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A periodic table for genetic codes

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This paper presents a new version of a periodic table for genetic codes using a 'Leibnitz Number' as a codon number or anticodon number, which is a natural binary code number and hence outwardly similar to the Gray code binary number. In the obtained periodic table or in the reformed table (a cube-shaped periodic table), the proteinaceous amino acids not only have periodicity, but also occupy mirror-symmetrical positions with respect to the xy-plane. Moreover, the cube-shaped periodic table allows a partial explanation of non-standard genetic codes and some predictions about providing potential candidates for non-standard genetic codons to be discovered in the future. By making a new format of a two-dimensional periodic table for anticodons as the primary reference point, all of the anticodon pairing with multiple codons can be intimately related to a mirror-symmetrical arrangement of amino acids with relation to the yz-plane in the two-dimensional periodic table.

In the later section two new indexes, the Inversion Number and the Miracle Number, are introduced to show that the codon numbers and anticodon numbers play a fundamental role in the structure underlying the genetic code table. These characteristic features, such as periodicity and mirror symmetry of the indexes, hold true for not just the Watson–Crick base-pairs, but also for the non-Watson–Crick base-pairs.

Furthermore, in the mammalian mitochondrial genetic code, some basic rules identical/similar to the standard genetic code can be disclosed. These results, including symmetric quality of amino acids and Inversion Numbers, suggest the necessary conditions for the existence of life systems. Additionally, the proposed periodic table can successfully understand the previous studies, such as codon ring, mutation ring, and biosynthetic pathways.

KEY WORDS: genetic code, periodic table, mirror symmetry, codon number, new indexes (IN, MN)

1. Introduction

While more recent molecular biology increasingly moves on to the structural, functional and modelling subjects of biopolymers, in particular as does the case in protein chemistry, some scientists have still pursued the earlier subjects of whether the standard genetic code and the non-standard genetic code bear new intriguing texture besides the base-pairing, why the specific codon assignments take their actual form and more [1–5]. The latter uses numerical analysis and algebraic/statistical approach to connect the genetic code with the physical properties of amino acids such as their polarity and bulkiness and hence to find some different patterns or periodicity in the genetic code. This paper is among the latter work. Unlike the previous studies, however, I try

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to discover some rules of the genetic code based on an idea analogous to the elemental periodic table. My paper is most similar to Swanson's [1] but differs from it both in numbering the genetic code and in analyzing them. The former relies on Leibnitz Numbers (a natural binary code number), which were given each of the 64 hexagrams by G.W. von Leibnitz when he discovered the binary system in the I-Ching [6], and the latter does on Gray code binary numbers.

In section 2 I describe how to construct a periodic table for genetic codes via one-to-one correspondence between the genetic codes and 6-digit binary numbers. At the same time, the validity of the correspondence between nucleic acid bases and 2-digit binary numbers will be confirmed there. In the periodic table obtained in this way, an ordered arrangement of codon number results in periodicity of amino acids.

In section 3, a new format of three-dimensional periodic table is presented, in which amino acids can be arranged to have mirror symmetry with respect to the xy-plane. In the new table a codon are placed on one of the $4 \times 4 \times 4$ lattice points of a cube, and therefore I term it a cube-shaped periodic table. One will see that this mirror symmetry plays a primary role in the later sections than the third.

In sections 3–6, the mirror symmetry is typically used to examine the genetic code. More specifically, in section 3 the symmetry is used to show that codons paring with first-base-modified anticodon occupy characteristic positions in the cube-shaped periodic table, and in sections 4 and 5, to classify non-standard genetic codes and to derive their rules. Furthermore, in section 6, it is used to explain anticodons pairing with multiple codons.

In sections 7 and 8, in order to show that the codon numbers and the anticodon numbers play a key role in the genetic code table, as atomic numbers do so in the elemental periodic table, I introduce two new indexes, Inversion Number (IN) and Miracle Number (MN), which can be calculated using the binary codon numbers and binary anticodon numbers.

In section 9, these indexes have not only the afore-mentioned periodic/symmetric qualities in the periodic table but also a new type of operational rules within their indexes. As some of these standard genetic codes rules are shared with mammalian genetic codes', these findings are strongly suggestive of the necessary condition for the existence of life systems, together with interpretation that mitochondria will come from a few symbionts including archaea.

In section 10, the previous results, including codon ring and mutation ring (Swanson [1]), amino acid polarity (Jungck [2]), weight diagram (Bashford et al. [3]), Siemion numbers (Siemion et al. [4]) and biosynthetic pathway (Knight et al. [5]), will be correlated with my findings.

As mentioned above, this paper examines the potential structure underlying the genetic code based on a conception analogous to the elemental periodic table. As is known, the amazing growth in computing power available to scientists over the past few decades has made the elemental periodic table progressively less important to scientific research, because such computer power has allowed the researchers to carry out theoretical calculations of the physical or chemical properties of molecules based on the first principle

of quantum mechanics. However, the elemental periodic table is still valuable in that it allows scientists to intuitively or systematically experience natural phenomenon. From this same reason, a periodic table for genetic code would also be highly useful if scientists could have access to it so that biological phenomenon could be intuitively or systematically understood, I believe so.

2. Basic principles of the periodic table for genetic codes

The numbers to be assigned to the codons and anticodons are the Leibnitz Numbers (shown in figure 1), which range from 0 to 63 (0 occurs just before the 6 o'clock position). To construct a periodic table for genetic codes requires three steps: the first is to characterize codon-anticodon base-pairing; the second is consequently to make one-to-one correspondence between nucleic acid bases and 2-digit binary numbers; the last is to examine scheme-independence on results obtained.

2.1. Characteristics of standard genetic codes base-pairing

To achieve purpose of this section necessitates classification of base-pair types in the standard genetic codes. The classified result is shown in table 1, which is obtained from summarization of table presented in figure 9. Identification of anticodon modified bases needed for this classification will be explained in section 8.

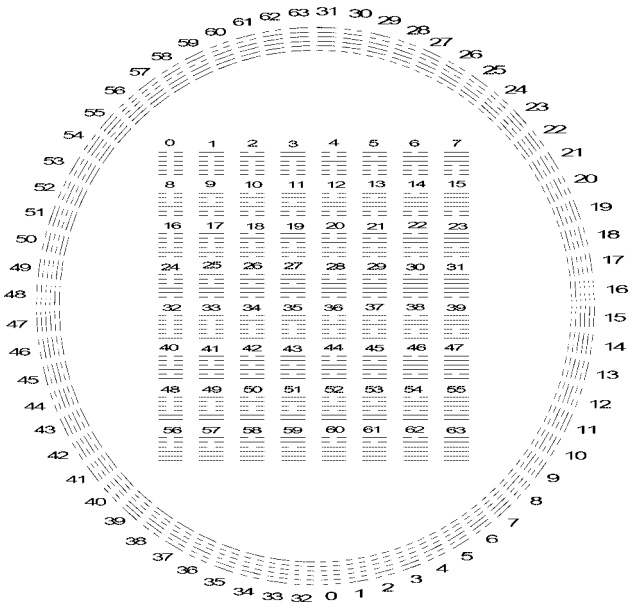

Figure 1. Leibnitz Numbers and circular diagram of the 64 hexagrams in the I-Ching. The number for each hexagram was first given by G.W. von Leibnitz.

Table 1
The base-pair types of the standard genetic codes and their populations and percentage.

The base-pair types		Frequency	
Bases[1)]	B.N. rep.[2)]	Pop.[3)]	P.C.[4)]
C–G	00–10	85	46.4
C–Q	00–10	4	2.2
A–U	01–11	70	38.3
G–U	10–11	15	8.2
Q-U	10–11	4	2.2
I–U	10–11	1	0.5
G–A	10–01	1	0.5
I–A	10–01	1	0.5
L–A	00–01	1	0.5
I–C	10–00	1	0.5

Note: Bases[1)]: Q, I and L are queuosine, inosine and 2-lysylcytidine, respectively; B.N. rep[2)]: binary number representation of bases; Pop.[3)]: populations; P.C.[4)]: percentage.

Table 1 has two notable features as follows: first, there is no base-pair between uracil (U) and cytosine (C); second, most base-pairs are the Watson–Crick type (87%) – namely, 38% of adenine (A) and U, and 49% of guanine (G) and C. There are about 10% of other base-pairs of G and U, which are the non-Watson–Crick type base-pair.

2.2. One-to-one correspondence between nucleic acid bases and 2-digit binary numbers

Two features of table 1 allow the interpretation that the genetic codes will use the binary system, because the first feature that two bases, U and C, do not pair with each other corresponds to electrically switching-off and the second feature of forming the base-pair to electrically switching-on. Specifically, if each base can be assigned to a 2-digit binary number (for example, C(00), U(11), G(10), and A(01)), then the above mentioned features of the standard genetic codes are completely replaced with two conditions: first, if the binary numbers of two compared bases share no common figure between any positions, which may be different from each other or not, then switch off; that is, there is no bonding between the codon and anticodon bases, such as C(00) and U(11); second, if the binary numbers of two different compared bases share at least a single common figure, though they exist at different positions such as G(10) and A(01), then switch on; that is, form a hydrogen-bond between the codon and anticodon bases.

Such similarity between the nucleic acid bases and the 2-digit binary numbers is summarized in table 2. As the result, these ideas lead to the following formulae as

Table 2
Classification of the base-pair types between codon and anticodon bases in the standard genetic codes and of the combination between 2-digit binary numbers, and correspondence between the two.

Bases	Binary numbers
Groups forming hydrogen-bond (HB)	Groups including the common figure (CF)
(C, A, G)	(00, 01, 10)
(U, A, G)	(11, 01, 10)
Group free from formation of HB	Group including no CF
(C, U)	(00, 11)

Note: Classification of bases is based on table 1.

Table 3
Periodic table of the genetic codes (N-scheme).

Codon No.	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Codon	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
	C	C	C	C	A	A	A	A	G	G	G	G	U	U	U	U
	C	A	G	U	C	A	G	U	C	A	G	U	C	A	G	U
Amino acid	P	P	P	P	H	Q	Q	H	R	R	R	R	L	L	L	L
Codon No.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Codon	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
	C	C	C	C	A	A	A	A	G	G	G	G	U	U	U	U
	C	A	G	U	C	A	G	U	C	A	G	U	C	A	G	U
Amino acid	T	T	T	T	N	K	K	N	S	R	R	S	I	I	M	I
Codon No.	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47
Codon	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
	C	C	C	C	A	A	A	A	G	G	G	G	U	U	U	U
	C	A	G	U	C	A	G	U	C	A	G	U	C	A	G	U
Amino acid	A	A	A	A	D	E	E	D	G	G	G	G	V	V	V	V
Codon No.	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63
Codon	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U
	C	C	C	C	A	A	A	A	G	G	G	G	U	U	U	U
	C	A	G	U	C	A	G	U	C	A	G	U	C	A	G	U
Amino acid	S	S	S	S	Y	–	–	Y	C	–	W	C	F	L	L	F

Note: Codon No. 33: G ← 1st base (5′); C ← 2nd base; A ← 3rd base (3′).

conversion schemes from the former representation into the latter:

$$\{\mathrm{C}, \mathrm{U}\} = \big\{(00), (11)\big\} \quad \text{and} \quad \{\mathrm{G}, \mathrm{A}\} = \big\{(10), (01)\big\}. \tag{1}$$

The scheme (2-digit numbers) in table 1, C(00), U(11), G(10), and A(01), is one of four possible schemes in formulae (1).

Table 4
Periodic table of the genetic code (R-scheme).

Codon No.	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Codon	C	A	G	U	C	A	G	U	C	A	G	U	C	A	G	U
	C	C	C	C	A	A	A	A	G	G	G	G	U	U	U	U
	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
Amino acid	P	T	A	S	H	N	D	Y	R	S	G	C	L	I	V	F
Codon No.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Codon	C	A	G	U	C	A	G	U	C	A	G	U	C	A	G	U
	C	C	C	C	A	A	A	A	G	G	G	G	U	U	U	U
	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
Amino acid	P	T	A	S	Q	K	E	–	R	R	G	–	L	I	V	L
Codon No.	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47
Codon	C	A	G	U	C	A	G	U	C	A	G	U	C	A	G	U
	C	C	C	C	A	A	A	A	G	G	G	G	U	U	U	U
	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
Amino acid	P	T	A	S	Q	K	E	–	R	R	G	W	L	M	V	L
Codon No.	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63
Codon	C	A	G	U	C	A	G	U	C	A	G	U	C	A	G	U
	C	C	C	C	A	A	A	A	G	G	G	G	U	U	U	U
	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U
Amino acid	P	T	A	S	H	N	D	Y	R	S	G	C	L	I	V	F

Note: Codon No. 18: G ← 1st base (5′); C ← 2nd base; A ← 3rd base (3′).

Now, another matter to be noticed in this subsection is implicated in sequence of base triplets: namely, which base-triplet (the three-bases code) of ‘normal’ or reverse sequence can be used as genetic code base-triplets when 6-digit binary numbers are converted into base triplets, as shown below?

Decimal number	Binary number	Normal sequence	Reverse sequence
18	010010	ACG	GCA

Normal sequence (N-scheme) gives the conventional genetic code table to see it in molecular biology text. In contrast, reverse sequence (R-scheme) offers a new version of a periodic table for genetic code. The N-scheme (table 3) has no periodicity unlike the elemental periodic table, whereas the R-scheme (table 4) has it. As my findings described in the later sections is scheme-independent as explained in next subsection, I use the R-scheme in this paper, primarily because table 4 has periodicity. Then, note that the origin of a word “periodic” is attributed to rule 7 in section 9.1, which is scheme-independent, rather than table 4.

2.3. Scheme-independence upon the obtained results

In this paper a following scheme is used:

$$\mathrm{C}(00),\ \mathrm{U}(11),\ \mathrm{G}(10),\ \text{and}\ \mathrm{A}(01). \tag{2}$$

For all of other candidate schemes from formulae (1), I confirmed scheme-independence of the results by fully examining the scheme resulting from mutual replacement of the bases concerned; for example, a possible scheme C(11), U(00), G(10), and A(01) was examined by the mutual displacement of the two bases C and U in each part of this paper. Likewise, I also perfectly checked up each part of this paper for the N-scheme including four possible candidates.

Therefore even if this study is started with any one of the possible assigning schemes, the scheme chosen has no affect on the results described below and is not a crucial point to the conclusion of this article. Conversely, this paper shows only results independent from the candidate schemes. Thus, table 4 can be obtained as a periodic table of the genetic codes.

3. Rules derived from a cube-shaped periodic table

The more remarkable features of the genetic codes can be shown by figure 2, which is provided by reorganization of table 4 and, as mentioned in introduction, is termed a cube-shaped periodic table.

Consequently, figure 2 is permissive for the following two rules. The first rule is as follows:

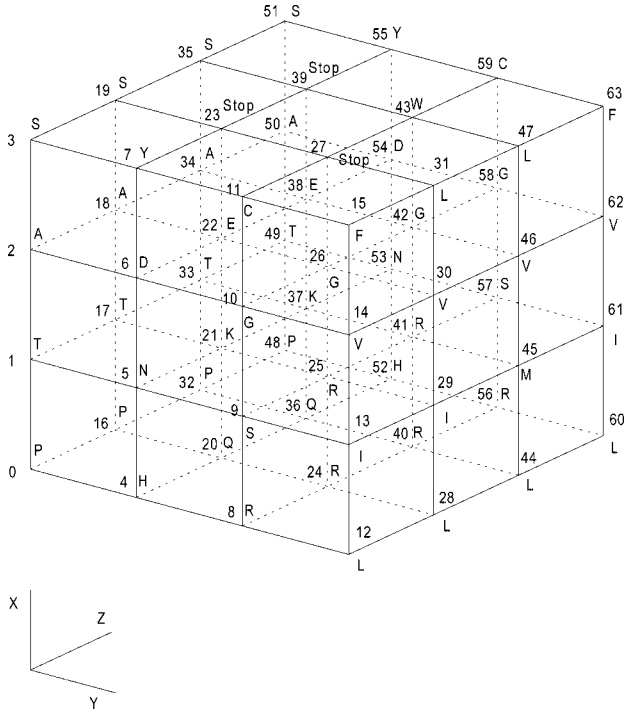

Figure 2. Cube-shaped periodic table of the standard genetic codes.

Rule 1. Amino acids in the cube-shaped periodic table are arranged in mirror symmetry in relation to the xy-plane (for the N-scheme, the yz-plane), with the exception of two pairs of codons – UGA and UGG, and AUA and AUG.

Of course, the exception of rule 1 also occurs at the same codons in any other candidate schemes including the N-scheme, whose codon numbers in the present scheme are as follows; UGA = 27, UGG = 43, AUA = 29, and AUG = 45.

Another feature in figure 2 is that leucine only has mirror symmetry with respect to the second plane (the yz-plane for the R-scheme; the xy-plane for the N-scheme) at two pairs of lattice points in figure 2. However, life systems do not always satisfy the symmetry with reference to the second plane. This is due to the fact that a high level of symmetry of amino acids in figure 2 will require fewer amino acids than available in a life system to support the multiplicity of proteins; specifically, full satisfaction of the second symmetry diminish kinds of amino acid up to the number of 16, and further satisfaction of the third symmetry leads to 8 kinds of amino acids. Therefore, I believe that the mirror symmetry seen in relation to the second plane will be merely a random occurrence. In the mammalian mitochondrial genetic code, rule 1 holds completely true without exception, unlike the standard genetic code. Similarly, the second plane symmetry of leucines corresponds precisely to the standard genetic code (see figure 3).

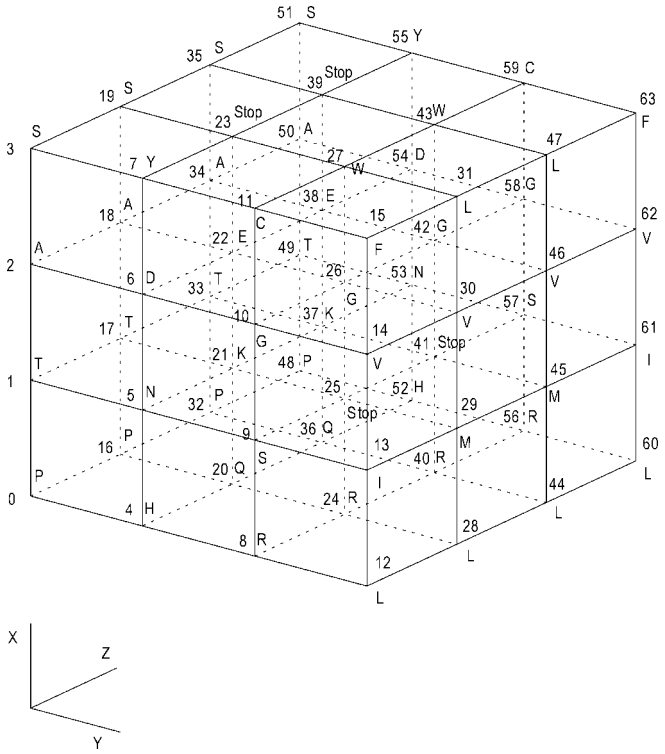

Figure 3. Cube-shaped periodic table of the mammalian mitochondrial genetic codes.

Therefore, I interpret that this mirror symmetry with respect to one plane will provide a suggestion for necessary conditions for the existence of life systems, because it has been mutually kept up in both life systems (mitochondria and their symbionts).

The second rule is relevant to an arrangement of the codons in the cube-shaped periodic table which pair with the anticodon including a modified base. Such anticodons are shown in table 5. In order to characterize their arrangements, they are highlighted in the cube-shaped periodic table; figure 4 is thus obtained.

From figure 4, the second rule can be readily derived.

Rule 2. With regard to the cube-shaped periodic table, the codons that pair with the first base-modified anticodon are located on two perpendicular planes which cross at right angles. In addition, these codons are arranged in mirror symmetry in relation to the yz-plane (for the N-scheme, the xy-plane).

Eight sites of highlighted codons (28 sites) in figure 4 break rule 2: three sites on the crossed-planes have no corresponding symmetric site; two sites of symmetric location are out of the planes; and the remainder (3 sites) show these composite breakings. I interpret this fact as follows: the most probable candidate anticodon of base-modification in the future would be found in the unmodified ones pairing with the six codons of an asymmetric arrangement. Concretely, with the exception of two

Table 5
Anticodons including a modified base.

Codon No.	Codon	Amino acids	Anticodons	Codon No.	Codon	Amino acids	Anticodons
4	CAC	H	^{1}QUG	26	GGA	G	^{8}UCC
5	AAC	N	^{1}QUU	28	CUA	L	^{3}UAG
6	GAC	D	^{1}QUC	29	AUA	I	^{9}LAU
7	UAC	Y	^{1}QUA	31	UUA	L	^{10}UAA
8	CGC	R	^{2}I CG	34	GCG	A	^{4}UGC
16	CCA	P	^{3}UGG	37	AAG	K	^{6}UUU
17	ACA	T	^{3}UGU	38	GAG	E	^{6}UUC
18	GCA	A	^{4}UGC	45	AUG	M	^{11}CAU
19	UCA	S	^{4}UGA	46	GUG	V	^{4}UAC
20	CAA	Q	^{5}UUG	52	CAU	H	^{1}QUG
21	AAA	K	^{6}UUU	53	AAU	N	^{1}QUU
22	GAA	E	^{6}UUC	54	GAU	D	^{1}QUC
24	CGA	R	^{2}I CG	55	UAU	Y	^{1}QUA
25	AGA	R	^{7}UCU	56	CGU	R	^{2}I CG

Note: This table is based on Muto's manuscript [7]. 1: queuosine (Q); 2: inosine (I); 3: not determined; 4: uridine-5-oxyacetic acid; 5: 2-thiouridine; 6: 5-methylaminomethyl-2-thiouridine; 7: 5-methoxycarbonylmethyluridine; 8: not determined; 9: 2-lysylcytidine (L); 10: 5-carboxymethylaminomethyl-2′-o-methyluridine; 11: N^4-acetylcytidine.

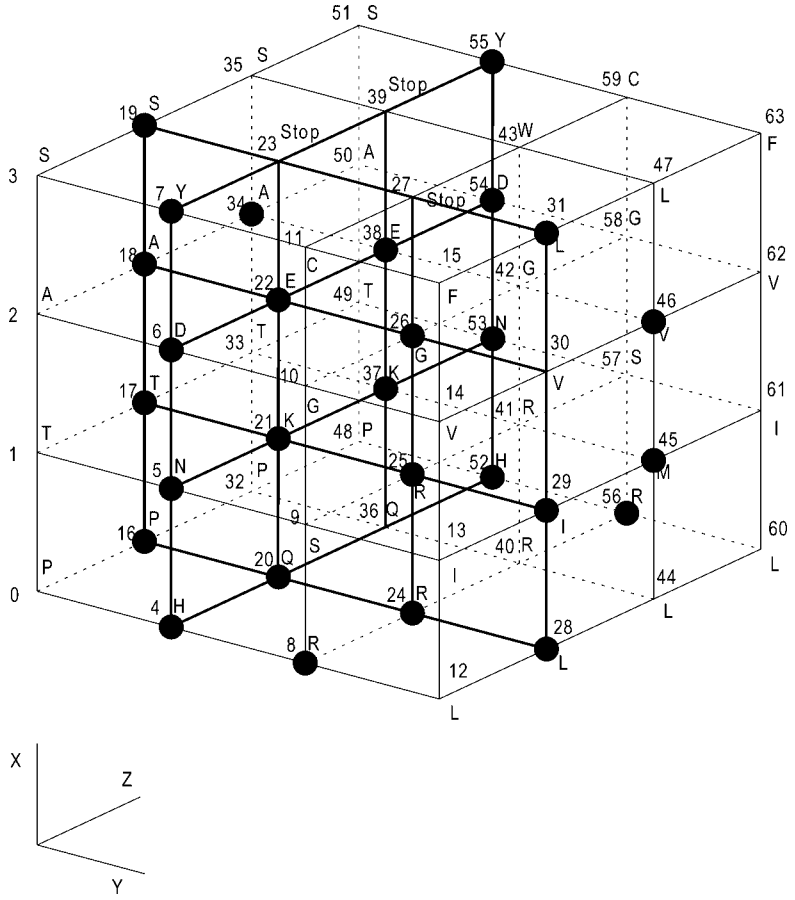

Figure 4. Codons (•) that pair with the anticodons contained in a modified base.

stop-codons UAA(23) and UGA(27), four codons UGC(11), GUA(30), ACG(33), and UGU(59) will be able to serve as pairing-partners of such candidate anticodons, where the number in parentheses is the codon number in the present scheme. These fine features are identical for those of the N-scheme.

Likewise, if non-standard genetic codons are highlighted in figure 2, then some observations of regularity of the non-standard genetic codes may emerge from the figure. In fact, when straight lines are properly drawn between the highlighted codons, it is possible to create four polygons, but three groups of polygons, which are arranged in mirror symmetry in relation to the xy-plane (figure 5) (for the N-scheme, the yz-plane). Thus, these polygons can be used to classify the non-standard genetic codes into three groups. How to make these polygons will be provided in the next section.

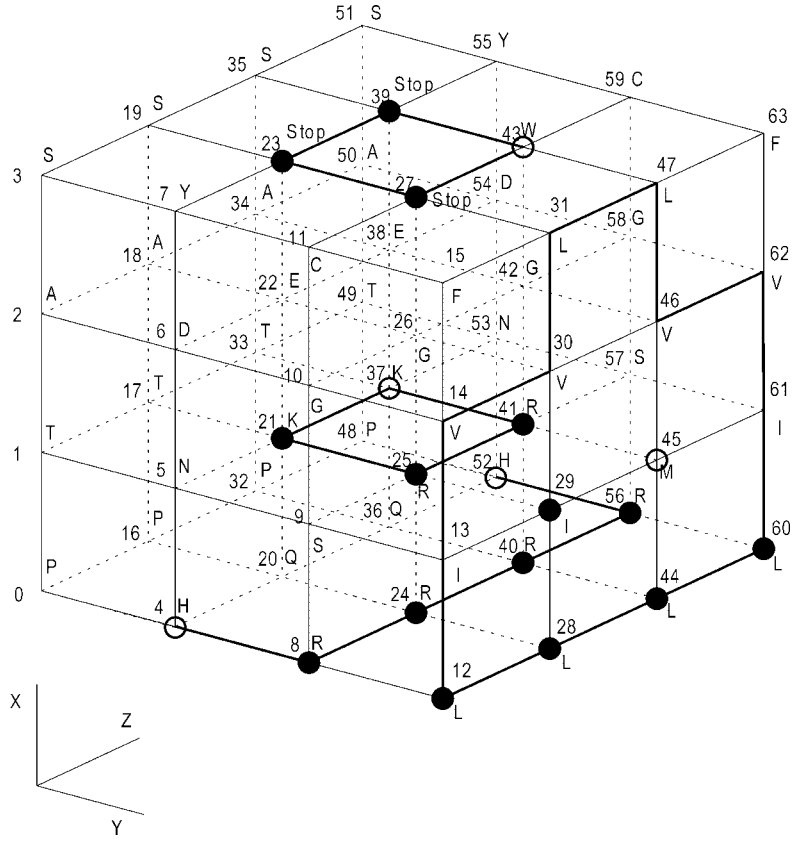

Figure 5. Non-standard genetic codons (●) shaping polygons.

4. Classification of the non-standard genetic codes

It is my opinion that classification of the non-standard genetic (non-SG) codes will be suggested by examining the replacement of a certain amino acid with other one in the evolutionary processes of proteins development; in other words, the rules of the non-SG codes in life systems will probably be contained those to replace some amino acids with other ones in proteins. Because the appearance of a non-SG code in the systems may cause a form of mutation and, consequently, it may allow the replacement of an amino acid with other one; thus a wide variety of mutations including such an episode will provide to biological organisms wholly new proteins needed in evolutionary processes. However, any amino acid in a protein will have been unable to be readily replaced with other one, but only a proper amino acid should have attained the qualifications for the replacement, for the replacement of such an amino acid with other one will have brought a critical, but not fatal, effect in maintenance of the life system. Table 6 shows groups of such potentially interchangeable amino acids, which was made by Miyata [8].

Now, as shown in figure 6, the highlighted genes coding amino acids in table 6 provide six shapes of figures with regard to the cube-shaped periodic table, and so the

Table 6
Classification of amino acids which have the potential to more easily undergo mutual replacement in the evolutionary processes of protein development.

Group	Amino acid	Volume	Polarity
1st	G	3	9.0
	A	31	8.1
	S	32	9.2
	P	32.5	8.0
	T	61	8.6
2nd	N	56	11.6
	D	54	13.0
	Q	85	10.5
	E	83	12.3
3rd	K	119	11.3
	H	96	10.4
	R	124	10.5
4th	V	84	5.9
	L	111	4.9
	I	111	5.2
	M	105	5.7
5th	F	132	5.2
	Y	136	6.2
	W	170	5.4
6th	C	55	5.5

Note: This table is based on Miyata's textbook [8].

six figures offer three groups of polygons, which are depicted in figure 5, to classification of non-SG codes without reserve (table 7). Roughly speaking, the three consist of one Stop-codons group and two groups of polygons in figure 6: the third and fourth groups.

It has important implications for this paper's context that each figure in figure 6 has mirror symmetry with reference to the xy-plane (for the N-scheme, the yz-plane), although the symmetry is, of course, attributed to rule 1. Because that leads not only to the same symmetry of three groups of non-SG codes polygons in the cube-shaped periodic table (see rule 3), but also to a suggestion that the evolutionary rule of proteins development might be closely related to mirror symmetry. Thus, such considerations lead to the next rule.

Rule 3. With regard to the cube-shaped periodic table, the polygons drawn by the lattice points of the highlighted non-SG codons have mirror symmetry with respect to the xy-plane (for the N-scheme, the yz-plane).

In the next section I will describe the non-SG codes' rules, including the mirror symmetry of their polygons, and will then predict non-SG codes to be newly discovered in the future using a few derived rules.

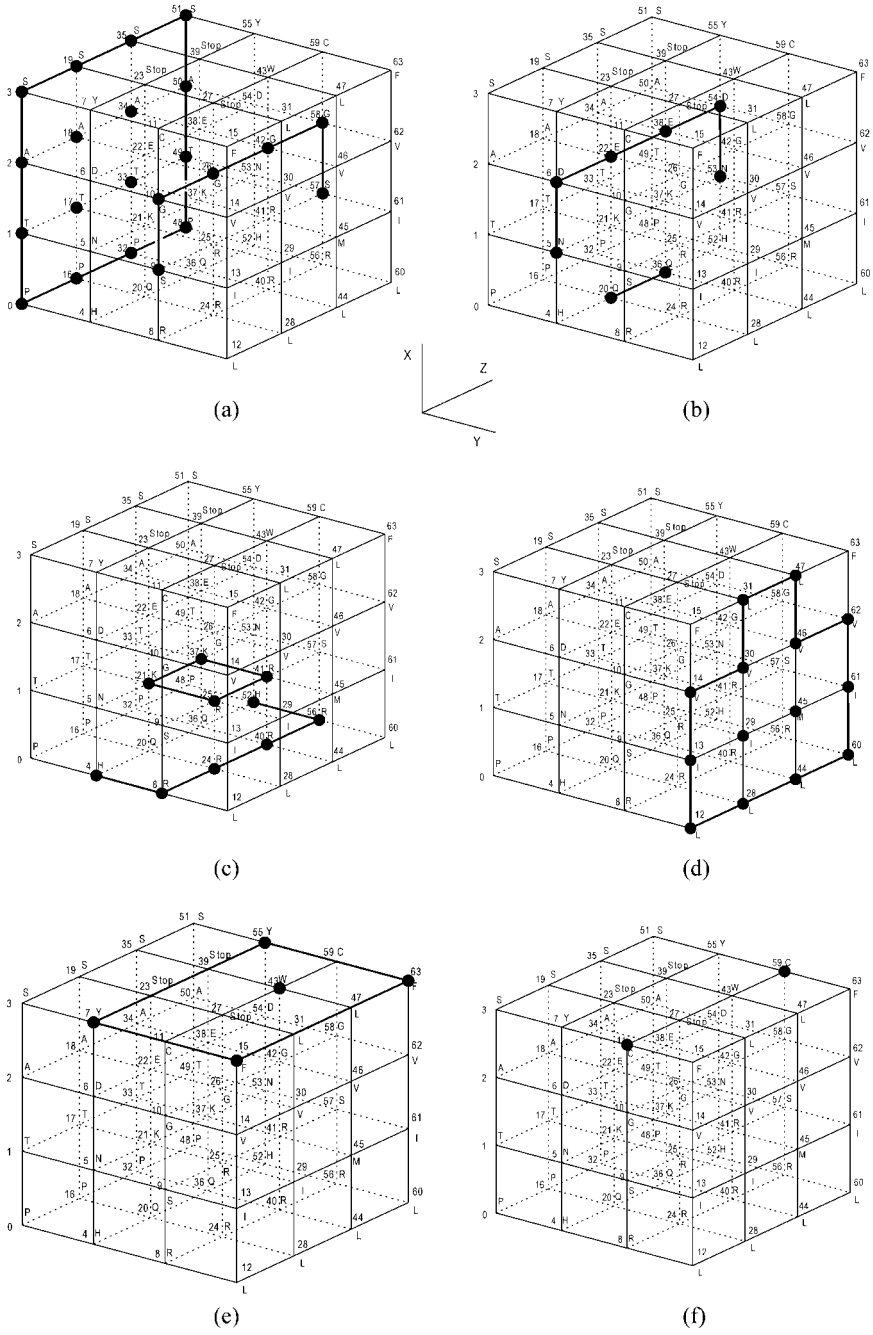

Figure 6. Amino acids (●) shaping polygons, which have the potential to more easily undergo mutual replacement in the evolutionary processes of protein development. (a) The first group. (b) The second group. (c) The third group. (d) The fourth group. (e) The fifth group. (f) The sixth group. For classification of amino acids, see table 6.

Table 7
Classification of the non-SG codes.

A. Mitochondrial variants

Group	Codon No. & Codon		Amino acid[1)]	Observed systems	Amino acid[2)]
1st	23	UAA	Y	Platyhelminths, *Dugesia japonica*,	Stop
	27	UGA	W	Ancestral mitochondrion, Chondrus crispus, Prymnesophytes	
	39	UAG	A, L	Chlorophytes	
2nd	21	AAA	N	Platyhelminths(1),	K
				Echinoderms(2)	
	25	AGA	Stop	Vertebrate	R
	41	AGG	S	Invertebrate	
			G	Chordata	
	8	CGC	Nonsense	Yeast,	R
	24	CGA			
	56	CGU			
	40	CGG		*Candida, Prototheca*	
3rd	29	AUA	M	Yeast,	I
				Metazoa except (1) and (2)	
	12	CUC	T	Yeast,	L
	28	CUA			
	44	CUG			
	60	CUU			

B. Nuclear variants

Group	Codon No. & Codon		Amino acid[1)]	Observed systems	Amino acid[2)]
1st	23	UAA	Q	*Ciliates*	Stop
	39	UAG		*Acetabularia, Retrovirus*	
	27	UGA	W	*Mycoplasma, Spiroplasma*	
			C	*Euplotes*	
			Se-C[3)]	*Escherichia coli*, Mammalia	
2nd	25	AGA	Nonsense	*Micrococcus*	R
	40	CGG		*Mycoplasma, Spiroplasma*	
	29	AUA		*Micrococcus*	I
3rd	44	CUG	S	*Candida*	L

Notes: This table was summarized using Osawa's textbook [9] and Ueda's [10] and Knight et al. [5] reports. Amino acid[1)] and amino acid[2)] are coded by a non-SG codon and SG codon, respectively. Se-C[3)]: Selenocysteine (the 21st amino acid).

5. Rules relating to non-SG codes

To find some rules of the non-SG codes is mediated by two subjects. One is involved in a rule of what codon is mutated to a non-SG code. However, as a general description of this rule is difficult, I conceive that the first candidates of a non-SG code will be among the codons of three groups of polygons in figure 5. That is based on an opinion that such candidate-codons will have conserved qualifications to be accepted by existing life systems as non-SG codes. Namely, such most potentially mutable codons will have conserved a role as the providers of a significant function in their evolutionary processes and thus will have a larger possibility to be discovered. And it is my opinion that any one of three groups of polygons in figure 5 will obey the mirror symmetry rule described in rule 3. This means that the void-lattice point of each polygon in figure 5 will be associated with non-SG codons to be newly discovered in the future.

The other necessary for attaining to a non-SG code's rule is what amino acid each of the candidate-codons selects. For this purpose, I exhibit two cubes with arrows drawn from non-SG codons to the nearest amino acid that is selected by that codon. They are shown in figures 7 and 8 which are composed of the first and second groups of non-SG

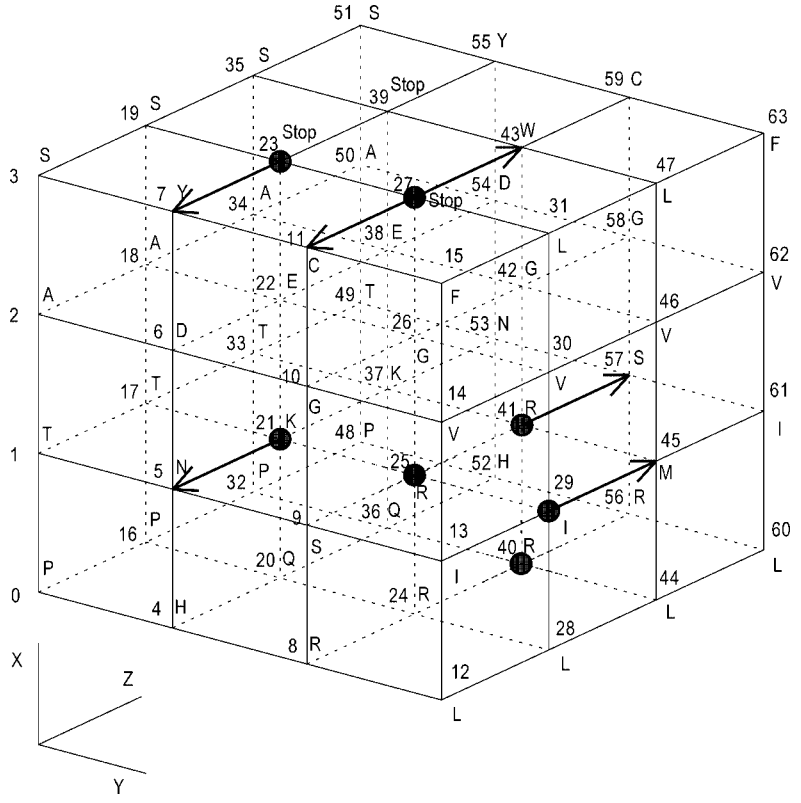

Figure 7. Non-SG codes (•) produced by a force acting on SG codes along the z-axis. The highlighted points without an arrow exhibit nonsense codons.

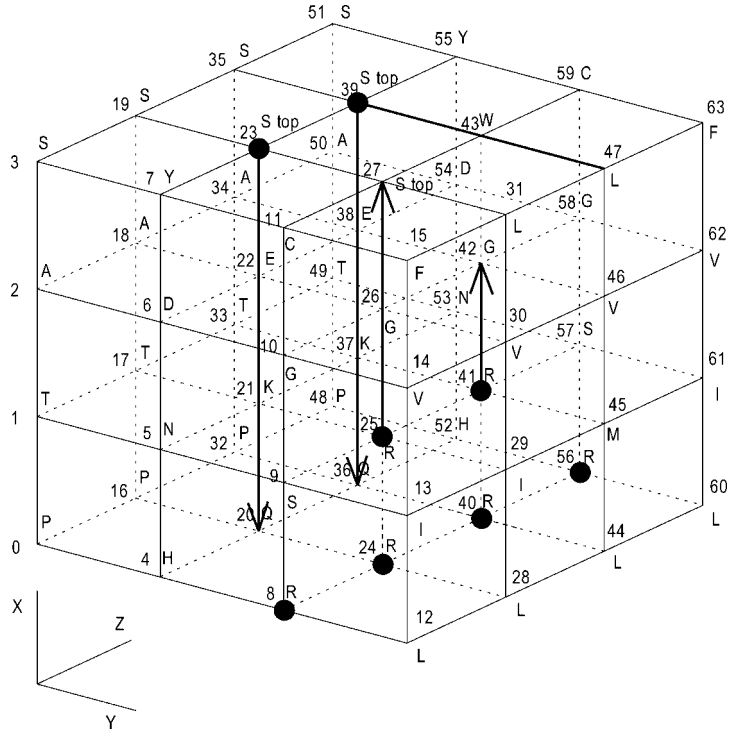

Figure 8. Non-SG codes (•) produced by a force acting on SG codes along the x- or the y-axis. The highlighted points without an arrow exhibit nonsense codons.

codons with the exception of AUA(29) codon. Concretely, in figure 7 AGG(41) and AUA codons belong to the second and third groups, respectively, and four of the rest to the first group; in figure 8 UAA(23) and UAG(39) codons belong to the first group, and two codons AGA(25) and AGG(41) to the second group, where the number in parenthesis is the codon number in the present scheme. Therefore, each figure contains both mitochondrial and nuclear variants.

Here, I should first explain the arrows shown in figures 7 and 8. I interpret an arrow as a 'force' or 'vector', and therefore their forces act on each of SG codons to cause a non-SG code, I think so.

In this way, one sees forces acting in the direction of the z-axis in figure 7 or the x- and the y-axes in figure 8 (for the N-scheme, the x-axis or the z- and the y-axes, respectively). Of course, they are not forces in real space but ones in abstract space, which will be described in a new theory to be developed in the future. Although being unable to develop here the theory, I believe that the findings in this paper will become formulated by it. Similar circumstances have been experienced previously for the elemental periodic table before establishment of quantum theory. Thus the force acting on a SG codon along each of the coordinate axes causes a non-SG codon.

The fact is, the mitochondrial Ala-encoding non-SG codon UAG only is neither shown in figures 7 or 8. This one alone of the first and second groups' non-SG codons

Table 8
Non-SG codes to be newly discovered in the future.

Group	Non-SG codes			Cell organs to be discovered	SG codes
	Codon No.& Codon		Amino acid		amino acid
1st	39	UAG	Y	Mitochondria	Stop
	43	UGG	Stop	Mitochondria, Nuclei	W
			C	Nuclei	
2nd	37	AAG	N	Mitochondria	K
	25	AGA	G S	Mitochondria	R
	41	AGG	W	Mitochondria	
3rd	28	CUA	S	Nuclei	L
	45	AUG	I	Mitochondria	M

arises from the effect of force having multicomponents. However, as it seems to me to be an exception to a rule, I believe that an above-mentioned interpretation still subsists. If so, that readily leads to rule 4.1 (hypothetical).

Rule 4.1. The force having only one component in the cube-shaped periodic table acts on a SG codon to make the first or second group's member of non-SG code.

Now, the third group of non-SG codes, with the exception of codon AUA, is not also shown in figures 7 and 8 both. Even though rule 4.1 provides a almost perfect explanation for the first and second groups in the non-SG code, it fails to explain the third group, with the exception of a mitochondrial AUA codon on which the force having only the z-axis component acts; that is, almost all of the third group of non-SG codon are closely related to forces having multi-components, whereas the first and second groups are intimately associated with forces having only one component. This means that the third group may have an unique role in the non-SG codes. Thus, another rule of the non-SG code is derived as follows:

Rule 4.2. The force having multi-components in the cube-shaped periodic table acts on a SG codon to make the third group's member of non-SG code.

It is true that almost all of the third group's codon in the non-SG code break rule 4.1, but 4 of 6 codon sites occupy mirror symmetric lattice-points (with reference to the xy-plane), and, in the first and second groups' codons, 6 of 17 codon sites satisfy the same condition. Therefore, if the polygons' symmetry rule (rule 3) of non-SG code can be extended to the arrangement of force-acting lattice-point, then it is possible to make

some predictions about providing a potential candidate for non-standard genetic codons to be newly discovered in the future.

Hypothesis 1. With regard to the cube-shaped periodic table, arrangement of force-acting lattice-points, whose force causes non-SG code, has mirror symmetry with reference to the xy-plane (for the N-scheme, the yz-plane).

This hypothesis and rule 3 give the most probable non-SG codes to be newly discovered in the future (table 8).

It is ultimately my opinions in this section that rules relating to the non-SG code (and probably revolutionary rules) will contain both hypothesis 1 and rule 3 as their parts and that table 8 will show consequently the most probable non-SG codes to be newly discovered.

6. Rules for the pairing of anticodons with multiple codons

For the purposes of this section, the conventional genetic code table is reorganized to make a new two-dimensional periodic table in which each of the codons has the same symmetric arrangement as it in the cube-shaped periodic table. Figure 9 is then attained.

In this case, two mirror symmetric sites with respect to the xy-plane in the cube-shaped periodic table are rearranged to ones in relation to the wavy line in figure 9, and two symmetric sites with respect to the yz- and zx-planes in the same periodic table to ones in relation to the 1st and 4th lines and in relation to the 2nd and 3rd lines in each of the 4×4 codon boxes of figure 9, respectively. Of course, each of the amino acids in figure 9 rightly has the same symmetric arrangement as it in the cube-shaped periodic table.

Another quality of figure 9 shows that their boxes have a tendency to be divided into two groups: one group contains modified anticodons, and the other unmodified ones only – or at least their boxes have a non-uniform distribution of anticodons with a modified base. That might indicate the possibility to discover new anticodons with a modified base, as well as figure 4 presented in section 3, although certainty for the existence of anticodon-base to be more easily modified is not guaranteed; If the episode is true, figure 9 will show the most probable candidates to discover new anticodons with a modified base; that is, an modified anticodon to be newly discovered in the future would be one of the unmodified anticodons in the box containing modified anticodons in figure 9. Here attention to each arrangement of unmodified anticodons in any box containing modified anticodon leads to observation that they are arranged at the positions involved in the mirror symmetry in relation to the yz-plane (for the N-scheme, the xy-plane). Therefore, further modification of their anticodons increases the boxes containing modified anticodons only in both the R- and N-schemes, and leads to more perfect satisfaction of rule 2.

In order to go forward this section, figure 9 is again reorganized using anticodons as the primary reference point and then figure 10 is obtained. The table requires anticodon numbers and accordingly the identification of anticodons including modified

C.No.[2] & Codon	Amino acid	Ant-cdn[3]	C.No.[2] & Codon	Amino acid	Ant-cdn[3]	C.No.[2] & Codon	Amino acid	Ant-cdn[3]	C.No.[2] & Codon	Amino acid	Ant-cdn[3]
0 CCC	P	GGG	1 ACC	T	GGU	4 CAC	H	[6]QUG	5 AAC	N	[6]QUU
12 CUC	L	GAG	13 AUC	I	GAU	8 CGC	R	[9]I CG	9 AGC	S	GCU
15 UUC	F	GAA	14 GUC	V	GAC	11 UGC	C	GCA	10 GGC	G	GCC
3 UCC	S	GGA	2 GCC	A	GGC	7 UAC	Y	[6]QUA	6 GAC	D	[6]QUC
16 CCA	P	[2]UGG	17 ACA	T	[2]UGU	20 CAA	Q	[7]UUG	21 AAA	K	[8]UUU
28 CUA	L	[2]UAG	29 AUA	I	[3]LAU	24 CGA	R	[9]I CG	25 AGA	R	[10]UCU
31 UUA	L	[1]UAA	30 GUA	V	GAC	27 UGA	Stop	–	26 GGA	G	[11]UCC
19 UCA	S	[5]UGA	18 GCA	A	[5]UGC	23 UAA	Stop	–	22 GAA	E	[8] UUC
35 UCG	S	CGA	34 GCG	A	[5]UGC	39 UAG	Stop	–	38 GAG	E	[8] UUC
47 UUG	L	CAA	46 GUG	V	[5]UAC	43 UGG	W	CCA	42 GGG	G	CCC
44 CUG	L	CAG	45 AUG	M	[4] CAU	40 CGG	R	CCG	41 AGG	R	CCU
32 CCG	P	CGG	33 ACG	T	CGU	36 CAG	Q	CUG	37 AAG	K	[8]UUU
51 UCU	S	GGA	50 GCU	A	GGC	55 UAU	Y	[6]QUA	54 GAU	D	[6] QUC
63 UUU	F	GAA	62 GUU	V	GAC	59 UGU	C	GCA	58 GGU	G	GCC
60 CUU	L	GAG	61 AUU	I	GAU	56 CGU	R	[9]I CG	57 AGU	S	GCU
48 CCU	P	GGG	49 ACU	T	GGU	52 CAU	H	[6]QUG	53 AAU	N	[6]QUU

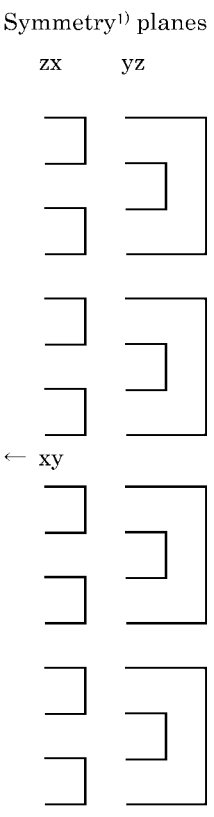

Figure 9. A new two-dimensional genetic code table for codons, with consideration of the symmetric arrangement of codon bases in the cube-shaped periodic table. Symmetry[1]: This symmetry operation is carried out on the cube-shaped periodic table; the two codons which are arranged in mirror symmetry with respect to the wavy line or which are connected with the solid line have mirror symmetric arrangement in relation to the respective plane (the *xy*-, *yz*- or *zx*-plane) of the cube-shaped periodic table. C.No.[2]: Codon number. Ant-cdn[3]: Anticodon, meaning of the modified bases of anticodons as in table 5.

A.C.No.[2] & Anti-cdn[3]	Amino acid	Codon	A.C.No.[2] & Anti-cdn[3]	Amino acid	Codon	A.C.No.[2] & Anti-cdn[3]	Amino acid	Codon	A.C.No.[2] & Anti-cdn[3]	Amino acid	Codon
0 CCC	G	GGG	1 ACC			4 CAC			5 AAC		
12 CUC			13 AUC			8 CGC			9 AGC		
15 [8]UUC	E	GAA GAG	14 [6]QUC	D	GAC GAU	11 [5]UGC	A	GCA GCG	10 GGC	A	GCC GCU
3 [11]UCC	G	GGA	2 GCC	G	GGC GGU	7 [5]UAC	V	GUG	6 GAC	V	GUC GUU GUA
16 CCA	W	UGG	17 ACA			20 CAA	L	UUG	21 AAA		
28 CUA	Stop	UAG	29 AUA			24 CGA	S	UCG	25 AGA		
31 UUA	Stop	UAA	30 [6]QUA	Y	UAC UAU	27 [5]UGA	S	UCA	26 GGA	S	UCC UCU
19 UCA	Stop	UGA	18 GCA	C	UGC UGU	23 [1]UAA	L	UUA	22 GAA	F	UUC UUU
35 UCG			34 [9]I CG	R	CGC CGA CGU	39 [2]UAG	L	CUA	38 GAG	L	CUC CUU
47 [7]UUG	Q	CAA	46 [6]QUG	H	CAC CAU	43 [2]UGG	P	CCA	42 GGG	P	CCC CCU
44 CUG	Q	CAG	45 AUG			40 CGG	P	CCG	41 AGG		
32 CCG	R	CGG	33 ACG			36 CAG	L	CUG	37 AAG		
51 [10]UCU	R	AGA	50 GCU	S	AGC AGU	55 UAU			54 GAU	I	AUC AUU
63 [8]UUU	K	AAA AAG	62 [6]QUU	N	AAC AAU	59 [2]UGU	T	ACA	58 GGU	T	ACC ACU
60 CUU			61 AUU			56 CGU	T	ACG	57 AGU		
48 CCU	R	AGG	49 ACU			52 [4]CAU [3]LAU	M I	AUG AUA	53 AAU		

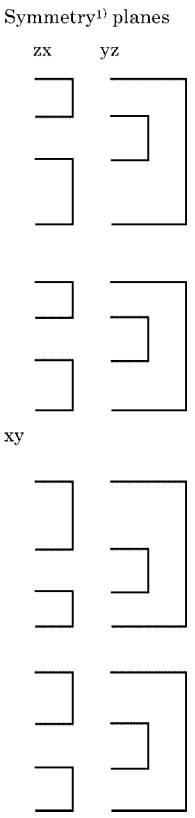

Figure 10. A new two-dimensional genetic code table for anticodons, with consideration of the symmetric arrangement of anticodon bases in the cube-shaped periodic table. Symmetry[1]: This symmetry operation is carried out on the cube-shaped periodic table; the two anticodons which are arranged in mirror symmetry with respect to the wavy line or which are connected with the solid line have mirror symmetric arrangement in relation to the respective plane (the *xy*-, *yz*- or *zx*-plane) of the cube-shaped periodic table. A.C.No.[2]: Anticodon number. Anti-cdn[3]: Anticodon, meaning of the modified bases of anticodons as in table 5.

bases, in particular, lysidine, queuosine and inosine, to attribute anticodon numbers to them. However, that won't be described here, but in section 8.

Figure 10 shows that there are some anticodons which do not pair with any codon and that this is especially true of ANN anticodons (anticodons with adenine at the first base), none of which pairs with a codon. Then, at what positions in figure 10 do their codons exist, which should have paired with such anticodons? The answer will be described below. As a result, the purposes of this section will be also achieved.

Here, focus your attention on amino acids in figure 10, and one learns that they have mirror-symmetric arrangement with respect to the yz-plane (for the N-scheme, the xy-plane) in the cube-shaped periodic table (rule 5); it includes examples such as amino acid L (leucine) of anticodons CAA(20) and UAA(23) and amino acid S (serine) of anticodons CGA(24) and UGA(27), where numbers in parenthesis are anticodon number in the present scheme. This rule is strongly supported by the existence of rule 1, as will be explained later.

Rule 5. Using anticodons as the primary reference point, amino acids in the new two-dimensional periodic table or the cube-shaped periodic table are arranged in mirror symmetry in relation to the yz-plane (for the N-scheme, the xy-plane).

If Watson–Crick base-pairing between codon and anticodon is postulated, then rule 5 can be utilized to assign a codon to each of the anticodons which have not usually paired with any codon; the 'native' position of their codons in figure 10 can be revealed. More specifically, the codons that was destined to pair with anticodons but separated from them have been paired with the other anticodons that occupy positions that are symmetrical to them with respect to the yz-plane in figure 10. As a result of this, some anticodons pair with two codons and others pair with no codon.

However, there are exceptionally two types of anticodons pairing with three codons. Two of the three codons have found anticodons either within the same box or at their codon's symmetrical position to form the Watson–Crick base-pair, but each of the third codons has failed to do so and found its partner anticodon at an asymmetrical position (an adjacent box in the R-scheme). To be specific, among three codons CGU, CGC and CGA which have paired with anticodon ICG(34), two codons CGU and CGC belong to the former, and the third codon CGA to the latter (anticodon: UCG(35) in an adjacent box). Similarly, among three codons GUC, GUU and GUA which have paired with anticodon GAC(6), two codons GUC and GUU belong to the former, and the third codon GUA to the latter (anticodon: UAC(7) in an adjacent box), where the numbers in parentheses are also anticodon numbers. As the result of this, the anticodons ICG and GAC have paired with three codons.

To sum up, the above description indicates that symmetric arrangement of amino acids in the cube-shaped periodic table for anticodons allows a systematical understanding that some codons pair with multiple anticodons.

Incidentally, the symmetry quality of rule 5 is related to the reverse side of a coin with rule 1, as rule 1 describes mirror symmetry of amino acids with respect to the

xy-plane in the cube-shaped periodic table for codons. That quality owes to a characteristic arrangement of codon-base in the cube-shaped periodic table as follows: mirror symmetry with respect to the xy-plane of the cube-shaped periodic table for codons can be seen between one codon and another codon of the same type but with the third base having guanine replaced by adenine (or uracil replaced by cytosine). The reverse is also true (adenine replaced by guanine or cytosine replaced by uracil); that is, this symmetry can be seen between the two codons which stand in the relation of 'transitional' replacement of the third codon base.

Similarly, if the same replacement is carried out at the first or second position of a codon, then the mirror symmetry will be seen with reference to the yz-plane or the zx-plane, respectively (I call this symmetry of transitional replacement between guanine and adenine or uracil and cytosine 'substitution-symmetry'). For example, to consider the symmetric relation between two codons UCG and UCA turns into a corresponding symmetric relationship between their anticodons CGA and UGA if their base-pairing is the Watson–Crick type. Therefore, the mirror symmetry of amino acids with respect to the xy-plane in the cube-shaped periodic table for codons changes into that with respect to the yz-plane in the cube-shaped periodic table for anticodons. In this case, substitution-symmetry between the two bases guanine and adenine at the third position of codons changes into that between the two bases cytosine and uracil at the first position of anticodons. Thus these considerations reveal the close relationship between rule 1 and rule 5. The corresponding events equally occur in the N-scheme.

In this way, the genetic codes can be more deeply understood through a periodic table. However, such an understanding is not as yet based on codon numbers and anticodon numbers, unlike an episode of chemical elements using their atomic numbers; it should be required to show that codon numbers and anticodon numbers play a significant role for understanding genetic codes. For these purposes, I will introduce two indexes in the next section, and will use them in the proposed periodic table to undertake a more deep understanding of the genetic codes.

7. Explanation of the two new indexes used: the Inversion Number and the Miracle Number

In the preceding sections, I described a new structure of the genetic codes from the standpoint of the symmetric quality underlying them. However, it is my opinion that the following sections should explicitly show that the codon numbers and anticodon numbers can play a key role in the proposed periodic table of the genetic codes as the atomic numbers in the elemental periodic table have done so; for example, the symmetric quality of the proposed periodic table should be closely linked to the codon numbers and anticodon numbers.

Here it is noteworthy to recall that the genetic codes are intimately associated with binary numbers (see section 2), that biological organisms are a certain kind of the information system and, in addition, that computational machinery as an artificial information system works on the binary system. Thus, it is examined in the following sections

Table 9
An example of calculations for IN and MN.

Amino acid	Codon & Anticodon	Codon No. & Deci. No.	Anticodon No. Binary number	MN	IN
T	Codon ACC Anti-C GGU	1 58	000001 111010	1 4 Sum = 5: odd	5
V	Codon GUC Anti-C GAC	14 6 Sum = 79	001110 000110	3 2 Sum = 5: odd	1 Sum = 6
A	Codon GCC Anti-C GGC	2 10	000010 001010	1 2 Sum = 3: odd	1
I	Codon AUC Anti-C GAU	13 54 Sum = 79	001101 110110	3 4 Sum = 7: odd	5 Sum = 6

Note: Deci. No.: Decimal number; Anti-C: Anticodon.

whether the binary codon numbers and binary anticodon numbers are the key factor in the periodic table of genetic codes. Then, I use Leibnitz Numbers as binary numbers, as mentioned in introduction.

For these purposes, I will introduce two indexes Inversion Number (IN) and Miracle Number (MN).

The calculation to obtain INs is described as follows: First, take a pair base and change its codon number (or anticodon number) from a decimal number to a binary number. Next, compare each position of the binary codon number with the corresponding position of the binary anticodon number, and count the number of positions that have different numbers. The total of the positions with different numbers is the IN of that pair base (see table 9). Therefore, the word "Inversion" comes from difference at the same positions of binary number.

The calculation to obtain MNs is described as follows: Count the number of ones (1's) present in the binary codon number (or anticodon number). The total number of ones is MN for that codon (or anticodon) (see table 9). I used the word "Miracle" as a few rules in which MNs participated gave me a marvelous feeling – they hold surprisingly true in spite of simplicity of its concept.

8. Identification of anticodon modified bases

In order to assign numbers to the anticodons, it is necessary to identify each of their modified bases as corresponding to one of the four nucleic acid bases. The bases that are applicable for this consideration are queuosine and inosine; they have been identified as guanine. This is done primarily because in figure 9 the majority of anticodons show mirror-symmetric arrangement or substitution symmetry relationship with respect to each of three planes (the xy-, yz-, and zx-planes). This assumption confers a high

level of symmetry on the arrangement of the first anticodon bases in figure 9 (or in the cube-shaped periodic table for codons); more specifically, in figure 9 the assumption brings substitution-symmetry with respect to the zx-plane to the arrangement of anticodons including queosine and inosine (or queosine and guanine). However, anticodon ICG which pairs with codon CGA (No. 24) scarcely satisfies these two symmetry. It should be noted that in Watson's textbook [11] inosine is identified as adenine, yet the identification has no effect on the numerical value of IN and MN; therefore this is not a crucial point for the following discussion. Other modified bases, containing lysydine, are bases with substituents and could be treated as unsubstituted bases without the slightest hesitation although anticodon LAU breaks a symmetry relation with respect to only one plane (zx).

9. The binary number logic rules

In this section, I first present a table of INs and MNs, which can be calculated for codons and anticodons under consideration in sections 7 and 8 (figure 11), and next derive from the table several basic rules that govern INs and MNs. As these rules are derived from the codon numbers and anticodon numbers, both the numbers can be accepted as key factors for the periodic table of genetic codes. Of course, these rules are scheme-independent. And I call these rules of INs and MNs the binary number logic rules.

9.1. IN related rules for the SG codes

From figure 11, the following five rules of IN can be derived. The first rule is as follows:

Rule 6. The vast majority of INs are one of the following three odd numbers: 1, 3 or 5.

These odd numbers seem to lead to a new classification of codons/anticodons. This is partly because all of the codons that are 1 and 5 as INs have a Watson–Crick base-pair. In contrast, all of 23 codons that form a non-Watson–Crick base-pair belong to the codon-group of 3 as INs. Another basis is that even if the second base of codon or anticodon in a certain group is replaced with any one of four nucleic acid bases, all codons belong to the original group before replacement and almost all of the resultant anticodons also belong to the original group before replacement; anticodons forbidden entry in the SG code are UUA and UCA for IN $= 1$, whose anticodons correspond to 'stop-anticodon'; UCG and CUA for IN $= 5$, the former is replaced with ICG (IN $= 4$) and the latter is 'stop-anticodon'; and UAU, CUU, CGC, CAC and CUC for IN $= 3$.

To seek biological meaning of this classification, table 6 is reorganized regarding the orderly relation among the electric polarity and size of amino acids. In the resultant table (table 10), the second base of amino acid-relevant anticodon and its IN are also listed together. Then anticodons ICG (IN $=$ 4) and GAC (IN $=$ 2) are placed at 5

Codon No.	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Amino acids	P	T	A	S	H	N	D	Y	R	S	G	C	L	I	V	F
IN	3	5	1	3	3	5	1	3	3	5	1	3	3	5	1	3
MN: Codon	0	1	1	2	1	2	2	3	1	2	2	3	2	3	3	4
Anti-C.*	3	4	2	3	4	5	3	4	2	3	1	2	3	4	2	3
MN sum	3	5	3	5	5	7	5	7	3	5	3	5	5	7	5	7
Codon No.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Amino acids	P	T	A	S	Q	K	E	–	R	R	G	–	L	I	V	L
IN	5	3	3	1	5	3	3	(1)	4	3	3	(1)	5	3	2	1
MN: Codon	1	2	2	3	2	3	3	4	2	3	3	4	3	4	4	5
Anti-C.*	4	5	3	4	5	6	4	(5)	2	4	2	(3)	4	3	2	4
MN sum	5	7	5	7	7	9	7	(9)	4	7	5	(7)	7	7	6	9
Codon No.	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47
Amino acids	P	T	A	S	Q	K	E	–	R	R	G	W	L	M	V	L
IN	1	3	3	5	1	3	3	(5)	1	3	3	5	1	3	3	5
MN: Codon	1	2	2	3	2	3	3	4	2	3	3	4	3	4	4	5
Anti-C.*	2	3	3	2	3	6	4	(3)	1	2	0	1	2	3	3	2
MN sum	3	5	5	5	5	9	7	(7)	3	5	3	5	5	7	7	7
Codon No.	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63
Amino acids	P	T	A	S	H	N	D	Y	R	S	G	C	L	I	V	F
IN	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
MN: Codon	2	3	3	4	3	4	4	5	3	4	4	5	4	5	5	6
Anti-C.*	3	4	2	3	4	5	3	4	2	3	1	2	3	4	2	3
MN sum	5	7	5	7	7	9	7	9	5	7	5	7	7	9	7	9

Figure 11. INs and MNs of the SG code. (·): IN or MN expected for Stop-codon. Anti-C.*: Anticodon.

and 3 as INs, respectively, by being made to conform the binary number logic rules, and represented by 1^4 and 1^2 in the table.

Table 10 shows that the second anticodon base can be closely correlated with the classification of amino acids in table 6: the majority of anticodons with uracil at the second base are closely linked to the second and third groups which contain amino acids of relatively larger electric polarity; among amino acids of smaller polarity, guanine belongs to the first group and adenine to the fourth group; but cytosine has no correlation with the second anticodon base. In contrast, table 10 indicates that INs themselves have no correlation with the classification of amino acids in table 6.

Table 10
Relationship between physical and chemical properties of amino acids and the second anticodon base.

a	Neutral												Acidic				Basic		
b	G	A	S	P	T	C	V	M	I	L	F	Y	W	D	N	E	Q	H	K	R
c	1					6	4				5			2				3		
d	C	G	$G^{\#}$	G	G	C	A	A	A	A	A	U	C	U	U	U	U	U	U	C
e	9	8	9	8	9	6	6	5	5	6	5	6	5	12	13	11	12	11	10	11
f	3	31	32	33	61	55	84	111	111	105	132	136	170	56	54	85	83	119	96	124
g^1	1	1	1	1			1			2				1			1			1
g^3	3	3	2^G	2	3	2	2	1	2	2	2	2		1	1	2		2	2	4
	1^C						1^2													
g^5			1^G	1	1				1	2			1		1		1			
	1^C																			1^4

Note: (a): Acidity/basicity of amino acids; (b): the kind of amino acids; (c): group number of classification of amino acids (see table 6); (d): the second base of anticodon coding amino acid, and $G^{\#}$ means that guanine G shares this position with cysteine C; (e): polarity of amino acid; (f): volume of amino acid; g^1, g^3, and g^5 are codon populations for 1, 3, and 5 of INs, respectively; 2^G, 1^C, and 1^G mean that they are codon populations for each of anticodons having different second base, but coding the same amino acid; 1^2 and 1^4 mean codon populations which come from 2 and 4 of INs, respectively.

More positive use of this classification of codons/anticodons might make them correlate with molecular evolution of the gene in the future because the resulting base-triplet arising from replacement of the second triplet base, which appear to be a dominant contributor to amino acids coded, belongs to the original triplet-group, and additionally because, particularly in the group of 1 as IN, most of the codon/anticodon base-pair (if 'anticodon' of stop-codon is postulated to follow the binary number logic rules, all of them) mutually share a common triplet form with another base-pair such as GCC/GGC and GGC/GCC. The former condition should be required by any life system to be persistently stable even if they are perturbed by surroundings, and the latter to start with minimal members of the primordial gene. However, it is beyond the aim of this paper to go into further detail concerning this problem.

The second rule in this subsection is also observed in figure 11:

Rule 7. There exist fundamental periodic patterns such as $(5, 3, 3, 1)$, $(1, 3, 3, 5)$, $(3, 5, 1, 3)$ or $(3, 3, 3, 3)$.

Similar periodic patterns also appear in the N-scheme and disorder of the pattern occurs only at two codons, CGA (IN = 4) and GUA (IN = 2).

This leads to a result of particular interest as rule 7 holds true for not just Watson–Crick base-pairs, but also for non-Watson–Crick base-pairs with the exception of the two codons CGA and GUA. The biological meaning of such events is, for now, poorly understood; yet I can partly provide a challenging idea for it.

Possible biological meaning for rule 7 will be found in the fact that all of the codons in the fourth horizontal row of the periodic chart of the SG code have the same numerical value as INs, which is 3. Twenty three of the 64 codons in the SG codes are non-Watson–Crick base-pairs. Seven codons of them locate on a period other than the fourth one. If each of their first anticodon base is replaced with other one to form a Watson–Crick base-pair, then the resultant anticodons can obey the binary number logic rules: INs of codons CGA (IN $= 4$) and GUA (IN $= 2$) change into 5 and 3, respectively, and those of the other remain unchanged. If similar replacement for anticodons pairing with 16 codons of the fourth period is performed, then their fundamental pattern $(3, 3, 3, 3)$ alters into $(3, 1, 5, 3)$. These mean that some codons destined to form a non-Watson–Crick base-pair refuse the 'original' pattern or the binary number logic rule and others retain it. This is particularly prominent in the fourth period: the codons of the fourth period tend to refuse the original pattern, whereas others appear to retain it although INs at two codons, CGA and GUA, alter. In other words, the fundamental periodic pattern $(3, 3, 3, 3)$ itself is probably required by biological organisms because they have preferred its pattern rather than the primary pattern of the Watson–Crick type. This idea will be reinforced by observing the same pattern in mammalian mitochondrial genetic codes, described in section 9.3. Thus, a challenging idea means that rule 8 may be one of the necessary conditions for existence of life systems although the rule 8 requires the most precise description when one regards the fundamental patterns of N-scheme; in the N-scheme the corresponding pattern is $(5, 3, 3, 3)$ (for C(00) and U(11) schemes) or $(3, 3, 3, 5)$ (for C(11) and U(00) schemes), but not $(3, 3, 3, 3)$, and one horizontal row of the periodic chart has consistently the same fundamental pattern as one in mammalian mitochondrial genetic codes. To my knowledge, this may provide the first indication of molecular, general relationship between the SG codes and mitochondrial genetic codes. Eventually, this pattern is expressed as the third rule in this subsection:

Rule 8. One horizontal row of the periodic chart of the SG codes has consistently the same fundamental pattern as one in mammalian mitochondrial genetic codes.

Another significant feature of the fundamental patterns is directly observed in figure 11 and consequently the fourth rule of this subsection is derived.

Rule 9. The sum of INs of two codons that are arranged in mirror symmetry with respect to the yz-plane (for the N-scheme, the xy-plane) in the cube-shaped periodic table is equal to 6, which corresponds to the maximum value of any IN.

The symmetric feature of INs should still be described. If INs are also displayed on the cube-shaped periodic table, then their mirror-symmetric arrangement can be readily observed (figure 12).

Thus, the last rule of this subsection can be obtained.

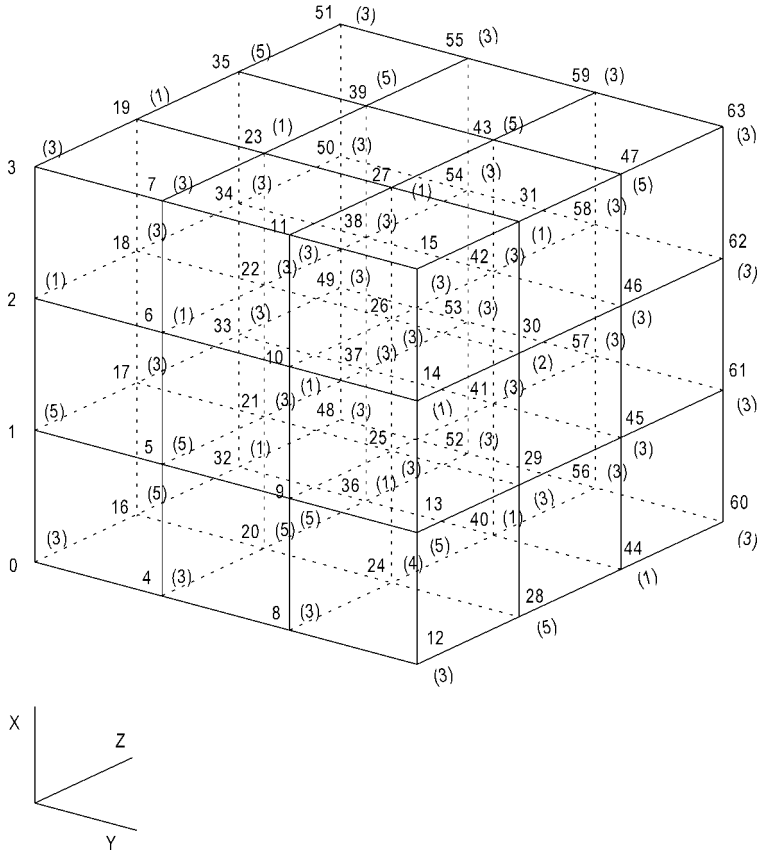

Figure 12. INs of the SG codes on the cube-shaped periodic table. IN is shown in parenthesis, and stop-codons' can be, then, decided from the binary number logic rules.

Rule 10. INs in the cube-shaped periodic table (of both the R- and N-schemes) are arranged in mirror symmetry in relation to the zx-plane with the exception of three pairs of codons: GCA and GUA, CAA and CGA, and UAG (stop) and UGG.

This symmetry rule is closely linked to rule 1 and so it seems also to be required for the existence of life systems from the standpoint of IN. The reason is based on the facts as follows: first, the zx-plane mirror symmetry of INs is equivalent to substitution symmetry of the second codon base from considerations in section 6 (rule 10); second, the preceding description in this subsection provides a suggestion that the second codon base appears to be a dominant contributor to amino acids; and third, the xy-plane mirror symmetry of amino acids is equivalent with substitution symmetry of the third codon base (rule 1). Therefore it seems to me that rules 10 and 1 represent the different aspects of a cognate event; hence the interpretation that rule 1 will provide a rationale for the necessary conditions for the existence of life systems will be also applicable to rule 10.

9.2. MN rule of the SG code

Only one rule of MNs can be observed in figure 11:

Rule 11. The sum of the MNs of the codon and anticodon that form a base pair is an odd number.

This rule means that if the MN of a codon is even, then the MN of the corresponding anticodon is odd. The reverse is also true. In addition, this rule still has exceptions at the codons CGA and GUA as well as rules 6–10 of INs. Its biological meaning is puzzling.

9.3. Rules for the INs and MNs of mammalian mitochondrial genetic codes

In this subsection, the INs- and MNs-related rules for the mammalian mitochondrial genetic codes (figure 13) are described, while being compared with those for the SG code. Their INs and MNs (figure 14) are determined on the scheme for the SG codes (formulae (1) in section 2.2) as the primary reference point although population of the base-pair types of mammalian mitochondrial genetic codes is slightly, but may be significantly, different from those of the SG codes.

Characteristic feature of figure 14 is that a horizontal row of the periodic chart has the same fundamental pattern of INs as the SG code. Most importantly, as described in rule 8, one common fundamental pattern consistently appears, for any schemes including R- and N-schemes, in a horizontal row of both the periodic chart of the SG codes and mammalian mitochondrial genetic codes ($(3, 3, 3, 3)$ for the R-scheme, and $(5, 3, 3, 3)$ or $(3, 3, 3, 5)$ for the N-scheme), and this relationship between the two genetic codes bore fruit of rule 8, together with interpretation that mitochondria will come from a few symbionts including archaea.

Now, three rules are described in this subsection and the first rule is obtained from figure 14 as the counterpart of rule 8:

Rule 12. A horizontal row of the periodic chart of the mammalian mitochondrial genetic code also has the same fundamental pattern of INs as the SG code.

The rule 12-related row is scheme-dependent: In the present scheme, it can be observed in the third period of the mitochondrial periodic chart, whereas it is in the fourth one of the SG chart. In this way, it can be seen in the different period of each periodic chart, and this holds true for other schemes of the R-scheme. More specifically, the mammalian mitochondrial genetic code has either the pattern in the second or the third period; the former is seen in the G(01) and A(10) schemes, and the latter in the G(10) and A(01) schemes. In contrast, the SG code has it either in the first or the fourth period; the former is seen in the C(11) and U(00) schemes, and the latter in the C(00) and U(11) schemes. Therefore, in the SG and mitochondrial periodic charts of R-scheme, the rule 12-related fundamental pattern appears in the different period. But

C.No.[2] & Codon	Amino acid	Anti-cdn[3]	C.No.[2] & Codon	Amino acid	Anti-cdn[3]	C.No.[2] & Codon	Amino acid	Anti-cdn[3]	C.No.[2] & Codon	Amino acid	Anti-cdn[3]
0 CCC	P	UGG	1 ACC	T	UGU	4 CAC	H	GUG	5 AAC	N	GUU
12 CUC	L	UAG	13 AUC	I	GAU	8 CGC	R	UCG	9 AGC	S	GCU
15 UUC	F	GAA	14 GUC	V	UAC	11 UGC	C	GCA	10 GGC	G	UCC
3 UCC	S	UGA	2 GCC	A	UGC	7 UAC	Y	GUA	6 GAC	D	GUC
16 CCA	P	UGG	17 ACA	T	UGU	20 CAA	Q	UUG	21 AAA	K	UUU
28 CUA	L	UAG	29 AUA	M	CAU	24 CGA	R	UCG	25 AGA	Stop	–
31 UUA	L	UAA	30 GUA	V	UAC	27 UGA	W	UCA	26 GGA	G	UCC
19 UCA	S	UGA	18 GCA	A	UGC	23 UAA	Stop	–	22 GAA	E	UUC
35 UCG	S	UGA	34 GCG	A	UGC	39 UAG	Stop	–	38 GAG	E	UUC
47 UUG	L	UAA	46 GUG	V	UAC	43 UGG	W	UCA	42 GGG	G	UCC
44 CUG	L	UAG	45 AUG	M	CAU	40 CGG	R	UCG	41 AGG	Stop	–
32 CCG	P	UGG	33 ACG	T	UGU	36 CAG	Q	UUG	37 AAG	K	UUU
51 UCU	S	UGA	50 GCU	A	UGC	55 UAU	Y	GUA	54 GAU	D	GUC
63 UUU	F	GAA	62 GUU	V	UAC	59 UGU	C	GCA	58 GGU	G	UCC
60 CUU	L	UAG	61 AUU	I	GAU	56 CGU	R	UCG	57 AGU	S	GCU
48 CCU	P	UGG	49 ACU	T	UGU	52 CAU	H	GUG	53 AAU	N	GUU

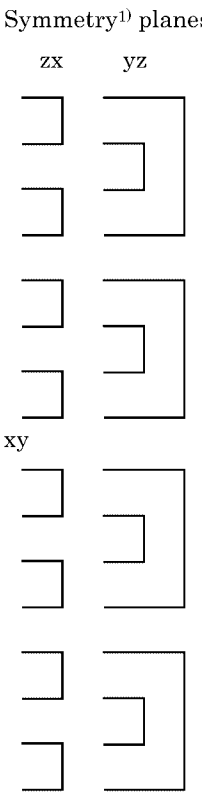

Figure 13. A new two-dimensional genetic code table for mammalian mitochondrial codons, with consideration of the symmetric arrangement of codon bases in the cube-shaped periodic table. Symmetry[1]: Meaning of codon's arrangement and symmetry as in figure 9. C.No.[2]: Codon number. Anti-cdn[3]: Anticodon, meaning of the modified bases of anticodons as in table 5.

Codon No.	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Amino acids	P	T	A	S	H	N	D	Y	R	S	G	C	L	I	V	F
δ #	1	1	1	1					1		1		1		1	
IN	4	4	2	2	3	5	1	3	4	5	2	3	4	5	2	3
MN: Codon	0	1	1	2	1	2	2	3	1	2	2	3	2	3	3	4
Anti-C.*	4	5	3	4	4	5	3	4	3	3	2	2	4	4	3	3
MN sum	4	6	4	6	5	7	5	7	4	5	4	5	6	7	6	7
Codon No.	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Amino acids	P	T	A	S	Q	K	E	–	R	–	G	W	L	M	V	L
δ #									1						1	
IN	5	3	3	1	5	3	3	(1)	5	(3)	3	1	5	3	3	1
MN: Codon	1	2	2	3	2	3	3	4	2	3	3	4	3	4	4	5
Anti-C.*	4	5	3	4	5	6	4	(5)	3	(4)	2	3	4	3	3	4
MN sum	5	7	5	7	7	9	7	(9)	5	(7)	5	7	7	7	7	9
Codon No.	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47
Amino acids	P	T	A	S	Q	K	E	–	R	–	G	W	L	M	V	L
δ #	3	3		3	3				3		3	3	3			3
IN	3	3	3	3	3	3	3	(3)	3	(3)	3	3	3	3	3	3
MN: Codon	1	2	2	3	2	3	3	4	2	3	3	4	3	4	4	5
Anti-C.*	4	5	3	4	5	6	4	(5)	3	(4)	2	3	4	3	3	4
MN sum	5	7	5	7	7	9	7	(9)	5	(7)	5	7	7	7	7	9
Codon No.	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63
Amino acids	P	T	A	S	H	N	D	Y	R	S	G	C	L	I	V	F
δ #	1	1	1	1					1		1		1		1	
IN	4	2	4	2	3	3	3	3	4	3	4	3	4	3	4	3
MN: Codon	2	3	3	4	3	4	4	5	3	4	4	5	4	5	5	6
Anti-C.*	4	5	3	4	4	5	3	4	3	3	2	2	4	4	3	3
MN sum	6	8	6	8	7	9	7	9	6	7	6	7	8	9	8	9

Figure 14. INs and MNs of the mammalian mitochondrial genetic code. $\delta^{\#}$ = Mitochondrial anticodon number minus Standard anticodon number. (·): IN or MN expected for Stop-codon. Anti-C.*: Anticodon.

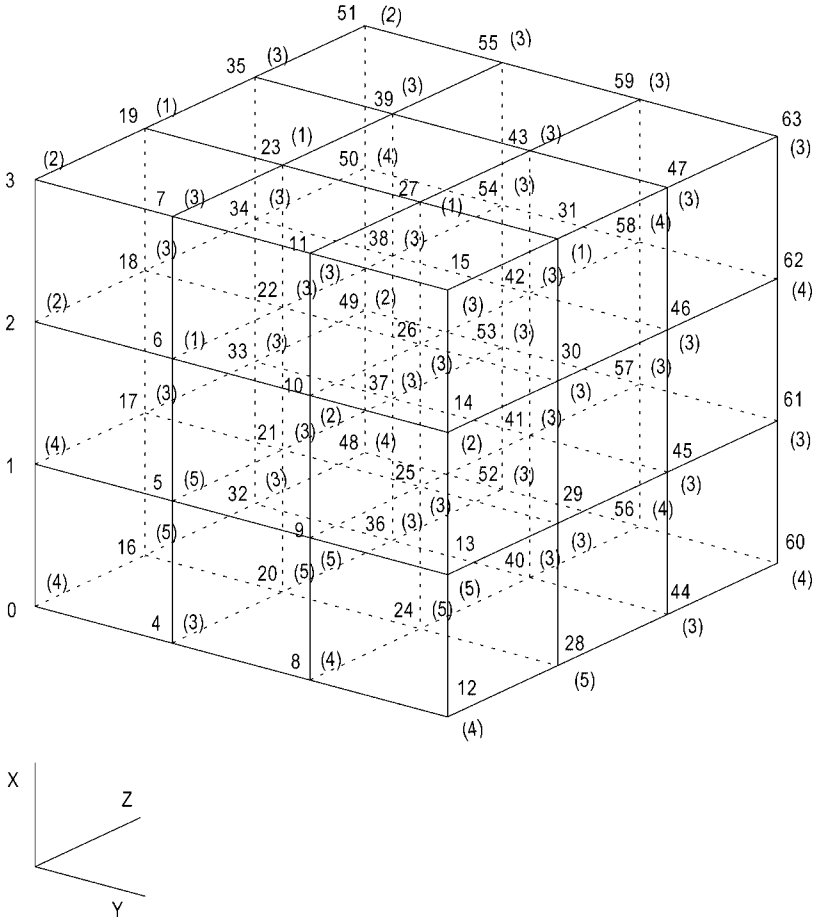

Figure 15. INs of the mammalian mitochondrial genetic codes on cube-shaped periodic table. IN is shown in parenthesis, and stop-codons' can be, then, decided from the binary number logic rules.

in two charts of the N-scheme, it appears in the same one while rule 8 holds still true for the scheme.

Another significance of INs' chart of the mammalian mitochondrial genetic codes is characterized by the same mirror symmetric feature (zx-plane) as the SG code, although the former has lower symmetry than the latter; concretely, there appears asymmetry of INs at 8 pairs of sites except asymmetry for stop codons (figure 15).

This lower symmetry may be largely due to adopting the present scheme reflecting table 2. However, I interpret this fact positively as follows: as a few rules of INs, including rule 12, can be seen in the mammalian mitochondrial chart within the present framework and so the two codes appear to cooperate, a certain symmetric quality of INs will be required for existence of life systems. This hypothesis will be reinforced by satisfaction of full symmetry of amino acids in the cube-shaped periodic table for mammalian mitochondrial genetic codes. Because if such a framework of the SG code

does not give any rule, or even in part a symmetric quality, to the mitochondrial genetic code, it seems to me then that two of any biological organisms will have been unable to make symbiosis between them.

The second rule in this subsection is concerned with MNs and only one rule can be observed in figure 14 like the SG codes:

Rule 13. When IN of a certain codon is even, then the sum of the codon and its partner anticodon's MNs is even, and when it is odd, then the sum of the related codon's and anticodon's MNs is odd.

This rule of even number can also be observed at two codons CGA and GUA of the SG code whose INs have 4 and 2, respectively, while an episode of odd number corresponds precisely to rule 11. Therefore, rule 13 is a general description of rule 11.

Thus, the number of the binary number logic rules is smaller in the mammalian mitochondrial genetic codes than in the SG codes within the present framework. However, the former codes appear to be harmoniously organized with the latter codes, because such a event as mentioned in rule 14 – a systematic change of their anticodon numbers relative to the corresponding SG codes – is also seen in figure 14.

Rule 14. When the mitochondrial anticodon is different from the corresponding SG code, the former's number in the same period of the periodic chart shifts by a definite number factor from the latter's numbers. The factor is either a number of α or β; one of the four periods is intimately associated with rule 8, and if the anticodon number of such a period varies by a factor of α, then the anticodon number of the rest varies by a factor of β.

The factors α and β depend on the scheme to be used and are partly, or wholly, different from those of the present scheme ($\alpha = 3$ and $\beta = 1$). For example, in other scheme C(11), U(00), G(10), and A(01), the values α and β change into -3 and -2, respectively. And this systematic change of anticodon numbers is noticeable in the R-scheme rather than in the N-scheme. In the latter scheme its feature is similar to rule 14, but 'consistently intricate'.

Ultimately, it is my opinion in sections 7–9 that although biological meaning of IN- and MN-related rules may be unclear, they indicate that codon numbers and anticodon numbers play a key role in base-pairing and consequently for the periodic table of the genetic codes.

10. Relationship with some previous studies

In this section the previous studies such as codon ring and mutation ring (Swanson [1]), amino acid polarity (Jungck [2]), Siemion numbers and weight diagram (Bashford et al. and Siemion et al. [3,4]), and biosynthetic pathways (Knight et al. [5]) are correlated with the proposed periodic table.

10.1. Codon ring and mutation ring

Swanson [1] used a Gray code binary number to assign a number to each codon. In figure 16, each of their numbers is positioned at Leibnitz Number of the same base triplet: for example, 28 and 4 of 'Swanson numbers' are 0 and 1 of Leibnitz Numbers, respectively.

Figure 16 shows systematic, but consistently intricate, arrangement of Swanson numbers: explicitly, four consecutive Swanson numbers are aligned on four lattice points in parallel with the z-axis, while concomitantly arranged to be constant in summation of two Swanson numbers which are at the mirror-symmetrical locations with respect to the

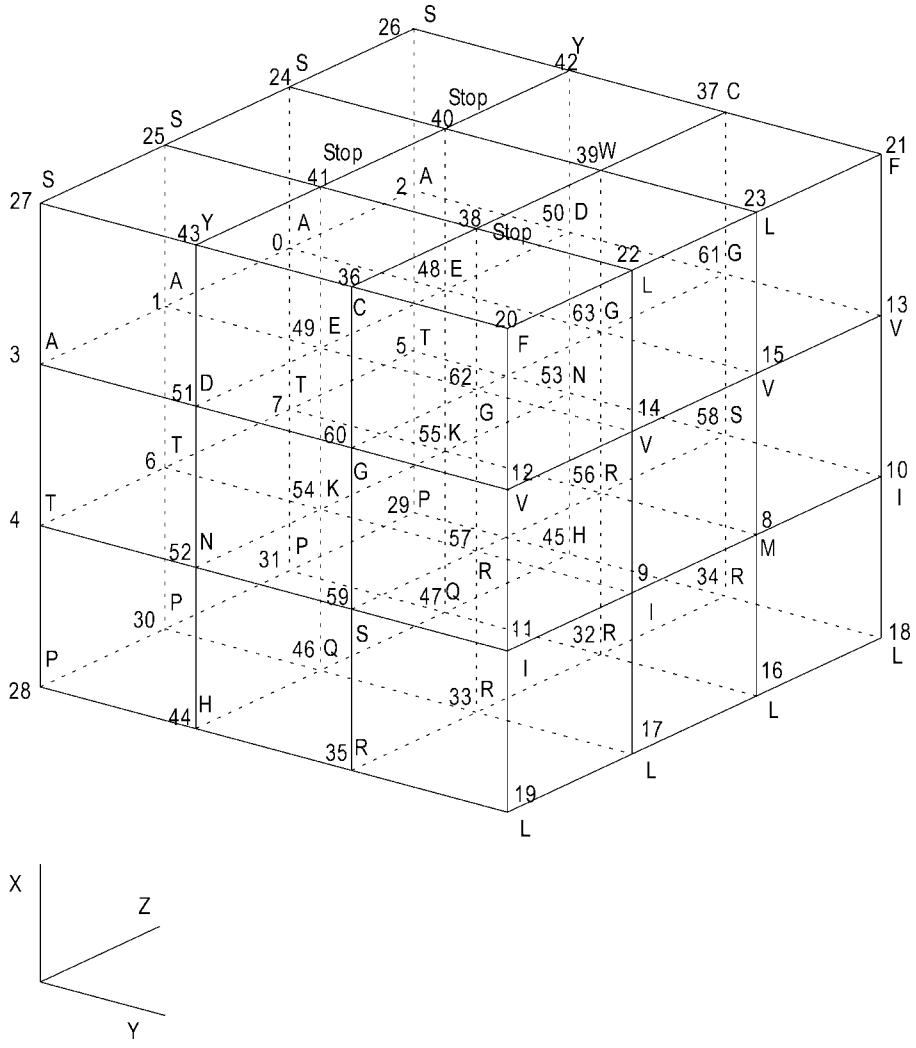

Figure 16. Swanson numbers on the cube-shaped periodic table. Each Swanson number is positioned at Leibnitz Number of the same base triplet.

yz-plane; and besides, four sets of the resultant values, 55, 87, 71, and 39, have great regularity in difference between the first and fourth, or the second and third, values, and the difference value, 16, concerning the sum of the within-top-plane Swanson number and within-bottom-plane Swanson number is identical to one of other sets concerning the sum of the within-(3–12–13–2)-plane number and within-(4–11–10–5)-plane number although the sum values of the former are entirely different from those of the latter, where the numbers in parenthesis are Swanson numbers in figure 16. These hold also true in the N-scheme. But, in the N-scheme, summation of two Swanson numbers must be performed for the codons at the mirror-symmetrical locations with respect to the *xy*-plane of the same plane as the R-scheme. Next, I describe relationship between the proposed genetic codes table and Swanson's codon ring. For this purpose, Leibnitz Numbers on Swanson's codon ring are shown (figure 17).

In figure 17, four Leibnitz Numbers sandwiched between two broken lines correspond to four consecutive Swanson numbers which are aligned on four lattice points in parallel with the *z*-axis in the cube-shaped periodic table. These four Leibnitz Numbers in figure 17 also have systematic, intricate arrangement.

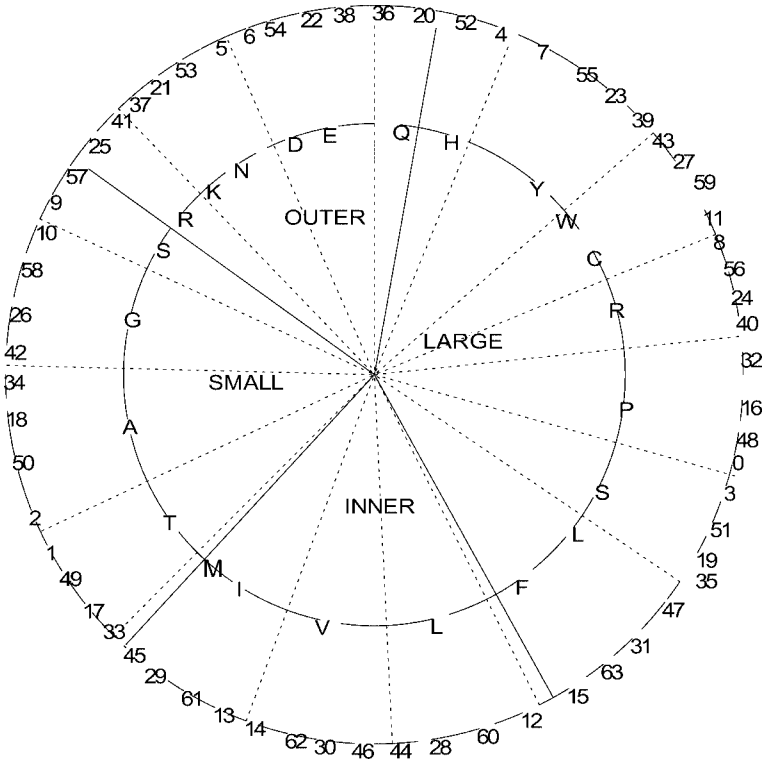

Figure 17. Leibnitz Numbers on Swanson's codon ring. Four groups of the codons sandwitched between two solid lines correspond to four families of amino acids classified on codon ring. Each of the codons sandwitched between two broken lines is positioned on a line in parallel with the *z*-axis in the cube-shaped periodic table.

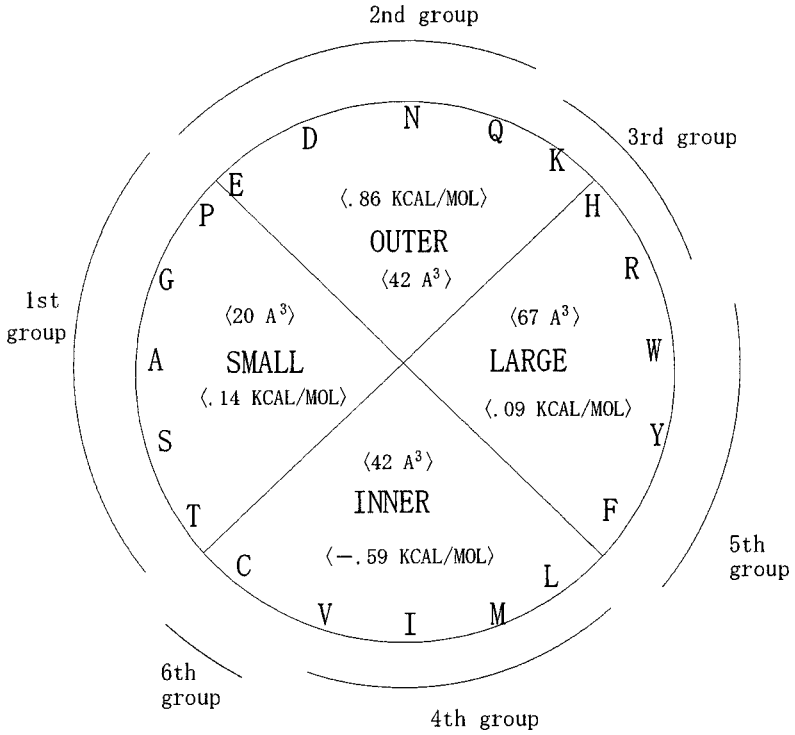

Figure 18. Swanson's mutation ring and classification of amino acids in table 6. Mutation ring exhibits a measure of amino acid similarity when any given amino acid may be replaced by each of the other 19 in protein sequences.

Table 11
Relationship between Swanson's mutation ring and classification of amino acids in table 6 or figure 6.

Groups of amino acids in mutation ring	Classification of amino acids in table 6 or figure 6
Small	The 1st group
Outer	The 2nd group, and lysine
Large	The 3rd group with the exception of lysine, and the 5th group
Inner	The 4th and 6th groups

Mutation ring (figure 18), which measures amino acid similarity, is intimately associated with table 6 (and hence figure 6) which shows classification of amino acids that have the potential to more easily undergo mutual replacement in evolutionary processes of proteins development. It is summarized in table 11 and both show a remarkable consistency.

10.2. Siemion's number and Woese's polarity

Siemion et al. [4] introduced a quantity (Siemion number) k, $k = 0, \ldots, 63$, which defined the so-called 'mutation angle' $\pi k/32$ for a particular assignment of codons (and hence of amino acids) in rank ordering. In figure 19, their numbers are positioned at Leibnitz Number of the same base triplet: for example, 38 and 33 of Siemion numbers are 0 and 1 of Leibnitz Numbers, respectively.

One can observe that an aspect of Siemion number is most similar to Swanson's. In effect, structural arrangement of Siemion number in the cube-shaped periodic table is analogous to Swanson's. Two sets of numbers differ solely in location of the four consecutive numbers in the cube-shaped periodic table: that is, the sum of two Siemion numbers at the mirror-symmetrical positions with respect to the yz-plane leads to the values of 63, 31, 63, and 95, and in this case the difference between the first and second, or the third and fourth, values gives constant values of 32 (for the mirror-symmetrical positions of the top and bottom planes) and 48 (for the corresponding positions of the (30–54–55–31)- and (33–57–56–32)-planes), where the numbers in parenthesis are Siemion numbers in figure 19. These situations in the N-scheme are also highly analogous to the R-scheme's. Next, to consider amino acid polarity from my viewpoint

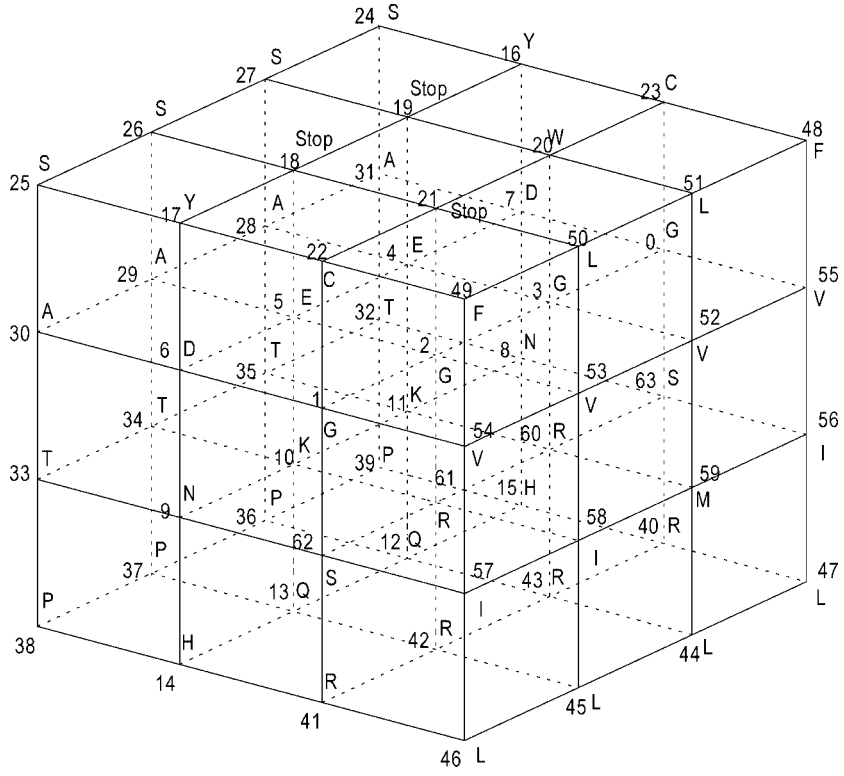

Figure 19. Siemion numbers on the cube-shaped periodic table. Each Siemion number is positioned at Leibnitz Number of the same base triplet.

		2nd anticodon base											
		A			G			C			U			
Weight diagram		ⓤ			Ⓒ			Ⓖ			Ⓐ			
Δ[3]	1st anti-c.[1] base	Anti-c.[1] (Codon) Number[2]	Amino acid	Woese's Polarity	Anti-c.[1] (Codon) Number[2]	Amino acid	Woese's Polarity	Anti-c.[1] (Codon) Number[2]	Amino acid	Woese's Polarity	Anti-c.[1] (Codon) Number[2]	Amino acid	Woese's Polarity	3rd anti-c.[1] base
0 (0)	A	21 (63)	F	5.0	25 (51)	S	7.5	17 (59)	C	4.8	29 (55)	Y	5.4	A
	G	22 (15)			26 (3)			18 (11)			30 (7)			
	C	20 (47)	L	4.9	24 (35)			16 (43)	W	5.2	28 (39)	Stop		
	U	23 (31)			27 (19)			19 (27)	Stop		31 (23)	Stop		
+16 (- 3)	A	37 (60)	L	4.9	41 (48)	P	6.6	33 (56)	R	9.1	45 (52)	H	8.4	G
	G	38 (12)			42 (0)			34 (8)			46 (4)			
	C	36 (44)			40 (32)			32 (40)			44 (36)	Q	8.6	
	U	39 (28)			43 (16)			35 (24)			47 (20)			
- 32 (+2)	A	5 (62)	V	5.6	9 (50)	A	7.0	1 (58)	G	7.9	13 (54)	D	13.0	C
	G	6 (14)			10 (2)			2 (10)			14 (6)			
	C	4 (46)			8 (34)			0 (42)			12 (38)	E	12.5	
	U	7 (30)			11 (18)			3 (26)			15 (22)			
+48 (- 1)	A	53 (61)	I	4.9	57 (49)	T	6.6	49 (57)	S	7.5	61 (53)	N	10.0	U
	G	54 (13)			58 (1)			50 (9)			62 (5)			
	C	52 (45)	M	5.3	56 (33)			48 (41)	R	9.1	60 (37)	K	10.1	
	U	55 (29)	I		59 (17)			51 (25)			63 (21)			
	Δ[4]	0 (0)			+4 (- 12)			- 8(+8)			+12(- 4)			

Figure 20. Anticodons, related-amino acids and Woese's polarity. Anti-c[1]: anticodon. Number[2]: Leibnitz Number. $\Delta^{3)}$, $\Delta^{4)}$: difference in Leibnitz Numbers between a certain box and a vertically upper or horizontally left-side box, respectively.

is a significant subject. Figure 20 shows Woese's polarity described by Jungck [2] or Szathmary [12], together with the related Leibnitz Numbers of anticodons and codons.

In 4×4 boxes of figure 20 four vertical columns from the left-hand toward the right-hand correspond to four codon groups Ⓤ, Ⓒ, Ⓖ, and Ⓐ of 'weight diagram' for the genetic code, respectively. And, these four codon groups, and hence amino acid groups, correspond to four planes in parallel with the zx-plane in the cube-shaped periodic table: Ⓒ to the (38–25–24–39)-plane, Ⓐ to the (14–17–16–15)-plane, Ⓖ to the (41–22–23–40)-plane, and Ⓤ to the (46–49–48–47)-plane, where the numbers in parenthesis are Siemion numbers in figure 19. One can also see neat regularity of Leibnitz Numbers between columns or rows (see $\Delta^{3)}$ and $\Delta^{4)}$ in figure 20). Such events do not emerge from Siemion's numbers.

10.3. Biosynthetic pathways

While regarding the related amino acid polarity, Knight et al. [5] describe biosynthetic pathways and related code assignment of three kinds of organisms: (a) Primitive sulfur-metabolizing bacteria (hypothetical), (b) Generalized prokaryotes, and (c) *Escherichia coli*. The three organisms share the fundamental structure of biosynthetic pathways and related codes, although differing in meticulous structure of them. Therefore, I invoke here primitive sulfur-metabolizing bacteria which have the simplest biosynthetic pathways structure (figure 21).

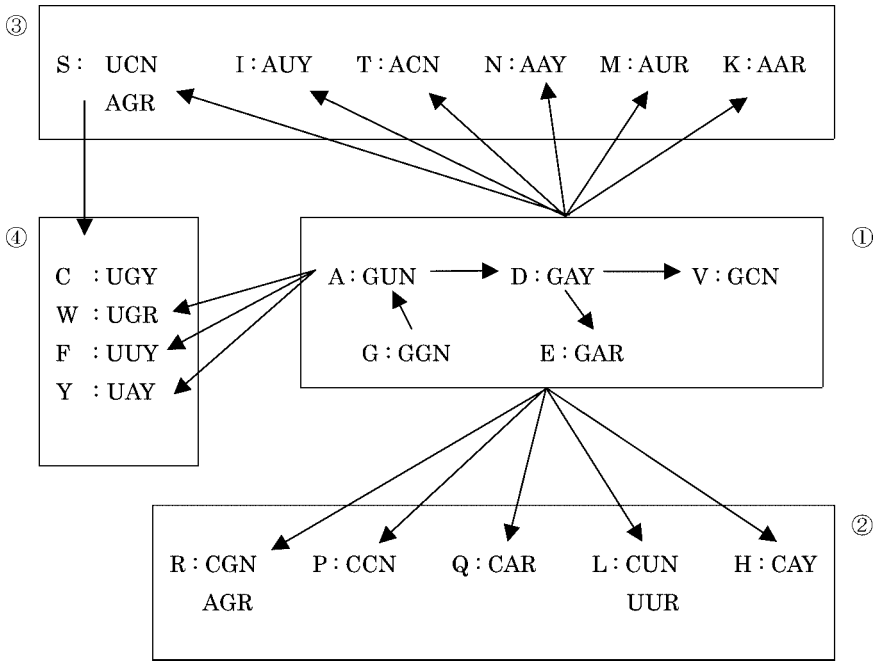

Figure 21. Biosynthetic pathways and code assignments of primitive sulfur-metabolizing bacteria. This figure is based on Knight et al. [5].

Table 12
Relationship between the biosynthetic pathways of primitive sulfur-metabolizing bacteria and related-planes in the cube-shaped periodic table.

Biosynthetic	The planes of cube-shaped periodic table			
pathways	Top	(2–14–62–50)#	(1–13–61–49)#	Bottom
① group		A:GUN, D:GAY, E:GAR, V:GCN, G:GGN		
② group	L:UUR		R:AGR	R:CGN, P:CCN, L:CUN, H:CAY, Q:CAR
③ group	S:UCN		S:AGR, I:AUY, M:AUR, T:ACN, N:AAY, K:AAR	
④ group	C:UGY, W:UGR, F:UUY, Y:UAY			

Note. (2–14–62–50)#: the numbers in parenthesis are Leibnitz Numbers.

Generally speaking, four within-rectangle codon groups ①–④ in figure 21 correspond to four in-plane codon groups in parallel with the yz-plane in the cube-shaped periodic table, figure 2: ① to the (2–14–62–50)-plane, ② to the bottom plane, ③ to the (1–13–61–49)-plane, and ④ to the top plane (the details: see table 12), where the numbers in parenthesis are Leibnitz Numbers in figure 2. Therefore, an arrow drawn between two rectangles roughly means a transition from one plane in parallel with the yz-plane in figure 2 to the other. This example is trivial success, but it gives simple features to the biosynthetic pathways.

Thus, the proposed periodic table, with special emphasis on the cube-shaped periodic table, seems to be successfully reconciled with the previous studies.

11. Conclusions

In this paper I proposed a periodic table for genetic codes which showed the periodicity and the mirror symmetric arrangement of amino acids. These characteristic features were observed in the SG code and also mostly in the mammalian mitochondrial genetic code; in particular, these features were shown more remarkably in the cube-shaped periodic table. As a result, it could be used to classify the non-SG codes and to discover some rules for them to obey. Furthermore, it was also used to make some predictions about non-SG codes to be newly discovered in the future, and to explain the rules for the pairing of anticodons with multiple codons.

Another feature of this paper was that by introducing two new indexes, IN and MN, and by showing several rules closely related to these indexes, it could be shown that codon numbers and anticodon numbers play a key role in base-pairing. In particular, INs in the SG codes table had periodicity, mirror symmetric quality and operational rules. Such properties of INs produced four fundamental periodic patterns such as (5, 3, 3, 1), (1, 3, 3, 5), (3, 5, 1, 3) and (3, 3, 3, 3). As one of these patterns was observed also in the mammalian mitochondrial genetic codes, I inferred that it would be essential for ex-

istence of life systems together with some sort of symmetry such as mirror symmetry of amino acids or INs. This hypothesis appeared to be reinforced by observing harmonic orchestration between the mitochondrial genetic codes and the SG codes, such as a systematic shift of the mitochondrial anticodon numbers in the periodic chart.

All of these features were independent of both the types of base-pair (Watson–Crick base-pair or not) and the possible schemes of bases (the R- and N-schemes). From these results it was my opinion that the periodic table of genetic codes would be valuable for understanding the functional properties of genetic codes.

And also my findings could be closely linked to the previous studies such as codon ring, mutation ring and Woese's polarity.

However, while such interesting results could be derived, two primary subjects, yet to be discussed in the future, remained unresolved. First, in the future will the genetic codes completely obey the binary number logic rules or the Watson–Crick base-pair? If they do completely satisfy these specifications, how will the genetic codes change after that? If the genetic codes must evolve and change by nature, and these changes are fatal to biological organisms, does that mean that biological organisms are in principle necessarily heading towards death? Could this be a correct interpretation? Second, can the periodic table of genetic codes be explained by a new basis as well as the elemental periodic table has been done? Regrettably, I have no idea for these subjects yet. This study was previously reported at the 23rd Symposium on Nucleic Acid Chemistry in 1996 (Gifu, Japan) [13,14].

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