Article

New Results in the Model of Bioharmony

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Abstract

This article describes some new results and considerations related to music harmony. For some years ago I developed a model of music harmony. As a surprising side product a model of genetic code predicting correctly the number of codons coding given amino-acid emerged. Since music expresses and creates emotions, one can ask whether genes could have moods characterized by these bio-harmonies. The fundamental realization could be in terms of dark photon triplets replacing phonon triplets for ordinary music.

The model relies on the geometries of icosahedron and tetrahedron and representation of 12-note scale as so called Hamiltonian cycle at icosahedron going through all 12 vertices of icosahedron. The 20 faces correspond to allowed 3-chords for harmony defined by given Hamiltonian cycle. This brings in mind 20 amino-acids (AAs). One has three basic types of harmonies depending on whether the symmetries of icosahedron leaving the shape of the Hamiltonian cycle is Z_6, Z_4 or Z_2. For Z_2 there are two options: $Z_{2,rot}$ is generated by rotation of π and $Z_{2,refl}$ by reflection with respect to a median of equilateral triangle. Combining together one harmony from each type one obtains union of 3 harmonies and if there are no common chords between the harmonies, one has 20+20+20 3-chords and a strong resemblance with the code table. To given AA one assigns the orbit of given face under icosahedral isometries so that codons correspond to the points of the orbit and orbit to the corresponding AA. 4 chords are however missing from 64. These one obtains by adding tetrahedron. One can glue it to icosahedron along chosen face or keep is disjoint. The model in its original form predicts 256 different harmonies with 64 3-chords defining the harmony. DNA codon sequences would be analogous to sequences of chords, pieces of music. Same applies to mRNA. Music expresses and creates emotions and the natural proposal is that these bio-harmonies correlate with moods that would appear already at molecular level. They could be realized in terms of dark photon triplets realized in terms of light and perhaps even music (living matter is full of piezo-electrets). In fact, also the emotions generated by other art forms could be realized using music of dark light.

The model of music harmony is separate from the model of genetic code based on dark proton triplets and one of the challenges has been to demonstrate that they are equivalent. This inspires several questions. Could the number of harmonies be actually larger than 256 as the original model predicts? One could rotate the 3 fused Hamilton's cycles with respect to each by icosahedral rotations other leaving the face shared by icosahedron and tetrahedron invariant. There are however conditions to be satisfied. There is purely mathematical restriction. If the fused 3 harmonies have no common 3-chords the number of coded AAs is 20. Can one give up the condition of having no common 3-chords and only require that the number of coded AAs is 20? There is also the question about the chemical realizability of the harmony. Is it possible to have DNA and RNA molecules to which the 3-chords of several harmonies couple resonantly? This could leave only very few realizable harmonies. The model predicts the representation of DNA and RNA codons as 3-chords. Melody is also an important aspect of music. Could amino-acids couple resonantly to the sums of the frequencies (modulo octave equivalence) of the 3-chords for codons coding for given AA? Could coding by the sum of frequencies appear in the coupling of tRNA with mRNA by codewords and coding by separate frequencies to the letterwise coupling of DNA and RNA nucleotides to DNA during replication and transcription? What about tRNA. Could tRNA correspond to pairs of harmonies with 20+20+444 codons? What about single 20+4=24 codon representation as kind of pre-tRNA? What is the origin of 12-note scale? Does genetic code force it? The affirmative answer to this question relies on the observation that 1-1 correspondence between codons and triplets of photons requires that the frequency assignable to the letter must depend on its position. This gives just 12 notes altogether. Simple symmetry arguments

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fix the correspondence between codons and 3-chords highly uniquely: only 4 alternatives are possible so that it would be possible to listen what DNA sequences sounds in given mood characterized by the harmony. What disharmony could mean? A possible answer comes from 6 Hamiltonian cycles having no symmetries. These disharmonies could express "negative" emotions.

Keywords: Bioharmony, model, music harmony, genetic code, TGD framework.

1 Introduction

This article describes some new results and considerations related to music harmony. Most of them have emerged during 2018.

Remark: In the sequel I will use the shorthand AA for amino-acids and shorthands DDNA, DRNA, DtRNA, DAA for the dark analogs of DNA, RNA, tRNA, and AA realizes as dark proton sequences with codon represented as dark proton triplet.

1.1 Some background

For some years ago I developed a model of music harmony [17] (see `http://tinyurl.com/yad4tqwl`), which should define map of dark codons to 3-chords represented as dark photon triplets and defining allowed 3-chords of music harmony (music of light and perhaps also of sound). The Appendix provides the tables describing the details of the harmonies.

1. The model relies on the geometries of icosahedron and tetrahedron and a representation of 12-note scale as so called Hamiltonian cycle at icosahedron going through all 12 vertices of icosahedron [5, 2, 4, 1, 3]. The 20 faces correspond to allowed 3-chords for harmony defined by given Hamiltonian cycle. This brings in mind 20 AAs.

   Single step of Hamiltonian cycle connecting vertices of a face of icosahedron (triangle) is assume to correspond to a scaling of the frequency by factor 3/2. This leads to a problem since 12 scalings of this kind does not quite given 7 octaves which reduced octave equivalence to the basic octave would give 12-note scale. The solution is to add single note slightly differing from 7 octaves and represented as vertex P of a tetrahedron glued to icosahedron along face. The Hamilton cycles are deformed so that they begin and end from this vertex. This also gives the missing 4 DNA codons realized as 3-chords and also defines unique ground note for the scales.

2. One obtains 3 basic types of harmonies depending on whether the symmetries of icosahedron leaving the shape of the Hamiltonian cycle is Z_6, Z_4 or Z_2. For Z_2 there are two options: $Z_{2,rot}$ is generated by rotation of π and $Z_{2,refl}$ by reflection with respect to a median of equilateral triangle.

   Combining together one harmony from each type one obtains union of 3 harmonies and if there are no common chords between the harmonies, one has 20+20+20 3-chords and a strong resemblance with the code table. To given AA one assigns the orbit of given face under icosahedral isometries so that codons correspond to the points of the orbit and orbit to the corresponding AA.

   4 chords are however missing from 64. These one obtains by adding tetrahedron. One can glue it to icosahedron along chosen face or keep is disjoint. The model predicts a highly unique and realistic model for numbers of DNA codons coding for a given AA. The model in its original form predicts two codes and also explains the fact that there are two additional AAs Pyl and Sec that appear as end-products.

3. AAs correspond to single 20-codon code, DNA and RNA to a union of 3 20-codon codes with symmetries Z_6, Z_4 or Z_2: here Z_2 would correspond to $Z_{2,rot}$ or $Z_{2,refl}$ and this would give to two two different codes.

4. The model in its original form predicts 256 different harmonies with 64 3-chords defining the harmony. DNA codon sequences would be analogous to sequences of chords, pieces of music. Same applies to mRNA.

   Music expresses and creates emotions and the natural proposal is that these bio-harmonies correlate with moods that would appear already at molecular level. They could be realized in terms of dark photon triplets realized in terms of light and perhaps even music (living matter is full of piezoelectrets). In fact, also the emotions generated by other art forms could be realized using music of dark light. [23]. Dark photons in various wavelength ranges and correspond to various values of h_{eff} would correspond to various sensory qualia and are represented at pineal gland ("third eye") as imagined sensory percepts [20]. They can be transformed to real sensory percepts at sensory organs by using DMT molecules as bridges allowing the propagation of dark photons (or the bio-photons resulting in their energy conserving transformation to ordinary photons) to sensory organs, where they generate genuine sensory experience identified as dream, psychedelic experience, hallucination, etc...

This summarizes the original article about geometric model of harmony [17] and contributions in online books [12, 10]. This chapter contains besides this article also some new results and considerations related to music harmony. Most of them have emerged during 2018.

1.2 Questions emerged during 2018

The model of music harmony is separate from the model of genetic code based on dark proton triplets [18] and one of the challenges has been to demonstrate that they are equivalent. One can raise several questions.

1. Could the number of harmonies be actually larger than 256 as the original model predicts? One could rotate the 3 fused Hamilton's cycles with respect to each by icosahedral rotations other leaving the face shared by icosahedron and tetrahedron invariant. There are however conditions to be satisfied.

   (a) There is purely mathematical restriction. If the fused 3 harmonies have no common 3-chords the number of coded AAs is 20. Can one give up the condition of having no common 3-chords and only require that the number of coded AAs is 20?

   (b) There is also the question about the chemical realizability of the harmony. Is it possible to have DNA and RNA molecules to which the 3-chords of several harmonies couple resonantly? This could leave only very few realizable harmonies.

2. The model predicts the representation of DNA and RNA codons as 3-chords. Melody is also an important aspect of music. Could AAs couple resonantly to the sums of the frequencies (modulo octave equivalence) of the 3-chords for codons coding for given AA? Could coding by the sum of frequencies appear in the coupling of tRNA with mRNA by codewords and coding by separate frequencies to the letterwise coupling of DNA and RNA nucleotides to DNA during replication and transcription? Could the emergence of DNA be interpreted as an evolutionary step from a holistic picture using codons as basic units (dark codons cannot be decomposed to letters) to more analytic picture in which letters are treated separately?

3. As I developed the model of bio-harmony [17] (see `http://tinyurl.com/yad4tqwl`) it did not occur to me that also the tRNA part of the dark code should have counterpart in the icosahedral model. Could tRNA correspond to pairs of harmonies with 20+20+4=44 codons? What about single 20+4=24 codon representation as kind of pre-tRNA? Could tRNA correspond to a union of 2 20-codon codes? Combining only 2 20-codon codes with 40 codons and tetrahedral code with

4 codons would give maximally 44-letter code and the upper bound for tRNAs is according to Wikipedia 45! Dark proton model predicts 40 DtRNAs suggesting that only the 40 isosahedral codons contribute to DtRNA code. The additional tRNAs could result from homonymy. The code sequences could be seen as a hierarchical sequence $3 \to 2 \to 1$ in this framework.

An important implication is that there are many realizations of DtRNA and tRNA harmony: (Z_6, Z_4), (Z_6, Z_2), (Z_4, Z_2) and Z_2 could be either $Z_{2,rot}$ or $Z_{2,refl}$. This could explain the homonymy of mRNA-tRNA pairing via difference in the chords in turn affecting biochemical counterparts. Note however that the chords for tRNA must be a subset of chords for mRNA so that RNA harmony determines tRNA harmony apart from the three choices (Z_6, Z_4), (Z_6, Z_2) or (Z_4, Z_2) giving rise to 3 different contexts. If DAAs code by 3-chords the AAs then this choice does not affect AAs.

4. What is the origin of 12-note scale? Does genetic code force it? The affirmative answer to this question relies on the observation that 1-1 correspondence between codons and triplets of photons requires that the frequency assignable to the letter must depend on its position. This gives just 12 notes altogether. Simple symmetry arguments fix the correspondence between codons and 3-chords highly uniquely: only 4 alternatives are possible.

   Hence it would be possible to listen what DNA sequences sounds in given mood characterized by the bio-harmony: the allowed 3-chords of harmonies with symmetries are given in [17] and I can provide the basic Python modules allowing to transform DNA sequences for given harmony to audible form using Garage Band program.

5. What disharmony could mean? A possible answer comes from 6 Hamiltonian cycles having no symmetries. These disharmonies could express "negative" emotions.

2 Some questions about the realization of the bio-harmony

In the sequel by I will proceed by posing questions related to the relationship between the 3 representations of genetic code [12] in terms of bio-molecules, their dark analogs represented as sequences dark proton triplets, and as 3-3-chords of bio-harmony.

2.1 What conditions pairings pose on the frequency triplets?

The realization of DDNA-DtRNA and DDNA-DAA pairings in terms of frequencies must involve a loss of information since the correspondence is many-to-one.

1. For DNA-mRNA pairing information is not lost and the pairing must be of form $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$. Note that the frequencies cannot be associated with the letters. It is however possible to consider the assignment of (f_1, f_2) to the first letter pair XY as a whole and f_3 to the third letter Z.

2. For DDNA-DAA and DmRNA-DAA pairing the natural hypothesis is $(f_1, f_2, f_3) \to f_1 + f_2 + f_3$. AA couples to the sum of the frequencies of the triplet. The simplest possibility is that the $f_1 + f_2 + f_3$ is same for all codons codin for given AA. One might say that AA sequence defines melody and mRNA sequence the accompaniment.If the sums for codons coding given AA are different they must couple resonantly to it. If there are several harmonies the sum must same for all realizable 3-harmonies or all chords of 3-chord harmonies coding for same AA couple to it resonantly. Since one has linear 1-D structures one might ask whether frequency differences coming as multiples of lattice frequencies are allowed. Second natural possibility is octave equivalence. mRNA-AA pairing would take place directly rather than with the mediation of of tRNA.

3. In the case of DmRNA-DtRNA pairing one one does not lose so much information since the number of dark DNAs is 40 (as also the 3-chords if tetrahedron does not contribute). One must remember that tRNAs are pairs of RNA like codons - call them RNA_t, and AAs. Therefore there pairing involves also the pairing mRNA-AA give by $(f_1, f_2, f_3) \to f_1 + f_2 + f_3$ and guaranteeing that the code is realized by this pairing alone irrespective of mRNA-RNA_t pairing. At chemical level the first to mRNA codons pair with tRNA anticodons according to the standard rules. Could RNA_t have completely passive role in carrying the AA? This cannot be the case since the last two letters of RNA_t couple in standard manner to the first two letters of mRNA.

   Remark: tRNA is analogous to melody + accompaniment using one of the 3 possible 2-harmonies for a given 3-harmony.

   Suppose that mRNA-RNA_t pairing corresponds to 3 possible choices of 2-harmonies as sub-harmonies of 3-harmony. This would suggest these different sub-harmonies define maps $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$ such that RNA_t pairs only with two sub-harmonies. For each choice RNA_t would correspond effectively to 40 sub-codons of the entire code (forgetting the tetrahedral part giving 4 additional codons). The three different realizations of the projection would give rise to the homonymy. Also the AA-trNA coupling would come out correctly.

DAAs would be different in the sense that they couple only to the sum of the frequencies. This is in accordance with bio-harmony in which AAs correspond to orbits of 3-chords for DNA under isometries rather than single 20-chord harmony. The coupling to the sum of frequencies is in accordance with the quantal interpretation as 3-dark-photon state whose energy is $E = h_{eff}(f_1 + f_2 + f_3)$ and couples to AA chemically via the transition to ordinary photons with the same energy.

This leaves some questions.

1. Could one consider the possibility that the chords of one of the 20-chord harmonies corresponds to AAs? There would be 3 basic types of AAs. This does not look plausible and the association of AAs with the orbits of 20-note chords is more natural and fits nicely with $f = f_{XYZ}$ picture.

2. It would be nice to assign notes to the individual letters of codons. This is not possible since codons with 2 or 3 identical letters would reduce to 2-chords or 1-chords. It is also impossible to assign frequencies with letters at dark level since letter decomposition does not exist. Thus the 3-chord has resonant interaction with the entire codon.

3. The symmetries of the genetic code however suggest that it might make sense to treat the first two letters XY of the codon as a single unit and the third letter as separate single unit. Could one assign to XY a 2-chord not reducible to frequencies for the letters X and Y, and to letter Z its own frequency. The frequencies of A, G, T, C as third letter must be different. Four 32 codons of standard code the AA would not be sensitive to the frequency of Z: this is possible if these frequencies are resonance frequencies of the same AA. For the remaining 32 codons the AA would not distinguish between frequencies of T and C *resp.* A and G so that the two frequencies would be both resonance frequencies of the corresponding AA.

2.2 Probabilistic estimates for single 20-chord harmony

One can make first some naive probabilistic estimates about single 20-chord harmony.

1. Given 20-chord harmony makes $20/220 = 1/11 \simeq 9$ per cent about al possible 3-chords. Three 20 chord harmonies would make $3 \times 9 = 27$ per cent about all possible 3-chords if there are no common chords so that the optimistic expectation might make sense. Of course, one cannot exclude the possibility that there are also triplets of 20-codon codes which gives smaller number of codons.

2. The total number of chords with different notes is $12 \times 11 \times /3! = 220$. Bio-harmony has 64 chords corresponding to faces of icosahedron: this is about 64/220 making 29 per cent of all possible 3-chords with different notes. Given bio-harmony thus throws out roughly 2/3 of all possible codons. This should be easy to test. For instance, does given gene correspond to a fixed bioharmony? Or does even entire genome do so. If bio-harmony is realized for non-nuclear genomes, it must satisfy rather strong constraints.

3. Given 20-chord harmony corresponds to 12 edges. Each edge is shared by two adjacent triangles. If all 20 triangles would contain just single face, there would be 24 triangles altogether. Therefore there must be triangles containing two subsequent edges of the cycle. Each triangle of this kind reduces the number of 24 neighbours by 2 units. Hence it seems that one must have at least 2 triangles with 2 edges at the cycle (two quints in the 3-chord).

   If there are more than 2 triangles of this kind, there must be triangles having no edges along the path. Each vertex of icosahedron is shared by 5 triangles and there are 5 edges starting from it.

4. The notion of Hamilton cycle generalizes to any graph and magnetic flux tube networks define such graphs as tensor networks. Why only icosahedron? Could one consider the possibility that any tensor network is characterized by harmonies characterize by Hamiltonian cycles and that one could assign some kind of codes with the combinations of these cycles? In the general case symmetries would be absent so that the notion of code in the proposed sense would fail: one could not identified codons as points at orbits of symmetry group. Rather, one can imagine that the notion of code could be defined quite generally in terms of orbits as AAs and points at them as DNAs coding them. For regular polygons in any dimension the symmetries are present and one could define the notion of code and also fuse the codes.

   For arbitrary tensor network the faces need not be symmetry related and one can also have faces that can be interpreted as higher-dimensional polytopes.

   One can also ask whether the icosahedron is realized physically. Icosahedral geometry is indeed very common in biology. Could the fusion of icosahedral and tetrahedral geometries have some concrete realization at molecular level?

2.3 Is the maximal number of codons for the fusion of 3 20-codon codes possible?

It has not earlier occurred to me to wonder whether the chords associated with the 3-different icosahedral harmonies giving 20 codons each correspond to 20+20+20=60 different chords as assumed. Could there be common 3-chords? This question could be answered by studying the Hamiltonian cycles at icosahedron.

Remark: Perhaps more important constraint than absence of common chords is the chemical realizability of the codes. If same mRNAs and DNAs realized different bio-harmonies then they must be able to respond resonantly to several 3-chords.

One can make naive probability estimates for a pair of codes to allow the maximal number of 60 codons. It seems natural to assume that the isometries of icosahedron (or their subgroup) can be applied separately and only the isometries acting on both in similar manner are symmetries. The situation would be the same as in the case of many-particle system: only the translations acting on all particles simultaneously remain symmetries and relative translations cease to be symmetries.

With this assumption the icosahedral group gives a large number of code pairs. For the fusion of 3 20-codon codes giving DNA/RNA the number is even higher. By choosing suitably the relative isometries it might be possible to obtain the maximal number of 60 different codons for the icosahedral genetic code. On the other hand, by a suitably choice of relative isometries one might have undesired common 3-chords. In any case, the earlier estimate 256 for the number of bio-harmonies [17] suggested to correlate with "emotional" states of the basic biomolecules is expected to change.

Before going to estimates one must consider some delicacies related to the notion of 12-note scale as Hamiltonian cycle.

1. One can regard the cycles as purely geometric objects without orientation or assign to them orientation. For two different orientations the scales would run in opposite directions as scalings by 3/2 along single edge of the cycle. If two codes have common edge, the scaling must be same along it. If the orientation of the second cycle is changed, the common edge ceases to be common.

2. The basic note of the 12-note scale at cycle can be chosen arbitrarily: this corresponds to the choice of the key in music (one could of course argue that the key does not make sense in 12-note scale if one has tempered scale with notes comes as powers of $2^{1/2}$ scaling of ground note rather than Pythagorean scale with rational ratios of notes).

   The fusion of tetrahedron to icosahedron selects one particular triangular face and brings in one additional vertex outside the icosahedron, call it P. It would be natural to assign the ground note as P. The isometries not affecting P would correspond to those of icosahedron leaving the common face invariant and isometries of tetrahedron leaving P un-affected and continuable to icosahedral isometries. One would have subgroup of icosahedral group as allowed isometries acting on the cycles to be fused.

3. If one assigns note sequences to the cycle by quint rule, cycles C_1 and C_2 can have common triangle in geometric sense but if the distances of the vertices A, B, C of the triangles from P measured as the number of edges of cycle portion connecting them are not same along C_1 and C_2, the triangles correspond to different chords and are thus orthogonal in the proposed description as many-fermion states.

4. To sum up, the states associated with triangles would be characterize by the position of triangle (20 values), by the notes of the triangle characterized by the distances from P, and the number 0, 1, 2 of the edges belonging to the cycle and should make easier to find ortogonal basis.

Again one can make probabilistic estimates: cycles are treated as purely geometric entities without orientation and without assignment of notes to the triangles.

1. Given cycles C_1 and C_2 what is the probability that they have at least one common edge as purely geometric entities without the sequence of notes? There are 30 edges so that given edge is shared with probability 1/30. If the edges of cycles were chosen randomly (certainly not true), the probability of having a common edge for two cycles would be $P(1) = 12/30$. The assumption of note sequence reduces this probability dramatically.

2. By the above estimate each cycle contains at least two triangles with 2 edges at the cycle with minimal angle between them. One can call these these edge pairs V-corners. Assume that for cycle C_1 one has V-corner ABC at vertex A, call it $V_{1,A}$. What is the probability that one one of the V-corners of C_2 is located at A co-incides with ABC. The probability of V-corner of C_2 to locate at A is 1/12 and the probability that the edge of C_2 from B is BC is is 1/4 so that the probability of having common V-corner is 1/48. If C_2 contains n V-edges the probability is naively $n/48$.

   This estimate takes into account only geometry. The situation changes if one assumes that the cycles are oriented. In this case one can have common V-corner if the local orientations of C_1 and C_2 are opposite at the V-corner. If one assumes that the external vertex P of the tetrahedron defines the ground note then the number of edges connecting P to A defining distance $d(P, A)$ must be same for C_1 and C_2.

3. Given C_1 and C_2 (and vertices A with same distance $d(P, A)$) it might be possible to perform suitable isometry for C_2 that there is common V-corner. Therefore not all possible combinations of three code types allowing relative isometries need not maximal number of 3-chords.

Remark: An interesting question is whether these can be allowed meaning that some codons are missing in the chemical realization of the dark codons in terms of ordinary DNA codons. Also the 1-1 pairing between dark DNA and and dark RNA would not be 1-1 if mediated by 3-chord resonance and one would have homonymy. This suggests that only codes without common chords can be allowed.

4. What about chords having 1 edge at cycle for two cycles C_1 and C_2? Let the edge be AB. As found, the naive probability for this is $P(1) = 12/30$. Both cycles must go through the third vertex C of the triangular face. The subsequent notes along cycle differ by a quint that is scaling of the frequency by factor 3/2. Notes are same if the numbers of the needed quints are same for C_1 and C_2 For C_1 the number $n_B > 1$ of quints is known. In the approximation that possible portions of C_1 represent n-step non-self-intersecting random walks from B to C, one must estimate the number of all non-self-intersecting n-step-paths from B to C and find what is the number of the paths leading to C. One can go from A to C with n_A steps and similar estimate applies.

5. The third possibility is that the one has 3 common vertices A, B, C forming a triangular face such that neither cycle contains any of its edges.

The cautious conclusion is that it is plausible that one can find 3 cycles having no common chords if one allows relative rotations of the cycles and that this condition is necessary for realizing the absence of homonymies at dark level. The automatic orthogonality of the Hamiltonian cycles cannot be excluded but would allow also codes with codons containing more than 3 letters so that one could have kind of super-DNA. Whether they can be realized chemically depends on whether there are biomolecules resonating with the the n frequency triplets involved. Octave equivalence for frequencies might give hopes about chemical realization of several harmonies. Therefore the evolution might be seen as gradual emergence of molecules able to pair with DDNA and one can even imagine artificial evolution by tailoring the frequencies involved (maybe cyclotron frequencies).

2.4 How the symmetries of the model of harmony could relate to those of the genetic code?

Genetic code has surprisingly strong symmetries. I have discussed a possible interpretation of these symmetries using analogies with particle physics and considered also a mechanism explaining their emergence earlier [8, 9]. The proposal was that 3-letter code emerged as a fusion of 2-letter code with 16 codons and 1-letter coded with 4 codons. In the recent framework, a more natural option is that the third codon of 3-letter code was originally passive and became active via symmetry breaking distinguishing first between UC and AG pairs and later between U and C *resp.* A and G. Note that for the standard code the breaking is minimal and caused by odd number of Start and Stop codons.

1. For vertebrate code one half of codons has very high symmetry in the sense that the two first letters dictate the AA for 32 cases. Exception is UUU, which codes for Phe or Leu for some modifications of the standard code. UUU $\rightarrow$ Leu means breaking of maximal symmetry.

2. There is also a second symmetry, which I have referred to as isospin symmetry. It is only slightly broken. For general codons XYU and XYC code for same AA as also XYA and ad XYG. For the standard code this symmetry is broken only in columns containing initiation codon or stop. The Start codon AUG codes also for met. UGA and UGG code for Stop and Trp. For the remaining codons one has slightly broken "isospin symmetry". The breaking of isospin symmetry is minimal for vertebrate code. The modifications of the code tend to break the isospin symmetry and even the maximal symmetry of 32 codons. This must be important.

If the model of genetic code based on music harmony [17] is correct, the symmetries for the model of music harmony should relate to those of genetic code.

1. How the symmetries of the genetic code relate to the symmetries of icosahedron (60-element group) and tetrahedron (permutation group S_4 with 24 elements) in the model of bio-harmony? Icosahedral symmetry group has 60 elements and has sub-groups $Z_2, Z_4, Z_5, Z_6 = Z_2Z_3$. Note that there are two Z_2:s having rotation by π and reflection as generators.

   The gluing of tetrahedron to icosahedral along single face reduces its group of symmetries to S_3 leaving the point P not belonging to icosahedron invariant. S_3 has as subgroups reflection group $Z_{2,refl}$ and Z_4 consisting of rotations.

2. What is the counterpart for maximal symmetry in icosahedral and tetrahedral groups? Do the 3-chords for codon XYZ decompose to two-chord characterizing XY and a note characteriing Z= A,U,C,G, which can depend on XY. The symmetry relating UC pair and AC pair could correspond to $Z_{2,refl}$ reflection symmetry, which is shared by icosahedral and tetrahedral groups. For 32 icosahedral codons the action of $Z_{2,refl} \times Z_{2,rot}$ would be trivial so that AA would not depend on the third letter at all. For most of the remaining codons the action of the symmetry group on icosahedral codons would reduce to $Z_{2,rot}$ permuting the third letters U and C *resp.* A and G. At the level of frequencies the sums of frequencies for codons coding for the same AA sould be same modulo octave equivalence.

   The addition of tetrahedron brings in 4 tetrahedral codons with one of them shared with icosahedron. Icosahedral $Z_{2,rot}$ does not make sense for these codons. Intriguingly, there are 4 codons in vertebrate code which break isospin symmetry AUA and AUG coding for I and Met/start and UGA and UGG coding for Stop and Trp. If these codons correspond to the tetrahedral codons which cannot have $Z_{2,rot}$ as isospin symmetry, the breaking of $Z_{2,rot}$ would follow from the breaking of symmetry induced by the attachment of tetrahedron to icosahedron.

2.5 What is the origin of 12-note scale?

One fundamental question is why dark photon realization of genetic code should involve 12-note scale as icosahedral model requires.

Remark: The gluing of tetrahedral codons gives 4 additional codons but if tetrahedron is glued to icosahedron along one of its faces, the additional vertex gives only one additional note, which should be very near to the 12:th one. This could relate to the basic problem observed already by Pythagoras that 12-note Pythagorean scale with rational valued frequency ratios does not quite close.

A popular article in Spacedaily with title "*Scientists crack how primordial life on Earth might have replicated itself*" (see `http://tinyurl.com/y92ng5vd`) led to a possible answer to the above question. The research paper [7] is titled "*Ribozyme-catalysed RNA synthesis using triplet building blocks*" and published in eLife (see `http://tinyurl.com/ya5qyjfn`).

It is possible to replicate unfolded RNA strands in Lab by using enzymes known as ribozymes, which are RNA counterparts of enzymes, which are amino-adic sequences. In the presence of folding the replication is however impossible. Since ribozymes are in general folded, they cannot thus catalyze their own replication in this manner. The researchers however discovered that the replication using RNA triplets - genetic codons - as basic unit can be carried out in laboratory even for the folded RNA strands and with rather low error rate. Also the ribozyme involved can thus replicate in codon-wise manner. For units longer than 3 nucleotides the replication becomes prone to errors.

These findings are highly interesting in TGD framework. In TGD the chemical realization of genetic code is not fundamental. Rather, dark matter level would provide the fundamental realizations of analogs of DNA, RNA, tRNA, and AAs as dark proton sequences giving rise to dark nuclei at magnetic flux tubes [21] (see `http://tinyurl.com/yalny39x`). Also ordinary nuclei correspond in TGD Universe to sequences of protons and neutrons forming string like entities assignable to magnetic flux tubes.

The basic unit representing DNA, RNA and tRNA codon and AA would consist of 3 entangled dark protons. The essential aspect is that by entanglement the dark codons do not decompose to products of letters. This is like words of some languages, which do not allow decomposition to letters. This

representation is holistic. As we learn to read and write, we learn the more analytic western view about words as letter sequences. Could the same hold true in evolution so that RNA triplets would have come first as entities pairing with dark RNA codons from from dark proton triplets as a whole? Later DNA codons would have emerged and paired with dark DNA codons. Now the coupling would have have been letter by letter in DNA replication and transcription to mRNA.

It is intriguing that tRNA consists of RNA triplets combined from AAs and analogs of mRNA triplets! The translation of mRNA to AAs having no 3-letter decomposition alone forces the holistic view but one can ask whether something deeper is involved. This might be the case. I have been wondering whether during RNA era RNA replicated using a prebiotic form of translational machinery, which replicated mRNA rather than translated RNA to protein formed from AAs (AAs) with AA serving as a catalyst.

1. During RNA era AAs associated with pre-tRNA molecules would served as catalysts for replication of RNA codons. The linguistic mode would have been "holistic" during RNA era in accordance with the findings of the above experiments. RNA codon would have been the basic unit.

2. This would have led to a smaller number of RNAs since RNA and RNA like molecules in tRNA are not in 1-1 correspondence. A more realistic option could have been replication of subset of RNA molecules appearing in tRNA in this manner.

3. Then a great evolutionary leap leading from RNA era to DNA era would have occurred. AA catalyzed replication of RNA would have transformed to a translation of RNA to proteins and the roles of RNA and AA in tRNA would have changed. [Perhaps the increase of h_{eff} in some relevant structure as quantum criticality was reached led to the revolution]

4. At this step also (subset of) DNA and its transcription to (a subset of) mRNA corresponding to tRNA had to emerge to produce mRNA in transcription. In the recent biology DNA replicates and is transcribed nucleotide by nucleotide rather than using codon as a unit so that helicases and DNA and RNA polymerases catalyzing replication and transcription should have emerged at this step. The ability of DNA to unwind with the help of helicase enzyme helping DNA to unwind is essential for the transcription and translation of DNA. Therefore helicase must have emerged together with the "analytic linguistic mode" as an analog of written language (DNA) decomposing codons to triplets of letters. This would been a crucial step in evolution comparable to the emergence of written language based on letters. Also the counterpart of RNA polymerase and separate RNA nucleotides for transcription should have emerged if not already present.

   An alternative option would involve "tDNA" as the analog of tRNA and the emergence of helicase and polymerases later as the transition from holistic to analytic mode took place.

   The minimal picture would be emergence of a subset of DNA codons corresponding to RNAs associated with pre-tRNA and the emergence of the analogs of helicase and DNA and RNA polymerases as the roles of AA and RNA codon in tRNA were changed.

5. How DNA could have emerged from RNA? The chemical change would have been essentially the replacement of ribose with de-oxiribose to get DNA from RNA and U$\rightarrow$ T. Single O-H in ribose was replaced with H. O forms hydrogen bonds with water and this had to change the hydrogen bonding characteristics of RNA.

   If the change of $h_{eff} = n \times h_0$ was involved, could it have led to stabilization of DNA? Did cell membrane emerge and allow to achieve this? I have proposed [21] (see `http://tinyurl.com/yalny39x`) that the emergence of cell membrane meant the emergence of new representation of dark genetic code based on dark nuclei with larger value of h_{eff}.

   Remark: One has $h = 6 \times h_0$ in the most plausible scenario [19, 22] (see `http://tinyurl.com/goruuzm` and `http://tinyurl.com/y9jxyjns`).

One can of course ask whether something simpler could be imagined by utilizing the potential provided by dark variants of bio-molecules present already from beginning and providing both genes and metabolism simultaneously.

1. Viruses are probable predecessors of cellular life. So called positive sense single stranded RNA (ssRNA) associated with viruses can form temporarily double strands and in this state replicate just like DNA (see `http://tinyurl.com/yc5f8b3t`). The resulting single stranded RNA can in turn be translated to proteins by using ribosomal machinery. RNA replication takes place in so called viral replication complexes associated with internal cell membranes, and is catalyzed by proteins produced by both virus and host cell.

   Could ribozyme molecules have catalyzed RNA replication during RNA era? For this option AA translation would have emerged later and the storage of genetic information to DNA only after that. There is however the question about the emergence of AAs and of course, DNA and RNA. Which selected just them from enormous variety of options.

2. Lipid membranes are formed by self-organization process from lipids and emerge spontaneously without the help of genetic machinery. It would be surprising if prebiotic life would not have utilized this possibility. This idea leads to the notion of lipid life as a predecessor of RNA life. In this scenario metabolism would have preceded genes (see `http://tinyurl.com/y7ehv8cq` and `http://tinyurl.com/y8nltb9e`). The basic objection against both genes-first and metabolism-first options is that they need each other!

3. In TGD framework the dark variants of DNA, RNA, AA, and tRNA would provide the analogs of genes and all basic biomolecules. They would also provide a mechanism of metabolism in which energy feed by (say) solar radiation creates so called exclusion zones (EZs) of Pollack [6] in water bounded by a hydrophilic substance. EZs are negatively charged regions of water giving rise to a potential gradient (analog of battery) storing chemically the energy provided by sunlight and the formation of these regions gives rise to dark nuclei at magnetic flux tubes with scaled down binding energy.

   When the p-adic length scale of these dark nuclei is liberated binding energy is liberated as metabolic energy so that metabolic energy feed giving basically rise to states with non-standard value $h_{eff}/h = n$ of Planck constant is possible. For instance, processes like protein folding and muscle contraction could correspond to this kind of reduction of h_{eff} liberating energy and also a transformation of dark protons to ordinary protons and disappearance of EZs.

   The cell interiors are negatively charged and this is presumably true for the interiors of lipid membranes in general and they would therefore correspond to EZs with part of protons at magnetic flux tubes as dark nuclei representing dark variants of basic biomolecules. Already this could have made possible metabolism, the chemical storage of metabolic energy to a potential gradient over the lipid membrane, and also the storing of the genetic information to dark variants of biomolecules at the magnetic flux tubes formed in Pollack effect.

4. In TGD framework biochemistry would have gradually learned to mimic dark variants of basic processes as a kind of shadow dynamics. Lipid membranes could have formed spontaneously in water already during prebiotic phase when only dark variants of DNA, RNA, AAs and tRNA, water, and lipids and some simple bio-molecules could have been present. The dark variants of replication, transcription and translation would have been present from the beginning and would still provide the templates for these processes at the level of biochemistry.

   Dark-dark pairing would rely on resonant frequency pairing by dark photons and dark-ordinary pairing to resonant energy pairing involving transformation of dark photon to ordinary photon. The direct pairing of basic biomolecules with their dark variants by resonance mechanism could have led to their selection explaining the puzzle of why so few biomolecules survived.

This is in contrast with the usual view in which the emergence of proteins would have required the emergence of translation machinery in turn requiring enzymes as catalyzers so that one ends up with hen-or-egg question: which came first, the translation machinery or proteins. In RNA life option similar problem emerges since RNA replication must be catalyzed by ribozymes.

5. Gradually DNA, RNA, tRNA, and AA would have emerged by pairing with their dark variants by resonance mechanism. The presence of lipid membranes could have been crucial in catalyzing this pairing. Later ribozymes could have catalyzed RNA replication by the above mentioned mechanism during RNA era: note however that the process could be only a shadow of much simpler replication for dark DNA. One can even imagine membrane RNAs as analogs of membrane proteins serving as receptors giving rise to ionic channels. Note however that in TGD framework membrane proteins could have emerged very early via their pairing with dark AA associated with the membrane. These membrane proteins and their RNA counterparts could have evolved into transcription and translation machineries.

   DNA molecules would have emerged through pairing with dark DNA molecules. The difference between deoxi-ribose and ribose would correspond to the difference between dark RNA and dark DNA manifesting as different cyclotron frequencies and energies making possible the resonant pairing for frequencies and energies. Proteins would have emerged as those proteins able to pair resonantly with dark variants of amino-acid sequences without any pre-existing translational machinery. It is difficult to say in which order the basic biomolecules would have emerged. They could have emerged even simultaneously by resonant pairing with their dark variants.

The communication between dark ordinary variants of biomolecules involves resonance mechanism and would also involve genetic code represented as 3-chords, music of light, and it is interesting to see whether this model provides additional insights.

1. The proposal is that 3-chords assignable to nucleotides as music of light with allowed 64 chords defining what I have called bio-harmony is essential for the resonance [23, 24, 22](see `http://tinyurl.com/ydhxen4g`, `http://tinyurl.com/yd5t82gq`, and `http://tinyurl.com/y9jxyjns`). The 3 frequencies must be identical in the resonance: this is like turning 3 knobs in radio. This 3-fold resonance would correspond to the analytic mode. The second mode could be holistic in the sense that it would involve only the sum only the sum of the 3 frequencies modulo octave equivalence assigning a melody to a sequence of 3-chords.

2. The proposal is that AAs having no triplet decomposition are holistic and couple to the sum of 3 frequencies assignable to tRNA and mRNA in this manner. Also the RNAs in tRNA could couple to mRNA in this manner. One could perhaps say that tRNA, mRNA and AAs codons sing whereas DNA provides the accompaniment proceeding as 3-chords. The couplings of DNA nucleotides to RNA nucleotides would rely on the frequencies assignable to nucleotides.

3. If the sum of any 3 frequencies associated with mRNA codons is not the same except when the codons code for the same AAs, the representation of 3-chords with the sum of the notes is faithful. The frequencies to DNA and RNA nucleotides cannot be however independent of codons since the codons differing only by a permutation of letters would correspond to the same frequency and therefore code for the same AA. Hence the information about the entire codon would be needed also in transcription and translation and could be provided either by dark DNA strand associated with DNA strand or by the interactions between the nucleotides of the DNA codon.

4. The DNA codon itself would know that it is associated with dark codon and the frequencies assignable to nucleotides could be determined by the dark DNA codon. It would be enough that the frequency of the letter depends on its position in the codon so that there would be 3 frequencies for every letter: 12 frequencies altogether.

What puts bells ringing is that this the number of notes in 12-note scale for which the model of bio-harmony [17, 23] (see `http://tinyurl.com/yad4tqwl` and `http://tinyurl.com/ydhxen4g`) based on the fusion of icosahedral (12 vertices and 20 triangular faces) and tetrahedral geometries by gluing icosahedron and tetrahedron along one face, provides a model as Hamiltonian cycle and produces genetic code as a by-product. Different Hamiltonian cycles define different harmonies identified as correlates for molecular moods.

Does each DNA nucleotide respond to 3 different frequencies coding for its position in the codon and do the 4 nucleotides give rise to the 12 notes of 12-note scale? There are many choices for the triplets but a good guess is that the intervals between the notes of triplet are same and that fourth note added to the triplet would be the first one to realize octave equivalence. This gives uniquely $CEG\sharp$, $C\sharp FA$,$DF\sharp B\flat$, and $DG\sharp B$ as the triplets assignable to the nucleotides. The emergence of 12-note scale in this manner would be a new element in the model of bio-harmony.

There are 4!=24 options for the correspondence between $\{A, T, C, G\}$ as the first letter and $\{C, C\sharp, D, D\sharp\}$. One can reduce this number by a simple argument.

(a) Letters and their conjugates form pyrimidine-purine pairs T, A and C, G. The square of conjugation is identity transformation. The replacement of note with note defining at distance of half-octave satisfies this condition (half-octave - tritonus - was a cursed interval in ancient music and the sound of ambulance realizes it). Conjugation could correspond to a transformation of 3-chords defined as

$$CEG\sharp \leftrightarrow DF\sharp B\flat \ , \quad C\sharp FA \leftrightarrow D\sharp GB \ .$$

(b) One could have

$$\{T, C\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \ , \quad \{A, G\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \ ,$$
$$\text{or}$$
$$\{T, C\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \ , \quad \{A, G\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \ .$$

.

(c) One can permute T and C and A and G in these correspondences. This leaves 8 alternative options. Fixing the order of the image of (T, C) to say $(C, C\sharp)$ fixes the order of the image of (A, G) to $(D, D\sharp)$ by the half-octave conjugation. This leaves 4 choices. Given the bio-harmony and having chosen one of these 4 options one could therefore check what given DNA sequence sounds as a sequence of 3-chords [17].

That the position the frequency associated with the nucleotide depends on its position in the codon would also reflect the biochemistry of the codon and this kind of dependence would be natural. In particular, different frequencies associated with the first and third codon would reflect the parity breaking defining orientation for DNA.

2.6 What disharmony could mean?

Harmonies - also those, which are sad (consider only passions of Bach) - are usually thought of as something beautiful. Could negative emotions really correspond to any bio-harmonies characterized by symmetries. In a discussion with Sini Kunnas I realized that also the notion of disharmony could make sense. There are indeed 6 Hamiltonian cycles without any symmetries [5, 2, 4, 1, 3]. I neglected them in the model of harmony because they would represent which one might call disharmony. Could one of the contributing 3 Hamiltonian cycles in bio-harmony correspond to this kind of dis-harmony and bring in 20 3-chords without any symmetries? If so the relationship between geometry and aesthetics would become very concrete. The alternative view would be that there are several harmonies realized simultaneously and thi creates disharmony.

The faces of the icosahedron belonging to the orbits of the symmetries of the harmony correspond to DNA codons coding for the same AA assignable to the orbit. The fact that there are no symmetries for these 6 bio-disharmonies, suggests one-to-one correspondence between DNA and AAs if also stop codon corresponds to ordinary AA.

2.7 How to concretely realize emotions as music of light?

Music expresses emotions and also create higher level emotions. As all art, it also induces experience of beauty. Since $h_{eff}/h = n$ [15, 16] serves as a kind of IQ in the evolutionary hierarchy, there are good reasons to expect that the emotions/feelings induced by music and other art forms are assignable to MB.

The dynamics of MB involves oscillations characterized by frequencies and in EEG frequencies are of key importance for the part of MB outside biological body. The communications from cell membrane to MB involve modulation of EEG frequencies identified as generalized Josephson frequencies by nerve pulse patterns [11] and would define a coding of sensory data to higher level emotions. The control signals from MB via DNA inducing gene expression would use dark photons at cyclotron frequencies to control BB. How to realize the music of genes represented as sequences of 3-chords of dark light as a communication tool between dark and ordinary DNA/RNA and possibly even dark and ordinary variants of tRNA and AAs?

1. Communication between ordinary and dark matter levels must be possible. This is guaranteed if the transition energy spectra at different levels of $h_{eff}/h = n$ hierarchy contain common transition energies so that a resonant interaction by exchange of dark photons becomes possible. This condition is extremely demanding and could explain why basic bio-molecules are selected amongst numerous alternatives [21] - this is indeed one of the hen-egg problems of pre-biotic evolution.

2. A hypothesis worth of studying is that the cyclotron transition energies of both ordinary DNA and RNA nucleotides and their dark variants represented as dark proton sequences are same [21]. Cyclotron transition energies should cover several octaves and the natural proposal is that magnetic field strength associated with the flux tube codes for the notes. In music experience roughly 10 octaves are needed corresponding to the range of audible sounds.

3. The cyclotron frequencies of DNA nucleotides A, T, C, G are very nearly the same and near 1 Hz for $B = B_{end} = .2$ Gauss since their masses do not differ much. Since the nucleotides are negatively charged, also the cyclotron energies for codons and codon sequences are around 1 Hz. $h_{eff} = h_{gr}$ hypothesis states that the cyclotron energies of DNA are in the energy range of bio-photons in visible and UV [16, 13, 14, 22].

There should be correspondences between a) the 64 ordinary DNA codons and allowed 3-chords and b) 64 dark variants of DNA codons and allowed 3-chords. These correspondences fix that between ordinary and dark codons. One would have triality.

1. To realize music of genes one the value of B must have values in a range of several octaves. The magnetic field strengths B associated with the flux tubes accompanying DNA strand should have a spectrum given by 12-note scale. Both 64 dark DNA codons and $4^3 = 64$ ordinary DNA codons should correspond to $20 + 20 + 20 + 4 = 64$ allowed 3-chords formed from the notes of 12-note scale.

2. Dark codons correspond to entangled states of 3 dark protons. The positions of dark protons are different so that ermutations of the positions of dark protons are involved. The invariance of 3-chord under permutations of notes would correspond to fermionic statistics. These permutations are lifted to braidings if dark protons are connected by flux tubes to some other system, for instance ordinary DNA.

   If the dark protons are ordered linearly along flux tube, it would seem that these these positions correspond to those of ordinary code letters. This does not make sense. If the letters of codon are

connected to the dark protons by flux tubes, the permutations of dark codons induce braiding of the flux tubes but do not affect the order of the letters of the ordinary codon. Braiding would become an essential part of the correspondence between ordinary and dark codons.

3. One should understand the correspondence of dark codons with the allowed 3-chords of a given harmony and also with the ordinary DNA codons. Bio-harmony is defined as a composite of 3 harmonies with 20 allowed 3-chords and having symmetries Z_6, Z_4, and Z_2 and of tetrahedral harmony with 4 chords. Tetrahedron can be regarded as disjoint object or attached to DNA, and this gives two variants of code.

   How could these the icosa-tetra-hedral Hamilton cycles relate to the physical realization of dark proton triplets? Each icosahedral cycle should give rise to 20 dark proton triplets. Why the icosahedral geometry with Hamiltonian cycle should make itself manifest in the quantum physics of dark proton triplet?

4. Could icosahedral geometry quite concretely correspond to a tensor network? The vertices of the icosahedron would be connected by a sequence of flux tubes connecting nearest neighbors to form a Hamiltonian cycle. Dark proton triplets would quite concretely be localized at the triangular faces of the icosahedron.

   Braided triplet of flux tubes would emerge from the vertices of an icosahedral triangle defining 3-chord and would connect it to the nucleotides of the corresponding ordinary DNA codon. Magnetic field strengths at these flux tubes would correspond to the notes of 12-note scale as defined by the Hamiltonian cycle in question. The permutations of the dark proton states at the vertices of the triangle would induce braidings of the flux tube triplet actually defining minimal braid in topological quantum computation (sic!) The braiding accompanying the states of 3 dark protons would make the correspondence with ordinary ordered DNA codons possible.

   Note that each dark proton triplet could be also connected (without braiding) to its conjugate dark proton triplet by a triplet of flux tubes so that one would obtain closed flux loops and one could speak of knots instead of braids.

   Remark: Braiding brings strongly in mind the many TGD inspired proposals for DNA as topological quantum computer [8, 12]: maybe DNA as topological quantum computer could be (also?) realized in this manner.

   What physical objects could the 20 vertices of icosahedron correspond to? Hydrogen bonded water clusters give rise to both tetrahedral and icosahedral structures. Could one associate dark proton triplets to the dark parts of these structures? Could one try to experimentally identity possible sequence of icosahedral water molecule clusters with vertices connected by hydrogen bonds associated with the DNA sequence? If the hydrogen bonds correspond to flux loops as suggested, they can be rather long (proportional to $h_{eff}/h = n$) so that even distant water molecules can become hydrogen bonds and one could have a fractal hierarchy of icosahedra.

5. Resonance condition suggests that at the level of ordinary DNA double strand the cyclotron energies of dark protons associated with the hydrogen bonds connecting DNA nucleotides correspond to those of flux tube triplets connecting ordinary and dark DNA codons. The magnetic field strengths associated with the dark flux tubes accompanying hydrogen bonds would correspond to those associated with the triangles of icosahedral triangle. This would make possible communication between the two dark sectors by dark-photon triplets as music of genes.

This leaves unanswered questions.

1. Why the 20+20+20=60 3-chords from 3 harmonies with different icosahedral symmetries (Z_6, Z_4, Z_2) and 4 chords from tetrahedral harmony would combine to form single bio-harmony with 64 chords? This requires the presence of 3 Hamiltonian cycles with different symmetries. Why all three different

symmetry types for DNA and RNA? Could the 20 AAs correspond to single symmetry type? Could tRNA codons correspond to two symmetry types?

2. How the 3-chords of dark photons could be played? 3-chord should be a collective effect affecting both dark and ordinary codon by inducing emission of 3-photon state like - like playing a chord by string instrument. The notes of the light chord need not emerge simultaneously but as arpeggios. Could there be a pulse travelling along the Hamiltonian cycle and picking all the cyclotron notes at the vertices containing dark proton and sending a cyclotron signal along flux tubes to ordinary DNA codon. This pulse would travel along dark DNA and play the music defined by dark DNA sequence.

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