Tracking the Origin OF LIFE'S Genetic Code

A seguel to "Revelations of a Biological Abacus"

Preamble

In a play of incredible irony, we find that amongst the findings of those scientists who currently seek a godless evolutionary explanation for the origin of life's genetic code, the 'criterion of divisibility by 037' should rather establish substantial links with a divine Creator, with His instructions concerning the Hebrews' 'wilderness experience', and with the numerical cryptogram associated with the opening words of the Judeo-Christian Scriptures.

Here we offer further evidences of the reality and significance of this criterion and also draw attention to further numerical data of a supportive nature. These features emerge from the study of, (i) the peer-reviewed paper, "A harmonic structure of the genetic code" [1] by MM Rakocevic and, (ii) the privately published article, "The numeric connections of the genetic code" [2] by J-Y Boulay. Whilst the finer details contained in these documents are, undoubtedly, matters for experts in the field, the informed layman may nevertheless participate in the essential truths revealed.

[1] M.M.Rakocevic "Journal of Theoretical Biology" 229 (2004) 221-234

[2] J-Y Boulay "The Numeric Connections of the Genetic Code": http://pagesperso-orange.fr/jean-yves.boulay/rap/eng/pagenucleon1.html

Rakocevic's contribution

A notable feature of Rakocevic's approach is his recognition of the fact that the constituent elements of the amino acids - H, C, N, O and S - are present in nature as *mixtures* of their respective isotopes. Thus, their molar masses (definition here) are not quite the whole numbers assumed by shCherbak (who based his results on the nucleon counts for each of the 20 canonical amino acids). Accordingly, Rakocevic fine-tunes the data as follows:

AMINO ACID	SYMBOL	MOLAR MASS
Alanine	Ala /A	89.09
Arginine	Arg/R	174.20
Asparagine	Asn/N	132.12
Aspartic acid	Asp/D	133.10
Cysteine	Cys/C	121.16
Glutamic acid	Glu/E	147.13
Glutamine	Gln/Q	146.14
Glysine	Gly /G	75.07
Histidine	His /H	155.15
Isoleucine	Ile /I	131.17
Leucine	Leu/L	131.17
Lysine	Lys /K	146.19
Methionine	Met/M	149.21
Phenylalanine	Phe/F	165.19
Proline	Pro /P	115.13
Serine	Ser/S	105.09
Threonine	Thr/T	119.12
Tryptophan	Trp/W	204.23
Tyrosine	Tyr/Y	181.19
Valine	Val /V	117.15

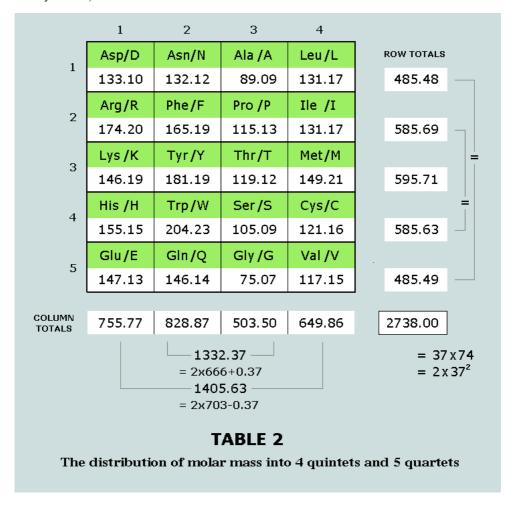
TABLE 1

The 20 amino acids with their 3- and 1-letter symbols and molar masses

[Observe here that when the constituent elements (C, H, N, O and S) are represented by their most abundant isotopes the integer part of each molar mass value corresponds precisely with the total nucleon count (i.e. protons + neutrons); the fractional part reflects the reality that other isotopes of these elements are present in the forms found to occur naturally]

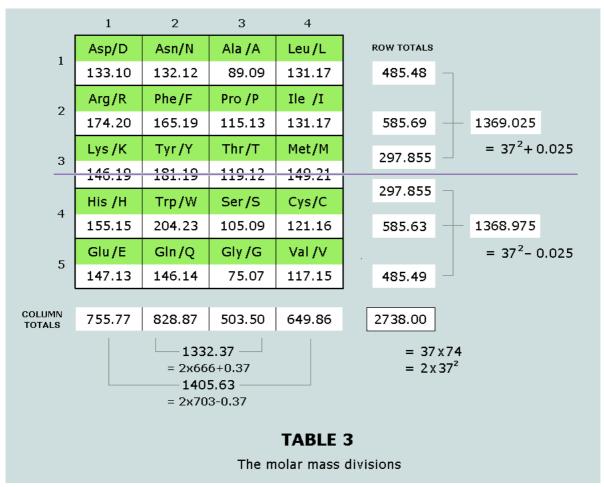
These data may be readily verified by accessing the links provided as an appendix to this page.

Rakocevic now sets out the data as a 5x4 matrix of molar masses (his reasons for choosing this particular arrangement are to be properly understood only by experts in the field; clearly, from the layman's point of view, the fact that they were accepted by a panel of his peers is all that really matters):

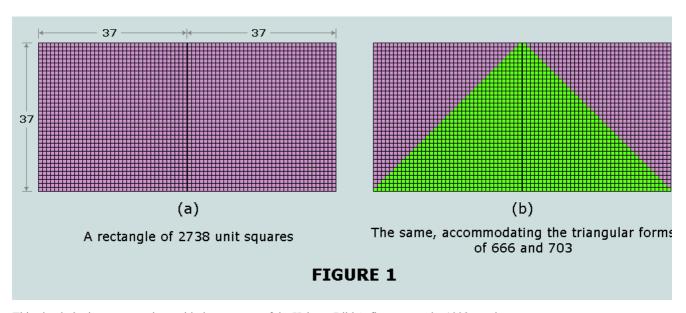


Observe here:

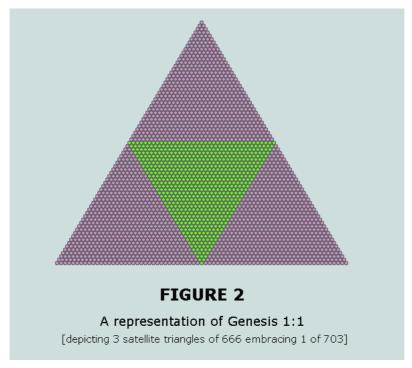
- the grand total of the molar masses of the 20 amino acids is 2738 = 37x74 = 2x37x37, precisely!
- the sum of columns 1 and 4 is 1405.63 = 1406 0.37 = (37x38) 0.37 = (2x703) 0.37
- the sum of columns 2 and 3 is 1332.37 = 1332 + 0.37 = (37x36) + 0.37 = (2x666) + 0.37
- alternating sums of the tabular elements (details here) yield 1331.45 and 1406.55, respectively, which again converge on the integers 1332 and 1406 this time with an orb of allowance of 0.55
- concerning the row totals: row 1 corresponds closely with row 5, and row 2 with row 4; we may therefore envisage the table's value, 2738, to be bisected by a horizontal line passing through the centre of the third row yielding the square of 37 both above and below, thus:



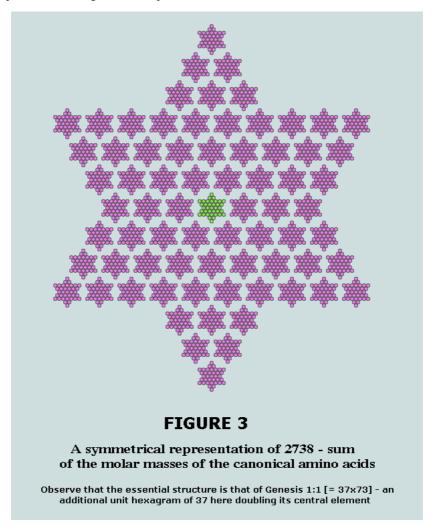
These divisions are captured in the following expressions of numerical geometry:



This clearly invites a comparison with the structure of the Hebrew Bible's first verse - the 1998 purple counters (representing the sum of the CVs of the opening 5 words) assembled into three equilateral triangles of 666, and the 703 green counters (sum of the CVs of the next two words, translated "... and the earth.") forming the central triangle.

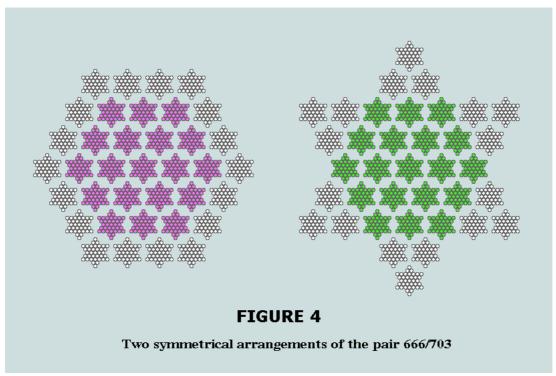


Further, some compound numerical geometries capture the same features:



Observe again, (i) that the doubling places 2x37 = 74, the value of the standard block) at the very centre of proceedings and, (ii) the sum of the ordinal positions of the letters of the English 'JESUS' also being 74, the Creator, most appropriately, occupies the same position!

The compound geometries here reveal 703 as a symmetrical hexagon of 19 units of 37-as-hexagram centrally placed within, first, a hexagon of 37 such units (representing a total of 1369 counters) and, again, within a hexagram of 37 of the same units. Clearly, the outlines of each of these larger figures comprise 18 units of 37-as-hexagram - a total of 666 counters.



Boulay's contribution

Here we return to the integer particle counts associated with the most abundant isotopes of the life-forming elements. Boulay begins by drawing attention to 2 anomalies in the universal genetic code:

- the rogue behaviour of the amino acid proline and,
- what he refers to as the 'rebel group' of codons

The proline problem

In common with shCherbak, Boulay's evidence rests upon a satisfactory resolution of the 'proline problem', i.e. the fact that it is the only amino acid that fails to conform with the generic formula



[R representing the 'radical' or 'side chain', and B the 'base' or 'standard block']

For 19 of the canonical amino acids the nucleon count for the standard block is 74, whereas that for proline is 73. shCherbak's solution involves moving a hydrogen atom (or proton) from R to B - thus standardising both atom and nucleon counts for B but decreasing those of R (respectively, 9 and 42) each by one. On the other hand, Boulay posits a neutron from R functioning as a proton as it connects to the base; the result - an extra proton (and atom) in B and one fewer neutrons in R. Clearly, both schemas leave the total nucleon count unaffected. There follows a summary of these proceedings.

					PAF	RTICLE	COU	NTS				
INVESTIGATOR	STANDARD BLOCK				SIDE CHAIN				TOTALS			
	Α	Р	N	Nc	Α	Р	N	Nc	Α	Р	Ν	Nc
shCherbak (S)	9	39	35	74	8	23	18	41	17	62	53	115
Boulay (B)	9	39	35	74	9	24	17	41	18	63	52	115

TABLE 4

A comparison of particle countings for the rogue amino acid proline [A = Atoms, P = Protons, N = Neutrons and Nc = Nucleons]

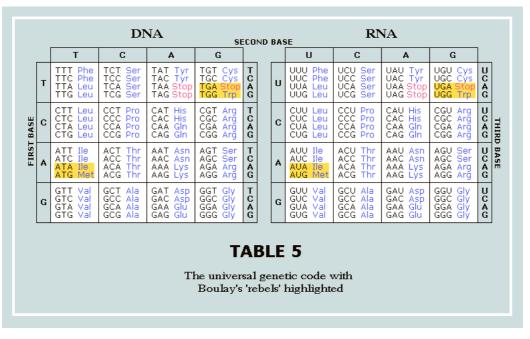
Boulay defends the validity of both these manoeuvres as follows:

"Without these two special countings, the very numerous and organised phenomena presented by shCherbak and Boulay disappear. (But they) are much too numerous and structured to be destroyed by an apparent contradiction of chemical arrangement."

Let us also observe that Rakocevic's approach, as outlined above, avoids the 'proline problem' entirely by focusing attention on phenomena associated with the molar weights of the amino acids rather than their particle counts. He therefore establishes the primacy of 037 quite independently of these conjectures. Thus, remarkably, the assumptions of both shCherbak and Boulay, in leading to the same conclusion, appear to be equally valid.

The 'rebel group'

As Table 5 reveals, it is generally the case that amino acid products are identical if the final base of the codon is either A or G, or T or C (or U or C). The exceptions are here highlighted: ATA/AUA delivers isoleucine (Ile/I), whereas ATG/AUG, methionine (Met/M); TGA/UGA, 'stop', and TGG/UGG, tryptophan (Trp/W). [In passing, we observe that only 61 of the 64 codons are producers of amino acids.]



Taking one of shCherbak's observations as an example of the significance of the foregoing, Boulay first points to this investigator's original table depicting the dominance of multiples of 37 among the particle counts of the 20 amino acids:

	Sub	set 1		Subset 2				
AMINO ACID	NUCLEONS IN BASE	NUCLEONS IN RADICAL	NUCLEON TOTAL	AMINO ACID	NUCLEONS IN BASE	NUCLEONS IN RADICAL	NUCLEON TOTAL	
Gly/G	74	1	75	Ser/S	74	31	105	
Ala /A	74	15	89	Cys/C	74	47	121	
Ser/S	74	31	105	Leu/L	74	57	131	
Pro /P	74	41	115	Ile /I	74	57	131	
Val /V	74	43	117	Asn/N	74	58	132	
Thr/T	74	45	119	Asp/D	74	59	133	
Leu/L	74	57	131	Gln/Q	74	72	146	
Arg/R	74	100	174	Lys/K	74	72	146	
				Glu/E	74	73	147	
				Met/M	74	75	149	
				His /H	74	81	155	
				Phe/F	74	91	165	
				Arg/R	74	100	174	
				Tyr/Y	74	107	181	
				Trp/W	74	130	204	
8	592 [4×4×37]	333 [3×3×37]	925 [5×5×37]	15	1110 [2x3x5x37]	1110 [2x3x5x37]	2220 [3×4×5×37	

TABLE 6

Two subsets of the amino acids which have nucleon numbers multiples of 37

[The 'rebel' products depicted in red]

The first subset comprises the 8 amino acids which are observed to be encoded 4 times in Table 5 - with the first two bases identical; in the second, the remainder which are encoded 1-, 2-, or 3-times - again, the first two bases being identical.

Now follow Boulay's additional observations involving the 'rebels':

	Sub	set 1				Sub	set 2	
AMINO ACID	TOTAL NUCLEONS	RELATED CODONS	NUCLEON GRAND TOTAL		AMINO ACID	TOTAL NUCLEONS	RELATED CODONS	NUCLEON GRAND TOTAL
Gly /G	75	2+2	300		(STOP)	(0)	(2+1)	(0)
Ala /A	89	2+2	356		Ser/S	105	2	210
Ser/S	105	2+2	420		Cys/C	121	2	242
Pro /P	115	2+2	460		Leu/L	131	2	262
Val /V	117	2+2	468		Ile /I	131	2+1	393
Thr/T	119	2+2	476		Asn/N	132	2	264
Leu/L	131	2+2	524		Asp/D	133	2	266
Arg/R	174	2+2	696		Gln/Q	146	2	292
					Lys/K	146	2	292
					Glu/E	147	2	294
					Met/M	149	2-1	149
					His /H	155	2	310
					Phe/F	165	2	330
					Arg/R	174	2	348
					Tyr/Y	181	2	362
					Trp/W	204	2-1	204
8	925 [5×5×37]	32 [4×8]	3700 [10×10×37]		16	2220 [3×4×5×37]	32 [2×16+2-2]	4218 [6×19×37]
			т	ABLE	7			

The same subsets with 'rebels' removed

Here, the 'Total Nucleons' (column 2) is a straight copy of 'Nucleon Total' (Table 6, column 4), and refers to a <u>single</u> occurrence of the related amino acid. However, each amino acid normally occurs <u>several times</u> as a codon product in the Genetic Code (see Table 5); the precise number of times is recorded in column 3, above. Thus, the 'Nucleon Grand Total' (column 4) is the product of the related columns 2 and 3.

For the first subset, the total of nucleons is, of course, a multiple of 37 because each amino acid (AA) normally occurs twice. For the second, though not all represented twice, the total is nevertheless a multiple of 37.

Some additional features of Boulay's work, worthy of close attention, are summarised in the following table:

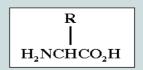
Particles	In the base of each amino acid	In all amino acids	In the 'rebel group'	In all amino acids without the 'rebel group'
NUCLEONS	74	7918	484	7434
	[= 37×2]	[=37x214]	[= 121×4]	[= 7×1062]
PROTONS	39	4264	260	4004
	[= 13x3]	[= 13x328]	[= 13×20]	[= 13x7x44]
NEUTRONS	35	3654	224	3430
	[= 7x5]	[= 7×522]	[= 7x32]	[= 7x7x7x10]

TABLE 8

Further interesting particle counts

Here we find that the particle sums for each of the amino acid bases and for the complete output of the 61 productive codons are multiples of 37 (the nucleons), 13 (the protons) and 7 (the neutrons). The derivation of these figures requires a scrutiny of the two following tables, in which is further revealed the potent fact that the total atom count is 1147, or 37x31.

Element	Approx Atomic Mass of most common isotope	Atomic Mass natural isotope mixture
Н	1	1.008
С	12	12.011
N	14	14.007
0	16	15.999
S	32	32.006



Amino acid: generic formula [side chain (R) and standard block (Std Blk)]

Atomic masses of the most common elements

AMINO	Emp	irical	Con	npos	ition	Atoms	Nucleons			DNA/RNA
ACID	С	Н	N	0	S	Atoms	Protons	Neutrons	Total	PF
Std Blk	2	4	1	2	0	9	39	35	74	61
Ala /A	3	7	1	2	0	13	48	41	89	4
Arg/R	6	14	4	2	0	26	94	80	174	6
Asn/N	4	8	2	3	0	17	70	62	132	2
Asp/D	4	7	1	4	0	16	70	63	133	2
Cys/C	3	7	1	2	1	14	64	57	121	2
Glu/E	5	9	1	4	0	19	78	69	147	2
Gln/Q	5	10	2	3	0	20	78	68	146	2
Gly /G	2	5	1	2	0	10	40	35	75	4
His /H	6	9	3	2	0	20	82	73	155	2
Ile /I	6	13	1	2	0	22	72	59	131	3
Leu/L	6	13	1	2	0	22	72	59	131	6
Lys/K	6	14	2	2	0	24	80	66	146	2
Met/M	5	11	1	2	1	20	80	69	149	1
Phe/F	9	11	1	2	0	23	88	77	165	2
Pro /P	5	10	1	2	0	18	63	52	115	4
Ser/S	3	7	1	3	0	14	56	49	105	6
Thr/T	4	9	1	3	0	17	64	55	119	4
Trp/W	11	12	2	2	0	27	108	96	204	1
Tyr/Y	9	11	1	3	0	24	96	85	181	2
Val /V	5	11	1	2	0	19	64	53	117	4

TABLE 9

Details of the particular compositions of the amino acids

AMINO	Parti	cles in the In	dividual Amino	Acids	DNA/RNA	Particles in the Products of the Genetic Code				
ACID	Atoms	Protons	Neutrons	Total	PF*	Atoms	Protons	Neutrons	Total	
Std Blk	9	39	35	74	61	549	2379	2135	4514	
Ala /A	13	48	41	89	4	52	192	164	356	
Arg/R	26	94	80	174	6	156	564	480	1044	
Asn/N	17	70	62	132	2	34	140	124	264	
Asp/D	16	70	63	133	2	32	140	126	266	
Cys/C	14	64	57	121	2	28	128	114	242	
Glu/E	19	78	69	147	2	38	156	138	294	
Gln/Q	20	78	68	146	2	40	156	136	292	
Gly/G	10	40	35	75	4	40	160	140	300	
His /H	20	82	73	155	2	40	164	146	310	
Ile /I	22	72	59	131	3	22/44	<mark>72</mark> /144	59 /118	131/262	
Leu/L	22	72	59	131	6	132	432	354	786	
Lys/K	24	80	66	146	2	48	160	132	292	
Met/M	20	80	69	149	1	20	80	69	149	
Phe/F	23	88	77	165	2	46	176	154	330	
Pro /P	18	63	52	115	4	72	252	208	460	
Ser/S	14	56	49	105	6	84	336	294	630	
Thr/T	17	64	55	119	4	68	256	220	476	
Trp/W	27	108	96	204	1	27	108	96	204	
Tyr/Y	24	96	85	181	2	48	192	170	362	
Val /V	19	64	53	117	4	76	256	212	468	

Totals	'rebels' included	1147	4264	3654	7918
locais	'rebels' excluded	1078	4004	3430	7434

TABLE 10

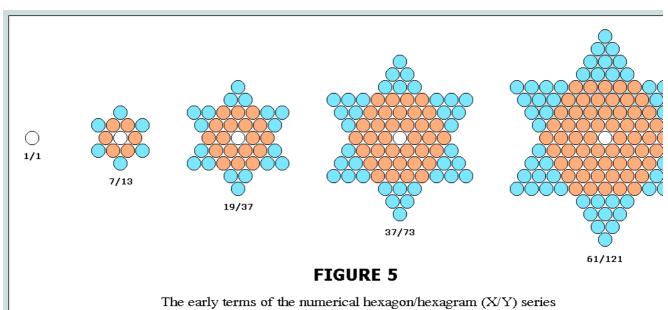
The particular implications of the amino acids appearing a total of 61 times as codon products

* PF represents 'product frequency'
i.e. the number of times a given amino acid appears
as a product in the DNA/RNA table of 64 codons

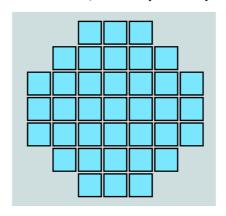
Observe here the splitting of the figures for isoleucine (Ile/I) because it features as a 'rebel' only once, but twice as a regular AA.

The figurate number associations

Boulay has clearly overlooked some additional, potentially significant, features of the foregoing results. For example, he might have pointed to the impressive pedigree of 37 as a number, *per se*, together with those matters of further interest and relevance that derive from its properties.

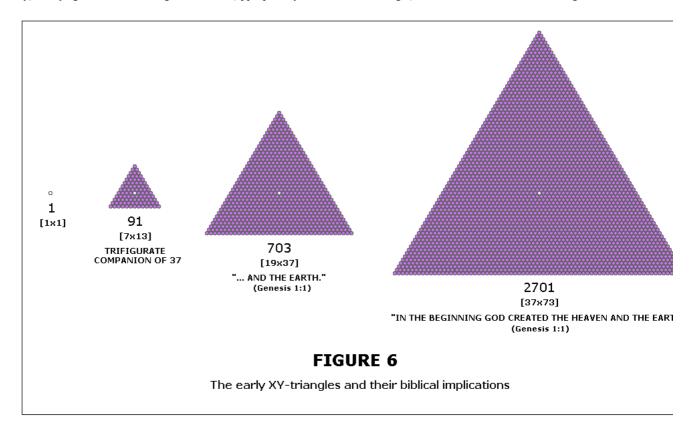


As revealed above, it is present in both hexagon and hexagram series of figurate numbers - a most rare event (there being only 2 more instances in the first million natural numbers). But it has yet a third symmetrical form as truncated square, thus:



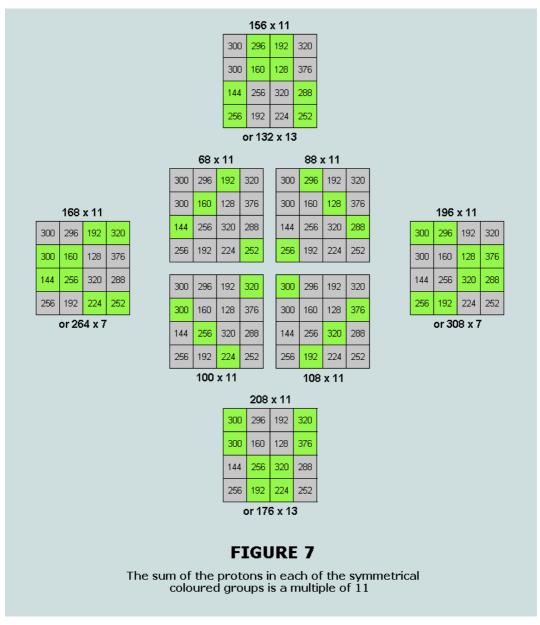
Clearly, therefore, 37 is a trifigurate number - sharing this exalted status with only one other number, 91. Interestingly, 91 = 7x13, i.e. the product of 2nd hexagon and related hexagram, as depicted above. But there are yet further examples selected from these series among the foregoing results; for example, 703 = 19x37; number of AA-producing codons = 61; large factor of nucleons in the rebel group = 121; and unadjusted proline nucleon count = 73.

One feature of considerable significance emerges here: namely, that the product of hexagon (X, say) by related hexagram (Y, say) always gives rise to a triangular number (appropriately termed an XY-triangle). This is made clear in the next figure.



The repunit associations

Boulay further draws attention to the interesting pattern depicted below in which 11 is revealed as a prominent feature of the proton sums of the canonical amino acids found in the genetic code table, 'rebels' excluded (proceed here for further details). Clearly, he has uncovered matters of some consequence.



Observe that 11 is the root prime for 2-digit repdigits, just as 37 is the root prime for 3-digit repdigits. Extending into 6-digit repunits, the entire set of [7, 11, 13, 37] is involved, as $111111 = 3 \times 7 \times 11 \times 13 \times 37$. Interestingly, the sum of the CVs of the Bible's first eight Hebrew words is 3003, or $3 \times 7 \times 11 \times 13 - 77$ th triangular number.

A final word from shCherbak

"Physics and chemistry are indifferent to the internal syntax of numerical language of arithmetic and, in particular, to the number system that this language employs. All they require from arithmetic is quantitative data. Absence of a privileged numerical system inherent to an object must therefore be a necessary condition of its natural origin. Recent research, however, has found an exception. That object is the universal genetic code. The genetic code turns out to be a syntactical structure of arithmetic, the result of unique summations carried out by some primordial abacus at least three and a half billion years ago. The decimal place-value numerical system with a zero conception was used for that arithmetic. It turned out that the zero sign governed the genetic code not only as an integral part of the decimal system, but also directly as an acting arithmetical symbol. Being non-material abstractions, all the zero, decimal syntax, and unique summations can display an artificial nature of the genetic code. They refute traditional ideas about the stochastic origin of the genetic code. A new order in the genetic code hardly ever went through chemical evolution and, seemingly, originally appeared as pure information like arithmetic itself."

[the abstract to his "The Arithmetic Origin of the Genetic Code" which appears (2008) as a chapter in the book "The Codes of Life" ISBN 978-1-4020-6340-4 (Online)]

Clearly, shCherbak has particularly in mind the eye-catching repdigits 111, 222, etc. which so frequently appear in the particle counts as described above. These represent multiples of 37 only as mediated by 10 in the decimal place-value system of numeration. And that system has only become known to man over the last millennium, or so; and only universally recognised and used by him within recent centuries. It must follow that the genetic code is an artefact. Whether directly, or by a process of infinite regression, its true Author must therefore be the Judeo-Christian Creator of all things. Significantly, the logic of shCherbak's argument is not extended by him to encompass this final step.

Conclusions

The reality of the appearance of 37 (now including its numero-geometrical analogues, 7, 13, 19, 61, 73 and 121, besides its multiples, 666 and 703), among the various particle counts of the 20 canonical amino acids is now supported in the writings of two experts in the field of genetics, viz. shCherbak and Rakocevic, and in the writings of a significant contributor to the nascent field of bioinformatics, Boulay. Clearly, these individuals have independently stumbled upon a matter of supreme importance, viz. that of directly relating the Creator with certain of the *modi operandi* of His Creativity!

So, on what rational grounds will Richard Dawkins *et al* continue to preach militant atheism? And, our team of investigators having inadvertently provided proof of the Being and Sovereignty of God, on what rational grounds will evolutionists continue to insist on 'dinosaurs before birds', when the Creator has clearly declared, 'birds before dinosaurs' (Genesis 1: 20-25)?!

Vernon Jenkins MSc

2010-03-22

Wikipedia Links for the properties of each of the canonical amino acids:

http://en.wikipedia.org/wiki/Alanine http://en.wikipedia.org/wiki/Arginine http://en.wikipedia.org/wiki/Asparagine http://en.wikipedia.org/wiki/Aspartic_acid http://en.wikipedia.org/wiki/Cysteine http://en.wikipedia.org/wiki/Glutamic acid http://en.wikipedia.org/wiki/Glutamine http://en.wikipedia.org/wiki/Glycine http://en.wikipedia.org/wiki/Histidine http://en.wikipedia.org/wiki/Isoleucine http://en.wikipedia.org/wiki/Leucine http://en.wikipedia.org/wiki/Lysine http://en.wikipedia.org/wiki/Methionine http://en.wikipedia.org/wiki/Phenylalanine http://en.wikipedia.org/wiki/Proline http://en.wikipedia.org/wiki/Serine http://en.wikipedia.org/wiki/Threonine http://en.wikipedia.org/wiki/Tryptophan http://en.wikipedia.org/wiki/Tyrosine

http://en.wikipedia.org/wiki/Valine