The Genetic code: Section III

Transformations between number–base systems

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17. Transformations between number-base systems (nb-x)

Bases - totals of ams \(\times 5\) x ES-numbers - Generative production of the 12-groups

1. Transformations of the codon-bases to the 12-groups of ams:

1.1 All geometrical dimensions should naturally be regarded as present in the cell simultaneously, on different levels, and interdependent through transformations into one another. One simple example is the geometries of proteins, forming linear threads (~ D1), sheets (~ D2) and globular forms (~ D3).

The thought that different d-degrees could be associated with different number base systems (nb-x), as nb-10, nb-8, nb-6 for \(x = 5, 4, 3\), led to a first test on mass of codon bases with remarkable results, figure 17-1 below. Further investigation showed also several connections with the ES-series. (Nb-x in text below often written as "-index figures. Figures in nb-8 and nb-6 are often rewritten with figures from nb-10.)

Fig 17-1: From mass of codon bases to the two 12-groups of ams:

<table>
<thead>
<tr>
<th>nb-10</th>
<th>nb-8</th>
<th>24 ams R</th>
</tr>
</thead>
<tbody>
<tr>
<td>G 151</td>
<td>(\rightarrow)</td>
<td>227</td>
</tr>
<tr>
<td>C 111</td>
<td>(\rightarrow)</td>
<td>157… sum 384 (\times) (\times 2 = 768 \sim 770)</td>
</tr>
</tbody>
</table>

\[ \begin{align*}
U 112 & \quad \rightarrow \quad 160 \\
A 135 & \quad \rightarrow \quad 207… \text{ sum } 367, \quad \times 2 = 734
\end{align*} \]

\(\downarrow\)

\(x 2 = 1018 \quad \rightarrow \quad 1772 = 24 \text{ B-chains unbound}\)

\(\times G + C \text{ transformed together } = 386 \text{ in nb-8.}\)

Hence, 4 sets of the 4 bases give the total sum of 24 unbound ams.

We find also that 2 x G+C-bases in nb-8 as 768 gives total sum 3276 in nb-6:

\[
\begin{align*}
\text{nb-10} & \quad \rightarrow \quad \text{nb-6} \\
768 & \rightarrow \quad \text{3276} \quad 24 \text{ ams } R + B, \text{ unbound (rewritten from 3320)}
\end{align*}
\]

The sum of the 4 bases in nb-8 = 752 \(+/1\):

\[
\begin{align*}
\text{nb-10} & \quad \rightarrow \quad \text{nb-6} \\
752 & \rightarrow \quad \text{2848} \quad 24 \text{ ams } R + B, \text{ bound (rewritten from 3050)}
\end{align*}
\]
Fig 17-2. From 752 as sum of ES-numbers 5', 4' and 3' to 2848 in nb-6:

\[ \begin{align*}
5' & \quad 292_{10} \rightarrow 1204_{6} - 244 = 960 \text{ U+A} \\
4' & \quad 252_{10} \rightarrow 1100_{6} + 244 = 1344 \text{ 24 B-chains bound} \\
3' & \quad 208_{10} \rightarrow 544_{6} = 544. \text{ C-C} \\
1' & \quad 100_{10} \rightarrow 224_{6} = 2848 \\
\end{align*} \]

2848 = 24 ams R + B bound

1.2 Some general annotations:

However strange the idea surely may seem for scientific "common sense", the many astonishing results here and below are rather difficult to dismiss as only haphazard. If they are not, if they reveal some connections on deep energy levels, they should represent one kind of references, one kind of guiding operators for potential growth - or just what is sometimes in the biochemical field is referred to as "affinities"?

All derived numbers shall naturally be regarded as nb-10-numbers, hence transformations as nb-10 → nb-8 may be repeated, illustrated for instance in the carbon-nitrogen cycle in the sun, from $^{12}$C to $^{14}$N to $^{16}$O, intermediate steps showing one way to perform such transformations.

It follows that all operations as multiplications are performed in nb-10. Indexes for x in nb-x are often used below to shorten the text. As mentioned above numbers in nb-8 and nb-6 are often rewritten with figures from nb-10.

A question is of course if such rewritings could be expressed in biochemical processes as for instance 20 equivalent with (~) 18 in nb-8 as -2H or 120 in nb-6 ~ 76 as -44 (CO2)?

Another question is how to interpret nb-16 in many examples below. If keeping to the thought of x in nb-x as first three numbers in the elementary chain 5' → 4' → 3' doubled, should nb-16 be regarded as 2 x 4 doubled or 2(5 + 3) doubled?

Fig Ti-1

\[ \begin{align*}
\leftarrow 16 \quad ? \\
\downarrow \\
10 \quad 8 \quad 6 \\
\end{align*} \]

A general feature may be noted: transformation of sums or whole units give larger numbers in lower nb-systems than their parts transformed and summed afterwards.

1.3 Halves of the 12-groups 770 and 734, -/+1 = 384 and 368:

**Fatty acids**, a first annotation here:

Cell membranes are an equally essential part of life as the genetic code. Two of the most common fatty acids give transformed to nb-6 three times these numbers 367 and 385, +/-1, a relation to R-chains of the 24 ams = 3/2 and simultaneously a relation d-degree 3 to 4(nb-6 to nb-8) with the assumed view above.

\[ \begin{align*}
\text{C16H32O2:} \quad 256_{10} \rightarrow 1104_{6} = 3 \times 368 \\
\text{C18H36O2:} \quad 284_{10} \rightarrow 1152_{6} = 3 \times 384, \text{ (Note: 1152 = 752 rewritten)}
\end{align*} \]
Cf. the hexagonal pattern in Table 0: fatty acids as a third way to read such a pattern.

From the numbers 384 and 368 in nb-10 transformed in two steps to nb-8 we get 2 sets of bases G and A in nb-8, as in opposite direction to the figure above and without C and U:

\[
\begin{align*}
384 \times \frac{1}{2} &= 192-10 \rightarrow 300-8 / 300-10 \rightarrow 454-8 = 2 \times 227 = 2 \text{ G-8} \\
368 \times \frac{1}{2} &= 184-10 \rightarrow 268-8 / 268-10 \rightarrow 414-8 = 2 \times 207 = 2 \text{ A-8}
\end{align*}
\]

1.4. Bases → totals:

1.4.1 Four times G+U and A+C to ~ B- and R-chains of total 3276:

Sums of R+B-chains together in nb-10:

\[
\begin{align*}
G1 + U1 &= C2 + A2 = 1468 \\
C1 + A1 &= G2 + U2 = 1808... \text{ Sums of coded amino acids (R + B)}
\end{align*}
\]

With exchanged partners these sums are given from 4 times the bases:

**Fig. 17-3**

<table>
<thead>
<tr>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>4 G-bases = 4 x 151 = 604</td>
<td>(\rightarrow 1134)</td>
</tr>
<tr>
<td>4 C-bases = 4 x 111 = 444</td>
<td>(\rightarrow 674...\text{sum 1808})</td>
</tr>
<tr>
<td>1 A-base = 135</td>
<td>(\rightarrow 207, \times 4 = 828)</td>
</tr>
<tr>
<td>1 U-base = 112</td>
<td>(\rightarrow 160, \times 4 = 640...\text{sum 1468})</td>
</tr>
</tbody>
</table>

In nb-10 we have groups of ams paired in keto-/amino types:

Here G- and A-bases have exchanged partners and bases A and U must be multiplied with 4 after transformation.

**Fig. 17-4**

<table>
<thead>
<tr>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>4 G = 604 (\rightarrow 1134)</td>
<td></td>
</tr>
<tr>
<td>1 U = 112</td>
<td>160, (\times 4 = 640, + 1134 = 1774 = \text{B-chains} + 2)</td>
</tr>
<tr>
<td>4 C = 444 (\rightarrow 674)</td>
<td></td>
</tr>
<tr>
<td>1 A = 135</td>
<td>207, (\times 4 = 828, + 674 = 1502 = \text{R-chains} - 2)</td>
</tr>
</tbody>
</table>

Rewriting 640 to 638 and 828 to 830 gives the right sums B 1772 and R 1504.
1.4.2 Two sets of bases from ES-numbers 5’, 4’ and 3’:

Fig. 17-5

<table>
<thead>
<tr>
<th>&quot;5’&quot;</th>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>252</td>
<td>10.3</td>
<td>444</td>
</tr>
<tr>
<td>&quot;4’&quot;</td>
<td>252</td>
<td>374</td>
</tr>
<tr>
<td>2 x &quot;3’&quot;</td>
<td>16-base</td>
<td>10-base</td>
</tr>
<tr>
<td>416</td>
<td>16.4</td>
<td>1046</td>
</tr>
</tbody>
</table>

Number 416 (2 x 3’, 208) is the one which added to 544 gives the A-U-group of ams. Cf. that U-base gets replaced by T-base in DNA, a CH2-group added for inward direction to DNA. (It could perhaps be compared with the interpretation of nb-16 as 2 x (3’ + 5’), a step backwards from 3’ to 5’, equivalent with inwards?)

2. The bases in the ES-chain:

Fig. 17-6

<table>
<thead>
<tr>
<th>10-base</th>
<th>8-base</th>
<th>(denotation here C₈ etc.)</th>
</tr>
</thead>
<tbody>
<tr>
<td>G 151</td>
<td>227</td>
<td></td>
</tr>
<tr>
<td>U 112</td>
<td>160</td>
<td></td>
</tr>
<tr>
<td>C 111</td>
<td>157...sum 544</td>
<td></td>
</tr>
<tr>
<td>A 135</td>
<td>207...sum 208</td>
<td>A₈ 207</td>
</tr>
</tbody>
</table>

U 160 + C 157 in nb-8 approximate number 2’ = 159 in the ES-series, together 317. In nb-10 number 385 is the interval 544 to 159. Here G-8 becomes the same interval to both bases U-8 + C-8. Cf. that G-base can bind to both:

Fig 17-7: The bases in nb-8 in the ES-chain:

```
\[
\begin{array}{cccccccc}
5^{23} & 4^{28} & 3^{23} & 2^{23} & 1^{23} & \times 10^2 \\
292 & 252 & 208 & 159/158 & 100 & 0 & ES-chain \rightarrow \\
\text{diff.} & 227 & G₈ & 317 = U₈ + C₈ (159 = U₈ - 1, 158 = C₈ + 1) \\
\end{array}
\]
```

These relations could be a reason why G+C-bases get connected with the 12-group 770 of ams in spite of all bases equally represented in this group.
3. 5 times ES-numbers:

3.1 The transformations between nb-10 and nb-8 of main codon groups of ams and 5 times the ES-chain numbers 5' - 4' - 3' are among the most astonishing:

**Fig 17-8: Main codon groups of ams from 5 times ES-numbers:**

<table>
<thead>
<tr>
<th>nb-10</th>
<th>nb-8</th>
</tr>
</thead>
<tbody>
<tr>
<td>C1 + U1 = 816</td>
<td>1460 = 5 x 292</td>
</tr>
<tr>
<td>G1 + A1 = 688</td>
<td>1260 = 5 x 252</td>
</tr>
<tr>
<td>G1 + C1 = 544</td>
<td>1040 = 5 x 208</td>
</tr>
<tr>
<td>U1 + A1 = 960</td>
<td>1680 = 5 x 336 (544 - 208)</td>
</tr>
</tbody>
</table>

816 and 688 is the division of R-chains of total sum 1504 of 24 ams, a division between purine and pyrimidine codon groups. As a division in step 5 - 4 here it precedes the one between complementary pairs G-C and U-A, which are attained from the secondary division of 544 in 336 and 208, a division in step 4 - 3.

Note also about 1344, the 24 B-chains bound, included in sum 2848:

1344 in nb-10 = 2500 in nb-8 = ES-numbers 5(292 + 208)

These relations seem to support the relevance of both the ES-chain and the thought that nb-transformations could be part of the reference system.

**Fig 17-9 5 x half of 752, number 688 as an interval:**

G+C, x 2 = 544 x 2; 10-base 8-base

<table>
<thead>
<tr>
<th>1088</th>
<th>1880</th>
</tr>
</thead>
<tbody>
<tr>
<td>1260 = 3360 / 1.460 = 5 x 376</td>
<td>5 x 252</td>
</tr>
<tr>
<td>1776</td>
<td>3360</td>
</tr>
</tbody>
</table>

There is also the feature that divisions stepwise as polarizations of numbers 816 in U1 + C1, separately transformed to nb-8 give 1260, next lower level, and this back to nb-10 and divided G1 and A1 gives 1040 in nb-8:
3.2 About the interval $84 = 292 \rightarrow 208$ in the ES-chain we have that $n \times 84$ ($n = 1, 2, 4$) times $10$ ($1040 \sim 840, 1680$ and $3360$) in nb-8 gives the groups $544, 960$ and $1776$ in nb-10:

$$Fig\ 17-11. \ n \times \text{interval} \ 84:\$$

$$\text{Interval} \ 292 - 208:$$

$$\begin{array}{c|c|c|c|c}
\text{nb-10} & \text{nb-8} & \text{ES-series} \\
24 \text{ B-chains à 74 A:} & 1776 & 336 \times 10 &= 4 \times 84, \times 10 \ (292 - 208) \\
\text{A+U-coded ams R:} & 960 & 168 \times 10 &= 2 \times 84 \ " \\
\text{G+C-coded ams R:} & 544 & 84 \times 10 &= 1 \times 84 \ "
\end{array}$$

3.3 5 times intervals in the exponent series in nb-8 give ams-groups -/+1:

$$Fig.\ 17-12 \ 5 \times \text{interval in the ES-chain:}$$

$$\begin{array}{c|c|c|c|c}
\text{Ams} & \text{10-base} & \text{8-base} & \text{Intervals in the exponent series:} \\
G1+1 & 192 & \leftarrow 300 = 5 \times \text{interval} & 60 = 292 - 352 = “5” — ("4 + 1") \\
A1-1 & 496 & \leftarrow 760 = 5 \times \text{interval} & 152 = 252 - 100 = “4” — “1” \\
U1+1 & 464 & \leftarrow 720 = 5 \times \text{interval} & 144 = 352 - 208 = (“4 + 1”) — “3” \\
C1-1 & 352 & \leftarrow 540 = 5 \times \text{interval} & 108 = 208 - 100 = “3” — “1”
\end{array}$$

3.4 Nb-6: 5 times the ES-numbers 5', 4' 3' in nb-6:

It gives the sum of U- plus A-coded ams R and also all C-atoms in R-chains in nb-10, divided on $G1 + A1 = 396$ and $U1 + C1 = 564$: 

$$\text{Steps of "polarisations" "5" \rightarrow "4" \rightarrow "3":}$$

$$\begin{array}{c|c|c|c|c}
\text{Steps} & \text{Ams} & \text{nb-10} & \text{nb-8} & \text{ES-numbers} \\
"5" & \text{C1 + U1:} & \leftarrow 816 & \text{1460} & 5 \times 292 \\
 & \text{C1:} & \downarrow & 353 & 541 \\
 & \text{U1:} & \downarrow & 463 & 717 \ldots 1258 \sim 1260 = 5 \times 252 \\
"4" & \text{G1 + A1:} & \leftarrow 688 & \text{1260} & 5 \times 208 \\
 & \text{G1:} & \downarrow & 191 & 277 \\
 & \text{A1:} & \downarrow & 497 & 761 \ldots 1038 \sim 1040 = 5 \times 208 \\
"3" & \text{G1 + C1:} & \leftarrow 544 & \text{1040} & 5 \times 208 \\
\end{array}$$
3.5 The parts above of 960 in nb-16 gives the total mass of bound ams in nb-8:

Fig. 17-14

<table>
<thead>
<tr>
<th>G1,A1 - G2, A2</th>
<th>6-base</th>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>G1,A1 - C2, U2</td>
<td>292</td>
<td>658</td>
<td>1222</td>
</tr>
<tr>
<td>G1,A1</td>
<td>688</td>
<td>2848</td>
<td>2848 = 24 ams bound</td>
</tr>
<tr>
<td>But</td>
<td>2 x 344</td>
<td>————&gt; 1504 x 2 = 2 x 24 ams B.</td>
<td></td>
</tr>
</tbody>
</table>

3.6 The numbers U1 + C1 = 816 and G1+ A1 = 688 read in nb-8 rewritten, give in two steps total 24 ams, R + B inbound in nb-8:

<table>
<thead>
<tr>
<th>nb-8</th>
<th>816 - 1016</th>
</tr>
</thead>
<tbody>
<tr>
<td>688</td>
<td>710 ... Sum 1726-8./ 1726-10 → 3276-8</td>
</tr>
</tbody>
</table>

4. Generation of the two 12-groups of ams with mixed and non-mixed codons:

4.1 Generative production of sums within 12-groups of ams:

Fig. 17-15a. The ES-chain, numbers 177 and 208:

\[
544 \leftarrow 177 \rightarrow 367 \quad 367 \times 2 = 734
\]

\[
292 \quad 252 \quad \text{208} \quad 159 \quad 100 \quad 49
\]

\[
385, \times 2 = 770
\]

Cf Table 2.3 in file 02.

Numbers 770 and 734 generated from 177 and 208:
- From 177 we get 385 in two steps nb-10 to nb-8:
- From 208 we get 734 in three such steps:
Fig. 17-15b
\[ \text{nb-10} \rightarrow 8 \quad \text{nb-10} \rightarrow 8 \]
\[ 177 \rightarrow 261 \rightarrow 385 \rightarrow x 2 = 770 \]
\[ \text{nb-10} \rightarrow 8 \quad \text{nb-10} \rightarrow 8 \quad \text{nb-10} \rightarrow 8 \]
\[ 208 \rightarrow 320 \rightarrow 318* \rightarrow 476 \rightarrow 734 \]
\[ \text{nb-10} \rightarrow 8 \quad \text{nb-10} \rightarrow 8 \]
\[ 208 \rightarrow 320 \sim 318* \rightarrow 476 \rightarrow 734 \]

* \( 318 = 2 \times 2', 159 \), from there only two steps:

Fig. 17-15c:
\[
\begin{align*}
2 \times 159: & \quad 10 \rightarrow 8 \text{-base} \quad 10 \rightarrow 8 \text{-base} \\
 & \quad 318 \rightarrow 476 \rightarrow 734 \rightarrow \text{RNA+Pair-coded ams}
\end{align*}
\]

In group 734 U+A-coded ams = 575, a number given through two steps nb-10 to nb-8, either as sum of 500 + Meth 75 or from 208 + interval 49: Meth that starts the protein synthesis are attained from the middle interval in the ES-chain:

Fig 17-15-d:
\[
\begin{align*}
\text{10} \rightarrow \text{8-base} \quad \text{10} \rightarrow \text{8-base} \\
208 \rightarrow 320 \rightarrow 500 \rightarrow 575 \\
\text{Interval 208-159:} & \quad 10 \rightarrow 8 \text{-base} \quad 10 \rightarrow 8 \text{-base} \\
 & \quad 49 \rightarrow 61 \rightarrow 75 \rightarrow \text{Meth, R. 75}
\end{align*}
\]

Note too that Meth leaves its outer CH3-goup at start of synthesis, \((-15 + 1)\), which gives R-chain = 61, the intermediate number in the figure above.

575 directly from 208 + 49 = 257 in only two steps:

Fig 17-15e:
\[
\begin{align*}
257 \rightarrow 381 \rightarrow 575 \\
\text{nb-10} \rightarrow 8 \quad \text{nb-10} \rightarrow 8 \]
\[ 208 \rightarrow 320 \rightarrow 318 \rightarrow \]

Number 75, R-chain of Meth:
In the ES-chain in nb-10 the number 75 = interval 292 - 367 (the sum in the middle of the chain). Transformed in two steps nb-10 to nb-8 it gives the number 159:

\[ 75 \rightarrow 113 \rightarrow 159 \quad (161 \text{ rewritten}) \]
4.2 A- and T-bases give the sum 575 of ams with non-mixed codons:

Starting numbers 177 and 208 in transformations, minus 1 in each, are the T- and A-bases in nb-8. With DNA-base T we get the sum 575 in two steps nb-10→8: (Cf. file 02.)

Fig. 17-16: $A+T$

\[
\begin{array}{c|c|c|c|c|c}
\hline
10-base & 8-base/10-base & 8-base & 10-base \\
\hline
A: & 135 & 207 & 207 & 317, +3 = 320 = AAU-UU-coded ams R \\
T: & 126 & 176 & 176 & 258, -3 = 255 = UU-UA-coded ams R \\
\hline
\end{array}
\]

The Exponent series: $317 = 2 \times 158.5, \sim 2 \times "2", 258 = 158 + 100, \sim "2 + 1".$

How explain the T-base here, a DNA-base giving A in RNA?

4.3 770-group from 4':

It can be added that $2 \times 252 (= 4' in the ES-chain)$ in nb-10 leads directly to 770 in nb-8: $2 \times 4' (252) = 504-10 \rightarrow 770-8$

4.4 Parts of 12-group 770 from halved ES-chain:

The division of group 770 in Cross- and Form-coded ams, 418 and 352, may be derived by dividing the whole ES-chain in step 4'-3' and halving these numbers:

Fig 17-17: From halved ES-parts to mixed codon groups

Cross-coded = 418 = $2 \times 209$; CA+CA+CU = 210, UG+UG+UC = 208,
Form-coded = 352 = $2 \times 176$; GA+GA+GU = 175, AG+AG+AC = 177.

The exponent series: \[
\begin{array}{c|c|c|c}
\hline
10-base & 8-base \\
\hline
292 & 544 \\
252 & 467 \\
208 & 159 \\
159 & 100 \\
\hline
\end{array}
\]

10-base: $\times \frac{1}{2} = 272$  8-base: $\downarrow$

8-base: $\downarrow$

544

418

$\downarrow$

=x \frac{1}{2} = 234. (round number)

467

352

= $2 \times 209$

208

159

100
4.5 Derivation of N- and Z-numbers within the two 12-groups of ams:

Fig. 17-18:

**G+C-group:** \( G_8 + C_8 = 384 \), difference transformed in 1 step:

\[
\begin{array}{c|c|c}
\text{10-base} & \text{S-base} & \text{= N-number in 770-group} \\
384 - G_{10}^{151} = 233 & 351 & \\
768 & 2 \times 253 & 772 - 770 = 768
\end{array}
\]

**A+U-group:** \( A_8 + U_8 = 367 \), difference transformed in 2 steps:

\[
\begin{array}{c|c|c}
\text{734} & \text{= N-number in 734-group} \\
367 - U_{10}^{112} = 255 & 327 & \\
377 - 112 = 265 & 411 - 409 & \\
367 - A_{10}^{135} = 232 & 350 - 348 & \\
348 \cdot 135 = 213 & 325 & \\
\end{array}
\]
18. More on totals and other notable transformations

- 1st to-2nd base

1. Total sum R+B-chains of 24 ams unbound = 3276:

3276 is about 1/10 of \(2^{15}\). In nb-16 it's CCC, which may be transcribed as
12.12.12 = 3072 (3 x 322 = 4 x 768) + 192 + 12:

Fig 18-1: Total sum of 24 ams R+B:

\[
\begin{align*}
\text{nb-16} & \quad \rightarrow \quad \text{nb-10} \\
\text{CCC} & \quad \downarrow \\
12.12.12 & \\
\text{CC} & \quad \rightarrow \quad \text{nb-10} \quad \rightarrow \quad \text{nb-8} \\
& \quad = \text{Trp, R+B,} \\
& \quad \text{the heaviest amino acid.} \\
& \quad 2 \times 314 \rightarrow 2848 = 24 \text{ ams R+B bound}
\end{align*}
\]

(2 \( \pi \times 100\): the bound 24 ams as a closed circle!)

12.12.12: An association goes to carbon \(^{12}\)C and the 3C-molecules from halved fructose in glycolysis from which first group of ams derives. Could we eventually read positions of the carbon atoms as decided and guided by oxygen \(^{16}\)O in some way?! Much of the process in glycolysis seems to be about a stepwise displacement of oxygen along the C-C-C-chain.

2. Why 24 ams?

One reason to suspect nb-transformations could be the 4 double-coded ams, if 20 ams have to be 24, then 4 ams must be repeated (!).

\[20-10 \rightarrow 24-8\]

3. H-atoms, 152 in R-chains: and the total of R 1504:

Number of hydrogen atoms in R-chains was 152 = interval 4'-1' in the ES-series.

\[
\begin{align*}
292 & \quad |<44>\|\quad 252 \quad |<44>\|\quad 208 \quad |<44>\|\quad 159 \quad |<44>\|\quad 100 \quad |<44>\|\quad 0 \\
& \quad |<44>\|\quad 108 \quad |<44>\|
\end{align*}
\]

This interval is divided \(4'-3' = 44\) and \(3'-1' = 108\): Transformed from nb-16 to nb-6 they give total Z-numbers of R-chains and N-numbers separately:
Fig 18-2: H-atoms:

\[ 44_{16} \rightarrow 152_{6} = \text{H in R-chains} \]

\[ 152 < \rightarrow 828 = \text{total Z in R-chains} \]

\[ 108_{16} \rightarrow 676_{6} = \text{N in R-chains} \]

Steps 44 → 152 = + 108
Step 108 → 676 = + 568...This sum is also = 676 = Z (or N) of atoms C, N, O, S.
Cf. 676 = 26^2 and the 2x^2-chain, file 13.

4. N-numbers in codon-groups of ams may lead to totals of ams:

Fig. 18-3: Neutron numbers to totals

<table>
<thead>
<tr>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>G1: N</td>
<td>86</td>
</tr>
<tr>
<td>C1: N</td>
<td>138</td>
</tr>
<tr>
<td>U1: N</td>
<td>213</td>
</tr>
<tr>
<td>A1: N</td>
<td>219</td>
</tr>
</tbody>
</table>

\[ \downarrow \quad 1018 \rightarrow 1772 \quad = 1772 = 24 \text{ B-chains} \]

<table>
<thead>
<tr>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>G2: N</td>
<td>187</td>
</tr>
<tr>
<td>C2: N</td>
<td>58</td>
</tr>
<tr>
<td>U2: N</td>
<td>190</td>
</tr>
<tr>
<td>A2: N</td>
<td>241</td>
</tr>
</tbody>
</table>

\[ \downarrow \quad 491 \rightarrow 753, \times 2 \quad = 1596 = 24 \text{ R-chains} + 2\text{H}^* \]

* 2 \times 491: 982 \rightarrow 1726

\[ \downarrow \quad 1726 \rightarrow 3276 \quad = 3276 = 24 \text{ ams R + B} \]

- 491, \sim 511, \sim 509 re-written, sum of 4 RNA-bases.
- (982 re-written = 1202, + 1018 = 2220 (nb-8). = 490 in nb-16.
- 490 in nb-15 = 1168 in nb-10 = 4 \times 292 in the exponent series, = 4 \times \text{inosine} + 4 \times \text{orotate} = \text{the sum of ams with 3rd base A/G (A or G) or U/C +1.)}

5. Number of C-atoms in R-chains as basis for divisions:

In file 04, para. 3, the ams were ordered after number of C-atoms in their R-chains and their mass summed. This division did not concern codon distribution but seemed related to the ES-series with certain assumptions. Here C for carbon. (8 ams with 4 C in R-chains got the sum 584 2 \times 292.)

Phe and Tyr are synthesized as 3C- plus 4C-molecules, hence positioned between 4C- and 3C-groups. Trp as 3C + 4C + 5C - 1C. Trp gets its B-chain from Ser, shares codon with Cys and can brake down to Ala, hence here regarded as "meeting the other way around", added to the 1C group.
Fig. 18-4a: Transformations along the ES-chain as a nxC-chain:

\[
\begin{array}{cccccc}
C4 & C3 + C0 & C2 & C1 & + C9 = Trp \\
584 & 198 & 306 & 162 & 124 & 130 \\
584 & 504 & 286 &
\end{array}
\]

\[
\begin{array}{c}
2 \times 544 \\
1088
\end{array}
\quad \quad
\begin{array}{c}
2 \times 208 \\
416
\end{array}
\]

\[
584 = 1088 - 584 + 198 + 306
\]

10-base $\rightarrow$ 8-base

\[
198 = 306
\]

10-base $\rightarrow$ 8-base

\[
\begin{array}{c}
306 \\
8\text{-base}
\end{array}
\quad \quad
\begin{array}{c}
286 \text{ (re-written)} \\
8\text{-base}
\end{array}
\]

\[
286 = 456 = 306 + 130 \ (\text{Trp})
\]

10-base $\rightarrow$ 8-base

\[
\begin{array}{c}
C2 \\
162 = 242
\end{array}
\]

\[
\begin{array}{c}
C1 \\
124 = + 174 = 416
\end{array}
\]

10-base $\rightarrow$ 8-base

\[
174 \rightarrow 256 = 124 + 130 + 2H
\]

10-base $\rightarrow$ 8-base

Fig. 18-4b: Cf. triplet sums, file 15, numbers 714 and 792:

\[
\begin{array}{cccc}
C4 & C3 + C0 & C2 & C1 + C9 \\
584 & 198 & 306 & 124 + 130 \ (\text{Trp}) \\
\end{array}
\]

\[
790 \sim C1 + U2
\]

\[
714 \sim C1 + A2
\]

(C here for ami groups)
Fig. 18-4c: \textit{nxC-atoms - three more details}:

The Exponent series:

\[
\begin{array}{cccccc}
292 & 252 & 208 & 159/158 & 100 \\
\downarrow & & & & \\
544 & 286 & 258 \rightarrow 258 (+1) & = C2 + C1 \\
& & & & \\
& & & & \\
& & & & \\
467 (208 + 259) & = C3 + C2 & \rightarrow = 305 + 162
\end{array}
\]

Different intervals in transformations through re-writings:

\[
\begin{array}{c}
584 \rightarrow 1088 \sim 1 \sim 890 \\
\downarrow & \\
198 \text{ out of re-writing}
\end{array}
\]

\[
\begin{array}{c}
584 \rightarrow 890 \\
306 = C3 + C0
\end{array}
\]

\textbf{Trp:}

\[
\begin{array}{c}
504 \leftarrow 416 \\
\downarrow & \\
88 \rightarrow 139 \text{ Trp}
\end{array}
\]

6. \textbf{B-chains:}

6.1 \textbf{Number 752, sum of first 3 numbers in the ES-chain:}

752 from nb-16 to nb-10 gives the total 1772 of 24 B-chains unbound:

\[
\begin{array}{c}
292-16 \rightarrow 658-10 \\
252-16 \rightarrow 594-10 \\
208-16 \rightarrow 520-10 \ldots \text{sum 1772, 24 B-chains unbound}
\end{array}
\]

Cf. that 752: nb-10 gave 2848 in nb-6, i.e., R+B-chains of 24 ams bound:

\textbf{Fig. 18-5:}

\[
\begin{array}{c}
\text{nb-16} \\
\frac{1}{2} \times 752 \rightarrow 886, \quad \times 2 = 1772, \text{24 unbound B-chains}
\end{array}
\]

6.2 \textbf{A single, unbound B-chain = 74:}

Two sets of the 4 RNA-bases, sum 1018, gave in nb-8 the sum of 24 B-chains unbound = 1772. A single unbound B-chain à 74 gives the sum of 2 bound B-chains.
Fig 18-6: From one unbound B-chain to two bound ones:

\[
\begin{align*}
\text{nb-10} & \quad \text{nb-8} \\
74 & \quad \longrightarrow \quad 112 = 2 \times 56 = 2 \text{ B-chains bound}
\end{align*}
\]

Cf. U\text{-base} = 112 A and exchange T to U in mRNA for synthesis.

6.3 Halvings of 2 x 5' 584 transformed to unbound and bound B-chains:

Fig. 18-7: From number 5' in the ES-chain to B-chains in groups of 6:

\[
\begin{align*}
\text{nb-10} & \quad \text{nb-8} \\
2 \times 292 & \quad \longrightarrow \quad 584 \rightarrow 1088 \sim 888, \ x \ 2 = 1776 = 24 \text{ B-chains à 74 A} \\
292 & \quad \longrightarrow \quad 444 = 6 \text{ B-chains à 74 A} \\
292, \ x \ \frac{1}{2} & \quad 146 \quad \longrightarrow \quad 222 - 3 \text{ B-chains unbound à 74 A} \\
\downarrow & \\
222 & \quad \longrightarrow \quad 336 = 6 \text{ B-chains bound à 56 A}
\end{align*}
\]

6.4 Total B-chains unbound times 2 from the 4 bases:

Fig. 18-8:

\[
\begin{align*}
\text{10-base} & \quad \text{8-base} \\
\text{4 G} & \quad 604 \quad \longrightarrow \quad 1134 \\
\text{4 C} & \quad 444 \quad 674...\text{sum} 1808 \sim 1810 \\
\text{4 U} & \quad 448 \quad 700 \\
\text{4 A} & \quad 540 \quad 1034...\text{sum} 1734
\end{align*}
\]

\[\rightarrow 3544 = 2 \times 1772, \text{ B-chains}\]
6.5 Total of bound B-chains = 1344 from the bases:

Fig. 18-9:

\[
\begin{align*}
10\text{-base} & \quad 8\text{-base} \\
194 & \quad \leftarrow 302 \quad 2 \times G \\
184 & \quad \leftarrow 270 \quad 2 \times A \\
146 & \quad \leftarrow 222 \quad 2 \times C \\
+ 148 & \quad \leftarrow 224 \quad 2 \times U \\
\hline
672 & \quad \Rightarrow x 2 = 1344, = 24 \text{ B-chains bound}
\end{align*}
\]

\[
\begin{align*}
388 & \quad \leftarrow 604 \quad 4 \times G \\
+ 352 & \quad \leftarrow 540 \quad 4 \times A \\
\hline
740 & \quad \Rightarrow 1344 \quad = 24 \text{ B-chains bound}
\end{align*}
\]

6.6 Inosine 136 in repeated steps gives B-chains bound or unbound:

Inosine or Hypoxanthine 136 A (1/4 x 544) may give both B-chain numbers 1344 and 1772 bound and unbound through 4 steps of transformations:

Fig. 18-10:

\[
\begin{align*}
10\text{-base} - 8\text{-base} \\
135 & \rightarrow 208
\end{align*}
\]

\[
\begin{align*}
10\text{-base} - 8\text{-base} / 10\text{-base} - 8\text{-base} / 10\text{-base} - 8\text{-base} \\
208 & \rightarrow 320 \quad 320 \rightarrow 500 \sim 480 \\
480 & \rightarrow 740 \quad 740 \rightarrow 1344
\end{align*}
\]

\[
\begin{align*}
10\text{-base} - 6\text{-base} / 10\text{-base} - 8\text{-base} / 10\text{-base} - 8\text{-base} \\
136 & \rightarrow 344 \quad 344 \rightarrow 530 \sim 528 \quad 528 \rightarrow 1020 \sim 1018 \quad 1018 \rightarrow 1772*
\end{align*}
\]

*Note that without rewritings 530 ~ 528 and 1020 ~ 1018 we get 1776 (24 x 74 A).
7. Displacements between 1st and 2nd base order: Numbers 220 - 26:

7.1 Relations between displacements 220 and 26:

Fig. 18-11:

\[ \text{G1 + A1} \quad \rightarrow \quad \text{G1 + A2} \]
\[ \text{C1 + U1} \quad \rightarrow \quad \text{C2 + U2} \]
\[ \text{G1 } \rightarrow \text{ G2 = 220}, \quad \text{C1 } \rightarrow \text{ C2 } = -220 \quad \text{G+C-coded ans = 544} \]
\[ \text{A1 } \rightarrow \text{ A2 = 26}, \quad \text{U1 } \rightarrow \text{ U2 = -26} \quad \text{A+U-coded ans = 544 + 2 x 208} \]

\[ 220 - 26 = 194, \text{ the difference } 4 \times 2 \text{ in the division of number } 416 \text{ in the exponent series, } (A+U) - (G+C): \]
\[ (A1 - G1) - (U1 - C1) = 194 - 2 = 306 - 110 \]
\[ (A2 - G2) - (U2 - C2) = 194 - 2 = 112 + 304 \]

\[ 194 = 2 \times 97; \text{ an } \text{HPO}^- \text{-group}; 194 \text{ also a charged ribose-}P\text{-group in nucleotides}. \]

Fig 18-12:

Number 220 divided \[ N = 100 (101), \text{ Z = 120 (119) in G-C-group} \]
\[ N = 23 (22), \text{ Z = 3 (4) in A-U-group}. \]

G+C-group:
\[ \begin{array}{cccc}
10-base & 8-base & 10-base & 8-base \\
\text{100} & \rightarrow & \text{144} & \rightarrow & \text{220} \\
\text{1} \rightarrow \text{displacement} & \text{Z-number} & \text{120} & \leftarrow \text{1} \\
\end{array} \]

The relations between displacement 220 in the G+C-group and 26 in the U+A-group could be explained through only a minus 1 in N- and Z parts and the results in nb-8 through transformations.

Regard number 144 in figure 18-11 above divided in 64 and 80:

Fig. 18-13: How the displacement 220 and 26 could be explained through -1:

\[ \begin{array}{cccc}
10-base & 8-base \\
\text{64} & \text{100 N} \\
\text{1} \rightarrow & \text{23 N} \\
\text{63} & \text{77} \\
\text{144} & \text{120 Z} \\
\text{1} \rightarrow & \text{3 Z} \\
\text{79} & \text{117 Z} \\
\end{array} \]

A1 - A2: \[ N = 22, \text{ Z = 4} \]

Fig. 18-14:

\[ \text{HPO}_2 = 64, \quad \text{PO}_2^- = 63, \quad \text{HPO}_3^- = 80, \quad \text{PO}_3^- = 79 \]
\[ 64 + 80 = 144 = 220 \text{ in nb-8, 77 + 117 = number 194, 220 - 194 = -26}. \]
7.2 The number 220 in displacements in group G+C:

Fig. 18-15:

**Number 220:** $G1 \rightarrow G2$, $C1 \leftarrow C2$, connected with the sum of ams G+C 544:

In relation to numbers of the exponent series:

\[
\begin{array}{ccc}
16\text{-base} & 10\text{-base} & 6\text{-base} \\
220 & 544 = 292 + 252 & 1040 = 5 \times 208 \\
292 & 84 & 220 = 5 \times 44, \text{the interval } 252 - 208. \\
208 & 544 \\
\end{array}
\]

220 in nb-15: a transition version or reference for the G+C-guided groups 544 between 1\textsuperscript{st} and 2\textsuperscript{nd} base order:

\[
\begin{align*}
544 + 220 &= 764 = C1 + G2 = 353 + 411, \text{ difference } 58 \\
544 - 220 &= 324 = G1 + C2 = 191 + 133, \quad -"- \quad 58
\end{align*}
\]

220 in nb-6: representing interval 84 (plus/minus) in the other context where number 544 is received in nb-6, from 208 in nb-10.

**A note:** Could different divisions of number 544 towards lower numbers in the exponent series be connected with different number base systems? For instance:

- 544 divided: 292, 252 = "5" - "4"
- 544 - "" - 336, 208 = ("5 + 4 - 3") - "3"
- 544 - "" - 177, 367 = ("5 + 4") - ("3 + 2") = ("3 + 2")

\[
\begin{array}{c|c|c}
10\text{-base} & 8\text{-base} \\
101 & 44 & 145 \\
\end{array}
\]

G1 = 292 + 101
C1 = 252 + 101
G1 = 367 - 176 = 191 = G1
C1 = 177 + 176 = 353 = C1

Number 220 as a nb-6 number: 6-base

\[
220 \sim 176, \quad G1 = 367 - 176 = 191
\]

Or: In 2\textsuperscript{nd} base order, using the interval 44 in the transformation nb-10 - nb-8 above? The 3\textsuperscript{rd} division of number 544 in the exponent series: 177 - 367;

\[
\begin{align*}
(\text{"5 + 4"}) & - (\text{"3 + 2"}) = 177 - 44 = 133 = C2, \\
(\text{"3 + 2"}) & = 367 + 44 = 411 = G2
\end{align*}
\]

8. The 4 double-coded ams, sum = 246

The sum of R-chains of the 4 ams with two different codons are "also" 246, i.e., the sum of displacements 220 and 26 above.

All 4 may become 37 in different nb-systems.

Fig. 18-16:

\[
\begin{array}{c|c|c}
10\text{-base} & 8\text{-base} \\
\text{Arg AG} & 101 & 145 = \text{Ser 31} + \text{Leu 57} + \text{Ile 57}
\end{array}
\]

\[
\begin{array}{c|c|c|c|c}
10\text{-base} & 8\text{-base} & 10\text{-base} & 6\text{-base} \\
\text{Arg AG} & 37 & 101 & 57 \\
\text{Ser AG} & 31 & 37 & \sim 57 = \text{Leu2, Ile2 in nb-10}
\end{array}
\]
19- P- phosphorous groups - Coenzymes - Nucleotides - Met AUG

1. P-groups, the single, "inorganic" phosphorous groups:

Fig 19-1: P-groups:

a. $\text{H}_2\text{PO}_4^-$ group, 97 A, $\text{PO}_3^{2-}$ group, 79 A, $\text{HPO}_3^-$ group = 80 A

10-base 8-base
$\text{HPO}_3^- $ group 80 $\rightleftharpoons$ 98 $\cong$ 120 $=$ $\text{H}_3\text{PO}_4$ 98 A
$\downarrow$
$=$ $\text{HPO}_3^- + \text{H}_2\text{O} = \text{H}_3\text{PO}_4$
$\text{H}_2\text{O}$ 18 $\rightleftharpoons$ 22, difference

10-base 8-base
$\text{PO}_3^{2-}$ group, 79 A: 79 $\longrightarrow$ 97 $\cong$ 117 $(79 + 117 = 2 \times 98 - 2 \text{H}_3\text{PO}_4)$
$\downarrow$
$\text{HPO}_3^- $ group, 80 A: 80 $\longrightarrow$ 120 $+$ 117
$\downarrow$
2 P-groups 79 + 80 = 159 $\longrightarrow$ 237 = 3 P-groups 79

(Energy storing in the bindings.)

8-base
79 $\cong$ 81 = + 2 H

b. Coenzyme groups:

$\text{H}_3\text{PO}_4 = 98 \longrightarrow$ 372 = ribose-P-P-P in coenzymes of bases (-TP)
$\text{HPO}_3^- = 80 \longrightarrow$ 292 = ribose-P-P = " " (-DP)

10-base
$\text{HPO}_3^- = 80 \longrightarrow$ 212 = ribose-P = " " (-MP)

c. NAD (664 A) - NADP (744 A) from P-groups:

16-base 6-base
$\text{H}_3\text{PO}_4$ : 98 $\longrightarrow$ 372 $\cong$ 412
9-18 $+$ $+$ $<$ difference 80 $\cong$ $\text{HPO}_3^-$
$\text{HPO}_3^- : 80 $\longrightarrow$ 292 $\cong$ 332
$=$ 664 744
$=$ NAD NADP in mb-10 system

16-base 10-base 8-base
NADP 744 $\longrightarrow$ 160 $\longrightarrow$ 3504
$=$ 2 $\times$ 372 $=$ 5 $\times$ 372
$=$ 12 $\times$ 292
372 = P-P-P-ribose, 292 = P-ribose.

d. The exponent series: 10-base 6-base
interval "3 - 2" = 49 $\longrightarrow$ 81 = $\text{H}_2\text{PO}_4^- $

A form of life was found some years ago, said to use arsenic instead of phosphorus (P), i.e. next higher element in the phosphorus group of elements in the periodic system. If so, it could of course lead to the conclusion that all such transformations between
masses including phosphorus are irrelevant and in any case no necessary condition for life as an eventual part of a reference system.
Yet, phosphorus could have had a decisive role at the very creation of the genetic code, while this not excludes further evolution?

2. Coenzymes of the bases, -MP, -DP, -TP:

2.1 Tables of masses of the coenzymes

Fig. 19-2: Survey

Survey of mass numbers (A) in base-10 system:

4 - 5 code bases, mass numbers, including +1 for bond to ribose:

G 151, A 135, U 112, C 111...Σ 509, +1 125...Σ 635

Sum of 2 x 24 bases, 1st and 2nd in the codons:

15 A + 13 U + 11 G + 9 C = 6141

Coenzymes of the code bases:

\[
\begin{array}{ccc}
-TP & -DP & -MP \\
GTP & 523 & GDP & 443 & GMP & 363 \\
ATP & 507 & ADP & 427 & AMP & 347 \\
UTP & 484 & UDP & 404 & UMP & 324 \\
CTP & 463 & CDP & 403 & CMP & 323 \\
\hline
1997 & 1677 & 1357 \\
TTP & 498 & TDP & 418 & TMP & 338 \\
\hline
= 2495 & 2095 & 1695 \\
\end{array}
\]

2.2 From 4 bases to their mass as coenzymes

Fig 19-3: 509 - 1357, 4 coenzymes -MP:

\[
\begin{array}{cccc}
4 \text{ RNA-bases} & 10\text{-base} & 8\text{-base} & 6\text{-base} \\
G & 151 & 227 & 411 & 411 \\
C & 111 & 157 & 303 & ~263 \\
A & 135 & 207 & 343 & 343 \\
U & 112 & 160 & 304 & ~264 \\
\hline
509 & 751 & 1361 & 1281 \\
\hline
\end{array}
\]

\[
751 \rightarrow 1357 = 4 \text{ RNA-nucleotides charged -1.}
\]

2.3 Expansion of bases nb-10 to nb-8 adds thePx-ribose groups:

Some transformations from sums of the bases to sums of their appearance as coenzymes are shown in figures below. Note expansions where 212-292-372 correspond to the P(P(P)-ribose groups:
Fig. 19-4: From the bases to coenzymes -MP, -DP, -TP

-MP:

\[
\begin{array}{c|c|c|c}
4 \text{ RNA-bases:} & 509 & \rightarrow & 751 \\
\text{separately transformed to} & 751 & \rightarrow & 1357 \\
& 4 \times 212 & & \\
212 = P-\text{ribose} & & \\
\end{array}
\]

-DP:

\[
\begin{array}{c|c|c|c|c}
2 \times 4 \text{ RNA-bases:} & 1018 & \rightarrow & 1772 & 1772 \\
= 2 \times 4 \text{ RNA-bases} & & & 3354 = 2 \times 1677 \text{ }^1 & \\
\text{as coenzymes -DP} & & 8 \times 292 & \rightarrow & \\
292 = P-P-\text{ribose} & \text{Ribose-P-P = -DP-form = 292 = "5" in the exponent series (= 131+80+81)} & (1772 = 24 \text{ amino B-chains}) & \\
\end{array}
\]

-TP:

\[
\begin{array}{c|c|c|c|c|c|c}
G_8+C_6: & 384 (386) & \rightarrow & 561 (\pm 1) & & & 1997 \\
A_8+U_8: & 367 & \rightarrow & 557... \text{Sum } 1158 = 1160 & \rightarrow & 2188 & \\
\downarrow & & & & & \downarrow \\
2188 & \rightarrow & 3994 = 2 \times 1997 & & & \\
\text{= 2 \times 4 RNA-bases as coenzymes -TP} & & & & & \\
\text{4 bases nb-10:} & 509 & \leftarrow & 4 \times 372 & \rightarrow & 1997 & \\
372 = P-P-\text{ribose} & & & & & \\
\end{array}
\]

2.4 5 bases to 5 coenzymes -TP:

Fig. 19-5:

\[
\begin{array}{c|c|c|c|c}
5 \text{ bases with T-base} & 635 & \rightarrow & 1173, \sim 973 & \rightarrow & 2495 = 5 \text{ bases as coenzymes -TP} \\
\downarrow & & & & & \\
5 \times 372 & \rightarrow & 1 & \left[2495, \sim 2.535 = 5 \times 507, \\
\text{= 5 x P-P-P-ribose} & & & & & \\
507 = \text{ATP}_{10} \right] \\
\end{array}
\]

2.5 4 RNA-bases giving 5 coenzymes -DP-MP in nb-6:

Fig. 19-6:

\[
\begin{array}{c|c|c|c|c|c}
G+C: & 262 & \rightarrow & 386 & & & \\
>753 / 753 & \rightarrow & 2095 & \rightarrow & 5 \text{ bases as coenzymes -DP} & \\
\downarrow & & & & & \\
\sim 1695 & \rightarrow & 5 \text{ bases as coenzymes -MP} & \\
\text{Re-writing gives } 5 \times 30, \sim 5 \text{ P-groups (HPO}_3^-) & & & & & \\
\end{array}
\]

\text{ }^1 \text{The number 1677 is used in the context of finding the exponent series for the RNA bases, which leads to the formation of coenzymes such as MP, DP, and TP. The process involves specific transformations of the RNA bases into coenzymes through various reactions.

The figure illustrates the conversion of bases into coenzymes, showing the steps from RNA bases to coenzymes through the intermediates -MP, -DP, and -TP. The respective equations and transformations are detailed, highlighting the role of these coenzymes in biological processes.

The numbers and symbols used in the figure represent specific biological processes and transformations, which are critical for understanding the roles of these coenzymes in cellular functions. The figure serves as a visual aid to comprehend the complex interactions between RNA bases and coenzymes, facilitating the study of biochemical pathways.}
2.6 From 751, the sum of 4 bases in nb-8, to 5 bases as coenzymes -TP and to 6141, the sum of 48 codon bases:

Fig. 19-7:

\[ \begin{array}{c}
10\text{-base} & \rightarrow & 8\text{-base} \\
751 & \rightarrow & 1357 = 4\text{ coenzymes -MP (G, A, U, C)} \\
\downarrow & & \\
1357 & \rightarrow & 2495 = 5\text{ bases as coenzymes -TP (including TTP)} \\
\downarrow & & \\
& & 5\text{-base} \\
& \rightarrow & 6141 = 48\text{ code bases, }1^{st}\text{ and }2^{nd}, \text{ for }24\text{ arms}
\end{array} \]

6141 \equiv 15\text{ A} + 13\text{ U} + 11\text{ G} + 9\text{ C}:

3. Nucleotides:

3.1 Survey of nucleotides in chain binding:

Fig 19-8:

Nucleotides in chain binding:

\begin{align*}
\text{RNA}: & \quad \text{G 345, A 329, U 306, C 305...} \quad \Sigma \ 1285, \text{ ionized -1 in P-groups} = 1281 \\
& \quad \text{cGMP = 345, cAMP = 329} \\
\text{DNA}: & \quad \text{G 329, A 313, T 304, C 289...} \quad \Sigma \ 1235, \text{ ionized -1 in P-groups} = 1231
\end{align*}

3.2 Two sets of the nucleotides from 2 sets of the bases (from file 17):

The four RNA-nucleotides in chain-binding and uncharged = 345, 329, 306 and 305 = 1285.

The four DNA-nucleotides (= 1285 - 4 x 16 + 14 in T-base) = 1235.

Two sets of RNA-nucleotides are given from 2 "times G- and C-bases in three steps nb-10 \rightarrow 8, as two sets of DNA-nucleotides from 2 times A- and U-base:

2G + 2C = 768 in nb-8:

\[768 - 10 \rightarrow 1400 - 8 / 1400 - 10 \rightarrow 2570 - 8 = 2 \times 1285 \sim \text{RNA-nucleotides}\]

2U + 2A = 734 in nb-8:

\[734 - 10 \rightarrow 1336 - 8 / 1336 - 10 \rightarrow 2470 - 8 = 2 \times 1235 \sim \text{DNA-nucleotides}\]
3.3 ES-number 752 gives in two steps the sum of 4 nucleotides in DNA and RNA:

Fig 19-9:

Nucleotides, 4 DNA 1235 + 4 RNA 1285 = 2520:

\[
\begin{align*}
4 \text{ bases in nb-8:} & \quad 752 \quad \rightarrow \quad 1360 \\
751/753 & \quad \downarrow \\
1360 & \quad \rightarrow \quad 2520 = 1285 + 1235
\end{align*}
\]

3.4 The 4 bound RNA-bases in nb-16 gives the 4 RNA-nucleotides in nb-10:

Fig. 19-10:

\[
\begin{align*}
4 \text{ RNA-bases bound} & \quad 16-\text{base} \quad 10-\text{base} \\
\quad 505 & \quad \leftarrow \quad 1285 \quad = \text{4 RNA-nucleotides, not ionized} \\
780 = 4 \times 195; & \quad \downarrow \\
\text{P-ribose-groups in chain bindings: ribose}131 + \text{HPO}_2\sim \quad 64
\end{align*}
\]

3.5 Bases read as nb-8-numbers, giving cGMP and cAMP in nb-10:

Fig. 19-11: \(\text{cGMP - cAMP}\):

\[
\begin{align*}
10-\text{base} & \quad 8-\text{base} \\
167 & \quad 247 \quad \text{A+U} \\
178 & \quad 262 \quad \text{G+C} \\
345 & \quad 509 \\
329 & \quad 509 \quad \text{cGMP = G-nucleotide} \\
\text{329 = cAMP = A-nucleotide} & \quad 6-\text{base}
\end{align*}
\]

*Base pair: \(262 \quad \Rightarrow \quad 674 = 2/3 \times 1011, \text{sum of exponent series.}
(674 also the number of atoms in 2 x 24 codon bases, 1st and 2nd, in the codons.)*

4. Met - codon AUG and tRNA-ends ACC:

AUG, the codon for Meth, leads the string at transcriptions from DNA. Chain-bound nucleotides AUG, transformed from nb-10 to nb-8 give the whole sum of 24 ams R, 1504. There is also the equivalence between the 4 bases 509 in nb-8, the A-nucleotide 329 in nb-10 and Meth 149 (R+B) in nb-16,
Fig 19-12: AUG, codon for Meth:

a. Meth as a kind of reference - or the opposite, the bases a reference to Meth?

<table>
<thead>
<tr>
<th>16-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>149</td>
<td>509</td>
</tr>
</tbody>
</table>

= 4 RNA-bases in base-10 system

<table>
<thead>
<tr>
<th>16-base</th>
<th>10-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>149</td>
<td>329</td>
</tr>
</tbody>
</table>

= cAMP, also = A-nucleotide

The exponent series:

<table>
<thead>
<tr>
<th>16-base</th>
<th>10-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>&quot;5&quot; = 292</td>
<td>658</td>
</tr>
</tbody>
</table>

= 2 x 329 (~ cAMP)

b. A-U-G-nucleotides separately transformed:

<table>
<thead>
<tr>
<th>Nucleotides</th>
<th>10-base</th>
<th>2-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>329 A</td>
<td>511</td>
<td>509</td>
</tr>
<tr>
<td>306 U</td>
<td>462</td>
<td>973</td>
</tr>
<tr>
<td>345 G</td>
<td>531</td>
<td>531</td>
</tr>
</tbody>
</table>

= 1504 = 24 ans K

The "triplet series" 543-432-321-210:

A+U+G: the mass numbers of the bases interpreted as base-8 numbers:

<table>
<thead>
<tr>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>93</td>
<td>135: A</td>
</tr>
<tr>
<td>74</td>
<td>112: U</td>
</tr>
<tr>
<td>+ 105</td>
<td>151: G</td>
</tr>
</tbody>
</table>

= 272 < 398

272 = 1/2 x 544, "5" + "4" in the exponent series

5. A-C-C - ends of tRNA:

A-C-C make up the common ends of tRNAs and one may ask why? The three bases (as unbound) give the sum 544 -/+1, the sum 5' + 4', 292 + 252 in the ES-series, when transformed in nb-8.

Fig 19-13: tRNA-ends ACC:

c. ACC-ends of tRNAs:

<table>
<thead>
<tr>
<th>nb-10</th>
<th>nb-8</th>
</tr>
</thead>
<tbody>
<tr>
<td>A+C+C-bases: 357</td>
<td>544 + 1</td>
</tr>
</tbody>
</table>

ES-series

A 135 \(\rightarrow\) 207 = 208 -1

or ACC: < 2 C 222 \(\rightarrow\) 356 = 544 - 208

Cf. mass numbers for A and C from Triplets, file 21;

012 + 123 = 135 (A-base), + 234 = 357. Two of the intervals in the steps = 2 x 111 (2 x C-base).
20. Additions to files 17 - 18

1. Rewritings

1.1 Rewriting G - C:

G- and C-bases transformed further to nb-6 becomes sums in later steps of the ES-chain, through rewritings, implying -44:

Fig. 20-1:

<table>
<thead>
<tr>
<th>544</th>
<th>460</th>
<th>367</th>
<th>259</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>292</td>
<td>252</td>
<td>208</td>
<td>159/158</td>
</tr>
</tbody>
</table>

G-base 151 = 411* - 367 = "3 + 2" re-written (367 = A_g + U_g) 1-108

C-base 111 = 303* - 259 = "2 + 1" re-written

*411 = sum of G2-coded ams.

Cf. 44 = the interval 252 - 208 = 4' - 3'. G1 + C1 = 544 divided 177 + 367:

C2 = 177 - 44 = 133

G2 = 367 + 44 = 411

1.2 Number 65 - 101 - 81, bases and codon-grouped ams:

Fig. 20-2:

292 - 101 = 191 = G1-coded ams R
252 + 101 = 353 = C1-coded ams R

\[ \sqrt{16\text{-base}} \rightarrow \text{10\text{-base}} \rightarrow \text{8\text{-base}} \rightarrow \text{6\text{-base}} \]

292 - 65 = 227 = C_g
272 + 65 = 337 = (U+C)_g

252 + 65 = 317 = C_g + U_g
272 + 65 = 337 = (U+C)_g

= 544

*Cf. ams-groups: 272 - 81 = 191 = G1. 544 - 81 = 463 = U1.


[U 112 and C 111 = 223, transformed together = 337-8.
Further transformed to nb-6 = 1011= total sum of the ES-chain in nb-10..]
1.3 Simple rewriting of $2 \times 5'$, $4'$, $3'$ in the ES-chain, taken as nb-8 numbers:

This rewriting gives closely the two sets of ams, sums of G1+G2, C+C2 etc.

$$2 \times 292-10: = 584. \quad 584-8 \sim 604 = G1 + G2 + 2; \quad \rightarrow 604 + 416 = 1020 = A1 + A2$$

$$2 \times 252-10 = 504, \quad 504-8 \sim 484 = C1 + C2 - 2; \quad \rightarrow 484 + 416 = 900 = U1 + U2$$

**Fig. 20-3:**

<table>
<thead>
<tr>
<th>8-base</th>
<th>$\implies$</th>
<th>8-base</th>
<th>Ams-groups R-chains in base-10 system</th>
</tr>
</thead>
<tbody>
<tr>
<td>2 x 292:</td>
<td>584</td>
<td>$\sim$ 604 =</td>
<td>G1 + G2 + 2</td>
</tr>
<tr>
<td>2 x 252:</td>
<td>504</td>
<td>$\sim$ 484 =</td>
<td>C1 + C2 - 2</td>
</tr>
<tr>
<td>2 x 208:</td>
<td>416</td>
<td>+ 604 = 1020 =</td>
<td>A1 + A2</td>
</tr>
</tbody>
</table>

| 8-base | 900 = U1 + U2 | (463 + 437) |

1.4 From A-base to 273, mean value of 2 ams R+B:

**Fig. 20-4:**

<table>
<thead>
<tr>
<th>10-base</th>
<th>8-base</th>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>A-base:</td>
<td>135</td>
<td>$\implies$ 207, $\sim$ 187 re-written</td>
<td>187</td>
</tr>
</tbody>
</table>

Mean value of 2 ams R+B in base-10 system

2. Parents of the codon bases, Inosine 136 and Orotate 156:

It was found (file 03) that the sum 292 of the parens to the base-types, when distributed to following numbers in the ES-chain, x 2, gave the codon-groups of ams C1 + U1 and G1 + A1:

**Fig. 20-5:**

| 292 | $\implies$ 252 | $\implies$ 208 | “5-4-3” in the exponent series |
| 1 $\implies$ + 156 $\implies$ + 136 | Orotate and Inosine added |

<table>
<thead>
<tr>
<th>Sums:</th>
<th>498</th>
<th>344</th>
</tr>
</thead>
<tbody>
<tr>
<td>x 2 =</td>
<td>816</td>
<td>688</td>
</tr>
<tr>
<td>= C1+U1</td>
<td>G1+A1</td>
<td></td>
</tr>
</tbody>
</table>

**Fig. 20-6:** The nb-10 and nb-8 numbers added (!), a curious operation:

<table>
<thead>
<tr>
<th>10-base</th>
<th>8-base</th>
<th>6-base</th>
<th>Mixed nb-10 + nb-8 numbers:</th>
</tr>
</thead>
<tbody>
<tr>
<td>Inosine</td>
<td>136 $\implies$ 208 $\implies$ 344</td>
<td>$\rightarrow$ 136 + 208 = 344, x 2 = 688 = G1 + A1</td>
<td></td>
</tr>
<tr>
<td>Orotate</td>
<td>156 $\implies$ 234 $\implies$ 416</td>
<td>$\rightarrow$ 156 + 234 = 390, = 408 read as nb-8, x 2 = 816 = C1+U1</td>
<td></td>
</tr>
</tbody>
</table>

3. Number 888 in different appearances:

**Fig. 20-7:**

- 888 in nb-10 = 543 + 345, numbers of the triplet series = 12 x B-chains = 74 A
- 888 in nb-8 = 1110₂ = 584 in nb-10 = 2 x 292 in the exponent series.
- 888 in nb-5 = 344 in nb-10 = 888 - 544. 344 x 2 = 688 = ams-groups G1 + A1.
- 344 in nb-6 = 136 (= Inosine) in nb-10 (1/4 x 344).
- 888 in nb-16 = 2184₁₀ = 4 x 546, 8 x 273 (the mean value of 2 ams R+B = 273)
4. Difference of bases in nb-10 and nb-8, read in nb-16, gives 2 x 272 = 544:

Fig. 20-8:

<table>
<thead>
<tr>
<th>nb-3</th>
<th>nb-10</th>
<th>16-base</th>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>G: 227</td>
<td>- 151 = 76</td>
<td>76</td>
<td>118</td>
<td>156</td>
</tr>
<tr>
<td>C: 157</td>
<td>- 111 = 46</td>
<td>46</td>
<td>70</td>
<td>106...sum 272</td>
</tr>
<tr>
<td>U: 160</td>
<td>- 112 = 48</td>
<td>48</td>
<td>72</td>
<td>110</td>
</tr>
<tr>
<td>A: 207</td>
<td>- 135 = 72</td>
<td>72</td>
<td>114</td>
<td>162...sum 272</td>
</tr>
</tbody>
</table>

374

544 = ans G+C (R)

5. DNA-bases transformed giver as intervals the G+C- and T+A-pairs and 752:

Fig. 20-9:

4 DNA-bases: 490 <--- 523 ---< 1013

490 <--- 262 ---< 752 = base pair A_{10}+T_{10}

base pair G_{10}+C_{10}

6. Sum of the whole ES-chain 1011:

6.1 N +3 and Z +3 from the ES-chain transformed separately and whole:

Fig. 20-10:

10-base 292 252 208 159 100

8-base 444 374 320 237 144

\[ \text{Sum = 1011} \]

10- to 8-base, whole sum: \[ \text{1011} \longrightarrow 1763 = \text{Z + 3} \]

752

\[ \frac{1}{2} \times 24 \text{ ans } R \]

Cf. sum 3282 and sum of triplet series in

6.2 DNA-bases as nb-6 numbers give the sum of the ES-chain:

Fig. 20-11:

10-base 67 43 59 + 34 = 223

6-base 151 111 135 126 T-base

223 ---< 1011 = the sum of the whole exponent series.

223 = C_{111} + U_{112}.\]
7. Totals, two mere operations

7.1 From ES-number 5' to 1/3 of the total 3276:

Fig. 20-12:

\[
\begin{align*}
\text{16.-base} & \quad \text{10.-base} & \quad \text{8.-base} \\
292 & \quad \rightarrow & \quad 444 \\
444 \times 4 & = 24 \text{ B-chains} & \text{à 74 A.}
\end{align*}
\]

7.2 G+C-bases transformed two times give 2 times total R 1504:

Fig. 20-13:

\[
\begin{align*}
\text{Base pair} & \quad \text{G+C} & \quad \text{262} & \quad \rightarrow & \quad 386 \\
\downarrow & \quad & \quad & \quad & \\
386 \times 4 & = 1544 & \quad \rightarrow & \quad 3008 \\
3008 & = 2 \times 1504, \text{ R-chains}
\end{align*}
\]

8. Individual R-chains of ams related through transformations?

Transformations often imply additional numbers equivalent with molecules, as e. g. plus CH2. There are formally of course a lot of transformations possible between individual ams, only some of which may correspond to biochemical relations. Some examples are shown in the figure below, here regarding R-chains:

It could be added that all four ams with double codons may transformed get the number 37: Ser AG 31-10 = 37-8, Arg AG 101-6 = 37-10, Ile and Leu 57-6 = 101-6 = 37-10, (file 18, para. 8).
Fig 20-14:

R-chains:

\[
\begin{array}{cccccccc}
10 \rightarrow 8 & 10 \rightarrow 8 & 6 \rightarrow 10 & 6 \rightarrow 10 & 6 \rightarrow 10 & 6 \rightarrow 10 \\
49 \rightarrow 5 & 9, \sim 61 \rightarrow 75 \rightleftharpoons 47 \leftarrow 31 \leftarrow 19 \leftarrow 15 \\
| Asp & Meth & Cys & Ser & Ala \\
| 10 \rightarrow 8 & 10 \rightarrow 8 & 10 \rightarrow 8 & 10 \rightarrow 8 & 10 \rightarrow 8 \\
73 Glu / Lys & 31 \rightarrow 37 \rightarrow 101 (\sim 61, \sim 57) & Ser & Arg \\
10 \rightarrow 6 & 10 \rightarrow 6 \\
49 \rightarrow 81 & 81 \sim 101 & 81 \sim 101 \\
8 \rightarrow 16 & 8 \rightarrow 16 \\
49 \rightarrow 31 = Ser & 49 \rightarrow 31 = Ser \\
101 (Arg) \rightarrow 65 & 8 \rightarrow 10 & 8 \rightarrow 10 \\
100 \rightarrow 64 & 53 \rightarrow 43 Pro before ring binding & 52 \rightarrow 42 Pro \\
108 \rightarrow 110 & 110 \rightarrow 42 & 8 \rightarrow 10 & 8 \rightarrow 10 \\
6 \rightarrow 10 & 6 \rightarrow 10 & 6 \rightarrow 10 & 6 \rightarrow 10 \\
| 8 \rightarrow 10 & 8 \rightarrow 10 & 8 \rightarrow 10 \\
108 \sim 88 \rightarrow 130 & 10 \rightarrow 8 & 10 \rightarrow 8 & 8 \rightarrow 8 & 8 \rightarrow 8 \\
| Trp & 59 \rightarrow 73 \rightarrow 111 \sim 91 & 111 \sim 107 & 111 \sim 107 \\
| 8 \rightarrow 10 & 8 \rightarrow 10 & 8 \rightarrow 10 \\
133 \rightarrow 91 & 93 \rightarrow 75 & 159 \rightarrow 113 \rightarrow 75 & 135 A \rightarrow 93 \\
Phe & Glu / Lys & Asp & Meth & Meth \\
6 \rightarrow 10 & 10 \rightarrow 8 & 10 \rightarrow 8 & 10 \rightarrow 8 \\
| Leu / Leu & Leu / Leu & Tyr \\
133 \rightarrow 57 \rightarrow 71 \rightarrow 107 & 10 \rightarrow 8 \\
8 \rightarrow 8 & 8 \rightarrow 8 & 8 \rightarrow 8 \\
44 \rightarrow 112 \sim 108 & 108 \sim 88 \rightarrow 130 & 130 \rightarrow 135 A \rightarrow 93 \\
| Trp & Trp & Only some of these steps would possibly have chemical correlations.
\end{array}
\]
21. I. Triplet series — II. An alternative series 151-111

I. The triplet series

I. Triplet series; intervals outwards - inwards:

1.1 Triplet chains in nb-8, transformed to nb-10:

The triplets as 4 numbers in two series, outwards and inwards (as 543-345, 432-234 etc., treated as nb-8-numbers, give in pairs in nb-10 sums 4 x 146, 3 x 146, 2 x 146, 1 x 146, the total 5 times 292 = 5' in the ES-chain.

Intervals in nb-10 "outwards - inwards" = 126, ½ x 252 (4').

Fig. 21-1:

<table>
<thead>
<tr>
<th>8-base</th>
<th>10-base</th>
<th>Sums</th>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>345</td>
<td></td>
<td>543</td>
<td></td>
<td>345</td>
</tr>
<tr>
<td>234</td>
<td>156</td>
<td>432</td>
<td>282</td>
<td></td>
</tr>
<tr>
<td>123</td>
<td>83</td>
<td>209</td>
<td>321</td>
<td></td>
</tr>
<tr>
<td>012</td>
<td>10</td>
<td>136</td>
<td>210</td>
<td></td>
</tr>
<tr>
<td>714</td>
<td>478</td>
<td>982</td>
<td>1506</td>
<td></td>
</tr>
</tbody>
</table>

982 = 2 x 491: 491-10 → 753-8
But 478-10 → 736-8.

Triplets read "inwards" approximate the 734-group of ams in middle of the ES-chain, hypothetically representing an inward direction in relation to the 770-group as outward directed.

Cf. for 982 file 18, figure 18-3 and for directions file 14, para 3, figure 14-2.

Fig. 21-2: Number 982:

<table>
<thead>
<tr>
<th>10-base</th>
<th>8-base</th>
</tr>
</thead>
<tbody>
<tr>
<td>355</td>
<td>543</td>
</tr>
<tr>
<td>282</td>
<td>432</td>
</tr>
<tr>
<td>209</td>
<td>321</td>
</tr>
<tr>
<td>136.....982</td>
<td>210</td>
</tr>
<tr>
<td>982</td>
<td>1726</td>
</tr>
<tr>
<td></td>
<td>1726</td>
</tr>
</tbody>
</table>
1.2 Codon bases read as nb-8-numbers give sums triplets in nb-10:

Fig. 21-3:

<table>
<thead>
<tr>
<th>4 DNA-bases</th>
<th>4 RNA-bases:</th>
</tr>
</thead>
<tbody>
<tr>
<td>10-base</td>
<td>8-base</td>
</tr>
<tr>
<td>G</td>
<td>105</td>
</tr>
<tr>
<td>C</td>
<td>73</td>
</tr>
<tr>
<td>T</td>
<td>86</td>
</tr>
<tr>
<td>A</td>
<td>93</td>
</tr>
<tr>
<td>Sum:</td>
<td>357</td>
</tr>
</tbody>
</table>

Triplet series "inwards"

2. Sums 1506 - 714 and intervals 792:

Fig. 21-4:

The Triplet chain "outwards" - "inwards";

\[
\begin{aligned}
543 & \rightarrow 345 \\
432...975 & \rightarrow 234 \\
321 & \rightarrow 123 \\
210...531 & \rightarrow 012 \\
1506 & \rightarrow 714 \\
792 & = 2 \times 714 \\
\end{aligned}
\]

Fig. 21-5: Total sum of R for 24 ams, sum 1506 -2 from 2 x 4 bases:

\[
\begin{aligned}
2 \times G & \rightarrow 302 \rightarrow 456 \\
2 \times C & \rightarrow 336...792 \\
2 \times U & \rightarrow 112 \times 2 \rightarrow 160 \times 2 = 320, \sim 318 \\
2 \times A & \rightarrow 135 \times 2 \rightarrow 207 \times 2 = 414, \sim 394...\text{sum 714}, \ldots 712
\end{aligned}
\]

3. Number n x 273 from codon bases; two other transformations:

273, the mean value of 2 ams R+B unbound:

\[
\begin{aligned}
\text{nb-16} & & \text{nb-10} \\
\text{C-base:} & 111 & \rightarrow 273
\end{aligned}
\]

The triplet chain with intervals 111: 543 - 432 - 321 - 210:
210-10 → 546-6 = 2 x 273.

From file 20: Number n x 111, the intervals in the triplet steps:

Fig. 21-6:

<table>
<thead>
<tr>
<th>16 base</th>
<th>10 base</th>
</tr>
</thead>
<tbody>
<tr>
<td>975</td>
<td>2421</td>
</tr>
</tbody>
</table>

\[1506 < 1-444 < 531 \rightarrow 1329\]

Compare: 666 \rightarrow 1638 \times 2 = 3276, = 24 ams R+B

4. The triplet series and number 1875:

Pairs of the triplets = 753 transformed as a number in nb-16 gives 1875 in nb-10.
All 4 triplets separately transformed, see figure below, give n x 273 as the differences.

Fig 21-7: Number 1875:

\[543_{16} \rightarrow 1347_{10}\]
\[432_{16} \rightarrow 1074_{10}\]
\[753 < > 1875\]
\[321_{16} \rightarrow 801_{10}\]
\[210_{16} \rightarrow 528_{10}\]

Intervals 1347 - 528 = 3 x 273 = 819, x 4 = 3276, total R+B of 24 ams.

The sums (pair wise added) reminds of the second spectral line of hydrogen from Balmer series, mentioned in Introduction: Formula \(\frac{1}{2}^2 - \frac{1}{4}^2 = 0.1875\). Cf. 210 and spectral line 0.21 (!).

Two other operations give relations between sums and intervals:

\(10 \log 1,875 \approx 0.273\ 00...\)

\(187.5^{2/3} \times 100 = 3275.93 \approx 3276, \text{total of 24 ams R+B}\)

\([1/4 \times \text{ES-chain numbers} = 73 - 63 - 52 - 39.75 - 25,\]
with exponent \(3/2 = 623.7 - 375. - 500. - 250.6. - 125\): sum ~1875 (1874.32.)

Note: 63 x 52 = 3276, total sum of 24 ams R+B. Cf “quark numbers” (in “17 short files”)

\(15/8 = 5 \times 3 \times 1/4 \times 2 = 1.875\)

24 ams R+B = 3276. = \(\text{409} \times 8.01\).

48 codon bases (1st nd 2nd) = 6141 = \(\text{409} \times 15.01\).
II. An alternative numeral series

Another series, from G- to C-base:

Such a series, not treated above, shows some interesting features:

151 - 141 - 131 - 121 - 111

First and last numbers = mass of G- and C-bases. The DNA-bases (+1 in A-base) are shown in figure below: 272 = 2 x 136 (~ Hypoxanthine), 252 = 2 x 126 = T-base:

**Fig 21-8: An alternative series G - to C:**

\[
\begin{array}{cccc}
292 & 272 & 252 & \rightarrow \text{ES-numbers} \\
151 & 141 & 131 & 121 & 111 \\
G & 2(A+1) & 2T & C
\end{array}
\]

With last three numbers doubled the sum in nb-10 = 2 x RNA-bases = 1018, in nb-8 = 1772, the 24 unbound B-chains.

All these numbers transformed to nb-8 give the triplet sums 975 (543 + 432) - 2 and 531 (321 + 210), sum 1504, 24 ams R:

**Fig. 21-9:**

The 12-groups 770 and 734 of ams are shown in the figure below. Here it may be noted that we get the 734-group in the middle of the chain as in the ES-series, with 2 times 208 in that chain included, corresponding to both 203-groups here.

**Fig 21-10:**

The ams groups 816 and 688 from -/+ last number 157:

973 - 157 = 816 = U1 + C1
531 + 157 = 688 = G1 + A1.
Some other paired groups of ams R from this alternative series:

**Fig. 21-11:**

With a last step in the chain: 101, plus/minus:

\[
\begin{align*}
10\text{-base} & \quad 8\text{-base} \\
101 & \rightarrow 145 \\
973 - 145 & = 828 = Z \text{ total 24 ams R} \\
531 + 145 & = 676 = N \text{ total 24 ams R} \\
973 - 157 & = 816 = A + U + 1 \\
531 + 157 & = 688 = G + C - 1
\end{align*}
\]

**Fig. 21-12:**

848 - 656 division:

\[
\begin{align*}
10\text{-base} & \quad 8\text{-base} \\
151 & \quad 227 \\
141 & \quad 215 \\
2 \times 131 & \quad 2 \times 203 = 406 = \text{Sum 848 = G2 + U2} \\
2 \times 121 & \quad 2 \times 171 = 342 \\
2 \times 111 & \quad 2 \times 157 = 314 = \text{Sum 656 = C2 + A2}
\end{align*}
\]

792-712:

Exponent series:

\[
\begin{align*}
215 + 171 & = 386 \\
203 + 203 & = 406 = \text{sum 792} = 2 \times 292 + 208 \\
227 + 171 & = 398 \\
157 + 157 & = 314 = \text{sum 712} = 2 \times 252 + 208
\end{align*}
\]

The doubled last steps re-written:

\[
\begin{align*}
203 - 183 & = -20 \\
171 - 169 & = 2 \\
157 & = \text{sum 531 - 22 = 509 = sum of 4 codon bases RNA} \\
127 & = \text{sum 531 - 22 = 509 = sum of 4 codon bases RNA}
\end{align*}
\]
22. Other substances

Fats — Sugar — Na-Cl, Na-K-pump

Some annotations about other substances:

1. Fatty acids

Two common fatty acids C18H36O2 = 284-10 \to 1152-6 (~752 rewritten) = 3 \times 384 and C16H32O2 = 256-10 \to 1104-6 = 3 \times 368 are already mentioned in file 17-1:

Fig. 22-1: Two common fatty acids

<table>
<thead>
<tr>
<th>10-base</th>
<th>6-base</th>
<th>Comp code on type groups of arms:</th>
</tr>
</thead>
<tbody>
<tr>
<td>C18 284</td>
<td>1152</td>
<td>= 3 \times 384 &gt; 3 \times 752 = 3/2 \times 24 arms R.</td>
</tr>
<tr>
<td>C16 256</td>
<td>1104</td>
<td>= 3 \times 368</td>
</tr>
</tbody>
</table>

384 + 1 \times 2 = Cross plus Form coded arms R. 384 = G_8 + C_8
368 - 1 \times 2 = DNA plus Pair coded arms R. 367 = A_8 + U_8

6-base 1152 \approx 752 re-written = \frac{1}{2} \times 24 arms R.

2. Carbohydrates:

Carbohydrates, some examples, transformations nb-16 \to 10 \to 8 or \to 6:
- \text{^{12}C} \to \text{H}_2\text{O} \to \text{HCOH} = 12-16 \to 18-10 \to 30-6, the building stone of sugar.
- \text{O}_2 \text{16 A} \to \text{H}_2\text{CO}_3 \text{62 A} (built into ribose): 32-16 \to 50-10 \to 62-8 = + 18, \text{H}_2\text{O}, + 12, \text{C}.
- Hexoses 180 in nb-10: In nb-16 180 = 384-10 (= 2 citrate à 192 or e.g. G-8 + C-8).
- A fructose in P-P-bonds = 178: 178-16 = 376-10 = \frac{1}{2} \times 752 in the ES-chain.
- Ribose 150 as a number in nb-16 = 336 in nb-10, 544 - 208 in ES-chain.
- A disaccharide 342 or two hexoses 180 from ES-numbers as intervals in transformation steps:
- 252-16 \to 594-10 = + 342, a disaccharide.
- 146-16 \to 326-10 \to 506-8 (ATP charged -1) = + 180, + 180.
Fig. 2-2: Sugar synthesis

**Sugar synthesis:**

\[
\begin{array}{c}
\text{16-base} & \text{10-base} & \text{8-base} \\
12 & 18 & 30 \\
C & \rightarrow & H_2O & \rightarrow & H-C-OH & \sim 1/6 \text{hexose}
\end{array}
\]

\[
\begin{array}{c}
\text{16-base} & \text{10-base} & \text{8-base} \\
32 = O_2 & \rightarrow & 50 & \rightarrow & 62 = H_2CO_3 & (62 \text{ also } = NO_3) \\
& & & \downarrow & & \text{incorporated at the sugar synthesis} \\
& & & \uparrow & & \text{ionized}
\end{array}
\]

\[
\begin{array}{c}
18 \rightarrow 24 \rightarrow 30 \\
H_2O \text{ (2 C, Mg ?)} & H-C-OH & \sim 1/6 \text{of hexose}
\end{array}
\]

**Sugar synthesis - the summation formula with following relations:**

\[
\begin{align*}
6 \text{CO}_2 + 6 \text{H}_2\text{O} & \rightarrow 6 \text{HCOH} + 6 \text{CO}_2 \\
372 & \rightarrow 372 \rightarrow \text{Cf. P-group 98 nb-16 to nb-6.}
\end{align*}
\]

\[
\begin{array}{c}
\text{16-base} & \text{10-base} & \text{8-base} \\
6 \text{H}_2\text{O}: & 108 & \rightarrow 264 = 6 \times \text{CO}_2 \\
& 180 = 6 \text{H-C-OH} & \leftarrow 264 = 6 \text{CO}_2 \\
6 \text{O}_2: & 192 & \rightarrow 390
\end{array}
\]

\[
\begin{array}{c}
\text{10-base} & \text{8-base} & \text{6-base} \\
6 \text{H}_2\text{O} & 108 & \rightarrow 154 \rightarrow 390 \ (-108 = 192) \\
& 146 & \text{Sum of intervals 46 + 146 = 192} \\
& 410 & \rightarrow 192 = 6 \text{O}_2, \text{in nb-10} \\
& 300 & > 108 = 6 \text{H}_2\text{O} \\
& 192 & \rightarrow 84 = 6 \text{CO}_2 \text{ in base-10} \\
& 264 = 6 \text{HCOH} \text{ in base-8 number}
\end{array}
\]

\[
\begin{array}{c}
1a) & 6 \text{H}_2\text{O} & 108 & \rightarrow 154 \rightarrow 390 \ (-108 = 192) \\
& 372 & \text{Sum of intervals 46 + 146 = 192} \\
& 146 & \rightarrow 192 = 6 \text{O}_2, \text{in nb-10} \\
& 410 & > 108 = 6 \text{H}_2\text{O} \\
& 300 & \rightarrow 192 = 6 \text{CO}_2 \text{ in base-10} \\
& 264 = 6 \text{HCOH} \text{ in base-8 number}
\end{array}
\]

Cf. numbers in the exponent series: 192, 146, 84, 108.

A simultaneous fixation of nitrogen occurs during which Molybdenum take part: Mo 42 Z, 96 A.

If presuming 2 Molybdenum atoms = 84 Z, 108 N = 192 A, same number as 6 O2, numbers of the transformation intervals above:

\[
\begin{align*}
\text{NO}_3^- = 62 \text{A}, x 6 & = 372 = 108 + 264 \text{ or } 180 + 192. \\
62 = 108 - 46, 146 - 84, \text{intervals above. NO}_3^- + \text{NO}_2^- = 62 + 46 = 108. \\
\alpha\text{-ketoglutarate, aminating amino acids} = 146.
\end{align*}
\]

**Hexoses as intervals - ? - in transformations within the exponent series, i. e.**

\[
\begin{array}{c}
\text{16-base} & \text{10-base} & \text{16-base} & \text{10-base} & \text{8-base} \\
252 & \rightarrow & 594 & 146 & \rightarrow 326 \rightarrow 506 (\sim \text{ATP}) \\
342 & \sim \text{disaccharide} & 180 & & 180 \sim \text{fructose/glucose}
\end{array}
\]

Cf. numbers in the exponent series: 192, 146, 84, 108.
3. Na-Cl and the Na-K-pump:

Na-Cl and Na-K-pump in the nervous system:

\[ \text{Na}^{11} (Z=11, A=23) \rightarrow \text{Cl}^{17} (Z=17, A=35) \rightarrow \text{K}^{19} (Z=19, A=39) \]

Cf. Na, Cl, K ionized, 10 e, 18 e: in nb-10 to nb-8 = +2, number for the transport of 2H through membranes.

Fig. 22-3:

<table>
<thead>
<tr>
<th>Element</th>
<th>Z</th>
<th>A</th>
</tr>
</thead>
<tbody>
<tr>
<td>Na</td>
<td>11</td>
<td>23</td>
</tr>
<tr>
<td>Cl</td>
<td>17</td>
<td>35</td>
</tr>
<tr>
<td>K</td>
<td>19</td>
<td>39</td>
</tr>
</tbody>
</table>

Z-numbers $\rightarrow$ Z-numbers $\leftrightarrow$ A-numbers:

A $\rightarrow$ Z:

\[ K^{39} \rightarrow 21 \rightarrow 11 \]

A:

\[ K^{39} \rightarrow 27 \rightarrow 23 \]

e-numbers:

\[ \text{Na}^+ \quad e = 10 \quad 12 = +2 \]
\[ \text{K}^+ \quad e = 18 \quad 22 = +4 \ldots \ldots \sim \text{H-wanderings} \]
\[ \text{Cl}^- \quad e = 18 \quad \sim \quad \text{through cell membrane} \]
\[ \text{H}_2\text{O}^{+} \quad A = 18 \quad 22^+ \]

*
Discussion

The amount of correlations between the genetic code and numeral series is difficult to regard as only random ones.

A general problem is of course that it still doesn't seem to exist any known biochemically accepted mechanisms that could "explain" construction along such numeral series, however established facts in the other mentioned examples. It could however be questioned in which sense the 2x2-series behind the periodic system is "explained", or the formula for spectral lines of hydrogen.) Facts are there. Science has only its models, as far as possible congruent with the facts.

With the hypothesis here that they really reveal features in how Nature organized the genetic code, what should it imply? About the elementary series 5→> 0, the series of valences for atoms in the genetic code could be remembered: P - C - N - O,S - H = valences 5 - 4 - 3 - 2 - 1. A-dimensional interpretation seems inevitable, with regard to exponents and to transformations between nb-systems.

How should the exponent 2/3 be explained? We have squares in the 2x²-chain behind the periodic system and intervals between inverted squares behind the spectral lines of hydrogen. These formulas concern electron shells of atoms, i. e. the property charge. With mass and charge most elementary assumed as a mutual relation D3 to D2, cubes become natural. We have mass as the energy form concentrated in atomic nuclei, charge expressed in the atomic shell with released energy in kinetic form. Why then inverted cubes? They lead inwards to a deeper level, as does the inward direction toward nucleus in an atom.

It may be remembered too that there are a similar inverted relation between radii and mass in neutron stars.

The many relations of disparate kinds to the 2x²-chain and other simpler chains support the interpretation of the genetic code as built on an elementary chain x = 5 - 0 with exponents of different degrees. With a dimensional view on the exponents, it could imply, either that such chains preceded the more elaborated ES-chain when the coding system emerged or could be regarded as simultaneously existing on underlying levels. It's possible to imagine a dimensional development from both ends of the chain towards step 3 - 2 in the middle with increasing agreement of mass distribution in the genetic code:

\[ x^4 \rightarrow x^3 \rightarrow [x^{3/2} \rightarrow \leftarrow x^{2/3}] \leftarrow x^2 \leftarrow x^1. \]

The mass distribution as described in section I often implied minus/plus lower numbers in the ES-series, correlating with features in the background model. It points to a two-way direction in he chain of both disintegration and synthesis. This could seem to conflict with the common view on evolution as a stepwise synthesis towards more complex and bigger units. Yet, a double-direction is natural in Nature, if we think of macrocosm, Big Bang and both processes in celestial Hx-clouds. It could be mentioned that even among physicists this opposite view of disintegration, starting from a whole, has been proposed. (There is a similar pattern of two-way direction in the protein synthesis, where tRNAs as from opposite strands of DNA meet mRNA "the other way around" at ribosomes in the "middle" of the process.) See figure 1 in section I, with dimensional interpretation of the forms from double direction (D4) in DNA to single-
stranded RNA as vector (pole 4b) outwards to ribosomes (D3) - meeting tRNAs (as "clover leaves" D2) and ams.

It's shown too that not only mass distribution on codon groups of ams correlates with the ES-chain but also other bases for mass division, for instance with main groups of atom kinds and the not codon-dependant B-chains as well as with several features in the origin of ams from stations in glycolysis - citrate cycle. This suggests an interpretation where the same principle scheme is developed on different levels or as representing different axes in a coordinate system when the genetic code emerged.

The single fact that the mass division on C-skeleton and other atoms (960 and 544) is the same as between main codon groups (U+A, 960 and G+C, 544) supports in itself the general suggestion that the code is built on a numeral series.

In several ways the results seems to agree with the coevolution theory [6, 7]. There is the relation with biochemical origins of ams from glycolysis and citrate cycle. There is the view of codon domains as totals, differentiated in following steps, even if the "codon domains" here is related to mass sums of ams. There is also the fact that G1-coded ams "arrive first" in the number chain as 5 out of about 7 ams assumed first in that theory: GG-GC-GU-GA-GA besides Ser UC and Phe UU..

Then about mass again, rejected as irrelevant for codon assignments: In addition to arguments in the Introduction it's reasonable to ask for instance why precisely these ams have been selected for coding, not other ones? The selection seems rather random. Why just this number of ams with oxygen as end groups, that number of ams with nitrogen? (Besides that both types and polar and non-polar ams surely have been necessary.)

Further, when much research in this field has been focusing on the "most stable" configuration of the coding system, one could naturally ask what the background is for this stability? One aspect is of course that the most common isotopes have shown up to be most stable. (When calculating with common mix of isotopes today, atomic weights should change the sum of R- plus B-chains of ams from 3276 → 3280 abbreviated, R-chains from 1504 → 1506, no more than the deviations of single units (u) in this analysis.) In addition, the analysis here mostly concerns groups of ams, i.e. sums were an individual deviation in mass might have a rather small influence.

The fact that Ileu sometimes gets mixed with Leu by tRNAs could also be mentioned, differing in structure but having the same mass and atoms.

Does the proposal for a guiding numeral series exclude such an individual invention among certain organisms as Pyl, called the 22nd ams, occupying a stop codon? Pyl add 108 to R-chain of Lys, i.e. the interval 3' to 1' in the ES-chain and could eventually be suspected as a "misreading" of the chain, leading to a compound, a new "word"?

The examples of transformations between nb-systems are astonishing and certainly provocative. They support however a general dimensional view in the creation of the code and actually too the relevance of the ES-chain. They seem to reveal a deep level in the reference system of a hitherto unknown kind, representing the very steps between dimensional degrees. In physical and biochemical terms they should imply something like mutual resonances between "mass fields" in different dimensional degrees, relations and fragmentation guided by geometrical and arithmetical rules. A problem is naturally the superfluity of such possible transformational relations.

If proposals in this paper are accepted as hypotheses, they will naturally raise many new
questions and lead to secondary hypotheses, which in their turn could be possible to test. The dimensional aspects, mostly omitted here, should reasonably, if elaborated further, have implications for protein structures and their different functions in cells. Whatever to believe about the arithmetic, something of that kind resembles life - in being very simple and very productive - and naturally multidimensional.

References

References, referred to in the text within brackets [ ]:

Since this research started in the beginning of 1980's, the main source used was:

A few data taken from

A selection of other articles dealing with the same topic:


END