Nature's Code

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This investigation started with a simple question; ''Why is it that Nature's cells predominantly use 20 standard amino acids to construct proteins during protein biosynthesis and yet the DNA code, composed of it's four bases allows a total of 64 triplet codons that could code for a maximum of 64 amino acids? '' There is no recognized limit in the availability of amino acids as there are known to be hundreds. Of course similar further questions are quick to follow such as why are there 4 building blocks to DNA, 2 strands to the DNA helix and the need for a specific chirality of these molecules that make both DNA and proteins. An exploration into whether certain geometric structures yield similar mathematical relationships revealed that octahedrons, cubes, tetrahedra and star tetrahedra may well do so. Subsequent collaboration with the quantum physicist Peter Rowlands has yielded similar relationships within specific fundamental theories of quantum mechanics. Application of these geometric principles has resulted in a geometric representation of a universal rewrite system that hints of an underlying process of Nature that reiterates constantly at higher and higher levels of organization.

Biological systems, though operating at the edge of chaos, are extremely ordered, whereas the tendency for nature is to become more disordered. Biology is, in effect, a race between order and entropy with the odds stacked in favour of entropy. So biological systems must create order, i.e. process information, with as much efficiency as possible. Theoretical studies by Freeland and Hurst suggest that the genetic code known on Earth has an extraordinary efficiency; of a million possible codes studied, only one could conceivably have been more efficient.[1-2] The genetic code we have inherited does not seem to be the product of pure chance; and it would appear, in fact, that the efficient processing of information requires certain algebraic and geometric structures, which are also found in systems organized at other scales, in particular, physics.

DNA, TRANSCRIPTION AND TRANSLATION

DNA is made up of 4 deoxyribonucleic acid bases (dNTPs): A, T, G and C. Two of these contain purines (A and G) and two pyrimidines (T and C). Within this double stranded, double helix structure of DNA, A pairs with T via a double bond and G pairs with C via a triple bond, i.e. the purines A and G pair with the pyrimidines T and C respectively. During the process of transcription the DNA unzips to expose the single strands and the enzyme RNA polymerase proceeds to make a reverse copy of one strand (the antisense coding strand). This copy replaces all the deoxyribonucleic acids with the ribonucleic acid bases A, U, G and C with the Ts being

replaced by Us, and the subsequent message (mRNA) is decoded by the protein machinery composed of ribosomes (made up of 65% rRNA and 35% protein) and transfer RNAs (tRNAs) during the process known as translation. The mRNA is translated into proteins by reading the RNA bases in groups of 3 known as triplet codons. The tRNAs each carry an anticodon that recognises a specific codon within the mRNA and each carries a specific amino acid. As the translation progresses a chain of amino acids is constructed that becomes a protein molecule. The number of triplet codons that can possibly arise from 4 bases is 4^3 or 64 but the number of amino acids nature uses is only 20.

THE FIVE PLATONIC SOLIDS

The 5 Platonic solids are the tetrahedron (4 sides, 4 vertices), cube (6 sides, 8 vertices), octahedron (8 sides, vertices), dodecahedron (12 sides, vertices) and the icosahedrons (20 sides, vertices) and interestingly, are the 5 resonance states of a sphere. The tetrahedron is a mathematical reciprocal of itself, the octahedron and the cube are reciprocals of each other as are the dodecahedron and the icosahedron. These 5 solids nest one inside the other ad infinitum (Fig 1).

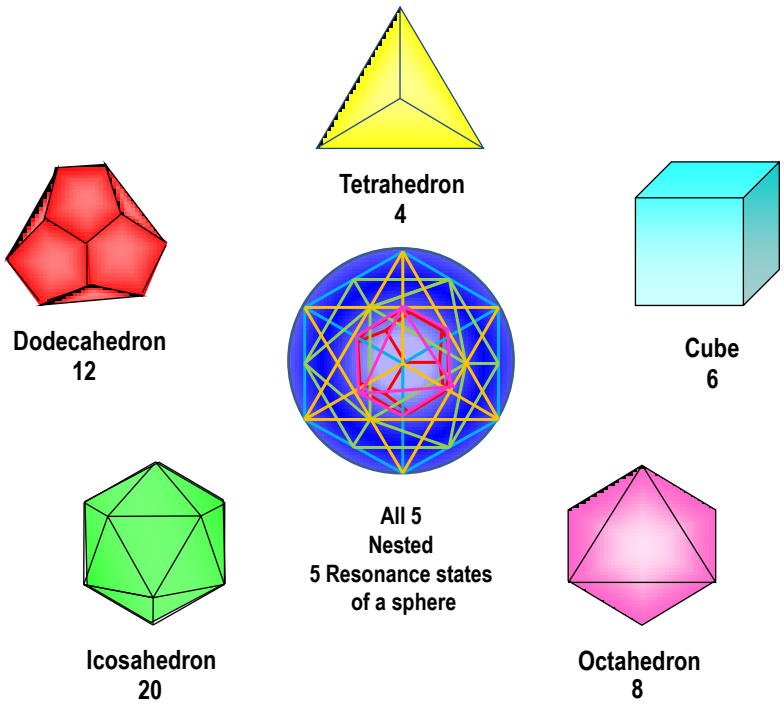


Fig 1. The 5 Platonic solids

THE PLATONIC SOLIDS AND THE DNA CODE

The four bases of DNA; A, T, G and C can be placed upon the four vertices of a tetrahedron (Fig 2) such that the tetrahedron can now be considered to contain, upon an information level, all the possible 64 (4^3) triplets defined by single stranded (sense) DNA or mRNA (U replacing T). Double stranded DNA can now be represented by interlocking a second tetrahedron to produce a star tetrahedron such that both the sense and antisense strands are combined with the correct base pairing of A to T and G to C that occur within the double helix (Fig 2). Three corners of a cube would also serve well here.[3]

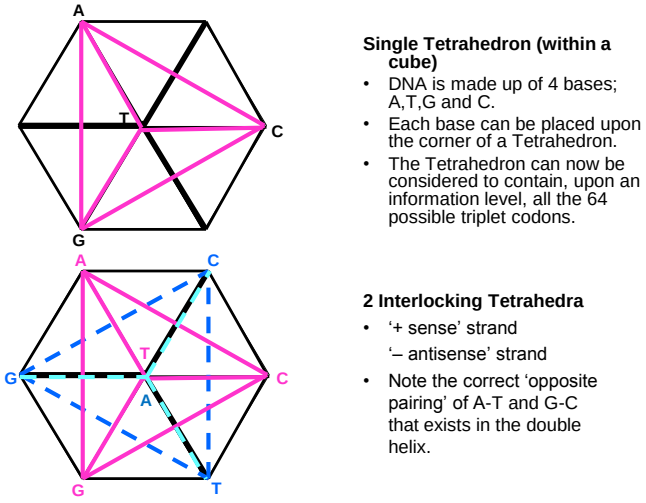


Fig 2. The geometry of single and double stranded DNA

2nd Position

1st Position 5'end	U		C		A		G		3rd Position 3'end
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC	Phe	UCC	Ser	UAC	Tyr	UGC	Cys	C
	UUA	Leu	UCA	Ser	UAA	STOP	UGA	STOP	A
	UUG	Leu*	UCG	Ser	UAG	STOP	UGG	Trp	G
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U
	CUC	Leu	CCC	Pro	CAC	His	CGC	Arg	C
	CUA	Leu	CCA	Pro	CAA	Gln	CGA	Arg	A
	CUG	Leu*	CCG	Pro	CAG	Gln	CGG	Arg	G
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	U
	AUC	Ile	ACC	Thr	AAC	Asn	AGC	Ser	C
	AUA	Ile*	ACA	Thr	AAA	Lys	AGA	Arg	A
	AUG	Met*	ACG	Thr	AAG	Lys	AGG	Arg	G
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	U
	GUC	Val	GCC	Ala	GAC	Asp	GGC	Gly	C
	GUA	Val	GCA	Ala	GAA	Glu	GGA	Gly	A
	GUG	Val*	GCG	Ala	GAG	Glu	GGG	Gly	G

Table 1. The 64 triplets, 20 amino acids and stop/start* codons

As previously mentioned, there are 64 (4^3) different possible triplets that can be obtained from four bases. These, theoretically could code for 64 different protein building blocks (amino acids) but generally Nature selects only 20 amino acids which can be coded for by 1 to 6 different triplets as shown in Table 1. If we now look at different higher order levels of tetrahedra (Fig 3), it can be seen that the second order is composed of one octahedron and four tetrahedra and the third order is composed of four octahedra and ten tetrahedra. If each triangular octahedral face is considered to represent a single triplet then each octahedron would have eight possible triplets and if each tetrahedron is considered to represent one amino acid we would have for a:-

- second order level tetrahedron : 8 triplet codons and 4 amino acids
- third order level tetrahedron : 32 triplet codons and 10 amino acids.

Introduction of a second interlocking tetrahedral form (Fig 3) to produce a star tetrahedron would now double these values to:-

- second order level star tetrahedron : 16 triplet codons and 8 amino acids
- third order level star tetrahedron : 64 triplet codons and 20 amino acids.

The third order level star tetrahedron now meets the requisite numbers of triplets possible from our 4 bases and also the total number of amino acids used by Nature to construct proteins.

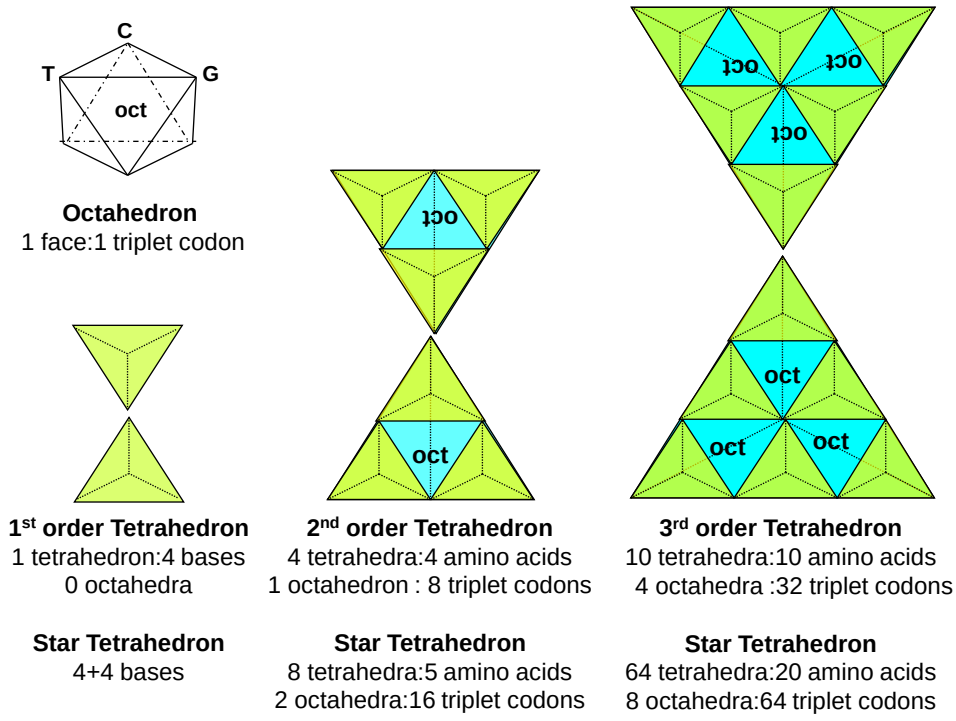


Fig 3. Higher order levels of tetrahedra and the genetic code.

Figure 4 gives a deeper insight into how the tetrahedra and octahedra pack within this star. Interestingly, there is a fractal nature to these diagrams, highlighting the reiteration of the star/octahedron/cube.

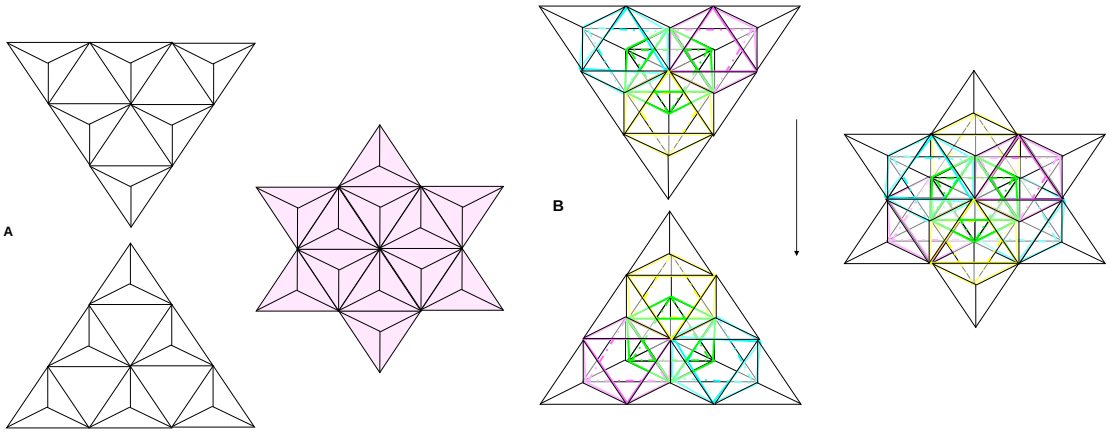


Fig 4. Packing within the star tetrahedron. A. The tetrahedra; B. The octahedra

The task now is to assign the correct placement of the triplets to give the appropriate amino acid represented by each tetrahedron. Figure 5 shows the beginnings of this procedure where

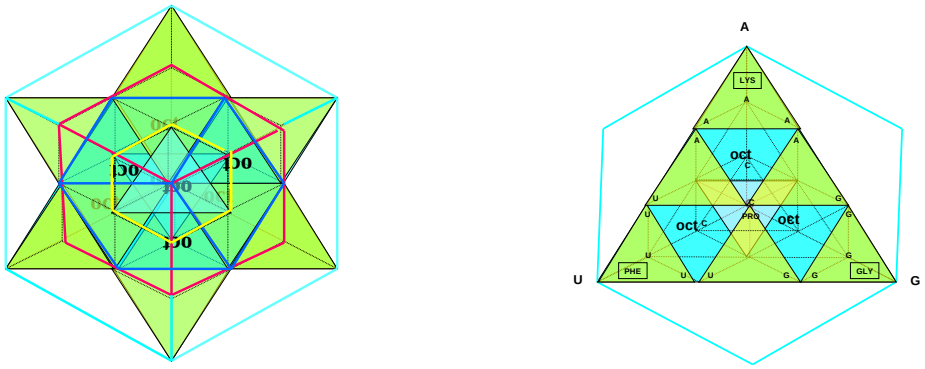


Fig 5. Cube reiteration and placement of the triplet codons

the corner tetrahedra can be nominated as the amino acid that relates to the triplet codon mirrored from the triangular face of an octahedron eg :-
UUU = phenylalanine (PHE)
GGG = glycine (GLY)
AAA = lysine (LYS)
CCC = proline (PRO)

THE UNIVERSAL REWRITE SYSTEM IN NATURE

There seems to be evidence that a universal rewrite system operates in nature at a fundamental level.[5-6] Essentially, this uses a create / conserve process to generate its own system of mathematical structure, based only on the permanent condition of zero totality, and not on any assumed pre-existing number system or algebra. A convenient, but not unique, representation of this mathematical structure is through an infinite Clifford algebra of nested quaternion systems ($\boldsymbol{i}_1$, $\boldsymbol{j}_1$, $\boldsymbol{k}_1$; $\boldsymbol{i}_2$, $\boldsymbol{j}_2$, $\boldsymbol{k}_2$, etc.), so that the successive units introduced at orders 2, 4, 8, 16, 32, 64 are

scalar, pseudoscalar, quaternion, multivariate vector (or complexified quaternion), double quaternion, and multivariate vector quaternion, with respective multiplication factors of (1, –1), (1, $\boldsymbol{i}_1$), (1, $\boldsymbol{j}_1$), (1, $\boldsymbol{i}_2$), (1, $\boldsymbol{j}_2$), (1, $\boldsymbol{i}_3$). Here, $\boldsymbol{i}_1$, $\boldsymbol{j}_1$ and $\boldsymbol{i}_1\boldsymbol{j}_1$ represent the quaternion operators $\boldsymbol{i}$, $\boldsymbol{j}$, $\boldsymbol{k}$; the incomplete quaternion set $\boldsymbol{i}_3$ represents the complex number i; while the products $i\boldsymbol{i}_2$, $i\boldsymbol{j}_2$ and $i\boldsymbol{i}_2\boldsymbol{j}_2$ become the multivariate vector units **i**, **j**, **k**.

Mathematically, the series continues to infinity, with (1, $\boldsymbol{j}_3$), (1, $\boldsymbol{i}_4$), etc., but, physically, we note the special significance of order 64, which introduces the algebra associated with the fundamental physical state, the fermion, that is the Dirac algebra or gamma matrices. This is the order needed to incorporate the component orders 2, 4, 8 and 16 as identifiable units, and, in physics, these orders are identifiable respectively with the fundamental physical parameters mass, time, charge and space. At this level, we observe, uniquely, an infinite number of *nilpotent* solutions, which, by squaring to zero, immediately produce the zero totality alphabet at this and all subsequent levels, and are distinguishable from each other by their higher order algebraic coefficients. Essentially, the combination of

time	space	mass	charge
pseudoscalar	vector	scalar	quaternion
i	**i j k**	1	$\boldsymbol{i}$ $\boldsymbol{j}$ $\boldsymbol{k}$

requires an algebra of 64 units (including + and – signs), but in the nilpotent structure we compactify these into five composite units (equivalent to the gamma matrices)

$$i\boldsymbol{k} \qquad \boldsymbol{i}\boldsymbol{i} \;\; \boldsymbol{i}\boldsymbol{j} \;\; \boldsymbol{i}\boldsymbol{k} \qquad 1\boldsymbol{j} \qquad \text{a)}$$

which are sufficient to generate the entire Dirac group, and associate these with new (composite) physical parameters, which we describe as energy (E), three components of momentum (**p**), and rest mass (m). The nilpotent structure

$$\left(\pm i\boldsymbol{k}E \pm \boldsymbol{i}\boldsymbol{i}p_x \pm \boldsymbol{i}\boldsymbol{j}p_y \pm \boldsymbol{i}\boldsymbol{k}p_z + 1\boldsymbol{j}m\right) = \left(\pm i\boldsymbol{k}E \pm \boldsymbol{i}\mathbf{p} + 1\boldsymbol{j}m\right).$$

now represents the fundamental unit of physics, the fermionic state. In quantum mechanics, the expression (± $i\boldsymbol{k}E$ ± $\boldsymbol{i}\mathbf{p}$ +1$\boldsymbol{j}m$) can represent either operator or amplitude and the nilpotent equation

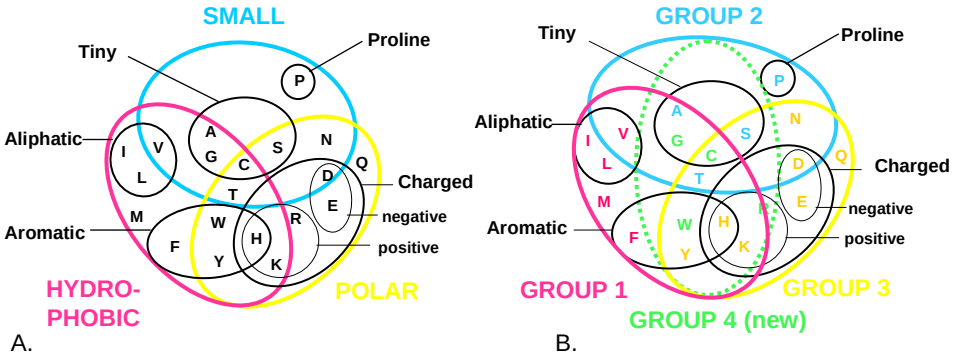
$$\left(\pm i\boldsymbol{k}E \pm \boldsymbol{i}\mathbf{p} + 1\boldsymbol{j}m\right)\left(\pm i\boldsymbol{k}E \pm \boldsymbol{i}\mathbf{p} + 1\boldsymbol{j}m\right) = 0. \qquad \text{b)}$$

has multiple meanings, including Pauli exclusion. We can also take –(± $i\boldsymbol{k}E$ ± $\boldsymbol{i}\mathbf{p}$ +1$\boldsymbol{j}m$) as the total ‘vacuum’ state, left by extracting the fermion from zero totality, so that equation (b) also implies that the fermion can only be defined at the same time as its vacuum state, and that the combination means that each fermion defines its own zero totality universe.

The creation of the nilpotent algebra by the compactification process outlined in (a) has many important consequences. Apart from introducing discreteness to otherwise continuous quantities such as time and mass, the compactification creates symmetry-breaking (between the quaternion units), as an 8-fold structure becomes 5-fold, and chirality because of the loss of independent information due to the reduction in sign variation; and the most significant physical quantity now becomes angular momentum, which is the only one structured at the highest level of the algebra – multivariate vector quaternion.

A significant aspect of the creation of the nilpotent state is that one of the quaternion sets remains incomplete. This is the one that appears as the complex factor on the energy or time term, and, by analogy, on the weak component of charge. A fermion is, in one sense, always

interacting to overcome this anomaly. Ultimately, its only complete way of doing this is by annihilation with the rest of the universe. However, a partial annihilation is produced by any of the processes of material aggregation which result in a bosonic-type state. The mechanism which results in the creation or destruction of (combined) bosonic from or into (uncombined) fermionic states is described as the harmonic oscillator. The harmonic oscillator is a classic indication of aggregation or complexity in a system. It is a statement that no system is ever 'closed'. All fermions interact with each other via discrete quantum transitions; *E* and **p** are never fixed. This lack of closure is an expression of the second law of thermodynamics, and is the driver for all processes.



GROUP 1	GROUP 2	GROUP 3	GROUP 4
Isoleucine : I	Proline : P	Glutamine : Q	Glycine : G
Leucine : L	Alanine : A	Asparagine :N	Cysteine : C
Valine : V	Serine : S	Tyrosine : Y	Tryptophan :W
Methionine:M	Threonine : T	Histidine : H	Arginine : R
Phenylalanin : F		Lysine : K	Serine :S
		Aspartate : D	
		Glutamate : E	

Properties of Group 4 Amino Acids	
Glycine	Smallest, most flexible, structure breaker, achiral.
Tryptophan	Largest, aromatic, rarest, absorbs uv light.
Arginine	Most basic, extensive delocalised charge, present in protein-nucleic acid interactions.
Cysteine	Disulfide bridge formation, typically extracellular, 1 of 2 S containing amino acids (other = methionine)

FIGURE 6. Grouping of the 20 amino acids. (A) Standard grouping according to chemical properties; (B) grouping dependent upon middle base of triplet codon; Tables show members of each group and the properties of the new group 4.

A significant aspect of the quantum harmonic oscillator is the spin ½ which is intrinsic to the fermionic state. The reason why it is ½ rather than 1 is because the fermion can only be defined at the same time as its vacuum partner, and the combination can in this sense be imagined as 'double helical'. The fermion / vacuum duality and spin ½ also makes the weak interaction ultimately dipolar, with the classic inverse fourth-power force which is characteristic of aggregating systems, including the Van der Waals force of molecular cohesion (and which gives stability between each twist of the double helix), and the hydrogen bonding which connects together the double strands of DNA.

As previously mentioned, the number of triplet codons that can possibly arise from 4 bases is 4^3 or 64 but the number of amino acids nature uses is only 20. Here we recognize a parallel with the 64 units of the Dirac algebra and the 20 components of the fermion state (fermion plus vacuum). At order 64, the 64 units of the rewrite algebra are composed of 32 + and 32 – parts,

and DNA can also be considered to carry 32 + codons and 32 – ones. This can be achieved by considering the 2 strands as mirror images where T, A, G and C are present on one strand; its opposite counterpart on the other strand would have the partners A, T, C and G. If the codons are now split into 2 groups, dependent upon the central base within the codon being either a purine or pyrimidine, we have 2 sets of 32 that are mirror images (order 32). Interestingly this produces 2 distinct groupings: one contains codons that code for amino acids that are predominantly nonpolar and the other those that are predominantly polar. These 2 groups can be split again to produce 4 groups dependent upon the central base within the triplet codon and reflect order 16 of the universal rewrite system. The division results in 4 groups of amino acids, two of which are distinctly polar and nonpolar with the other two showing a degree of overlap. In Fig. 6 we can see a standard text book diagram (A) showing the grouping of amino acids according to their chemical properties and, alongside, the resultant grouping obtained when the amino acids are grouped by the specific central base within the triplet codon (B). Remarkably, the two groupings are identical in the placement of each amino acid, depending on its specific chemical property, and now produce 4 distinct groups previously unconsidered.[3] The first group (distinctly nonpolar) contains all the 4 known start codons, the third group is distinctly polar (+vely and – vely charged) and the fourth group contains those amino acids with extremes in chemical behaviour. Similar grouping attempts made by placing emphasis upon the first or third codons yield an entirely random result. This is not unexpected for grouping dependent upon the third base, as this is known as the 'redundant' base.

GEOMETRY APPLIED TO THE REWITE ALGEBRA

The direct connection of biology with the rewrite structure is now apparent, with the key information being the number of nested 3-D systems, as we progress from, say, 2 (purines, A and G or pyrimidines T and C) and 4 bases (purines plus pyrimidines) (orders 2 and 4), to the formation of double stranded DNA (order 8) and then an unzipping of these strands to expose the –sense ssDNA to allow the production of a mRNA (+sense), i.e. transcription takes place (order 16). The mRNA is transported to the ribosomes where it is held in place by the ribosomal RNA as are the tRNAs that correspond to the appropriate triplet codons within the message. Of course there are also the actual interactions between the mRNA and the tRNAs and the tRNAs and their respective amino acids within the ribosome hence a four way interaction occurs to allow the translation process of all possible 64 codons to produce a protein molecule composed of the 20 amino acids (orders 32 and 64). Here the 8 fold symmetry breaks to produce the 5 fold symmetry relevant to the icosahedron and dodecahedron. In DNA replication, the double-strand DNA composed of all 4 bases (order 64) can be represented by the third order level star tetrahedron which meets the requisite numbers of triplets possible from our 4 bases and also the number of amino acids used by Nature to construct proteins. The breaking of symmetry is observed in the alpha DNA double helix itself which expresses a pentagonal based chiral structure. The geometric sequence is shown in Fig. 7. The equivalent algebraic structures are given in Table 2.

Order 8 here corresponds to the second order level tetrahedron with 8 triplet codons in an octahedron and 4 tetrahedral amino acids. Order 16 doubles this to a second order level star tetrahedron with 16 triplet codons in two octahedra and 8 tetrahedral amino acids. Order 32 produces a third order level tetrahedron with 32 triplet codons in 4 octahedra and 10 tetrahedral amino acids, while order 64 produces a third order level star tetrahedron with 64 triplet codons in 8 octahedra and 20 tetrahedral amino acids.

TABLE 2. The Rewrite Algebra.

Group Order	Algebraic Units	3-Dimensionality
Order 2	$(1, -1)$	$0 \times$ 3-D
Order 4	$(1, -1) \times (1, \boldsymbol{i}_1)$	$0.5 \times$ 3-D
Order 8	$(1, -1) \times (1, \boldsymbol{i}_1) \times (1, \boldsymbol{j}_1)$	$1 \times$ 3-D
Order 16	$(1, -1) \times (1, \boldsymbol{i}_1) \times (1, \boldsymbol{j}_1) \times (1, \boldsymbol{i}_2)$	$1.5 \times$ 3-D
Order 32	$(1, -1) \times (1, \boldsymbol{i}_1) \times (1, \boldsymbol{j}_1) \times (1, \boldsymbol{i}_2) \times (1, \boldsymbol{j}_2)$	$2 \times$ 3-D
Order 64	$(1, -1) \times (1, \boldsymbol{i}_1) \times (1, \boldsymbol{j}_1) \times (1, \boldsymbol{i}_2) \times (1, \boldsymbol{j}_2) \times (1, \boldsymbol{i}_3)$	$2.5 \times$ 3-D

The stages at order 8 and order 32 are key 'phase transitions', producing, respectively the first octahedron and then the first 3-D (tetrahedral) arrangement of 4 octahedra. Orders 16 and 64 produce the direct doubling that is characteristic of timelike transition between spatial states characterized by the hidden time component in the multivariate vector system, due to the additional pseudoscalar $0.5 \times$ 3-D. The cube reiteration in Figure 5 shows the exact parallel between the $1.5 \times$ 3-D and $2.5 \times$ 3-D structures when one complete 3-D system is mapped exactly onto another. Pentad (i.e. 5-fold) structures notably occur only at orders 32 and 64.

The rewrite system requires a double 3-D because an object is dual with the rest of the universe (or vacuum) in that the two combine to a zero totality. In particle physics, this means that a fermion has interactions with all other particles in the universe, and that these determine its final state. They also cause its changes. In a sense the vacuum is what the fermion will become, and we can picture it like two spaces interpenetrating each other in a way that cannot be visualised in 3-D, but can be in higher dimensions. So we have 'static' dimensions and changing ones, just as we have conserved (mass and charge) and nonconserved ones (space and time), or, alternatively, amplitude and phase, or fermion and vacuum. Because the 'phase' part includes the idea of change, it is like the set of moving biological coordinates, assumed by Illert in his $2 \times$ 3-D work on shells,[7] but we also need a rest frame of fixed coordinates which express what remains fixed, and as a reference. Significantly, the interaction with the rest of the universe in particle physics is through charge, which provides the second 3-D. Biology, with its self-replicating mechanisms, is even more obviously organised in this holistic way.

GEOMETRIC STRUCTURES APPLIED TO GENETICS AND CODING

The transcription and translation of the 64 codons of DNA into 20 amino acid building blocks of protein is analogous to the resolution of the 64 units of algebra into 20 in the fermionic nilpotent. This 20 can be considered as a group of 4 pentads and we have just described the

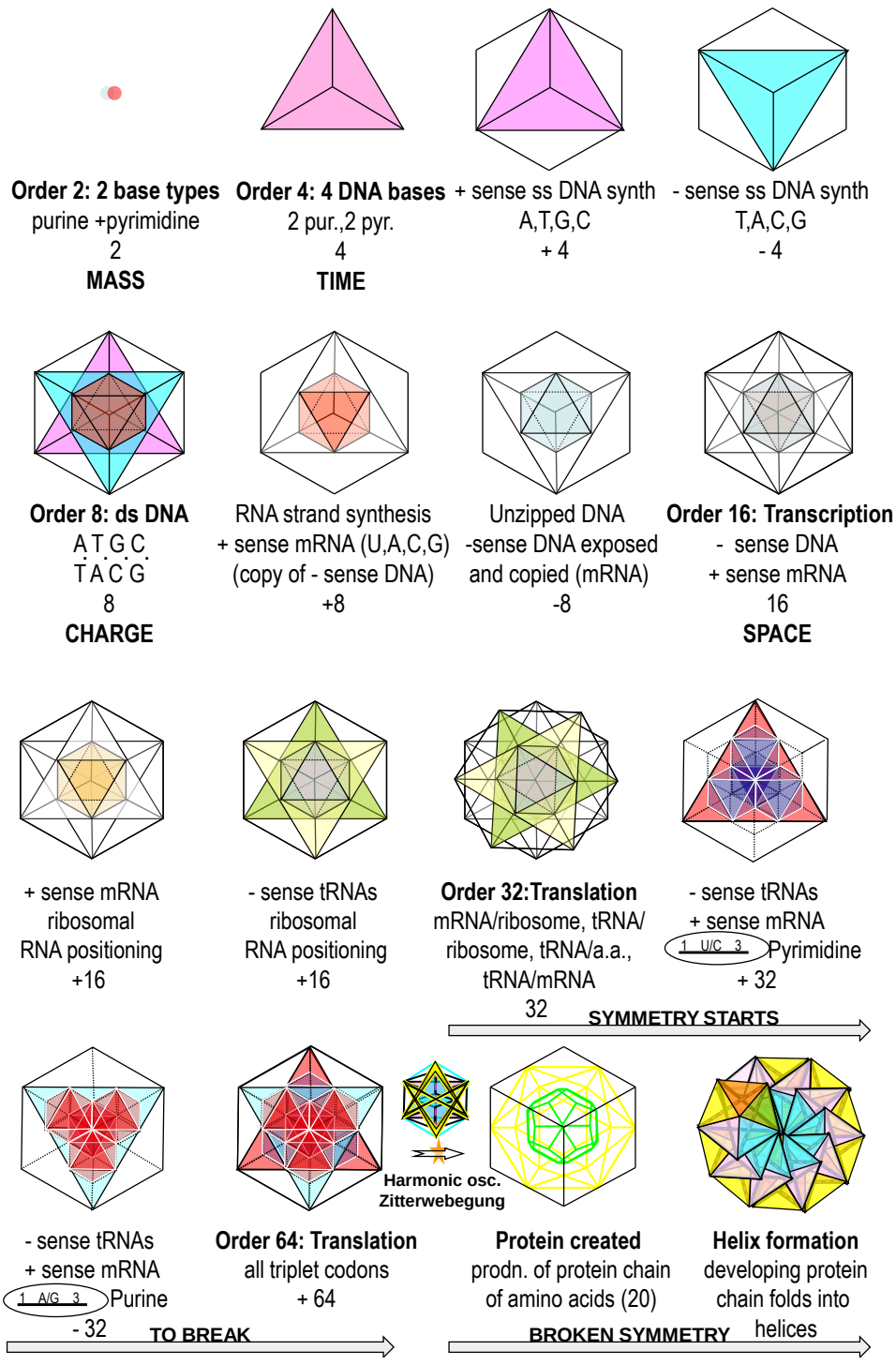


FIGURE 7. The rewrite geometry applied to physics and DNA, transcription and translation.

division of amino acids into 4 groups. It is also interesting here to note that there is a 'loss' of 4 units from the total of 64 ($\pm 1, \pm i$). In biology there are a series of 'stop codons' that do not translate into any amino acids but act as termination points in translation. These codons vary from one species to another but there are known to be 3 or 4 present within most genera. Perhaps the phase change observed at order 64, where we see the reiteration of the cube (in 2-D), is one that can be represented by the icosahedron. The icosahedron has 20 sides where each can represent one amino acid and each of the 20 component tetrahedra has 4 triangular faces that can represent a triplet codon giving the full complement of 60 codons. Another method can be applied to give the same figures by placing a tetrahedron upon each icosahedral face to produce a star icosahedron. The breaking of symmetry from an 8-fold to a 5-fold structure within the algebra can be geometrically described by the formation of a pentagonal disk composed of 5 tetrahedra (minus 7º 12'), and we are again reminded of the icosahedron where we can divide this structure into two such discs plus a ring of 10 tetrahedra which join them. What is remarkable is that 10 of these disks naturally pack to form one cycle of a double helical spiral, with the $10 \times 7º\ 12'$ ratcheting the dNTP pair to the next twist in the spiral, and if we now consider them as part of a string of icosahedra (albeit incomplete), and construct the internal reciprocal dodecahedra within them. The front two faces of those dodecahedra lie where the 10 dNTPs would be placed within a single cycle of the double helix of DNA. Amazingly, one disc even highlights 3 dNTPs thus implicating one triplet codon. In fact DNA has a distinctive pentagonal symmetry within its structure as shown in Fig 8. The top down view of an icosahedron (two joined overlapping pentagal discs) fits very well upon the computer generated scattergraph of DNA in the same way as the ring of 10 pentagonal disks, the outline of which constructs the outline of the icosahedron.[8] Fig. 8 B also shows the 8-fold symmetry breaking into two overlapping pentagons in a way which recalls the symmetry-breaking which forms the fermionic nilpotent in (a).

The structure of amino acids that make up a protein can also be considered as having a tetrahedral format. When the string of amino acids fold they form two fundamental structures namely helices and ß-pleated sheets (hexagonal lattices) and it is a combination of these that make up the proteins of all cells. Here, once again, we see the recurrence of helices and hexagons. The DNA helix is an alpha helix and is made up of bases that also exhibit selected chirality. Likewise proteins also show a selected chirality in that the amino acids are L–forms and their D–form counterparts are often toxic to cells. The protein helices are generally alpha forms. Interestingly, when actual pentagonal/pentameric proteins are considered from a functional aspect within a cell they appear to be involved in helix formation or moving motor type structures, e.g. the pentameric cap proteins within bacteria drive the formation of flagellin helices. Hexameric proteins by contrast form membranes and cell walls, i.e. are more static in nature.

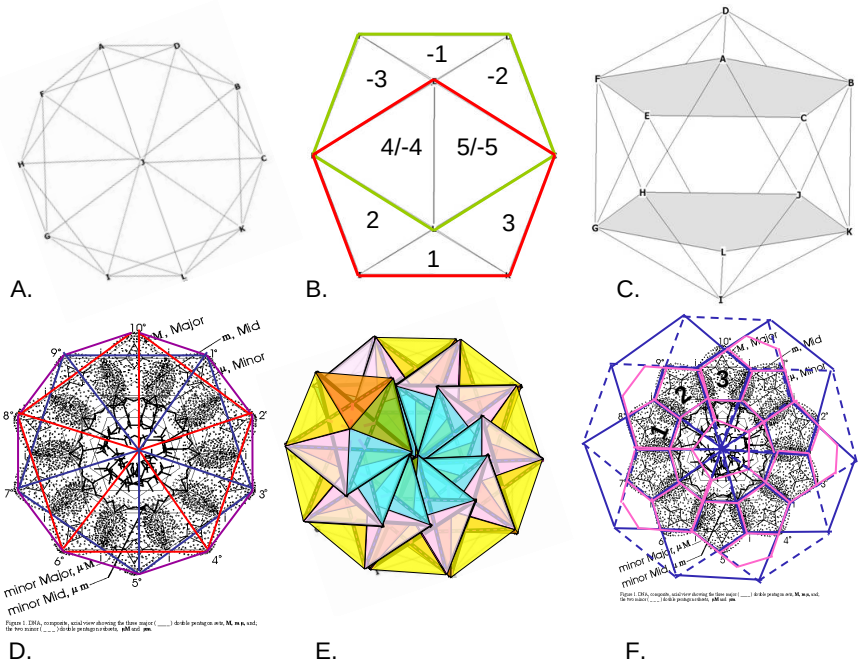


FIGURE 8. The icosahedron and the pentagonal geometry of DNA. A: top- down view; B: side view 1; C: side view 2; D: A overlaid onto scattergraph of DNA; E: Spiral of pentagonal disks overlaid (incomplete icosaheda) top-down view; F: E overlaid onto scattergraph of DNA (with internal dodecahedra–faces numbered identify dNTP positions).

CONCLUSION

It would appear that the fundamental rewrite system, with its 5-component nilpotent operator, displays in compactified form all the fundamental units of *natural process*. Summarising a large body of work, it is possible to show that, defining a nilpotent operator for physics simultaneously leads to the creation of point singularity and discreteness; compactification (from 8 units to 5) and chirality (as a result of the loss of some sign degrees of freedom in the compactification); symmetry-breaking (between the 5 units) and spontaneous symmetry-breaking (because of the chirality); (double) helicity and angular momentum (with its double 3-D nature); irreversibility (because of the chirality of the time and energy operators); 5-fold symmetry (cubical → spiral) and hence the Fibonacci sequence; and a harmonic oscillator-based tendency to aggregation and complexity (because of the pseudoscalar nature of the time / energy term needed for nilpotency). These, in fact, would appear to be universal processes, originating in the fundamental algebras and geometries of the rewrite system, and there are many indications that they apply in biology as well as in physics, in particular to the genetic code and its construction mechanism for proteins. Here, we see that the Dirac nilpotent fermion plus vacuum structure, with its four fundamental components (space, time, mass and charge), the 64 elements of its algebra, the double helical structure, chirality, and 5-fold broken symmetry (*E*, **p**, *m*), corresponds closely to the structure of the DNA / RNA genetic code, with its four bases A(denine), G(uanine), C(ytosine) and T(hymine)), 64 triplet codons, double helical structure, chirality, and 5-fold axial symmetry.

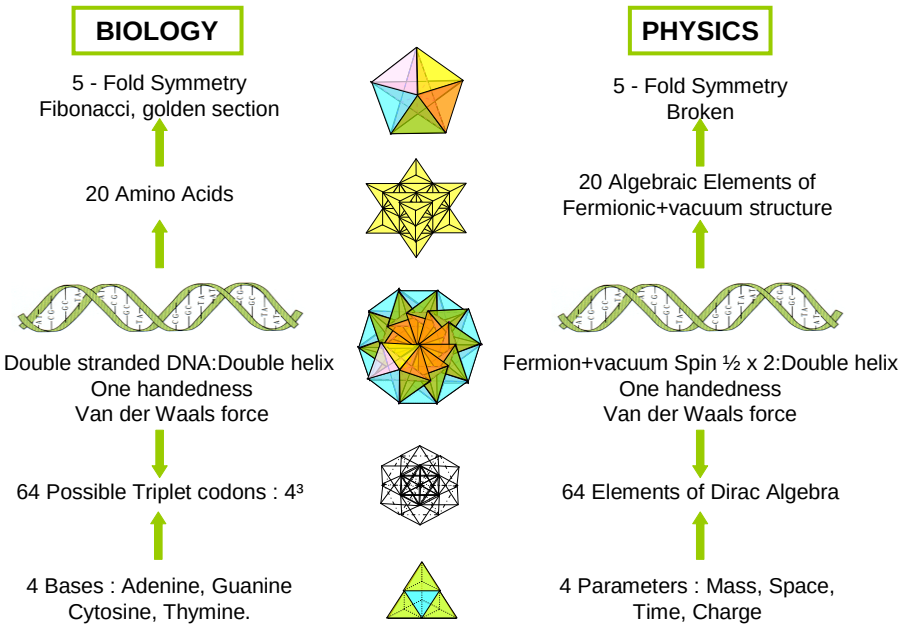


Fig 9. The unification of physics and biology

In summary, mathematical structures, both algebraic and geometric, related to the 'universal rewrite system', appear to define a universal process applicable to Nature, which operates in both physical and biological systems, and which may be described as 'Nature's code'.

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