

The 55-entity triangular genetic code matrix and the 3 to 2 ratio

The genetic code as a geometric algebra biological system

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Abstract: From the table of the standard genetic code at 64 codons, 61 amino acids and 3 Stop signals, it is invested a reduced triangular matrix of the genetic code comprising just twice fifty-five entities. In relationship with number theory, many symmetrical and asymmetrical geometric sub-configurations of this triangular matrix show that the amino acids are distributed very singularly in various 3 to 2 value ratios according to the concept of their numbering, a concept recently introduced by the author in a published article.

Keywords: genetic code, symmetry, amino acid numbering, fractal, nucleobases, set theory, molecular biology, number theory.

1. Introduction

Today, it is now firmly established that living matter is organized via a called “universal” genetic code and that this genetic code encodes only, and very precisely, twenty proteinogenic amino acids. This number is not arbitrary, it is equal to $5x$. More precisely this number of 20 entities is equal to $3x + 2x$ entities with a value of x equal to 4.

In its entirety, the genetic code is organized into sixty-four coding entities to which correspond sixty-one amino acids and three nonsense signals. These three different values are therefore in no way equal to $5x$ entities. . It turns out that each amino acid is associated with a seemingly random number of codons.

In fact, codons are usually encoded with codons at the same first two identical nucleobases. In this universal genetic code, each amino acid is associated with a set of codons with two identical first bases varying from 1 to 4 codons.

Three amino acids are encoded with more than one of these sets at the same first nucleobases. Arginine, Leucine and Serine encoded by these 4-codon sets are also encoded with 2-codon sets.

We therefore propose, to consider only a reduced genetic code of these smaller sets since for these three AAs*, a set of larger codons also encodes them. We therefore subtract from the initial 64 codons these three times two codons and we do not consider the three "Stop" codons either. Thus, we lighten the initial genetic code of 9 codons and therefore keep only 55 codons for the coding of the 20 amino acids.

This residual number of 55 codons is therefore equal to $5x$ entities with a value of x equal to 11. Thus, we reduce the genetic code to $5x$ coding entities, the DNA triplets, and to $5x$ coded entities, the canonical amino acids. We therefore propose a matrix of the genetic code of 55 triplets for 55 amino acids.

The number 55 is very special in number theory. This is directly related to the decimal system. It is in fact a triangular number with value T_{10} . That is, it is the sum of the first strictly positive ten numbers from 1 to 10.

The study of a lighter genetic code configured in a triangular matrix of 55 entities reveals many singular phenomena in the distribution of amino acids differentiated according to the concept of their numbering proposed and introduced in the article “*Numbering of the twenty proteinogenic amino acids and new alphanumerical nomenclature proposal to them*” [1].

* To simplify, in some parts of text and tables, AA (or AAs) is used to replace amino acid appellation.

2. Two sets of proteinogenic amino acids

In preview papers [1 – 2 and 3], using two very different approaches, we identified two sets of amino acids of respective size 3 to 2. In these previous articles, from two different but converging ways, we therefore created a set of 12 AAs opposing, in a ratio of 3 to 2, to 8 other AAs. Before continuing our investigations, we must recall here this double concept: that of AA numbering and the concept of the ultimate genetic code.

2.1. Numbering of the twenty canonical amino acids

In preview published paper “*Numbering of the twenty proteinogenic amino acids and new alphanumeric nomenclature proposal to them*” [1], we have demonstrated that a large number of different amino acid attributes arrange themselves numerically in exact 3/2 value ratios according to a numbering system of the twenty proteinogenic amino acids. We will then show that this numbering is closely related to the configuration of the matrix of the ultimate genetic code by transcending the ultimate 3/2 ratio.

From a subtle numbering of the 64 codons of the universal genetic code, we propose a numbering (from 0 to 19) of the twenty amino acids. These two numbering systems, including the first proposed by Professor Sergey Petoukhov [4], are very directly dependent on the physico-chemical properties of the four nucleobases that make up DNA. They are therefore very legitimate to be used for the study of the genetic code mechanism. When we number the twenty amino acids, which are, very importantly, 5x in number, then we classify them into two symmetrical sets of 12 (or 3x) and 8 (or 2x) entities.

2.1.2. Petoukhov’s numbering of the 64 genetic code codons

In his investigations of the genetic code [3] Sergey Petoukhov assigns a number from 0 to 63 to each of the sixty-four codons. This Petoukhov numbering is directly dependent on the physico-chemical properties of the four DNA coding bases. Using a very sophisticated method, Sergey Petoukhov manages to classify the full sixty-four codons set using a binary language (or alphabet, we invite the reader to consult the full article by Sergey Petoukhov [3]). Depending on whether each nucleobase can undergo deamination or not, Sergey Petoukhov assigns them either the value 1 or the value 0 as illustrated Figure 1. Also, depending on whether each nucleobase can undergo depurination or not, Sergey Petoukhov assigns them either the value 0 or the value 1.

nucleobases	Adenine	Thymine	Guanine	Cytosine
Possible deamination: yes = 1 no = 0	1	0	0	1
Possible depurination: yes = 0 no = 1	0	1	0	1

Figure 1: Method of assigning a double binary value to the four DNA nucleobases according to Sergey Petoukhov [4].

This double criterion makes it possible, for each codon, to create a six-digit binary number by juxtaposition of two three-digit numbers as described in Figure 2.

physico-chemical criteria →	possible deamination yes = 1 no = 0			possible depurination yes = 0 no = 1			
	codon →	A	T	G	A	T	G
binary convert →		1	0	0	0	1	0
	ATG Met 34 100010						
							ATG = 100010 = 34

Figure 2: Method of assigning a number to codons according to Sergey Petoukhov. See Figures 1 and 3 also.

Sergey Petoukhov then classifies very subtly in superimposed squares of 4, 16 and 64 boxes the 64 codons and numbers them in the order of the bases G→T→A→C for the first, second and third bases. In this numbering imagined by Sergey Petoukhov, the GGG codon thus bears the number 0 (binary 000000) and the CCC codon the number 63 (binary 111111). Figure 3 illustrates this complete numbering of the 64 genetic code codons set.

We would like to support here the importance that Sergey Petoukhov [4] gives to these criteria of deamination and depurination. It is in fact largely through these criteria that the four nucleobases can "mutate" within DNA chains, also allowing the evolution of living organisms.

	111	110	101	100	011	010	001	000
111	CCC Pro 63 111111	CCA Pro 62 111110	CAC His 61 111101	CAA Gln 60 111100	ACC Thr 59 111011	ACA Thr 58 111010	AAC Asn 57 111001	AAA Lys 56 111000
110	CCT Pro 55 110111	CCG Pro 54 110110	CAT His 53 110101	CAG Gln 52 110100	ACT Thr 51 110011	ACG Thr 50 110010	AAT Asn 49 110001	AAG Lys 48 110000
101	CTC Leu 47 101111	CTA Leu 46 101110	CGC Arg 45 101101	CGA Arg 44 101100	ATC Ile 43 101011	ATA Ile 42 101010	AGC Ser 41 101001	AGA Arg 40 101000
100	CTT Leu 39 100111	CTG Leu 38 100110	CGT Arg 37 100101	CGG Arg 36 100100	ATT Ile 35 100011	ATG Met 34 100010	AGT Ser 33 100001	AGG Arg 32 100000
011	TCC Ser 31 011111	TCA Ser 30 011110	TAC Tyr 29 011101	TAA Stop 28 011100	GCC Ala 27 011011	GCA Ala 26 011010	GAC Asp 25 011001	GAA Glu 24 011000
010	TCT Ser 23 010111	TCG Ser 22 010110	TAT Tyr 21 010101	TAG Stop 20 010100	GCT Ala 19 010011	GCG Ala 18 010010	GAT Asp 17 010001	GAG Glu 16 010000
001	TTC Phe 15 001111	TTA Leu 14 001110	TGC Cys 13 001101	TGA Stop 12 001100	GTC Val 11 001011	GTA Val 10 001010	GGC Gly 9 001001	GGA Gly 8 001000
000	TTT Phe 7 000111	TTG Leu 6 000110	TGT Cys 5 000101	TGG Trp 4 000100	GTT Val 3 000011	GTG Val 2 000010	GGT Gly 1 000001	GGG Gly 0 000000

Figure 3: Numbering of the 64 codons according to Sergey Petoukhov genetic code investigations [4] and distinction (grey areas) of the first appearance of each of the 20 coded amino acids. See Figures 1 and 2 also.

2.1.3. Numbering of the twenty proteinogenic amino acids

From this numbering system, in order to assign a number to each of the twenty proteinogenic amino acids, the most logical procedure is therefore proposed here, which is to follow the order of appearance of the amino acids according to this numbering of the codons (from 0 to 63) of the table by Sergey Petoukhov (Figure 3).

Only one number
assigning to amino acids

Pro	Pro	His	Gln	Thr	Thr	Asn	Lys
Pro	19 Pro	18 His	17 Gln	Thr	16 Thr	15 Asn	14 Lys
Leu	Leu	Arg	Arg	Ile	Ile	Ser	Arg
Leu	Leu	Arg	Arg	13 Ile	12 Met	Ser	11 Arg
Ser	Ser	Tyr	Stop	Ala	Ala	Asp	Glu
Ser	10 Ser	9 Tyr	Stop	Ala	8 Ala	7 Asp	6 Glu
Phe	Leu	Cys	Stop	Val	Val	Gly	Gly
5 Phe	4 Leu	3 Cys	2 Trp	Val	1 Val	Gly	0 Gly

Figure 4: Assigning a single only one number to each of 20 proteinogenic amino acids in the table of the complete genetic code. See Figure 3 also.

By this process, it is thus assigned (Figure 4) number 0 to Glycine, number 1 to Valine and to Proline, the last amino acid to appear according to this order of numbering of the sixty-four genetic code codons, 19 as number. Also, as we give the explanation in Appendix A6, we now designate the twenty AAs by a 5-character alphanumeric symbol.

2.1.4. Symmetrical break-up of the 20 AAs in ratio 3 to 2

Now that we have determined a numbering of amino acids by assigning them a unique and personal number, we propose to isolate these twenty entities in two sets of unequal size. We therefore distinguish, in Figure 5, a first set of 12 entities then a second set of 8 other entities. As illustrated in Figure 5, these two sets then oppose each other in a ratio of value 3/2.

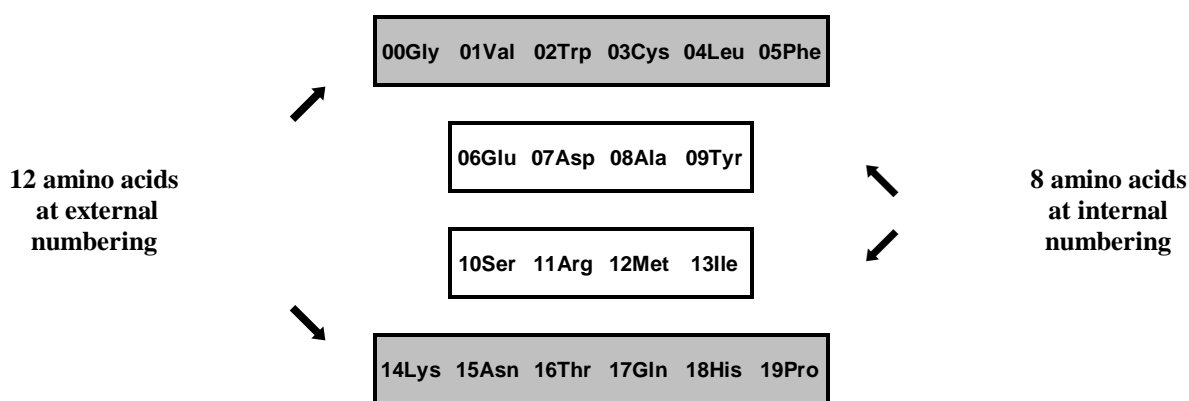


Figure 5: Conventional representation of 20 proteinogenic amino acids numbering in symmetry graphics. Since their numbering, symmetrical break-up of the 20 AAs into two sets of 2 times 6 versus 2 times 4 entities. See Figure 4 also.

Thereby, using symmetry graphics, each of the 20 amino acids is symmetrically positioned to the one of opposite numbering in relation to the numbering order of these 20 AAs: 00Gly versus 19Pro, 01Val versus 18His, etc.

Also, we therefore isolate two numbering zones:

- an area called “external” with inside the first six and last six numbered AAs (from 0 to 5 and from 14 to 19),
- an area called “internal” with inside the two times four centrally numbered AAs (from 6 to 13).

2.2. The ultimate genetic code concept

In preview published paper “Symmetry and Asymmetry of The Ultimate Genetic Code Matrix” [3], we introduced the concept of the ultimate genetic code. Here is a brief overview. From the matrix of 64 double entities of the universal genetic code, we isolate just twenty double entities corresponding quite simply to the twenty proteinogenic amino acids and them corresponding twenty DNA biplets.

2.2.1. The ultimate genetic code table construction

To this purpose, we use a mechanism for filling in the initial table of the universal genetic code by retaining only one triplet for each of the twenty amino acids. Also we do not consider stop signals (nonsense).

AAA	Lys	GAA	Glu	TAA	-	CAA	Gln
AAG	Lys	GAG	Glu	TAG	-	CAG	Gln
AAT	Asn	GAT	Asp	TAT	Tyr	CAT	His
AAC	Asn	GAC	Asp	TAC	Tyr	CAC	His
AGA	Arg	GGA	Gly	TGA	-	CGA	Arg
AGG	Arg	GGG	Gly	TGG	Trp	CGG	Arg
AGT	Ser	GGT	Gly	TGT	Cys	CGT	Arg
AGC	Ser	GGC	Gly	TGC	Cys	CGC	Arg
ATA	Ile	GTA	Val	TTA	Leu	CTA	Leu
ATG	Met	GTG	Val	TTG	Leu	CTG	Leu
ATT	Ile	GTT	Val	TTT	Phe	CTT	Leu
ATC	Ile	GTC	Val	TTC	Phe	CTC	Leu
ACA	Thr	GCA	Ala	TCA	Ser	CCA	Pro
ACG	Thr	GCG	Ala	TCG	Ser	CCG	Pro
ACT	Thr	GCT	Ala	TCT	Ser	CCT	Pro
ACC	Thr	GCC	Ala	TCC	Ser	CCC	Pro

Figure 6: Vertical or horizontal filler mechanism generating the ultimate genetic code (in base order A → G → T → C).

The mechanism for filling the genetic code table can be done line by line as described in Figure 6 but also column by column while always respecting the order of the bases A-G-T-C. This filling order generating the ultimate genetic code is related to the

degree of affinity of the bases between them: in relation to Adenine, the first base considered in the table of the genetic code (first row, first column), the second base, Guanine, is the other base of the same nature (A and G both being purines), the third, Thymine, is the complementary base (of the double DNA chain) to Adenine and the fourth and last base, Cytosine, is the opposite base: neither of the same nature nor complementary to Adenine.

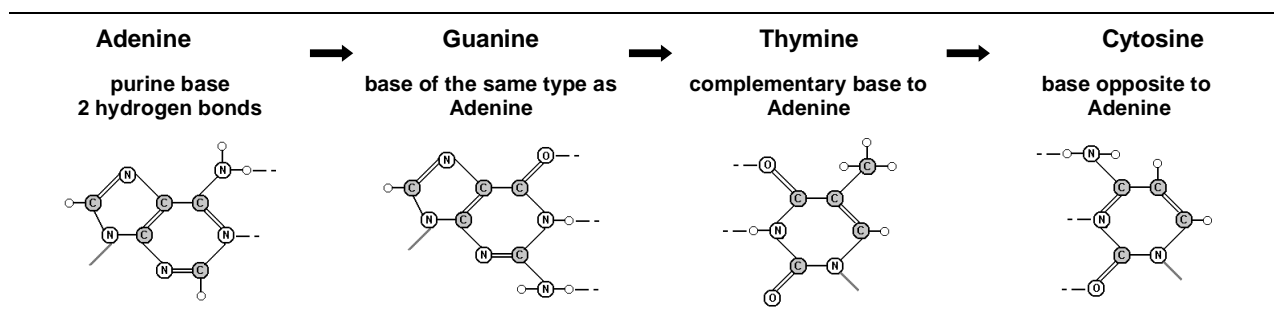


Figure 7: Classification of the four DNA bases in order A→G→T→C according to their degree of affinity.

This filling rule has an influence on the selected position of three amino acids which are normally present in two boxes of the complete table of the genetic code: SER, ARG and LEU (see Figure 6).

These different paths, always respecting the order of the bases A-G-T-C and progressively isolating, one after the other, twenty codons and twenty coded ones, produce the same final table of the ultimate genetic code as presented in Figure 8: twenty unique codons associated with twenty unique proteinogenic coded amino acids.

Generation of the ultimate genetic code						The ultimate genetic code: 20 codons - 20 coded AAs			
AAA Lys	GAA Glu	TAA -	CAA Gln	AA Lys	GA Glu	TA Tyr	CA Gln		
AAG Lys	GAG Glu	TAG -	CAG Gln	AA Asn	GA Asp	TA Tyr	CA His		
AAT Asn	GAT Asp	TAT Tyr	CAT His	AG Arg		TG Trp			
AAC Asn	GAC Asp	TAC Tyr	CAC His	AG Ser	GG Gly	TG Cys			
AGA Arg	GGA Gly	TGA -	CGA Arg	AT Ile		TT Leu			
AGG Arg	GGG Gly	TGG Trp	CGG Arg	AT Met	GT Val	TT Phe			
AGT Ser	GGT Gly	TGT Cys	CGT Arg	AC Thr					
AGC Ser	GGC Gly	TGC Cys	CGC Arg	AC Thr	GC Ala				CC Pro
ATA Ile	GTA Val	TTA Leu	CTA Leu						
ATG Met	GTG Val	TTG Leu	CTG Leu						
ATT Ile	GTT Val	TTT Phe	CTT Leu						
ATC Ile	GTC Val	TTC Phe	CTC Leu						
ACA Thr	GCA Ala	TCA Ser	CCA Pro						
ACG Thr	GCG Ala	TCG Ser	CCG Pro						
ACT Thr	GCT Ala	TCT Ser	CCT Pro						
ACC Thr	GCC Ala	TCC Ser	CCC Pro						

Figure 8: Generating, from the table of the universal genetic code, of the table of the ultimate genetic code. See Figures 6 and 7 also.

In this ultimate genetic code, it is no longer considered the third coding base but only the first two, i.e., for each of the twenty AAs, a biplet of two nucleobases.

2.2.2. The ultimate genetic code table

The final association of the symmetrical and asymmetrical groups of two boxes containing either three or two amino acids form two groupings (or coding areas) of eight boxes containing respectively a total of twelve and eight amino acids (as well as twelve and eight codons respectively).

These two groupings are therefore opposed in a duality whose ratio is equal to 3/2. This phenomenon (this ratio) is thus conventionally called "The ultimate 3/2 ratio". Figure 9 graphically introduces the concept of the ultimate 3/2 ratio into the entire table of the ultimate genetic code.

The ultimate genetic code matrix

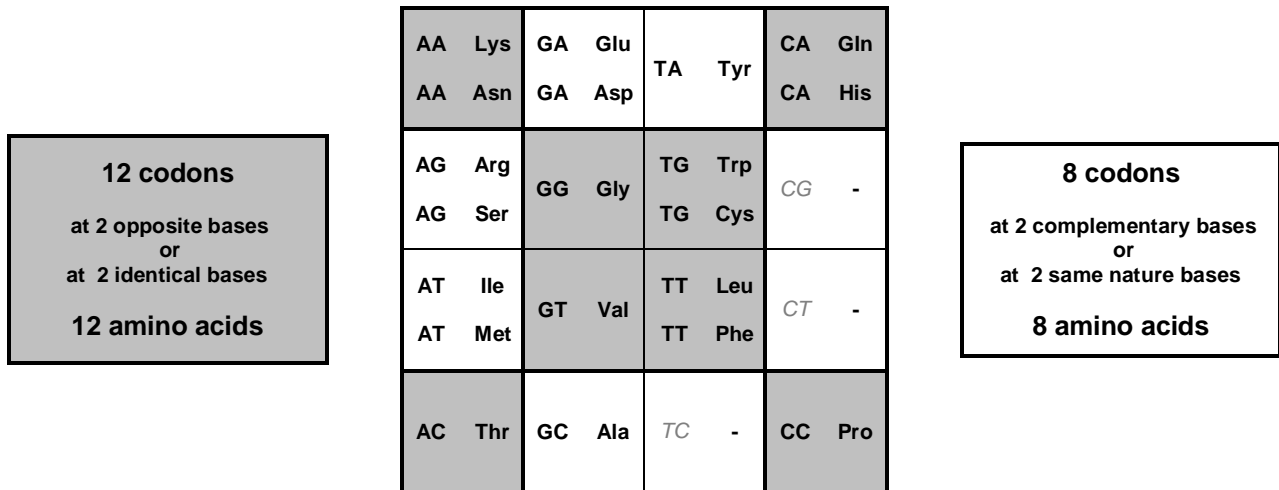


Figure 9: The ultimate genetic code concept: 12 amino acids and 12 codons with 2 opposite or identical bases versus 8 amino acids and 8 codons with 2 complementary or similar bases.

2.3. Amino acid numbering and ultimate genetic code matrix

By introducing the concept of ultimate genetic code, we were able to conclude that the matrix of this optimized code is organized into two areas of 12 versus 8 entities. What we call the ultimate 3/2 ratio. Using the concept of numbering the twenty proteinogenic AAs, we have also defined two areas of 12 versus 8 entities.

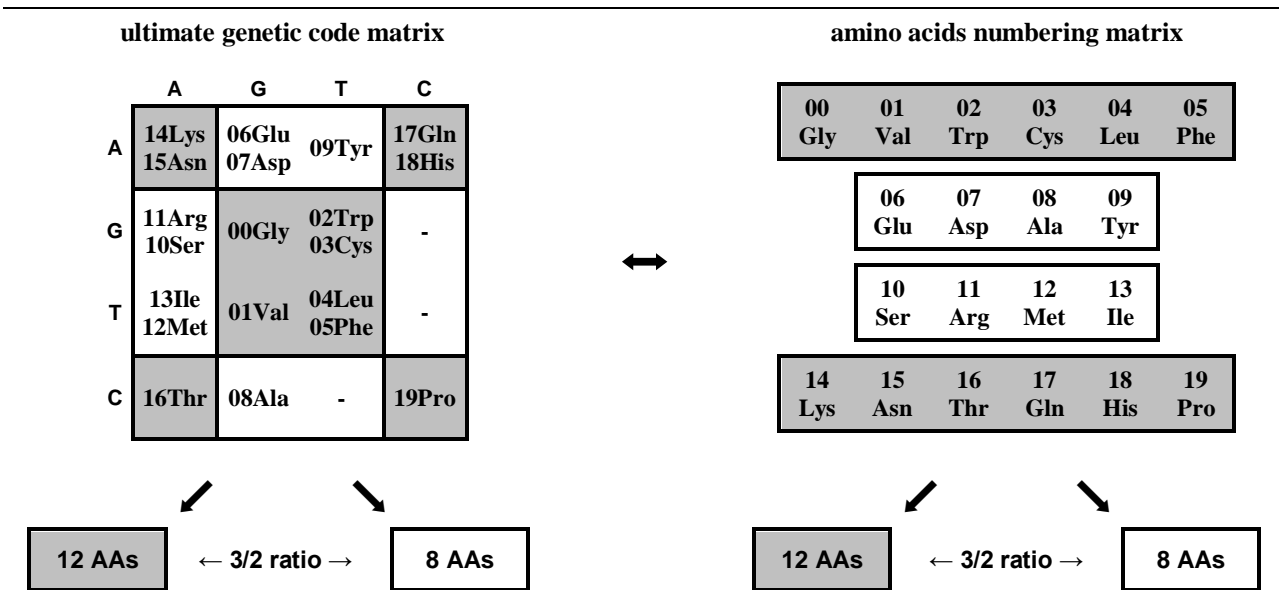


Figure 10: The two convergent matrix of the ultimate genetic code concept and the AA numbering concept.. See Figures 5 and 9.

As we can discover in Figure 10, it turns out that these two double areas are coincident. In fact, the 12 amino acids with two identical bases or two opposite bases are entirely those with external numbering. The 8 AAs with two bases of the same nature or with complementary bases are entirely those with internal numbering. This phenomenon amplifies these two twin concepts which we merge into the genetic concept of ultimate ratio 3 to 2.

We will can now study the distribution of these two defined sets of amino acids in a triangular matrix of the genetic code of 55 entities.

3. The triangular genetic code matrix

In relationship with number theory, with set theory, genetic code is singularly organized. We demonstrate this through a geometric study of a genetic matrix of size T_{10} , or 55 entities. This matrix is legitimately constructed from the eight-by-eight boxing square genetic code table as it appears in the biochemistry literature.

3.1 Lighter genetic code table

In its entirety, the genetic code is organized into sixty-four coding entities to which correspond sixty-one amino acids and three nonsense signals. These three different values are therefore in no way equal to $5x$ entities. It turns out that each amino acid is associated with a seemingly random number of codons.

In fact, codons are usually encoded with codons at the same first two identical nucleobases. In this universal genetic code, each amino acid is associated with a set of codons with two identical first bases varying from 1 to 4 codons.

Three amino acids are encoded with more than one of these sets at the same first nucleobases. Arginine, Leucine and Serine encoded by these 4-codon sets are also encoded with 2-codon sets.

**Square complete genetic code table:
64 codons to 61 AAs and 3 Stop signals**

63 CCC 19Pro	62 CCA 19Pro	61 CAC 18His	60 CAA 17Gln	59 ACC 16Thr	58 ACA 16Thr	57 AAC 15Asn	56 AAA 14Lys
55 CCT 19Pro	54 CCG 19Pro	53 CAT 18His	52 CAG 17Gln	51 ACT 16Thr	50 ACG 16Thr	49 AAT 15Asn	48 AAG 14Lys
47 CTC 04Leu	46 CTA 04Leu	45 CGC 11Arg	44 CGA 11Arg	43 ATC 13Ile	42 ATA 13Ile	41 AGC 10Ser	40 AGA 11Arg
39 CTT 04Leu	38 CTG 04Leu	37 CGT 11Arg	36 CGG 11Arg	35 ATT 13Ile	34 ATG 12Met	33 AGT 10Ser	32 AGG 11Arg
31 TCC 10Ser	30 TCA 10Ser	29 TAC 09Tyr	28 TAA Stop	27 GCC 08Ala	26 GCA 08Ala	25 GAC 07Asp	24 GAA 06Glu
23 TCT 10Ser	22 TCG 10Ser	21 TAT 09Tyr	20 TAG Stop	19 GCT 08Ala	18 GCG 08Ala	17 GAT 07Asp	16 GAG 06Glu
15 TTC 05Phe	14 TTA 04Leu	13 TGC 03Cys	12 TGA Stop	11 GTC 01Val	10 GTA 01Val	9 GGC 00Gly	8 GGA 00Gly
7 TTT 05Phe	6 TTG 04Leu	5 TGT 03Cys	4 TGG 02Trp	3 GTT 01Val	2 GTG 01Val	1 GGT 00Gly	0 GGG 00Gly

**Square lighter genetic code table:
55 codons to 55 AAs → $5x$ codons to $5x$ AAs**

63 CCC 19Pro	62 CCA 19Pro	61 CAC 18His	60 CAA 17Gln	59 ACC 16Thr	58 ACA 16Thr	57 AAC 15Asn	56 AAA 14Lys
55 CCT 19Pro	54 CCG 19Pro	53 CAT 18His	52 CAG 17Gln	51 ACT 16Thr	50 ACG 16Thr	49 AAT 15Asn	48 AAG 14Lys
47 CTC 04Leu	46 CTA 04Leu	45 CGC 11Arg	44 CGA 11Arg	43 ATC 13Ile	42 ATA 13Ile	41 AGC 10Ser	40 AGA 11Arg
39 CTT 04Leu	38 CTG 04Leu	37 CGT 11Arg	36 CGG 11Arg	35 ATT 13Ile	34 ATG 12Met	33 AGT 10Ser	32 AGG 11Arg
31 TCC 10Ser	30 TCA 10Ser	29 TAC 09Tyr	28 TAA Stop	27 GCC 08Ala	26 GCA 08Ala	25 GAC 07Asp	24 GAA 06Glu
23 TCT 10Ser	22 TCG 10Ser	21 TAT 09Tyr	20 TAG Stop	19 GCT 08Ala	18 GCG 08Ala	17 GAT 07Asp	16 GAG 06Glu
15 TTC 05Phe	14 TTA 04Leu	13 TGC 03Cys	12 TGA Stop	11 GTC 01Val	10 GTA 01Val	9 GGC 00Gly	8 GGA 00Gly
7 TTT 05Phe	6 TTG 04Leu	5 TGT 03Cys	4 TGG 02Trp	3 GTT 01Val	2 GTG 01Val	1 GGT 00Gly	0 GGG 00Gly

Figure 11: Complete genetic code (64 codons) and lighter genetic code (55 codons) with only, for each AA, consideration of the largest codons sets with the first two identical nucleobases. This original configuration of the genetic code is linked to the concept of numbering the 20 AAs: see text and illustrations in Chapter 2.

As illustrated Figure 11, we therefore propose, to consider only a reduced genetic code of these smaller sets since for these three AAs, a set of larger codons also encodes them. We therefore subtract from the initial 64 codons these three times two codons and we do not consider the three "Stop" codons either. Thus, we lighten the initial genetic code of 9 codons and therefore keep only 55 codons for the coding of the 20 amino acids.

3.2. Triangular genetic code matrix construction

This residual number of 55 codons is therefore equal to $5x$ entities with a value of x equal to 11. Thus, we reduce the genetic code to $5x$ coding entities, the DNA triplets, and to $5x$ coded entities, the proteinogenic amino acids. We therefore propose a matrix of the genetic code of 55 triplets for 55 amino acids.

The number 55 is very special in number theory. This is directly related to the decimal system. It is in fact a triangular number with value T_{10} . That is, it is the sum of ten numbers from 1 to 10.

Thus, as illustrated in Figure 12, from the square table of the genetic code reduced to 55 entities, we construct a triangular matrix of 10 lines. These ten lines are progressive in size from 1 to 10 columns. This triangular matrix is therefore of size T_{10} and therefore includes 55 boxes.

In this triangular matrix, we arrange the 55 residual codons (64 -9) in the order of their previously introduced numbering, i.e. in the order of the original table by Sergei Petoukhov [4] so from number 0 to number 63 (See Figure 3). These 55 codons are therefore classified into a triangular number sequence of T_{10} as size. In each of these 55 boxes, 55 coded amino acids therefore also appear, associated with their respective codon.

Square lighter genetic code:
55 codons to 55 AAs → 5x codons to 5x AAs

63 CCC 19Pro	62 CCA 19Pro	61 CAC 18His	60 CAA 17Gln	59 ACC 16Thr	58 ACA 16Thr	57 AAC 15Asn	56 AAA 14Lys
55 CCT 19Pro	54 CCG 19Pro	53 CAT 18His	52 CAG 17Gln	51 ACT 16Thr	50 ACG 16Thr	49 AAT 15Asn	48 AAG 14Lys
47 CTC 04Leu	46 CTA 04Leu	45 CGC 11Arg	44 CGA 11Arg	43 ATC 13Ile	42 ATA 13Ile	41 AGC 10Ser	40 AGA 11Arg
39 CTT 04Leu	38 CTG 04Leu	37 CGT 11Arg	36 CGG 11Arg	35 ATT 13Ile	34 ATG 12Met	33 AGT 10Ser	32 AGG 11Arg
31 TCC 10Ser	30 TCA 10Ser	29 TAC 09Tyr	28 TAA Stop	27 GCC 08Ala	26 GCA 08Ala	25 GAC 07Asp	24 GAA 06Glu
23 TCT 10Ser	22 TCG 10Ser	21 TAT 09Tyr	20 TAG Stop	19 GCT 08Ala	18 GCG 08Ala	17 GAT 07Asp	16 GAG 06Glu
15 TTC 05Phe	14 TTA 04Leu	13 TGC 03Cys	12 TGA Stop	11 GTC 01Val	10 GTA 01Val	9 GGC 00Gly	8 GGA 00Gly
7 TTT 05Phe	6 TTG 04Leu	5 TGT 03Cys	4 TGG 02Trp	3 GTT 01Val	2 GTG 01Val	1 GGT 00Gly	0 GGG 00Gly

The 55-entity triangular genetic code matrix
55 codons to 55 AAs → 5x codons to 5x AAs

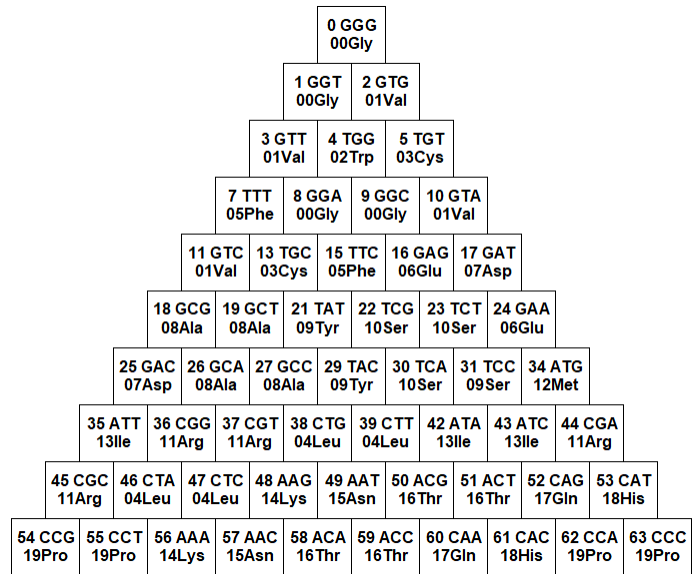


Figure 12: From lighter genetic code (55 codons), construction of the triangular genetic code matrix in triangular number sequence.

3.3. Triangular genetic code matrix and the two sets of AAs

in the published article “*Numbering of the twenty proteinogenic amino acids and new alphanumeric nomenclature proposal to them*” [1] and in preview preprint “*Symmetry and Asymmetry of The Ultimate Genetic Code Matrix*” [3], it has been widely demonstrated that the twenty proteinogenic amino acids are organized in varied and singular arithmetic arrangements with a ratio of 3/2. This considering the two twice concepts of AA numbering and the ultimate genetic code.

We will now demonstrate that the same geometrically arithmetic phenomena operates within the triangular matrix of the genetic code newly introduced here.

AA numbering
and ultimate genetic code matrices

00Gly 4	01Val 4	02Trp 1	03Cys 2	04Leu 4	05Phe 2
06Glu 2	07Asp 2	08Ala 4	09Tyr 2		
10Ser 4	11Arg 4	12Met 1	13Ile 3		
14Lys 2	15Asn 2	16Thr 4	17Gln 2	18His 2	19Pro 4

33 codons
33 AAs ← 3/2 ratio → 22 codons
22 AAs

AA 2 AA 2	GA 2 GA 2	TA 2 CA 2	CA 2 CA 2
AG 4 AG 4	GG 4	TG 1 TG 2	-
AT 3 AT 1	GT 4	TT 4 TT 2	-
AC 4	GC 4	-	CC 4

Triangular genetic code matrix

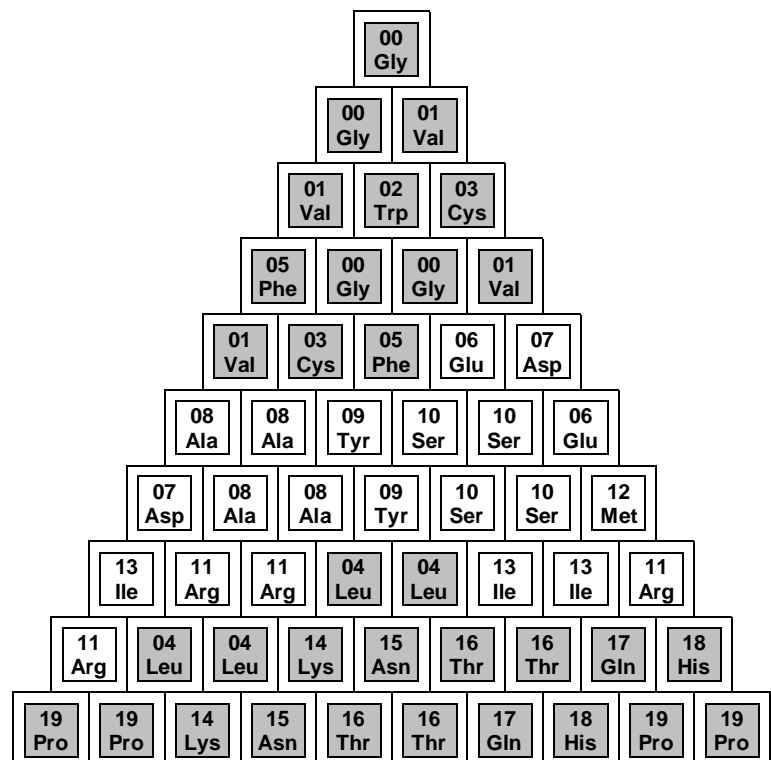


Figure 13: Distribution of amino acids in the 55-entity triangular genetic code matrix according to twice concept of AA numbering and to ultimate genetic code. See Figures 5, 9 and 12.

In Figure 13, the two sets of amino acids previously defined according to a double concept are clearly identified. In the interest of simplifying geometric demonstrations, there is no longer any mention of the respective codons (DNA triplets) of the coded AAs. It is therefore simply studied here the distribution of the twenty proteinogenic amino acids in this 55-entity triangular genetic code matrix.

We are therefore studying a triangular matrix of $5x$ entities, also $3x + 2x$ entities with x equal to 11. As it appears immediately in Figure 13, it turns out that $3x$ AAs with external numbering are opposed to $2x$ AAs with internal numbering. In fact, in this matrix there are 33 AAs of external numbering versus 22 of internal numbering, this in an exact ratio of value 3 to 2.

As we introduced in Chapter 2.3 and illustrated Figure 10, the set of AAs with external numbering merges with that of AAs with identical or opposite nucleobases (DNA bipelets of the called "genetic code ultimate"). Also, that of AAs with external numbering merges with that of AAs with two nucleobases of the same nature or complementary. To simplify the demonstrations, we will now just name these two sets of outer numbering AAs and inner numbering AAs. In all graphic demonstrations, the outer AAs will be distinguished in grey and the inner AAs in white.

4. Triangular genetic code matrix and 3 to 2 ratio

Inside the 55-entity triangular matrix of the genetic code, $3x$ AAs at outer numbering and $2x$ AAs at inner numbering therefore oppose each other overall. Numerous and varied symmetrical and asymmetrical divisions of this entire matrix show a very sophisticated organization of the genetic code linked to the concept of numbering the twenty proteinogenic amino acids. Indeed, in all of the configurations proposed, the two sets of amino acids previously defined according to their numbering are always distributed in exact ratios of value $3/2$. These configurations consist of complementary subsets of the 55-entity triangular matrix. these configurations are geometrically arranged in a symmetrical or asymmetrical way but also by entanglement of these two notions.

4.1. Linear configurations

In Figure 14, the 55-entity genetic code matrix is split into two subsets of 25 and 30 boxes. This is done by alternating the ten different lines of this matrix. In these two $5x$ entities areas, outer AAs and inner AAs oppose in exact $3/2$ ratios.

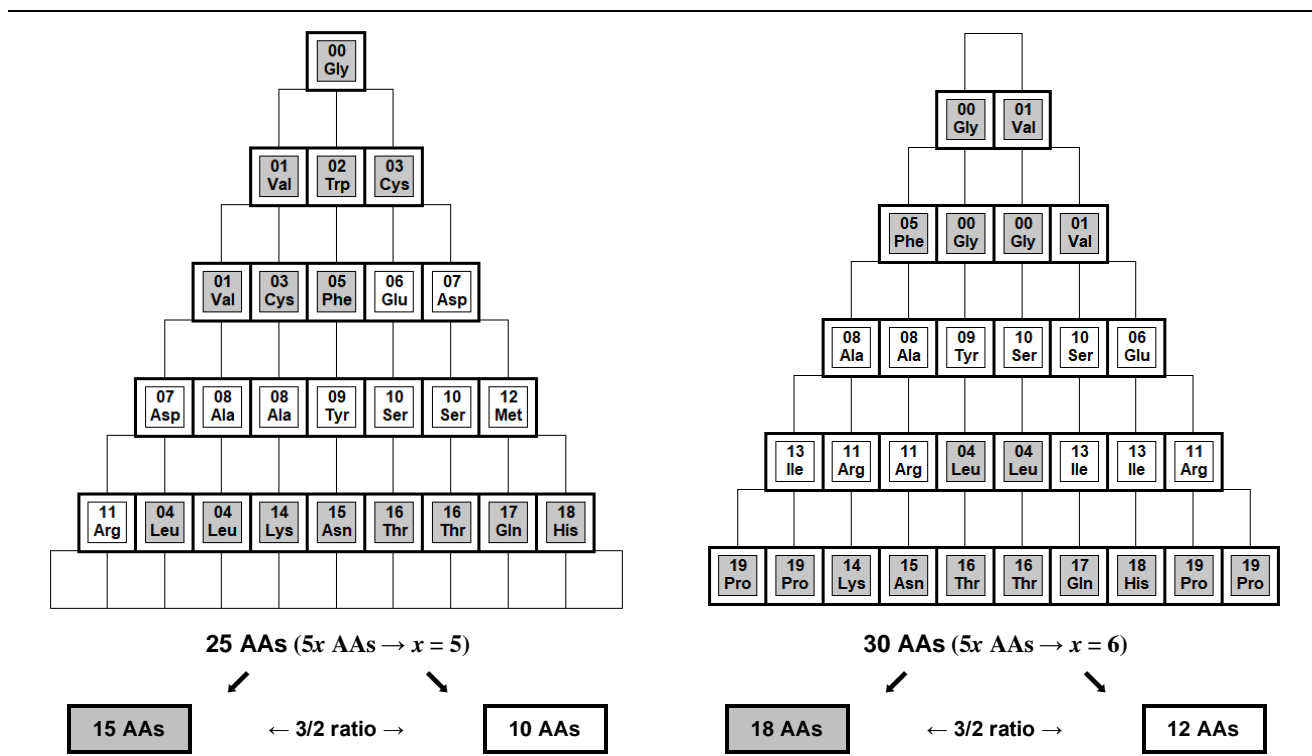


Figure 14: Distribution of outer numbering AAs and inner numbering AAs in 3 to 2 ratios into linear sub configurations of the triangular genetic code matrix.

4.2. Diagonal configurations

The 55-entity triangular matrix graphically has three vertices. As a first investigation, we have, Figure 14, alternately isolated lines perpendicular to the top vertex of this matrix. Figure 15 then 16, we alternately isolate the ten diagonals perpendicular to each of the two low vertices of this matrix. This, exactly as in the first linear configuration.

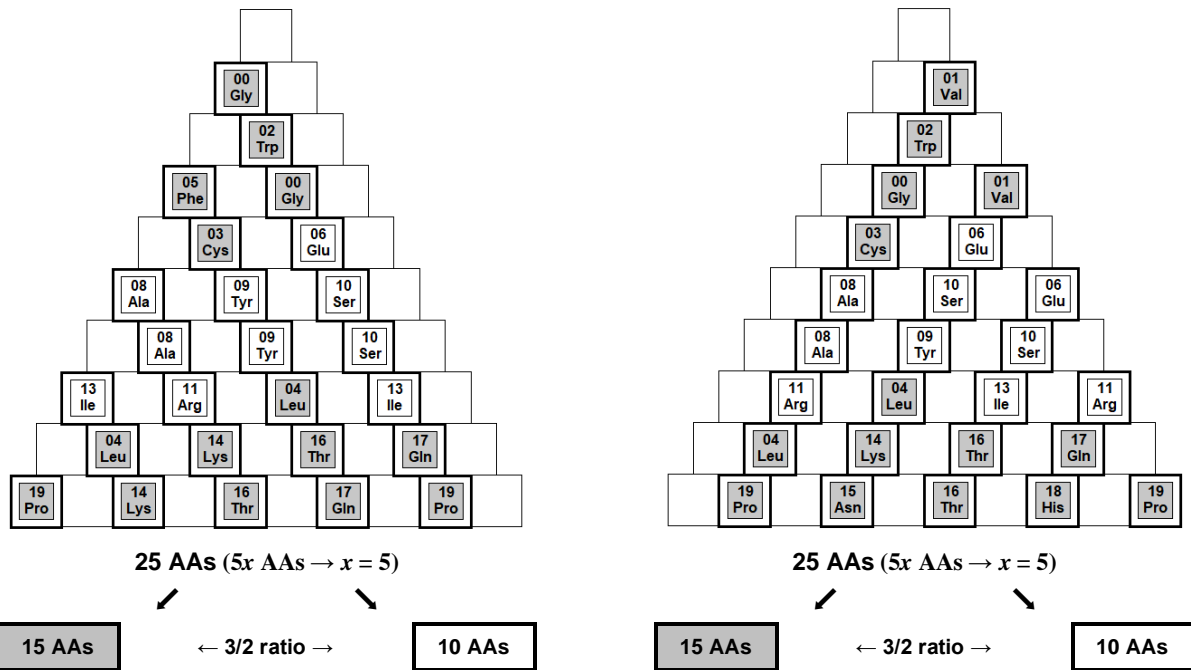


Figure 15: Distribution of outer numbering AAs and inner numbering AAs in 3 to 2 ratios into diagonal sub configurations of the triangular genetic code matrix.

Doing this, it then appears as illustrated Figures 15 and 16 that the two different sets of amino acids respectively described as outer and inner are opposed in exact ratios of value 3/2.

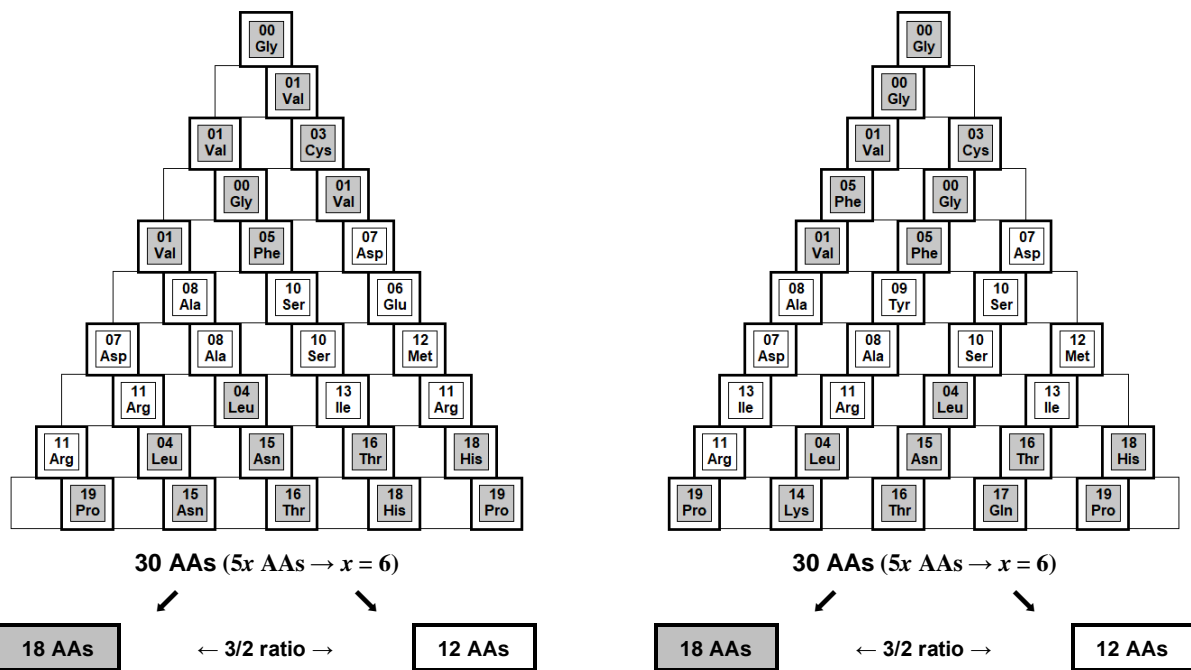


Figure 16: Distribution of outer numbering AAs and inner numbering AAs in 3 to 2 ratios into diagonal sub configurations of the triangular genetic code matrix.

4.3. Mixed sub-configurations

It is known that a triangular number is the sum of four other triangular numbers. So T_{10} is equal to $3T_5 + T_4$. Indeed, triangular number 55 is equal to $15 + 15 + 15 + 10$.

By crossing the linear diagonals of Figure 14 with diagonal configurations introduced in Figures 15 or 16, sub-configurations of size T_5 and T_4 are created. This creates, as illustrated in figure 17, three sub-configurations of size T_5 (15 AAs) and one of size T_4 (10 AAs).

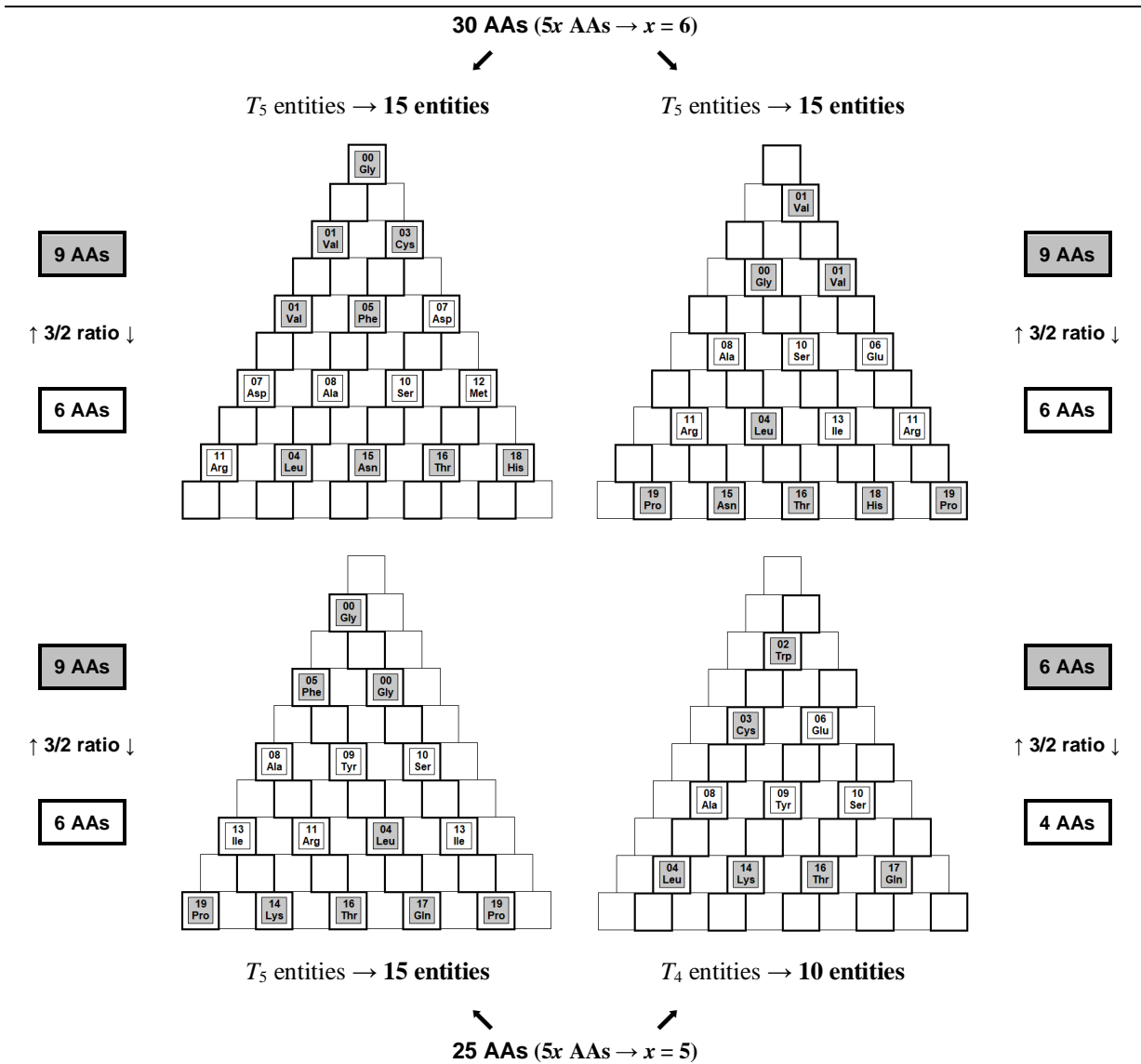


Figure 17: Crossed sub-configurations of T_5 and T_4 as size with inside each, an exact ratio of value $3/2$ between the outer AAs and the inner AAs.

These four sub-configurations are more precisely the source of the linear and diagonal configurations introduced previously. Indeed, their different associations produce the arrangements of Figures 14 to 16 which are $15 + 15$ entities ($T_5 + T_5$) or $15 + 10$ entities ($T_5 + T_4$) as size.

Within these four sub-configurations, the two sets of amino acids described as outer and inner also oppose each other in an exact ratio of value $3/2$ with either 9 versus 6 AAs or 6 versus 4 AAs.

5. Triangular to rectangular genetic code matrix

In accordance with their inner or outer numbering, we have just demonstrated a very sophisticated organization of the distribution of the two numbering sets of canonical amino acids within the 55-entity triangular matrix of the genetic code. The number 55 is therefore a triangular number. It is also a semi prime which is equal to 5 times 11.

Triangular genetic code matrix
1+2+3+4+5+6+7+8+9+10 entities

Rectangular genetic code matrix
5 times 11 entities

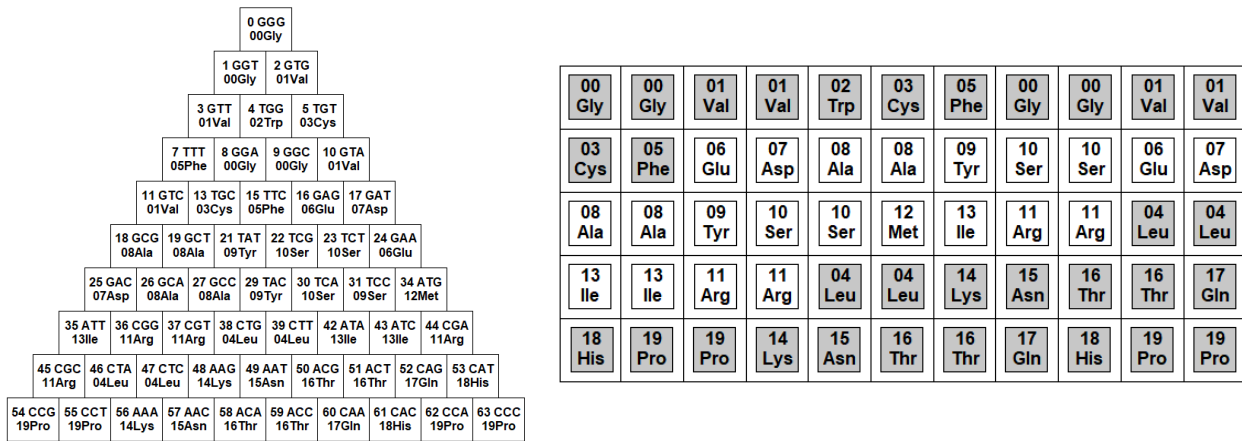


Figure 18: Redeployment of the 55-entity triangular matrix of the genetic code into a rectangular matrix of 5 by 11 entities as size.

The redeployment, Figure 18, of the triangular matrix of the genetic code into a rectangular matrix of 5 by 11 entities in size generates some similar singular geometric phenomena according to the AA numbering concept isolating them in two sets of 3/2 in size.

5.1. Vertical configurations

The alternating division of the eleven columns of this rectangular matrix produces two configurations of 30 and 25 entities. Just like in the previous configurations of the triangular matrix. It also appears that, Figure 19, the two sets of amino acids oppose each other again in ratios of value 3/2 with respectively 18 versus 12 AAs in the configuration of 30 entities (6 columns) and 15 versus 10 AAs in that of 25 entities (5 columns).

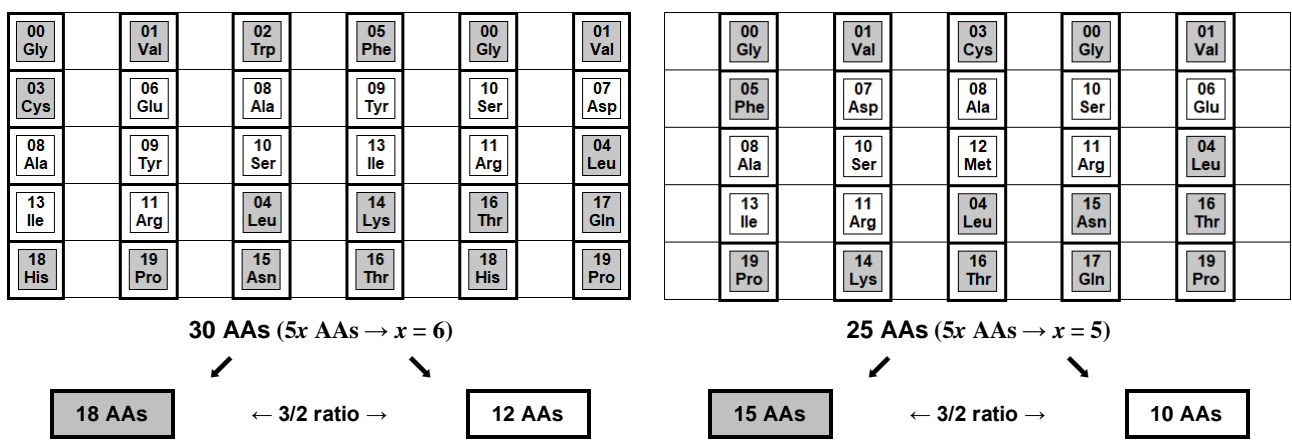


Figure 19: Distribution of outer versus inner numbering AAs in 3 to 2 ratios inside alternate columns of the rectangular genetic code matrix.

5.1.1. Triangulated vertical sub-configurations

As has already been demonstrated in a similar manner in Figure 17 for other configurations of the triangular matrix, these two initial vertical configurations can be split into four smaller ones of dimensions T_5 or T_4 .

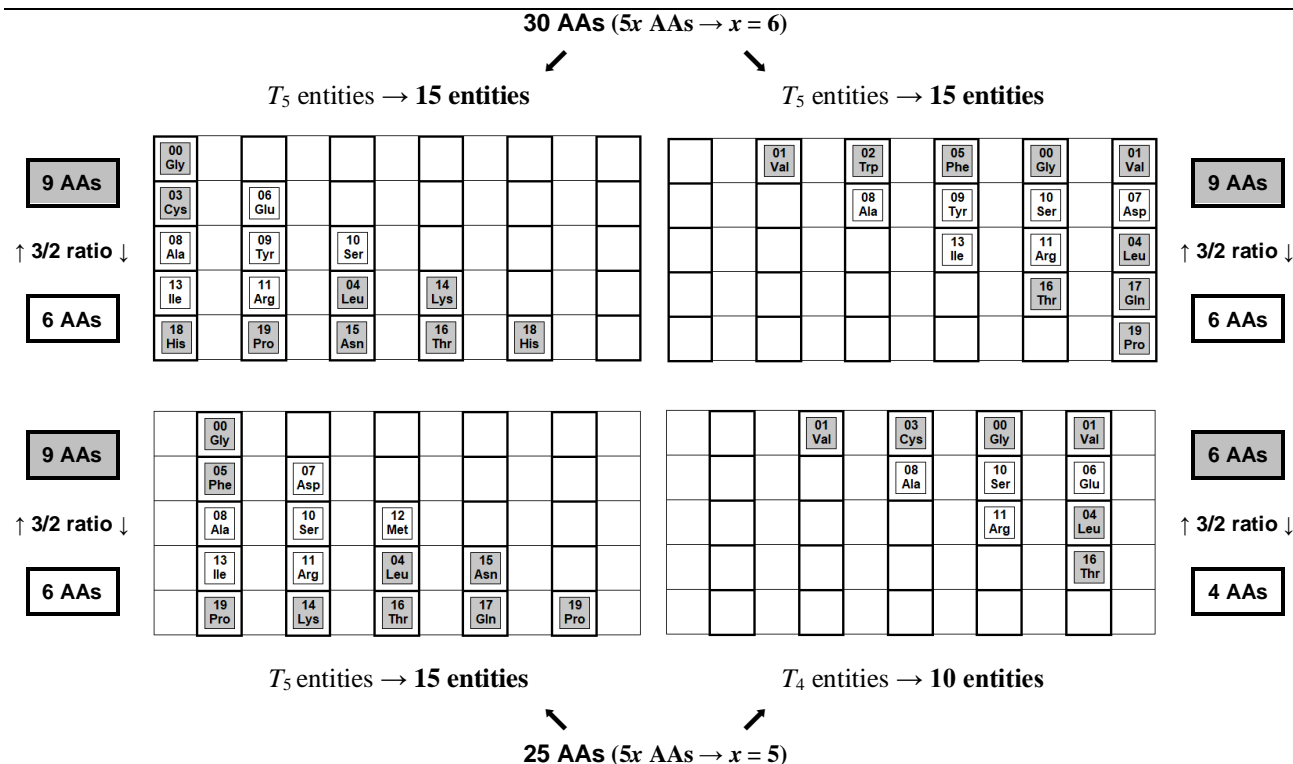


Figure 20: Alternating asymmetric triangulated sub-configurations of T_5 and T_4 as size with inside each, an exact ratio of value $3/2$ between the outer AAs and the inner AAs. See Figure 19. See Figure 17 also to comparison.

Within these four triangulated sub-configurations, Figure 20, the two sets of amino acids described as outer and inner also oppose each other in an exact ratio of value $3/2$ with either 9 versus 6 AAs or 6 versus 4 AAs.

5.1.2. T_4 and T_5 triangulated vertical configurations

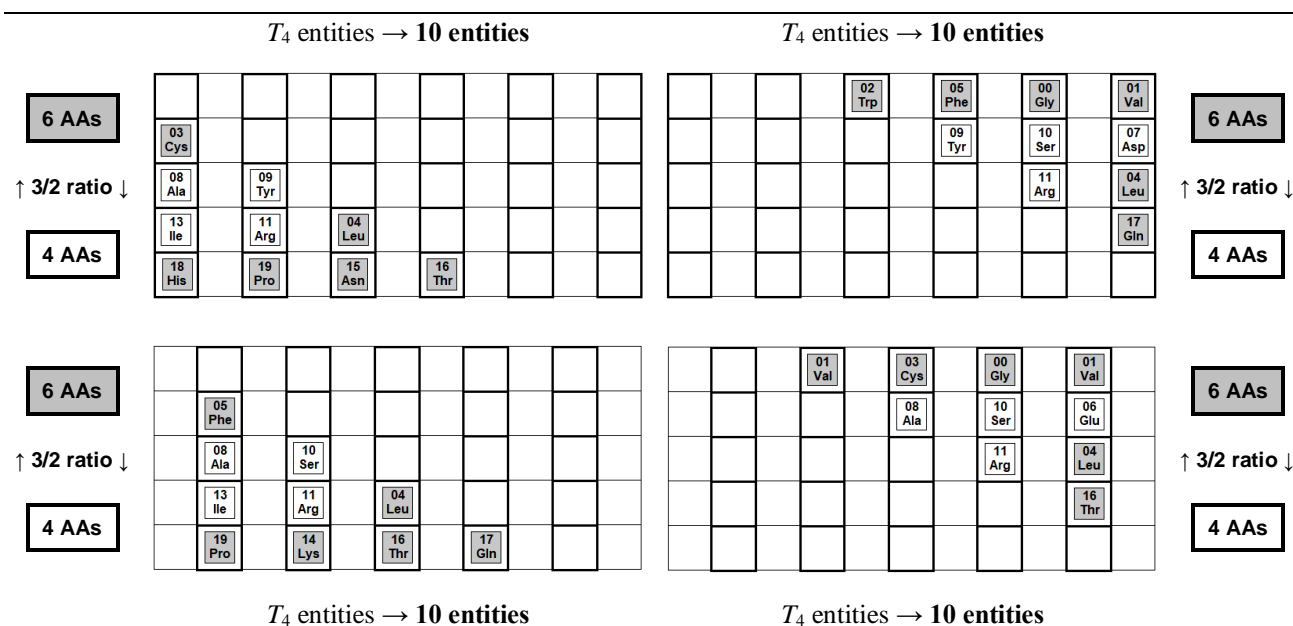


Figure 21: Alternating asymmetric triangulated sub-configurations of T_4 as size with inside each, an exact ratio of value $3/2$ between the outer AAs and the inner AAs. See Figures 20 and 22 also.

In Figures 21 and 22, the asymmetric sub-configurations of size T_4 and T_5 all have the same arithmetic characteristics. They are always made up of $3x$ outer numbering AAs and $2x$ inner numbering AAs.

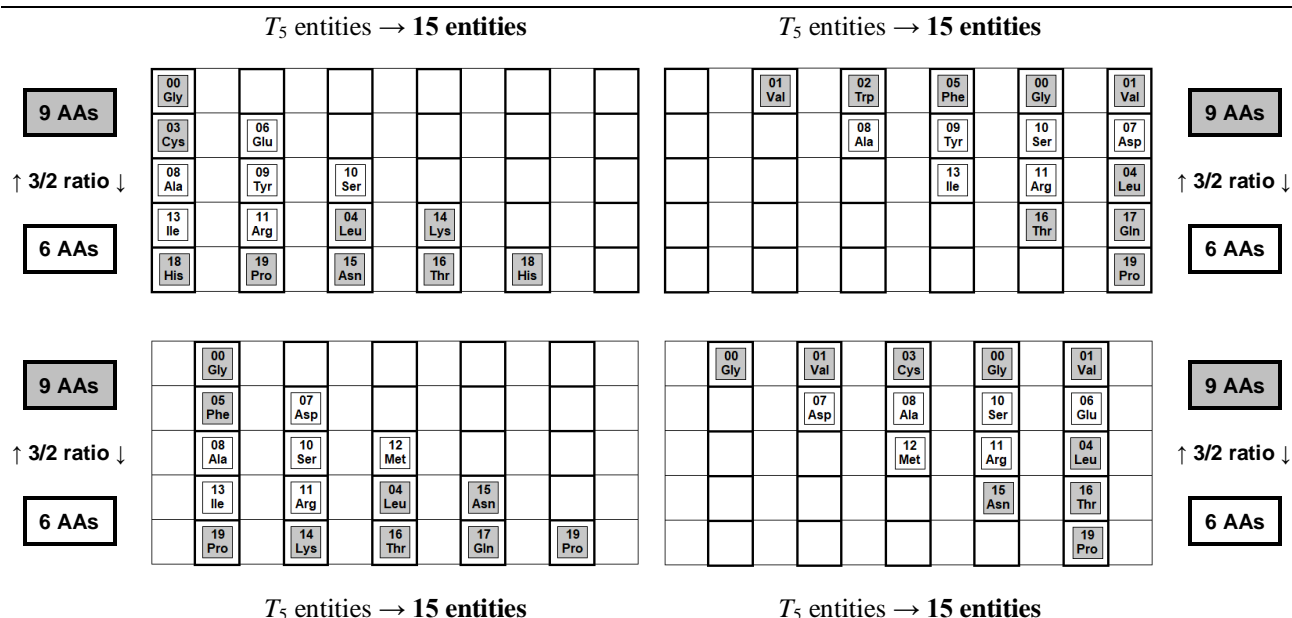


Figure 22: Alternating asymmetric triangulated sub-configurations of T_5 as size with inside each, an exact ratio of value $3/2$ between the outer AAs and the inner AAs. See Figures 20 and 21 also.

5.2. Alternating horizontal configurations

As we constructed sub-configurations of the triangular matrix by alternating six and five columns of five entities (5 AAs), we construct here horizontal sub-configurations of five times six and five times 5 AAs, this therefore by regularly alternating semi-lines. As can be seen in Figure 23, by this process, it is therefore possible to construct four sub-configurations that are respectively asymmetrical or symmetrical to each other.

In each of these four geometric configurations, the two sets of amino acids oppose each other in an exact ratio of value $3/2$. Thus the configurations of five semi-lines of six entities contain 18 outer numbering AAs versus 12 inner AAs. These composed of five semi-lines of five entities contain 15 outer numbering AAs versus 10 inner AAs.

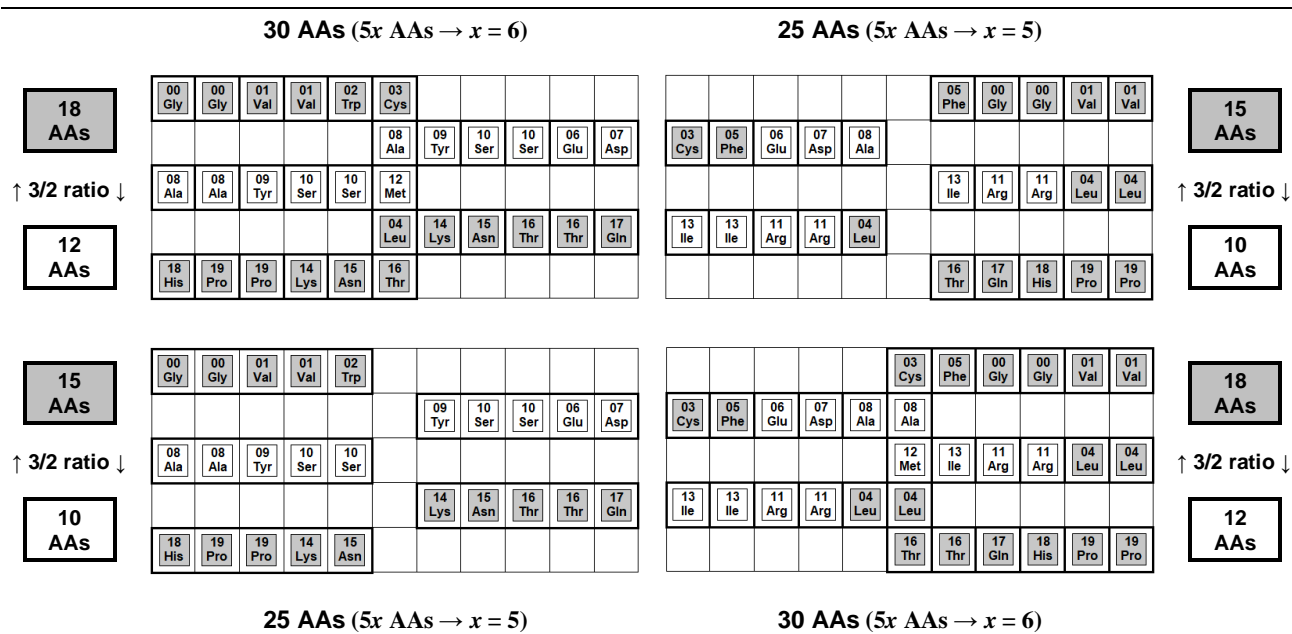


Figure 23: Four alternating sub-configurations of two times five semi-lines of 6 and 5 AAs with inside each, an exact ratio of value $3/2$ between the outer AAs and the inner AAs.

5.3. Mixed configurations

As was done in Chapter 4.3 with the triangular matrix, the mixing of the alternating vertical and horizontal configurations of the rectangular matrix (of size 5 by 11 entities), results in the same arithmetic arrangements between the two predefined sets of amino acids.

Thus, in Figure 24, just as happened in Figure 17 about triangular matrix, this mixing generates sub-configurations of size T4 and T5 (10 and 15 entities) where the outer AAs and inner AAs still oppose each other in exact ratios of value 3/2 with, depending on the case, 9 versus 6 AAs and 6 versus 4 AAs.

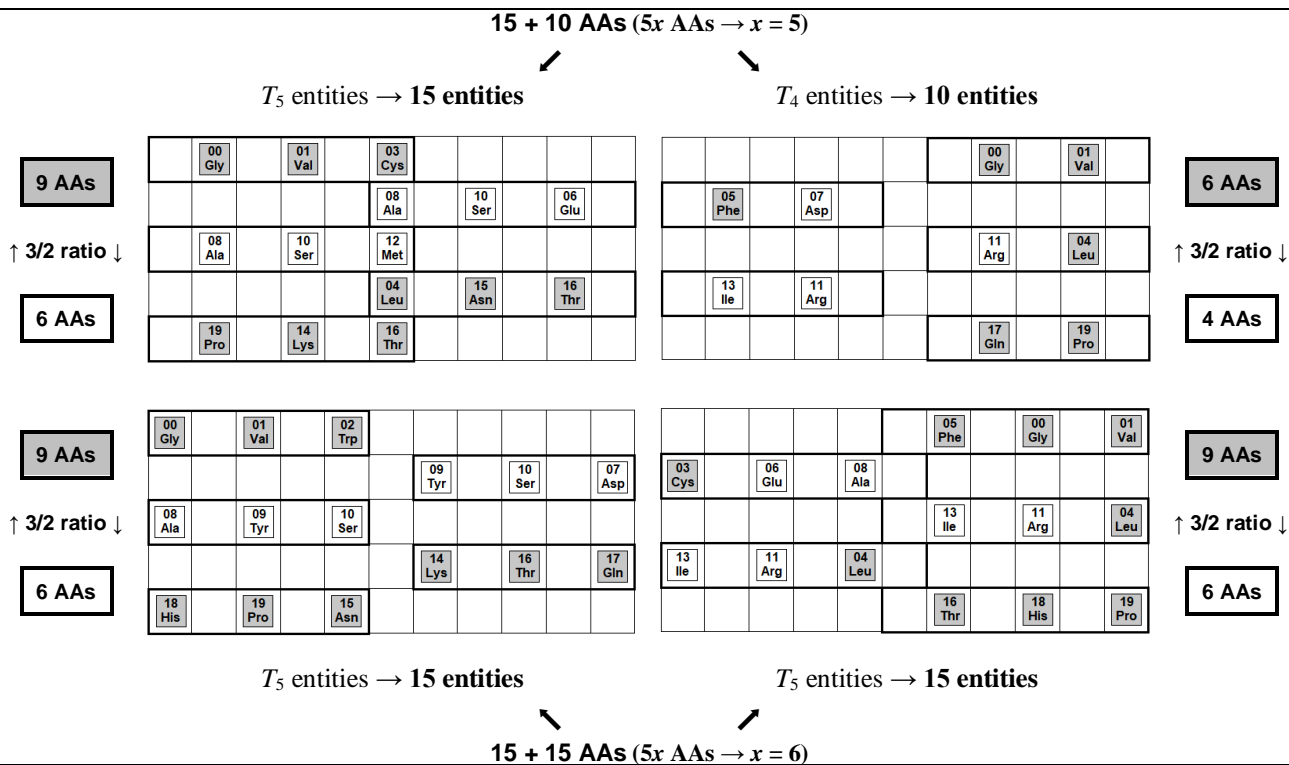


Figure 24: Mixed vertical and horizontal sub-configurations of the rectangular matrix with inside each, persistence of an exact ratio of value 3/2 between the outer AAs and the inner AAs. See Figures 19 and 23. See Figure 17 for comparison.

6. Recombined triangulation of rectangular sub-matrices

We will now demonstrate a very powerful organization of the genetic code as a geometric algebra structure. The previously invested rectangular matrix of size 5 by 11 entities can otherwise be considered as an assembly of two times five semi-lines of complementary sizes two by two as illustrated Figure 25. In relationship with decimal system, this actually corresponds to ten rows whose sizes vary from 1 to 10 entities.

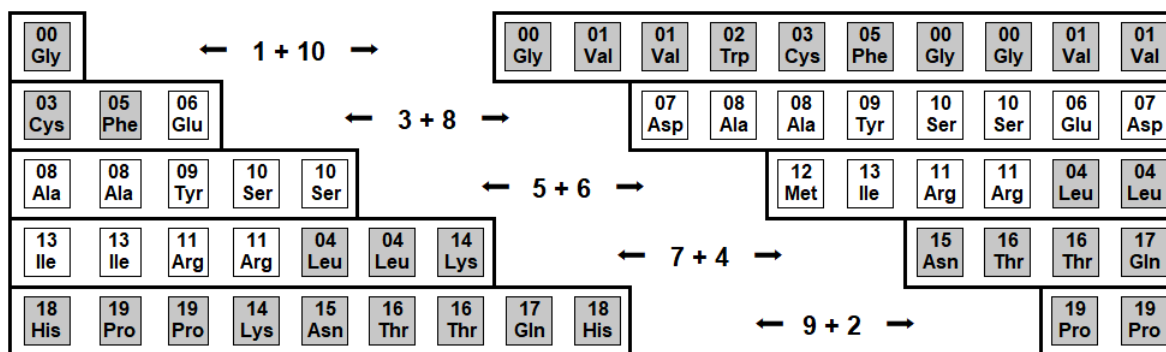


Figure 25: Original rectangular matrix dissociation in two parts according to complementary sizes of sub-rows.

6.1. Recombined triangulation

As illustrated in Figure 26, the two times five complementary rows (at 11 in size) can be redeployed into two triangular sub-matrices.

In accordance with the numbering of the amino acids, these two sub-matrices are organized exactly as those introduced in Figure 14, that is to say like the original triangular matrix of the genetic code, a matrix reduced to 55 entities.

In these two triangular sub-matrices, the two sets of amino acids oppose each other in an exact ratio of value 3/2 with 15 outer AAs versus 10 inner AAs for one and 18 outer AAs versus 12 inner AAs for the other sub-matrix.

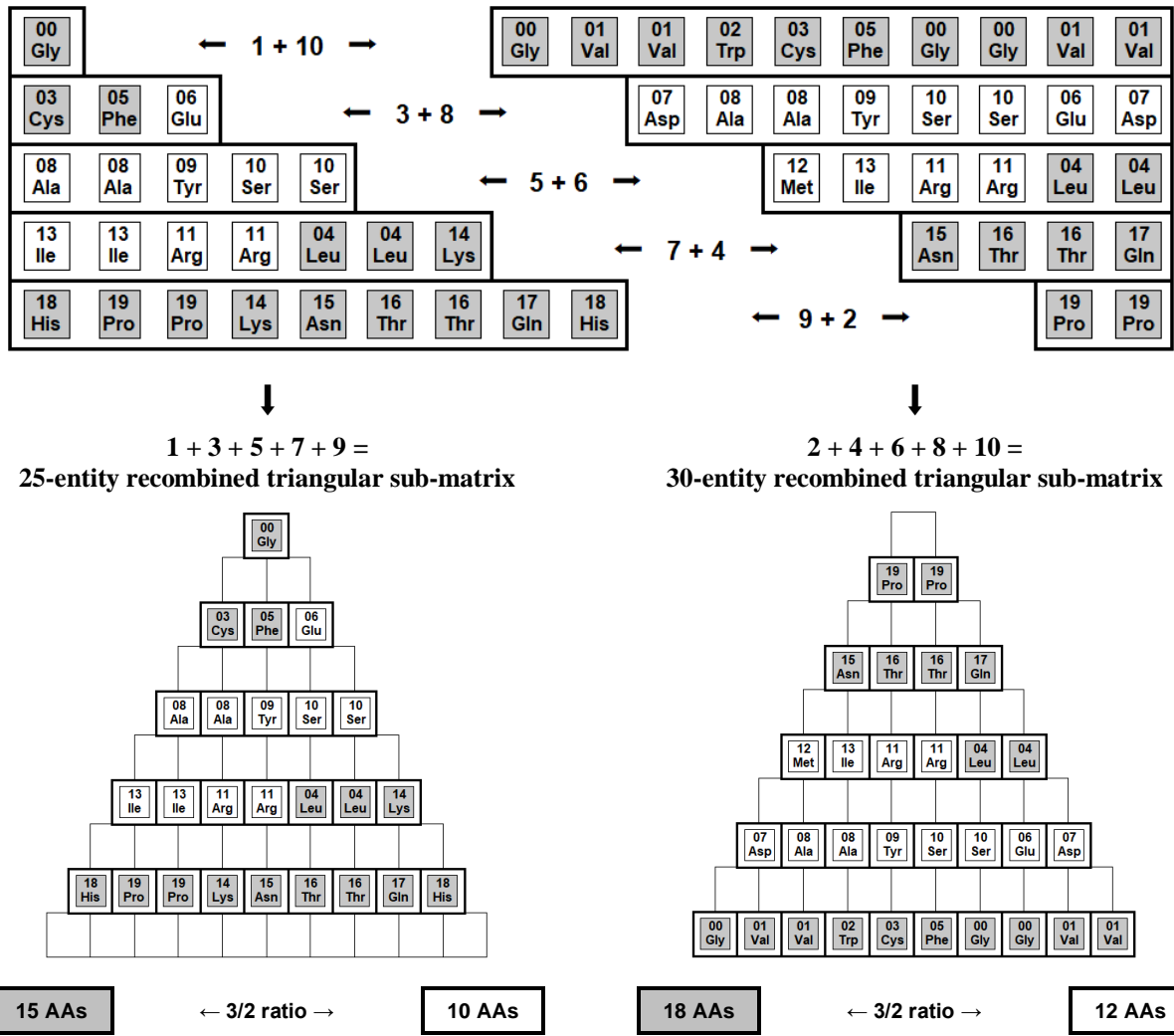


Figure 26: Recombination of two triangular sub-matrices from two rectangular sub-matrices.

Thus, Figure 27, from the original rectangular matrix, then from these two triangular sub-matrices, a completely new triangular matrix of 55 entities can be reconstructed.

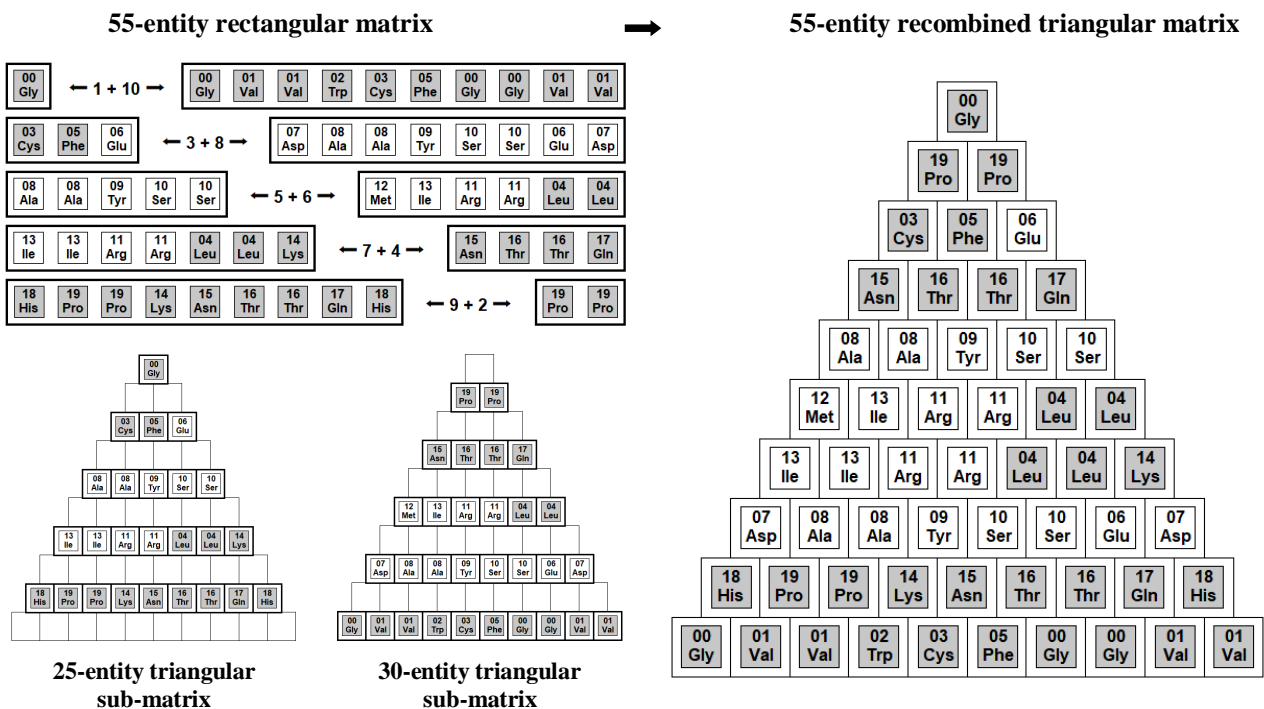


Figure 27: Recombination of a completely triangular matrix of 55 entities.

6.2. Diagonal configurations

As the original matrix introduced Chapter 3, this new 55-entity triangular matrix graphically has three vertices. In the same way as with this original matrix, we alternately isolate the ten diagonals perpendicular to the two low vertices of this recombined triangular matrix. Doing this, it then appears as illustrated Figure 28 that the two different sets of amino acids respectively described as outer and inner are opposed in exact ratios of value $3/2$.

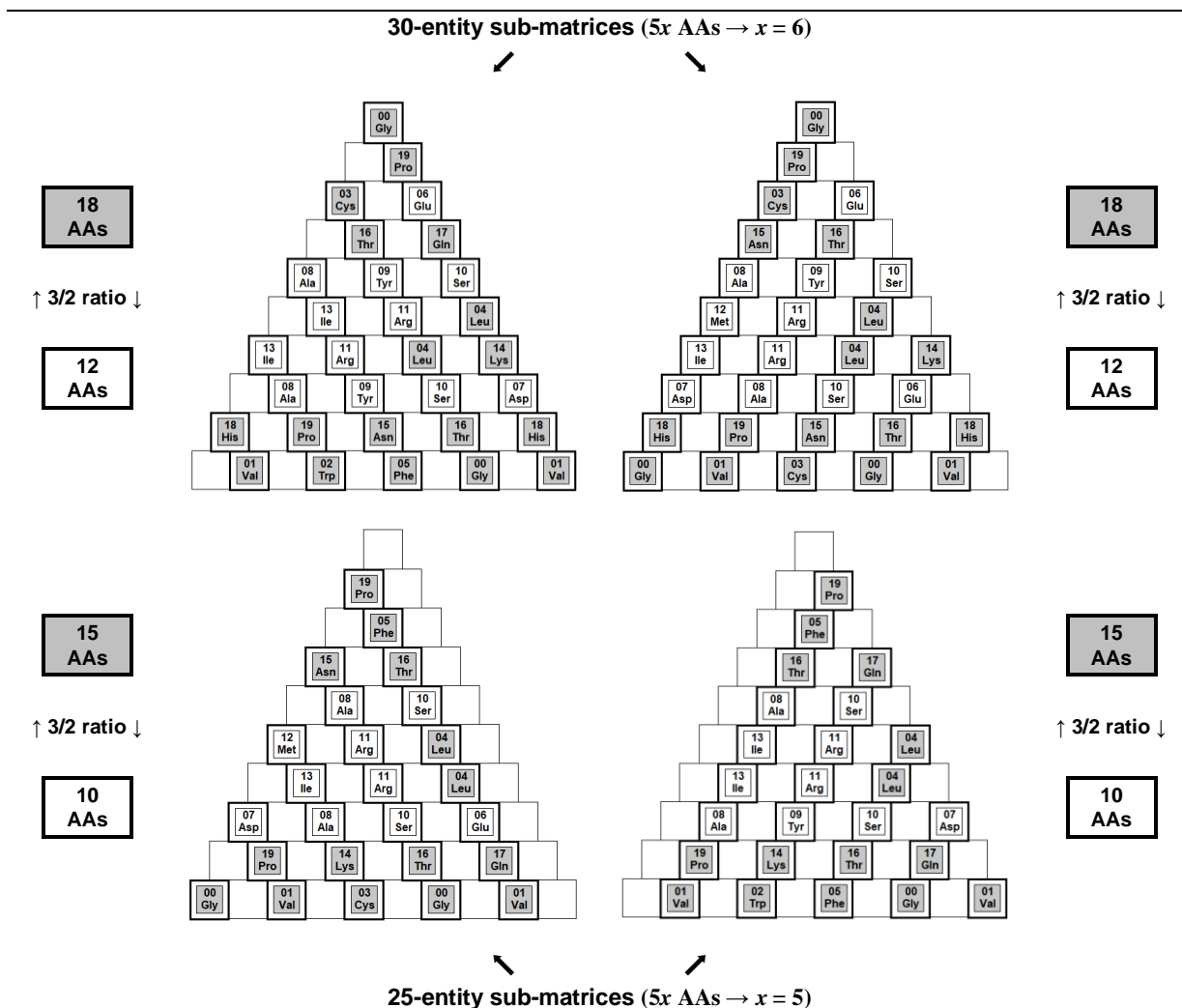


Figure 28: Distribution of outer numbering AAs and inner numbering AAs in 3 to 2 ratios into diagonal sub-configurations of the recombined triangular genetic code matrix. See Figures 15 and 16 to comparison.

This geometric algebra phenomenon is perfectly identical to that operating within the original matrix. This while the different AAs are in very different arrangements in the two matrices considered.

6.3. Mixed sub-configurations

Also, still like with the original matrix, by crossing the linear diagonals of Figure 26 with diagonal configurations introduced in Figure 28, sub-configurations of size T_5 and T_4 are created. This creates, as illustrated in figure 29, three sub-configurations of size T_5 (15 AAs) and one of size T_4 (10 AAs).

These four sub-configurations are more precisely the source of the linear and diagonal configurations introduced previously. Indeed, their different associations produce the arrangements of Figure 28 which are $15 + 15$ entities ($T_5 + T_5$) or $15 + 10$ entities ($T_5 + T_4$) as size.

Within these four sub-configurations, the two sets of amino acids described as outer and inner also oppose each other in an exact ratio of value $3/2$ with either 9 versus 6 AAs or 6 versus 4 AAs.

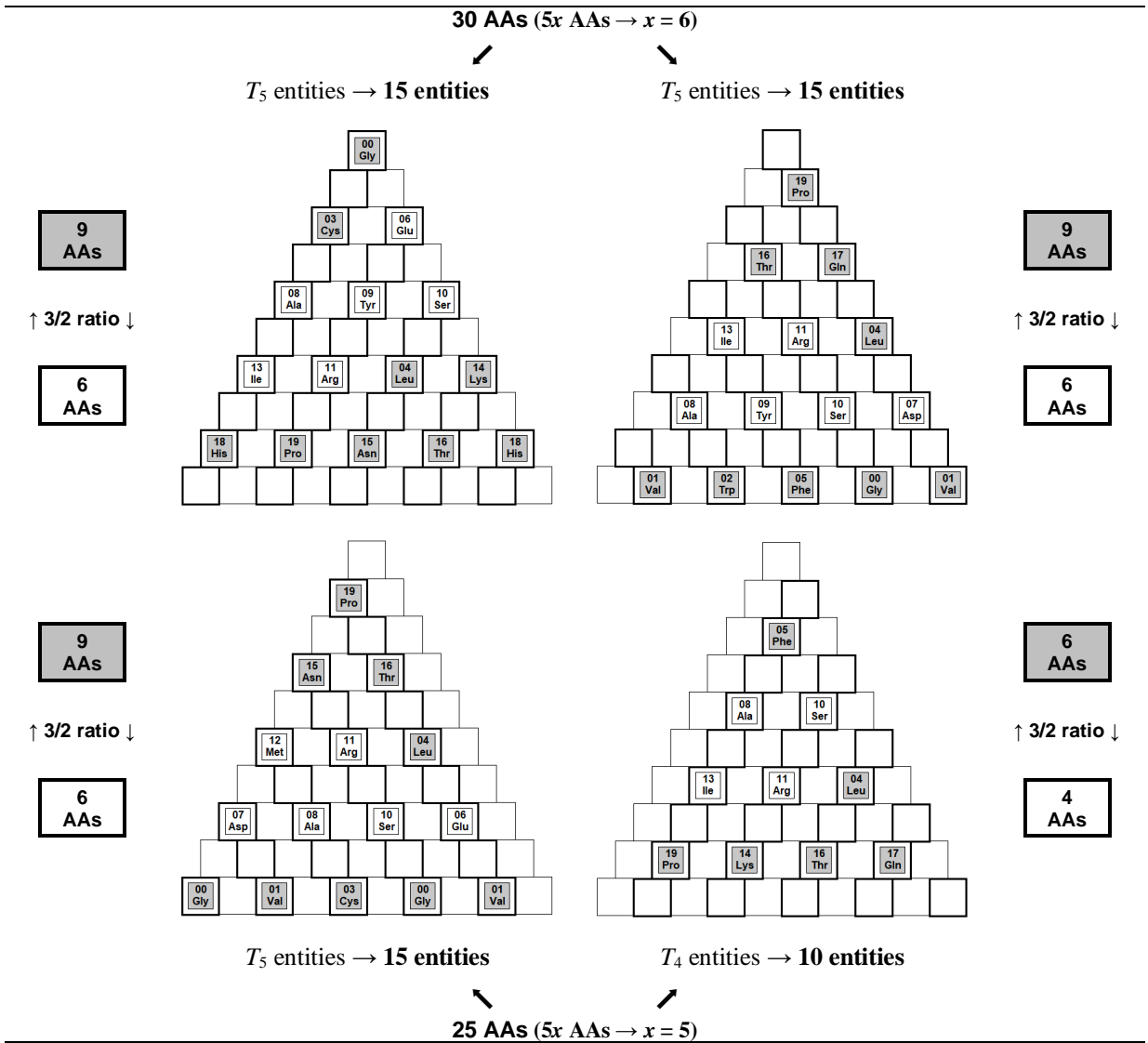


Figure 29: Crossed sub-configurations of T_5 and T_4 as size with inside each, an exact ratio of value $3/2$ between the outer AAs and the inner AAs. See Figure 17 to comparison.

6.4. Second recombined triangulation of rectangular sub-matrices

Once again, the original rectangular matrix of size 5 by 11 entities can otherwise be considered as an other assembly of two times five semi-lines of complementary sizes two by two as illustrated Figure 30. This actually corresponds to ten rows whose sizes vary from 1 to 10 entities. This, in reverse way of the previous configuration illustrated in Figure 25, so in start-up with dissociation of 2 versus 9 entities instead 1 versus 10 in the previous configuration.

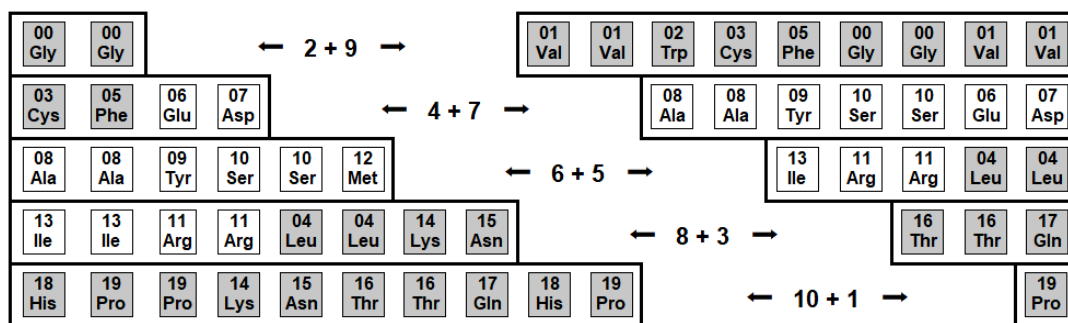


Figure 30: Second rectangular matrix dissociation in two parts according to complementary sizes of sub-rows.

As illustrated in Figure 31 and exactly in the algebra geometrical way introduced Figure 26, the two times five complementary rows (at 11 in size) can be redeployed into two triangular sub-matrices. In accordance with the numbering of the amino acids, these two sub-matrices are organized exactly as those introduced in Figure 14, that is to say like the original triangular matrix of the genetic code, a matrix reduced to 55 entities. In these two other triangular sub-matrices, the two sets of amino acids

oppose each other in an exact ratio of value 3/2 with 15 outer AAs versus 10 inner AAs for one and 18 outer AAs versus 12 inner AAs for the other sub-matrix.

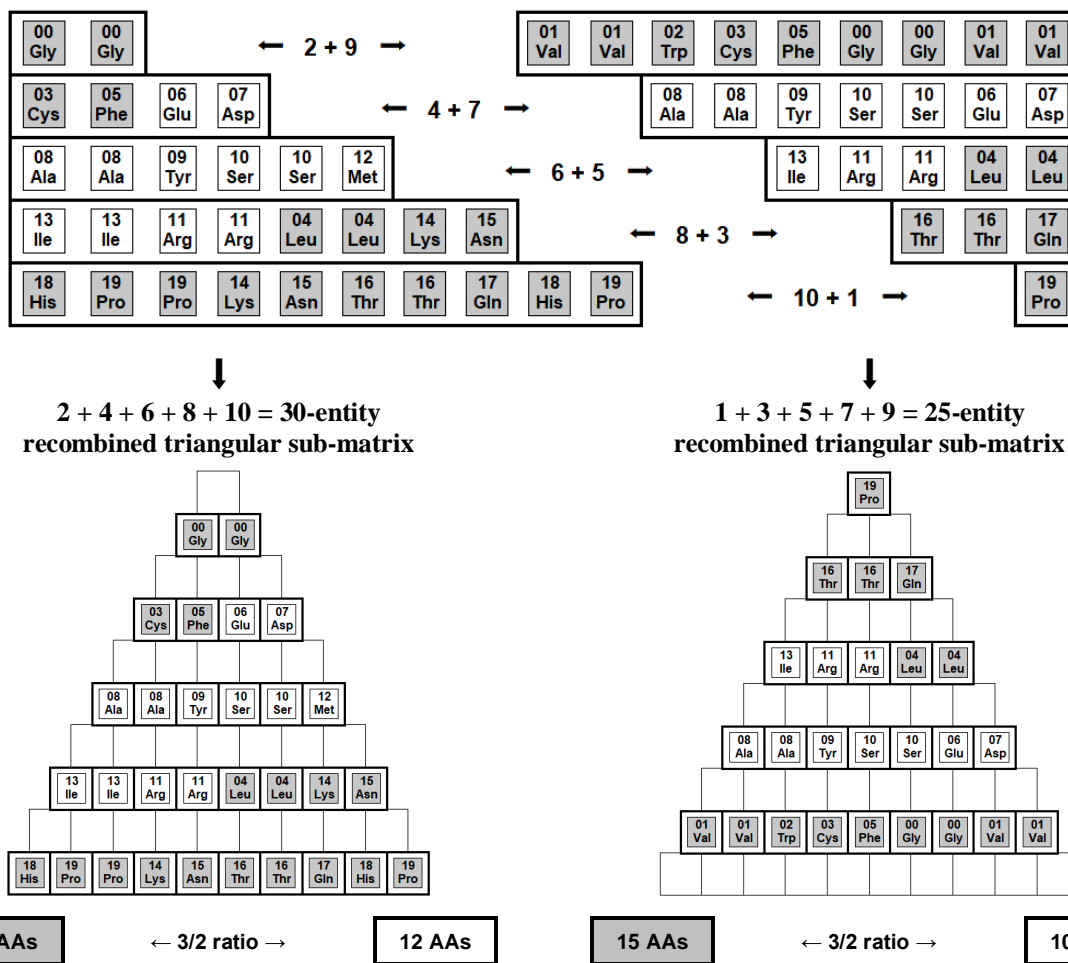


Figure 31: Recombination of two triangular sub-matrices from two rectangular sub-matrices.

Thus, Figure 32, from the original rectangular matrix, then from these two triangular sub-matrices, a completely new triangular matrix of 55 entities can be reconstructed.

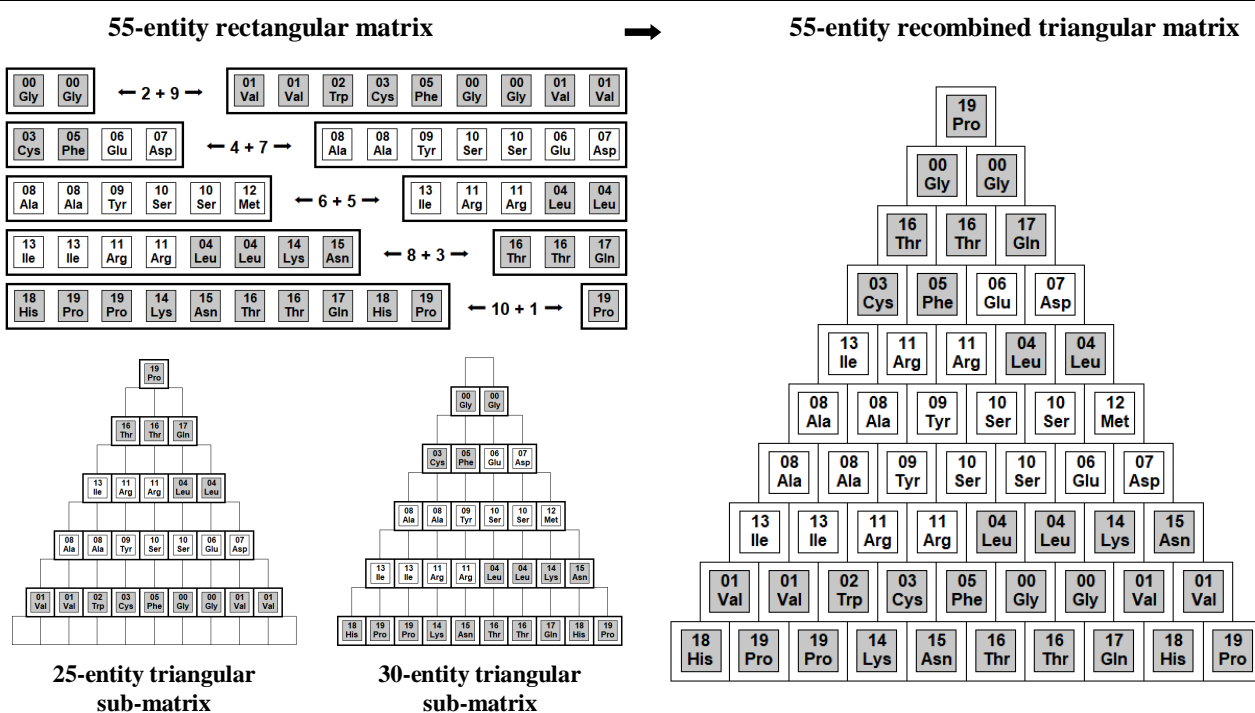


Figure 32: Recombination of a second completely triangular matrix of 55 entities.

6.4.1. Diagonal configurations

As the original matrix introduced Chapter 3, this new 55-entity triangular matrix graphically has three vertices. In the same way as with this original matrix but also the one previous recombined in Figure 27, we alternately isolate the ten diagonals perpendicular to the two low vertices of this second recombined triangular matrix. Doing this, it then appears as illustrated Figure 33 that the two different sets of amino acids respectively described as outer and inner are opposed in exact ratios of value 3/2.

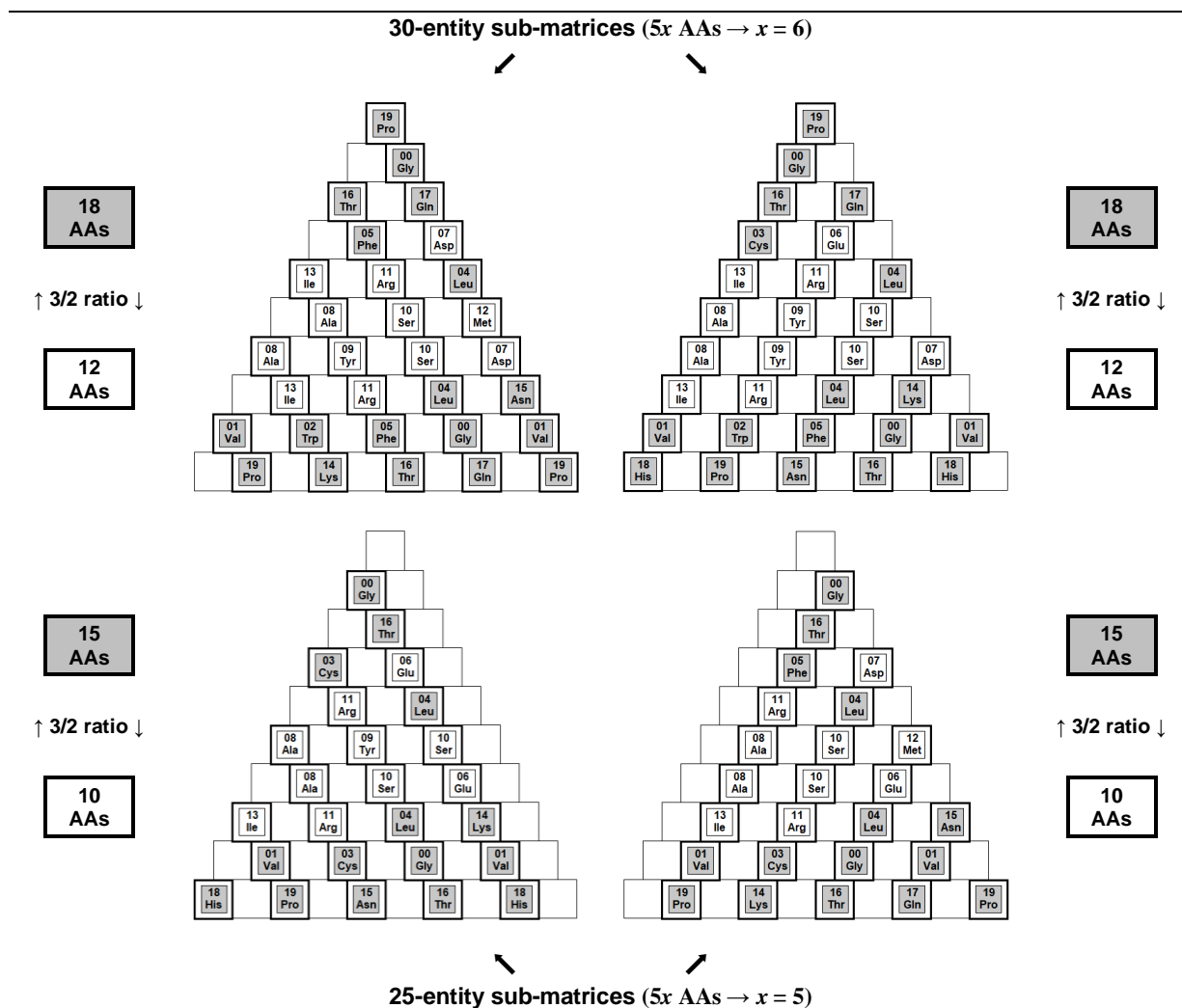


Figure 33: Distribution of outer numbering AAs and inner numbering AAs in 3 to 2 ratios into diagonal sub-configurations of the second recombined triangular genetic code matrix. See Figures 15, 16 and 29 to comparison.

Again here, this geometric algebra phenomenon is perfectly identical to that operating within the original matrix. This while the different AAs are in very different arrangements in the two matrices considered.

6.4.2. Mixed sub-configurations

Also, still like with the original matrix, but also the one previous recombined in Figure 27, by crossing the linear diagonals of Figure 31 with diagonal configurations introduced in Figure 33, sub-configurations of size T_5 and T_4 are created. This creates, as illustrated in Figure 34, three sub-configurations of size T_5 (15 AAs) and one of size T_4 (10 AAs).

These four sub-configurations are more precisely the source of the linear and diagonal configurations introduced previously. Indeed, their different associations produce the arrangements of Figure 33 which are 15 + 15 entities ($T_5 + T_5$) or 15 + 10 entities ($T_5 + T_4$) as size.

Within these four sub-configurations, the two sets of amino acids described as outer and inner also oppose each other in an exact ratio of value 3/2 with either 9 versus 6 AAs or 6 versus 4 AAs.

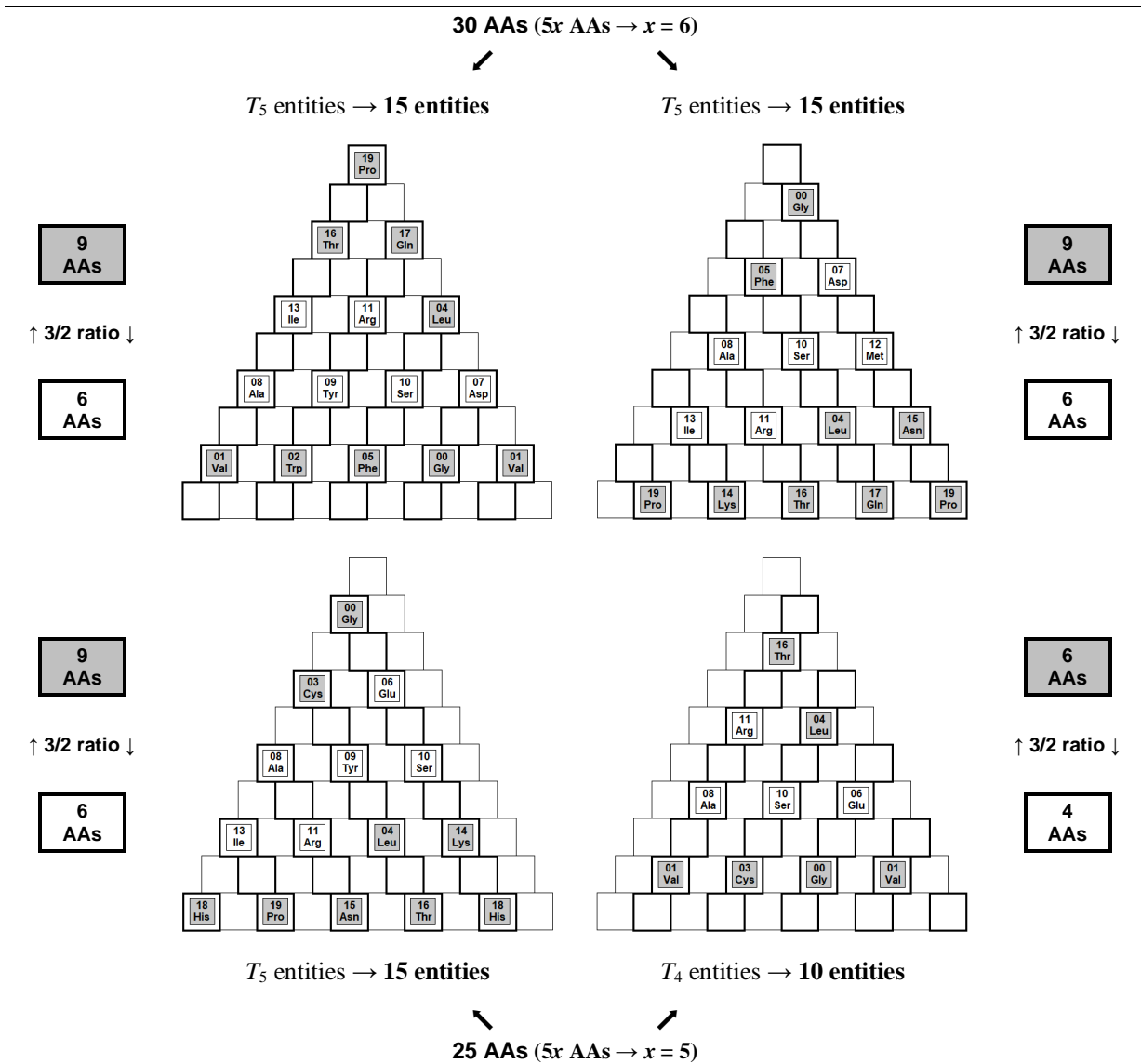
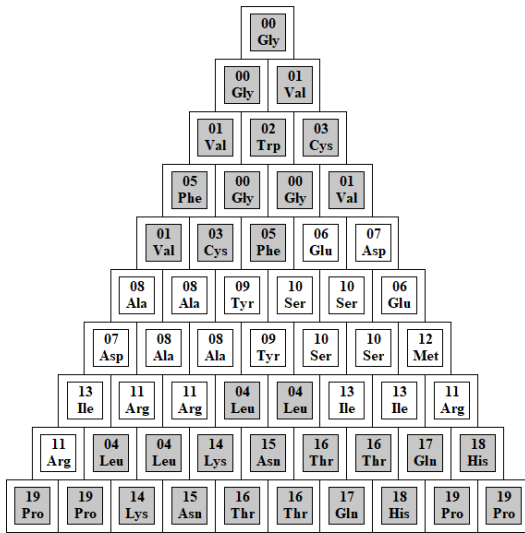


Figure 34: Crossed sub-configurations of T_5 and T_4 as size with inside each, an exact ratio of value $3/2$ between the outer AAs and the inner AAs. See Figure 17 to comparison.

7. Ultimate genetic code and 55-entity matrix

Until now, we have differentiated the twenty canonical amino acids into two sets according to their numbering which can be external or internal. Inside the 55-entity triangular genetic code matrix, in the matrix, there are therefore 33 outer AAs and 22 inner AAs. We demonstrated in Chapter 3, according to the concept of the ultimate genetic code of 20 entities, that the set described as outer also corresponds to AAs whose biulet is made up of 2 identical nucleobases or two opposite nucleobases. By the same way, the AA set described as inner also corresponds to AAs whose biulet is made up of 2 of same nature nucleobases or 2 complementary nucleobases. This is illustrated in more detail in Figure 35.

55-entity triangular genetic code matrix



counting of the 55 AAs of lighter genetic code inside the 20-entity ultimate genetic code

	A	G	T	C
A	14Lys 2 15Asn 2	06Glu 2 07Asp 2	09Tyr 2	17Gln 2 18His 2
G	11Arg 4 10Ser 4	00Gly 4	02Trp 1 03Cys 2	-
T	13Ile 3 12Met 1	01Val 4	04Leu 4 05Phe 2	-
C	16Thr 4	08Ala 4	-	19Pro 4

Figure 35: Distribution of the 55 entities of lighter genetic code inside the 20-entity ultimate genetic code. See Figures 12, 13 and 36 also.

In previous demonstrations, we identified, each time, sub-sets of 18 versus 12 and 15 versus 12 entities according to the different geometric configurations proposed within the 55-entity triangular genetic code matrix. As shown in Figure 36, these four different values correspond to the four different ways in which nucleobases can assemble into the biphlets of the ultimate genetic code. In fact, in this table of the genetic code called as ultimate, it turns out that 18 AAs have identical nucleobases and that 12 AAs have nucleobases of the same nature. Also, in this ultimate table, 15 AAs have opposite nucleobases and 10 have complementary nucleobases.

30 AAs* at biphlets** with 2 DNA bases which are:

	A	G	T	C
A	2 2			
G		4		
T			4 2	
C				4

identical

	A	G	T	C
A				
G		2 2		
T				
C				

of same nature

	A	G	T	C
A				
G		4 4		-
T				-
C				-

	A	G	T	C
A	14Lys 2 15Asn 2	06Glu 2 07Asp 2	09Tyr 2	17Gln 2 18His 2
G	11Arg 4 10Ser 4	00Gly 4	02Trp 1 03Cys 2	-
T	13Ile 3 12Met 1	01Val 4	04Leu 4 05Phe 2	-
C	16Thr 4	08Ala 4	-	19Pro 4

25 AAs* at biphlets** with 2 DNA bases which are:

	A	G	T	C
A				2 2
G			1 2	-
T		4		-
C	4			-

opposite

	A	G	T	C
A				2
G				-
T	3 1			-
C		4		-

complementary

	A	G	T	C
A	14Lys 2 15Asn 2	06Glu 2 07Asp 2	09Tyr 2	17Gln 2 18His 2
G	11Arg 4 10Ser 4	00Gly 4	02Trp 1 03Cys 2	-
T	13Ile 3 12Met 1	01Val 4	04Leu 4 05Phe 2	-
C	16Thr 4	08Ala 4	-	19Pro 4

18 AAs

← 3/2 ratio →

12 AAs

15 AAs

← 3/2 ratio →

10 AAs

Figure 36: Distinction of the four subsets of amino acids according to the reciprocal nature of the DNA bases of the ultimate twenty-biphlet genetic code. *AAs of the 55-entity lighter genetic code inside. ** Biphlets of the 20-entity ultimate genetic code. See Figure 12, 13 and 35 also.

We can therefore consider, depending on the nature of the respective bases which encode them, two sets of amino acids where those qualified as externally numbered are opposed in a ratio of value 3/2 to those qualified as internal:

- 25 AAs whose codons are with 2 DNA bases which are opposite or complementary,
- 30 AAs whose codons are with 2 DNA bases which are identical or of same nature.

7.1. Two rectangular matrices

In Figure 37, the two different sets of previously defined amino acids are identified, This within the 55-entity rectangular genetic code matrix. Doing this, we can create two rectangular matrices of 25 and 30 entities. Here we continue to distinguish amino acids into inner and outer according to the concept of their numbering. In the 25-entity matrix, all the outer AAs, numbering 15, are those associated with 2 opposite bases of the ultimate genetic code and all the inner AAs, numbering 10, are those associated with 2 complementary bases. In the 30-entity matrix, all the outer AAs, numbering 18, are those associated with 2 identical bases of the ultimate genetic code and all the inner AAs, numbering 12, are those associated with 2 bases of the same nature.

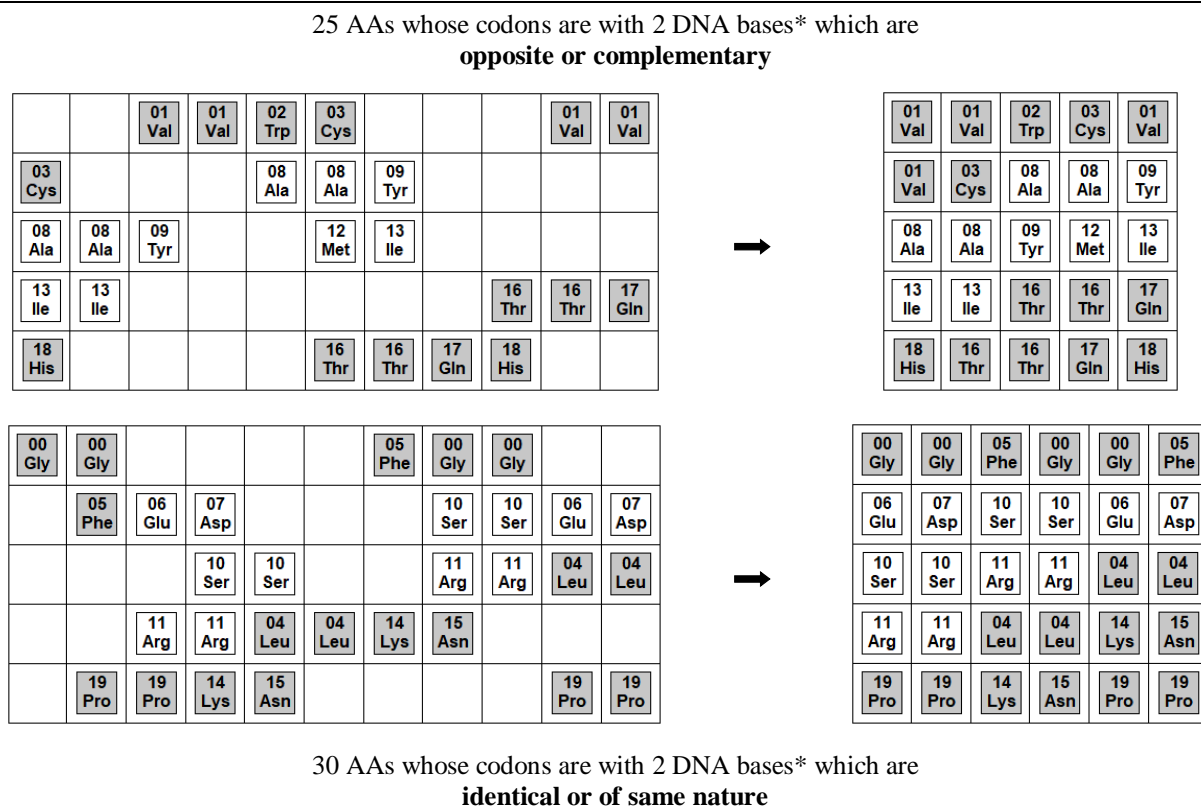


Figure 37: From the original 55-entity triangular genetic code matrix, creation of two matrices of 25 and 30 entities according to ultimate genetic code. See Figure 35 and 36 also. * Ultimate genetic code.

7.2. The 3/2 ratio and the 25-entity matrix

In this section, in the matrix of 25 entities, we oppose different sets of each 5x entities. We do this with a value of x equal to 0 to 5. It appears in the following figures that we can geometrically oppose sub-matrices whose values of x are complementary to 5.

We also simultaneously oppose sub-matrices of the same size (same x's value) of opposite mirror configurations. these sub-matrices consist of 5 rows whose geometric arrangement is regularly alternated but with an equal value of x (from 0 to 5) as length.

We voluntarily present an empty sub-matrix of zero entities which completes the full one of 25 entities. In fact, this matrix is equal to five time 0x as size with a value of x equal to 5.

It then appears that in all these sub-matrices, the AAs always oppose each other in number in an exact ratio of value 3/2 depending on whether they are outer numbering or inner numbering.

Thus, we can also say that, in all these sub-matrices, the AAs with bipelets made up of opposite nucleobases are always 3x in number and that those with bipelets made up of complementary nucleobases are always 2x in number.

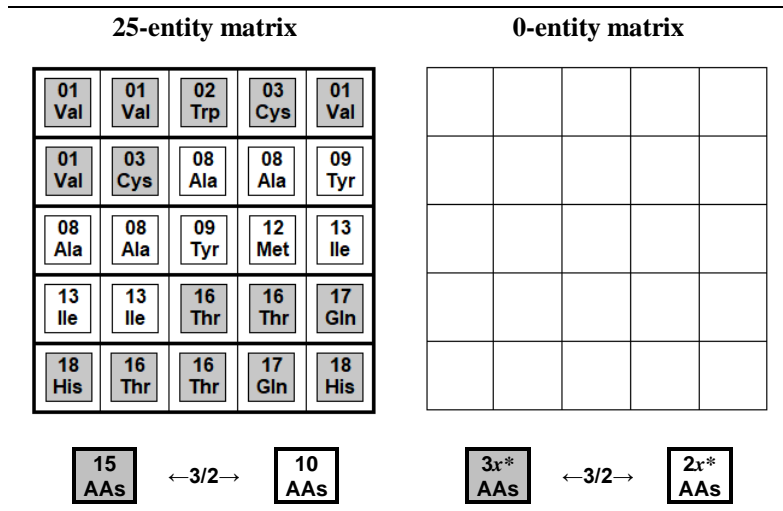


Figure 38: Sub-matrices to 25 versus 0 entities. * x = 0. AAs whose codons are with 2 DNA bases** which are opposite or complementary. **Ultimate genetic code.

Figure 38, which may seem strange, actually shows an empty matrix of 25 boxes. This is not an anomaly. This empty matrix completes the series of different other sub-matrices introduced in Figures 39 and 40.

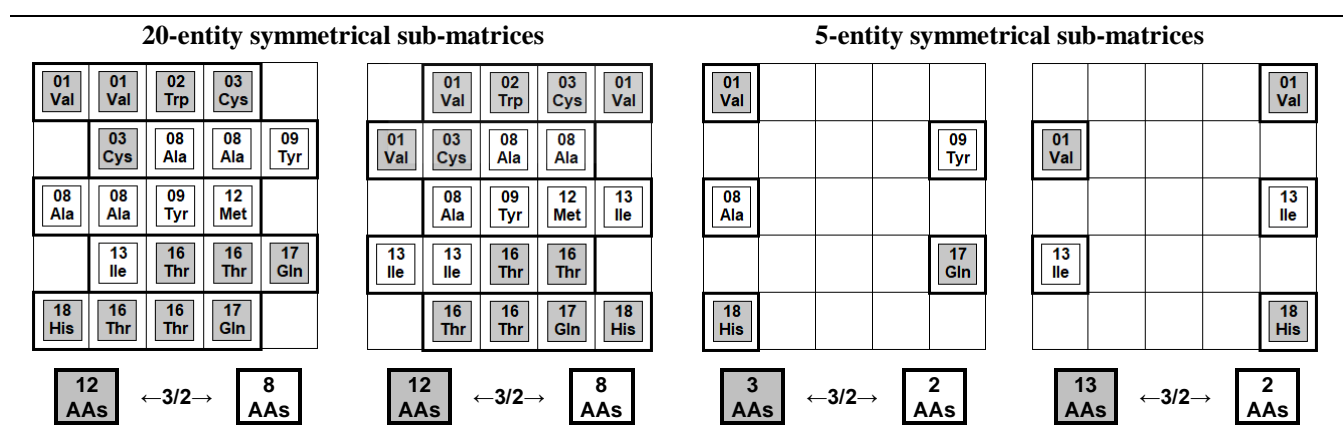


Figure 39: Symmetrical sub-matrices to 20 versus 5 entities. AAs whose codons are with 2 DNA bases* which are opposite or complementary. *Ultimate genetic code.

Thus, made up of five time 0x entities to five time 5x entities, these different symmetrical sub-matrices are always organized in a 3/2 ratio according to the predefined numbering nature of the 20 canonical amino acids.

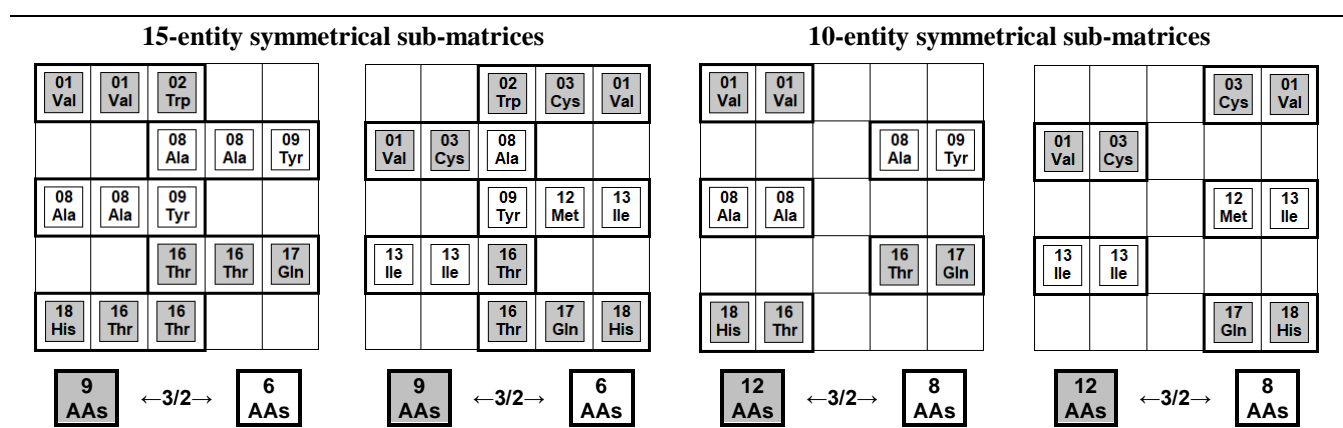


Figure 40: Symmetrical sub-matrices to 15 versus 10 entities. AAs whose codons are with 2 DNA bases* which are opposite or complementary. *Ultimate genetic code.

7.4. Recombined triangulation

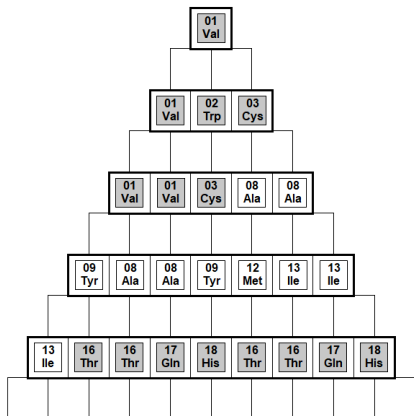
From the two rectangular sub-matrices just invested, we reconstruct here a new triangular matrix of 55 entities. As illustrated in Figure 44, we therefore create two triangular sub-matrices of 25 and 30 entities by alternating successive rows. These sub-matrices are therefore of the same configuration as that previously introduced.

25 AAs whose codons are with 2 DNA bases* which are **opposite or complementary**

01 Val	01 Val	02 Trp	03 Cys	01 Val
01 Val	03 Cys	08 Ala	08 Ala	09 Tyr
08 Ala	08 Ala	09 Tyr	12 Met	13 Ile
13 Ile	13 Ile	16 Thr	16 Thr	17 Gln
18 His	16 Thr	16 Thr	17 Gln	18 His

$$1 + 3 + 5 + 7 + 9 =$$

25-entity recombined triangular sub-matrix



15 AAs

← 3/2 ratio →

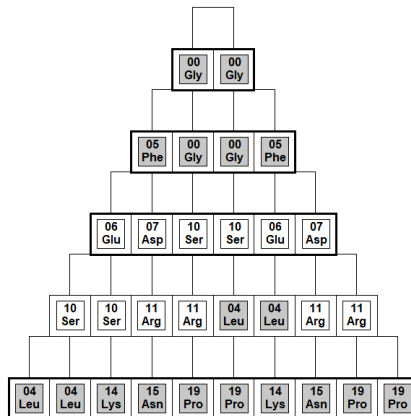
10 AAs

30 AAs whose codons are with 2 DNA bases* which are **identical or of same nature**

00 Gly	00 Gly	05 Phe	00 Gly	00 Gly	05 Phe
06 Glu	07 Asp	10 Ser	10 Ser	06 Glu	07 Asp
10 Ser	10 Ser	11 Arg	11 Arg	04 Leu	04 Leu
11 Arg	11 Arg	04 Leu	04 Leu	14 Lys	15 Asn
19 Pro	19 Pro	14 Lys	15 Asn	19 Pro	19 Pro

$$2 + 4 + 6 + 8 + 10 =$$

30-entity recombined triangular sub-matrix



18 AAs

← 3/2 ratio →

12 AAs

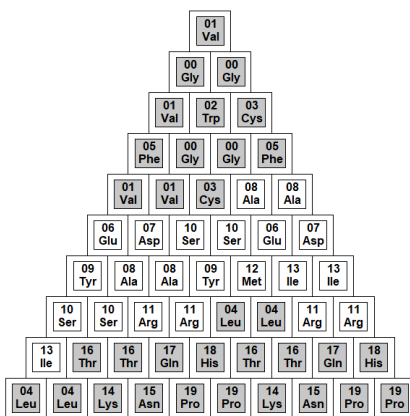


Figure 44: From the two rectangular matrices which are in agreement with the nature of the bases of the ultimate genetic code, recombined linear alternate triangular sub-matrices then a full 55-entity triangular matrix.

7.4.1. Diagonal sub- configurations

As the original matrix introduced Chapter 3, this new 55-entity triangular genetic code matrix graphically has three vertices. In the same way as with this original matrix but also the one previous recombined in Figure 27, or the one in Figure 32 again, we alternately isolate the ten diagonals which are perpendicular to the two low vertices of this last recombined triangular matrix. Doing this, it then appears as illustrated Figure 45 that the two different sets of amino acids respectively described as outer and inner are opposed in exact ratios of value 3/2.

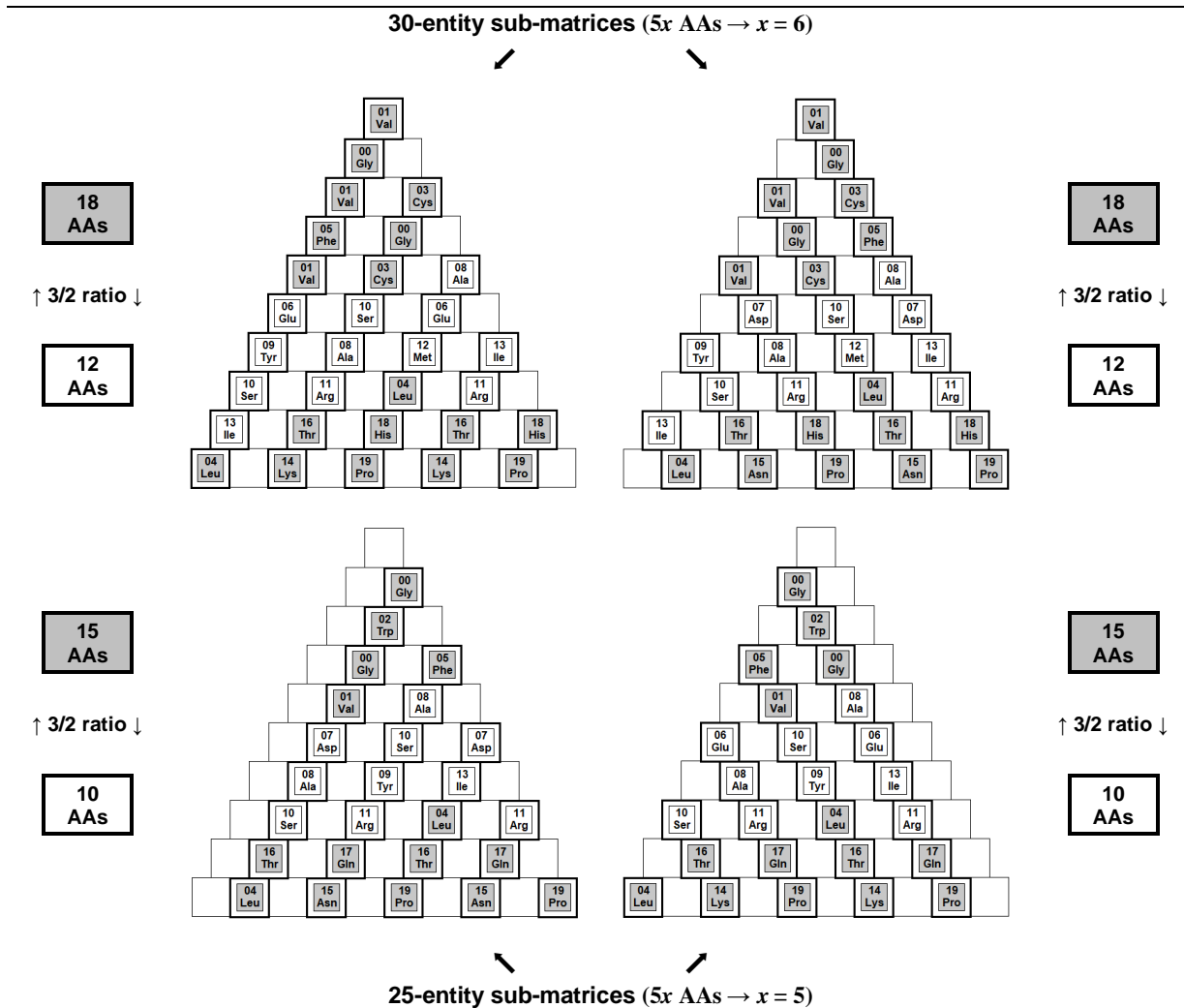


Figure 45: Distribution of outer numbering AAs and inner numbering AAs in 3 to 2 ratios into diagonal sub-configurations of a recombined triangular genetic code matrix in agreement with the nature of the bases of the ultimate genetic code. See Figure 44 Also.

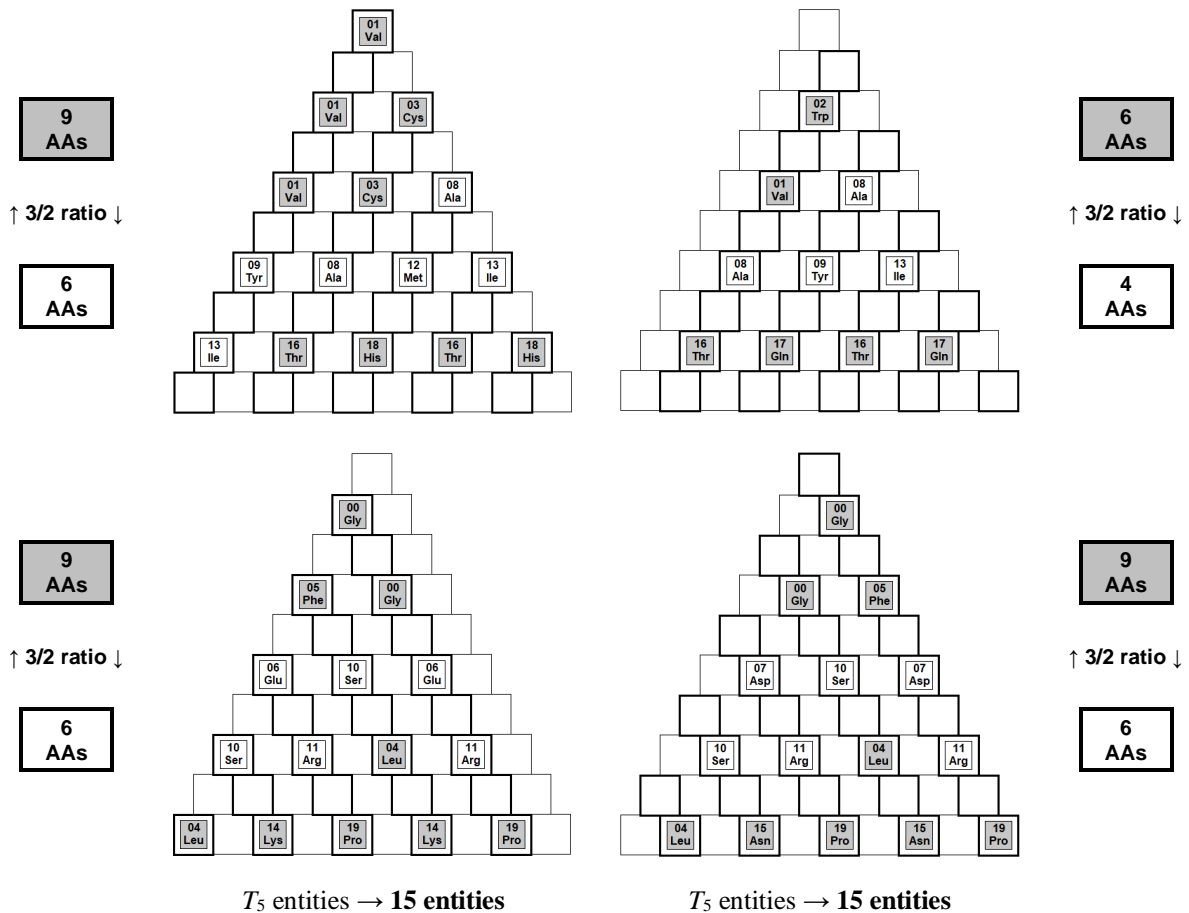
7.4.2. Mixed sub-configuration

As has already been done for this type of triangular sub-matrix (Figure 17 Chapter 4, Figure 29 Chapter 6, etc.), we cut them by alternating their diagonals in one direction and the other. Thus we form four sub-matrices of size T_5 or T_4 as component. It then appears, Figure 46, that the AAs qualified as outer and those qualified as inner oppose each other again in ratios of the exact value $3/2$ in these alternate diagonal sub-matrices. Thus, Figure 46, in agreement with the nature of the bases of the ultimate genetic code, 9 AAs versus 6 or 6 versus 4 are opposed according to the different sub-configurations of size T_5 or T_4 .

25 AAs ($5x$ AAs $\rightarrow x = 5$) whose codons are with 2 DNA bases* which are opposite or complementary

T_5 entities \rightarrow 15 entities

T_4 entities \rightarrow 10 entities



T_5 entities \rightarrow 15 entities

T_5 entities \rightarrow 15 entities

30 AAs ($5x$ AAs $\rightarrow x = 6$) whose codons are with 2 DNA bases* which are identical or of same nature

Figure 46: In agreement with the nature of the bases of the ultimate genetic code, crossed sub-configurations of T_5 and T_4 as size with inside each, an exact ratio of value $3/2$ between the outer AAs and the inner AAs. * Ultimate genetic code.

8. Genetic code and number theory

The genetic code as a geometric algebra biological system, this is the subtitle of this article. In this section we justify this ambitious theory.

8.1. Genetic code and remarkable identity

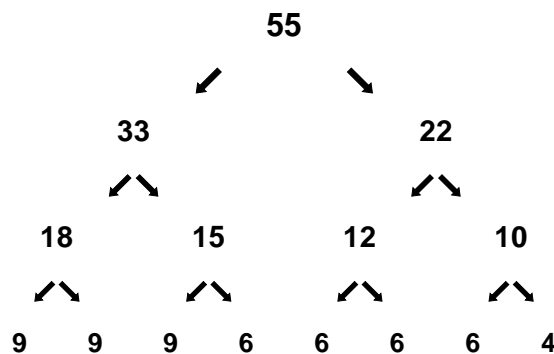


Figure 47: Final values of entities which make up the 55-entity triangular genetic code matrix according to the numbering of the AAs and their geometric distribution within numerous configurations. See Figure 46 as an example.

In the varied and numerous demonstrations of this article, we have largely demonstrated that the AAs qualified as outer and those qualified as inner are opposed in number in different ratios of value $3/2$ inside the 55-entity triangular genetic code

matrix. From larger configurations towards thinner and thinner, the same three final values are always found: nine, six and four. This fractal-type distribution is illustrated in Figure 47. These three final values are not something, they correspond to a^2 to ab and to b^2 where a and b have the respective values 3 and 2.

In final configurations, we observed that the entire matrix of 55 entities can be divided into zones of size T_5 and T_4 , i.e. sub-configurations of 15 and 10 entities. Thus, these various ratios opposing the outer and inner AAs previously defined according to their numbering are organized in the remarkable identity $(a + b)^2 = a^2 + 2ab + b^2$ where a and b have the respective values 3 and 2. Figure 48 explains this arithmetic organization operating inside the genetic code considering this triangular matrix.

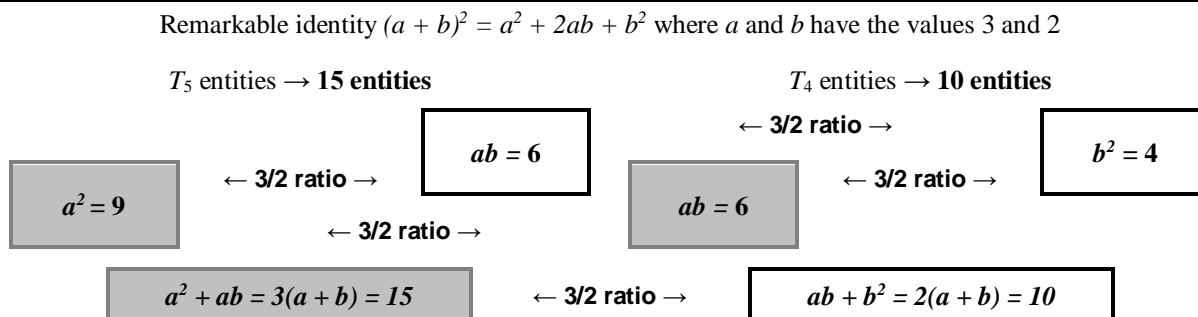


Figure 48: Remarkable identity revealed in the count of AAs inside final sub-configurations of the 55-entity triangular genetic code matrix. See Figure 46 and 47 also.

In appendix, Figure A4, about shell and subshell amount of the five living matter atoms constituting canonical amino acids, an identical arithmetical phenomena can be observed.

8.2. Hydrogen bonds and number theory

In Chapter 3 we introduced the concept of the 55-entity genetic code matrix. We did this by removing from the 64-entity square table genetic code the smallest groups of codons with identical first two bases encoding amino acids also encoded with larger codon sets (See Chapter 3). We therefore subtracted two codons for Serine, Arginine and Leucine. We also subtracted the three nonsense codons. Thus, we constructed a *lighter square genetic code matrix* with only 55 entities.

As can be seen in Figure 49, it turns out that all of the nine codons subtracted from the complete matrix have a first nucleobase, either Adenine or Thymine, but never a first Cytosine or Guanine base. Thus, in this lighter genetic code matrix, all of the codons whose first DNA base has connected with three hydrogen bonds (C or G) are considered, i.e. 32 codons while those whose first DNA base has connected with two hydrogen bonds (A and T) are 23 in number (→ 32 - 9 codons).

32 codons with C or G as first DNA base in lighter square genetic code matrix 10 encoded amino acids

63 CCC 19Pro	62 CCA 19Pro	61 CAC 18His	60 CAA 17Gln	59 ACC 16Thr	58 ACA 16Thr	57 AAC 15Asn	56 AAA 14Lys
55 CCT 19Pro	54 CCG 19Pro	53 CAT 18His	52 CAG 17Gln	51 ACT 16Thr	50 ACG 16Thr	49 AAT 15Asn	48 AAG 14Lys
47 CTC 04Leu	46 CTA 04Leu	45 CGC 11Arg	44 CGA 11Arg	43 ATC 13Ile	42 ATA 13Ile	41 AGC 10Ser	40 AGA 11Arg
39 CTT 04Leu	38 CTG 04Leu	37 CGT 11Arg	36 CGG 11Arg	35 ATT 13Ile	34 ATG 12Met	33 AGT 10Ser	32 AGG 11Arg
31 TCC 10Ser	30 TCA 10Ser	29 TAC 09Tyr	28 TAA Stop	27 GCC 08Ala	26 GCA 08Ala	25 GAC 07Asp	24 GAA 06Glu
23 TCT 10Ser	22 TCG 10Ser	21 TAT 09Tyr	20 TAG Stop	19 GCT 08Ala	18 GCG 08Ala	17 GAT 07Asp	16 GAG 06Glu
15 TTC 05Phe	14 TTA 04Leu	13 TGC 03Cys	12 TGA Stop	11 GTC 01Val	10 GTA 01Val	9 GGC 00Gly	8 GGA 00Gly
7 TTT 05Phe	6 TTG 04Leu	5 TGT 03Cys	4 TGG 02Trp	3 GTT 01Val	2 GTG 01Val	1 GGT 00Gly	0 GGG 00Gly

23 codons with A or T as first DNA base in lighter square genetic code matrix 10 encoded amino acids

63 CCC 19Pro	62 CCA 19Pro	61 CAC 18His	60 CAA 17Gln	59 ACC 16Thr	58 ACA 16Thr	57 AAC 15Asn	56 AAA 14Lys
55 CCT 19Pro	54 CCG 19Pro	53 CAT 18His	52 CAG 17Gln	51 ACT 16Thr	50 ACG 16Thr	49 AAT 15Asn	48 AAG 14Lys
47 CTC 04Leu	46 CTA 04Leu	45 CGC 11Arg	44 CGA 11Arg	43 ATC 13Ile	42 ATA 13Ile	41 AGC 10Ser	40 AGA 11Arg
39 CTT 04Leu	38 CTG 04Leu	37 CGT 11Arg	36 CGG 11Arg	35 ATT 13Ile	34 ATG 12Met	33 AGT 10Ser	32 AGG 11Arg
31 TCC 10Ser	30 TCA 10Ser	29 TAC 09Tyr	28 TAA Stop	27 GCC 08Ala	26 GCA 08Ala	25 GAC 07Asp	24 GAA 06Glu
23 TCT 10Ser	22 TCG 10Ser	21 TAT 09Tyr	20 TAG Stop	19 GCT 08Ala	18 GCG 08Ala	17 GAT 07Asp	16 GAG 06Glu
15 TTC 05Phe	14 TTA 04Leu	13 TGC 03Cys	12 TGA Stop	11 GTC 01Val	10 GTA 01Val	9 GGC 00Gly	8 GGA 00Gly
7 TTT 05Phe	6 TTG 04Leu	5 TGT 03Cys	4 TGG 02Trp	3 GTT 01Val	2 GTG 01Val	1 GGT 00Gly	0 GGG 00Gly

Figure 49: Distinction of the codons in the lighter square genetic code matrix according to the nature of the four DNA bases which can be with three (C and G) or two (A and T) hydrogen bonds. See Figure 1 also.

It also appears, in this distinction of the 55 residual codons in two sets of unequal size, that the twenty canonical amino acids are nevertheless in equal quantity in these two sets. Thus, 10 different AAs are in the C or G first base codon set and 10 different others are in the A or T first base codon set.

8.2.1. Palindrome number 55: 32 versus 23 codons

It turns out that the number 55 is a triangular number, which makes it possible to generate the numerous geometric algebra configurations which were introduced in the various previous chapters. This number 55 is as well a palindrome number. It is too a particular palindrome number since it is made up of five tens and five ones. This double value in fifth makes it possible to generate oppositions of its digital components in a value ratio of 3/2.

Thus, as can be seen in Figure 50, the mirror numbers 32 and 23, which represent the respective quantity of codons previously isolated according to the nature of the nucleobases with two or three hydrogen bonds, oppose their ten and unit in ratios 3/2 both between themselves and inside their digital structure.

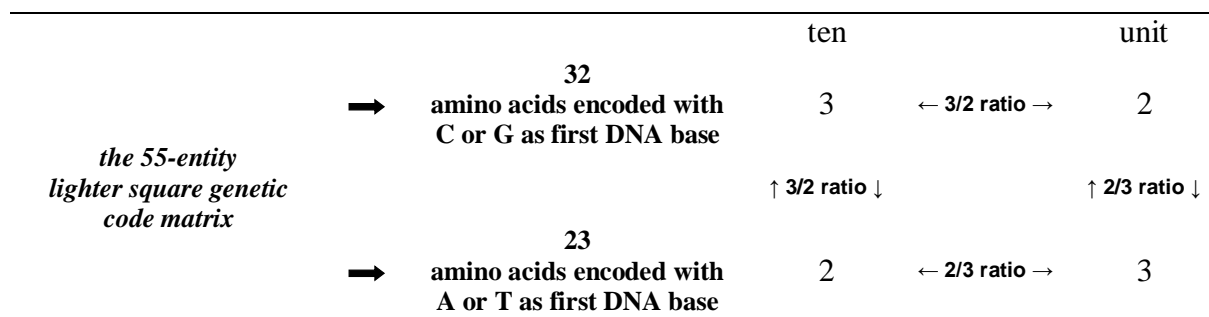


Figure 50: Crossed ratios of 3/2 value according to digital structure of the two mirror number 32 and 23, amount of codons depending of the nature of the first DNA base in the 55-entity lighter square genetic code matrix.

8.2.2. Ten versus ten AAs and AA numbering concept

Inside each previously defined two sets of 32 and 23 codons of the lighter square genetic code matrix there are therefore 10 different amino acids. As illustrated in Figure 51, these two 10-AA sets are distributed in a value ratio of 3/2 according to AA numbering concept (or also superposed ultimate genetic code concept).

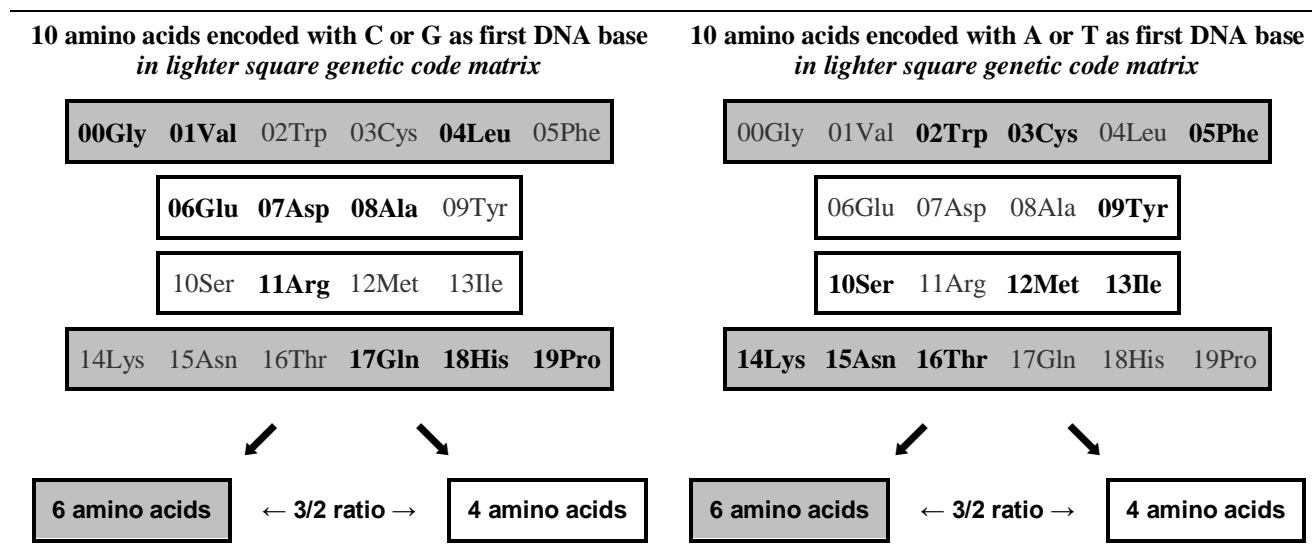


Figure 51: According to AA numbering concept and depending of the nature of the first DNA base in the 55-entity lighter square genetic code matrix, distribution of two 10-AA sets in 3/2 ratios.

8.3. First ten chemical elements and living matter

Here we find the value 55, a triangular number with value T_{10} , in a singular observation linking physics, biology and number theory.

8.3.1. Six non-organic versus four organic chemical elements

It turns out that four of the six primordial organic chemical elements (H, C, N, O, P and S) are among the first classified ten atoms. Thus, among these first 10 (i.e. 5x elements) elements, in a ratio of value 3/2, six are not organic and four participate in the organization of living matter as constituents of the twenty canonical amino acids and also of nucleotides.

The cumulative value of the atomic numbers (Z), also called nuclear charge numbers, of the first ten elements is mathematically equal to $5x$ with $x = 11$, i.e. a cumulative charge equal to 55.

The first ten chemical elements										
6 non-organic chemical elements						← 3/2 ratio →	4 organic chemical elements			
Helium	Lithium	Beryllium	Boron	Fluorine	Neon		Hydrogen	Carbon	Nitrogen	Oxygen
2	3	4	5	9	10		1	6	7	8
33 cumulated atomic numbers (33 protons)						← 3/2 ratio →	22 cumulated atomic numbers (22 protons)			

Figure 52: Opposition, in 3/2 ratios, of the 6 non-organic chemical elements and 4 organic chemical elements about their respective cumulated atomic number (Z).

It is found, there again, that the cumulated value of the nuclear charges of the six inorganic elements opposes that cumulated of the four organic chemical elements in a ratio of exact value 3/2. Indeed, as shown in Figure 52, the six inorganic elements total 33 nuclear charges (33 protons) and the four organic elements which are Hydrogen, Carbon, Nitrogen and Oxygen total 22 nuclear charges (22 protons). Since all the other phenomena presented previously, it seems very unlikely that this ratio will appear there also by simple chance. The very singular new observations that we are going to introduce strongly support this idea.

8.3.2. The 55-entity triangular matrix of the first ten chemical elements

As we have already done with the table of the lighter genetic code, we propose here a triangular matrix formed with the 55 cumulative charges (atomic numbers Z) of the first ten chemical elements.

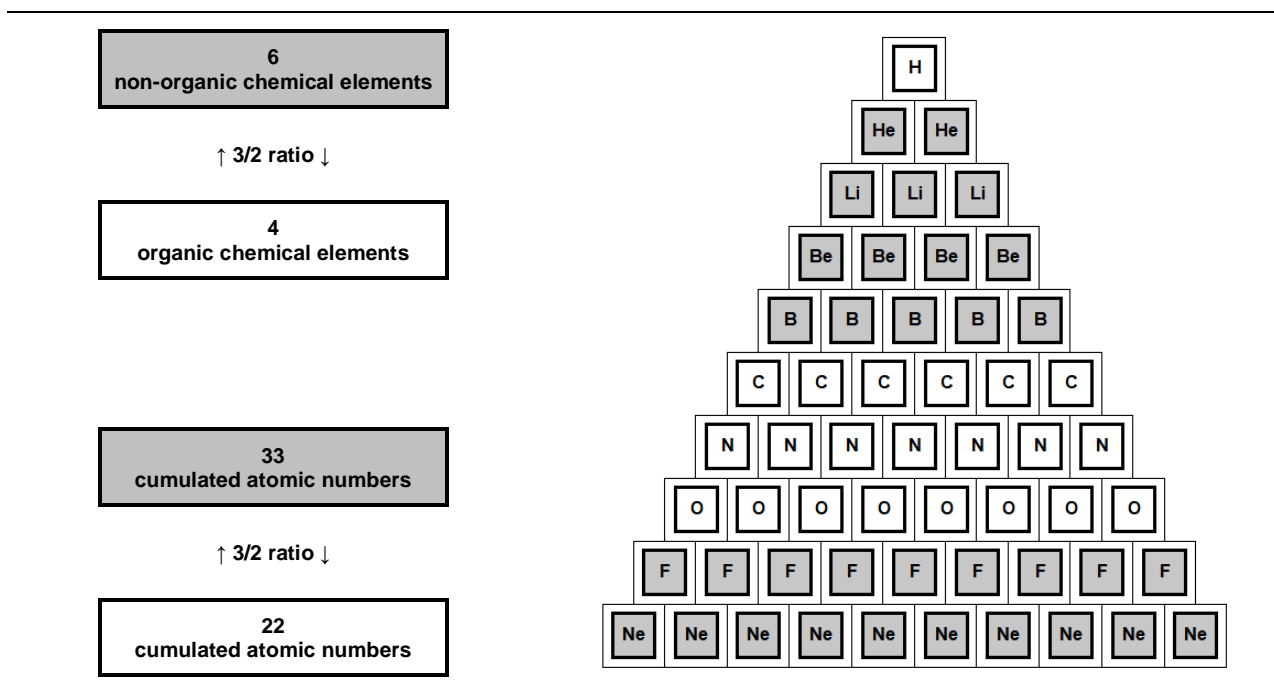


Figure 53: Distribution of nuclear charges (atomic number) in a 55-entity triangular matrix according to non-organic or organic properties of the first ten chemical elements. See Figure 52 also.

As we recall and as it is more visible in Figure 53, the 33 cumulative atomic numbers of the six non-organic elements are opposed to the 22 cumulative atomic numbers of the four organic elements.

Also we recall that a triangular number is the sum of four other triangular numbers. So T_{10} is equal to $3T_5 + T_4$. Indeed, triangular number 55 is equal to $15 + 15 + 15 + 10$. Thus, the 55-entity triangular matrix of size T_{10} representing the cumulative atomic numbers of the first 10 elements can be symmetrically divided into four triangular areas of size T_5 or T_4 .

As illustrated in Figure 54, the symmetrical association of these zones two by two generates two sub-matrices of 25 and 30 entities where the organic and non-organic elements oppose their cumulative atomic number in exact ratio 3/2.

Here the different values considered (18 versus 12 and 15 versus 10) remain the same as those previously presented throughout the numerous geometric algebra demonstrations made about amino acid distributions inside the 55-entity genetic code matrix.

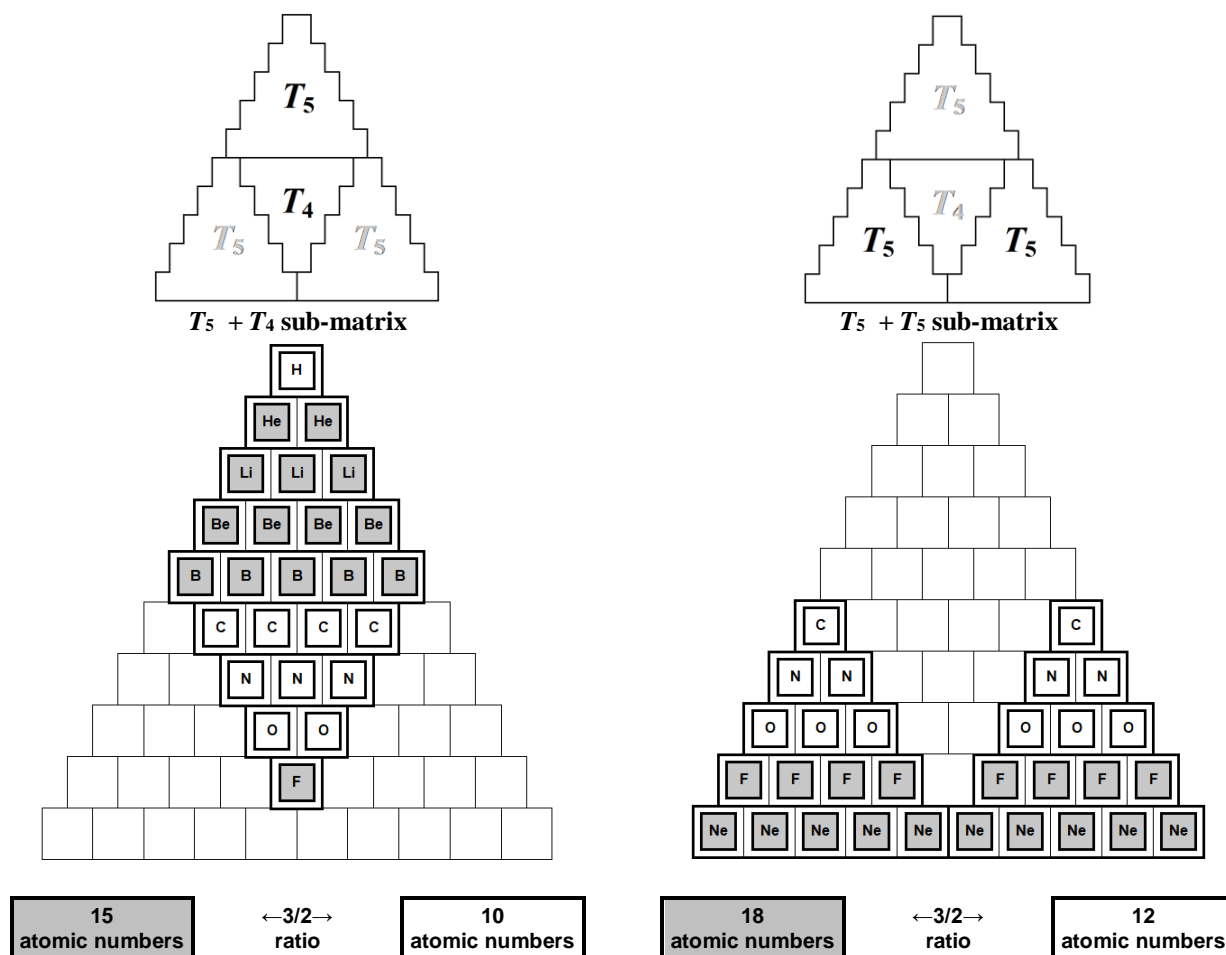


Figure 54: Opposition in perfect ratios of value $3/2$ of the cumulative atomic numbers of the organic and non-organic first ten chemical elements in symmetrical sub-matrices of sizes $2T_5$ and $T_5 + T_4$.

About this last 55-entity triangular matrix other numerous phenomena of geometric algebra similar or identical to those concerning the triangular matrix of the genetic code operate. Not presented here and because it is not the topic of this article, these phenomena will be the subject of a future paper by the author.

8.4. Domination of the $3/2$ ratio in living matter organization

As a preliminary conclusion, it seems essential to us to speak about the importance of the arithmetic ratio of value $3/2$ in the organization of the genetic code and more largely in the organization of the living matter.

The ultimate genetic code concept and the one of numbering of the twenty proteinogenic amino acids is not the only concepts to generate singular arithmetic phenomena opposing the entities of the genetic code in various ratios of value $3/2$. In a preview paper "*Genetic code, quantum physics and the $3/2$ ratio*" [5], we have revealed in great detail, a multitude of arithmetic arrangements of the components of the genetic code in this $3/2$ ratio.

For example, we are drawing attention to the fact that Glycine, which is simply like an amino acid base, has all these various components at $5x$ in number (10 atoms, 40 protons, 75 nucleons, etc.) and that these can be opposed in $3x$ and $2x$ in number. The same phenomena are also observed in the composition of the five atoms constituting the twenty proteinogenic amino acids (Hydrogen, Carbon, Nitrogen, Oxygen and Sulphur) which can also be opposed in various ratios of $3/2$ values. Finally, depending on whether or not they are organic, the first ten chemical elements also oppose their nuclear charge number (atomic number) in a ratio of value $3/2$. These many observations confirm the main idea of this article that the genetic code, confused AAs and nucleobases, is arithmetically organized according with the ratio $3/2$. Some of these singular phenomena are more fully illustrated in the appendix at the end of this paper.

Also, various other genetic code investigations from many authors are in relationship with the subject of this paper especially about ratio 3 to 2, symmetry, listing of proteinogenic amino acids or more generally connections between number theory and the genetic code. As example and not limited to, some of these investigations are listed in references [9 to 17].

From this reference list, we draw particular attention to two of our previous preprints. In "*Preproinsulin molecule and numbering of the twenty proteinogenic amino acids*" [7], we demonstrate that the amino acid sequence of the 110-amino acid preproinsulin, the initial product of the translation of insulin mRNA, is in close dependence with the twice concept of the

numbering of the twenty proteinogenic amino acids and the ultimate genetic code. In fact, It turns out that the orders of occurrence of the various preproinsulin amino acids, both direct and inverse sequence, are organized in numerous ratios of exact value $3/2$. This, according to the amino acid numbering concept. The degree of abundance of these amino acids in this initial single-chain molecule reveals same numerical rational phenomena.

In "*Amino acid numbering, ultimate numbers and the 3/2 ratio*" [8], we demonstrate relationships between the mechanism of the genetic code, of the field of Biology, and the number theory field, of which more precisely the notion of *ultimate number* [18 and 19], one of the four classes of Mathematics entities proposed to constitute the set of whole numbers. These connections are revealed in an physico-arithmetic organization of the genetic code in various ratios of $3/2$ value as global configurations.

9. Discussions and conclusions

It is universally recognized that living matter is primarily organized into a genetic code allowing the construction of protein chains composed of assemblies of almost only twenty different canonical amino acids. This genetic code corresponds to sequences of three nucleobases out of four possible to twenty different amino acids and these different possible sequences, called codons, are sixty-four in number. According to their own structures, the four DNA bases then the sixty-four codons that they form can be digitized. We have demonstrated that this digitalization allows the creation of a numbering of these codons and that this then allows the creation of a numbering of the twenty canonical amino acids.

We insist on the fact that this digitalization of codons from 0 to 63 in decimal system depends on essential criteria of deamination and depurination, criteria that the four nucleobases can more or less "mutate" within DNA chains, also allowing the evolution of living organisms.

The reduction of the table of the square genetic code into a triangular matrix of 55 entities makes it possible to reveal an organization of living matter as a geometric algebra biological system. Through this triangular matrix, this organization of the genetic code is entirely dominated by a geometric algebra constraint in a multitude of entangled ratios of $3/2$ as exact value.

All these geometric algebra mechanisms depend themselves and simultaneously on the numbering of the codons and those of the twenty canonical amino acids.

Thus, although, at base, these are physico-chemical properties, we can proclaim that living matter, in its genetic organization, in reality uses purely mathematical mechanisms.

This powerful new demonstration reinforces all the previous papers [1-2-3-5-7-8] introduced by the author, revealing each time and under numerous aspects an organization of living matter into digital entities.

This may open the way to a new branch of science considering living matter as a pure algebra biological system. Also, since this sophisticated mathematical organization of living matter depends on the physical properties of the chemical elements generated since the Big Bang, we can say that it is the purpose of cosmic evolution.

From this, we also hypothesize that what governs the genetic code, just like what governs the quantum structure of matter in its evolution towards the chemical elements, is of timeless origin, that is to say post Big Bang and even trans Big Bang.

References

1. Jean-Yves Boulay. Numbering of the twenty proteinogenic amino acids and new alphanumerical nomenclature proposal to them. *Symmetry: Culture and Science* Volume 34, Number 1, pages 061-086. 2023. https://doi.org/10.26830/symmetry_2023_1_061.
2. Jean-Yves Boulay. Numbering of the twenty proteinogenic amino acids: 3/2 ratios inside the genetic code. 2022. <https://www.researchgate.net/publication/363952852>.
3. Jean-Yves Boulay. Symmetry and Asymmetry of The Ultimate Genetic Code Matrix. 2023. <https://www.researchgate.net/publication/375923785>.
4. S.V. Petoukhov. Genetic Code and the Ancient Chinese Book Of Changes. *Symmetry: Culture and Science* Vol. 10, Nos. 3-4, p. 211-226. 1999. <https://www.researchgate.net/publication/285143425>.
5. Jean-Yves Boulay. Genetic code, quantum physics and the 3/2 ratio. 2020. <https://www.researchgate.net/publication/343064455>.
6. Sweet R.M., Eisenberg D. Optimized matching hydrophobicity (OMH). *J. Mol. Biol.* 171:479-488. 1983; [https://doi.org/10.1016/0022-2836\(83\)90041-4](https://doi.org/10.1016/0022-2836(83)90041-4).
7. Jean-Yves Boulay. Preproinsulin molecule and numbering of the twenty proteinogenic amino acids. 2023. <https://www.researchgate.net/publication/369880921>.
8. Jean-Yves Boulay. Amino acid numbering, ultimate numbers and the 3/2 ratio. 2022. <https://www.researchgate.net/publication/364374047>.
9. Ming Liu. Biosynthesis, structure, and folding of the insulin precursor protein. Volume20, IssueS. 2Supplement: Update on Islet Hormone Production: A Tribute to Donald Steiner. Proceedings of the 19th Servier - IGIS Symposium, St Jean Cap Ferrat, France, 22 - 25 March 2018. <https://doi.org/10.1111/dom.13378>.
10. S.V. Petoukhov. The Bi-periodic Table of Genetic Code and Number of Protons, Foreword of K. V. Frolov, Moscow, 258. 2001.
11. Then, A., Mácha, K., Ibrahim, B. et al. A novel method for achieving an optimal classification of the proteinogenic amino acids. *Sci Rep* 10, 15321, 2020; <https://doi.org/10.1038/s41598-020-72174-5>.
12. Wohlin A. Numerical analysis of 3/2-relations in the genetic code and correlations with the basic series of integers 5-0. *Biomed Genet Genomics* 1, 2016; <https://doi.org/10.15761/BGG.1000118>.
13. Petoukhov S., He M. Symmetrical Analysis Techniques for Genetic Systems and Bioinformatics: Advanced Patterns and Applications. IGI Global, Hershey, USA, p. 271, 2009; <https://doi.org/10.4018/978-1-60566-124-7>.
14. Darvas G., Koblyakov A.A., Petoukhov S.V., Stepanyan I.V. Symmetries in molecular-genetic systems and musical harmony. *Symmetry Culture and Science*, vol. 23, №3-4, p. 343, 2012; http://symmetry.hu/scs_online/SCS_23_3-4.pdf.
15. Petoukhov S.V. Genetic code, musical harmony, stochastic resonance and the Ancient Chinese book of I-Ching. Editor-in-Chief Solar G. p. 160-180, 2022, . Published by: The First Clinic of Acupuncture and Natural Medicine of G.Solar, Ltd, Samorin, Slovak Republic. ISBN 978-80-974284-1-9. EAN 9788097428419. This publication was created thanks to support from the European Union Erasmus program, project number 2020-1-SK01-KA202-078222; <https://www.acuclinic.eu/ecompodium/>.
16. Petoukhov S. The principle “like begets like” in algebra-matrix genetics and code biology. 2023. <https://www.researchgate.net/publication/373812983>.
17. Tidjani Négadi. Fibonacci-Like Sequences Reveal the Genetic Code Symmetries, also When the Amino Acids Are in a Physiological Environment. 2024. <https://www.researchgate.net/publication/377310535>.
18. Jean-Yves Boulay. The ultimate numbers and the 3/2 ratio. Just two primary sets of whole numbers. 2023. <https://www.researchgate.net/publication/339943634>.
19. Jean-Yves Boulay. New whole number classification and the 3 to 2 ratio. 2023. <https://www.researchgate.net/publication/341787835>.

APPENDIX

Many of phenomena presented here are taken from the author's previous paper: *Jean-Yves Boulay. Genetic code, quantum physics and the 3/2 ratio. 2020. [5]*. Other phenomena is from various J-Y Boulay papers listed in references. This appendix is of a global theme and sometimes without direct references to the different chapters introduced previously. Its important relationship, however, is the organization of the genetic code around a numerical constraint revealed in an exact ratio of value 3 to 2.

A1. Anatomy of Glycine as 3/2 ratio

A1.1. Glycine as glycined base

Within the mechanism of the genetic code and therefore among the twenty amino acids, Glycine is distinguished by its absence of radical. Its radical is reduced to a simple hydrogen atom which in a way simply closes the "base" structure common to each amino acid. The quantum study of this *glycined base*, identifying with Glycine, reveals singular arithmetic arrangements of its different components.

A1.2. Modules of Petoukhov

The notion of modules is an original system proposed by Sergey Petoukhov [3 and 8] to describe the structure of biological molecules. According to this genetic code researcher, in organic chemistry, module is a group formed of just one non-hydrogen atom with possibly its satellite hydrogen atoms attached. Also, Sergey Petoukhov considers Sulphur as constituted in a twice module.

A1.3. Detailed structure of Glycine

Figure A1 describes the structure of Glycine (or saturated base called *glycined base*) according to many criteria including its chemical composition, modular, but also atomic. It turns out that Glycine consists of 40 protons, either $5x$ protons or $(3 + 2)x$ protons.

This glycined base also consists of 5 groups or modules, i.e. $(3 + 2)x$ chemical groups. In Glycine, the number of protons is therefore an exact multiple of 8 (5 times 8 protons) and it turns out that the average number of protons per chemical group (or Petoukhov module) is therefore 8. For two groups (CH₂ and O), the amount of protons is exactly 8 whereas for the other three groups, these proton amounts are 9 or 6 (NH₂ → 9, OH → 9 and C → 6). The differentiation of these two types of modules, made up or not made up of 8 protons reveals a multitude of oppositions of the different natures of the components of Glycine (glycined base) in always an arithmetical ratio of 3/2 value.

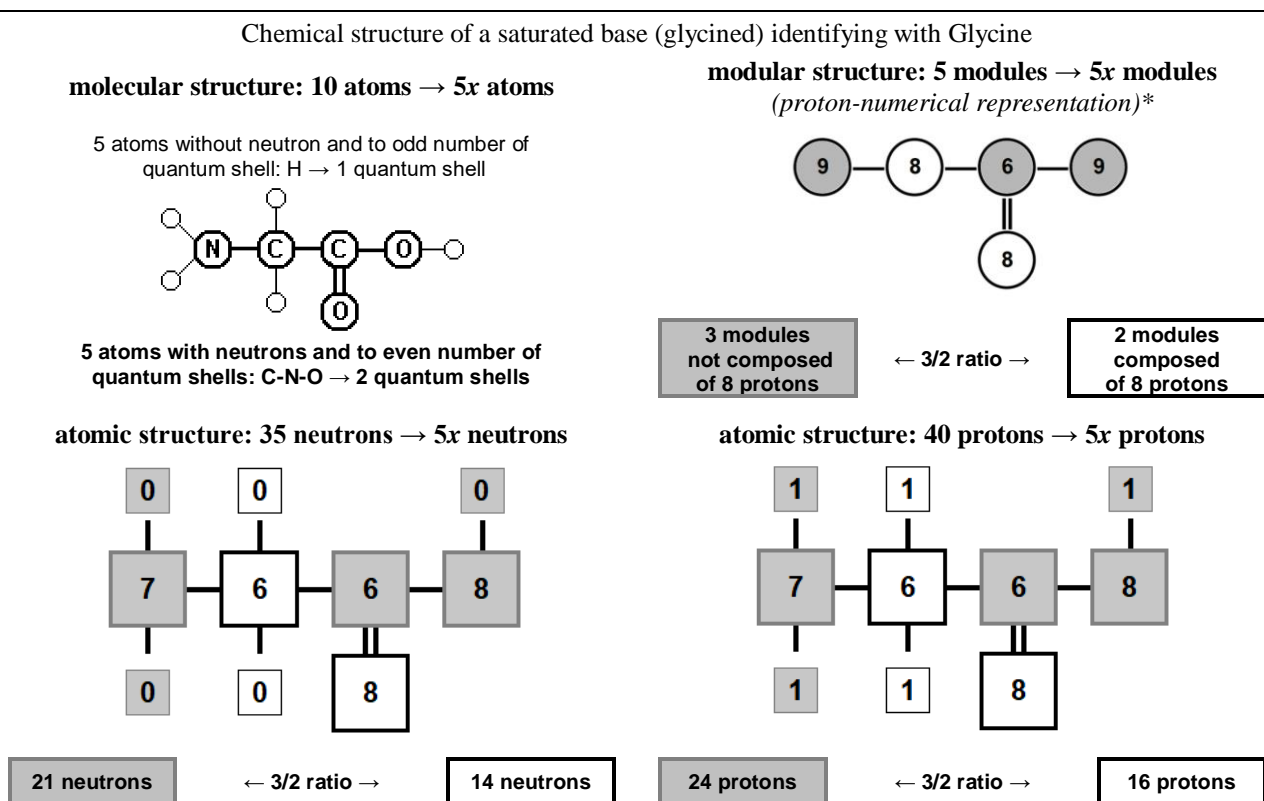


Figure A1: Chemical, modular and atomic structure of a saturated base identified with the amino acid Glycine: 5 modules, 10 atoms, 40 protons and 35 neutrons. See also Figure A2. * inspired representation from Sergey Petoukhov [4 and 10].

Glycine is made up of a multitude of entities whose numbers are all multiples of five. Thus the glycined base consists of five modules, two times five atoms, five of which have one electron shell (H) and five at two shells (C, N and O). Also Glycine consists of 5 times 15 nucleons (75) including 5 times 7 (35) neutrons and 5 times 8 (40) protons. Valences of these different components are also in numbers which are equal to $5x$ entities.

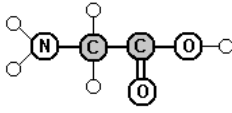

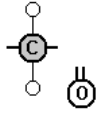
Glycine entities	Total entities number	Entities account in 3 no 8-proton modules	Entities account in 2 8-proton modules
			
5 modules	5 $5x \rightarrow x = 1$	3 $3x \rightarrow x = 1$	2 $2x \rightarrow x = 1$
10 atoms	10 $5x \rightarrow x = 2$	6 $3x \rightarrow x = 4$	4 $2x \rightarrow x = 4$
5 non-hydrogen atoms (at even number quantum shells)	5 $5x \rightarrow x = 1$	3 $3x \rightarrow x = 1$	2 $2x \rightarrow x = 1$
5 hydrogen atoms (at odd number quantum shells)	5 $5x \rightarrow x = 1$	3 $3x \rightarrow x = 1$	2 $2x \rightarrow x = 1$
75 nucleons	75 $5x \rightarrow x = 15$	45 $3x \rightarrow x = 15$	30 $2x \rightarrow x = 15$
40 protons	40 $5x \rightarrow x = 8$	24 $3x \rightarrow x = 8$	16 $2x \rightarrow x = 8$
35 neutrons	35 $5x \rightarrow x = 7$	21 $3x \rightarrow x = 7$	14 $2x \rightarrow x = 7$
20 valences (cumulated by atom)	20 $5x \rightarrow x = 4$	12 $3x \rightarrow x = 4$	8 $2x \rightarrow x = 4$
15 valences in non-hydrogen atoms	15 $5x \rightarrow x = 3$	9 $3x \rightarrow x = 3$	6 $2x \rightarrow x = 3$
5 valences in hydrogen atoms	5 $5x \rightarrow x = 1$	3 $3x \rightarrow x = 1$	2 $2x \rightarrow x = 1$

Figure A2: Distribution of the prime attributes (to $5x$ in number) of Glycine. Arrangement in $3/2$ ratios according to module proton number which can be equal to 8 or not to 8.

Also, it therefore appears, Figures A1 and A2, that the different constituents of Glycine, always $5x$ in number, are always at 3 same x entities in the set of three modules (chemical groups) with number of protons not equal to 8 and always of amount at 2 same x entities in the set of two modules whose number of protons is equal to 8.

A2. Five living matter atoms

Proteinogenic amino acids (and nucleotides) are just constituted by arrangements of five different atoms. The opposition of the values of Carbon, Nitrogen and Oxygen to those of Hydrogen and Sulphur (Phosphorus for nucleotides in DNA), always generates an arithmetic ratio of value $3/2$ according to multiple criteria studied.

A2.1. Quantum anatomy of the five living matter atoms

The table in Figure A3 lists the impressive series of quantum situations in which this remarkable duality takes place between sets of $3x$ entities versus $2x$ entities. Thus, the ratio for the numbers of electron subshells ($1s, 2s, 2p, 3s, 3p$) is $3/2$. It is still $3/2$ if we detail the subshells of those where the quantum number $l = 0$ of those where the quantum number $l = 1$. Also, the ratio for the numbers of orbitals is $3/2$. It is still on $3/2$ if we detail the orbitals of those where the quantum number $m = 0$, of those where the quantum number $m = -1$ and those where the quantum number $m = 1$.

This ratio is always $3/2$ if we detail the orbitals of those where the quantum number $l = 0$ of those where the quantum number $l = 1$. Also, the maximum number of electrons that can orbit inside all of the electronic shells of these two groups of atoms is still in a ratio of $3/2$: thirty electrons can orbit inside the electronic shells of Carbon, Nitrogen and Oxygen versus twenty on the electron shells of Hydrogen and Sulphur (Phosphorus for DNA bases).

For this last criterion, the distinction of the electrons which can orbit either on the first internal shell (2 electrons for each of the five atoms) or on the set of the other (external) shells always opposes the different values in ratios $3/2$: 6 versus 4 electrons for the inner shell and 24 versus 16 for the other shells.

Quantum criteria:	Atoms to even number of electron quantum shells			Atoms to odd number of electron quantum shells	
	Carbon 1	Nitrogen 1	Oxygen 1	Hydrogen 1	Sulphur* 1
Number of atoms	3 atoms			← 3/2 ratio →	2 atoms
Number of electron shells (K, L, M)	Carbon 2	Nitrogen 2	Oxygen 2	← 3/2 ratio →	Hydrogen 1 Sulphur* 3
	6 electron shells			← 3/2 ratio →	4 electron shells
Number of subshells (1s, 2s, 2p, 3s, 3p)	Carbon 3	Nitrogen 3	Oxygen 3	← 3/2 ratio →	Hydrogen 1 Sulphur* 5
	9 subshells			← 3/2 ratio →	6 subshells
Number of subshells where the quantum number $l = 0$	Carbon 2	Nitrogen 2	Oxygen 2	← 3/2 ratio →	Hydrogen 1 Sulphur* 3
where the quantum number $l = 1$	1	1	1	← 3/2 ratio →	0 2
	6 subshells where $l = 0$ 3 subshells where $l = 1$			← 3/2 ratio →	4 subshells where $l = 0$ 2 subshells where $l = 1$
Maximum number of orbitals	Carbon 5	Nitrogen 5	Oxygen 5	← 3/2 ratio →	Hydrogen 1 Sulphur* 9
	15 orbitals			← 3/2 ratio →	10 orbitals
Number of orbitals where the quantum number $m = 0$	Carbon 3	Nitrogen 3	Oxygen 3	← 3/2 ratio →	Hydrogen 1 Sulphur* 5
where the quantum number $m = -1$	1	1	1	← 3/2 ratio →	0 2
where the quantum number $m = 1$	1	1	1	← 3/2 ratio →	0 2
	9 orbitals where $m = 0$ 3 orbitals where $m = -1$ 3 orbitals where $m = +1$			← 3/2 ratio →	6 orbitals where $m = 0$ 2 orbitals where $m = -1$ 2 orbitals where $m = +1$
number of orbitals where the quantum number $l = 0$	Carbon 2	Nitrogen 2	Oxygen 2	← 3/2 ratio →	Hydrogen 1 Sulphur* 3
where the quantum number $l = 1$	3	3	3	← 3/2 ratio →	0 6
	6 orbitals where $l = 0$ 9 orbitals where $l = 1$			← 3/2 ratio →	4 orbitals where $l = 0$ 6 orbitals where $l = 1$
Maximum number of electrons orbiting on quantum shells	Carbon 10	Nitrogen 10	Oxygen 10	← 3/2 ratio →	Hydrogen 2 Sulphur* 18
of which the first shell (internal)	2	2	2	← 3/2 ratio →	2 2
of which the outer shell (s)	8	8	8	← 3/2 ratio →	- 8+8
	30 electrons 6 electrons 24 electrons			← 3/2 ratio →	20 electrons 4 electrons 16 electrons

Figure A3: 3/2 ratio of the electron shells and subshells, orbitals and maximum numbers of electrons according to the parity of the number of electron shells of the five atoms constituting the twenty amino acids (* Or Phosphorus for DNA).
Other 3/2 ratios generated in relation to the values of the different quantum numbers of the electrons.

Thus, fourteen different quantum criteria oppose, in a duality of ratio 3/2, the five atoms constituting the twenty amino acids (and also constituting the four DNA nucleotides with the Phosphorus in place of Sulphur). The fact that the genetic code is organized only with these five different atoms in this duality is therefore not random. The perfect complementarity of the quantum characteristics of Hydrogen and Sulphur (Phosphorus in DNA) is particularly remarkable.

These last two atoms have indeed very different quantum characteristics (in contrast to Carbon, Nitrogen and Oxygen with common characteristics) which however complement each other perfectly to always oppose in a 3/2 ratio to three other atoms, constituents of amino acids (and DNA bases). For example, Sulphur has a maximum number of nine orbitals versus only one for Hydrogen. These two very different values nevertheless complement each other (10 orbitals) to oppose in a duality of ratio 3/2 to the three times five quantum orbitals of Carbon, Nitrogen and Oxygen (15 orbitals).

Thus, the 3/2 ratio is revealed at the bottomest of the subatomic structure of the constituents of the twenty amino acids that are on the one hand the three atoms of Carbon, Nitrogen and Oxygen and on the other hand the two atoms of Hydrogen and Sulphur. It is therefore remarkable to note that these same phenomena are found in DNA, another mechanical component of the genetic code, where the quantum properties of the Phosphorus mimic those of Sulphur.

A2.2. Five living matter atoms and remarkable identity

Thus, these various ratios opposing the subshells and shells and transversely, the two categories of atoms previously defined according to the parity of their number of quantum shells, are organized in the remarkable identity $(a + b)^2 = a^2 + 2ab + b^2$ where a and b have the respective values 3 and 2.

Figure A4 explains this arithmetic organization operating in the quantum structure of the five elements working within the genetic code.

Remarkable identity $(a + b)^2 = a^2 + 2ab + b^2$ where a and b have the values 3 and 2

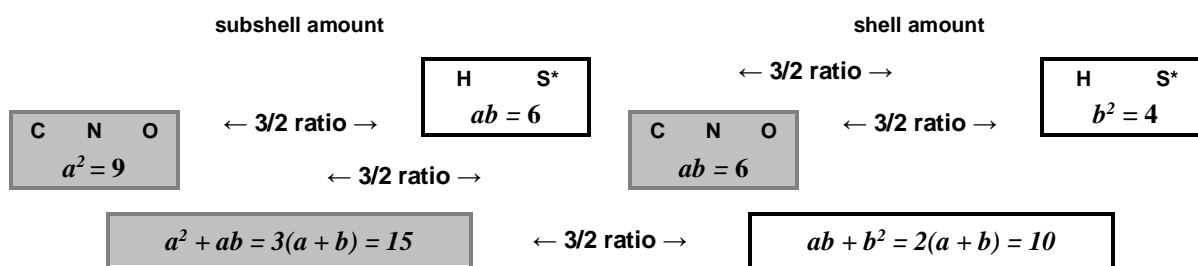


Figure A4: Remarkable identity revealed in the count of subshells and quantum shells of the five elements H, C, N, O and S (*or P in DNA). See Figure A3. See Figure 48 to comparison.

Thus, the quantity of subshells in C, N and O corresponds to the value a^2 of the remarkable identity and the quantity of subshells in H and S corresponds to the value ab . The quantity of quantum shells in C, N and O also corresponds to the value ab and that in H and S corresponds to the value b^2 . These different values therefore transcend into these equal ratios:

$$(a^2/ab) = (ab/b^2) = (a^2+ab)/(ab+b^2)$$

$$(3^2/6) = (6/2^2) = (3^2+6)/(6+2^2)$$

$$(9/6) = (6/4) = (15)/(10)$$

In a similar fashion, this remarkable identity therefore also operates in the counts of electrons according to their azimuthal quantum number and according to their magnetic number. In these electron counts, the values are just double and, for a and b at the root values 3 and 2, the respective and transcendent values are equal to:

$$2a^2 \rightarrow 2ab \rightarrow 2ab \rightarrow 2b^2$$

$$18 \rightarrow 12 \rightarrow 12 \rightarrow 8$$

A3. Alphanumeric symbol of the 20 proteinogenic amino acids

We have therefore firmly established, in many aspects, that the various characteristics of the twenty canonical proteinogenic amino acids are closely linked to their numbering, which itself depends on their DNA codification as proposed at the beginning of the article. This is why we suggest here, to enrich the current nomenclature applied to these twenty entities, the creation of new standardized alphanumeric symbols making it possible to identify these twenty proteinogenic amino acids.

In first preview papers [1 and 2], we initially numbered these entities from 0 to 19 and we attached their respective number to their three-letter alphabetic symbol. For example, we have described Valine as *1Val* and Arginine as *11Arg* so by respectively four and five characters.

For the sake of standardization (and even formalization), we propose, as illustrated Figures A5 and A6, to describe all the twenty AAs with five characters, two of which are numeric and three alphabetical. So we add the number symbol 0 (zero) to the first ten AAs numbered from 0 to 9. By this, for each AA, we therefore propose a unified symbol of 2 digits + 3 letters.

Conventional nomenclature		Proposed alphanumeric symbol into 5 characters	
Trivial name	→	<i>Glycine</i>	
Symbol (three letters)	→	<i>Gly</i>	→ <i>00Gly</i>
One letter symbol	→	<i>G</i>	

Figure A5: Conventional nomenclature and alphanumeric symbol proposal to proteinogenic amino acids into 5 characters: 2 digits + 3 letters. Here Glycine as example. See Figure A6 also.

The in Figure A6 therefore lists all of the 20 proteinogenic amino acids involved in the mechanism of the universal genetic code. It is table therefore described, from the conventional nomenclature, the trivial name, the symbol in 3 letters and the one letter symbol. To this is added, for each AA, its alphanumeric symbol of 5 characters that we propose as a new standardized and official nomenclature.

The 20 proteinogenic amino acids conventional nomenclature:			Alphanumeric symbol proposal
<i>Trivial name</i>	<i>symbol</i>	<i>one letter symbol</i>	
Glycine	Gly	G	00Gly
Valine	Val	V	01Val
Tryptophan	Trp	W	02Trp
Cysteine	Cys	C	03Cys
Leucine	Leu	L	04Leu
Phenylalanine	Phe	F	05Phe
Glutamic acid	Glu	E	06Glu
Aspartic acid	Asp	D	07Asp
Alanine	Ala	A	08Ala
Tyrosine	Tyr	Y	09Tyr
Serine	Ser	S	10Ser
Arginine	Arg	R	11Arg
Methionine	Met	M	12Met
Isoleucine	Ile	I	13Ile
Lysine	Lys	K	14Lys
Asparagine	Asn	N	15Asn
Threonine	Thr	T	16Thr
Glutamine	Gln	Q	17Gln
Histidine	His	H	18His
Proline	Pro	P	19Pro

Figure A6: Conventional nomenclature and alphanumeric symbol proposal to the twenty proteinogenic amino acids into 5 characters: 2 digits + 3 letters.