GENETIC CODE AS A HARMONIC SYSTEM: TWO SUPPLEMENTS

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Abstract.

The paper represents two supplements to the source paper, q-bio.OT/0610044, with two new series of harmonic structures of the genetic code, determined by Gauss arithmetical algorithm through atom number balances. By this the determination itself appears as a connection between Gauss algorithm and polarity of molecules (about polarity: in Suppl. 2).

SUPPLEMENT 1

1. Introduction. In this supplement we give a new series of harmonic structures of the genetic code, determined by Gauss arithmetical algorithm as it is shown in the source paper (Rakočević, 2006a), q-bio.OT/0610044. In source paper beside others, we showed that 16 non-contact canonical amino acids (AAs), in an amino acid molecule size order, are determined by a Gauss’ arithmetical algorithm. In this supplement however we show that the same is valid – for the same 16 non-contact amino acids – for their coding order (ordinal number) in Genetic Code Table (GCT). The difference is in the fact that here are valid only two last steps from the said Gauss’ algorithm. Namely, from all Gauss’ algorithm quantums – 11, 21, 31, 41, ( ), 61, 71, 81, 91 – only two last steps are here in the „game“; the quantums „81“ and „91“ as well as their arithmetical mean 86±0. (Cf. source paper-Figure 1 and see the positions of quantums 86±1 in source paper-Figure 1.1.) As in source paper, all determinations are realized through principle of minimum change, i.e. through the unit atom number balances in first or in the second position of the digit-number-notation, respectively (x±00, x±01; x±10), (y±00, y±01; y±10).
2. Results and Discussion. In following 16 illustrations (Tables) are given the results of calculations of atom number within amino acid side chains; the calculations, related to the amino acid system built either from only 16 non-contact or from all 20 AAs (16 non-contact plus 4 contact AAs). By this the rest of four contact AAs make: Glycine (G), Proline (P), Valine (V) and Isoleucine (I). After our hypothesis (Hypothesis 1) there are some other possibilities of the amino acid splitting into 4 special and 16 other AAs; such a splitting which is related to the atom number balances (x±00, x±01; x±10), (y±00, y±01; y±10). The possible examples are: Serine (S), Threonine (T), Cisteine (C) and Methionine (M) as chalcogene AAs (chalcogene because they possess oxygen or sulfur in molecule side chains); then carboxylic AAs and their amide derivatives: Aspartic acid (D), Glutamic acid (E), Asparagine (N) and Glutamine (Q); four aromatic versus 16 aliphatic etc.

Table 1 [left]. This Table is analog with Table 1.2 in source paper. The 16 non-contact AAs arranged into two octets, correspondingly to their ordinal number in GCT, i.e. correspondingly to ordinal number of belonging codons; the first octet on the left and the second one (in the sequence up/down) on the right. The calculation for the ordinal numbers for all 16 amino acids (their sums) is given just down (16+20 = 36 and 48 + 52 = 100).

Table 2 [right]. All is the same as in previous Table, except the second octet (on the right) is given in a vice-versa sequence (down/up).
**Remark 1:** For the terms „contact“ and „non-contact“ AAs as well as for all other new terms see source paper q-bio.OT/0610044.

**Remark 2:** Hypothesis 1 follows from the idea that quantum „4“ represents the first possible case for the existence of one pair of pairs (cf. legend given for Figure 1 in source paper). On the other hand the equation $16 + 4 = 20$, corresponding to square equation $x^2 + x = 20$, is one and only case from the family of metallic means, in relation to the Golden mean (Rakočević, 1998, 2004a; 2006b – Table 2), which corresponds with the middle point in the Harmonic multiplication table.

The first two Tables (Tables 1 & 2) show a correspondence with the natural numbers series from one side and with the Gauss’ arithmetical algorithm from the other side (with quantums “81” and “91” and their arithmetic mean 86±0 and/or 86±1).

|     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|
| 06  | 04  | 05  | 07  | 12  | 13  | 14  | 11  |
| 04  | 05  | 07  | 10  | 12  | 13  | 14  | 11  |
| 05  | 07  | 10  | 13  | 14  | 11  | 12  | 13  |
| 03  | 11  | 15  | 11  | 12  | 13  | 14  | 15  |
| 08  | 11  | 17  | 16  | 15  | 13  | 10  | 09  |
| 02  | 13  | 08  | 10  | 09  | 16  | 15  | 13  |
| 01  | 14  | 11  | 09  | 08  | 16  | 15  | 13  |
| 07  | 15  | 18  | 15  | 13  | 10  | 09  | 08  |

|     |     |     |     |     |
|-----|-----|-----|-----|
| Odd | 37  | 43  | 81  |
| Even| 44  | 48  | 91  |

|     |     |     |     |     |
|-----|-----|-----|-----|
| Odd | 37  | 50  | 81  |
| Even| 44  | 41  | 91  |

Table 3 [left]. The Table follows from Table 1, so that the left octet is given here in a sequence of molecule sizes. In spite of the fact that the sequence of ordinal numbers is disrupted, the odd/even quantums are the same as in Table 1, that means: 16, 20, 48 and 52, but in a vice versa arrangement.

**Table 4 [right].** This Table follows from Table 2 at the same manner as the Table 3 follows from Table 1. Notice that 76 equals 86 – 10 and 96 equals 86 +10.
The amino acid pairs in odd row positions, in Table 1, are larger than the pairs in even row positions. (For example, the amino acid pair F-Q with 25 atoms is larger than L-N with 21 atoms; then the amino acid pair M-K with 26 atoms is larger than S-D with 12 atoms, etc.) Notice also that atom number within side chains of “odd” AAs is determined with multiples of number 6 (8 x 6 = 48 and 9 x 6 = 54). [Cf. these two quantums (48 and 54) with the same quantums in Figure 2.1 in source paper.]

Table 5 [left]. The choice of non-contact AAs from GCT. Each next amino acid chooses its own pair-member from all four columns of GCT; on the other words, each amino acid from the left octet is chosen together with its chemically corresponding pair-member in the right octet. Except a determination with quantums “81” and “91” there is a determination with “half” quantums (81 – 1):2 = 40 and (91 + 1):2 = 46 in forms: 40±10 and 46±10. In spite of the fact that the sequence of ordinal number is disrupted, the odd/even quantums (sums) are only in a balance change (±11)

Table 6 [right]. All is the same (mutatis mutandis) as in previous Table, except the pairing process which is arranged horizontally as well vertically. This Table is analog with source paper-Tables 1.1 and 2.1.
Table 7 [left]. This Table follows from Table 6 at the same manner as source paper-Figure 1 follows from source paper-Table 1.1. (Cf. quantums 29, 36, 49 and 58 in source paper-Fig. 1.)

Table 8 [right]. The same is valid as for previous Table; except, the contact AAs are added.

Table 9 [left]. This Table follows from Table 5 (as Table 3 from Table 1).

Table 10 [right]. This Table follows from Table 9 at the same manner as Table 6 from Table 5.

The sum of two (above mentioned) quantums in Table 1 equals: \(48 + 54 = 102\) atoms within 8 molecules, where 102 represents a half of total atom number.
within 20 canonical AAs, i.e. within their side chains. On the other hand “even” AAs in Table 1 possess 70 atoms which quantum together with the quantum of 32 atoms, existing in four contact AAs (G 01+ P 08 + V 10+ I 13 = 32) equals 102 atoms still once; 102 atoms within 12 molecules. (Proportion 1:1 for atom number and 2:3 for molecule number.) [For proportion 1:1 cf. Marcus (1989) and Stakhov (1989); for proportion 2:3 cf. Moore (1994).] All other illustrations follow analogously and logically – next from previous – as it is shown in their legends.

Table 11 [left]. This Table follows from Table 10 at the same manner as source paper-Figure 1 follows from source paper-Table 1.1.

Table 12 [right]. The same is valid as for previous Table; except, the contact AAs are added.
Table 13 [left]. The order as in Table 5 except a distinction into aliphatic versus aromatic AAs (the first must be aliphatic AAs as in source paper-Table 1.1)

Table 14 [right]. This Table follows from Table 13 at the same manner as Table 10 follows from Table 9.

Table 15 [left]. This Table follows from Table 14 at the same manner as source paper-Figure 1 follows from source paper-Table 1.1.

Table 16 [right]. The same is valid as for previous Table; except, the contact AAs are added.
SUPPLEMENT 2

1. Introduction. In this supplement we give still a set of harmonic structures of the genetic code, determined by Gauss arithmetical algorithm as it is shown in the source paper (Rakočević, 2006a), q-bio.OT/0610044. In source paper beside others, we showed that polarity of amino acids (AAs) indirectly is determined by Gauss arithmetical algorithm. Namely, the polar AAs are positioned (within a 4 x 5 amino acid system) as a separate entity, in the form of a specific “island” surrounded by non-polar AAs (source paper – Figure 2.1). By this, the four ambivalent AAs, i.e. polar and nonpolar at the same time (glycine, proline, tryptophan and histidine)¹ are positioned in a snug “string” at the very edge of the system.

In this supplement, however, we show a direct determination, i.e. a direct connection between Gauss arithmetical algorithm and polarity of amino acid molecules, including their positions in standard Genetic Code Table (GCT). In such a case the connection itself appears to be followed by a strict atom number balance through the existence of new four amino acid classes.

2. Results. The starting step is the choice of one and only single amino acid pair, G-P (Table 1); single pair because glycine is one and only amino acid within glycinic stereochemical type and proline also one and only, but within prolinic stereochemical type (about four stereochemical types see in Popov, 1989 and Rakočević & Jokić, 1996). Follow two pairs of aromatic AAs, first H-W and second F-Y. As the first pair is H-W because the quartet G-P/H-W represents ambivalent AAs – polar and nonpolar at the same time (cf. Footnote 1). The next steps are comming in relation to the AAs sequence, such as it occurs in the first column of GCT.

As a noteworthy is the fact that after four ambivalent come four extrem AAs, extrem just from the aspect of polarity: F-Y/L-R. Phenylalanine is the most nonpolar amino acid of all four aromatic AAs and Leucine (together with

¹ Glycine: after hydropathy is polar; after cloister energy and polar requirement is non-polar; Proline: after hydropathy and cloister energy is polar; after polar requirement is non-polar; Tryptophan: after hydropathy and polar requirement is polar; after cloister energy is non-polar. Hydropathy (Kyte & Doolittle, 1982); cloister energy (Swanson, 1984); polar requirement (Woese et al., 1966; Konopel’chenko and Rumer, 1975). Really regarding, histidine as a „semi-ambivalent“ amino acid since it has neither positive nor negative value in cloister energy, but its value is equal to zero (Figure 5 in Swanson, 1984). About the pairing process of AAs through Hydropathy and Cloister energy see Survey 1 in Rakočević & Jokić, 1996, and about ambivalence of glycine and proline see Section 3.3 in Rakočević, 2004b.
Isoleucine) is the most nonpolar of all aliphatic AAs (after hydropathy). On the
other hand, Tyrosine is extrem because its polarity comes not only from the
aromatic ring but from a polar functional group (OH); and arginine is extrem
through its very massive guanidino group – very massive, and very polar at the
same time.

As we can see from equations 1-4 and from Table 2, the four extreme AAs
are the same AAs that we know from the balance distinction between polar/nonpolar\(^2\) and inner/outer AAs in GCT, with the reading: 22 molecules,
222 atoms within amino acid side chains and 420 atom within whole molecules,
etc. (Rakočević, 2000, 2006c):

\[
\begin{align*}
(n) & \quad 4V+1M+3I+4A+2L+4I+2F+2C = 22 \\
& \quad 40+11+39+16+26+52+28+10 = 222 \quad (420) \quad (1) \\
(o) & \quad 4V+1M+3I+4A+2Y+4R+1W+2C = 21 \\
& \quad 40+11+39+16+30+68+18+10 = 232 \quad (421) \quad (2) \\
(p) & \quad 4G+2K+2N+4P+2Y+4R+1W+2E+2D+2R+2S+2H+4S = 39 \\
& \quad 04+30+16+32+30+68+18+20+14+32+34+10+22+22+20 = 372 \quad (723) \quad (3) \\
(i) & \quad 4G+2K+2N+4P+2L+4I+2F+2E+2D+4T+2R+2S+2Q+2H+4S = 40 \\
& \quad 04+30+16+32+26+52+28+20+14+32+34+10+22+22+20 = 362 \quad (722) \quad (4) \\
(p) & \quad 6S+4T+2N+2Q+2D+2K+6R+2Y = 28 \\
& \quad 30+32+16+22+14+20+30+102+30 = 297–1 \quad (549–1) \quad (5) \\
n) & \quad 4G+4P+1W+2H+4A+6L+4V+3I+2C+1M+2F = 33 \\
& \quad 04+32+18+22+16+78+40+39+10+11+28 = 297+1 \quad (594+1) \quad (6) \\
\end{align*}
\]

Equations (5) and (6) show the relations which are more than a balance; a
specific relationship of the amino acid “heads” and “bodies” (all “heads” and all
“bodies”) from one side and the wholeness of molecules from the second side.
So, the distribution of atom number is the following. In polar AAs molecules
there are exactly as many atoms as in the heads of all molecules, minus one atom
\((61 \times 9 = 549)\). In the “nonpolar” molecules (nonpolar plus ambivalent) there are
as many atoms as in the bodies, i.e. side chains of all 61 molecules, plus one
atom \([(297+1) + (33 \times 9 = 297) = 594+1]\). On the other hand, in the bodies of

\(^2\) Polar/nonpolar AAs after their hydropathy (cf. Footnote 1).
polar as well as of non-polar molecules, there is 297±1 atoms, exactly as in first (297-1) and second half (297+1) of standard GCT\(^3\). Thirdly, in the heads of non-polar molecules there are exactly as many atoms as it is the half of the atom number in the bodies of all molecules (33 x 9 = \(\frac{1}{2} \times 9\)) of 594, while in the heads of polar AAs there are as many as it is the half of 504, which number is the modular pair (in module 9) of number 504.

**Remark 1.** Number 504 represents the sum of each two and two (out of eight in total) branches on the 6-bit binary tree (Figure 1 in Rakočević, 1998), or of two and two octets in GCT as follows: in two central octets there are: 24+25+...+31 = 220 and 32+33+...+39 = 284 (220+284 = 504); in next two octets there are: 16+17+...+23 = 156 and 40+41+...+47 = 348 (156+348 = 504); within the first to last pair of octets there are: 8+9+...+15 = 92 and 48+49+...+55 = 412 (92+412 = 504); Finely, within the last octet pair we have: 0+1+...+7 = 28 and 56+57+...+63 = 476 (28+476 = 504)(cf. Table 3).

**Remark 2.** The number 504 represents the sum of the first two friendly numbers (the first pair): 220+284 = 504. On the other hand, Shcherbak has shown (1994) that within the set of 23 AAs, the eight four-codon AAs possess 592+333 = 925 nucleons, where 592 is a half of the third friendly number (1184 = 2 x 592)
\(^4\). But Shcherbak also showed that within side chains of all 23 AAs there are 1443 of nucleons (333 nucleons within four-codon AAs plus 1110 within non-four-codon AAs), where 1443 is a sixth part of the sum of first four perfect numbers [1443 x 6 = 8658 = (7770+0888) = 6+28+496+8128] (About determination of the genetic code with the perfect and friendly numbers see in Rakočević, 1997).

Parallel with the atom number balance there is a molecule number balance as follows: the unit distances between the number of molecules: 22-21 = 1 and 40-39 = 1 in equation (1) in relation to equation (2) and equation (4) in relation to equation (3), respectively; then the double units distances between the number of

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\(^3\) Table 2 appears to be the standard GCT if the texture (dark tones) is excluded. In such a manner the left half of GCT make 32 amino acid molecules encoded by 32 NYN codons, whereas the right half make 29 amino acid molecules encoded by 29 NRN codons, plus three stop codons. Within 32 amino acid molecules (side chains) there are 297-1, and within 29 molecules 297+1 of atoms.

\(^4\) The forth friendly number is the number 1210 as a product of 10 x 11\(^2\). The third and forth friendly numbers make the second friendly number pair.
molecules: 33-22 = 11 and 39-28 = 11 in equation (6) in relation to equation (1) and equation (3) in relation to equation (5), respectively.

Table 1. First four AAs are ambivalent, next four “extreme” (as it is explained in the text) and other AAs in a chemically determined order and arrangement.

| G 01 | H 11 | F 14 | L 13 | I 13 | M 11 | V 10 |
|------|------|------|------|------|------|------|
| P 08 | W 18 | Y 15 | R 17 | K 15 | C 05 | A 04 |
| Q 11 | N 08 | S 05 | T 08 |      |      |      |
| E 10 | D 01 |      |      |      |      |      |

After first two AAs quartets in Table 1 (G-P/H-W and F-Y/L-R) follow other AAs through a chemically relevant relation: two source aliphatic AAs (L-I)\(^5\) and two amino derivatives (R-K); then two sulfur AAs (M-C) and two source aliphatic still once (V-A). The next two are the chalcogen AAs: S-T in a continuation to M-C; amino acid T also in contact with A as two methyl derivatives. At the end come two carboxylic AAs (D-E) whose amide derivatives, as nitrogen compounds, hold a connection with other two nitrogen derivatives (R-K).

\(^5\) Notice that F-L make also a chemical pair through the same structural motive – the first possible branching (iso-butane in relation to toluen structural motive). Here lies the reason why benzene ring is excluded from the set of aromatic AAs.
Table 2. The amino acids within three diagonals are inner, and other – outer AAs. On the other side, within bordered space are polar AAs and other – nonpolar AAs (polar/nonpolar after hydropathy: Kyte & Doolittle, 1982).

| 1st lett. | 2nd letter | 3rd lett. |
|-----------|------------|-----------|
| U         | A          | G         |
| UUU       | UCU        | UAU       |
| UUG       | UGC        | UGU       |
| UUA       | UCA        | UAG       |
| UUG       | UCG        | CT        |
| C         | A          | G         |
| CUU       | CCA        | CGC       |
| CUC       | CCG        | CT        |
| CUA       | CAA        | CGA       |
| CUG       | CAG        | CT        |
| A         | A          | G         |
| AUU       | ACC        | AGC       |
| AUC       | ACA        | AGG       |
| AUA       | AAC        | AGG       |
| AUG       | AAA        | AGG       |
| G         | A          | G         |
| GUU       | GCU        | GAU       |
| GUC       | GCC        | GAC       |
| GUA       | GCA        | GAA       |
| GUG       | GCG        | GAG       |

Table 3. The eight octets within 6-bit binary-code tree (Rakočević, 1998) as well as within GCT are determined with the first pair of friendly numbers (220 & 284) and third perfect number (496). For details see the text, especially Remarks 1 & 2.
Table 4 [left]. This Table follows from Table 1. Atom number determination in relation to Gauss’ algorithm (explanation in the text).

Table 5 [right]. All is the same as in previous Table, except the determination by nucleon number. Notice a symmetry determination through module 9: 595 versus 660.

|     | G   | 01  | 08  | P   | G   | 001 | 041 | P   |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | H   | 11  | 18  | W   | H   | 081 | 130 | W   |
|     | F   | 14  | 15  | Y   | F   | 091 | 107 | Y   |
|     | L   | 13  | 17  | R   | L   | 057 | 100 | R   |
|     | I   | 13  | 15  | K   | I   | 057 | 072 | K   |
|     | M   | 11  | 05  | C   | M   | 075 | 047 | C   |
|     | V   | 10  | 04  | A   | V   | 043 | 015 | A   |
|     | T   | 08  | 05  | S   | T   | 045 | 031 | S   |
|     | Q   | 11  | 08  | N   | Q   | 072 | 058 | N   |
|     | E   | 10  | 07  | D   | E   | 073 | 059 | D   |
| Odd | 49  | 50  |     |     | O   | 264 | 293 |     |
| Even| 53  | 52  |     |     | E   | 331 | 367 |     |
|     | 102 | 102 |     |     |     | 595 | 660 |     |

From Table 1 follows Table 4 (in relation to Table 5), first row on the left and second row on the right, plus AAs from third and fourth rows – three outer (T, Q, E) on the left and three inner (S, N, D) on the right. As we see AAs in odd and even positions make four AAs groups with atom number directly determined by Gauss’ arithmetical algorithm (Table 6). Namely, in source paper (source paper – Figure 1) we showed that within four amino acid rows there are so many atoms as in 10th and 20th Gauss’ pair (in relation to middle point “51”: 10th pair as 41-61 and 20th pair as 31-71 atoms). And here we see that within four amino acid rows are so many atoms as in 01st and 02nd Gauss’ pair (01st pair as 50-52 and 02nd pair as 49-53 atoms).
Table 6 [left]. The Table follows from Table 4: two outer columns as odd/even positions in left column of table 4, and two inner columns as odd/even positions in right column of table 4, respectively.

Table 7 [right]. As previous one, this Table also follows from Table 4: first five and last five AAs as two outer columns, and 5 & 5 amino acids as two inner columns. The atom number quantums “50” and “52” are the same as in previous Table (Table 6), whereas two other quantums (73 = 71 + 2 and 29 = 31 – 2) correspond to the Gauss pair 31-71 through a deviation of ±2 (minus first and second step; plus first and second step).

The sum of two quantums in Table 1 equals: \(48+54 = 102\) atoms within 8 molecules, where 102 represents a half of total atom number within 20 canonical AAs, i.e. within their side chains. On the other hand “even” AAs in Table 1 possess 70 atoms which quantum together with the quantum of 32 atoms, existing in four contact AAs (G 01+ P 08 + V 10+ I 13 = 32) equals 102 atoms still once; 102 atoms within 12 molecules. (Proportion 1:1 for atom number and 2:3 for molecule number.) [For proportion 1:1 cf. Marcus (1989) and Stakhov (1989); for proportion 2:3 cf. Moore (1994).] All other illustrations follow analogously and logically – next from previous – as it is shown in their legends.

3. Conclusion for both Supplements. Bearing in mind that the order of amino acids in presented Tables, in both Supplements, is given in correspondence with the order of codons in GCT, it makes sense to speak about genetic code as a harmonic system. On the other side, presented harmonic structures provide evidence to support the hypothesis, given in a previous paper (Rakočević, 2004b), that genetic code was complete from the very beginning as the condition for the origin and evolution of the life.
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