The realization of genetic code in terms of dark nucleon and dark photon triplets

February 24, 2022

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Abstract

I have worked for more than 10 years with a proposal for two kinds of realizations of the genetic code. The first realization, bioharmony model, represents genetics as light 3-chords consisting of dark photons. The second realization is in terms of dark proton or nucleon triplets forming closed or open strings. I have considered several variants of both realizations but the details have remained poorly understood and I have spent a considerable time on wrong tracks.

It however seems that the dust is finally settling (I am writing this in the beginning of 2022). One can see the dark nucleon model as a generalization of the quark model of nucleon and Δ baryons obtained by replacing u and d quarks with dark nucleons. Galois confinement solves the statistics problem. The nucleons are connected by pionic flux tubes to form a closed string-like entity. The dark variants of DNA, RNA, tRNA, and amino-acids (AAs) follow as a prediction. In the sequel, the notation DDNA, DRNA, DtRNA, DAA will be used for the dark variants of the basic information molecules. One can also understand the small symmetry breaking associated with the genetic code.

A concrete realization of bioharmony in terms of the dark nucleon model for codons emerges. The small symmetry breaking effects - the members of doublet that should code for the same amino acid (or act as stop codons), code for different amino acid (or amino acid and stop), are understood. Also the differences between vertebrate and bacterial codes are understood.

Contents

1 Introduction

I have worked for more than 10 years with a proposal for a realization of the genetic code in terms of dark proton or nucleon triplets forming closed or open strings. I have considered several variants of the code but the details have remained poorly understood and I have spent a considerable time on wrong tracks. Also the contents of this chapter reflect this wandering.

It however seems that the dust is finally settling (I am writing this in the beginning of 2022). One can see the model as a generalization of the quark model of nucleon and Δ baryons obtained by replacing u and d quarks with dark nucleons. The color group solving the statistic problem for Δ baryon is in the receint case solved by Galois confinement involving Galois group Z_3 assignable to the codons.

1.1 Basic notions and ideas

The basic notions behind the models of genetic code and of biomolecules rely on the notion of dark matter as $h_{eff} = nh_0$ phases of ordinary matter predicted by number theoretic vision. $n = h_eff/h_0$ serves as a measure for algebraic complexity and as a kind of universal IQ.

Dark matter at the magnetic body (MB) has large h_{eff} so that it is quantum coherent in long scales and acts as a master controlling ordinary biomatter. The control dynamics at dark level is very simple as compared to the biochemical dynamics, which is a kind of shadow dynamics.

Galois confinement is an essential element of the picture. Physical states are singlets under the action of the Galois group associated with the real polynomial with rational coefficients permuting the roots of the polynomial defined a 4-surface in M^8_c and mapped by $M^8 - H$ duality to $M^4 \times CP_2$. Among other things, this implies that the quark momenta, which are algebraic integers in an extension of rationals defined by the polynomial, sum up to an ordinary integer when the momentum scale corresponds to the largest ramified prime assignable to the extension.

Galois confinement provides a universal mechanism for the formation of bound states. Dark codons as dark nucleon- and dark photon triplets are Galois confined states behaving like a single quantum unit. Dark 3N-nucleons and dark 3N-photons define dark genes.

1.2 Two models of the genetic code based on dark particles

Both models are based on Galois confinement providing a universal mechanism for the formation of bound states in TGD Universe.

1.2.1 Bioharmony model

The faces of icosahedron and tetrahedron (and octahedron) are triangles. They would correspond to 3-chords made of dark photons, which in turn represent genetic codons. m

Communications are by dark 3N-photons representing genes and are based cyclotron 3N-resonance. Information coded in the frequency modulation of cyclotron frequencies. The chords serve as address and the message is coded to the frequency modulation. The outcome is sequence of resonances giving rise to pulses. Nerve pulse patterns could emerge by this mechanism.

Biophotons are ordinary photons resulting from the decay of dark N-photons to ordinary photons.

1.2.2 Codons as dark 3-nucleons

This work led to a more detailed model of the realization of the genetic code in terms of dark nucleon triplets forming a linear structure as the dark counterpart of linear biomolecule pairing and parallel with it.

The nucleons are connected by pionic flux tubes carring charge $0, \pm 1$ to form a closed string-like entity carrying angular momentum 0,1, or 2. The dark variants DDNA, DRNA, DtRNA, DAA of DNA, RNA, tRNA, and and amino acids (AA) follow as a prediction. AAs correspond to non-rotating analogs of N (p,n) and Δ, DNA and RNA to rotating analog of Δ, and tRNA to rotating analog of N.

Also the pairings between dark information molecules can be understood to a high degree, and the chemical and functional differences between DNA and RNA could reflect the differences between DDNA and DRNA. The almost exact T-C and A-G symmetries of the third letter of the genetic codon could be seen as reflection of almost exact spin or isospin symmetry. The latter option was considerd in [K1] but this work strongly favors spin symmetry. One can understand the numbers of DDNAs coding for given DAA and also the the breaking of spin symmetry. The number of DtRNAs is the minimal 32 and this predicts 1-to-many character of DtRNA-tRNA pairing which would induce wobble base pairing.

1.3 The relationship between the two models of genetic code?

The precise relation between the two models of genetic code remained poorly understood for a long time. The connection came from the realization of bioharmony model as so-called icosa-tetrahedral tessellation of hyperbolic 3-space H^3, which corresponds to either mass shell in momentum space or light-cone proper time constant hyperboloid [L8]. H^3 allows an infinite number of tessellations as analogs of 3-D lattices in the Euclidean 3-space E^3.

1. Basic biomolecules would correspond to linear sub-lattice-like structures of the icosahedral tessellation formed from triplets of icosahedron, tetrahedron and octahedron. One can say that DDNA codon X is associated with icosahedron-pair and corresponds to a face. This face represents X in the bioharmony model and also the entangled dark nucleons at its vertices represent X.

2. The cyclotron frequencies for the nucleons of X correspond to the frequencies of a dark 3-photon emitted by the dark 3-nucleon. This picture generalizes to genes represented as dark 3N-codons and dark 3N photons emitted in their communications involving 3N-resonance and frequency modulation yielding a series of resonance peaks at the end of the receiver as an analog of nerve pulse pattern.

3. Hamiltonian cycle must be physically realized at the icosa-tetrahedron which would serve as the basic structure for all dark counterparts of the information molecules. The simplest option is that the Hamiltonian cycle corresponds to a closed flux tube going through all vertices of the tetra-icosahedron. If the cyclotron frequencies, that is magnetic field strengths, are scaled by factor 3/2 (and scaled down to the same octave by octave equivalence) at each step along the cycle, the model of bioharmony is realized in terms of cyclotron frequencies. The codon realized as 3 dark nucleons associated with corresponds to the codon realized as dark photon triplet.

4. This picture generalizes to DtRNAs and DAAs. DtRNAs would have as active faces those DtRNA codons, which pair with DmRNA codons. DAAs would have at active faces those DtRNA codons which pair with them. Common dark codon would make pairing by dark 3-photon resonance possible. DtRNA could attach to correct DmRNA during translation and for DAA to correct DtRNA. Ordinary biomolecules would be paired with their dark variants so that dark variants of basic processes would induce their biochemical variants as a kind of shadow dynamics. The pairing by 3N-resonance could be a completely general mechanism involved with biocatalysis.

A concrete realization of bioharmony [**?**]n terms of the dark nucleon model for codons emerges. The small symmetry breaking effects - the members of doublet that should code for the same amino

acid (or act as stop codons), code for different amino acid (or amino acid and stop), are understood. A crucial piece of the puzzle is that one particular chord $CEG\sharp$ has identical intervals between the notes in even tempered scale. Also the failure of the Pythagorean quint cycle (notes are obtained by scaling the basic frequency by power powers of (3/2) and using octave equivalence) to close, which bothered Pythagoras, is in an essential role. Also the differences between vertebrate and bacterial codes are understood.

2 Dark nucleon realization of the genetic code and basic information molecules

In this section I will represent the arguments leading to the recent (2022) view about dark nucleon realization of the genetic code and dark counterparts of basic information molecules DNA,RNA,tRNA, and amino acids.

2.1 The basic vision and the first guess

The basic vision is that dark matter and magnetic body (MB) serves as a master controlling the dynamics of the ordinary biomatter so that its dynamics is shadow dynamics, and the huge complexity of living matter could reduce to relatively simple control dynamics at the level of MB.

Biomolecules are information molecules and dark matter has a higher "IQ" than ordinary matter measured as the dimension $n = h_{eff}/h_0$ of the extension of rationals associated with the space-time regions characterizing the system measuring also the scale of quantum coherence. Therefore the natural expectation is that basic information molecules have dark counterparts and genetic code is realized at a darl level so that the chemical realization would be a secondary realization.

1. I started with a proposal [K4, K6, K3, K7] that dark codons could correspond to dark nucleons, that is dark quark triplets, assignable to open or closed string like objects (flux tubes). This led to the proposal for the basic group theoretical decomposition DDNA and DRNA codons in terms of group representations of $SU(2)_I \times SU(2)_R$ as $(4_I \otimes 4_s \oplus 2_I \otimes 2_s) \otimes (5_s \oplus 3_s) = [(3/2,-3/2)_I + (1/2,-1/2)_I] \otimes (4_s \oplus 2 \otimes 2) \otimes (5_s \oplus 3_s) = 64_{DNA} \oplus 64_{RNA}$. In the quark model, this corresponds in fermionic degrees of freedom to nucleon N and Δ assuming color degrees of freedom to get statistics right. $5 \oplus 3$ could be assigned to 2 *rho*-meson-like bonds for an open string-like object.

2. The realization of $4 \times 4 \oplus 2 \oplus 2$ in terms of quark color triplets is not physically plausible and the challenge is to realize $4 \times 4 \oplus 2 \oplus 2$ and $5 \oplus 3$ physically in terms of more plausible dark states. The natural guess is that this realization involves dark protons and neutrons. u and d would be replaced with p and n.

3. Color would be absent and since the Δ is completely symmetric, antisymmetry required by Fermi statistics must be realized by bringing in some new degrees of freedom. Galois confinement is suggestive in the TGD framework [L8, L9, L10, L11, L12]. Z_3 is a natural guess for the Galois group in the case of codons and one has 3 states in geometric degrees of freedom and 3-nucleon state, which is Z_3 singlet would be antisymmetric.

   Since the induced spinors do not have color as spin-like quantum numbers, one must leave open the possibility that even ordinary color confinement has this kind of description as a description at space-time level (as opposed to the descriptions at embedding space and "world of classical worlds" (WCW) level).

2.2 The charge DNA as a guideline

A strong constraint comes from the observation that DDNA and DRNA codons have charge -3.

1. If DDNA and DNA form parallel string-like structures, this strongly suggests that there is a neutralizing charge +3 associated with the dark codon paired with the ordinary codon. This charge could be assigned either to 3 protons or 3 nucleons if there is some additional charge allowing to take care that the total charge is 3 units in the case of DDNA and DRNA.

If also the notions of DAA and DtRNA make sense, charge neutrality for them is a plausible option. Of course, the additional charges could be dynamical in the same way as the charges of corresponding bio-molecules.

2. The compensating charge could be assigned to meson-like states with charges $0, \pm 1$. They could be meson-like bonds connecting the dark nucleons to a string-like object. ρ mesons with spin 1 and charges $(0, \pm 1)$ and pions with spin 0 and charges $(0, \pm 1)$ are the natural candidates. For closed string-like objects one would have 3 bonds and for open string-like objects 2 bonds.

   For ρ mesons associated with two bonds one would have spin representations $3 \otimes 3 = 5 \oplus 3 \oplus 1$. One should somehow get rid of the spin singlet if one assumes the proposal considered above. Spin-statistics represents the second problem: Bose-Einstein statistics does not allow 3.

   For $3 \otimes 3 \otimes 3 = (7 \oplus 5 \oplus 3) \oplus (5 \oplus 3 \oplus 1) \oplus 3$ associated with closed string-like objects, the number of states is quite too high. The only completely symmetric representation is 7 whereas 1 is antisymmetric. Thus it seems that the ρ-meason option is not realistic so that only pionic realization remains.

   This leaves open only the possibility that $5 \oplus 3(\oplus 1)$ corresponds to the rotational degrees of freedom of a closed or open string-like object.

2.3 Dark nucleons or dark protons?

Are both dark p and n needed or are dark protons enough as mildly suggested by the model [L1] of Pollack effect [I3, L1, I5, I4]? Could one build the needed states using only dark protons and suitably chosen bonds?

1. Could number theoretic Galois degrees of freedom [L7, L6, L3, L4, L9, L11, L12] come to rescue? The analog of isospin could be assigned with Galois degrees of freedom. For 3-D algebraic extension of rationals replacing color, the extension increases the algebraic dimension of the 3-space consisting of rational points by factor $n = 3$ to nd, $d = 3$. The dimension of number theoretic spinors would be $2^{n(d-1)}/2 = 2^3$, which is much larger than the dimension $d = 2$ of isospin spinors in 3-D space. One could speak of Galois-spin or G-spin. Nucleon isospin is therefore a more reasonable candidate.

2. The objection against the dark nucleon-triplet picture is that, in the standard nuclear physics, neutrons are not thought to be important in living matter. Note however that the dark electroweak length scale scaled by h_{eff}/h_0 could be much longer than the ordinary weak scale, even of the order of cell length scale.

   Weak gauge bosons would be effectively massless below the dark weak scale and weak interactions associated with the dark pion-like bonds would be as strong as electromagnetic interactions. This could explain the mysterious large chirality breaking effects in living matter.

3. One can also ask whether the dark neutron is effectively a dark proton plus pionic bond so that dark protons would be the basic building bricks after all. One cannot exclude the possibility that this applies also to the neutrons of ordinary nuclei [K5, K4]. This does not however conform with charge +3 for DDNA codons . This would leave the option that the dark neutron is an ordinary proton plus dark π^- bond.

2.4 Dark variants of information molecules as analogs of nucleon and Δ obtained by replacing quarks with dark nucleons

Could the dark analogs of N and Δ with quarks replaced by nucleons give rise to the genetic code and dark analogs of the basic information molecules?

1. The analogs of N and Δ would give 2 spin doublets (counterparts of p and n as ppn and pnn) and 4 spin 4-plets as a counterpart of Δ (ppp,ppn,pnn,nnn): altogether 20 states, which brings into mind AAs. Note that pion bonds could modify the charges for ordinary nucleons.

2. The analogs of N and Δ can be tensored with $A = 5_s \oplus 3_s \oplus 1_s$ or $B = 5_s \oplus 3_s$. $\Delta \otimes B$ would give $[(3/2, -3/2)_I \oplus (1/2, -1/2)_I] \otimes (5_s \oplus 3_s)$: these two 64-plets could be identified as DDNA and DRNA.

   $N \otimes 1$ could give 20 AAs. For both options, $N \otimes B = (2_I \oplus 2_s) \otimes (5_s \oplus 3_s)$ would give 20+12=32 states, which is the minimal number of tRNA codons. The number of chemical tRNA codons is larger than 40 so that DtRNA-tRNA pairing would be 1-to-many. This could induce the wobble base pairing [I1].

3. DDNA and DRNA would correspond to the analogs of Δ nucleons with rotation. For instance, ppp and ppn as counterparts of Δ^{++} and Δ^+ could correspond to DDNA and pnn and nnn as counterparts of Δ^- and Δ^0 could correspond to DRNA. This implies charge asymmetry which should relate to the differences between DNA and RNA. DtRNA would correspond to N with rotation. DAA would correspond to Δ and N without rotation, which should relate to the different functions between AAs and molecules DNA, RNA, and tRNA.

   Remark: Note that pionic bonds would guarantee that the total charge of DDNA and DRNA codons is 3 units.

2.5 Angular momentum of the nuclear string as origin of $5 \oplus 3 \oplus 1$

One must understand the origin of $5 \oplus 3 \oplus 1$ or of $5 \oplus 3$. There are 3 scenarios to consider. Closed string scenario favors $5 \oplus 3$ but does not predict AAs. Open string scenario favors $5 \oplus 3 \oplus 1$ and allows the identification of dark counterparts of all basic biomolecules. If ρ mesons do *not* give rise to $5 \oplus 3 \oplus 1$, both closed and open strings can be considered.

1. What came first into mind was that the bonds between protons are analogous to ρ mesons. This would allow only an open string option. There is however a problem with statistics: 3 is antisymmetric (analogous to the cross product of 3-vectors).

   This suggests that the bonds are pionic and do not contribute to the spin but allow to obtain desired total charges for 3 proton states. Charge neutrality is attractive for AAs and would require maximum neutralizing charge -3 so that only the closed string option with ordinary nucleons plus dark pionic bonds remains. Even dynamical charges would be possible also at the level of dark bio-molecules and one can consider the possibility that the MB controls the charge state of the basic biomolecules.

2. Concerning the identification of $5 \oplus 3(\oplus 1)$, the rotational degrees of freedom of string seem to be the only reasonable option. 1 and 5 could correspond to spin 0 and spin 2 states of the Regge trajectory and 3 to spin 1 state of a possibly exchange degenerate trajectory. What is encouraging is that only the bosonic spins 0, 1, and 2 and fermionic spins 1/2 and 3/2, which are in a very special role physically would be needed.

To sum up, closed strings with dark nucleon triplets and stringy rotational degrees of freedom allow us to predict the dark counterparts of all basic information molecules as analogs of nucleon and Δ states with pionic bonds. The number of dark tRNA codons is predicted to be minimal and equal to 32, and the considerably larger number of the chemical tRNA codons implying that dark tRNA-tRNA pairing is 1-to-many. This would explain wobble base pairing.

2.6 Various pairings of the information molecules

The basic vision is that the dynamics of the MB induces the dynamics of the biological body and the observed chemical pairings are induced by dark pairings. One should therefore understand the DDNA-DRNA, DRNA-DtRNA, and DtRNA-DAA pairings.

1. DDNA-DRNA pairing is obtained trivially. DDNA-DAA pairing is induced by DRNA-DtrNA pairing and DtRNA-AA pairing.

2. The decomposition $2 \times (20 \oplus 12)$ for DRNA suggests a natural pairing with tRNA identified as $20 \oplus 12$. The spin contents of the codons are however different and the situation is more complex. This leads to a model for the breaking of the (A,G) symmetry of the third codon

in RNA-AA pairing. The pairing of DtRNA with DAA requires pairing of $20 \oplus 12$ with 20. $20 \to 20$ is a natural pairing but how to realize $12 \to 20$?

3. Could icosa-tetrahedral realization of the genetic code in terms of dark photon triplets (bioharmony) [K2] [L5, L8] help here? In this realization the faces of icosahedron and tetrahedron identifiable as 3-chords correspond to codons and 3 isohedral Hamiltonian cycles providing a model for 12-note scale and the unique tetrahedral Hamiltonian cycle are needed for the realization of bioharmony as genetic code.

   Icosahedron has 20 faces and 12 vertices defining Hamiltonian cycles essential for the realization in terms of bioharmony. Hamiltonian cycles have Z_6, Z^4 or Z^2 as a symmetry group: Z_2 can correspond to reflection of rotation by π. Z_6 has 3 orbits with 6 faces and 1 orbit with 2 faces. Z_4 has 5 orbits with 4 faces. Z_2 has 10 orbits with 2 faces.

   Could the missing faces correspond to the missing orbits for one of these symmetry groups: a) to 6-orbit and 2-orbit for Z_6 or b) 2 4-orbits for Z_4 or c) 4 2-orbits for Z_2. Z_6 and Z_4 Hamiltonian cycles are unique and part of any realization. Option b) is more symmetric than option a) and is a more promising candidate.

Consider now the pairings of type DX-X.

1. All dark pairings as a bound state formation by Galois confinement [L11, L12] would involve formation of a composite $P_n \circ P_{n-1} \circ ... \circ P_1$ of the polynomials P_i determining at M^8 level the 4-surfaces of systems participating in the interaction. This implies that Galois groups extend to a larger group having the Galois groups of composites as normal subgroups.

2. The already mentioned charge asymmetry reflecting the violation of the weak isospin symmetry between DDNA and DRNA could explain why DNA *resp.* RNA involves deoxyribose *resp.* ribose molecule and the nucleotide T is replaced with U in RNA. The instability of RNA molecules and the rarity and short life-time of double RNA strands could derive from the properties of DRNA .

   The almost exact T-C and A-G symmetries of the third letter of genetic codon could also reflect almost exact isospin symmetry as proposed in [K1]. The number of DtRNAs is the minimal 32 and this predicts 1-to-many character of DtRNA-tRNA pairing which would induced wobble base pairing.

   Dark base pairing could involve an extension of Galois group Z_3 of codon to Z_6 of codon pair. This could make DDNA double strand stable and perhaps induce the stability of DNA double strand. DDNA double strand would permanently be in the bound state with Z_6 as the Galois group of the dark base pair. This would support the view that DDNA is above DRNA in the dark master-slave hierarchy.

   Also the functional differences between DNA and RNA could relate to the differences of their dark counterparts. The DDNA double strand with larger h_{eff} would represent a higher evolutionary level than the DRNA strand.

3. The number of DtRNA molecules is 32, and minimal one, so that DtRNA-tRNA pairing is not unique. This explains the wobbling of RNA-tRNA pairing [I1]. Does the wobble phenomenon have some biological function or does it signal that dark tRNA-tRNA pairing has not yet evolved to its final form?

   That tRNA as such does not represent information storage but plays a role of servant in the translation process, supports the first view. The basic function of dark tRNA in the translation is unique but it is less risky to have several manners to perform this function: hence the large number of ordinary tRNAs.

2.7 A model for the symmetry breaking of the genetic code

The model predicts that the numbers of DRNA and DtRNAs are 64 and 32 respectively. This condition does not force DRNA-DtRNA correspondence to be 2-1 in a codon-wise way. This is however true in an excellent approximation as becomes clear by looking at the code table.

For the third letter, RNA-AA correspondence has an exact U-C symmetry and almost exact A-G symmetry. There are only 2 exceptions. TTX 4-plet decomposes to 3× ile + 1 met: (A,G) doublet for the third codon splits to (ile,met). The (A,G) doublet in TGX splits to (stop,trp). Both stop codons and met as a start codon are therefore very special.

In bacterial genetic codes also the (A,G) doublet in TGX, which usually corresponds to (stop,stop), corresponds sometimes to (stop,pyl) doublet so that CG symmetry is broken. Also the (A,G) doublet usually mapped to (stop,trp) can be mapped to (sec,trp). The interpretation would be that a stop codon is obtained if DtRNA corresponding to UAG or UGA does not pair at all with tRNA. If it pairs, UAG codes for pyl and UGA codes for sec.

One should understand this symmetry breaking.

1. Since iso-spin and spin are involved, either isospin or spin symmetry breaking is suggestive. In the nucleon sector the situation is completely symmetric between spin and isospin. In the string sector, the situation is different for DDNA, DRNA and DtRNA.

2. The earlier interpretation for (U,C) and (A,G) doublets was as isospin doublets and isospin symmetry breaking. The conjugations $G \leftrightarrow C$ and $U \leftrightarrow A$ were interpreted as an analog of particle-antiparticle conjugation.

   The following model leads to the proposal that (T,C) doublet corresponds to spin doublet 2_s and (A,G) doublet to pseudo-spin doublet $(3/2, -3/2)$. As if rotational symmetry would have reduced to axial symmetry.

   At the level of DNA, DRNA and DtRNA, the natural possibility is that (T,C) doublet corresponds to 2_s and (A,G) doublet to the spin symmetry violating $(3/2, -3/2)_s$. (T,C) and (A,G) could form an isospin doublet.

3. An important point to note is that (3× ile,met) and (stop,stop), (stop,trp) dot correspond to identical situations since 2 iles correspond to (T,C) for which there is no symmetry breaking. Actually one has 3 (A,G) symmetry breakings.

Consider now the identification of spin- and isospin contents of various dark information molecules.

1. Suppose that the spin symmetry is not broken at DDNA and DRNA level but isospin 4-plet $4_I = (3/2, 1/2, -1/2, -3/2)$ splits into pseudo-doublets $2_{I_1} = (1/2, -1/2)$ and $2_{I_2} = (3/2, -3/2)$. If DDNA were maximally symmetric it would correspond to $2_{I_1} = (1/2, -1/2)$. Which option one chooses, does not matter in the sequel so that this option is selected.

   This would give

$$DDNA = 2_{I_1} \otimes [4_s \otimes (5_s \oplus 3_s)] \ ,$$
$$DRNA = 2_{I_2} \otimes [4_s \otimes (5_s \oplus 3_s)] \ .$$

2. DtRNA and DAA correspond to

$$DtRNA = 2_I \otimes [2s \otimes (5_s \oplus 3_s)] \ ,$$
$$DAA = 4_I \otimes 4_s \oplus 2_I \otimes 2_s \ .$$

3. One would expect that the pairing minimizes the breaking of rotational symmetry meaning that spins are the same for paired dark molecules if possible and the spin difference is minimized otherwise. To get some idea about the symmetry breaking, one can decompose the tensor products for the spin representations

$$DRNA = 2_{I_2} \otimes (8_s \oplus 2 \times 6_s \oplus 2 \times 4_s \oplus 2 \times 2_s) \ ,$$
$$DtRNA = 2_I \otimes (6_s \oplus 2 \times 4_s \oplus 2_s) \ .$$

   The representation contents are different and the number of spin states for DRNA is twice that for DtRNA so that the symmetry breaking relates to spin pairing rather than isospin pairing.

The first thing to notice is that $2 \times 2_s$ for DRNA naturally projects to 2_s for DtRNA. Also $2 \times 6_s$ projects to 6_s . Bothe decomposis however have $2 \times 4_s$:s so that 8_s must pair with $2 \times 4_s$. Symmetry breaking must localize to this pairing.

8_s is not present in DtRNA and forces a pairing between different spins. This should cause the violation of spin symmetry for dark (A,G) doublets in the sense that they couple to different DAAs, which in turn requires that they couple to different DtRNAs.

1. One can decompose 8_s as

$$8_s = (7/2, -7/2)_s \oplus (5/2, -5/2)_s \oplus 4_{s_1} \quad .$$

   8_s should correspond to $2 \times 4_s$ in DtRNA. The pseudo 4-plet 4_{s_1} pairs with 4_s in a spin conserving manner.

2. What is left is $2_{I_2} \otimes [(7/2, -7/2)_s \oplus (5/2, -5/2)_s]$, which should pair $2_I \times 4_s$. This pairing cannot conserve spin and the 2-1 symmetry must be violated in the sense that the DRNAs paired with $(3/2)_s$ and $-(3/2)_s$ are different. One can ask whether the change of the magnitude of the spin component is minimal in the DRNA-DtRNA pairing.

3. At the level of DAA and DtRNA, ile could correspond to the first DtRNA doublet $((3/2)_I \otimes (1/2, -1/2)_s$ and $(3/2)_I \otimes (3/2)_s$ as a singlet and met to $(3/2)_I \otimes (-3/2)_s$ as a singlet. $(stop, stop)$ and $(stop, trp)$ could correspond to $(3/2)_I \otimes (3/2, -3/2)_s$ and $(-3/2)_I \otimes (3/2, -3/2)_s$. Spin symmetry breaking would therefore mean that different DRNAs pair with DtRNAs in the doublet $(3/2, -3/2)_s$.

How do DRNAs and DtRNAs correspond to each other in the (A,G) symmetry violating sector? In the absence of symmetry breaking DRNA-DtRNA pairing is 2-1 in a codon-wise way if DRNA with opposite values 3/2 and -3/2 of isospin pair with the same DtRNA. Symmetry breaking would mean that some DRNAs with spins 3/2 and -3/2 pair with different DtRNAs and therefore with different DAAs for some (A,G) doublets $(3/2, -3/2)_s$. For the (T,C) doublets $(1/2, -1/2)_s$ this would not occur.

1. There are 8 spin symmetry violating DRNAs and 8 DtRNAs corresponding to $UA(A, G)$ and $UG(A, G)$ and $UA(T, C)$ and $UA(A, G)$ (3× ile+ met). $UA(T, C)$ is strictly speaking not spin symmetry violating but ile corresponds to DRNA triplet instead of doublet. As if the DRNA doublet paired with 2 DtRNAs pairing with met would pair with DtRNAs coding for ile and met.

   There are 2 $[(7/2, -7/2)_s \oplus (5/2, -5/2)_s]$ multiplets at the DRNA side. At the DtRNA side one has pseudo doublets $(3/2, -3/2) \oplus 2_{s_1}$, $s_1 = (1/2, -1/2)$. There are two of these corresponding isospin doublet 2_{I_1}.

2. Since there are 3 UCAG 4-plets with symmetry breaking, the symmetry violation is not independent of the value of isospin for $(3/2, -3/2)_I$ for DRNA and $(1/2, -1/2)_I$ for DtRNA. Symmetry breaking for isospin should localize to the DRNA side. There are several options (3,0), (0,3), (2,1) (1,2) for the numbers of symmetry breakings for DRNA multiplets. One can restrict in the sequel to a single value of isospin, say 3/2.

3. One should find symmetry violating pairing between these 8 DRNAs and 8 DtRNAs. $[(7/2, -7/2)_s \oplus (5/2, -5/2)_s]$ should be mapped to $(3/2, -3/2)_s \oplus 2_{s_1}$. Assume that the spin difference between paired DRNA and DtRNA is as small as possible.

   (a) (T,C) doublet without symmetry breaking would correspond to the pairing

$$(5/2, -5/2)_s \to (1/2, -1/2)_s \quad .$$

   (T,C) symmetry is not violated if the both doublets correspond to the same DAA and DtRNA.

(b) (A,G) doublet could correspond to the pairing

$$(7/2, -7/2)_s \to (3/2, -3/2)_s \quad .$$

Now the members of the doublets would correspond to different DAA.

(c) For instance, the DRNA corresponding to the second met in (met,met) in absence of symmetry breaking, would pair with DtRNA, which pairs with ile. The symmetry present at the DRNA level would be broken by the pairing.

In the case of (stop,trp) doublet, the same would occur. This would also happen in the replacements (stop,stop) $\to$ (stop,pyl) and (stop,trp)$\to$ (sec,trp). Now the DtRNA in question would not pair at all with tRNA and AA or it would be with exotic tRNA pairing with an exotic AA.

3 Connection between dark nucleon code and bioharmony

The model of genetic code based on bioharmony has evolved through many sidetracks [K2] but the the version discussed in [L2, L5, L8] is roughly consistent with the original model and also gives a connection with the model of dark nuclear code.

3.1 Bioharmony and resonance mechanism for dark photon communications

The faces of icosahedron and tetrahedron (and also octahedron appearing in the model of genetic code as icosa-tetrahedral tessellation of hyperbolic space H^3 [L8]) are triangles. The proposal is that they somehow correspond to 3-chords made of dark photons, which in turn represent genetic codons.

Communications by dark 3-photons represent codons. 3N-photons represent in turn genes. The communications rely on cyclotron 3N-resonance so that the vertices of the faces of icosa-tetrahedron must contain charged particles coupling to a magnetic field. The magnetic field strengths at flux tubes associated with charged particles would determine the cyclotron frequencies.

Information is encoded to the frequency modulation of cyclotron frequencies. The chords serve as addresses much like in computer language LISP. If the modulations of 3N frequencies are identical and in synchrony, the outcome of the receiver consisting of 3N charged particles is a sequence of 3N-resonances giving rise to an 3N-pulse sequence. Nerve pulse patterns could emerge by this mechanism.

One can also consider 3N-signals for which only $M < 3N$ modulations are identical and in synchrony. In this manner communications to subsets of the receiver are possible. For instance, some subset of codons of dark gene or dark protein can be selected as a receiver, possibly controlled. This selection could de-entangled the receiver to de-entangled coherent pieces.

There is a direct connection with empiria. Biophotons, whose origin remains poorly understood, can be identified as ordinary photons resulting from the decay of dark 3N-photons to ordinary photons.

The realization in terms of dark nucleons looks more plausible if also DtRNA and DAAs are realized in terms of icosa-tetrahedral picture. This is because the amino acids are often neutral unlike DNA nucleotides, which are negatively charged. The dark charge assignable to the icosa-tetrahedron can be controlled by pionic bonds with charges $0, \pm 1$ so that it can be 3 units for DDNA and vanish for amino acids. A natural proposal is that the charge of icosa-tetrahedron compensates the charge of the amino acid and tRNA.

There are pairings of type DX-DY. The pairings DDNA-DRNA, DRNA- DtRNA and DtRNA-DAA induce the biochemical dynamics of transcription and translation. There are also pairings DX-X. DDNA-DNA and DRNA-RNA unique DtRNA-tRNA pairing is 1-to-many and relates to the wobble phenomenon. The pairings between dark nucleon variants of biomolecules and corresponding dark 3N-photons make possible biocommunications and control.

3.2 Details of the bioharmony model

Consider now a more detailed bioharmony model of the genetic code based on the geometries of icosahedron and tetrahedron.

1. Icosahedron has 12 vertices and 20 faces, which are triangles. The idea is that the 12 vertices correspond to the notes of 12-note scale. Tetrahedron has 4 vertices and 4 faces and is self-dual whereas the dual of icosahedron is dodecahedron having 20 faces and 12 faces.

2. 12-note scale can be represented as a Hamiltonian cycle at an icosahedron going once through all vertices. The frequencies at the neighboring points as edges of a face in cycle relate by a frequency scaling of 3/2: this gives rise to the Pythorean variant of quint cycle.

   Octave equivalence means the identification of frequencies differing by a multiple of octaves. Octave equivalence can be used to reduce all frequencies to a single octave. If the scaling is exactly 3/2 at all steps there is a slight-breaking of octave equivalence since $(3/2)^{12}$ does not quite correspond to an integer number (7) of octaves. Pythagoras was well aware of this.

   Given cycle assigns to faces 3-chords defining a harmony with 20 chords assignable to the faces of the icosahedron. For dodecahedron there is only single harmony with 12 chords and 20-note scale which could correspond to Eastern scales. For the tetrahedron the Hamiltonian cycle is unique.

3. Icosahedral Hamiltonian cycles can be classified by symmetries. The group Z_6, Z_4, or Z_2 (rotation by π or reflection) as a group of symmetries

The connection with the genetic code emerges in the following manner.

1. The natural idea is that the faces of the icosa-tetrahedron correspond to both 3-chords and genetic DNA/RNA codons. If the orbits of faces could correspond to amino acids (AAs), the DNA codon would code for amino acid AA if the corresponding face is at the orbit corresponding to AA.

2. One wants 64 DNAs: Z_6,Z_4 ja Z_2 cycle give rise to 20+20+20 =60 DNa codons. Tetrahedron gives the remaining 4 codons.

3. Does one obtain a correct number of AAs? Do the numbers of faces at the orbits correspond to numbers of DNAs coding for the corresponding AA?

   (a) Z_6 decomposes to 3 6-orbits and 1 2-orbit ()$3 \times 6 + 2 = 20$). There are 3 AAs coded by 6 DNAs. 2-orbit corresponds to AA coded by two DNAs.

   (b) Z_4 decomposes to 5 4-orbits. There are 5 AAs coded by 4 codons.

   (c) Z_2 corresponds to 10 2-orbits predicting 10 AAs coded by 2 codons.There would be 11 2-orbits altogether. There are 9 AAs coded by 2 codons.

   Some kind of symmetry breaking is present as in the case of dark nucleon code. 2 AA doublets must split to singlets. If (ile,ile,ile,met) coded by UAX could correspond to (ile,ile) and (met,met) such that (met,met) is split to (ile,met). In absence of symmetry breaking one would have 11 doublets as predicted.

4. There are also 4 tetrahedral codons.

   There is (stop,stop) doublet (UAA, UAG) and (stop,trp) doublet (UGA,UGG). These doublets could correspond to the faces of the tetrahedron. Only one face would code for amino acid in the vertebrate code. Other faces would not have corresponding tRNA?

   For bacterial codes, the situation can be different. Pyl and sec appear as exotic amino acids. Could (UAA,UAG) for code for (stop,pyl) and (UGA,UGG) for (sec,trp) instead of (stop,trp)? Orientation preserving rotations form a 12-element group having Z_2 and Z_3 as subgroups. For Z_2 the orbits consist of 2 vertices and for Z_3 of 3 vertices (face) and 1 vertex. Z_3 symmetry could correspond to trp as singlet and vertebrate stop codons as triplet. For bacterial pyl and sec Z_2 with symmetry breaking is suggestive.

3.3 Bioharmony, dark nucleon code, and icosa-tetrahedral code as a tessellation of H^3

Bioharmony model involves icosahedron and tetrahedron. This looks ugly unless there is some really deep reason for their emergence. One can also ask why not also octahedron having triangular faces.

Hyperbolic 3-space H^3 has interpretations as a mass shell of Minkowski space M^4 at the level of M^8 and as light-cone proper-time constant surface at the level of H. The 4-surface X^4 in M^8 contains mass shells of M^4 corresponding to the roots of the polynomial P defining X^4. Hence one expects that H^3 plays a key role in quantum TGD both discretized momentum as defining a cognitive representation with momenta, which are algebraic integers associated with extension of rationals defined by P. H^3 has infinite discrete subgroups of the Lorentz group analogous to discrete groups of translations in E^3 as isometries and H^3 allows an infinite number of tessellations (lattices). Perhaps the simplest tessellation is icosa-tetrahedral tessellation involving also octahedrons and thus all triangular Platonic solids. This tessellation could give rise to genetic code by induction of tesselation to 3-surfaces or lower-D objects such as linear biomolecules, and cell membranes [L8]. I do not however understand the mathematical details well enough but the following discussion is general.

Consider first the model for DDNA and DRNA allowing us to understand the connection between dark nucleon and dark photon realization of the genetic code physically.

1. The realization of DDNA/DRNA/DtRNA/DAA could correspond to a sequence of icosahedron-tetrahedron pairs at H^3 contained by the 4-surface $X^4 \subset M^8$ and its H images which is also H^3.

2. Each icosa-tetrahedron would contain a dark codon realized both as a face and dark nucleon triplet associated with it. The dark photon chord associated with the face must be the same as the codon defined by dark nucleon triplet. The dark nucleon triplets correspond to cyclotron frequency triplets, which in turn correspond to dark photon 3-chords associated with the Hamiltonian cycles.

3. The cyclotron frequencies are determined by magnetic fields at flux tubes so that Hamilton cycles must correspond to flux tube patterns. The simplest hypothesis is that the Hamilton cycle is a closed flux tube connecting all vertices of the icosahedron. Dark codon triplet corresponds to a face. It does have 1 or 2 flux tube edges if the corresponding chord contains 1 or two quints and otherwise no flux tube edges. Therefore cyclotron frequencies cannot be always associated with the edges of the triangle.

   The simplest option is that the Hamiltonian flux tube following the vertex at the cycle defines the cyclotron frequency associated with the vertex. The harmony depends on the orientation of the cycle and for 8-note scale roughly corresponds the transformation from major to minor. The variation of flux tube thickness implies frequency modulation crucial for communications.

   The realization of the Hamilton cycle requires that the magnetic field strength along the cycle is scaled by factor 3/2 to give a Pythagorean quint cycle. For an evenly tempered quint scale the scaling is $2^{5/12}$.

4. An interesting question relates to the relation of DDNA strand and its conjugate. The change of the orientation of the Hamiltonian cycle changes the chord of the harmony. For the ordinary 8-note scale one can roughly say that major and minor chords are transformed to each other. The orientation reversal could correspond to time reversal. The fact that the orientations of two DNA strands are opposite suggests that DNA and conjugate DNA are related by the orientation reversal of the Hamiltonian cycle inducing the map $G \to C$, $U \to A$ a the level of DNA letters. The conjugation does not imply any obvious symmetry for the corresponding amino acids as the inspection of the code table demonstrates.

How could the Hamiltonian cycle determine the DtRNA codons?

1. DRNA codons pair with 32 DtRNA codons and DtRNA codons pair with trNA codons in 1-to-many manner. Therefore DRNA-DtRNA pairing could be universal and 2-1, although

not in a codon-wise manner. This pairing should be the same for both bioharmony and dark nucleont triplets.

2. The pairing by 3-resonances requires that DtRNA icosa-tetrahedron contains the DRNA codons, which pair with DtRNA codon. There would be 2 DRNA codons in DtRNA icosahedron for most DtrNA codons and 1 codon for DtRNA pairing with DAA corresponding to met and trp. The number 32 of DtRNA implies in the case of icosa-tetrahedral code that there are 10+10-10=30 icosahedral DtRNAs and only 2 tetrahedral DtRNAs so that two faces of tetrahedron cannot correspond to DtRNA codon so that corresponding DRNAs must serve as stop codons.

   One of the DtRNAs could correspond to trp. The second one would correspond to a stop codon in the vertebrate code: either the DtRNA codon is not present at all or or it does not pair with tRNA. TAG and TGA can code for pyl and sec in some bacterial versions of the code and in this case the corresponding dark DRNA codon would be represented at the DtRNA tetrahedron.

3. For bioharmony DDNA-DAA correspondence means that AAs correspond to orbits of the faces of icosahedron under the subgroup Z_6, Z_4, or Z_2 which could correspond to reflection or to a rotation by π.

   Since DRNA-DtRNA correspondence is 2-1 although not codon-wise, the natural first guess is that Z_2 orbits of the faces define the DRNA codons at the DtRNA icosahedron so that it would contain 2 codons for most DtRNAs. At the DtRNA tetrahedron the only option is Z_1 so there is a symmetry breaking.

   If Z_2 corresponds to a reflection, the orbit always contains 2 codons. If Z_2 corresponds to a rotation by π, it might happen that the face invariant under π rotation and the orbit would consist of a single point. Could this explain why one has (ile,ile,ile,met) instead of (ile,ile) and (met,met)? The rotation axis should go through the invariant face and since the face is a triangle, π rotations lead out of the icosahedron. Therefore the answer is negative.

Ile-met problem deserves a separate discussion.

1. The pairing of Z_2 related DDRNA faces with two different DtRNAs coding for ile and met rather than two mets means Z_2 symmetry breaking at the level of bioharmony. Could the fact that AUG acts as a start codon relate to this? Could it be that both AUG and AUA cannot act as start codons? It is difficult to invent any raeson for this.

2. The symmetry breaking could occur in DtRNA-DAA pairing and replace Dmet with Dile. Is it possible that the 3-chords for coding for ile and second met are nearly identical so that the resonance mechanism selects ile instead of met? Could the situation be similar for the codons coding for (stop,stop) and (stop,trp) and cause the coding of pyl or sec in some situations? The scale for the quint cycle model with octave equivalence does not quite close. Could this have some role in the problem?

3. Since similar ambivalence occurs for stop codons assigned to the tetrahedral Hamiltonian cycle, one can look at the tetrahedral Hamiltonian cycle. In this case one has 3-quint cycle and a given edge of the cycle corresponds to a scaling by $(3/2)^3$ so that 4 steps gives $(3/2)^{12}$, which is slightly more than 7 octaves. For the quint scale in Pythagorean sense, one obtains 4 notes in the same octave.

   Exact octave equivalence corresponding to equally tempered scale in which half-note corresponds to frequency scaling $2^{1/12}$, implies that there is only one 3-chord $CEG\sharp$: this would explain why there are 3 stop codons in the vertebrate code!

   The original guiding idea in the attempts to understand the fusion of icosahedral and tetrahedral codes was that the tetrahedron is effectively glued to the icosahedron along one face. This is consistent with the icosahedral quint cycle only if the common face contains no edges of the icosahedral cycle but contains tetrahedral flux edges with $(3/2)^3$ scaling. This would give strong constraints on the common face.

If bacterial codes correspond to Pythagorean scale, there would be two different 3-chords since $CEG\sharp$ and $EG\sharp C$ are not quite the same. The reason is that the frequency ratios of chords are powers of $3/2)^{12}$. This situation is completely exceptional.

In the quint scale there are small differences between the 4 chords. Could this explain why only one of these 3-chords codes for AA (trp) in vertebrate code and pyl or sec is coded instead of stop in bacterial codes? Amusingly, the chord $CEG\sharp$ ends many finnish tangos and therefore acts like a stop codon!

Could bacteria have a perfect pitch and live in a Pythagorean world? Could the transition to multicellulars mean the emergence of an algebraic extension of rationals containing $2^{1/12} \simeq 1.059($, which is considerably larger than to $(3/2)^{12}/2^7 \simeq 1.0136$)! Could people with perfect pitch have in their dark genome parts using Pythagorean scale or can they tune the magnetic flux tube radii to realize Pythagorean scale?

4. Could the ile-met problem have a similar solution? The chords associated with ile and met would differ by ascaling with $(3/2)^3$ or $(3/2)^6$ using octave equivalence. These chords are not quite the same: could it happen that the 3-chord associated with the second met is nearer to that for ile? These 3-chords do not contain quint scaling and should correspond to the special chords for which no edge belongs to a Hamiltonian cycle.

Also DtRNA-DAA pairing is based on the 3-resonance.

1. DAA icosahedron must contain the DtRNA codons pairing with DAA. This raises the question whether DDNAs could have a direct resonant coupling to DAAs. Could this pairing occur in DDNA-DAA occurring in transcription (`https://cutt.ly/QPP46St`) so that pieces of DDNA and DAA associated with an enzyme involved could pair with each other by 3N-resonance at DDA-DAA level? At the chemical level the base-amino acid interactions are extremely complex involving stereochemistry and formation of hydrogen bonds (`https://cutt.ly/RPP7plM`) so that the reduction of these interactions to 3N-resonance would mean a huge simplification.

2. Could this resonance pairing serve as a universal mechanism of bio-catalysis and take place for various enzymes and ribozymes? One example are promoters and enhancers involved with the transcription. Enhancers and promoters induce a highly non-local process generating a chromosome loop in which two portions of DNA become parallel and near to each other and dark 3N-photons could explain the non-locality as an outcome of quantum coherence in long scales.

3. Why would DDNA-DAA pairing not occur? 3N-resonance relies on cyclotron frequencies and therefore on the magnetic field strength determined by the radii of the monopole flux tubes. One explanation would be that the frequency scales of DAA and DDNA are slightly different. Could the attachment of DRNA to translation machinery scale the magnetic field strengths of the flux tubes and their cyclotron frequencies so that only dRNA-DtRNA and DtRNA-DAA couplings are possible.

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