quantization one has $B \propto 1/S$, S the area of flux tube cross section (which for monopole flux tubes is closed 2-surface). The variation of the thickness/area of the flux tube, second motor action of MB, would allow to vary cyclotron frequencies.

2. The ideal situation concerning the coupling to ordinary matter would be that same chemical transition with fixed energy for given molecule could couple to several frequencies. This would be achieved if the cyclotron energy is constant.

   The condition that the cyclotron energies in a coupling to a given molecule do not depend on the frequency requires that $h_{eff,i}$ at flux tube i compensates this dependence. MB can vary the value of B to vary frequencies and the value of $h_{eff,i}$ to keep energy unaffected. The areas S and length L of flux tubes are varied so that the volume remains unaffected. $B \propto 1/S$ and $L \propto h_{eff}$ by Uncertainty Principle. $E_c \propto \hbar_{eff} B = constant$ implies that L/S is constant. S increases like $S \to x^2 S$ and $L \to x^2 L$ in the scaling changing $f_c \to f_c/x^2$. The magnetic energy $E_{magn} = B^2 SL \propto L/S$ of the flux tube is not changed. Kind of energy criticality would be in question - one would have a large

number of flux tube configurations with the same energy and volume ideal for control purposes. Quantum criticality is actually basic dynamical principle of quantum TGD allowing to predict the spectrum of various coupling parameters.

3. Besides cyclotron frequences Josephson energies are central in TGD based model of nerve pulse and EEG. Josephson energy $E_J = ZeV$ and cyclotron frequency $f_c = ZeB/m$ do not depend on h_{eff}. An attractive possibility is that cyclotron photons couple to Josephson junctions meaning that they become Josephson photons and then transform to ordinary photons inducing molecular transitions.

4. In the case of bio-harmony the frequencies would be rational multiples of basic frequency and by separating common numerator they are certain integer multiples $f_i = n_i f_0$ of a basic frequency f_0. The integers n_i have decomposition to products of powers of certain primes: $n_i = \prod p_i^{k_i}$ and each of p_i appears as some maximal power $k_{i,max}$. If one has $n = \prod_i p^{k_{i,max}} n_0$ one can obtain $h_{eff,i} = h_{eff}/n_i$. In this manner one would obtain the desired independence of $E_{c,i}$ on f_i. For Pythagorean scale only primes $p = 2$ and $p = 3$ would be involved.

All codons coding for given AA could have same coupling energy. Unless the values of Planck constants and frequencies associated with flux tubes coupling to given codon are fixed, one could have same transition energy for all letters but this is an unrealistic condition. Transition energies are naturally different and can code for letters if not even codons. For this option only the correct combination of frequencies and values of $h_{eff,i}$ allows resonant coupling.

The 3-chords associated with different harmonies would naturally correspond to the same energy. The physics of emotions would not be directly visible at the level of chemistry: chemist would certainly agree with this. The values of Planck constants would characterize the frequencies: I have indeed speculated that nucleotides could be labelled by values of h_{eff}. Number theory would be essential for the understanding life at the level of genes: Galois groups would characterize the nucleotides. Galois groups code for complexity at the level of dark matter so that the behavior guided by the MB of molecule would depend on the $IQ = n = h_{eff}/h_0$ of MB.

2.2 The independence of cyclotron energy on frequency and Nottale hypothesis

Is the independence of interaction energy on frequencies consistent with $h_{gr} = GMm/v_0$ hypothesis [2] [9, 10, 11]? Here one might encounter difficulties. The division by n_i should change one of the parameters appearing in the formula. The interpretation has been m corresponds to the dark proton mass at the end of the flux tube connecting it to large mass M. If so m cannot be varied.

Could M be varied?

1. The parameter $v_0 \simeq 2^{-11}$ can be varied by powers of two, which do not affect the notes identified by octave equivalence.

2. Could M correspond to atomic or molecular mass in good approximation equal to sum of atomic numbers A of atoms involved? The divisors of the total atomic number A_{tot} would define the allowed integers n_i characterizing the frequencies of Pythagorean scale in the model of bio-harmony. One must have $h_{gr}/h > 1$ with requires $M > \hbar/Gm = 1.3 \times 10^{19} m_p v_0$. For $v_0 = 2^{-11}$ this corresponds to $M > \hbar/Gm = 6 \times 10^{15} m_p$. The scale of a water blob with $A = 20$ containing this number of protons is about 70 μ, which is of order cell size. One can wonder how A_{tot} could be kept as divisible by n_i characterizing the frequencies of the Pythagorean scale. The problem is that an addition of one proton spoils the divisibility conditions completely.

3. The solution of the problem could be based on a more precise view about h_{eff} [20]. The understanding of the variation of Newton's constant - too large to be due to experimental errors - led to the realization of the meaning of the fact that space-time surfaces can be regarded simultaneously

coverings of n_2-fold M^4 and n_1 fold CP_2 and that one has $n = n_1 n_2$ in $h_{eff}/h_0 = n$ and n_1 would have interpretation as the number of flux tubes which are parallel in M^4 and can be even disjoint. This would give $h_{gr} \propto n_1$ and the factors of n_1 should correspond to the integers characterizing the notes of the 12-note scale. One could perhaps say that effectively single proton is replaced with n_1 protons located at different flux tubes so that also proton mass becomes $n_1 m$. One would have effectively a Bose-Einstein condensate like state of n_1 protons (at different flux tubes).

4. In the Pythagorean representation of octave the notes correspond to powers $(3/2)^k$, $k = 0, 1, ..., 11$, if $3/2)^{12} \simeq 2^7$ is not included. The corresponding integers are $3^k 2^{11-k}$. Only powers of primes $p = 2$ and $p = 3$ are involved and one just have $n_1 \propto 3^{11} 2^{11}$. If one increases the number of octaves involved to 14 to get a representation for chords needed to avoid the mapping of two dark codons to same 3-chords, one must have $n \propto 3^{23} 2^{23} = 6^{23}$. One can consider also simpler representations using integers expressible in terms of powers of primes $p = 2, 3, 5$ but one must give up exact quint cycle in this case. Interestingly, a good guess for the standard value h of h_{eff} is as $h = 6h_0$ [14, 17].

5. Small p-adic primes $p = 2$, $p = 3$ and perhaps also $p = 5$ (Golden Mean) are expected to be of special importance in TGD inspired biology [8]. $p = 2$ seems to appear everywhere and there is also support for $p = 3$ in biology [5, 6] (see `http://tinyurl.com/ycesc5mq`): great evolutionary leaps seem to correspond to time scales coming in powers of 3.

6. The branching of the flux tube bundle to n_i sub-bundles $N_i = n/n_i$ could correspond to the reduction $h_{eff} \to h_{eff}/n_i$. This could be seen as reduction of h_{eff}. One can also consider phase transitions reducing n to n/n_i.

3 Homonymy of the genetic code

In the following I will discuss briefly the basic facts about genetic code at Wikipedia level with emphasis on the poorly understood aspects of the code. There are two interesting phenomena: synonymy and homonymy. Synonymy means several names for AA or tRNA codon so that that several RNAs are mapped to the sama AA or tRNA codon: the understanding of the genetic code is the understanding of synonymy.

Homonymy means that the same RNA codon can correspond to several tRNAs or even AAs. A general TGD based view about homonymy differing from that discussed in [18] based on the recent understanding of the interaction between various representations of the genetic code is described below.

3.1 Variations of the genetic code

There exists also as many as 31 genetic codes (see `http://tinyurl.com/ydeeyhjl`) and an interesting question is whether this relates to the context dependence. Mitochondrial codes differs from the nuclear code and there are several of them. The codes for viruses, prokaryotes, mitochondria and chloroplasts deviate from the standard code. As a rule, the non-standard codes break U-C or A-G symmetries for the third code letter. Some examples are in order (see `http://tinyurl.com/puw82x8`).

1. UUU can code Leu instead of Phe and CUG can code Ser rather than Leu. In bacteria the GUG and UUG coding for Val and Leu normally can serve as Start codons.

2. UGA can code to Trp rather than Stop: in this case the broken symmetry is restored since also UGG codes for Trp.

3. There is variation even in human mitochondrial code (see `http://tinyurl.com/puw82x8`). In 2016, researchers studying the translation of malate dehydrogenase found that in about 4 per cent of the mRNAs encoding this enzyme the UAG Stop codon is naturally used to encode the AAs Trp and

Arg. This phenomenon is known as Stop codon readthrough (see `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5133446/`).

4. There is also a variant of genetic code in which there are 21st and 22nd AAs Sec and Pyl coded by Stop codons. UGA can code for Sec and Stop in the same organism. UAG can code for Pyl instead of Stop and introduces additional breaking of A-G symmetry for the third letter (UAA to Stop and UAG to Pyl).

3.2 Wobble base pairing

Wobble base pairing (see `http://tinyurl.com/y73se8vs`) emerges from the observation that the number of tRNAs pairing with mRNAs is smaller than 45 and considerably smaller than that of mRNAs. The needed minimum number of tRNAs is 32. Therefore the RNA-tRNA pairing cannot be 1-1 and some mRNA codons must correspond to several tRNA codons.

Remark: One could ask whether mRNAs code for tRNAs just like DNAs code for AAs. Homonymy for mRNA-tRNA pairing implies that the pairing can be many-to-1 only in given context.

1. According to the standard code, the first two bases of mRNA codon corresponds to two last bases of tRNA anti-codon and obey standard code. Wobble base pairing hypothesis applies to the pairing of the 3rd mRNA base to the 1st base in tRNA anticodon. At the level of chemistry the hypothesis is that the position of the first tRNA anticodon base pairing with the third mRNA base is variable and allows it to pair with several bases appearing as 3rd base in mRNA. This homonymy would be due to "wobbling" of the position of the first tRNA anticodon.

2. In the original model for wobble base pairing tRNA bases contain besides standard A, C, G, U also inosine I as a modification of G obtained by dropping NH_2 from the 6-cycle of G. It has turned out that there are actually variants of C and 5 variants of U (see `http://tinyurl.com/y73se8vs`). The large amount of homonymy for tRNAs forces to ask whether chemistry alone really dictates the genetic code.

3. The first tRNA letter is assumed to be spatially wobbling so that the association of tRNA with RNA is not unique and mRNA-tRNA pairing involves both synonymy and homonymy as the two tables for the pairing of the 1st 5' anticodon base of tRNA and 3rd 3' codon base of mRNA show. In the second column bold letters for mRN bases allow to read the standard pairing with tRNA codons in the first column and non-bold letters allow to deduce the non-standard behavior.

4. The first table (see `http://tinyurl.com/y73se8vs`) represents the original Watson-Crick proposal.

   (a) The pairings of the 3rd letter of mRNA codon to the 1st letter of tRNA anti-codon are following.

   - U $\rightarrow$ G.
   - G $\rightarrow$ U
   - {A, C or U} $\rightarrow$ I.

   The 2nd and 3rd tRNA letters A and C are paired with the 1st and 2nd mRNA letters in the canonical manner. There are only 3 tRNA letters, which implies that the number of tRNAs is smaller than maximal.

   (b) There is single 1-to-many pairing: U$\rightarrow$ {G, I} giving rise to 2-fold homonymy.

5. Revised pairing rules (see `http://tinyurl.com/y73se8vs`) are more complex since the number of tRNA bases is larger (U has 5 variants and C has 2 variants). All mRNA letters have 1-to-many pairing. Even if one counts the variants of U as single U there is 4-fold homonymy for U and homonymies for other codons. For A one has 9-fold homonymy.

These variations do not induce variation in DNA → AA pairing if the AA associated with the homonyms of tRNA are identical. This seems to be the case almost always since the variation of the genetic code is surprisingly small. This raises the question whether there is some mechanism eliminating to high degree the expected effects of homonymy in mRNA→ tRNA pairing.

4 TGD view about homonymies

One should understand the homonymies of the genetic code [18]. One can imagine homonymies at the level of DDNA-3-chord and DRNA-3-chord correspondences and between RNA-AA and RNA-tRNA correspondences.

4.1 Homonymies for DRNA-3-chord correspondence

It is possible that homonymies are present already at the dark photon level in the sense that the sub-harmonies have common chords.

1. Are the icosahedral orbits for different symmetry groups Z_6, Z_4, Z_2 disjoint? If they contain common triangles, the outcome is homonymy for dark codons unless one can scale the 12-note scales with respect to each other (different keys) to avoid common chords.

   This question finds an answer from the tables of [13] representing the chords. If the two scales considered contain 3-chords with the same frequency ratios this can happen. Z_6 harmony contains chords of same type with whole note intervals: $C_x, D_x, E_x, ...$, $x = m, 6, 9$ coding the frequency ratios as is done in popular music. If second harmony contains several types such that they are not separated by a multiple of whole note interval, at least one common chord is unavoidable also for shifted harmonies.

2. From the tables 1 and 2 of Appendix one finds that for Z_6 and 2 Z_4 harmonies this is indeed the case and they have 2-chords involving 2 quints in common: 6-orbit and 4-orbit containing $x = 9$ 3-chords have 2 common chords. One has homonymy at dark level. If entire orbits are mapped to the same AA there would be 8 AAs in the same multiplet. Some DDNA and DRNA codons are mapped to the same 3-chord of dark photons. This problem is shared by all 3 models of bio-harmony.

3. For the unique Z_6 harmony and 3 $Z_{2,rot}$ (table 3 of Appendix) of harmonies common chords can be avoided by shifting the latter harmonies by a half-note. The reason is that the chords of same type are now separated by a multiple of whole note interval. For $Z_{2,refl}$ harmonics (table 4 of Appendix) the chords of same type are separated by odd number of half-notes so that common chords are unavoidable since 3-chords of the same type appear. There are also common chords with Z_4 harmony.

4. Z_6 and $Z_{2,rot}$ harmonies possess no common chords by a shift by odd number of half notes. Z_4 and $Z_{2,rot}$ and Z_4 and Z_6 possess at least 2 common chords. $Z_{2,refl}$ possesses more common chords with Z_4 and Z_6.

   The fusion of Z_6, Z_4, and $Z_{2,rot}$ harmonies with 2 common chords between in $Z_6 \cap Z_4$ $Z_4 \cap Z_{r,rot}$ seems seems to be best that one can achieve. This would give $1 \times 2 \times 3 = 6$ harmonies altogether unless one obtains new harmonies by by relative shifts of the key.

How to solve the problem?

1. The above described homonymies involving 6-plets involve either 6-plet or 2-plet as second multiplet so that these deviations cannot be due to homonymy at the level of DRNA-3-chord correspondence.

2. Should one take seriously the puzzle that teased Pythagoras and led him to seriously consider that the structure of the Universe based on rationals has serious flaw in it. 12 quints give slightly more than 7 octaves: one has $(3/2)^{12} = 129.746337890625$ rather than $(3/2)^{12} = 128$ so that one obtains slightly more than octave under octave equivalence.

   Why not represent notes as powers of algebraic number $2^{1/12}$ and this is indeed done in practice (in rational approximation of course) but very musical people notice the difference and dislike this representation. There should be something deep in the representation of the scsale in terms of rationals as TGD indeed predicts. Note that a strict resonance is not required, it represents only the optimal situation.

3. Repeating the quint cycle gives slightly displaced chords: one can of course do this several times [21]. Could these slightly displaced chords represent DDNA and RNA codons as 3-chords otherwise mapped to the same chords? This would also mean that the corresponding DNAs and RNAs correspond to 3-chords with at least one note differing only slightly. This kind of notes is shared by 5 chords in icosa-tetrahedral harmony. The addition of second quite cycle means that the integers $n_i = 2^k 3^{23-k}$ characterize the notes of the 3-chords and $2^k 3^{23-k}$ and $2^{k+12} 3^{11-k}$ represent the nearby notes.

4. The minimal modification would replace only minimum number of notes in the problematic chords with new ones. A stronger modification would replace the problematic chords with displaced variants with notes in the second quint cycle. One could also do the same for all chords and say that the number of codons for non-problematic dark codons is doubled.

   One could also consider the doubling of each letter of the codon so that each chord would be replaced with 8 almost copies except in the case of homonymic AAs. A non-homonymic AA coded by n RNAs would be coded by $8n$ 3-chords. If the frequency differences are small enough this is not seen at the level of transition energies of AAs: this must be the case for non-homomymous AAs. For homonymous RNAs the energy differences must be seen and remove the homonymy. This DRNA-3-chord homonymy would be analogous to the RNA-tRNA homonymy.

5. One can consider the problem from a different perspective. For Hachimoji DNA [3] (see `http://tinyurl.com/y2mcjb4r`) the number of DNA letters seem to double so that codon is replaced with 8 codons. An explanation based on the Pythagorean dilemma was discussed in [21]. In the model it was however assumed that the doubling of dark DNA and DNA is real being due to the possibility of having also negatively charged color bonds between dark protons so that dark proton is effectively dark neutron (this might happen even in ordinary nuclear physics in nuclear string model [7]). The Pythagorean double covering of 3-chords could describe the doubling of codons. The doubling would not occur for the codons for which one has the homonymy - a prediction, which could be perhaps tested.

4.2 The map DRNA-DtRNA by 3-chords

The map $64 \to 40$ for DRNA-DtRNA inducing the corresponding map for $RNA - tRNA$ is not unique since there are many manners to reduces 64 to 40. Could this relate to tRNA-RNA homonomy? Consider icosa-tetrahedral code $20 + 20 + 20 + 4 = (3 \times 6 + 2) + (5 \times 4) + (10 \times 2) + (3 + 1)$ as example.

1. Suppose Z_2 is the divisor group (also Z_4 and $Z_3 \subset Z_6$ can be considered) so that the orbit can split to two and two tRNAs are associated with given amino-acid coded by n codons. At the first step one can take $20_1 + 20_2 + 20_3 + 4 \to 20_1 + 10_2 + 10_3 + 4 = 44$. Also $10_1 + 20_2 + 10_3 + 4$ and $10_1 + 10_2 + 20_2 + 4$ can be considered. Since Z_n has Z_2 as subgroup, the simplest manner to achieve $20_k = 10_k$ is to divide all orbits to 2 Z_2 cosets. This can be carried out in 3 manners.

2. One must get rid of 4 tRNAs. This can be achieved in several manners. In $20_1 = 3 \times 6 + 2$ one could have $6 + 2 \to 3 + 1$: there are 3 alternatives. In $20_2 = 5 \times 4$ one could have $5 \times 4 \to 3 \times 4 + 2 + 2$ (10 manners). In $20_3 = 10 \times 2$ one can take two 2:s to 1 (45) manners.

3. Could all these maps be realized and could they correspond to different maps at the level of dark codons? If the independence of resonances energies on frequencies is true with an appropriate choice of $h_{eff,i}$, it would seem that in all these cases same chemical tRNA is possible.

4.3 Homonymies for RNA-AA correspondence

There are two basic types of homonymies involving bio-molecules.

1. RNA-AA correspondence can vary somewhat and there are 31 variants of genetic code. RNA-tRNA homonymies are common and wobble phenomenon could be regarded as as such homonomy. This homony is poorly understood.

   I made the first attempt to understand homonymies in [18] but failed to realize one absolutely essential feature. Despite RNA-tRNA homononmies there are practically no RNA-AA homonymies. They might be completely absent for given genetic code. There must be a simple explanation for this.

2. In TGD framework the genetic code is replaced with 3 codes. There is DRANA-DtRNA code mapping 64 DRNA codons to 40 DtRNA codons and $DtRNA - DAA$ code mapping 40 DtRNA codons to 20 DAAs. The composition of these codes gives DRNA-DAA code inducing the RNA-AA code.

   The highly non-trivial fact is that one has what mathematician would call commuting triangle: RNA-tRNA-AA = RNA-AA for given code. All the homonymies of RNA-tRNA code are possibly completely compensated for given $RNA - AA$ code. This must have simple explanation and once one has made this question, one also knows its answer in TGD framework.

3. For Hamiltonian cycles the $n(A)$ codons coding for given AA corresponds to orbit of a fixed codon at the orbit having symmetry group $Z_{n(A)}$. Genetic code maps the codons at the orbit to the AA corresponding to the orbit and replaces the symmetry group Z_n with trivial group $Z_n/Z_n = Z_1$.

   Remark: There are 6 chaotic icosahedral Hamiltonian cycles with symmetry group Z_1 so that therefore 20 amino-acids each coded by single codon. Could one interpret the 20 amino-acids with the chaotic representation of chaotic icosahedral Hamiltonian cycle?

   For RNA-tRNA correspondence similar process is possible. Now one replaces Z_n/Z_k where k is factor of n.

   Consider icosa-tetrahedral code as an example. $k = 2$ is simplest choice since it divides $n = 6, 4, 2$ for icosahedral codes but not for tetrahedral code for which one has $n = 3$: (ile, ile, ile, met) would naturally correspond to the 2 orbits under tetrahedral Z_3. This symmetry appears only for icosa-tetrahedral option. For other options one can explain it as an outcome of symmetry breaking for doublets and (ile,ile) and symmetry broken (ile,met) would have ile in common. This looks un-natural.

   One can indeed construct $64 \to 40$ map for DRNA and DtRNA codons by replacing some orbits with their Z_2 cosets but this map is not completely unique. This is possible for all code candidates, which all contain Z_6 and Z_4 symmetric icosahedral harmonies giving rise to amino-acids corresponding to 3 6-orbits and one 2-orbit for Z_6 symmetry and 5 4-orbits with Z_4 symmetry. The remaining orbits are 3-orbit and 1-orbit for tetrahedral symmetry broken to Z_3 and 2-plets for Z_2 orbits.

There are are however codes for which RNA-AA correspondence is non-standard. As explained above, the simultaneous replacement UUC-Leu → UUC-Phe and UUG-Leu → UUG-Ser can take place. Also AUG-met → CUG-met and GUG-met → GUG-met can occur.

A general explanation could be as follows. If the two homonymous amino-acids - Phe and Leu and Leu and Ser in the first example and met and Leu and Val in the second example- have very nearly same transition energy, and if the 3-chords correspond transition energies of AA irrespective of frequencies, homonymy becomes possible.

This problem can be avoided if the tRNA pairing second AA with the RNA codon is not present. Both options might be realized in the same organism. It could also happen that second AA is so far from energy resonance that it is only rarely translated.

4.4 Homonymies for RNA-tRNA correspondence

Could the possibility of several harmonies/moods with different chords increase the number of tRNA codons from the minimal value 40? Are these homonymies forced by necessity or do their reflect freedom of MB to choose? Do dialects emerge already at the molecular level and do they have some practical advantage?

1. Could the possibility of several moods demand more than the minimal number of tRNAs. Harmonies correspond to different collections of triplets (n_1, n_2, n_3) characterizing the chord.

   It was however already noticed that the variation of the Planck constants $h_{eff} \to h_{eff}/n_i$ associated with the flux tubes can modify the cyclotron energies. This would mean that the emotions are not directly seen at the level of molecular transitions as bio-chemist would certainly argue. If energy resonance couples dark photons to ordinary matter it could be possible to guarantee the coupling energy does not depend on the values of frequencies of the 3-chord at flux tubes. This would suggest that there is no motivation to increase the number of tRNAs for the lack of required resonance energies.

2. Could a large number of tRNAs as mediators of RNA-AA pairing be something chosen intentionally by MB rather than being forced by chemical limitations. Could surplus of different tRNAs be a safer option when some tRNAs are not produced. In natural languages there is large number of dialects and new are born all the time.

   No hard-wired correspondence would exist at chemical level. MB would be to some degree creative and able to build tRNAs from the stuff that it happens to find from the lab! Biology could be creative already at RNA-tRNA level and this flexibility could emerge from the intelligence coded by $h_{eff} = n$: the larger the number of factors of n the higher the intelligence of the system would be.

   This flexibility might also explain the homonymy at RNA-AA level and different genetic codes as a formation of dialects.

5 About the 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 vertices of the graph used. The most plausible realization of the harmony is as icosahedral harmony [13] (see `http://tinyurl.com/yad4tqwl` and `http://tinyurl.com/yyjpm25r`).

1. Icosahedron (see `http://tinyurl.com/l5sphzz`) 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 equivalene). Icosahedron

allows a large number of inequivalent Hamiltonian cycles and thus harmonies characterized by the subgroup of icosahedral group leaving the cycle invariant. This group can be Z_6, Z_4, or Z_2 which acts either as 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. I call this harmony bio-harmony. The predicted number of DNA codons coding for given amino-acid is the number of triangles at the orbit of given triangle and the numbers are those for genetic code.

4. How to concretely realize the fusion of harmonies? Perhaps the simplest realization that I have found hitherto is based on union of tetrahedron of 3 icosahedrons obtained by gluing tetrahedron to icosahedron along its face which is triangle. The precise geometric interpretation of this realization has been however missing and I have considered several variants. I have proposed that the model could explain the two additional amino-acids Pyl and Sec appearing in Nature.

   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 (see `http://tinyurl.com/puw82x8`). This symmetry breaking should be understood.

5.1 Why 3 icosahedral harmonies and 1 tetrahedral harmony?

The following argument suggests a more detailed solution of these problems than proposed earlier.

1. The copies of icosahedron would differ by a rotation by multiples of $2\pi/3$ (Z_3) around axis through the common triangular face. This face unlike the other faces remains un-affected. Also tetrahedron remains un-affected so that it is counted only once.

   If the 3 copies of the icosahedral common face are counted as separate (this is important!), one obtains 20+20+20 faces from icosahedron. If also tetrahedral shared faces is counted as separate, tetrahedron gives 4 faces: 64 codons altogether as required. One obtains 19 orbits from the 3 icosahedra and 1 orbit from tetrahedron: 20 orbits as counterparts of amino-acids altogether.

2. But can one really counter the 4 common faces as separate? One must do so. Could these faces be interpreted as somehow special codons? Maybe as stop codons or start codons for the vertebrate genetic code which also corresponds to the realization of DNA, RNA ,tRNA, and amino-acids as dark proton triplets so that DNA sequences would correspond to dark proton sequences. Could the shared codons be assigned with various modifications of the vertebrate code involving also exotic amino-acids Pyl and Sec.

3. Consider first the tetrahedral face. If the common face is removed from the 4-face orbit of tetrahedron, the orbit has only 3 faces and correspond to an amino-acid coded by 3 DNA codons. ile is the only such amino-acid and the interpretation could be that one ile corresponds to the 3 tetrahedral faces and met acting as start codon to the fourth shared face.

4. Also 3 icosahedral amino-acids corresponding to orbits containing the shared face can lose 1 codon each. To nake this more concrete, one can look for the deviations from the vertebrate code.

(a) There are 10 doublets if the doublet UAA, UAG acting as stop codons is counted as doublet coding for stop regarded formally as amino-acid.

(b) The second member in the doublet UGA, UGG coding for tyr in code table could correspond to a common face and act as a stop codon.

(c) For the modifications of genetic code UAG coding for stop can code for Pyl and UGA coding for stop can also code for Sec. UGA can also code for trp so that there would not be any symmetry breaking in this case. Could UAG and UGA correspond to common faces for two icosahedra?

(d) There is also third icosahedral shared face. CUG coding for leu can also code for ser. Could this correspond to the third exceptional codon associated with the icosahedral part of the code?

5. If the answers to the questions are affirmative, all basic deviations from the vertebrate code can be understood. The translation of the codons associated with shared face would be unstable for some reason.

   (a) 3-chord representation is more fundamental than the chemical one. This could mean that the chords associated with the shared faces are very near to each other so that the correspondence between 3-chord representation and chemical representation of codons becomes unstable if based on triple resonance.

   (b) The proposal has indeed been that the 13th vertex implied by tetrahedron corresponds to a note very near to one of the notes of 12-note scale - this note is necessary since the 12-note scale defined by quints gives 12th note slightly more than octave under octave equivalence as discovered already by Pythagoras.

   If this picture is correct, the symmetry breaking of the genetic code would be due to the presence of the face common to icosahedron and tetrahedron and reflect the problem discovered already by Pythagoras. The rational number based Pythagorean scale defined by quints is special: people with absolute pitch prefer it over the well-tempered scale involving powers of irrational number $2^{1/12}$ requiring extension of rationals.

5.2 Could stop codons correspond to dissonant 3-chords?

One can approach the situation also from the point of view of harmony - or rather, dis-harmony: could dissonance 3-chords act as stop codons. The 3-chords of icosahedral harmonies can be classified to three groups depending on whether the triangle representing the chord contains 0, 1, or 2 sides [13]: in in other words, whether the chord contains 0 , 1, or 2 quints. The harmonies can be labelled by the triplet (n_0, n_1, n_2) telling the numbers of chords with 0, 1, and 2 quints.

1. The unique Z_6 harmony necessarily present in the bio-harmony has $(2, 12, 6)$. It has two augmented chords (transposes of $C_{aug} = CDG\sharp$) containing two major thirds and defining the 3-chord of a harmony assignable to triangle). This beautiful chord to which finnish tangos so often end, cannot be regarded as dissonance.

2. The 2 Z_4 harmonies have $(n_0, n_1, n_2) = (0, 16, 4)$ and $(4, 8, 8)$. For the latter harmony one has genuine dissonances since the the highest and lowest note of 3-chord are separated by major or minor third. The chords with 0 quints labelled by script "ex1","ex2",...,"ex6" (for the notation see [13]) are dissonances in this sense. "ex7" and "ex8" ($CDF\sharp$ and $CDG\sharp$) cannot be regarded as dissonances in this sense.

3. The 3 $Z_{2,rot}$ harmonies have $(0, 16, 4)$, $(2, 12, 6)$, and $(4, 8, 8)$. Both 2-plets and 4-plets contain 2 dissonances.

4. There are 3 $Z_{2,refl}$ harmonies with $(2,12,6)$ and 1 with $(4,8,8)$. These harmonies have genuine dissonances. Interestingly, $(2,12,6)$ corresponds to a doublet for which only the second member corresponds to dissonance.

5. For tetrahedral harmony single step should correspond to 1/4:th of octave (using suitable power of 3/2 as a rational approximation) so that the notes at the vertices of tetrahedron should correspond to $CE\flat F\sharp$ defining C_{dim}. This does not appear in the icosahedral code table as 0-quint chord. Although the triangles of tetrahedron and icosahedron would be shared in some sense, the chords cannot be same. This support the idea that ile triplet and met are coded by tetrahedral faces.

The chords containing 0 quints appearing in Z_4 and Z_2 harmonics can be regarded as dissonant. The minimization of dissonance would give a fusion of the unique Z_6 harmony $(2,12,6)$, unique Z_4 harmony $(0,16,4)$ and unique $Z_{2,rot}$ harmony $(0,16,4)$. Bio-harmony would be unique and contain no dissonances. Recall however that the proposal is that bio-harmonies serve as correlates for moods realized even at the level of basic bio-molecules.

For other options one would have dissonant chords. $Z_{2,refl}$ harmony $(2,12,6)$ has only single dissonant chord. Since stop codons would naturally correspond to dissonances, this observation raises some questions.

1. Could the dissonant chord of $Z_{2,refl}$ harmony $(2,12,6)$ correspond to the triangle shared by tetrahedron and icosahedron? Could this correspond to (stop,trp) pair with stop coded by dissonant chord "ex"7 ($CDF\sharp$ defining part of D7 chord). This would fix the code to contain Z_6 harmony $(2,12,6)$, unique Z_4 harmony $(0,16,4)$ and unique $Z_{2,refl}$ harmony $(2,12,6)$. There would be single dissonance coding for stop in stop,trp doublet.

2. The doublet coding for stop should formally code for amino-acid. One cannot realize this doublet as a doublet of dissonances with "ex"n, with $n \in \{1,..,6\}$ for single bio-harmony. The second member of this doublet could however correspond to the shared triangle.

This tentative picture should be of course checked. There are also cycles without any symmetries. Could these chaotic cycles be interpreted as disharmonies.

5.3 How could the representations of genetic code as dark 3-chords and nucleotide triplets relate?

One of the poorly understood aspects of the model is how the various representations of the code relate.

5.3.1 Frequency coding of nucleotides is not possible

Frequency coding of nucleotides would look natural but it is easy to see that it is in conflict with bio-harmony.

1. The representations as dark proton triplets and dark photon triplets do not involve decomposition to ordered triplet of letters as the ordinary chemical representation does. Dark protons are entangled and one cannot order them and there is no obvious ordering of the frequencies of dark photons.

   This is not a problem for the correspondence between dark proton triplets and dark photon triplets and one can even imagine assignment of dark cyclotron photons with 3 parallel flux tubes acting as wave guides. This could mediate the interaction between dark variants of basic biomolecules with same value of h_{eff} as frequency resonance.

2. The interaction between ordinary DNA/RNA/tRNA and its dark variant should involve the transformation of dark photon triplet associated with flux tube triplet emanating from dark bio-molecule to ordinary photons (possibly bio-photons) and energy resonance would be involved. Is the energy

resonance involved with the formation of the dark-ordinary pairs or with the sustainment of these pairings? The example of benzene suggests sustainment.

3. The assumption that energy resonance is involved with dark-ordinary pairing indeed leads to problems. The first guess would be that ordinary photon triplet somehow carries information about the position of nucleotide in the codon. The 4 nucleotides would correspond to 4 frequencies with frequency scale depending on the position inside the codon. There are indeed 12 frequencies in the 12-note scale so that 3 frequency scales with 4 frequencies associated with each of them would give 64 combinations of frequencies.

   Frequency coding of nucleotides however leads to a problem. The first two letters of the codon are known to determine the amino-acid coded by it to a high degree since the third letter typically distinguishes between 1 or 2 amino-acids only, and labels codons at the orbit of DNA codon defining amino-acid. Therefore for DNA codons coding same amino-acid the first two frequencies should be same. This is not the case for bio-harmony for the simple reason that the frequencies of 3-chords along the orbit defining amino-acids are different. Only the frequency ratios defining the type of the chord are same along the orbit.

   The frequency ratios determine the correspondence so that the correspondence can be only between *entire* dark and ordinary codons, and cannot be reduced to correspondence between frequencies and letters. Holism does not reduce to reductionism.

5.3.2 Does the impossibility of frequency coding of nucleotides lead to problems with the models of replication and transription?

This becomes a potential problem in the model for DNA replication and transcription to RNA.

1. The basic picture about bio-catalysis in TGD framework is following. U-shaped magnetic flux tubes emanate from the reactants and can reconnect to form a pair of flux tubes connecting the reactants. The shortening of the flux tube pair by a reduction of h_{eff} brings the reactants together and liberates the energy needed to kick the reactants over the potential wall making the reaction rate extremely low otherwise.

   The U-shaped flux tubes or flux tube triplets would be associated with dark codons of dark DNA accompanying DNA strand, and would be formed as the flux tube pair(s) connecting the strands split by the reversal of reconnection. The h_{eff} associated with resulting U-shaped flux tubes associated with replicating strands would increase requiring metabolic energy. They would get longer and could act as tentacles scanning the environment to spot similar flux tubes assignable to nucleotides or codons by resonance.

2. In the standard picture one assumes that nucleotides defining the letters of the codons appear as non-correlated molecules in the environment, and that each codon is built by a stepwise process in which letters attach to it. The letters can respond only to single frequency and cannot "know" which position to attach to. Thefrequency coding is not consistent with the idea that dark photon triplet assigned with the dark codon gives rise to energy resonance with the letters one by one.

   Could the triple resonance occur as single step and attach all 3 nucleotides in single step? Or could the triple resonance be a collective frequency resonance with dark codon already attached to the ordinary codon in the environment. Ordinary-dark pairing by energy resonance would sustain rather than generate DNA strand since otherwise the Coulomb repulsion due to the large negative charge of DNA does not allow stability.

3. The problem is that it is nucleotides seem to appear in the environment rather than codons. Could the nucleotides of the environment actually form loose codons connected to dark codons by long flux tubes with large value of h_{eff}? Could the reduction of h_{eff} bringing nucleotides together induce

the reduction of flux tube lengths giving rise to ordinary codon? If the reduction of h_{eff} for flux tubes occurs nucleotide-by nucleotide, one would have consistency with the standard picture. The simplest picture is following.

Dark codons are paired with the loose variants ordinary codons. The opening of DNA double strand leads to the splitting of the flux tube pairs connecting the ordinary codons of strands to U-shaped flux tubes, which reconnect with U-shaped flux tubes coming dark codons paired with loose ordinary codons. The reduction of h_{eff} d pairs nucleotides of loose codons with those of ordinary codons.

4. The pairs of dark codons and loose codons would be analogous to tRNA molecules. One can imagine even pre-tRNA molecules with loose coupling of RNA and amino-acid so that replication and transcription would be very similar topological processes. Also RNA transcription and translation of RNA to amino-acids would rely on similar mechanism. The only difference would be that only the second - active - strand would form U-shaped flux tubes connecting with dark RNA codons.

5.3.3 What about remote DNA replication

This model could also explain remote replication of DNA for which Montagnier et al have reported evidence [4]. Also remote transcription is predicted to be possible. I have already earlier considered a model of remote replication [12] in an article written together with Peter Gariaev who has reported this kind phenomenon already earlier. I have discussed the findings of Montagnier et al in [22].

1. The experiment involves two vessels, call them A and B. A contains genes and B only nucleotides - at least according to the standard picture. There is irradiation using 7 Hz frequency not far from the lowest Schumann frequency having a nominal value of 7.8 Hz. What happens is that the replicas of genes appear in B. It is also reported that the DNA generates em radiation possibly responsible for the information transfer.

2. The proposed model for the ordinary DNA replication generalizes easily to describe also remote replication. The new element would be that the U-shaped flux tubes from A would extend to B - here 7 Hz radiation could be essential - , would be parallel to each other, and have same average length, which is natural if they have same value of h_{eff}. Also the experimental arrangement could favor parallel flux tubes. In B the dark codons paired with loose codons formed from ordinary nucleotides would be present, and their U-shaped flux tubes would reconnect with those coming from A. Remote replication could take place: here it is essential that the U-shaped flux tubes are parallel and have very nearly the same length.

   The TGD interpretation would be that the Earth's magnetic body is involved and generates quantum coherence in the length scale at least the size of the system studied. The reported em radiation would naturally relate to the dark photon triplets representing the codons.

5.3.4 Is ZEO needed to understand the replication?

In TGD one must give up thinking in terms of standard ontology of bio-chemistry in which the process is a kinetic process governed by differential equations for the populations of molecules and proceeding in step-wise manner nucleotide by nucleotide. ZEO suggests temporal holism - at least at the level of single dark codon, which cannot be built building brick by building brick.

1. An open question is in which time scale this temporal quantum holism holds true: in the time scale of addition of single codon or in the time scale of replication of gene or something else? In the following the possibility that temporal holism holds in the time scale for the pairing of dark codons.

2. In ZEO one could have state function reduction in which initial state corresponds to dark codon plus population of nucleotides and final state to dark codon paired with the ordinary codon formed

from 3 nucleotides in energy resonance with the codon formed from nucleotides. What matters are only the initial and final states.

3. If "big" state function reduction (BSFR) is in question, the final state would correspond to a superposition of deterministic time evolutions leading from the outcome of the reduction to geometric past, possibly but not necessary to a state in which nucleotides do not form codon paired with the dark codon.

4. The process would create strong correlations between the position of nucleotides of the codon and between the positions of codon and its dark variant and therefore a generation of entanglement. Unitary evolutions followed by "small" state function reductions (SSFRs) would generate a state as a superposition of the states satisfying the criteria of the desired final state and other states and BSFR would select the desired final state. It could be followed by BSFR returning the original arrow of time but doing nothing for the state.

6 Appendix: Tables of basic 3-chords for the icosahedral harmonies with symmetries

The tables below give list for the three types of 3-chords for the 11 harmonies possessing symmetries. One must remember that the reversal of the orientation for the cycle induces the transformation $C \leftrightarrow C$, $F\sharp \leftrightarrow F\sharp$, $H \leftrightarrow C\sharp$, $F \leftrightarrow G$, $D \leftrightarrow B\flat$, $E \leftrightarrow G\sharp$, $A \leftrightarrow D\sharp$ and produces a new scale with minor type chords mapped to major type chords and vice versa. Also one must remember that all 3-chords except those which are simple majors or minors lack the third so that their emotional tone remains uncharacterized. For instance, $C6$ does could be replaced with $Cm6$ and $G7$ with $Gm7$. The reader can check the chords by direct inspection of the figures. The convention used is that vertex number one corresponds to C note.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(2, 12, 6)	$(Faug, Gaug)$	$(Cm, Dm, Em, F\sharp m, G\sharp m, B\flat m)$,	$(C9, D9, E9, F\sharp 9, G\sharp 9, B\flat 9)$.
		$(F6, G6, A6, B6, C\sharp 6, D\sharp 6)$.	

Table 1: Table gives various types of 3-chords for harmonies with Z_6 rotational symmetry. Note that half-octave shift is an exat symmetry. Note that $G^{aug} = CEG\sharp, F^{aug}$ act as bridges between the groups related by half octave shift. The chords have been arranged so that they form orbits of Z_6. "Amino-acid chords" correspond to preferred chords at the orbits.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(0, 16, 4)		$(D7, D6, G\sharp 7, G\sharp 6)$,	$(B\flat 9, B9, E9, F9)$.
		$(G4+, A9-, C\sharp 4+, D\sharp 9-)$,	
		$(Emaj7, Gmaj7, B\flat maj7, C\sharp maj7)$,	
		$(C9-, A9-, F\sharp 9-, D\sharp 9-)$.	
(4, 8, 8)	$(Cex3, Eex2, F\sharp ex3, B\flat ex2)$.	$(Dmaj7, E9-, A7, A6)$,	$(B\flat 9, F9, C9, G9)$.
		$(G\sharp maj7, B\flat 9-, D\sharp 7, D\sharp 6)$.	$(E9, B9, F\sharp 9, C\sharp 9)$.

Table 2: Table gives various types of 3-chords for the two harmonies with $Z_4 = Z_2^{rot} \times Z_2^{refl}$ symmetry. 4-plets represent the orbits. First cycle has no harmonic loners. Second cycle gives rise to bio-harmony (4, 8, 8) for which 0-quint chords are dissonant.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(0, 16, 4)		$(Em, B\flat m), (Cm, F\sharp m),$	$(D9, G\sharp 9),$
		$(G6, C\sharp 6), (A6, D\sharp 6),$	$(E9, B\flat 9).$
		$(D4+, G\sharp 4+), (B4+, F4+),$	
		$(Cmaj7, F\sharp maj7), (G6-, C\sharp 6-).$	
(2, 12, 6)	$(Aex4, D\sharp ex2).$	$(Am, D\sharp m), (G9-, C\sharp 9-),$	$(C9, F\sharp 9),$
		$(C4, F\sharp 4), (E4+, B\flat 4+),$	$(A9, D\sharp 9),$
		$(Dmaj7, G\sharp maj7),$	$(D9, G\sharp 9).$
		$(Bmaj7, Fmaj7).$	
(4, 8, 8)	$(Aex2, Hex8, D\sharp ex2, Fex8).$	$(D7, G\sharp 7), (Amaj7, D\sharp maj7),$	$(G9, C\sharp 9), (A9, D\sharp 9),$
		$(A4+, D\sharp 4+), (E7, B\flat 7).$	$(B9, F9), (E9, B\flat 9).$

Table 3: Table gives various types of 3-chords for harmonies with Z_2 rotation symmetry acting as half-octave shift. The doublets represent 2-chord orbits.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(2, 12, 6)	$(F\sharp ex3, Hex4),$	$(Am, D\sharp), (A6, D\sharp 7),$	$(C9, F9), (B9, F\sharp 9),$
		$(D7, B\flat 6), (G6-, Fmaj7),$	$(E9-, C\sharp 9).$
		$(D4+, B\flat 9-), (E9, G\sharp 4+),$	
(2, 12, 6)	$(Dex4, Hex4).$	$(F, Fm), (C6-, B\flat maj7),$	$(C9, D\sharp 9),$
		$(D7, G\sharp 6), (Gmaj7, D\sharp 6-).$	$(D\sharp 9, C\sharp 9),$
		$(C\sharp 4-, A4+), (E4+, F\sharp 6).$	$(E9, B9).$
(4, 8, 8)	$(Fex1, D\sharp ex3, G\sharp ex1, Aex2).$	$(E7, E6), (Amaj7, B9-),$	$(D9, B9), (C9, C\sharp 9),$
		$(G, C\sharp m), (D7, F\sharp 6).$	$(F9, G\sharp 9), (D\sharp 9, B\flat 9).$
(2, 12, 6)	$(Hex3, Eex7).$	$(D7, G\sharp 6), (G, D\sharp m),$	$(C9, D\sharp 9),$
		$(F, Fm), (C6-, B\flat maj7),$	$(D9, C\sharp 9),$
		$(A9-, C\sharp 4+), (E7, F\sharp 6).$	$(E9, B9).$
(2, 12, 6)	$(F\sharp ex2, Fex3).$	$(F, B\flat m), (C7, G\sharp 6),$	$(B\flat 9, D\sharp 9),$
		$(Amaj7, B9-), (E6, E7),$	$(C9, C\sharp 9),$
		$(G, C\sharp m), (D7, B6).$	$(D9, H9).$

Table 4: Table gives various types of 3-chords for harmonies with single reflection symmetry.

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