Progress in the understanding of the icosa tetrahedral realization of the genetic code

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Abstract

TGD leads to two models of the genetic code. The first model emerges from a model of music harmony based on the combination of icosahedral and tetrahedral geometries. The second model relies on the representation of the genetic codons as entangled triplets of dark protons at the monopoles flux tubes defining the dark variant of DNA accompanying the ordinary DNA.

It took quite a long time to understand why both icosahedra and tetrahedra are needed and how the two models are related. The solution of the puzzle came from a universal model of the genetic code based on a completely unique tessellation of 3-D hyperbolic space H^3 realized as the light-cone proper time constant hyperboloid of the Minkowski space. This icosa tetrahedral tessellation (ITT) (known also as tetrahedral-icosahedral tessellation) makes sense in all scales and I have proposed its realization at the level of DNA. The model involves several intuitive elements and the best way to proceed is to try to improve the existing understanding and to identify the possible weaknesses of the model.

This article provides an answer to the question how many icosahedrons, octahedrons and tetrahedrons meet at the vertex of ITT: the answer comes by studying the vertex figure of ITT: these numbers are 12, 30, and 20. The study of the vertex figure of ITT suggests that the ITT can be constructed as a "blow-up" of the icosahedral tessellation (IT) by replacing icosahedral vertices with tetrahedra and dodecahedral vertices by pentagons and adding between icosahedral tetrahedra and dodecahedra octahedra as analogs of edges. Icosahedral and dodecahedral bioharmonies correspond to 12-note *resp.* assignable to Western *resp.* Eastern music. One can ask whether octahedral 4-codons should also be allowed.

The picture provided by RID is consistent with the earlier notion of "super-icosahedron". The model of the genetic code generalizes: besides the icosahedral Hamilton cycles (HCs) and codons for the three icosahedral codes and the tetrahedral HC and corresponding codons, also a unique dodecahedral HC and associated 5-codons plus pentahedral HC and codons are in principle possible. The fundamental region deduced from RID corresponds to a sequence of 10 or 12 DNA codons as proposed already earlier on the basis "super-icosahedron model".

The model allows us to understand the symmetry breaking of genetic codons. In particular, tetrahedral codons correspond to 3 stop codons and the codon coding for trp. A given codon corresponds either to I/T or D/pentahedron. The fundamental region represents a sequence of 10 or 12 DNAs so that all codons of the Hamiltonian cycle are used and the HC corresponds to a section of DNA. Fundamental region represents both DNA strands.

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1 Introduction

TGD leads to two models of the genetic code. The first model emerges from a model of music harmony based on the combination icosahedral and tetrahedral geometries [K1] [L2]. The second model relies on the representation of the genetic codons as entangled triplets of dark protons at the monopoles flux tubes defining the dark variant of DNA accompanying the ordinary DNA [L1].

It took quite a long time to understand why both icosahedra and tetrahedra are needed and how the two models are related. The solution of the puzzle came from a universal model of the genetic code based on a completely unique tessellation of 3-D hyperbolic space H^3 realized as the light-cone proper time constant hyperboloid of the Minkowski space. This icosa tetrahedral tessellation (ITT) (known also as tetrahedral-icosahedral tessellation) makes sense in all scales and I have proposed its realization at the level of DNA in [L4]. The model involves several intuitive elements and the best way to proceed is to try to improve the existing understanding and to identify the possible weaknesses of the model.

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I am not a professional hyperbolic crystallographer and my view of ITT (see this) relies on guesswork guided by physical and biological intuition based on what I call icosa tetrahedral model for the genetic code. In this article I represent some results based on using standard results from Platonic solids to deduce the numbers of tetrahedrons, octahedrons and icosahedrons emanating from a given vertex of the tessellation. The study of the vertex figure of ITT leads to a rather plausible guess for a manner to obtain ITT as a "blow-up" of icosahedral tessellation (IT).

The improved understanding of the icosa tetrahedral tessellation allows to answer some long standing questions related to the detailed realization of the genetic code. It however turns out that the notion of the super-icosahedron discussed in [L4] is not consistent with the improved view. However the 3-D generalization of the vertex figure of the ITT as its inverse image under projection permutes the numbers for the Platonic solids appearing in the super-icosahedron.

This article provides an answer to the question how many icosahedrons, octahedrons and tetrahedrons meet at the vertex of ITT: the answer comes by studying the vertex figure of ITT: these numbers are 12, 30, and 20. The study of the vertex figure of ITT suggests that the ITT can be constructed as a "blow-up" of the icosahedral tessellation (IT) by replacing icosahedral vertices with tetrahedra and dodecahedral vertices by pentagons and adding between icosahedral tetrahedra and dodecahedra octahedra as analogs of edges. Icosahedral and dodecahedral bioharmonies correspond to 12-note *resp.* assignable to Western *resp.* Eastern music. One can ask whether octahedral 4-codons should also be allowed.

The picture provided by RID is consistent with the earlier notion of "super-icosahedron". The model of the genetic code generalizes: besides the icosahedral Hamilton cycles (HCs) and codons for the three icosahedral codes and the tetrahedral HC and corresponding codons, also a unique dodecahedral HC and associated 5-codons plus pentahedral HC and codons are in principle possible. The fundamental region deduced from RID corresponds to a sequence of 10 or 12 DNA codons as proposed already earlier on the basis "super-icosahedron model".

The model allows us to understand the symmetry breaking of genetic codons. In particular, tetrahedral codons correspond to 3 stop codons and the codon coding for trp. A given codon corresponds either to I/T or D /pentahedron. The fundamental region represents a sequence of

10 or 12 DNAs so that all codons of the Hamiltonian cycle are used and the HC corresponds to a section of DNA. Fundamental region represents both DNA strands.

2 More precise views about some aspects of the icosa tetrahedral realization of the genetic code

The improved understanding of the icosa tetrahedral tessellation allows to answer some long standing questions related to the detailed realization of the genetic code.

2.1 What does the fundamental domain of ITT look like?

One basic question is how many tetrahedra (T), icosahedra (I) and octahedra (O) emerge from a given vertex of ITT.

2.1.1 The first guess was wrong as always

The wrong guess was that one can answer this question just from the knowledge of the solid angles associated with vertices of these Platonic solids. The solid angles are naturally defined as ratios of spherical areas to the radial distance squared and at the limit of very small hyperbolic radial distance approaching Euclidean distance, the total solid angle at this limit is 4π as in the Euclidean case.

However, the metric in the radial direction is non-Euclidean for the negatively curved hyperbolic 3-space H^3 the edges from the vertex diverge whereas in Euclidean spherical geometry they converge. Note that H^3 has 3-D rotation group as isometries so that the notion of Platonic solid applies also in H^3.

The lines emanating from the vertex are shared by neighboring T, O, and I emanating from the vertex. Two neighboring lines are associated with a triangular face shared by two Platonic solids involved.

The basic condition for the numbers $n(i)$ of the Platonic solids involved is $\sum_{i\in\{T,O,I\}} n_i\Omega_i = 4\pi$. Consider first the *Euclidean* case. One can find the general formulas for the solid angles from Wikipedia (see this).

1. Platonic solids are classified by 2 integers $\{q,p\}$ stating that q $p-$polygons meet at a given vertex. In the recent case one has only 3-polygons, that is triangles, for all Platonic solids involved. One has

$$[q(T),q(O),q(I)] = [3,4,5] \quad , \quad [p(T),p(O),p(I)] = [3,3,3] \quad .$$

2. Dihedral angle angle is the interior angle between the faces of the Platonic solid and satisfies the general formula

$$\theta(q,p) = 2asin(\frac{cos(\pi/q)}{sin(\pi/p)}) \quad .$$

In the *Euclidean* case the solid angle at the vertex is given as

$$\Omega(q,p) = q\theta(q,p) - (q-2)\pi \quad .$$

3. Suppose that all vertices are identical as the fact that there is only a single vertex figure. The vertex of vertex figure, call it V, involves $n(T) \equiv n(3)$ tetrahedrons, $n(O) \equiv n(4)$ octahedrons and $n(I) \equiv n(5)$ icosahedrons. The sum of the solid angles equals to 4π, which gives

$$\sum_{q\in\{3,4,5\}} n(q)[q\theta(q,3) - (q-2)\pi] = 4\pi \quad .$$

This gives

$$\sum_{q\in\{3,4,5\}} n(q)\ qasin(\frac{cos(\pi/q)}{sin(\pi/p)}) - (n(3)+2n(4)+3n(5))\pi = 4\pi \ .$$

4. In the Euclidean case, one can guess the solution to the condition by starting from the icosa tetrahedral model [L1, L2] for the genetic code, which is a fusion of 3 icosahedral codes associated with Hamiltonian cycles (HCs) with symmetry groups Z_6, Z_4, Z_2 and of a single tetrahedral code defined by the unique tetrahedral HC. In the proposed model based on ITTs [L3, L4], the octahedron is passive and does not contribute to the code. A reasonable guess based on this model is $n(I) = 3$ and $n(T) = 1$.

   The normalized vertex solid angles are

   $$\frac{[\Omega(3), \Omega(4), \Omega(5)]}{4\pi} = [0.043871, 0.1082, 0.2097] \ .$$

   The consistency condition is

   $$\frac{n(T)\Omega(T) + n(O)\Omega(O) + n(I)\Omega(I)}{4\pi} = 1 \ .$$

   This leaves only the guess $[n(T), n(O), n(I)] = [1, 3, 3]$ under consideration giving for the sum the value 0.9974 in the accuracy used partially determined by the approximation $\pi \simeq 3.1415926535897$.

2.1.2 The vertex figure for ITT contains the needed information

The vertex figure V codes the information about the fundamental domain as one can easily see in the case of say cube. Consider now the vertex figure V for ITT.

1. The vertex figure is obtained by cutting a 3-sphere around a vertex is a 2-D object to which the vertices as edges and faces of the fundamental region of the solid are projected. For ITT, the vertex figure is rhombicosidodecahedron (RID) (see this). This is an Archimedean solid, one of thirteen convex isogonal nonprismatic solids constructed of two or more types of regular polygon faces.

   RID has *20 disjoint triangular* faces (as also I has), *30 square* faces , which share their corners with other square faces, *12 disjoint pentagonal* faces (as D has), 60 vertices, and 120 edges. The numbers of faces are much larger than in the Euclidean case.

   The 20 triangular faces correspond naturally to intersections of 20 T:s with the sphere, the 30 square faces to the intersections with 30 octahedra, and 12 pentagons to the intersections with 12 icosahedra. From V one finds squares and common edges with triangles and pentagons.

2. The illustrations of RID (see this) gives a 2-D analog for what it means that the tessellation has different 3-D Platonic solids as building bricks. Interestingly, the faces of RID are faces of the duals of the Platonic solids T, O and and I. In RID the triangles are disjoint and share sides with squares.

   Since RID and ITT are combinatorially closely related, this suggests that the disjoint triangles of RID correspond disjoint T:s of ITT and the squares of RID having sharing only corners correspond to O:s of ITT sharing only edges whereas D:s would correspond to I:s.

Could an analog for the construction of RID allow to deform the hyperbolic icosahedral tessellation (IT) to ITT?

1. The construction would rely on the correspondence *triangle - self dual T, pentagon - I as dual of D, square - O as dual of cube*. One could generalize the correspondence to *triangle→ T , pentagon → I, and square → O*.

   The recipe would be as follows. Start from the hyperbolic icosahedral tessellation (IT) $\{(3, 5, 3\}$ with 3 I:s $\{5, 3\}$ meeting at each edge. One could blow-up the icosahedral vertices

to T:s and glue to the faces of a given T 4 O:s. O:s would also share faces with other T:s and I:s but not with O:s if there is a combinatorial analogy with RID.

2. The inspection of the RID shows that T:s and I:s do not have common faces and meet only at V. O:s share faces with I:s and T:s. Besides the vertex figure there are also T:s,I:s, and O:s emerging from the origin. They have triangular 3 ,4, 5 triangular faces respectively and they contribute to the genetic code. Second important point is that RID contains only one half of the vertex figure. The natural interpretation would be that these halves correspond to DNA strands. This however requires that the fundamental domain is realized at the magnetic body.

3. The maximally symmetric solution to the condition $\sum_{i\in\{T,O,I\}} n_i\Omega_i = 4\pi$ would be

$$\Omega_i = \frac{4\pi}{(n(T)+n(O)+n(I))} = \frac{4\pi}{62} \quad .$$

2.2 Some progress in the detailed realization of the genetic code

ITT emerged as a mathematization of the icosa tetrahedral realization of the genetic code and it is interesting to see whether the new results allow us to gain some understanding about the issues related to the detailed realizations.

In the original vision [K1], it was unclear whether there are 3 different I:s or only a single I realizing one of the 3 HCs at time. Also the relationship between T and I was unclear. The proposal was that there is a single I and T that shares a common face with it. The idea about a common face was however somewhat fuzzy and I have discussed several ways to understand the details of the genetic code, in particular those assignable to stop codons.

Also the selection of a single active triangle as a representation of the codon was adhoc. The natural idea is that the Hamiltonian cycle selects all codons so that the fundamental region represents a portion of DNA: in fact 10 codons.

2.2.1 The revised view of the genetic code

The number 12 of pentagons is the number of the faces of D, the number of squares is the number of O:s and the number of edges of I, and the number 20 T:s is the number of faces of I. This conforms with the idea of blow-up in which vertices of I are replaced with T:s.

The structure of RID suggests a rather dramatic revision of the view about how the genetic code is realized at the level of ITT assignable to the magnetic body of DNA double strand. The interpretation that O:s serve in the role of edges is attractive and suggests that there are no codons associated with them. The role of the possible O codons as edges means that they are determined by I and D codons and that the Hamiltonian cycle for the squares is not a useful concept. Furthermore, there is no analog of edge between O codons which intersect at their corners.

This leads to the following picture.

1. Codons are associated with RID, that is with both the intersections of T:s, O:s, and I:s with the S^2 and also with the triangles emanating from the vertex V to RID. One can interpret the 20 triangles and 12 pentagons and 30 squares as potential genetic codons.

2. The notion of Hamiltonian cycle generalizes for the blow-ups and the edges of the cycle connects the blow-up vertices: 20 triangles for the blow-up of D and 12 pentagons for the blow-up of D. There are also tetrahedral with 1+3 vertices and codons with 1+5 vertices. For I:s having triangles as vertices there is a larger number of Hamiltonian cycles. For D:s having pentagons as vertices there is only one Hamiltonian cycle. Hamiltonian cycles represent a piece of DNA strand.

   Octave Equivalence implies that the frequency scaling in transition between two neighboring vertices for $2^{1/V}$, where the number of vertices is $V = 12$ *resp.* $V = 20$ for the I *resp.* D type

Hamilatonian cycle is $2^{1/20}$. This corresponds to the micro scales used in Eastern music. For the tetrahedral cycle it is $2^{1/4}$: this corresponds to the chord $C, E, G\sharp$. For its analog for D, the scaling is $2^{1/6}$.

3. RID and its mirror image needed to obtain the fundamental domain represent the 20 DNA icosahedral codons or 12 dodecahedral codons.

In [L4], I proposed a heuristic model for the 10-codon piece of DNA sequence a candidate for the fundamental region of IIT. The idea was that it corresponds to what I called super-icosahedron (SI) having icosahedrons as 12 super-edges, tetrahedrons as 20 super-faces, and 30 octahedrons as super-vertices. What is worrying is that 2 DNAs would be missing so that there would be 10 Is.

The guess was essentially correct: the RID has 20 regular disjoint triangular faces (as also I has), 30 square faces, which share their corners with other square faces, 12 regular disjoint pentagonal faces (as D has) plus 60 vertices, and 120 edges. The triplet (20 triangles, 30 squares, 12 pentagons) contains the same numbers as appear in SI. The correct identification of SI could indeed be as the fundamental domain of ITT if one glues to RIDs together (consider cube as an simple example). ITT could be seen as a 3-D combinatorial lift of RID obtained by the inverse of the projection to the sphere defining the vertex figure (triangle $\rightarrow$ T, square $\rightarrow$ O, pentagon $\rightarrow$ I): this is supported by the view what vertex figure means. Could the sequence of 12 DNAs correspond to (20 T:s, 30 O:s, 12 I:s) as the 3-D inverse image of the RID?

2.2.2 Solutions of some problems provided by the new view

The model of genetic code has suffered from some cronic problems.

1. If each vertex of IT is replaced with T in the blow-up identified as ITT, a single icosahedral triangle of IT would be replaced with 3 T:s. A natural identification is in terms of a genetic codon with 3 letters, one T per letter.

2. The icosahedral realization leads the following problem. The icosahedral HC with Z_6 symmetry corresponds to 3 Z_6 orbits with 6 triangles and one orbit with 2 triangles (6+6+6+2=20). This corresponds to 5 amino acids (AAs) identified as orbits of Z_6. The HC with Z_4 symmetry contains 5 orbits with 4 triangles ($5 \times 4 = 20$) and gives 5 AAs. The HC with Z_2 symmetry gives 10 orbits and therefore 10 AAs. One has 19 AAs altogether. One AA is missing.

3. Tetrahedral cycle involves 4 triangles and Z_3 symmetry is natural. The triangle opposite to V would give a codon coding for single AAs and the remaining triangles related by Z_3 symmetry corresponding to 3 ordinary DNA codons. The frequencies of these dark codons differ only by order and this suggests that they code for a single AA (vertex of T and the vertices opposite to it). The triplet could correspond to stop codons coding for no physical AA. The singlet codon could correspond to the missing AA, most naturally trip. Another less plausible option corresponds to (ile,ile,ile,met). One cannot interpret this multiplet as a symmetry broken quadruplet since there are 5 quartets. The interpretation as a symmetry breaking of (met,met) (ile, met) however works.

4. There are also problems related to the chemical realization of the dark code. There are several slightly different chemical realizations of the code, which are not complete and violate the symmetries, which are exact for the dark realization. Also the number of stop codons van vary.

2.2.3 Representation of codons as 3-chords

There are also questions related to the HC and its realization and also the realization of the codons as cyclotron frequency triplets.

1. Icosahedral HC corresponds to a sequence of 12 vertices to which one can assign T:s. The basic idea of bioharmony is that one assigns to each vertex a note of 12-note scale and the notes associated with the triangular faces define the 20 chords of the harmony for a given T as dark counterparts of DNA codons.

   The 12 edges connecting the faces in the simplest model corresponds to a scaling of frequency by 3/2 or by $2^{7/12}$ corresponding to Pythagorean and well-tempered scales (HC as quint cycle module octave equivalence). Various HCs correspond to different realizations of the genetic code in terms of 3-chords realized as cyclotron frequency triplets assignable to the triangular faces of I and interpreted as different harmonies as representations of moods: this aspect is absent in the standard view.

2. How the cyclotron frequencies are assigned with the vertices of I. One could consider the situation also from the point of view of IIT as a blow-up of IT. Each vertex of I has T as a blow-up. One should assign a cyclotron frequency with this particular vertex of T.

3. Could one assign the frequency triplets with the 3 T:s associated with the blow-ups of the triangular face of I? A given cyclotron frequency is most naturally associated with the vertex which it shares with an active I. This seems necessary since the letters of the codon defined by the 3 T:s should be independent. Octave equivalence allows only one frequency triplet unless the order of frequencies $C, E, G\sharp$ matters. At the level of DNA it matters but at the level of AAs it does not. The T triplets could correspond to different DNA codons coding for the same AA.

4. The situation is very similar for the start codon and stop codons. The start codon of the gene coding for the met is very special. Could one assign the start codon to the triangle opposite to the active vertex of T, so that it would effectively reduce to a doublet and the three codons coding for ile to the other faces of T?

What DNA codons do the T codons correspond to? One can consider two options for which T codons would code for DNA triplet and singlet and there would be no symmetry at the level of T.

1. At the level of the ordinary DNA, T codons could correspond to 3 stop codons and a codon coding trp or to 3 ile codons and met. There would be symmetry breaking for the I quartet giving rise to (ile,ile,ile, met) but this is not possible since there are 5 AAs coded by 4 DNAs. Therefore this option fails.

2. For the second option dark T codons correspond to DNA codons coding for (ile,ile,ile,met). One doublet would code for (stop,stp) and a second doublet would break Z_2 symmetry and code for (stop,trp). This option might also allow us to understand the small deviations from the standard genetic code for which stop codons occasionally code for a real AA.

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