Article

Homonymy of the Genetic Code from TGD Point of View

Matti Pitkänen [1]

Abstract

Peter Gariaev and colleagues have applied the linguistic notions of synonymy and homonymy to genetic code. Also the notion of syhomy fusing these concepts is introduced. Homonymy is visible in mRNa-tRNA pairing and induced by the 1-to-many pairing of the third mRNA nucleotide with tRNA nucleotide. The homonymy in mRNA-AA (AA for amino-acid) pairing is also present albeit rare. The codons for the standard code can be divided to two classes. For 32 codons the first two letters fix AA completely. For the remaining 32 codons this is not the case. There is however almost unbroken symmetry in that U and C *resp.* A and G code for the same AA. The breaking of this symmetry is minimal appearing only for 3 4-columns of the code table and present for A-G only. The deviations from the standard code as a rule break A-G or T-C symmetry or re-establish it. The notion of homonymy is highly interesting from TGD point of view. TGD leads to two basic proposals for non-chemical realization of genetic code predicting the numbers of DNA codons coding for AA rather successfully. The first proposal relies on TGD based view about dark matter as $h_{eff}/h = n$ phases of ordinary matter and identifies counterparts of DNA, RNA, tNRA, and AAs as entangled dark proton triplets. Second proposal emerged from the model of music-harmony based on fusion of icosahedral and tetrahedral geometries. Codons are represented as photon triplets (dark or ordinary) defining the allowed 3-chords of given harmony defined by Hamilton cycle at icosahedron extended to Hamilton cycle to the fusion of icosahedron with tetrahedron along common face. Photon triplets give rise to resonant coupling giving rise to physical pairing of biomolecule and its dark counterpart. Remarkably, there are 3 different realizations of tRNA in terms of 3-chords. There is large number of bio-harmonies corresponding to Hamiltonian cycles. Since music expresses and creates emotions, the proposal is that a realization of emotions at molecular level adding additional degrees of freedom not visible at the level of chemistry is in question. This might give rise to a context dependence of the code. The proposal is that genetic code at dark level extends to a sequence DDNA $\rightarrow$ DmRNA $\rightarrow$ DtRNA $\rightarrow$ DAA of horizontal pairings analogous to projections is fundamental one. Codon-codon pairings are realized via dark photon triplet resonance and mRNA-AA pairing by resonant coupling to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of 3-chord frequencies: the codons coding same AA would have frequencies f_{XYZ} differing only by a multiple of octave. One might perhaps say that AA sequence defines melody and mRNA sequence the accompaniment. There is context dependence and homonymies already in DmRNA-DtRNA pairing and due the fact that DtRNA corresponds to a 2-harmony which is sub-harmony of 3-harmony and can be chosen in 3 different manners. The vertical pairings DDNA $\rightarrow$ DNA, DmRNA $\rightarrow$ mRNA, etc. also mediated by frequency couplings induce ordinary genetic code and horizontal pairings in DNA $\rightarrow$ mRNA $\rightarrow$ tRNA $\rightarrow$ AA. DAA $\rightarrow$ AA pairing dictates mRNA $\rightarrow$ AA pairing and mRNA $\rightarrow$ tRNA homonymy does not matter and actually makes the translation safer by increasing the number of tRNAs performing the same task. The rather rare homonymies in DNA-AA pairing can be understood as accidental degeneracies. AA couples resonantly to the sum $f_{XYZ} = f_1 + f_2 + f_2$ of frequencies associated with codon XYZ and it can occur that the sum frequencies can be identical for two codons.

Keywords: Genetic code, DNA, RNA, synonymy, homonymy, TGD.

1 Introduction

This article was motivated by the article of Peter Gariaev [7] about the linguistic notions of synonymy and homonymy applied to genetic code (for other works of Gariaev and collaborators on the linguistic aspects

[1]Correspondence: Matti Pitkänen `http://tgdtheory.com/`. Address: Rinnekatu 2-4 A8, 03620, Karkkila, Finland. Email: matpitka6@gamail.com.

of DNA see [5, 4]). In another article by Peter Gariaev and Ekaterina Leonova-Gariaeva to be published in Open Journal of Genetics the notion of syhomy fusing these concepts is introduced. Homonymy is visible in mRNa-tRNA pairing and induced by the 1-to-many pairing of the third mRNA nucleotide with tRNA nucleotide. The homonymy in mRNA-AA (AA for amino-acid) pairing is also present albeit rare and might be explainable in terms of context dependence of this pairing.

The article summarizes much what is known about the theoretically poorly understood role of the third nucleotide of mRNA in the translation of mRNA to AAs. That many tRNAs correspond to same mRNA - synonymy - is not surprising since the number of tRNAs is smaller than that of mRNAs. There is however also homonymy present - the third nucleotide of mRNA can correspond to several tRNAs. If the AAs associated with homonymous tRNAs are same, the is no homonymy in mRNA-AA pairing. This is not quite always the case but the deviations are surprisingly small.

The article emphasizes the fact that the codons for the standard code can be divided to two classes. For 32 codons the first two letters fix AA completely. For the remaining 32 codons there is almost unbroken symmetry in that U and C *resp.* A and G code for the same AA. This symmetry is broken only for the the three 4-columns of the code table containing Stop codon or Start codon coding also for met: this symmetry breaking is unavoidable given that the number of both start and Stop codons is odd. This symmetry breaking is minimal and applies only to A-G whereas T-C symmetry is exact. For the deviations of the code from the standard code the deviation as a rule breaks A-G or T-C symmetry or re-establishes it.

The notion of homonymy is extremely interesting from TGD point of view. TGD leads to two basic proposals predicting the numbers of DNA codons coding for AA rather successfully.

1. The first proposal [15] relies on TGD view about dark matter as $h_{eff}/h = n$ phases of ordinary matter [9, 11, 12][16, 17] motivated by adelic physics extending physics to include also the correlates of cognition [16] [17]. The empirical motivation comes from several sources, in particular from the findings of Pollack [1] discussed in [14]. One can understand the formation of negatively charged regions - exclusion zones (EZs) - as being due to the transformation of part of protons to dark protons residing at magnetic flux tubes.

   Dark genetic code would be realized in ters of dark proton sequences - to be denoted by DDNA, DmRNA, DtRNA, and DAA - would provide dark analogs of DNA, mRNA, tRNA, and AA. Biochemistry would emerge as a shadow of the much simpler dynamics of dark matter at flux tubes and genetic code would be induced by dark code code. The dark code would be sequence DDNA $\rightarrow$ DmRNA $\rightarrow$ DtRNA$\rightarrow$ DAA of pairings.

2. Second model of genetic code emerged accidentally from a geometric model of music harmony [13] (see `http://tinyurl.com/yad4tqwl`) involving icosahedral (12 vertices-12-note scale and 20 faces-number of AAs) and tetrahedral geometries leading to the proposal that DNA codons and possibly also AAs correspond to 3-chords defining the harmony and obtained as unions of 20+20+20 3-chords associated with icosahedral 20-chord harmonies with symmetries Z_6, Z_4, Z_2 plus tetrahedral 4-chord harmony. There is large number of these harmonies bringing in additional degrees of freedom.

   Remark: This model has obviously analogies with the notion of wave genome introduced by Peter Gariaev [2, 3, 6].

   Since music both expresses and creates emotions the proposal is that these harmonies assigning additional hidden degrees of freedom to the magnetic bodies of DDNA, DRNA, etc... serve as correlates of emotions also at the molecular level. This emotional context could also give rise to context dependence of the code if several harmonies are realizable chemically. Taking seriously TGD inspired theory of consciousness [18] and model of emotions [19] (see `http://tinyurl.com/ydhxen4g`), one might say that the details of the code might depend slightly on the "emotional" state of DNA, RNA, and possibly other molecules.

In the sequel I will consider the following proposal for the various pairings of dark DNA and ordinary DNA visualizable as a 2×4-matrix with two rows representing DDNA, DmRNA, DtRNA, DAA *resp.* DNA, mRNA, tRNA, AA.

1. The proposal is that genetic code at dark level extends to a sequence DDNA $\rightarrow$ DmRNA $\rightarrow$ DtRNA $\rightarrow$ DAA of horizontal pairings analogous to projections is the fundamental one, and realized via dark photon triplet resonance expect for the coupling to DAA for which coupling is based on the sum $f_{XYZ} = f_1 + f_2 + f_3$ of 3-chord frequencies. One might perhaps say that AA sequence defines melody and mRNA sequence the accompaniment. The frequencies f_{XYZ} for codons coding same AA would be same modulo octave multiple. There is context dependence and homonymies already in DmRNA-DtRNA pairing and due the fact that DtRNA corresponds to a 2-harmony as sub-harmony of 3-harmony and can be chosen in 3 different manners. Also this choice - perhaps by state function reduction - could correlate with emotional state.

2. There are also vertical mappings DDNA $\rightarrow$ DNA, DmRNA $\rightarrow$ mRNA, DtRNA $\rightarrow$ tRNA and DAA $\rightarrow$ AA. These pairings would induce the horizontal pairings DNA $\rightarrow$ mRNA $\rightarrow$ tRNA $\rightarrow$ AA at the chemical level. The homonymy at mRNA-tRNA level would have no effects on DNA-AA pairing.

3. Apart from mRNA-AA pairing all these pairings would be realized dynamically in terms of 3-chords (f_1, f_2, f_3) and giving rise to a resonant coupling between members of the pair connected by magnetic flux tubes to single dynamical unit carrying the dark photon triplets at the frequencies characterized by the 3-chord. The model for musical harmony [13] leading also to a realization of genetic code suggests the existence of a large number of harmonies.

   It is not however obvious whether these harmonies can be realized bio-chemically since the 3-chords must be resonance 3-chords for bio-molecules. For DNA-AA and mRNA-AA correspondence the constraints are the slightest ones since they couple to $f_{XYZ} = f_1 + f_2 + f_3$: AAs could have emerged in rather early stages of the prebiotic evolution. One cannot even exclude the possibility f_{XYZ} are same for different harmonies. Slight chemical modifications of DNA and mRNA and AA analogous to wobbling for tRNA might allow to realize the slightly different collections of 3-chords defining the harmonies.

4. The model leads to an explanation for the homonymy of mRNA $\rightarrow$ tRNA pairing as being induced by the mRNA-tRNA homonymy realized already at dark level. The rather rare homonymies in DNA-AA pairing can be understood as accidental degeneracies. AA couples resonantly to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of frequencies associated with codon XYZ, and one can have $f_{X_1Y_1Z_1} = f_{X_2Y_2Z_2}$ modulo octave multiple for two codons. DAA coded by DDNA codes for AA and tRNA serves only in the role of transferring DAA-AA pairs and attaching them to DmRNA-mRNA pairs: the mRNA-AA pairing would be determined completely by dark molecules. It is actually advantageous to have tRNA homonymy since it can happen that the concentration of particular certain kind of tRNA is low.

5. What distinguishes between DNA and RNA and between codons and anti-codons is not obvious in the harmonic model. The most plausible identification for the map mapping codons to anti-codons is reflection symmetry of the icosahedron permuting opposite faces. An internal reflection changing the orientation of the scale could map DNA to RNA: this makes sense if the chords can be regarded as arpeggios.

6. The vision of biological evolution as chemical evolution in which dark variants of genetic code gradually find biological representations suggests a concrete model for RNA era. At that era AAs would have catalyzed mRNA replication possibly as non-faithful process. This era might have preceded tRNA era with mRNA replaced with tRNA analog corresponding to to the fusion of two 20-chord representations. The era before this could have been era with single 20-chord representation and corresponding tRNAs and amino-acids.

2 Some background

In the following I will discuss briefly the basic facts about genetic code at Wikipedia level with emphasis on the poorly understood aspects of the code.

2.1 Variations of the genetic code

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

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

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

3. There is variation even in human mitochondrial code (see `http://tinyurl.com/puw82x8`). In 2016, researchers studying the translation of malate dehydrogenase found that in about 4 per cent of the mRNAs encoding this enzyme the UAG Stop codon is naturally used to encode the AAs Trp and Arg. This phenomenon is known as Stop codon readthrough (see `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5133446/`).

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

2.2 Wobble base pairing

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

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

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

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

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

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

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

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

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

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

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

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

3 Two TGD based realizations of genetic code

During years I have considered several visions about genetic code. Two of them have allowed to build concrete contacts with the empirical reality. They are realized in terms of dark protons sequences [15] and in terms of 3-chords of bio-harmony [13].

3.1 Dark realization of genetic code

The first TGD view about this is based on the dark realization of the genetic code [15] (see `http://tinyurl.com/jgfjlbe`). This relies on general vision that dark matter and magnetic flux tubes - magnetic body (MB) - controls the biochemistry and that biochemical realization need not be complete.

1. TGD proposal is that dark proton sequences - dark nuclei - at magnetic flux tubes parallel to DNA strands provide the fundamental realization of the genetic code. Dark proton triplets would represent the analogs of DNA, mRNA, tRNA, and AAs. There would be 64 DDNAs, 64 DmRNAs, 40 DtRNAs and 20 DAAs. Dark codon cannot be separated to a product of letters but is an entangled state of 3 dark protons. There is a linguistic analogy: in primitive languages entire words are holistic basic units having no decomposition to letters.

2. DDNA, dmRNA, dtRNA, and DAA would control their biochemical variants and would be associated flux tubes carrying dark proton sequences. Dark code would dictate what happens at the chemical level. Chemistry would be a shadow of dark dynamics. Transcription and translation would take place at dark level.

One can argue that this assumption is too strong. It requires that also the Stop codon codes for DAA and this in turn requires at the level of chemistry to an analog of tRNA attaching to the Stop codon. For standard realization of the genetic code there are indeed 2 release factors RF1, RF2 which are proteins not involving RNA (see `http://tinyurl.com/ydcgnlb3`) attaching to Stop codons and stopping the translation. RF1 recognizes UAA and UAG. RF2 recognizes UAA and UGA.

There is also release factor RF3 binding to GTP (not appearing in RNA) and leading to a dissociation of RF1/RF2 after peptide release. Therefore RF3 does not play a role of tRNA. Note that both release factors recognize UAA so that the map from RNA codon to release factor is 1-to-2.

The 1-to-many character of mRNA-AA association requires hidden degrees of freedom for DDNA affecting the genetic code by changing DAA $\rightarrow$ ordinary AA pairingat the level of chemistry.

3. If there is **no** homonymy at the dark level, one would have the following picture to start with.

   Remark: One could of course ask whether the dark variants of the 3 codes unique - are there several dialects possible already at this level. The degeneracies of dark codons coding for dark codon at lower levels down the ladder DNA-mRNA-tRNAA-As are unique but how many codes satisfying this condition are possible? In the sequence dark code is however assumed to be universal.

   (a) Dark genetic code decomposes to a sequence of three many-to-one codes without context dependence/homonymy: DDNA $\rightarrow$ DmRNA, which is 1-to-1, DmRNA $\rightarrow$ DtRNA, which is 64-to-40 and DtRNA $\rightarrow$ AA, which is 40$\rightarrow$ 20.

   (b) Chemical representation of dark variants of biomolecules is induced by the dark-chemical pairing, which can be context dependent to some degree. This in turn would induce context dependence of mRNA-tRNA pairing and possibly tRNAA-A pairing and as a consequence also that of mRNAA-A pairing. It is important to notice that the DX-X pairing involves transformation of dark photons to ordinary photons. The proposal is that the ordinary photons are bio-photons with much higher frequencies. The transition reducing the value of $h_{eff}/h = n$ would allow energy preserving transformation of extremely low frequency photons with large n and to bio-photons inducing molecular transitions.

   Remark: mRNA-AA correspondence is basically induced by DAA $\rightarrow$ AA correspondence.

   (c) One could say that there are several dialects each free of homonymies in their own context. Even the genes or the two strands of DNA might speak different dialects. What could be the quantum physics behind these dialects? At which level one can find the contexts causing the dialects? In TGD framework magnetic body (MB) carrying dark matter suggest itself.

   One can ask whether DDNA and DRNA, and maybe DtRNA and DAA could have a context defined by internal degrees of freedom, which varies in the situation when same DNA/RNA codes for 2 different AAs or AA and stopping sign. Magnetic body (MB) would naturally give rise to these new integral degrees of freedom.

3.2 The notion of magnetic body carrying dark matter and resonance as a mechanism of pairing

Pairing is the basic mechanism of molecular biology appearing in DNA replication, translation, and transcription. Pairing could be based on resonance coupling by dark photons propagating along magnetic flux tubes connecting the pairing systems.

The pairing between DDNA and DmRNA and DDNA and ordinary DNA would rely on resonance. More generally both dark and ordinary variants of the basic biomolecules would be characterized by collections of frequencies and if the frequencies are same the objects pair with each other. The 3-letter structure of the genetic codon suggests that resonance coupling occurs simultaneously for 3 frequencies defining the 3-chord. The pairing objects able to pair must be characterized by same the 3-chord.

1. DDNA, mRNA, tRNA, and AAs would pair horizontally. These horizontal pairings together with vertical pairings of dark molecules to their ordinary counterparts (DDNA →DNA, DmRNA → mRNA- DtRNA → tRNA, DAA → AA would induce the horizontal pairings of DNA, mRNA, tRNA, and AAs.

2. All these pairings would rely on resonant coupling and the structure of codons suggests that 3-chords of frequencies are involved.

3. The first idea was that there is no context dependence at the level of horizontal pairings. It turned out that there are naturally 3 different DmRNA-DtRNA pairings for a given harmony for mRNA. This induces context dependence at the level of chemistry and would due to variation of the collection of 3-chords characterizing DtRNA.

3.3 The geometric model for music harmony and genetic code

For some years ago I developed a model of music harmony [13] (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 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. 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 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 notice 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. It turns out that 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 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. 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. Since music expresses emotions and produces them, the proposal is that these

harmonies correspond to different molecular emotional states. The fundamental realization could be in terms of dark photon triplets replacing phonon triplets for ordinary music. Geometrically the two codes can be described as attachment of tetrahedron to icosahedron along face or as union of the two. Icosahedron corresponds to 60 DNAs and tetrahedron to 4 DNAs.

During writing of this article I learned that the number of harmonies could be different, probably larger. There is however the question of the chemical realizability of the harmony: it is not at all clear whether there exist biomolecules to which the 3-chords of several harmonies could couple resonantly.

4. As I developed the model of bio-harmony [13] (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. AAs correspond to single 20-codon code, DNA and RNA to 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.

   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.

3.3.1 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 coding 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.

3.3.2 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?

3.3.3 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 [13] 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).

3.3.4 Could harmonies form a Hilbert space

The condition that there are no common 3-chords brings in mind orthogonality and suggests that harmonies as Hamiltonian cycles could be defined as quantum states in suitable Hilbert space.

1. One could define inner product for Hamiltonian cycles as the number of common chords suitably normalized so that the norm of cycle of cycle equals to one. The number of common chords in the norm squared is 20 in the icosahedral case and 24 for the fusion of icosahedral and tetrahedral codes. Could Hilbert space picture for cycles make sense? The fusion of 2 (tRNA) or 3 (DNA) codes does not however naturally correspond to quantum superposition but rather tensor product.

2. Could one think that each cycle correspond to a 20-fermion product state with 3-chord characterizing the state of given triangle created by fermionic oscillator operator so that product P of 20 fermionic oscillators assignable to the triangles would create the harmony? The fusion of cycles C_1 and C_2 would be obtained by product P_1P_2. By fermionic statistics the resut would be zero if there are common cycles.

These considerations are purely formal and have no implications for what follows.

3.4 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, 10]. 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 [13] is correct, the symmetries for the model of music harmony must 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.

3.5 What distinguishes between codons and anti-codons and between DNA and RNA?

The icosahedral model should provide answer to several questions not considered yet.

1. The model for the genetic code in terms of dark proton sequences both DNA and RNA are predicted. This should be the case also in the icosahedral model. The 3-chords for DNA and RNA should be the same but there should be some inherent distinction between the two realizations.

2. Besides the active DNA strand there is also the inactive DNA strand (no transcription to mRNA) consisting of anti-codons. What does anti-strand correspond in the representation consisting of 3-chords? The chords assignable to the anti-strand should exist but there should be some difference between chords and anti-chords. Why this strand is inactive? mRNA is produced only via the

pairing of RNA codons with active DNA strand. Could RNA_t as part of tRNA and counterpart of anti-RNA be unable to form stable strands in the recent biological environment and could lonely RNA_t codons fail to exist stably so that the transcription of DNA anti-strand to RNA_t strands would be impossible.

3. What does anti-DNA anti-RNA and anti-tRNA mean at the level of dark proton sequences?

I have approached these problems from particle physics point of view by using analogies and they might be helpful in the attempts to answer these questions [10]. There are two mirror symmetries in the icosahedral harmony: 3-D reflection with respect to origin and change of the direction of the 12-note scale. Could these reflection symmetries help to understand the situation?

1. The symmetry mapping letters to antiletters (T $\leftrightarrow$ A, G $\leftrightarrow$ C) is mirror symmetry like charge-parity symmetry CP of particle physics equivalent with time reversal T by CPT theorem. CP is mysteriously broken: we have matter but where is the antimatter?

   The biological analogy with matter-antimatter asymmetry is that strand is active but anti-strand is passive - no transcription to mRNA. This would be the case if anti-RNA does snot exist as stable sequences. This would also explain why RNA does not replicate and does not form stable double helices.

2. Codons and conjugate letters for DNA are related by the CP like transformation (T $\leftrightarrow$ A, G $\leftrightarrow$ C). There should exist an icosahedral symmetry realizing this symmetry. Icosahedron allows also 3-D reflection through the origin as a symmetry (see `http://tinyurl.com/y8capjz7`). It permutes the opposite faces of icosahedron and extends the icosahedral rotation group with 60 elements to a group with 120 elements. The extended symmetry should preserve the set of 3-chords: they should be identical for DNA codon and anticodon.

   Harmony and anti-harmony for DNA would differ in that the attached tetrahedron would be at opposite face for the anti-codon representation since the reflection maps the tetrahedron to the opposite face. Could one see this as an analog of matter antimatter asymmetry? For double DNA strand anti-codons would correspond to icosahedron with tetrahedron attached to the opposite face. This symmetry should map the codons to their anticodons and there should be no fixed codon - this is indeed the case since there are no fixed faces.

   Icosahedral reflection should however leave the chords invariant apart from transponation by some power of 3/2 in order to leave the harmony invariant: codons and anticodons would be in different key in order to resonate. Icosahedral reflection would be an additional symmetry of the Hamiltonian cycles. The tetrahedron attached to the opposite face in reflection would be shifted back in transponation.

mRNA should have icosahedral realization with same 3-chords. What distinguishes mRNA from DNA at icosahedral level? Could only mRNA exists as stable sequences and anti-mRNA fails to exist in this manner? This would be analog of CP breaking and the codons RNA_t in tRNA would correspond to anti-RNA_t existing only as single codon attached to AA. Could also the 4 tetrahedral anticodons for RNA_t (anti-tRNA) fail to exist (this would give 40 tRNA codons as also dark proton model predicts). Otherwise one would have 44 RNA_t codons.

DNA and mRNA differ only in single aspect: the letter T is replaced with letter U. How the replacement of U $\rightarrow$ T (and the replacement of riboses with de-oxy-riboses) is visible in the icosahedral harmony if the set of chords remained the same? Why RNAs would have resonant 3-chord coupling with the dark variant of RNA but not with that of dark variant of RNA if the chords are same.

Could the order of notes along the Hamiltonian cycle distinguish between DNA and RNA? The chords would remain the same but the order of notes in the chord would change.

1. If the reversed scale proceeded downwards in quarts (quint backwards, say C-G to C-G), the 3-chords would be same for the scales and the two scales are identical. Could one imagine that 3-chords are "played" as arpeggios! The order of arpeggio (upwards downwards in scale) would be opposite for up-chord and down-chord. RNA_t would define down-chords for mRNA up-chords but they would not form stable sequences and 4 anti-chords might be even missing.

2. If it proceeds in quints, the chords for the harmonies would not be same in general (for instance C-G upwards quint is replaced with C-F downwards quint). The scalings $(3/2)^k$ are replaced by scalings $(3/2)^{12-k}$ and the cycle becomes mirror image retaining its shape so that it is still a cycle and since the shape is preserved the symmetries are preserved too. Chords are in reflected positions and related by the map $(k_1, k_2, k_3) \to (12-k_1, 12-k_2, 12-k_3)$. The chords are obviously different so that DNA and mRNA cannot differ in this manner.

   The scale and its quint-reversed counterpart differ much like major and quint scales as one easily finds (consider only the upwards scale Cmajor scale $CDEFG...$ in C major and the downwards Cminor scale $CB\flat A\flat G...$). They could therefore correspond to two different moods rather than mRNA-RNA.

3. TGD and TGD inspired theory of consciousness bringing observer part of physical system relies on zero energy ontology (ZEO). In ZEO the scale and its quint reversal could correspond to two different arrows of time for zero energy states. As self dies in state function reduction to the opposite boundary of causal diamond (CD), it is predicted to reincarnate with reversed arrow of time [18]. Death is a sad event: could it be that the death of sub-self representing mental image is experienced by self as sad event and that in bio-harmony time reversal would change joy to sadness?

This relates in an interesting manner to the earlier speculations in TGD inspired view about pre-biotic life.

1. The proposal made in [10] is that during RNA era preceding DNA era RNA replicated and AAs associated with pre-tRNA served as catalyst and later stole the stage so that RNA replication became translation. The greatest betrayal in the history of life! At this moment also DNA had to emerge. Otherwise RNA and life would have disappeared.

   Amusingly, also in cosmology CP symmetry was broken, when antimatter and matter annihilated and what remained was matter (there was slight imbalance originally).

2. Could one think that before the breaking of the analog of CP symmetry the tetrahedral part of the code was not present and the number of mRNA codons was 60. mRNA and anti-mRNA realized as mRNA_t had common chords related by icosahedral reflection symmetry. Also the 1st letter of mRNA_t was just like the other letters.

   In the transition A and C as 1st letters disappeared and were replaced with G,U and I (in Watson-Crick scenario). The 4 tetrahedral codons containing Start and Stop codons emerged in the transition.

   In the symmetry breaking DNA with opposite direction of the scale (the reversed scale proceeded downwards as quarts rather than quints) and arpeggios emerged. Perhaps this required the replacement of U with T and perhaps also of riboses with de-oxy-riboses.

3. Was the letter mRNA letter U replaced with DNA letter T in this transition. Did this make possible the existence DNA as double strands but not stable as single strands but only in presence of cell membrane. Did the 4 additional tetrahedral codons responsible for the breaking of the analog of isospin symmetry (A $\leftrightarrow$ G and T $\leftrightarrow$ C) associated with the stop and Start codons emerge in this transition. Before the transition the entire mRNA strand was able to replicate. mRNA-AA pairing was present and AA served as a catalyst for replication.

4. Did the 4 additional tetrahedral codons responsible for the breaking of the analog of isospin symmetry (A $\leftrightarrow$ G and T $\leftrightarrow$ C) associated with the stop and Start codons emerge in this event so that 60-codon realization of the code was replaced with 64 codon realization. If Start and Stop emerged in this event the entire mRNA strand replicated before it.

5. Was the letter mRNA letter U replaced with DNA letter T in this transition. Did this make possible the existence DNA as double strands stable in the presence of nuclear or cell membrane but not stable as single strand. Did the 4 additional tetrahedral codons responsible for the breaking of the analog of isospin symmetry (A $\leftrightarrow$ G and T $\leftrightarrow$ C) associated with the stop and Start codons emerge in this transition. Before the transition the entire mRNA strand would have been able to replicate. mRNA-AA pairing was present and AA would have catalysed the replication.

6. Was the homonymy present in mRNA replication before the transition. The updated scenerio for mRNA-tRNA correspondence allows the replication albeit not in 1-1 manner (see `http://tinyurl.com/y73se8vs`). Was the letter I present at that period: was it part of both mRNA and rNA$_t$ or of only RNA$_t$ giving therefore rise to a leakage?

If RNA era in the proposed sense was realized, what happened before it?

1. One imagine that before RNA era the RNA$_t$ - not necessary identical with its recent form - as a realization of 2-harmony (or perhaps of all 3 different types of 2-harmonies) with 40 codons was realized and was able to replicate with AAs serving as catalysts attached to RNA$_t$.

   Only the complementary RNA$_t$ was able to appear as sequences: tetrahedral codons were absent. In the transition from 2-harmony to 3-harmony both DNA and full RNA emerged. Replication of RNA$_t$ transformed to translation of AAs. This vision would be more in spirit with the idea about the gradual emergence of biological representations of the dark variants of biomolecules.

2. One could go even further and ask whether this period was preceded by a period during which pre-tRNA identifiable as single 20-codon representation choosable in 3 manners. Pre-tRNA $\leftrightarrow$ AA correspondence would have been 1-1. AAs would have decomposed to three types corresponding to these 3 choices. For instance for the code with Z_6 symmetry only 4 AAs would have been present. For the details of harmonies see the Appendix of [13] (see `http://tinyurl.com/yad4tqwl`).

4 Context dependence from TGD point of view

The original idea was that context dependence and homonymy are absent at the level of dark variants of various codons and AAs and would result from the pairing with chemical counterparts of dark codons. More precisely: the horizontal dark DX-DY pairings would be context independent and would not depend on emotional state whereas the vertical DX-X pairings are induced by DX-DY pairings and induce X-Y pairings. This is obviously something new from the point of biology as chemistry paradigm.

It however turned out that the context dependence appears very naturally at the dark level. DtRNA bio-harmony allows naturally 3 different representations as 2-harmonies realized as sub-harmonies of 3-harmony associated with DNA and mRNA. One would have 3 basic context already at this level.

One can imagine at least 3-sources of context dependence and expression of emotions by gene expression.

1. Several bio-harmonies are possible and DX and X would couple by different resonant 3-chords for each harmony. It is of course possible that very few of these bioharmonies - perhaps only one - are realized at the level of DNA and mRNA. This would explain the uniqueness of DNA and mRNA codons in biological sense.

   If several bioharmonies are realized for DNA then both mRNA, RNA$_t$ and AA must have resonance couplings to all these bioharmonies. For AA this is satisfied if $f_{XYZ} = f_1 + f_2 + f_3$ is same (perhaps

modulo octave equivalence) for all harmonies involved or if AA has all all the frequencies f_{XYZ} as resonance frequencies. For mRNA $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$ pairing would require even larger spectrum of resonant 3-chords at the level of chemistry. Hence it is quite possible that only single 3-harmony is realized for DDNA, DmRNA, and DAA. If several harmonies are present, the evolution would have gradually invented the biomolecules having the needed spectrum and would still be in progress.

2. The situation with DtRNA is different. The DmRNA-DtRNA pairings would involve 3 different unions of 2 20-chord harmonies. This choice implies context dependence already at dark DNA level and could be the fundamental reason for mRNA-tRNA homonymy. What is however important that the decomposing of tRNA to (RNA_t,AA) pairs guarantees automatically genetic code via $f_{XYZ} = f_1 + f_2 + f_3$ coupling. AA dictates the pairing unlike usually thought.

3. If the frequencies are cyclotron frequencies determined by the magnetic fields at flux tubes, the variation of magnetic field strength due to the variation of flux tube thickness changes the frequency scale. This could be also seen as emotional expression (in analogy with membrane potential in biology inducing variation of Josephson frequencies and varying the degree of alertness in neurons).

   The gradual variation of magnetic fields strengths during evolution could explain the slight differences in the genetic code. Evolution would be clearly in question in the sense that the symmetries of the code are maximal for the nuclear code. It will be found that also this mechanism is needed in order to understand all deviations of the code.

4.1 Context dependence as "emotional expression" at molecular level?

Using the attribute "emotional" certainly raises eyebrows and I will drop even the quotation marks in the following. Reader can freely add them.

4.1.1 Basic guide lines

Consider first the basic guidelines

1. One plausible possibility is that genetic code as DNA-AA pairing is unique in given context - whatever it is physically - but there exist what one might call dialects just like slight modifications of vertebrate genetic code. There is homonymy, which however disappears when context is taken into account: same mRNA can correspond to two AAs or AA and stop. The homonymy is associated with mRNA-tRNA pairing for the third mRNA letter which is many-to-one and 1-to-many. Which the actual choice depends on context as in ordinary language.

2. Wobble base pairing is the model explaining both the many-to-1 and 1-to-many pairings. An interesting finding is that for 32 codons the pairing does not depend on third letter at all. I have proposed long time ago a model in which 2-letter code emerged first and then fused with 1-letter code to give 3-letter code. A more plausible interpretation is as activation of the 3rd letter in 3-letter code. The wobble base pairing and homonymy would have emerged in this fusion of codes.

3. From the tables of Wikipedia at article (see `http://tinyurl.com/y73se8vs`) for standard code one can read when the pairing of the third letter is many-to-one and 1-to-many. If it is 1-to-many and unless the resulting tRNA anticodons correspond to the same AA, the outcome can be several AAs.

   This does not lead to 1-to-many mRNA $\to$ AA if the RNAs associated with tRNAs in mRNA $\to$ tRNA pairing couple with the same AA. The pairing between mRNA and AAs is 1-to-many rather rarely and could be accidental. It seems that there is a principle taking care that the deviations from the standard code get minimized.

4. The homonymy for mRNA-AA pairings is very rare. This suggests that it is accidental and disappeared during the evolution.

4.1.2 The origin of mRNA-tRNA homonymy and mRNA-AA homonymy

mRNA-tRNA homonymy is clearly exceptional and the proposal that tRNA bio-harmony corresponds to a fusion of 2 20-chord codes together with the fact that there are 3 basic types of these codes could explain this.

1. Suppose that DtRNA harmony corresponds to a sub-harmony of full bio-harmony for DDNA and DRNA as a fusion of two sub-cycles from the union of 3 cycles defining DDNA and DRNA harmony. One can make this choice in 3 manners corresponding to the choices (Z_6, Z_4), (Z_6, Z_2) and Z_4, Z_2. These 3 basic choices would naturally explain the DtRNA-tRNA homonymy without the dependence on emotional state. This would not however explain the deviations from the standard code.

   In the case DtRNA- tRNA pairing it is enough that tRNA couples resonantly only to the 3-chord representatives associated with one 2-harmony appearing as sub-harmony of 3-harmony that is selected and defines the context. This obviously allows larger number of tRNAs satisfying the resonance conditions. This could relate to the homonymy.

   The function of tRNA as an agent transferring DAA-AA pair and attaching it to DmRNA-mRNA pair. Hence tRNA homonymy is desirable - it can happen that the concentration of particular certain kind of tRNA is low so that second kind of tRNA coupling to same mRNA can handle the job.

2. tRNA homonyms for the first anticodon of tRNA would reflect the emotional state of DDNA/mRNA. Why only the third? This might relate to the idea about fusion of 2-letter codes and 1-letter codes. For 2-letter code there would be no "emotional expression" and no context dependence. The emergence or perhaps better, the activation of additional letter at the level of chemical expression, would have brought in the chemical emotional expression.

Consider now mRNA-AA homonymy. This homonymy is rather rare and could be accidental.

1. If AA couples to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of the frequencies characterizing the codon $X_1Y_1Z_1$, it can happen that one has $f_{X_1Y_1Z_1} = f_{X_2Y_2Z_2}$ modulo octave multiple so that besides codon $X_1Y_1Z_1$ also the wrong codon $X_2Y_2Z_2$ codes for the same AA. Of course, this condition might hold true only approximately. This could explain mRNA-AA homonymies as accidental.

2. There is however an objection against the proposal. If the frequencies f_{XYZ} are identical in octave equivalence for all codons coding for AA, the accidental degeneracy would suggests that the entire mRNA multiplet containing $X_2Y_2Z_2$ codes for AA. Typically however only one member of the mRA multiplet codes for wrong AA.

   Should one give up the idea that the members of mRNA multiplet satisfy $f_{X_1Y_1Z_1} = f_{X_2Y_2Z_2}$. If so, AA would have the frequencies f_{XYZ} of mRNA multiplet as distinct resonance frequencies. For instance, could one think that the A-G and T-C breakings at the level of frequencies are present although they are not large enough to make themselves visible in the mRNA-AA correspondence (say for the mRNA 4-plets coding for same AA). This is the case if AA has all these frequencies as resonance frequencies. Also the number of octaves distinguishing between $X_1Y_1Z_1$ and $X_2Y_2Z_2$ matters somewhat. In this case the accidental resonance condition for wrong AA could be satisfied for single member of mRNA multiplet only.

4.1.3 A concrete objection against the model

One can try to understand the possible dependence of code on the emotional state by looking the numbers of 3-harmonies obtained as fusion of Z_6, Z_4 and Z_2 symmetries. One can find explicit tables for the codes in the Appendix of [13] (see `http://tinyurl.com/yad4tqwl`).

1. A crucially important thing to notice is that Z_6 harmony is unique. This harmony allows 3 6-plets for which 6 DNAs code for single AA. There is also one doublet. Therefore the codons associated 3 6-plets and doublet should always code the same AA unless the magnetic fields at flux tubes determining the cyclotron frequencies van vary. It is easy to verify that this prediction is correct for the nuclear code.

   For non-nuclear codes the situation is different. There are 3 6-plets and they code for Leu, Ser, and Arg. These 6-plets should be stable under the modifications of the standard code. This rule is however broken in at least two cases:

   (a) For CUG coding for Ser instead of Leu. Ser is coded usually by UCG. Both DAA and AA couple to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of the 3-chord frequencies. The simplest explanation already discussed is that DSer and DLeu have accidentally $f_{CUG} = f_{UCG}$ modulo octave multiple. T

   (b) UUG coding for Stop rather than Leu. Stop is coded usually by UGG. Accidental degeneracy would be the explanation also now. Stop identified as release factor FR1 or FR2 playing the role of AA and possibly having also dark AA counterpart would have $f_{UGG} = f_{UUG}$.

2. All deviations from the standard code could be determined solely by the accidental degeneracies for the frequencies f_{XYZ} associated with two codons coding for different AAs or AA and stop. For standard code they would have been eliminated almost completely by evolution: as noticed earlier, even in human mitochondrial code there is this kind of homonymy.

3. For 3-chords with Z_4 as isometry group one has 2 different harmonies, which means non-trivial conditions on DNA and mRNA since the 3-chords of all these harmonies must act as resonance chords. In principle homonymy becomes possible for DDNA $\rightarrow$ DNA and DmRNA $\rightarrow$ mRNA pairings but is not realized. Either coupling to both harmonies is possible or there are no DNAs or mRNAs coupling resonantly to all 3-chords of either harmonies so that only 1 harmony is realized completely. This is important if one requires uniqueness of the genetic code.

4. For 3-chords having Z_{rot} isometries there are 3 harmonies and for Z_{refl} 5 harmonies. This gives increasingly stronger conditions on resonant couplings. The uniqueness of the code suggests that only a subset of possible harmonies is possible. Also the probability of homonymy for DAA-AA pairing increases and might explain 21st and 22nd AAs Pyl and Sec coupling to non-standard representation. Deviations typically occur for the doublets as indeed found.

What is interesting that if one loosens the conditions and allows different couplings and allows several 3-harmonies, it is in principle possible to have larger number of DNA and mRNA codons than usually. Also analogs of AAs can be considered. Frequency coding relates interestingly to extended genetic codes with 4 or 5 codons (see `http://tinyurl.com/ycsfgu7n`) and nucleic acid analogues (see `http://tinyurl.com/y8tj8hsm`).

4.2 Is the notion of reading frame consistent with the proposed realizations of the genetic code?

Reading frame (see `http://tinyurl.com/yb6wr3d7`) represents also a context dependence of the code. Reading frame begins with the Start codon and new reading frame can begin at second or third letter of codon. There must be also Stop after $3 \times n$ letters also in the new reading frame.

Shifting of reading frame by 1 or 2 units can take place for viral, prokaryote, and mitochondrial genomes but for some reason not in nuclear genome. Shift makes sense if the first codon is Start codon. For human genome MT-AOT8 and MT-ATP6 are examples of reading frames for mitochondrial genes coding for different proteins. The interesting question is why the shift occurs only at the level of viruses, prokaryotes, and mitochondria and chloroplasts.

Does the notion of reading frame make sense for the two models of genetic code? Consider first the representation of 64 codons as 3-chords. If all 64 codons are are realized as chords, shift does not produce chords not belonging to the harmony. Since the notes of chords cannot correspond to the letters the shift is highly non-trivial since it is not only shifted decomposition of notes to triplets but change also the notes.

Is this possible at the level of DmRNA? At the dark level code words do not have decomposition to letters. Dark proton triplets should re-organize in a new manner into triplets. If the dark protons inside proton triplet are connected by colored bonds to form color singlet, the shift would produce colored 3-proton states unless also the color structure of the states is re-organized so that it is consistent with the shift at the level of codons. Kind of phase transition would take place and induce the change of the reading frame.

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