

A 5-dimensional Structure and Transformations between Number-base Systems as possible guiding Principles behind the Genetic Code

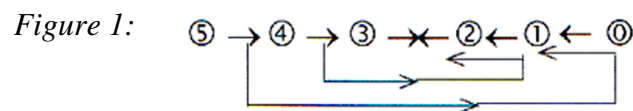
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ABSTRACT

Background of this research was an elementary 5-dimensional model or conceptual structure, suggested by the author for interpretations in theoretical physics. The model, with some redefinitions, implies a development through polarising steps towards entities of lower degrees, $5 \rightarrow 4 \rightarrow 3 \dots$ with debranched degrees being translated to external motions or meeting "the other way around"...



The thought was that such a model, if valid, also should reveal itself in some form in sciences of superposed levels, not least in a "main stream" development towards life and the nearly "universal" genetic code. Adding the natural idea that numbers are given from this underground of dimensions.

This paper shows two things:

1. - that a simple "5-dimensional" chain, $5 - 4 - 3 - 2 - 1 - (0)$ with the exponent $2/3$, $\times 100$, generates many mass sums of codon grouped amino acids, indicating a dynamic, mathematical pattern. (G+C-coded amino acids for example "arriving" first in step 5-4, in accordance with a common assumption.)

2. - that an operator for transformations between number base systems also seems to be involved, as to and from the base-10 to base-8 to base-6 systems. The codon bases generate mass sums for codon-grouped amino acids for example, and much more of that kind. If such an operator exist, it is reasonably connected with different dimension degrees. Perhaps a factor in what is called "affinities" or developments towards heavier molecules? Surely a more revolutionary fact if more than hazard and probably difficult to accept.

There are several connections too between the exponent series and these transformations in part II.

Simple first tests of the suggestions here would be to proof or refute the importance of mass numbers and ordinary isotopes in liquids used to precipitate amino acids: Do other isotopes of C-N-O or H change the results?

Keywords:

codon distribution, amino acid, mass analysis, dimension, arithmetical pattern

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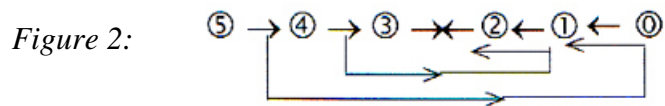
Introduction:

Subject field for this research is the nearly universal genetic code and the question whether it is a “frozen hazard” or hides some internal logic.

There are opposite views on this matter and the discussion has gone on for some decades now. It hasn't been easy to find many correlations between the codons and biochemical properties of the amino acids they code for, besides some rough tendencies.

Starting point here - as for many others in the field - is the hypothesis or belief that life - and thus its central genetic code - shouldn't be a hazard.

The special background here was an elementary 5-dimensional model or conceptual structure suggested by the author for interpretations in theoretical physics. The model, with some redefinitions of the concept “dimension” and the 4th dimension degree, implies a development through polarising steps towards entities of lower degrees, $5 \rightarrow 4 \rightarrow 3 \dots$ with debranched degrees being translated to external motions or meeting “the other way around”...



The thought was that such a model — or whichever other model in theoretical physics, if valid, also should show up in some form in sciences of superposed levels, not least in a “main stream” development towards life and the nearly universal genetic code. Adding the natural idea that numbers are given from this underground of dimensions.

With this short mention of the background model, it's necessary to point out that the following results in no way demand acceptance or any closer understanding of the model. The results are there “in their own right”.

Yet, there is a property in the results of plus/minus lower numbers in the presented number chain below, named the “exponent series”, that seems to mirror the idea of debranched dimension degrees meeting “the other way around”, which gives cause for including the figure above.

Some general presumptions:

- It's reasonable to expect that the genetic code has deep roots in physics and quantum mechanics and that multidimensional aspects are a natural part of any interpretation.
- It's equally reasonable to expect that similar patterns could show up on different levels of sciences. (Cf. chaos research.)
- It's also a possible view that “the whole” in some sense come first, even if only on a deep pre-material level: the whole a starting point, reading nature in the direction of differentiations. Such a view has been suggested in theoretical physics too. It can be regarded as a background to the following pages as mainly concerned with groups of amino acids.

The research here started with a table of 24 codons and connected amino acids, 4 amino acids regarded as double-coded, codons differing in 1st, and/or 2nd base or *type* of base (A, G) or (U, C) in 3rd position. It doesn't regard the question of evolution of the genetic code, but it seems probable that this approach concerns a rather late phase in this evolution, not contradicting other findings regarding earlier phases. There are signs too that the actual genetic code in itself consists of different levels.

The investigation is carried out in simple arithmetic. Interested scientists in bioinformatics and theoretical biology could regard the results as a material for further developments and interpretations.

Table 1:**Codons and A-, Z-, N-numbers in side chains of 20 plus 4 amino acids [1]:**

Codons where A or G (A/G) in 3rd position makes no difference, or U or C (U/C) in 3rd position, are counted as one, which gives 24 codons.

A = mass number, Z = protons, N = neutrons; ordinary isotopes.

1 st base	2 nd base	Ams	N	Z	A	A	Z	N	Ams	1 st base	2 nd base
G1	G	Gly	-	1	1	1	1	-	Gly	G	G2
	C	Ala	6	9	15	101	56	45	Arg ₁	C	
	U	Val	18	25	43	130	69	61	Trp	U	
	A	Asp	28	31	59	47	25	22	Cys	U	
	A	Glu	34	39	73	31	17	14	Ser ₂	A	
					Σ 5	411	224	187		6	Σ
C1	G	Arg ₁	45	56	101	15	9	6	Ala	G	C2
	C	Pro	18	24	42	42	24	18	Pro	C	
	U	Leu ₁	24	33	57	31	17	14	Ser ₁	U	
	A	Gln	33	39	72	45	25	20	Thr	A	
	A	His	38	43	81						
					Σ 5	133	75	58		4	Σ
U1	G	Cys	22	25	47	43	25	18	Val	G	U2
	G	Trp	61	69	130	57	33	24	Leu ₁	C	
	C	Ser ₁	14	17	31	57	33	24	Leu ₂	U	
	U	Leu ₂	24	33	57	91	49	42	Phe	U	
	U	Phe	42	49	91	57	33	24	Ileu ₁	A*	
	A	Tyr	50	57	107	57	33	24	Ileu ₂	A*	
					Σ 6	437	247	190		7	Σ
A1	G	Ser ₂	14	17	31	73	39	34	Glu	G	A2
	G	Arg ₂	45	56	101	59	31	28	Asp	G	
	C	Thr	20	25	45	72	39	33	Gln	C	
	U*	Ileu ₁	24	33	57	81	43	38	His	C	
	U*	Ileu ₂	24	33	57	107	57	50	Tyr	U	
	U	Meth	34	41	75	58	31	27	Asn	A	
	A	Lys	31	42	73	73	42	31	Lys	A	
	A	Asn	27	31	58						
					Σ 8	523	282	241		7	Σ

* Ileu 1: AU-U/C, Ileu 2: AU-A, codon differing only in 3rd base type.

Abbreviations and ways of writing:

Ams = amino acids (ama = amino acid)

20 ams --> 24 codons: i.e. 4 ams with double codons:

Arg1, 2: codons CG + AG-A/G;

Ser1, 2: codons UC + AG-U/C;

Leu1, 2: codons CU + UU-A/G; and

Ileu1, 2: codons AU-A +AU-U/C, only differing in types of 3rd base

Codons where A or G in 3rd position makes no difference (written -A/G are counted as one and the same, as codons where U or C in 3rd position (-U/C) makes no difference.

R = R-chain(s) = the side chains or "radical chain" of amino acids =
= the differing part of ams not taking part in the peptide binding.

B = B-chain(s) = "ground chain" =

= the similar parts of ams which through condensation combines to peptide chains.

Sums: All sums refer to mass number A where not anything else is mentioned.
They refer to R-chains where not anything else is denounced.

G1 - C1 - U1 - A1 = groups of ams coded by G-C-U-A respectively as first base.
G2 - C2 - U2 - A2 = " " " " " " as second base.

Types of codons, with respect to 1st and 2nd base, used denominations:

"Cross-codons" = GU-UG-AC-CA Val - Cys, Trp - Thr - Gln, His

"Form-codons" = GA-UC-AG-CU Asp, Glu - Ser1 - Arg2, Ser2- Leu1

"Pair-codons" = GG-UU-AA-CC Gly -Phe, Leu2 - Asn, Lys - Pro

"RNA-codons" = GC-UA-AU-CG Ala - Tyr - - Meth, Ile1, Ile2 -Arg1

6 ams in each group.

"The exponent series", the 5-4-3-2-1-0-chain of numbers with exponent 2/3, x 100:
= $5^{2/3} \times 100$, $4^{2/3} \times 100$ etc.

In some places a shortened way of writing these numbers is used: "5", "4" etc.,
the elementary numbers within quotation marks.

Λ = sign for inversion of numbers

~ = sign for "equivalent with" or "the same number as" or "circa".

3rd base:

8 ams with G or A in 3rd place: A/G, or either A or G, for instance Glu GA-A/G, and
Meth AUG

8 ams with U or C in 3rd place: U/C, for instance Asp GA-U/C

8 ams with indifferent base (G-C-U-or A) in 3rd place = "2-base-coded"

"0-bases" = U, C (T)

"00-bases" = G, A, referring to the forms: single or double rings.

All troublesome longer chemical terms are avoided as far as possible. For instance:
H is used instead of hydrogen, O instead of oxygen etc.

First observations from Table 1 (R-chains):

The mass sums for group G+C-coded ams as for A+U-coded ams becomes the same in 1st and 2nd base ordering:

$$\begin{aligned} G1 + C1 &= G2 + C2 = \mathbf{544} \\ U1 + A1 &= U2 + A2 = \mathbf{960} \end{aligned}$$

This implies that the sums of amino acids (ams) exchanged between the groups are the same. A table over these exchanged ams, the Cross-coded and the Form-coded, reveals a mathematical pattern which suggests some deeper logic behind the connection between codons and mass sums of ams:

Table 2: Cross- and Form-codons, total sum of mass units in R-chains 770:

GA Glu	CA His	UG Trp	AG Arg →	385 heavier *
GA Asp	CA Gln	UG Cys	AG Ser →	209 lighter
<u>GU Val</u>	<u>CU Leu</u>	<u>UC Ser</u>	<u>AC Thr</u> →	176
<u>175</u>	<u>210</u>	<u>208</u>	<u>177</u>	
385		385		

* The heavier ams: 3rd base A/G, lighter ams: 3rd base U/C, with exception of the CA-pair His – Gln. Third row: “2-base-coded”.

- The sum is divided equally (+/-1) horizontally and vertically.
- G1 + A1 groups give the same sum as Form-coded ams, **352**. GA+AG+CU+UC,
U1 + C1 the same sum as Cross-coded ams, **418**: CA+UG+GU+AC.
- Z-sum of the whole group = **418 +1**, N-sum **352 -1**.
- There is a factor 11 involved:
Numbers 3^3 ----- 2^3 , 27 — 8: Sum 35, x 11 = 385. Difference 19, x 11 = 209,
2 x 8, x 11 = 2 x 88 = 176. (GU + AC = 88, CU + UC = 88)
(Numbers 27 - 8 have been said to appear in group theories of elementary
particle physics. This mentioned without any closer knowledge in that field.)
- There is also in vertical and horizontal additions a division of the number 385
= 5 x 77 in **3 x 77**, **2 x 77**:

$$\begin{aligned} \text{GA Glu} + \text{CA His} &= 154 = \mathbf{2 \times 77} \\ \text{UG Trp} + \text{AG Arg} &= 231 = \mathbf{3 \times 77} \end{aligned}$$

$$\begin{aligned} \text{GA Asp} + \text{CA Gln} + \text{GU Val} + \text{CU Leu} &= 231 = \mathbf{3 \times 77} \\ \text{UG Cys} + \text{AG Ser} + \text{UC Ser} + \text{AC Thr} &= 154 = \mathbf{2 \times 77}. \end{aligned}$$

(Cf. factors 5 and 7 with the number of ams in G+C-group and A-U-group respectively.)

Two short annotations here on these observations:

- a) Why a factor 11 in these groups in table 2?
The other codon type groups, RNA-coded + Pair-coded ams, with total sum of 734,

(as 770 - 2 H₂O), did not reveal such an interesting pattern. (One should have to count with hydroxyproline and hydroxylysine for instance, + 4 H to get some similarity. The difference between the two codon type groups could eventually imply that there is different levels or stages involved in the actual scheme.

There are in fact 4 other groups which can be combined to $n \times 11$:

AU: Meth + Ile = 132; AA + GG: Lys + Asn, + Gly = 132; $\underline{UU} + \underline{UA}$: Phe + Tyr (out of Phe chemically) 198; $\underline{CC} + \underline{CG}$, Pro + Arg (can transform into one another): 143.

Sum 11 x 55. To compare with the group 11 x 70. Remains Ile₂, Leu₂, Ala, 129 A.

(With the "21" ams with Selen instead of Ile₂ and a Se-isotope 78, this gives an addition of 165, these groups becomes 11 x 70 too.)

So why a factor 11? Avoiding speculations, it's only possible here to refer to some unknown roots in physics.

b) The division of the whole sum in N — Z in Cross- plus Form-coded ams in table 2 above was the same as between G1+A1-groups and U1+C1-groups respectively -/+1: N = 352 -1, Z = 418 +1.

There are several other examples of equal (or +/-1) number divisions as along quite different co-ordinate axes of polarisations. (See the www-address referred to below.) Just to mention the most obvious one: the division of mass of ams (R) between kinds of atoms:

S+O+N+H = **544**, the same number as G+C-coded ams
C-atoms = **960**, - " - A+U-coded ams

Such similarities seem to point towards an interpretation where a "whole" is differentiated along separate co-ordinate axes, representing different types of polarities.

The "triplet series":

One more observation should be mentioned here from earlier research: that a "triplet series" approximates mass sums of the 24 ams:

$$\begin{array}{r} \underline{543} \quad - \quad \underline{432} \quad - \quad \underline{321} \quad - \quad \underline{210} \quad \text{Sum } 1506 \\ = \quad \underline{G + C, -1} \quad \underline{963} = \underline{U + A, +3} \end{array}$$

$$\begin{array}{r} 210 = \text{Z-number } \underline{UG-UC-AC-AG}, +1 \quad = \text{G, C in } 2^{\text{nd}} \text{ position} \\ 321 = \text{Z-number } \underline{UU-UA-AU-AA}\text{-coded}, +2 \quad \uparrow \\ 432 = \text{N-number } \underline{A1+U1}\text{-coded} \quad \uparrow \\ 543 = \text{A-number } \underline{G+C}\text{-coded ams } -1 \quad \uparrow \end{array}$$

$$\begin{array}{r} \text{The triplet series expanded: } \underline{987 + 876 + 765 + 654 + 543 + 432 + 321 + 210} \\ = \quad \quad \quad 3282 \quad \leftarrow \quad | \quad \rightarrow \quad 1506 \\ \text{interval:} \quad \quad \quad \underline{1776} \\ \quad \quad \quad \quad \quad \quad \quad 24 \times 74 \end{array}$$

The numbers shall be compared with the total sum **3276** (R+B-chains), B-chains = **1772** after reduction of 1 H in Pro, Lys and Arg_{1,2}, R-chains = **1504**.

Intervals in each step **111**, **3/2 x 74**, the number of unbound B-chains, (a reason for the need of 3 ams to form the smallest peptides?).

*Some more results from this earlier research can be found here:
http://u5d.net/ama/subama/Subpages/list_contents.html
http://www.u5d.net/booklets/bch_protein_synthesis.html

Part I: The “Exponent Series”

1. The exponent series and codon grouped amino acids:

The observations above and others led to further search for patterns in the attribution of codons to amino acids. The following version of an elementary “5-dimensional chain” with an exponent $2/3$ was tested. With a factor $\times 100$ it was surprisingly found to easily generate many of codon grouped mass sums among the $20 + 4$ amino acids:

$$\text{a.} \quad = \quad 5^{2/3} \text{ — } 4^{2/3} \text{ — } 3^{2/3} \text{ — } 2^{2/3} \text{ — } 1^{2/3} \text{ — } 0, \quad \times 100$$

$$= \quad 292,4. \quad 252,0. \quad 208,0. \quad 158,7. \quad 100$$

$$\text{abridged:} \quad \underline{292} \quad \underline{252} \quad \underline{208} \quad \underline{159} \quad \underline{100}$$

$$\text{Sum:} \quad \quad \quad \underline{752} \quad \quad \quad \underline{259}$$

$$\text{Sum} \quad \quad \quad \underline{544} \quad \quad \quad \underline{\times 2 = 416}$$

Three first numbers in steps “5-4-3” = 752, $\times 2 = 1504$ = the whole sum of 24 ams, R-chains.

Two first numbers in steps “5” + “4” = 544 is the sum of G+C-coded ams.
“5” + “4” + 2 x “3” = 544 + 416 = 960 = A+U-coded ams

Written in another way:

$$752 - 208 = 544 = \text{G+C-coded ams}$$

$$752 + 208 = 960 = \text{U+A-coded ams}$$

- b.** Cross- plus Form-coded. ams = $2 (544 - 159) = 2 \times 385 = 770$
RNA- plus Pair-coded ams = $2 (208 + 159) = 2 \times 367 = 734$

$$\begin{array}{ccccccc} & 544 & & 367 & & & 2 \times 367 = 734 \\ / & & \backslash & / & \backslash & & = \text{RNA+Pair-coded ams} \\ 292 \text{ — } & 252 \text{ — } & 208 \text{ — } & 159 \text{ — } & 100 & & \\ \underline{544} & | < \text{ — } & | & \text{ — } & > | & & 2 \times 385 = 770 \\ & & 385 & & & & = \text{Cross+Form-coded ams} \end{array}$$

- c.** C1 + U1-coded ams = 816 = $544 + 1/2 \times 544 = 2 (252 + 208) - 1/2 \times 208$
G1 + A1-coded ams = 688 = $960 - 1/2 \times 544 = 2 \times 292 + 1/2 \times 208$

$$\begin{array}{ccccccc} & & & \times 1/2 = 104 & & & \\ & & & | & & & \\ 292 \text{ — } & 252 \text{ — } & 208 \text{ — } & 159 \text{ — } & 100 & & \\ \underline{292} & & \underline{460} & & & & 2 \times 292 + 104 = 688 = \text{G1 + A1} \\ & & & & & & 2 \times 460 - 104 = 816 = \text{C1 + U1} \end{array}$$

- d. C2 + U2-coded ams = 570 = 2(544 - 259)
G2 + A2-coded ams = 934 = 2(208 + 259)

$$\begin{array}{cccccccc}
 & \mathbf{544} & \longleftarrow & \mathbf{285} & \longrightarrow & \mathbf{259} & & \mathbf{2 \times 285 = 570} \\
 / & & & \backslash & & / & & \backslash \\
 292 & \text{---} & 252 & \text{---} & 208 & \text{---} & 159 & \text{---} & 100 \\
 & & & & | & & & & | \\
 & & & & \mathbf{467} & & & & \mathbf{2 \times 467 = 934} \\
 & & & & & & & & \mathbf{= G2 + A2-coded ams}
 \end{array}$$

- e. G1-coded ams = 292 - 100, - 1 = 191 "5 - 1"
C1-coded ams = 252 + 100, + 1 = 353 "4 + 1" (101 = Arg CG, charged)¹⁾
- C2-coded ams = 292 - 159 = 133 "5 - 2"
G2-coded ams = 252 + 159 = 411 "4 + 2"

$$\begin{array}{cccccccc}
 | & \longleftarrow & \mathbf{C2 \ 133} & \longrightarrow & | & & & \mathbf{C2 = 292 - 159 = 133} \\
 | & & & & | & & & \mathbf{G2 = 252 + 159 = 411} \\
 | & & & & | & & & \\
 | & & \mathbf{G2 \ 411} & & | & & & \\
 / & & & & \backslash & & & \\
 292 & \text{---} & 252 & \text{---} & 208 & \text{---} & 159 & \text{---} & 100 \\
 | & & | & & & & & & | \\
 | & \longleftarrow & \mathbf{G1 \ 191} & \longrightarrow & | & 101 & & & \mathbf{G1 = 292 - 101 = 191} \\
 | & & | & & | & & & & | \\
 \backslash & 252 & \text{---} & \mathbf{C1 \ 353} & \text{---} & 101 & / & & \mathbf{C1 = 252 + 101 = 353}
 \end{array}$$

- f. U2-coded ams = 544 - 208 + 100, +1 = 544 - 107 = 437
A2-coded ams = 416 + 208 - 100, -1 = 416 + 107 = 523 (107 = Tyr UA)¹⁾

$$\begin{array}{cccccccc}
 & & \mathbf{x \ 2 = 416} & & & & & \mathbf{416 + 208 - 100, +1 = 437 = U2} \\
 & & | & & & & & \\
 292 & \text{---} & 252 & \text{---} & \mathbf{208} & \text{---} & 159 & \text{---} & 100 \\
 & \mathbf{544} & & \mathbf{2 \times = 416} & & & \mathbf{100} & & \mathbf{544 - 208 + 100, -1 = 523 = A2}
 \end{array}$$

¹⁾ About Arg and Tyr, see 2.d, page 13.

- g. **Groups U1 and A1:** There are different ways to derive the groups:
g1. Division of number 208 in 2 x 104:

$$\begin{array}{l}
 \mathbf{U1 = 463 = 460 + \frac{1}{2} \times 208 = 564, - 101.} \\
 \mathbf{A1 = 497 = 292 + \frac{1}{2} \times 208, = 396, + 101.}
 \end{array}$$

$$\begin{array}{cccccccc}
 & 104 & & & & & & \mathbf{All \ G1+A1-coded \ ams = 2 \times 292 + 104 = 688} \\
 | & \text{---} & & & | & & & \mathbf{All \ C1+U1-coded \ ams = 2 \times 460 - 104 = 816} \\
 | & & & & | & & & \\
 | & & & & | & & & \\
 | & & \mathbf{104} & & | & & & \\
 / & & & & \backslash & & & \\
 292 & \text{---} & 252 & \text{---} & 208 & \text{---} & 159 & \text{---} & 100 \\
 \mathbf{292} & & \mathbf{460} & & & & \mathbf{100} & & \mathbf{460 + 104 - 100 = 438, - 1 = U1} \\
 & & & & & & & & \mathbf{292 + 104 + 100 = 496, +1 = A1}
 \end{array}$$

g2. Division of number 544 in 2 x 272:

$$\begin{aligned} U1 &= 191 (\sim G1) & + 272 &= 463 \\ A1 &= 353 (\sim C1) + 416, & - 272 &= 497 \end{aligned}$$

$$\begin{array}{r} \text{A } 500 \\ \hline | \\ | \quad \text{U } 460 \quad | \\ | \quad | \quad || \\ \text{"5"} \text{---} \text{"4"} \text{---} \text{"3"} \text{---} \text{"2"} \text{---} \text{"1"} \\ | \quad | \\ 292 \quad 252 \quad 208 \\ G+101 \quad C-101 \quad | \\ \backslash 544 / \quad \times 2 = 416 \\ 2 \times 272 \end{array}$$

h. "Pure" A-U-codons and "pure" G-C-codons, 1st and 2nd positions:

$$\begin{aligned} \text{Ams with only G and/or C in 1}^{\text{st}} \text{ and 2}^{\text{nd}} \text{ position} &= 159 \text{ (GG + GC + CG + CC)} \\ \text{Ams with only U and/or A in 1}^{\text{st}} \text{ and 2}^{\text{nd}} \text{ position} &= 2 \times 208 + 159 = 575 \end{aligned}$$

$$\begin{array}{r} 367 \\ / \quad \backslash \\ \times 2 = 416 \quad \backslash \\ 292 \text{---} 252 \text{---} 208 \text{---} 159 \text{---} 100 \end{array} \quad \begin{array}{l} 416 + 159 = 575 = \text{A-U-group} \\ = 159 = \text{G-C-group} \end{array}$$

Main purpose on the following pages in part I is only to illustrate and investigate such number relations between this "exponent series" and amino acids from different aspects of division: codon groupings and some biochemical ones. It's hard to believe that all these relations are only accidental.

If not, why an exponent 2/3 and a "constant" x 100? Without pretending any ability to interpret the grounds for it, it's only possible here to suggest that the roots should be found in underlying levels of theoretical physics. The exponent series as a structuring principle could express laws in the same sense as Kepler's laws for the planets (where $A = T^{2/3}$ times a constant) or the equations for the spectral lines of hydrogen...?

If accepting a 5-dimensional model as a background, the results here could have implications for the analysis of structures and functions of proteins, however complicated as they may be.

The way of generating ams sums through minus/plus numbers of lower "degrees" remind of what is said about the background model and the figure in the introduction concerning debranched degrees, meeting "the other way around". (There is also a similarity in such a chain with exothermic reactions, as in steps 5→4→3, versus endothermic ones.)

Why the 4 double-coded ams, (2 of them in table 2, Arg AG and Ser AG)? One aspect could be that a given underlying mathematical scheme should be filled up.

Another possible aspect is that the "triplet series", approximating the numbers of amino acid totals, and the exponent series eventually represent different underlying levels in such schemes.

2 Internal divisions in codon groups, intervals in the exponent series and sums of groups in 1st and 2nd base order:

a. The division of the number 385 of Cross- and Form-coded ams (table 2):

209 and 176, -/+1 = 208 and 177 in the exponent series:

$$\begin{array}{r}
 544 \leftarrow 177 \rightarrow 367 \\
 / \quad \backslash \quad / \quad \backslash \\
 292 - 252 - 208 - 159 - 100 \\
 | \leftarrow 40 \rightarrow | \leftarrow 1 \rightarrow | \\
 \quad \quad \quad 44 \\
 | \leftarrow 133 \rightarrow | \leftarrow 59 \rightarrow | \\
 \quad \quad \quad 152 \rightarrow |
 \end{array}$$

- **177 = 133 + 44:** (292 - 159 = 133, 252 - 208 = 44)

-

2 x 44 -/+1 GU Val, **43** A, + AC Thr, **45** A

2 x 44 = CU Leu, 57 A (Val + 14, CH2) + UC Ser 31 A (Thr - 14, CH2)

- **UG = 177** (Trp + Cys).

UG + UC = **208**. Ser UC = 177 - 208 = **31**.

- **133 - 1 = 132 = GA** (Glu + Asp) = **AG** (Arg2 + Ser2) in this table.

- **152 + 1 = 153 = CA** (His + Gln). His 2 x 40 + 1, Gln (133-59) - 2.

[Individual number relations in the RNA- plus Pair-coded groups:

133 - 59 = 74, +/-1 Meth 75, Lys 73

59 - 1, - 2 = Asn 58, Ile1, Ile2, Leu1, Leu2 57

252 - 159 = 93, - 2 = Phe

208 - 100, - 1 = Tyr

44, - 2 = Pro. 44 - 59 = 15 = Ala. 100 + 1 = Arg. + Gly 1.]

b. Divisions within codon groups G1 + A1 = 688 and C1 + U1 = 816:

$$\begin{array}{r}
 \leftarrow 104 \leftarrow 104 \leftarrow | \\
 | \quad | \quad || \\
 \underline{292} - \underline{252} - \underline{208} - 159 - 100 \\
 + \underline{104} \quad + \underline{104} \\
 \hline
 \underline{396} \quad \underline{356}
 \end{array}$$

A division of one 208 number as example of processes also "inwards higher degrees" in the exponent series.

G1 + A1 = 688 = 292 + 104 = **396**, + **292**

C1 + U1 = 816 = 252 + 104 = **356**, + **252**, + **208**

G1 + A1:

396 = GA+GG + AA +AG = ams with only G or A in 1st and 2nd position

292 = GU+GC + AU +AC = ams with U or C as 2nd base.

396 = 3 x 132: GA = 132, AA+GG = 132, AG = 132.

C1 + U1:

356 = U1 without Tyr 107

252 = C1 without Arg 101 **208** = Arg + Tyr = CG + UA (complementary codons)

The distribution of atoms in these groups gives the same number divisions:

$$\begin{array}{rclcl} \underline{G1+A1=688}: & \mathbf{C-atoms} & = & \mathbf{396}. & \underline{U1+C1=816}: & \mathbf{C-atoms} & = & \underline{\mathbf{356 + 208}} \\ & \mathbf{N+O+S+H} & = & \mathbf{292}. & & \mathbf{N+O+S+H} & = & \mathbf{252} \end{array}$$

c. Intervals in the exponent series: more derivations of ams groups:

$$\begin{array}{cccccc} \frac{2 \times 272}{\text{"5} \quad 4} & & \frac{367}{3} & & \frac{259}{2} & & \frac{259}{1} & & 0 & \rightarrow \text{sums} \\ 292 \text{ --- } | \text{ --- } 252 \text{ --- } | \text{ --- } 208 \text{ --- } | \text{ --- } 159 \text{ --- } | \text{ --- } 100 \text{ --- } | \text{ --- } 0 & & & & & & & & & \\ & 40 & & \mathbf{44} & & 49 & & \mathbf{59} & & \rightarrow \text{intervals} \\ | \text{-----} \mathbf{84} \text{ -----} > | & & & & & & & & & \\ & & | \text{-----} \mathbf{152} \text{ -----} > | & & & & & & & \end{array}$$

Interval 59 -/+1:

Crossing additions as if counting on two sets of ams, in both 1st and 2nd base order.

$$G1 - 58 = C2 \quad U1 + 60 = A2$$

$$C1 + 58 = G2 \quad A1 - 60 = U2$$

Interval 44 = 252 - 208 = "4 - 3" and code base groups in 2nd base order:

$$544 - 367, - 44 = 133 = C2\text{-coded ams}$$

$$208 + 159, + 44 = 411 = G2\text{-coded ams}$$

$$272 + 208, - 44 = 436 = U2\text{-coded ams} - 1$$

$$272 + 208, + 44 = 524 = A2\text{-coded ams} + 1$$

Interval 152 = "4 - 1" and pairs of codon groups in 2nd base order:

$$C2 + U2 = 570 = 2(544 - 259) = 2 \times \mathbf{285}$$

$$\mathbf{285 - 152} = 133 = C2$$

$$\mathbf{285 + 152} = 437 = U2$$

$$G2 + A2 = 934 = 2(208 + 259) = 2 \times \mathbf{467}$$

$$\mathbf{467 - 208 + 152} = 411 = G2$$

$$\mathbf{467 + 208 - 152} = 523 = A2$$

Interval 84 = 292 - 208 = "5 - 3":

Crossing additions as if counting on two sets of ams:

$$U+A: 960, - \mathbf{84} = \mathbf{876} = C1 + A2$$

$$G+C: 544, + \mathbf{84} = \mathbf{628} = G1 + U2. \quad (C1 + 84 = U2)$$

$$C2 + U2 = 2 (544 - 259) = 570, \quad + 84 = 654 = G1 + U1 = C2 + A2 - 2$$

$$G2 + A2 = 2 (208 + 259) = 934, \quad - 84 = 850 = C1 + A1 = G2 + U2 + 2$$

In general terms these number operations as +/- 84 ("5" — "3") could express a process outwards - inwards: "5 → 4 → 3 — 3 → 4 → 5".

d. Tyr and Arg:

Referring to the derivation of single codon base groups (*le, f, page 9*), sums of the R-chains were received through plus/minus intervals 100 +1, 108 -1, representing A-numbers of R-chains for Arg and Tyr:

$$G1 = 292 - 101 \quad U2 = 544 - 107$$

$$C1 = 252 + 101 \quad A2 = 416 + 107.$$

$$\begin{array}{cccccc}
 292 & - & 252 & - & 208 & - & 159 & - & 100 & - & 0 \\
 "5" & & 4 & & 3 & & 2 & & 1 & & 0" \\
 & & & & \leftarrow & & & & \leftarrow & & \\
 & & & & 107 + 1 & & & & 101 - 1 & & \\
 & & & & \text{Tyr } 107 & & & & \text{Arg } 101 & & \text{R-chains}
 \end{array}$$

It could perhaps be possible to identify these intervals with these ams: Arg then presumed as debranched from a G1-codon, connected as it is with Gly GG in creatinephosphate, and Tyr as debranched from a U2-codon as derived from Phe UU? (Tyr - Arg make up the end of the α -chain of hemoglobine.)

[In the background model the last step 1 → 0 is interpreted as a step from d-degree 1 into motions. It has been told that Arginine is especially rich in the tails of sperms.]

However, number 101 appears also in other contexts.

The derivation of U1- and A1-groups of ams was a bit more complicated, including division of number 208 in 2 x 104:

$$A1: 292 + 104 = 396, + 101 \text{ (cf. Arg AG)} = 497$$

$$U1: 252 + 104 = 356, + 107 \text{ (cf. Tyr UA)} = 463$$

A simpler way to derive these sums is through imaging that Cys UG, 47 A, has moved from an A1-code (Ser AG - or Meth AUG?) to an UG-code:

$$A1 = 544 - 47 \text{ (Cys)} = 497,$$

$$U1 = 416 + 47 = 463. \quad \text{But number 47 not in the exponent series.}$$

e. Additions of two sets of ams, 1st and 2nd base order:

If counting with two sets of ams, both in 1st and 2nd base order, it gives the following simple derivations of G1 + G2, A1 + A2 etc.:

$$\begin{array}{ll}
 "5" & 2 \times 292 = 584 \quad - 100 = 484 = C1 + C2 - 2 \\
 "4" & 2 \times 252 = 504 \quad + 100 = 604 = G1 + G2 + 2 \\
 "3" & 2 \times 208 = 416 + 584 \quad - 100 = 900 = U1 + U2 \text{ (U1+U2 from the C-groups)} \\
 "3" & 2 \times 208 = 416 + 504 \quad + 100 = 1020 = A1 + A2 \text{ (A1+A2 from the G-groups)}
 \end{array}$$

3. Some general first comments on observations in the Exponent series:

a. Number of ams in each group G - C - U - A:

$$5 + 4 + 3 = 12, \quad \times 2 = 24$$

$$\begin{array}{c} | \quad \quad \backslash \quad / \\ 5 \quad \quad 7 \end{array} \quad 5 + 5 \text{ ams G1 + C1}, \quad 7 + 7 \text{ ams U2 + A2} \quad (5 \times 77 = 385.)$$

$$A1 = 2 \times 4, \quad U1 = 2 \times 3, \quad G2 = 2 \times 3, \quad C2 = 2 \times 2$$

These numbers of ams could support the general suggestion here of a “5-dimensional” chain such as the exponent series behind the g4enetic code.

The quotient between A+U-bases and G+C-bases in RNA has been said to be circa 1,4. (Concerned higher species?) The quotient in that case seems related to a single set of ams - *including* the 4 double-coded ams, essential to observe.

b. **G1-coded ams come first** in experiments by laboratories, so one says. — as in the derivation of mass according to this exponent series.

It has also been said that there seems to have been a “press” towards more A-T (U-A)-rich codons during first unicellular development (although not unambiguous) [3]. Here it’s possible to see this as a development in the steps “5” → “4” → “3”, a direction in the process.

c. **292, = “5” in the exponent series, is the sum of Inosine 136 A+ Orotate 156 A** from which the 4 code bases derive [1].

Note the complementary features in their construction:

(See http://www.u5d.net/booklets/bch_bases_synthesis.html.)

d. **146 = 292/2 = α-ketoglutarate** (uncharged), an essential station in the citrate cycle, from which the ams Glu (146 A charged) directly derives, and Glu has a central role for the ammoniating of amino acids [1, 2]. (146 also the A-number of Lys, R+B.)

e. **146 is also the number of base pairs of DNA rolled up on each of the Histone conglomerates** in the chromosomes. (Histones are also of 5 kinds). [4]

Is this just a coincidence? The same number on quite different levels of units? According to the first hypothesis here, it could be an example of the same underlying mathematical, multidimensional structure, steering the processes on both lower and higher levels.

Number of amino acids 20 → 24, with 4 double-coded ams:

There are 5 + 4 + 3 in the codon type groups: 6 of each kind, but arranged 4 x 3 in Cross-plus Formcoded ams. In RNA- plus Pair-coded ams the A+U-groups dominate with 8 ams. A simple view on the 4 double-coded ams could be the counting: 5 x 4 = 20 → 4 x 3 x 1 = 24, referring to the background model where higher dimension degrees (d-degrees) transform into lower ones. This is another eventual aspect, besides the role of the double-coded ams to fill up a scheme. (Compare also Part II: 20 in a base-10 system = 24 in a base-8 system.)

{Perhaps worth a note too is the possibility of reading ams sums from a simple “5-chain”:

$$\begin{array}{ccccccc} 5 & - & 4 & - & 3 & - & 2 & - & 1 & - & 0 \\ 5 & & 4 & & & & 6 & & & & \\ & & & & & & & & & & \end{array} \quad \frac{5-4-6, \times 6}{5-4-6} = 3276 = 24 \text{ ams R+B}$$

$$5-4-6 \quad \times 5, \quad \frac{+5}{5} = 2735, \quad 20 \text{ ams R+B.} \quad 5-4-6 \quad \times 1 - \frac{5}{5} = 4 \text{ double-coded ams R+B}$$

4. 3rd base groupings of the amino acids (R-chains):

$$\begin{array}{rcl}
 3^{\text{rd}} \text{ base A/G (+A or G)} = 8 \text{ ams} = \text{mass sum of R-chains} & \mathbf{638} & \\
 & & > \mathbf{1169} \\
 3^{\text{rd}} \text{ base U/C} = & = 8 \text{ ams} = & \text{-- " --} & \mathbf{531} \\
 3^{\text{rd}} \text{ base indifferent} & = 8 \text{ ams} = & \text{-- " --} & \mathbf{335} > \mathbf{335}
 \end{array}$$

It's possible to derive the two main groups -/+ 1 from the exponent series too:

$$\begin{array}{rcl}
 752 - 416 = 544 - 208 = \mathbf{336}, & - 1 = \text{indifferent } 3^{\text{rd}} \text{ base} & \\
 752 + 416 = 960 + 208 = \mathbf{1168}, & +1 = \text{A/G (or G) + U/C, } 3^{\text{rd}} \text{ base} &
 \end{array}$$

This sum **1168 = 2 x 584. 4 x 292:**

$$\begin{array}{rcl}
 G1 + A1 = \mathbf{688}, & \text{minus the "2-base-coded" ams (104)} & = \mathbf{584}. \\
 C1 + U1 = \mathbf{816}, & \text{minus the "2-base-coded" ams (231)} & = \mathbf{584}, +1
 \end{array}$$

Note that number 1168 (+1) in 2nd base order is divided
 $2 \times 416 = G2 + A2$, and $544 - 208 = 336$, $+1 = U2 + C2$.

Inosine + Orotate x 4 = 1168: Is it a coincidence ?

A/G + (A or G) in 3rd position seem to refer to their origin in Inosine, U/C as equivalent in 3rd position to Orotate, and there is 8 ams in each group.

The first, main division in 3rd codon base grouping could be thought of as governed by these origins of the bases, giving (as would be proper) 2 sets of these groups:

$$\begin{array}{rcl}
 \text{Codon bases A and G from Inosine,} & \mathbf{136 A:} & 8 \times 136 = 1088 = \mathbf{2 \times 544} \\
 \text{Codon bases U and C from Orotate,} & \mathbf{156 A:} & 8 \times 156 = \mathbf{1248} = \mathbf{2 \times 624} \\
 & & \Sigma = \mathbf{2 \times 1168}
 \end{array}$$

However, the division *within* these groups does not accord with the right one. In numbers of the exponent series this could be written:

$$\begin{array}{rcl}
 544 & + 93 & = 637 = \text{A and or G as } 3^{\text{rd}} \text{ base} - 1 \\
 544 - 208 & & = 336 = \text{indifferent } 3^{\text{rd}} \text{ base} + 1 \\
 416 + 208 = 624, & - 93 & = 531, \text{ U or C as } 3^{\text{rd}} \text{ base}
 \end{array}$$

[Why 93 ? **93** is the interval 252 — 159, "4" — "2" in the exponent series. It could eventually too be interpreted as a position, inviting the "21st amino acid", UGA, with Se, 93 A (if isotope 78) to fill a scheme in this respect: a variation of Cys, UG, with 3rd base U/C. (?)]

An association: The "2-base-coded" are 6 out of 10 in the G+C-group, 2 out of 14 in the U+A-group. With the aspect of debranched degrees as numbers, it gives the chain

$$\begin{array}{cccc}
 2 & \text{---} & 6 & \text{---} & 10 & \text{---} & 14, & \text{reminding of the orbitals } \mathbf{s, p, d, f} & \text{ in electron shells...} \\
 \uparrow & & \uparrow & \text{---} & \downarrow & & \downarrow & & \\
 \uparrow & \text{---} & & & & & \downarrow & &
 \end{array}$$

(Cf. Ams with "2-base-codons" in G1+C1-group = 259, "2" + "1" in the exponent series.)

The “2-base-coded” in each group:

$$\begin{array}{l} \text{G1+ A1: } \text{GG+GC} + \text{GU+AC} = \mathbf{104} \\ \text{U1+ C1: } \frac{\text{CC+CG}}{\mathbf{159}} + \frac{\text{CU+ UC}}{\mathbf{176}} = \mathbf{231} \end{array}$$

159 the part of RNA+Pair-coded ams,
176 the part of the Cross+Form-coded.

104 = “2-base-coded” of G1 + A1 = $\frac{1}{2} \times \mathbf{208}$,
231, -1 (if Arg uncharged) = “2-base-coded” of C1 + U1 = $\frac{1}{2} \times \mathbf{460}$ (= **252** + **208**).

There is the same division -/+2 within the “2-base-coded” ams in 2nd base ordering:
 G2 + A2 = 934, - **102** = $\frac{832}{2} = 2 \times 416$
 C2 + U2 = 570, - **233** = $\frac{337}{2}$, = 336 +1. 584 +/- 248 = 832, 336. 248 = 584 - 336.

Inosine and Orotate added to number 292:

Adding the mass numbers of these parents of the codon bases to 292 = “5”, to the next numbers in the exponent series, “4” and “3”, the sums x 2 become the totals for G+A-coded ams and U+C-coded ams respectively:

$$\begin{array}{l} \text{G1 + A1} = 688 = \mathbf{2 \text{ Inosine} \rightarrow 136} + \mathbf{2 \times 208} \quad (2 \text{ Inosine} = 272 = \frac{1}{2} \times 544) \\ \text{C1 + U1} = 816 = \mathbf{2 \text{ Orotate} \rightarrow 156} + \mathbf{2 \times 252}. \quad (2 \text{ Orotate} = 312 = \frac{3}{2} \times 208) \end{array}$$

“5”	“4”	“3”	“2”	“1”
292	252	208	159	100
↓→	<u>+ 156</u>	<u>+ 136</u>		
	= 408	= 344		
	x 2 = 816	x2 = 688		
	C1+U1	G1+A1	ams sums,	R-chains

Could there be a direct involvement of these parents to the bases in the “whole” of a pre-amino acid configuration? The question will be returned to in part II.

Referring to the main division again, one general assumption seems to be that the mass numbers of the two molecules Inosine and Orotate are very closely connected - in one direction or the other ? - with the groups of R-chains of ams, — and the exponent series.

The arithmetic seems to support the general presumption in the introduction that numbers reign, more or less irrespective of what they represent.

Another eventual interpretation of 3rd base dividing:

"5 ——— 4 ——— 3 ——— 2 ——— 1 ——— 0"
\ 544 / 208 159 100
272+272 367 259
↓ ——— + ——— ↑ ——— ↑

$$\text{A/G-coded ams: } \mathbf{272} + \mathbf{367} = 639, \quad - 1 = \mathbf{638}$$

$$\text{U/C-coded ams: } \mathbf{272} + \mathbf{259} = \mathbf{531}$$

5. The B-chains, the similar part of all amino acids:

If the exponent series in many ways seem to steer mass numbers in the genetic code, it isn't the case for the separate, unbound amino acids. There is no connections as it seems between *codon grouped* whole ams, with B-chains included, and this series, and this can be regarded as very natural: The genetic code is a code for proteins, for bound ams where the B-chains form an own "co-ordinate axis" and of this reason may be analysed separately from the R-chains. It makes it reasonable - from the viewpoint of the genetic code - to look at the development in the direction of fragmentation through H₂O as additions.

However, looking at the B-chains separately from codons, sums of B-chains seem connected with the exponent series too:

The numbers of B-chains:

In unbound ams: (H)HN - CH - COO(H) = **74 A**, -1 in Arg 1 and 2, Lys and Pro. [1]

In ams bound through condensation: HN - CH - CO = **56 A**

$$544 - 100 = 444 = 6 \text{ B-chains } \hat{=} 74 \text{ A,}$$

$$544 - 208 = 336 = 6 \text{ B-chains bound } \hat{=} 56 \text{ A}$$

$$208 - 100 = 108 = 6 \text{ H}_2\text{O } \hat{=} 18 \text{ A}$$

$$544 - 101 = 443, \times 4 = 1772, \text{ the sum of } 24 \text{ B-chains.}$$

(There are the number 101 again, but hardly - or only in Arg1,2, not in Lys, Pro, - connected with Arg (charged), as perhaps could be the case in the groups of R-chains (G1 = 292 - 101, C1 = 252 + 101).

Number 74 could be defined as an interval of second order:

$$\begin{array}{ccccccccc} 292 & & 252 & & 208 & & 159 & & 100 \\ | & & | & & | & & | & & | \\ \leftarrow & & \leftarrow & & \leftarrow & & \leftarrow & & \leftarrow \\ & & 133 & & 74 & & 59 & & \\ & & & & & & & & \text{Asp R+B} = 133, \text{ Asp R-chain} = 59 \end{array}$$

Is there anything in the division of the B-chains that could support the simple interpretation or reading above? So it seems:

For the bound ams, there is first the simple dividing:

$$\begin{array}{ccccccc} 544 & \text{---} & | & \text{---} & 208 & \text{---} & | & \text{---} & 100 \\ & & 336 & & & & 108 & & \\ & & 6 \times 56 & & & & 6 \times 18 \text{ (H}_2\text{O)} & & \text{- deducted through condensation.} \end{array}$$

For unbound B-chains:

$$\begin{array}{ccccccccc} 292 & & 252 & & 208 & & 159 & & 100 & & 0 \\ | & & | & & | & & | & & | & & | \\ 544 & \leftarrow & & \leftarrow & & \leftarrow & & \leftarrow & & \leftarrow & 100 \\ \text{intervals} & & 177 & & & & 267 & & & & \\ & & 177 / 6 = 29,5 & & & & 267 / 6 = 44,5 & & & & \end{array}$$



Condensation raises the border of division half a step, from 367 to 208. The half unit 0,5

seems to mirror the fact that the H-atom in the COOH-end changes position to the NH₂-end, giving the plus-charged and the minus-charged ends in peptides...

The division *within* bound B-chains à 56 A could naturally be thought of as across the position for condensation, which could give:

$$\frac{\text{CH(R)}}{13} \text{—NH—} \frac{\text{CO}}{43} = 13 \text{—} 43.$$

	Exponent series:
6 x 13 = 78, - 1 = 77	= 544 - 467 (467 = 208 + 259 + 100),
6 x 43 = 258, +1 = 259	(544 - 208 = 336, - 259 = 77.)

Some other notes:

- a) The number of B-chains from the exponent series was grouped in 6: Two of the number series giving the R-chains with the operation below are not enough for the B-chains:

$$\begin{aligned} 544 + 208, \times 2 &= 1504 = 24 \text{ R-chains} \\ 544 - 208, \times 2 &= 672 = 12 \text{ B-chains bound} \end{aligned}$$

Should the first three steps in the exponent series eventually be read both forward and backwards, (as in the “triplet series 5-4-3 + 3-4-5 = 888, x 2 = 24 unbound B-chains)? Eventually connected in some way with the opposite directions of R-chains in proteins?

- b) There are other ways deriving groups of unbound B-chains for G+C-coded and A+U-coded ams: 2 x 5 and 2 x 7 B-chains:

$$\begin{array}{rcccccccc} & & & & & & \underline{259} & & \\ 292 & - & 252 & - & 208 & - & 159 & - & 100 & - & 0 \\ & & & & & & \text{<—107—>} & \text{<—101—>} & & & \\ 292 - 101 & = & 191 & = & \text{R-chains G1 (5 ams)} & & & & & & \\ 292 - 107 (\sim \text{next interval}) & = & \mathbf{185}, \times 2 & = & \mathbf{370}^* & = & 5 \text{ B-chains à } 74. & & & & \\ & & & & \mathbf{259}, \times 2 & = & \mathbf{518} & = & 7 \text{ B-chains à } 74. & & \end{array}$$

$$\begin{aligned} \text{*Cf. R-chains of groups: } & \text{UG} + \text{GU} + \text{UU} + \text{GG} = \mathbf{370 - 1} \\ & \text{AC} + \text{CA} + \text{AA} + \text{CC} = \mathbf{370 + 1}. \end{aligned}$$

- c) All R-chains of ams with A-base in 1st or 2nd position = **888 + 1**, ~ 12 B-chains.
All R-chains with C in these positions = 444. x 2 = **888**.

Could there eventually exist some deep number connection with the common A-C-C-end of t-RNAs?

- d) Number 336 = 3 x 112, 112 the A-number of the U-base, the sum of 2 bound B-chains. Is it a coincidence that T in DNA is replaced by the U-base at start of the protein synthesis? There are of course chemical aspects of this replacement too: the hydrophobic CH₂-group deducted for outward direction of RNA. Yet, the number itself may represent an essential, underlying arithmetical scheme?

- e) **56**, the number of bound B-chains, x **3/2** = 84, the interval 292 — 208.
74, the number of unbound B-chains, x **3/2** = 111, number 544 - 100, divided in 4.
111 also = A-number for the C-base - and the interval in the “triplet eries”.

The factor 3/2 could be regarded as an expression for an intimate connection between B-chains, as always lacking 1/2 - and therefore the urge for growing chains?

6. N-Z-divisions:

The first observations from table 1 showed that the sums of G+C-coded ams and A+U-coded ams become the same in 1st and 2nd base order. It also shows that N- and Z-sums only differ with +/-1 between 1st and 2nd base ordering. This latter observation led to the investigation below: How is the difference distributed in each codon base group? Is there some interesting information hidden behind the similarities?

$$\begin{array}{rcccl}
 \text{A} & & & & \text{A} \\
 \hline
 \text{G1: } 191 & \xrightarrow{+(100+1) \text{ N}} & \mathbf{292} & \xrightarrow{+ (120-1) \text{ Z}} & 411 \text{ G2} \\
 & & & & \\
 \text{C1: } 353 & \xrightarrow{- 100 \text{ N}} & \mathbf{253} & \xrightarrow{- 120 \text{ Z}} & 133 \text{ C2} \\
 & & & & \\
 \text{U1 } 463 & \xleftarrow{- 3 \text{ Z}} & \mathbf{460} & \xleftarrow{- 23 \text{ N}} & 437 \text{ U2} \\
 & & & & \\
 \text{A1: } 497 & \xleftarrow{+ (3+1) \text{ Z}} & \mathbf{501} & \xleftarrow{+ (23-1) \text{ N}} & 523 \text{ A2}
 \end{array}$$

The numbers from the exponent series appear (+1 in C- and A-groups) and it seems as if this series rules over the N-Z-division too, dividing the N-/Z-distribution, if reading A- and U-groups backwards from 2nd to 1st ordering. (Cf. number of ams equally divided between G1 and C1, 5+5, +/-1 in 1st base ordering, but between U2 and A2, 7+7. -/+ 1 in 2nd base ordering.)

Numbers 500, 460:

$$\begin{array}{r}
 \text{A } \mathbf{500} = 292 + 208 \quad \rightarrow \text{A-numbers R: A1} = 500 - 3 \\
 | \quad \quad \quad | \quad \quad \quad | \quad \quad \quad | \quad \quad \quad | \\
 | \quad \quad \quad | \quad \quad \quad | \quad \quad \quad | \quad \quad \quad | \\
 \text{"5"} \quad \quad \quad \text{"4"} \quad \quad \quad \text{"3"} \quad \quad \quad \text{"2"} \quad \quad \quad \text{"1"} \quad \quad \quad 0 \\
 \mathbf{292} \quad \quad \quad \mathbf{252} \quad \quad \quad 208 \\
 \text{G} \quad \quad \quad \text{C} \\
 \mathbf{292 + 500 = 792}, \quad - 1/2 \times 208 = \mathbf{688} = \mathbf{G1 + A1} \\
 \mathbf{252 + 460 = 712}, \quad + 1/2 \times 208 = \mathbf{816} = \mathbf{C1 + U1}
 \end{array}$$

Cf. the triplet series, 543+432+321+210 = 1506, with +1 in numbers for C- and A-groups. 012+123+234+345 = **714**, 712 +2. Interval 1506 - 714 = **792**.

Adding Z- and N-numbers crosswise, counting with two sets of ams, gives these same numbers:

$$\begin{array}{l}
 \text{G1 Z} + \text{G2 N}, 105 + 187 = \mathbf{292}, \quad \text{C1 Z} + \text{C2 N} = 195 + 58 = \mathbf{253}. \\
 \text{U2 Z} + \text{U1 N}, 247 + 213 = \mathbf{460}. \quad \text{A2 Z} + \text{A1 N} = 282 + 219 = \mathbf{501}
 \end{array}$$

The complementary additions give the numbers 310 - 233 - 440 - 519:

They are given by -/+ the **interval "2 - 1" = 59** in the exponent series (-/+ 1).

Interval 49 in the middle step: "3" — "2" : 208 – 159:

This interval, -/+ **49** (+/-1) gives the N-Z-division between main codon groups G+C, A+U:

			<u>1st base order</u>	<u>2nd base order</u>
292	- interval 49	= 243	= N - 1, G+C-groups	- 2 G+C
252	+ interval 49	= 301	= Z + 1, - " -	+ 2 G+C
544 / 2: 272 + 208	- interval 49	= 431	= N - 1, A+U-groups	+ 0 A+U
" 272 + 208	+ interval 49	= 529	= Z + 1, - " -	+ 0 A+U

Receiving numbers of ams groups through plus/minus intervals in the exponent series (see also page 13) could support the suggested view on “the whole” in terms of a coordinate system, axes pointing in opposite directions (signs +/-), representing polarities as different properties. Intervals between intervals as a mix:

$$\underline{\text{“5 - 4”}} = 40 \leftarrow \text{19} \longrightarrow 59 : \underline{\text{“2 - 1”}}$$

H-atoms in R-chains = 152 = 8 x 19:

In the displacements above from 1st to 2nd base order the difference N - Z = 19 -/+1. The H-atoms are distributed on the individual codon groups with circa

$$\begin{aligned} 1/8 - 2/8 - 2/8, 3/8 &= 19 - 38 (-1) - 38 (-1) - 57 (+2): \\ &\quad \text{G1 - C1} \quad \text{U1} \quad - \quad \text{A1} \\ &\quad \text{C2 - G2} \quad \text{A2} \quad - \quad \text{U2} \quad (\text{C2 17, G2 37, A2 41, U2 57}) \end{aligned}$$

With this division of H-atoms it's possible to derive the N- and Z-numbers of the individual codon base groups +/-1 (+/- 2 in the last A-base group with Lys AA and Arg AG charged).

$$\begin{aligned} \text{Examples:} \quad \text{G1: } 191 \text{ A, } - 19 &= 172, \times \frac{1}{2} = 86 \text{ N,} \quad + 19 = 105 \text{ Z.} \\ \text{A1: } 497 \text{ A, } - 57 &= 440, \times \frac{1}{2} = 220 = \text{N} + 1, + 57 = 277 = \text{Z} - 1 \end{aligned}$$

How could this distribution of H in eighth be interpreted in relation to the exponent series? Perhaps it's guided from a more elementary level? $(15/8)^{2/3} \times 100 = 152$. $15/8 = (5 \times 3 \times 1)/(4 \times 2)$.

The whole sums N and Z in 24 R-chains:

$$\begin{aligned} 2 \times 544 - 259 &= \mathbf{829} = \mathbf{Z \text{ total} + 1} \quad \text{or} \quad \text{“4 + 3 + 3 + 2”} = 460 + 367 = 827 = \text{Z} - 1 \\ 2 \times 208 + 259 &= \mathbf{675} = \mathbf{N \text{ total} - 1} \quad \frac{\text{“3 + 3 + 2 + 1”} = 416 + 259}{\text{H} = \text{“4”} - \text{“1”} = 152} = \text{N} - 1 \end{aligned}$$

Other examples of crosswise additions, this one giving equal (or +2) divisions N--Z:

$$\begin{aligned} \text{N-number:} \quad \text{G1 + U1} &= 299 &= 299 &= \text{A2 + C2} \\ &\underline{\text{G2 + U2} = 377} &= 377 &= \text{A1 + C1} \\ \text{Z-number:} \quad \text{G1 + U1} &= 355 \quad +2 &= 357 &= \text{A2 + C2} \\ &\underline{\text{G2 + U2} = 471 \quad +2} &= 473 &= \text{A1 + C1} \end{aligned}$$

Crosswise addition N-Z between G2-C2-groups, U2-A2-groups gives the same numbers as Cross-plus Formcoded 770, RNA- plus Pair-coded 734:

$$\begin{aligned} \underline{\text{G2: N + C2: Z}} = 262 &\rightarrow \mathbf{734} \leftarrow \underline{\text{U2: N + A2: Z}} = 472. && \text{Interval } 208 + 2. \\ \underline{\text{G2: Z + C2: N}} = 282. &\rightarrow \mathbf{770} \leftarrow \underline{\text{U2: Z + A2: N}} = 488. && \text{Interval } 208 - 2. \end{aligned}$$

Summing-up: Even without a deeper interpretation of the rather intricate N-Z-relations above, a bit like lace-making in the crosswise additions, it's possible to see them connected both with codons and with the exponent series as a suggested structuring principle.

Number 246, sum of displacements in N+Z from 1st to 2nd base order:

In G-C-groups **220**, in A-U-groups **26**. One way to get these numbers, abbreviated:

$$\text{G-C: } 5^{4/3} - 4^{4/3}, \underline{\times 100} = \mathbf{220}. \quad \text{A-U: } (5+3)^{4/3} - (4+3)^{4/3}, \underline{\times 10} = \mathbf{26}.$$

Could the exponent 4/3 represent an underlying level? (Cf. page 29, b, d.)

246 happens to be the sum of the 4 double-coded ams too (R-chains): Any connection? The question is returned to in part II.

8. Biochemical aspects as basis of mass division:

a. R-chains grouped with respect to kind of atoms CHx only or + N-O-S:

9 ams with only CHx-groups (+ Gly, only H)	= 420
Gly, Ala, Val, Leu 1, Ile 1, Ile 2, Pro, Phe, Leu2	> 888 = 2 (544 - 100)
8 ams with S and O-atoms (and no N):	= 468
Meth, Cys, Ser1, Ser2, Thr, Tyr, Asp, Glu	
7 ams with N-atoms, including Gln, Asn:	= 616 > 616 = 2 (208 + 100)
Trp, Asn, Gln, Arg1, Arg2, His, Lys	= 416 -2, + 2 Arg A 101

This way to group the R-chains in rough accordance with the exponent series could mirror the more fundamental development from CHx-groups to carbohydrates to amination, replacing oxygen O with nitrogen N.

Arranging the groups according to the reference [1] in nonpolar ams (= the one with only CHx-groups) versus polar ams plus ams “with polarising effect” gives

$$420 \text{ ——— } 1084 (468 + 616) = 2 \times 416 +4, 2 \times 544 - 4.$$

(An association: Could eventually a similar chemical characterisation be motivated which divide the ams in 8-8-8-groups? Some decades ago there was a view on the strong force that it seemed to involve 8 gravitational like potentials, 8 complex, resembling electromagnetic ones – and 8 simple, attraction like potentials: the number of 24, as the amino acids here. The amino acids as the strong force on a superposed level!?)

b. Glycolysis - citrate cycle: derivations of ams from these stations [1, 2]:

Can such an investigation, although not unambiguous, reveal some pattern?

Here is Ala, GC, regarded as derived from Oxaloacetate (can also derive from Pyruvate). Ser2, the same (AG-codon presumed), since there is another way (outside the main steps) from Oxaloacetate via Homoserine to 3-P-glycerate.

<i>Glycolysis</i>			<i>Citrate cycle</i>		
<i>3-P-glyc.</i>	<i>P-enolpyruvate</i>	<i>Pyruvate</i>	<i>Oxaloacetate</i>	<i>α-ketoglutarate</i>	
Gly GG	Trp UGG	Val GU	Ala GC	Glu GA	
Ser1 UC	Tyr UA	Ile1 AU	Asp GA	Gln CA	
Cys UG	Phe UU	Ile2 AU	Asn AA	Lys AA	
Meth AUG		Leu2 UU	Thr AC	Pro CC	
		Leu1 CU	Ser2 AG	Arg1 CG	
				Arg2 AG	
				His CA*	
<u>U1 (U2)+G1</u>	<u>U1</u>	<u>U2</u>	<u>G1 - A1</u>	<u>C1 - A1 +G1</u>	
154	328	271	208	543	
1/2 x 960 +2		1/2 x 544 -1			
<hr/>			<hr/>		
752 +1			752 -1		

* (His derives from A-base but can break down to this station [1].)

With Gly from some ams in α-keto-group the division should become totally equal.

- Sum of all ams with U in 1st or 2nd position is 752, exactly half of the total sum and = “5” + “4” + “3” in the exponent series. All ams with U-containing codons derive

from glycolysis, which as a suggestion has connection with the fact that UTP - UDP... is the coenzyme working with carbohydrates [1].)

- According to numbers, it seems as if the whole process from breaking down fructose to α -ketoglutarate and Glu, as mainly responsible for amination, should be read backwards, with start at number 543 (544 - 1). α -ketoglutarate has as said before the number $292/2 = 146$ uncharged.

The directions of the process from glycolysis outside mitochondria to the citrate cycle inside these is also inwards in this sense, which give cause for seeing the process backwards - as from higher to lower dimension degrees as outwards in the background model.

- With Ala removed to the glycolysis side, the division in numbers become 768 - 736, +/- 2H reminding of the similar division in codon type groups: 770 - 734, but - essential to say, without any connections with codons.

Yet, main codon grouping of ams gives sums from the exponent series:

		<u>1st base grouping</u>		<u>2nd base grouping</u>	
		<u>G+C</u>	<u>A+U</u>	<u>G+C</u>	<u>A+U</u>
Glycolysis:	753: ←	<u>100 + 1</u>	<u>752 - 100</u>	<u>208 + 1</u>	<u>544</u>
		↑	↓	↑	↓
Citrate cycle:	751: →	<u>544 - 100 - 1</u>	<u>208 + 100</u>	<u>336 - 1</u>	<u>416</u>

Mass number distribution above: displacements from 1st to 2nd base ordering:

G1+C1 ↔	G2+C2:	Glycolysis	-	108
- " - ↔	- " -	Citrate cycle	+	108
A1+U1 ↔	A2+U2	Glycolysis	+	108
- " - ↔	- " -	Citrate cycle	-	108
(108 = 208 - 100 = "3 - 1"-interval.)				

108 = 6 x 18 (H₂O). -/+ H₂O an essential aspect on these processes.

Distribution of atoms in R-chains of ams, expressed in numbers of the exponent series:

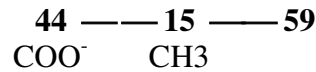
<u>Glycolysis,</u>	<u>Citrate cycle</u>	
= <u>47 C = 564</u>	<u>33 C = 396</u>	(Cf. divisions page 11.)
252 + 208, + 104	← = 292 + 104	
	diff. 168	
<u>S+O+N+H</u>	<u>S+O+N+H</u>	
<u>188 + 1</u>	<u>356 - 1</u>	
= 292 - 104, + 1	→ = 252 + 104, - 1	
	diff. 168, - 2	

It could be essential to add that many numbers from the exponent series dealt with here appear in the glycolysis - citrate cycle, for instance:

104, 3-phospho-glycerate charged,
2 x 44, pyruvate uncharged,

192 (292 - 100) isocitrate uncharged,
 146, as mentioned above, = α -ketoglutarate uncharged,
 100, succinyl charged,
 101 succinyl uncharged,
 2 x 58 = 116, succinate
 and 59, the essential incorporated group $\text{CH}_3 - \text{COO}^-$, charged*.

*Cf. intrvals in the exponent series: 252 —|— 208 — 159 —|—100



Compare **Ala, 15 A (R)**, as derivable “across” the border outside/inside mitochondria.

c. Codons with U as 1st or 2nd base: all in stations of the glycolysis:

As suggested above it could be connected with the role of UTP (-DP...) as the active coenzyme in reactions of carbohydrates?

The sum 752 of U-containing codons (1st and 2nd position) is divided in this way:

$$\begin{array}{rcl} \text{Cross- + Form-coded ams with U in codons} & = & \mathbf{308}. \text{ The rest} = 462 = \mathbf{460} + \mathbf{2} \\ & & \uparrow \qquad \qquad \qquad \uparrow \\ \text{RNA- + Pair-coded ams with U in codons} & = & \mathbf{444}. \text{ The rest} = 290 = \mathbf{292} - \mathbf{2} \end{array}$$

Arrows for the reading direction of numbers related the exponent series.

$$444 = 544 - 100, \quad 308 = 208 + 100$$

$$\begin{array}{r} \mathbf{444} \qquad \mathbf{308} \\ \underline{544 - 100} \quad \underline{208 + 100} \\ \mathbf{292} \quad - \quad \mathbf{252} \quad - \quad \mathbf{208} \quad - \quad 159 \quad - \quad 100 \quad - \quad 0 \quad \text{Exponent series} \\ \mathbf{292} \qquad \qquad \mathbf{460} \end{array}$$

There is the same division too between the rest (no codons with U), if this rest is divided in G1+C1 \longleftrightarrow A1:

$$\begin{array}{l} \mathbf{444} = \text{G1} + \text{C1}, \text{ ams without U-containing codons} \\ \mathbf{308} = \text{A1}, \text{ ams without U-containing codons} \end{array}$$

d. P-ribose-groups in nucleotides - and why triplets of bases?

The P-ribose-groups in chain binding = **195** uncharged, 194 charged (64 or 63 + 131):

$$\mathbf{584}, \mathbf{2 \times 292} \text{ in the exponnt series} = \mathbf{3 \times 195 - 1}.$$

This number from the exponent series could be one aspect on the cause for triplets of the bases in codons.

$$\mathbf{(H)PO}_2 = 64 \text{ A}, \times 3 = 192 = \mathbf{292 - 100}, \text{ Ribose-group} = 131 \text{ A}, \times 3 = \mathbf{292 + 101}.$$

Also: in the AMP-transportation of B-chains to t-RNA, the B-chains have mass value 73, half of number 146: 24 B-chains = 6 x number 292 = “5”.

9. The codon bases in relation to the exponent series:

It was earlier observed that the two molecules from which the bases derive in developed organisms [1], Inosine and Orotate, with masses (A-numbers) 136 and 156, give the sum 292, the first number in the exponent series.

Is it also possible to relate the mass numbers of the codon bases to this series? Below some annotations, not meant in themselves to convince of such a relation:

G-base:	151 A,	included +1 for bond to ribose
C-base:	111 A,	- “ -
U-base:	112 A	- “ -
A-base:	135 A,	- “ - Sum RNA-bases 509 A
T-base:	126 A,	- “ - Sum DNA-bases (T instead of U): 523 A

RNA-bases:

The 4 RNA-bases bound = **505**, ~ $1/2 \times 1011$, sum of the whole exponent series.

DNA-bases: 4 x the mass numbers of the DNA bases:

4 x C-base	= 544 - 100	("5+4 - 1")	
4 x G-base	= 504 + 100	("4+4 +1")	
4 x A-base +1	= 544	("5+4")	Why 4 of them.
4 x T-base - 1	= 500	("5+3")	Cf. further part II.

N-Z-division in 4 DNA-bases, sum 523 A, to compare with the exponent series:

Z:	272 = 544/2	G+C: 136,	A+T 136
N:	251 = 252, -1	G+C: 126,	A+T 125

Mean value of a base pair of DNA

happens to be the quotient: **544 / 208, x 100 = 261,5.**

Synthesis of Inosine and Orotate from which the bases derive [1]:

It starts with Asp (one “half” of Orotate, for U- and C-bases), with Gly (as a centre in Inosine, for A-, G-bases):

Asp 133 A, Gly 75 A (R+B-chains):

133 + 75 = 208 = "3" in the exponent series.

133 = 292 - 159, 75 = 367 - 292.

The synthesis has several complementary features. One kind of complementarity could be seen in the fact that these numbers are inversions:

$$133 \wedge 75 \text{ (x } 10^x\text{)}.$$

The exponent 2/3 applied to mass numbers of codon bases:

Since the exponent 2/3 (with a constant x 100) gave the “exponent series” from a fundamental “5-dimensional” chain 5-4-3-2-1, the question arose if the exponent could work as an “operator” (with a term from vector analysis) even on other fundamental life substances as here the codon bases.

As shown below it gives sums from the exponent series (with and without a “constant” x 10). However, it’s left to mathematicians and scientists in the field of bioinformatics to eventually find out if such operations and results make sense in a deeper, integrated logic:

Bases bound, with exponent 2/3:

$$\begin{array}{r} 292 \quad - \quad 252 \quad - \quad 208 \quad - \quad 159 \quad - \quad 100 \quad - \quad 0: \\ \hline 544 \quad \quad \quad \backslash \quad / \\ \quad \quad \quad \quad \quad \quad 460 \end{array}$$

$$G: 150^{2/3} \times 10 = 282,31.$$

$$A: 134^{2/3} \times 10 = 261,86 \dots \text{sum } \mathbf{544},17. = 544 = 292+252 = "5 + 4"$$

$$U: 111^{2/3} \times 10 = 230,97.$$

$$C: 110^{2/3} \times 10 = 229,58 \dots \text{sum } \mathbf{460},54. = 460 = 252+208 = "4 + 3"$$

$$T: 125^{2/3} \times 10 = 250$$

$$C: 110^{2/3} \times 10 = 229,58 \dots \text{sum } 479,58. = \mathbf{480} = \mathbf{960} \times \frac{1}{2} = \frac{1}{2} \times "5 + 4 + 3 + 3"$$

$$282,31^{2/3} + 261,86^{2/3} + 230,97^{2/3} + 229,58^{2/3} = 159,10 \approx \mathbf{159}. ("2")$$

$$150^{2/3} + 134^{2/3} + 111^{2/3} + 110^{2/3} = 100,5. \approx \mathbf{100}. ("1").$$

10. Separate R-chains of amino acids with exponent 2/3:

With the same, certainly vague hypothesis as above, about the exponent perhaps acting as an operator even on more "polarised" number levels, the separate amino acids with exponent 2/3 were tested (*Table 3, page 72*). The R-chains with exponent 2/3 give numbers from 1 to 25,66. The sums gather in numbers of the "3" - "2"-step in the exponent series, perhaps of interest in a further dimensional analysis:

R-chains: the 24 numbers summed = 367. = 208 + 159 = "3 + 2".

$$\begin{array}{r} "5" \quad "4" \quad "3" \quad - \quad "2" \quad "1" \quad 0 \\ 292 \quad 252 \quad \mathbf{208} \quad \mathbf{159} \quad 100 \quad 0 \\ \hline \quad \quad \quad \backslash \quad / \\ \quad \quad \quad \quad \quad \quad \mathbf{367} \end{array}$$

(More exactly: **366,787**.)

$$3^{2/3} + 2^{2/3}, \times 100 = \mathbf{366,748}.)$$

Divided on code base groups:

$$\Sigma [\text{ams}^{2/3}]: \quad C1: 84,6 \quad 106,1: \quad U1 \quad \Sigma \mathbf{191}. \quad (\sim "5 - 1")$$

$$A1: 124,1 \quad 52,0: \quad G1 \quad \Sigma \mathbf{176}. \quad (\sim "4 + 1" \times \frac{1}{2})$$

$$\Sigma \quad \mathbf{208,7} \quad \mathbf{158,1}$$

$$\quad \quad \quad \backslash \mathbf{366,8} /$$

$$\sim "3" \quad "2"$$

R- plus B-chains in peptide binding, with B-chain = 56 A for each ams
(*Table 4, page 73*):

$$C1: 125,7 \quad 155,3: \quad U1 \quad \Sigma 281$$

$$A1: 192,0 \quad 102,5: \quad G1 \quad \Sigma 294,5$$

$$\Sigma \quad \mathbf{317,7} \quad \mathbf{257,8}$$

$$\quad \quad \quad \downarrow \backslash \mathbf{575,5} / \quad \downarrow$$

$$\sim \mathbf{2 \times "2"} \quad \sim \mathbf{"2 + 1"} \quad (2 \times 159), (158 + 100)$$

Cf. Just dividing this whole sum **2848** in two, in bound B-chains and R-chains. or halving, the results with exponent 2/3 adds to **253**, ~ number "4" +1:

With the type of operation: 2848, $x 1/4 = 712: \rightarrow 712^{2/3}$, $x 4 = 2 \times 159 (+1)$:

Dividing it in $3 \times 2 = 6$ gives the sum	365 , ~ 367, " 3 + 2 " in the exponent series
Dividing it in $4 \times 3 = 12$, gives the sum	460 , " 4 + 3 " - " - "
Dividing it in $5 \times 4 = 20$, gives the sum	545 . ~ 544 " 5 + 4 " - " - "
Dividing it in $5 \times 5 = 25$ - " - "	2 x 294 . (2 x 292 +3) 2 x " 5 " + 3,5.
Dividing it in $4 \times 4 = 16$ - " - "	2 x 253 . (2 x 252 +2) 2 x " 4 " +2
Dividing it in $3 \times 3 = 9$ - " - "	2 x 209 (2 x 208 +2). 2 x " 3 ", +2.
Dividing it in $2 \times 2 = 4$ - " - "	2 x 159 +1 . 2 x " 2 ", +1
Dividing it in $1 \times 1 = 1$ - " - "	2 x 100 +1 2 x " 1 " +1

Such number relations seem to show on a close, inverse relation between a "fragmentation" principle and the dimension degree (using the view from the background model) with exponent 2/3. This in the context of bound amino acids. Other numbers as 3276, sum of unbound ams, or 1504, the sum of R-chains, don't give such a pattern. Number 2848 doesn't seem to be a random one. Interpretations of these operations and results remain.

11. Other substances from the exponent series? Some transmitters:

It's reasonable to ask whether there are other central substances in life chemistry that could show patterns connected with the exponent series. Here only observations of transmitters, a few of the well-known ones. Their mass numbers make up about half of numbers in the exponent series as shown below.

If relying on this little selection, it would perhaps be possible to see them analogous to forces: assuming that a polarisation into "halves" is necessary to get an active force, not neutralised by its opposite force.

<i>The exponent series</i>		<i>Transmitters</i>
"5"	= 292 = 2 x 146	146 = Acetylcholine
"4 + 1"	= 352 = 2 x 176	176 = Serotonin
"3"	= 208 = 2 x 104	104 = Choline
"3"	= 208 = 2 x 104	104 - 1 = γ -Aminobuturate
"4"	= 252 = 2 x 126	126 - 1 = Taurine
"5"	= 292 = 2 x 146	146 +1 = Glu
"5 + 3 + 2"	= 659 = 2 x 329 (+1)	329 = Cyclic AMP
"3 + 2"	= 367 = 2 x 183 (+1)	183 = Adrenaline
"5 + 4 - 3"	= 336 = 2 x 168	168 +1 = Noradrenaline
"3 + 1"	= 308 = 2 x 154	154 -1 = Dopamine

Some of the numbers in the exponent series:

		interval			
	Acetyl~ = 43	44		adrenaline	
				183	
	acetylcholine		choline / \		
"Poles" = 1/2:	146		104	79	
	292	252 — ---	208	159	100
	"5"	"4"	"3"	"2"	"1"
			<----->		
			108, -1 = Tyr, R		
			(Dopa - Noradrenaline- Adrenaline out of Tyr)		

12. Special arithmetical annotations related to the exponent series:

a. Transformation from proportional distribution of mass to the exponent series:

How is the mass of the 24 ams (R) distributed on codon groups in relation to a proportional division and how is a proportional division related to the exponent series?

Triplet numbers 5-4-3, $\times 2 = 10 - 8 - 6$: sum 24 ams.
Number of ams: **G1 + C1 = 10 = 5 + 5, A1 = 8, U1 = 6.**

Following operations transform a proportional division into the exponent series:

$$\begin{array}{r} 10/24 \times 1504 = 627. \rightarrow 627^{2/3} = 73,26 \rightarrow 73 \times 4 = 292. = 5^{2/3} \times 100 \\ 8/24 \times 1504 = 501. \quad 501^{2/3} = 63,11 \quad 63 \times 4 = 252. = 4^{2/3} \times 100 \\ \underline{6/24 \times 1504 = 376.} \quad \underline{376^{2/3} = 52,09} \quad \underline{52 \times 4 = 208. = 3^{2/3} \times 100} \\ \text{Sum} \quad 1504 \quad \text{Sum} \quad 188,43 \quad \text{Sum} \quad 1504 / 2 \end{array}$$

With the interval "5" - "3" in the series (= 84) seen as transferred from "5" to "3", the results give about the main groups (cf. numbers, page 19):

$$\begin{array}{l} 292 - 208 = 84: \quad 10/24 \times 1504 = 627, - 84 = 544 - 1. \quad (G+C -1) \\ \quad \quad \quad 8/24 \times 1504 = 501. \quad = 500 +1 \quad (A1 +4), \quad (292 + 208, +1) \\ \quad \quad \quad \underline{6/24 \times 1504 = 376, + 84 = 460.} \quad (U1 - 3). \quad (252 + 208) \end{array}$$

It can be noted too that even without reference to the sum 1504, the quotients with 24 x 10^3 approximate numbers of the exponent series. The whole then $3/2 \times 10^3$ (1500), as for instance with Arg2 + Lys uncharged, Glu and Asp charged:

$$\begin{array}{l} 7/24 = 0,292., \times 10^{+3}. \times 2 = 584. \quad \quad \quad 292 + 250 = G1 + C1 -2, \\ 6/24 = 0,250 \times 10^{+3} \times 2 = 500 \quad (2 \times 252 -4) \quad + 2 \times 208 = U1 + A1 -2 \\ \underline{5/24 = 0,208., \times 10^{+3} \times 2 = 416.} \quad \text{.....intervals in the steps 84} \\ 2/24 = 0,083., \times 10^{+3} \times 2 = 2 \times 84 \quad (-1). \end{array}$$

b. First intervals in the exponent series with exponent 3/2:

An inverted exponent, applied to first intervals in the exponent series, "re-establishes" first 2 - 3 numbers in the series. Interval 44 gives number 292 as a kind of feed back:

$$\begin{array}{ccccccc} 292 & \text{---|} & 252 & \text{---|} & 208 & \text{---|} & 159 & \text{---} & 100 \\ & & \underline{40} & & \underline{44} & & \underline{49} & & \\ & & & & 84 & < \text{---} & 35 & \text{---} > | & \end{array}$$

$$40^{3/2} = 252,98. = 253.$$

$$44^{3/2} = 291,86. = 292. \text{Sum } 544 +1.$$

|

$$\text{Third number ?}: 84 - 49 = 35, \rightarrow 35^{3/2} = 207,06. = 208 -1$$

$$84^{3/2} = [292 - 208]^{3/2} = 770. = \text{Cross- plus Form-coded ams.}$$

Some numbers from such a chain:

$$\begin{array}{cccccc}
 5^4 & & 4^4 & & 3^4 & & 2^4 & & 1^4 \\
 625 & \text{---} & 256 & \text{---} & 81 & \text{---} & 16 & \text{---} & 1 & \text{---} & 0 \\
 \hline
 & & \mathbf{962} & \text{A + U, +2} & & = & 5^4 + 4^4 + 3^4 & = & 625 + 256 + 81 & = & 962 \\
 \hline
 & & \mathbf{544} & \text{G + C} & & = & 5^4 & - & 3^4 & = & 625 - 81 = 544
 \end{array}$$

$$256 - 81 + 16 = \mathbf{191 = G1}$$

$$256 + 81 + 16 = \mathbf{353 = C1} \dots \text{(From this chain some other ams numbers too.)}$$

P-group and its energy-storing bonds in step 3-2:

$$\begin{array}{cccc}
 3^4 & \text{---} & 2^4 & & 1^4 \\
 \text{H}_2\text{PO}_3^- & & 81 & \sim & 16 \dots & 1 & \text{Sum 98: H}_3\text{PO}_4
 \end{array}$$

e. Comparison with a "2-figure-chain":

There is other ways operating with a fundamental "5-dimensional" chain, which give similar numbers as the exponent series (sometimes +1, +2 as in the triplet series). This supports the idea of such a series at bottom, behind the pattern of the genetic code.

Here the elementary chain 5 - 4 - 3 - 2 - 1 - 0 with a superposed level 9-7-5-3-1. Additions of 2-figure-numbers "downwards" and "upwards":

$$\begin{array}{cccccc}
 \underline{18} & \underline{14} & \underline{10} & \underline{6} & \underline{2} & \rightarrow \text{ orbitals in electron shells} \\
 \\
 9 & & 7 & & 5 & & 3 & & 1 & \rightarrow 975 + 531 = \mathbf{1506} = 24 \text{ ams R +2} \\
 / & & \backslash / & & \backslash / & & \backslash / & & \backslash / & & \backslash \\
 5 & & 4 & & 3 & & 2 & & 1 & & 0/00 \\
 \underline{95+94} & \underline{74+73} & \underline{53+52} & \underline{32+31} & \underline{11+10} & & & & & \rightarrow \text{Downward reading:} \\
 189 & & \mathbf{147} & & 105 & & 63 & & 21 & = 525. \text{ (If } 2 \times 21 = 546, \text{ G + C +2.)} \\
 \underline{94+74} & \underline{73+53} & \underline{52+32} & \underline{31+11} & & & & & & \\
 \mathbf{168} & & \mathbf{126} & & 84 & & 42 & & & = 420 \\
 & & & & & & & & & > & = \mathbf{960} \text{ (A + U)} \\
 108 + 96 + 84 + 72 + 60 + 48 + 36 + 24 + 12 & = 540 & \rightarrow \text{Upward reading } 59 + 49 \text{ etc.}
 \end{array}$$

Comparisons with numbers in the exponent series:

$$\begin{array}{l}
 189 - 1 = 1/4 \times (\mathbf{292} + \mathbf{252} + \mathbf{208}) = 1/4 \times 752 \\
 168 = 1/2 \times \mathbf{336} \text{ (544 - 208)} \\
 147 - 1 = 1/2 \times \mathbf{292} \\
 126 = 1/2 \times \mathbf{252} \\
 105 - 1 = 1/2 \times \mathbf{208} \\
 84 = \mathbf{292} - \mathbf{208}, \text{ etc.}
 \end{array}
 \left. \begin{array}{l} \\ \\ \\ \\ \\ \end{array} \right\} \text{ steps 4-3-2 here } \sim 5 - 4 - 3 \text{ in the exponent series}$$

$$\begin{array}{cccccc}
 \underline{168} & \underline{147} & \underline{126} & \underline{105} & \underline{84} & \underline{63} & \underline{42} & \underline{21} \\
 \mathbf{544 + 2} & & & & \mathbf{208 + 2} & & &
 \end{array}$$

$$189 + 168 + 147 + 126 + 105 + 84 = \mathbf{819}, \times 4 = \mathbf{3276}, \mathbf{24 \text{ ams, R+B.}}$$

$$\text{Mean value 2 ams, unbound, R+B,} = \mathbf{273} = \mathbf{147} + \mathbf{126}.$$

(Numbers **168, 147, 126** look like A-number x 10 + Z-number of the atoms O, N, C: 16-8, 14-7, 12-6. If this wasn't just a funny way of reading, there would be found an internal division in the Z-sum of N and in the A-sum of O-atoms (9-7) and C-atoms (7-5)! And the first half of the chain inwards illustrates the C→N→O-cycle of fusion in the sun, the second half inwards 21 - 42 - 63 - 84 = D - He - Li - 2 alpha... as a more elementary line of fusion! The role of Bohr 10-5?)

3276, the total sum of 24 unbound amino acids, R+B-chains:

Additions downwards in last 4 steps: 52 + 32 = 84 etc., and exponent 3/2:

$$\begin{array}{ccccccccc} & 9 & & 7 & & 5 & & 3 & & 1 \\ & / & \backslash & / & \backslash & / & \backslash & / & \backslash & / \\ 5 & & 4 & & 3 & & 2 & \mathbf{63} & & 1 & \mathbf{21} & 0 \text{ (/00)} \end{array}$$

$$84^{3/2} = \underline{770}. \quad 63^{3/2} = \underline{500}. \quad 42^{3/2} = \underline{272}. = \frac{1}{2} \times 544 \quad 21^{3/2} = \underline{96}. = \frac{1}{2} \times 192$$

Sum **1638**, x 2 = **3276** (3276,7.) = 24 ams R+B.

Sum 1504 of R-chains of ams out of horizontal reading:

Reading the chains above horizontally, up and down between levels, as a wave *, in the first 5-4-3-steps to the middle of the chain (the upper 5), gives the squares of the codon type groups +/-1:

Forwards ~ outwards:

$$5-9-4-7-3-5 \rightarrow \sqrt{\quad} = \mathbf{771}. = \text{Cross- plus Form-coded ams +1}$$

Backwards ~ inwards:

$$5-3-7-4-9-5 \rightarrow \sqrt{\quad} = \mathbf{733}. = \text{RNA- plus Pair-coded ams -1}$$

> 1504.

(* Could wave functions in quantum mechanics eventually be interpreted as oscillations between different levels, superposed and polarised ones??)

f. The Golden Section:

There are examples of the Fibonacci series in nature. How about the Golden section which gives similar results? Do such relations appear in the exponent series?

Some approximated number relations ($\sqrt{5}/4$, $+1/2 = \underline{1,618...}$, shortened gs):

$$\begin{array}{ll} 208 \times \text{gs} = 336,5 \times \text{gs} = 544,5. & \\ + 367 \times \text{gs}^2 = 960,8. & (367 = 208 + 159), \frac{1}{2} \times \text{RNA- plus pair-coded)} \\ = 575 \times \text{gs}^2 = 1505. & (\text{Pure A-U-codons: } 575 = \text{AA+AU+UU+UA}) \end{array}$$

$$\begin{array}{l} \text{"2"} = \underline{158,74...} \\ \sim 1344 \left\{ \begin{array}{l} \times \text{gs} = 256,8,.. \\ \times \text{gs} = \mathbf{416}. \\ \times \text{gs} = \mathbf{672}. (2 \times 336) \\ \times \text{gs} = \mathbf{1088}, (2 \times 544), \\ \times \text{gs} = \mathbf{1760}. (\text{total sum Z of 24 ams, R+B}) \\ \times \text{gs} = \underline{\mathbf{2848}}. = 24 \text{ ams in ring binding R+B} \end{array} \right. - \sim 1504, 24 \text{ ams R-chains} \\ \text{B-chains} \\ \text{bound} \end{array}$$

$$\times \text{gs} = 8 \times 24^2$$

Part II

Transformations between number-base systems**Introduction:**

The background of this search for patterns in the genetic code was the 5-dimensional model or conceptual structure mentioned in part I. The model included a development from higher dimension degrees (d-degrees) through polarisations into complementary poles of lower degrees. During the investigation of the exponent series the vague idea arose that such steps between d-degrees in some way could be connected with different number base systems, 5 - 4 - 3 with base-10, -8, -6 systems.

First tested numbers was the mass numbers (A)90 of the codon bases of RNA. Surprisingly and curiously these transformations generated the numbers of codon type groups, halved: the numbers 385 (+/-1) and 367. With separate or added sums in the transformations, they gave both the R-chains and B-chains of the 24 amino acids.

Accidental or not? The question led to the investigations and results in this part II. It also revealed connections with the exponent series. More aspects on the transformations are given after a presentation of first results below.

Just one thing should be mentioned here: a number as $2848 = 24$ ams with bound B-chains, appearing as a base-6 number, should as such properly be written 3252. "Re-writing" numbers, using the higher base-10 figures, are frequently used here and discussed later.

An introducing figure

The whole sum of 24 unbound amino acids, R- plus B-chains: 3276

$$\begin{array}{ccc} \text{16-base} & & \text{10-base} \\ \text{CCC} & \longrightarrow & \text{3276} \\ \downarrow & & \\ 12.12.12 & & \text{(The mass number of C-atoms in displacements of base-16, the A-number of } ^{16}\text{O, oxygen: as a 3C-piece giving all ams!)*} \end{array}$$

$$\begin{array}{ccc} & & \text{10-base} \\ & & \text{204} = \text{Trp R+B,} \longrightarrow \text{the heaviest ams} \\ \text{CC} & \longrightarrow & \\ & & \text{10-base} \quad \text{8-base} \\ \text{CC} & \longrightarrow & \text{204} \quad \longrightarrow \quad \text{314} (\sim \pi\text{-number} \times 100) \\ & & \downarrow \\ \text{16-base} & & \text{8-base} \\ \text{314} & \longrightarrow & \text{1424} \\ (\sim \pi \times 100) & & \times 2 = \text{2848, 24 ams in peptide ring binding} \end{array}$$

* The division of fructose in glycolysis gives C3-pieces, molecules with 3 C-atoms, and oxygen atoms moving between them...

All but one amino acid derives from the glycolysis and the citrate cycle where 1C- and 2C-pieces are added and C1-molecules (CO₂) is secreted. [1].

Isocitrate with 6 C-atoms, uncharged = 192 = C0 as a HEX-number (292 - 100 in the exponent series.).

1. The four RNA-bases transformed to the sum of 24 amino acids:

4 x 4 RNA-bases give the total of 24 ams, R + B unbound, 1504 (R) + 1772 (B) = 3276. Note that these transformations give reason for counting with the reduction of 4 H in B-chains Arg1, 2, Lys and Pro in accordance with the reference [1].

	<u>10- base</u>	<u>8-base</u>	<u>Decimal multiplication:</u>	<u>Amino acids</u>
G-base:	151 A =	227		
			> 384 , <u>x 2 = 768</u> (~770)	Cross+Form-coded ams R
C-base:	111 A =	157		
			> 1504 (-2)	= 24 R-chains (-2)
U-base:	112 A =	160		
			> 367 , <u>x 2 = 734</u>	RNA+Pair-coded ams R
<u>A-base:</u>	<u>135 A =</u>	<u>207</u>		
Sum:	509		751 (753)	
2 x 509 = 1018 A = 1772 —————> 1772 = 24 B-chains unbound				

Mean value of the 4 transformed bases, divided or added pairs, 751-753: = 752:

This is the sum of the first 3 numbers in the exponent series.

$$\frac{10\text{-base}}{752} \longleftrightarrow \frac{6\text{-base}}{2848} = 24 \text{ ams R+B, bound}$$

Whole sum 3276 as a base-6 number from only G₈+C₈:

G+C-numbers received in nb-8 read as base-10 numbers.

$$2 \times 384 = \frac{10\text{-base}}{768} = \frac{6\text{-base}}{3276} = 24 \text{ ams R+B unbound}$$

G and C transformed together give 386 = 384 +2:

A first example of the difference received at transforming whole versus divided numbers. The base pair A + U gives no difference in this regard.

$$\begin{array}{l} \text{G + C:} \quad \frac{10\text{-base}}{262} \text{ A = } \frac{8\text{-base}}{386}, \quad \times 2 = \text{Cross- plus Form-coded ams } \underline{+2} \\ \text{A + U:} \quad \frac{247}{\underline{367}} \text{ A = } \frac{367}{\underline{753}}, \quad \times 2 = \text{RNA- plus Pair-coded ams} \end{array}$$

Move of the nb-8 numbers of the 4 bases to nb-16:

$$\begin{array}{l} \text{G+C, +1} \quad \frac{16\text{-base}}{384, +1} \quad \frac{10\text{-base}}{901} \\ \text{A+U} \quad 367 \quad 871\text{....sum } 1772 \quad = 24 \text{ B-chains, unbound} \end{array}$$

Numbers of ams: 20 ams --> 24 ams with 4 double-coded:

$$\frac{10\text{-base}}{20} \text{ ams} \longrightarrow \frac{8\text{-base}}{24} \text{ ams} = +4 \text{ double-coded ams}$$

This transformation seems to be one of possible explanations to why there are 4 double-coded ams, in the way of counting used in this paper.

2. First comments on an eventual interpretation and aspects on operations:

If the results above and on following pages are more than a chance, *if* assuming that they reveal some underlying principle in molecular development, how to interpret it?

A very general suggestion, the only possible here, is to see it as a factor in what is called affinities, and as a principle behind growth towards larger molecules and structures.

There is of course no magic transformation of masses and atoms on a material level. The numbers received in base-8, base-6 etc. should be regarded as base-10-numbers and they are operated here (additions, multiplications...) in our ordinary base-10 system.

This implies that the transformations only represent or function as a kind of architect drawings, which reveals mutual relations between materialised structures.

The principle should originate in a multi-dimensional dynamic process of some kind (such as the 5-dimensional model behind this paper), the transformations outlining possible developments in different dimensional degrees.

(It's also possible to imagine that all numbers and biochemical properties, as energy levels, pH-values, ionisations, threshold values of other kinds etc. ultimately, at bottom derive from numbers of dimension degrees.)

More concrete aspects to observe in the following transformations:

a) **Selection of number base systems:** With the background in a 5-dimensional model, only operations between base-10, -8, -6 and 16 ($10 + 6$) are treated here, as doubled values of d-degrees $5 - 4 - 3$, which doubled in the exponent series gave the sum of 24 ams R. What should then 16 represent? Possibly $10 + 6$ (?) as there sometimes in the exponent series seemed to be a kind of "feed back" between "3" and "5":

There are of course no theoretical reasons for the exclusion of other number base systems as 4 and 2 or perhaps odd numbers?

←	16 ?	—
↓		↑
10	— 8	— 6

b) Transformations of **divided or whole numbers:**

Operations as additions and multiplications may be applied before or after a transformation, with quite different results.

At transformations to a lower base system, a **split mass** most often gives a smaller sum than transformation of the whole mass:

10-base	8-base	single base ₈
G 151, x 2 = 302 ———>	= 456 = 2 x 227	<u>+ 2</u>
U 112, x 2 = 224 ———>	= 340 = 2 x 160	<u>+ 20</u>
C 111, x 2 = 222, ———>	= 336 = 2 x 157	<u>+ 22</u>
A 135, x 2 = 270 ———>	= 416 = 2 x 207	<u>+ 2</u>

Just as a suggestion, such reductions could be thought of as connected with chemical processes. For instance:

+/- 2 could represent +/- 2H,
 +/- 20 (in base-8 system) ———> = 16 in base-10 system, ~ ¹⁶O
 H₂O = 18 A (base-10) ———> = 22 (base-8), difference 4:
 Compare 4 H x 2 out of the citrate cycle ?

c) **Re-writing** of numbers in lower base systems, allowing figures of higher base systems, implies a reduction as pointed out in the introduction above. A new example: 416 as a base-8-number = 396, twenty units lower, but the same number translated to base-10. Number 1160 as a base-8 number may be written 960, the sum of ams R in A-U-groups, or 958.

How to interpret such reductions? Just as an arithmetic formalism - or with a meaning in an underlying dimensional process? Eventually interpretable in terms of biochemical intermediate substances?

d) This question above is more adequate when it comes to the **transformation gaps or intervals**, between a number and its transformed appearance. With the hypothesis that these transformations reveal an underlying principle, the intervals represent a measure of the growth - or in the other direction of reductions. In which number base systems should they be interpreted? Optional? One example:

Number 208 ("3" in the exponent series), base-10 = 320, base-8. Interval or gap = 112: reading it as a base-8 number it represents 74, as a base-10 number just 112, transformed to base-6 = 304. All these numbers are interesting in connection with ams, (cf. e.g. page 64) and could point out interesting relations in processes or structures in an eventual further investigation of the hypothesis.

e) Another simple question concerns the **moving of a number**, received for instance as a base-8 number, moved unchanged to base-10, transformed again etc. It's perhaps no problem with accepting such repeated operations, since the received numbers all must be regarded in the base-10 system (*e1* below).

But what should a move or jump to base-16 of that same number imply (*e2*)?

e1) One example of repeated steps base-10 to -8:

<u>10-base</u>	<u>8-base</u>	/	<u>10-base</u>	<u>8-base</u>	/	<u>10-base</u>	<u>8-base</u>	/	<u>10-base</u>	<u>8-base</u>
208	→ 320, ~318	318	→ 476	476	→ 734.....	734	→ 1336	
212	→ 324		+ 324	→ 504		504	770	770	→ 1402	
418	← 642	← =	642	→ 1202, ~ 982	982	→ 1726.....	1726	→ 3276	

734 = RNA+Pair-coded ams R

770 = Cross+Form-coded ams R. 3276 = 24 ams R+B unbound.

Re-writings = reduction -2, - 220 = - 222 = 3 x 74 (B-chains unbound).

A difference at start of 4 (H) grows to a difference of 36 (as 2 H₂O) between the codon type groups.

With a 5th step of reduction, inwards, **418** as a base-8 number leads to **272**, half the number 544 ("5" + "4") in the exponent series.

e2) 16-base 10-base Nmber 318 from transformations in *e1*:
 318 → 792* Are there possible jumps between non
 consecutive dimension degrees which could imply that the number 318 moved to
 number base-16 as to another branch of development on the same "tree"? Or should it
 be read as a different number in another context, only with the same formal appearance?
 Such a question is just noted here, not answered. *792 is the difference between the
 triplet series outwards an inwards: 2(543 + 210) - 2(012 + 345).

- Arrows in operations means reading or transformation direction.
- In text rows below number-base system is shortened nb-10, nb-8 etc.
- Sometimes index figures is used to mark the number base, as A₈ for the mass of the A-base transformed to nb-8 = 207.

3. From codon bases to amino acids, some more examples:

- a. Two steps of transformation, connected with the role of the A-base in protein synthesis?

$$\begin{array}{rcccl}
 \text{10-base} & \text{8-base} & & \text{10-base} & \text{8-base} \\
 \text{A-base: } \mathbf{135} & \longrightarrow & 207, \sim 187 \text{ re-written} & 187 & \longrightarrow & \mathbf{273} & \times 12 = 3276 \\
 & & & & & \downarrow & \\
 & & & & & \text{Mean value of 2 ams R+B in base-10 system} &
 \end{array}$$

- b. Codon grouped ams, R+B, from 4 x 4 RNA-bases:

$$\begin{array}{l}
 \text{10-base sums:} \quad G1 + U1 = \mathbf{1468} = A2 + C2 \\
 \quad \quad \quad \quad A1 + C1 = \mathbf{1808} = G2 + U2
 \end{array}$$

These same two sums may be received, but with an exchange between U- and C-bases and with the multiplication *after* the transformation in the case of A- and U-bases:

$$\begin{array}{rcccl}
 & \text{10-base} & \text{8-base} & & \\
 4 \text{ G-bases} = 4 \times 151 = & 604 & \longrightarrow & 1134 & \\
 4 \text{ C-bases} = 4 \times 111 = & 444 & \longrightarrow & 674 \dots \text{sum } \mathbf{1808} & \\
 \\
 1 \text{ A-base} & = 135 & \longrightarrow & 207, \times 4 = 828 & \\
 \underline{1 \text{ U-base}} & = 112 & \longrightarrow & 160, \times 4 = 640 \dots \text{sum } \mathbf{1468} &
 \end{array}$$

If U- and C-base change partner, the sum is divided in nearly R- and B-chains:

$$\begin{array}{rcccl}
 \text{10-base} & \text{8-base} & & & \\
 4 \text{ G} = 604 & \longrightarrow & 1134 & & \\
 1 \text{ U} = 112 & 160, & \times 4 = 640, & + 1134 = \mathbf{1774} \sim \text{B-chains} & +2 \\
 4 \text{ C} = 444 & \longrightarrow & 674 & & \\
 \underline{1 \text{ A} = 135} & 207, & \times 4 = 828, & + 674 = \mathbf{1502} \sim \text{R-chains} & -2
 \end{array}$$

Re-writing 640 ~638, 828 ~830 gives the right sums B **1772**, R **1504**.

- c. 4 x RNA-bases separately transformed give also 2 x 24 B-chains:

$$\begin{array}{rcccl}
 & \text{10-base} & \text{8-base} & & \\
 4 \text{ G} & 604 & \longrightarrow & 1134 & \\
 4 \text{ C} & 444 & & 674 \dots \text{sum } 1808 \sim 1810 & \\
 & & & & > \mathbf{3544} = 2 \times \mathbf{1772}, \text{ B-chains} \\
 4 \text{ U} & 448 & & 700 & \\
 4 \text{ A} & 540 & & 1034 \dots \text{sum} & 1734
 \end{array}$$

- d. One pair of codon bases G + C, times 4, gives through 2 steps 2 x 24 ams, R-chains:

$$\begin{array}{rcccl}
 & \text{10-base} & \text{8-base} & & \\
 \text{Base pair} \quad G+C & \mathbf{262} & \longrightarrow & 386 & \\
 & & & \downarrow & \\
 & & & \mathbf{386} & \\
 & \times 4 = 1544 & \longrightarrow & \mathbf{3008} & \quad \mathbf{3008} = 2 \times \mathbf{1504}, \text{ R-chains}
 \end{array}$$

4. Starting codon AUG — and the common end of t-RNA, A-C-C:

The amino acid Meth, codon AUG, is starting the protein synthesis. Why? Its end group CH₂ (-14) is deducted and gives it then the same mass number that the A-base, 135 (R+B). The A-base as coenzyme has the central role of transporting ams to the t-RNAs, the end of which is the bases A-C-C. Why? Are there any chemical explanations? Or could the transformations below point towards a deeper one?

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

$$\begin{array}{l} \text{16-base} \\ \mathbf{149} = \text{Meth, R+B} \end{array} \longrightarrow = \begin{array}{l} \text{8-base} \\ \mathbf{509} \end{array} = 4 \text{ RNA-bases in base-10 system}$$

$$\begin{array}{l} \text{16-base} \\ \mathbf{149} \end{array} \longrightarrow \begin{array}{l} \text{10-base} \\ \mathbf{329} \end{array} = \text{cAMP, also = A-nucleotide}$$

The exponent series:

$$\text{"5"} = \begin{array}{l} \text{16-base} \\ 292 \end{array} \longrightarrow \begin{array}{l} \text{10-base} \\ 658 \end{array} = 2 \times \mathbf{329} (\sim \text{cAMP})$$

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

	<u>10-base</u>	<u>8-base</u>	<u>The "triplet series"</u>
Nucleotides:	$\mathbf{329}$ A	$\mathbf{511} \sim \mathbf{509}$ (4 RNA-bases)	543-432-321-210:
	$\mathbf{306}$ U	462.....Σ. $\mathbf{973}$	= 543 + 432 - 2
	<u>$\mathbf{345}$</u> G	<u>531.....</u> $\mathbf{531}$	<u>= 321 + 210</u>
	$= \mathbf{1504}$	$= \mathbf{24 \text{ ams R}}$	

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

<u>10-base:</u>	<u>8-base:</u>	
93 ←	135: A	
74 ←	112: U	
+ <u>105</u> ←	<u>151: G</u>	
= $\mathbf{272}$ ←	398	$\mathbf{272} = \frac{1}{2} \times \mathbf{544}$, "5" + "4" in the exponent series

c. A+C+C = the similar end of t-RNAs to which the amino acids are transported:

A+C+C-bases:	<u>10-base</u>	<u>8-base</u>	
	$\mathbf{357}$	$\mathbf{544} + \mathbf{1}$	
ACC: <	A	135 →	207 = <u>Exponent series</u> 208 - 1
	2 C	222 →	336 = 544 - 208 > $\mathbf{544 - 1}$

d. 1504, sum of 24 ams R, – related to cGMP ionized (?) :

cGMP: role in the protein synthesis ?

$$\text{cGMP}^- \quad \begin{array}{l} \text{16-base} \\ 344 \end{array} \longrightarrow \begin{array}{l} \text{10-base} \\ 836 \end{array} \longrightarrow \begin{array}{l} \text{8-base} \\ \mathbf{1504} \end{array} = 24 \text{ ams R}$$

5. From codon bases to nucleotides and coenzymes of the bases:

In following transformations the mass numbers of the bases generates numbers of nucleotides and coenzymes, in some cases in an astonishing simple way.

They concern sums of the nucleotides and coenzymes as if separation, fragmentation and re-arrangements in the genetic code were a later history.

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

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

$$G \ 151, \ A \ 135, \ U \ 112, \ C \ 111 \dots \Sigma \ 509, \ +T \ 126 \dots \Sigma \ 635$$

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

$$15 \ A + 13 \ U + 11 \ G + 9 \ C = \mathbf{6141}$$

Nucleotides in chain binding:

$$\underline{\text{RNA:}} \ G \ 345, \ A \ 329, \ U \ 306, \ C \ 305 \dots \Sigma \ \mathbf{1285}, \ \text{ionized -1 in P-groups} = \mathbf{1281}$$

$$\text{cGMP} = 345, \ \text{cAMP} = 329$$

$$\underline{\text{DNA:}} \ G \ 329, \ A \ 313, \ T \ 304, \ C \ 289 \dots \Sigma \ \mathbf{1235}, \ \text{ionized -1 in P-groups} = \mathbf{1231}$$

Coenzymes of the code bases:

<u>-TP</u>		<u>-DP</u>		<u>-MP</u>	
GTP	523	GDP	443	GMP	363
ATP	507	ADP	427	AMP	347
UTP	484	UDP	404	UMP	324
CTP	483	CDP	403	CMP	323
	1997		1677		1357
TTP	498	TDP	418	TMP	338
=	2495		2095		1695

a. Transformations to nucleotides:

$$4 \ \text{RNA-bases} \quad \begin{array}{c} \underline{16\text{-base}} \\ \leftarrow \text{---} \rightarrow \\ \text{bound} \end{array} = \mathbf{505} \quad \begin{array}{c} \underline{10\text{-base}} \\ \leftarrow \text{---} \rightarrow \\ \text{bound} \end{array} = \mathbf{1285} = 4 \ \text{RNA-nucleotides, not ionized}$$

$$\downarrow$$

$$780 = \mathbf{4 \times 195}$$

↓
P-ribose-groups in chain bindings: ribose 131 + HPO₂⁻ 64.

b. 4 RNA-nucleotides ionized -1 = 1281:

4 RNA-bases	<u>10-base</u>	<u>8-base</u>	<u>6-base</u>	
G	151	227	411	411
C	111	157	303	~ 263
A	135	207	343	343
U	112	160	304	~ 264
	509	751	1361	1281
	↓	↓	~ 1357	↓
	751	1357		= 4 RNA-nucleotides
	↓	↓		charged -1.
	(4 coenzymes RNA, -MP)			

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

$$\begin{array}{rcccl}
 & \underline{10\text{-base}} & & \underline{8\text{-base}} & \\
 4 \text{ bses in nb-8:} & \mathbf{752} & \longrightarrow & \mathbf{1360} & \\
 751/753 & & & & (5 \times 272 \text{ from the exponent series}) \\
 & \downarrow & & & \\
 & \mathbf{1360} & \longrightarrow & \mathbf{2520} & = 1285 + 1235
 \end{array}$$

d. Bases read as nb-8 numbers \rightarrow nucleotides G, A:

$$\begin{array}{rcccl}
 & \underline{10\text{-base}} & & \underline{8\text{-base}} & \\
 167 & \longleftarrow & 247 & \text{A+U} & \\
 178 & & 262 & \text{G+C} & \\
 \hline
 & \mathbf{345} & & \mathbf{509} & \mathbf{345 = cGMP = G-nucleotide} \\
 < 674^* & & & & \\
 & \underline{\mathbf{329}} & \longleftarrow & \underline{509} & \underline{\mathbf{329 = cAMP = A-nucleotide}} \\
 & \underline{10\text{-base}} & & \underline{6\text{-base}} & \\
 * \text{Base pair: } & \mathbf{262} & \longrightarrow & \mathbf{674} & = 2/3 \times 1011, \text{ sum of exponent series.} \\
 & & & & (674 \text{ also the number of atoms in } 2 \times 24 \text{ codon bases, } 1^{\text{st}} \text{ and } 2^{\text{nd}}, \text{ in the codons.})
 \end{array}$$

e. 5 coenzymes -TP from 5 bases:

$$\begin{array}{rcccl}
 & \underline{10\text{-base}} & & \underline{8\text{-base}} & & \underline{6\text{-base}} & \\
 5 \text{ bases} & 635 & \longrightarrow & 1173, \sim 973 & \longrightarrow & \mathbf{2495} & = \mathbf{5 \text{ bases as coenzymes -TP}} \\
 \text{with T-base} & | & & & & | & \\
 & \longleftarrow & \mathbf{5 \times 372} & \longrightarrow & & & [2495_6 \sim 2535 = 5 \times 507. \\
 & & = 5 \times \text{P}\sim\text{P}\sim\text{P-ribose} & & & & 507 = \text{ATP}_{10}]
 \end{array}$$

f. From 4 codon bases, separately transformed to the sum 751 (page 36) to numbers 1357 - 2495 and 6141:

$$\begin{array}{rcccl}
 & \underline{10\text{-base}} & & \underline{8\text{-base}} & \\
 \mathbf{751} & \longrightarrow & \mathbf{1357} & = \mathbf{4 \text{ coenzymes -MP (G, A, U, C)}} \\
 & & & & \\
 & \downarrow & & & \\
 \mathbf{1357} & \longrightarrow & \mathbf{2495} & = \mathbf{5 \text{ bases as coenzymes -TP (including TTP)}} \\
 & & & & \\
 & & & & \underline{6\text{-base}} \\
 & & & & \mathbf{6141} = \mathbf{48 \text{ code bases, } 1^{\text{st}} \text{ and } 2^{\text{nd}}, \text{ for } 24 \text{ ams}}
 \end{array}$$

g. 5 bases as coenzymes, -DP-form = 2095 as a 6-base sum from the 4 RNA-bases:

$$\begin{array}{rcccl}
 & \underline{10\text{-base}} & \underline{8\text{-base}} & \underline{8\text{-base}} & \underline{6\text{-base}} \\
 \text{G+C: } \mathbf{262} & \longrightarrow & \mathbf{386} & & \\
 & & & >753 / 753 \longrightarrow & \mathbf{2095} \longrightarrow = \mathbf{5 \text{ bases as coenzymes -DP}} \\
 \text{A+U: } \mathbf{247} & \longrightarrow & \mathbf{367} & & \downarrow \\
 & & & & \underline{\sim \mathbf{1695}} \longrightarrow = \mathbf{5 \text{ bases as coenzymes -MP}} \\
 & & & & \text{Re-writing gives } - 5 \times 80, \sim 5 \text{ P-groups (HPO}_3^-)
 \end{array}$$

Coenzymes of the 4 RNA-bases, survey:**-MP:**

$$\begin{array}{rcccl}
 & \underline{10\text{-base}} & & \underline{8\text{-base}} & / & \underline{10\text{-base}} & & \underline{8\text{-base}} \\
 4 \text{ RNA-bases:} & \mathbf{509} & \longrightarrow & 751 & & 751 & \longrightarrow & \mathbf{1357} \\
 \text{- separately} & | & & & & & & = 4 \text{ RNA-bases} \\
 \text{transformed to 751} & | & & & & & & \text{as coenzymes -MP} \\
 & \longleftarrow & \mathbf{4 \times 212} & \longrightarrow & & & & \\
 & & 212 = \text{P~ribose} & & & & &
 \end{array}$$

-DP

$$\begin{array}{rcccl}
 & \underline{10\text{-base}} & & \underline{8\text{-base}} / \underline{10\text{-base}} & & \underline{8\text{-base}} \\
 2 \times 4 \text{ RNA-bases:} & \mathbf{1018} & \longrightarrow & 1772 & & 1772 & \longrightarrow & 3354 = \mathbf{2 \times 1677} \text{ } ^1) \\
 & | & & & & & & = 2 \times 4 \text{ RNA-bases} \\
 = 2 \times 4 \text{ RNA-bases} & & & & & & & \text{as coenzymes -DP} \\
 & \longleftarrow & \mathbf{8 \times 292} & \longrightarrow & & & & \\
 & & 292 = \text{P~P ~ribose} & & & & &
 \end{array}$$

Ribose-P~P = -DP-form = 292 = "5" in the exponent series (= 131+80+81)

(1772 = 24 ams B-chains)

-TP:

$$\begin{array}{rcccl}
 & \underline{10\text{-base}} & & \underline{8\text{-base}} & & \underline{10\text{-base}} & & \underline{8\text{-base}} & & \underline{6\text{-base}} \\
 G_8+C_8: & 384 (386) & \longrightarrow & 601 (-/+1) & & & & & & 1997 \\
 A_8+U_8: & 367 & \longrightarrow & 557\dots \text{Sum } \mathbf{1158 \sim 1160} & \longrightarrow & \mathbf{2188} & & & & \\
 & & & & & \downarrow & & & & \\
 & & & & & \mathbf{2188} & \longrightarrow & 3994 = \mathbf{2 \times 1997} & & \\
 & & & & & & & \downarrow & & \\
 & & & & & & & = 2 \times 4 \text{ RNA-bases} & & \\
 & & & & & & & \text{as coenzymes -TP} & & \\
 4 \text{ bases nb-10:} & 509 & \longleftarrow & \mathbf{4 \times 372} & \longrightarrow & 1997 & & & & \\
 & & & 372 = \text{P ~P ~ P-ribose} & & & & & &
 \end{array}$$

It seems as if the formation of the -TP-form of the coenzymes in some way involves the 4 complementary bases as well. An observation is also that number **601** above in nb-10 = 1997 in **nb-6**. It's possible to get all 4 -TP coenzymes from only one base pair. (And in nb-6 number 601 should be the same as 557 re-written.)

4 x 372 = 1488, transformed to nb-8 = 5 x 544, 2720, the sum of 24 ams R transformed to nb-8 (2720 = 1460 + 1260, page 45).

1488 in nb-6 = **416** in nb-10, also a number from the exponent series.

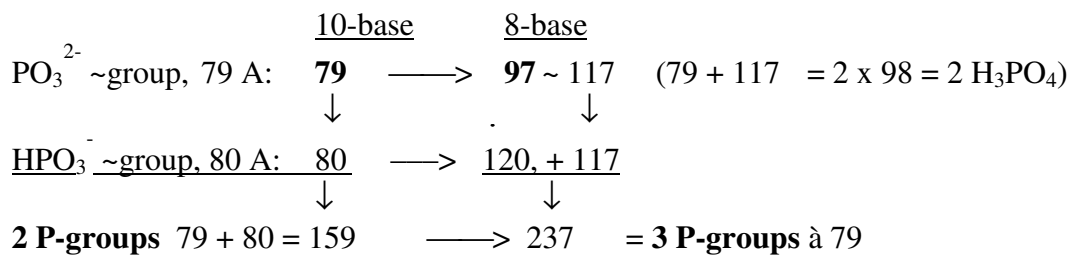
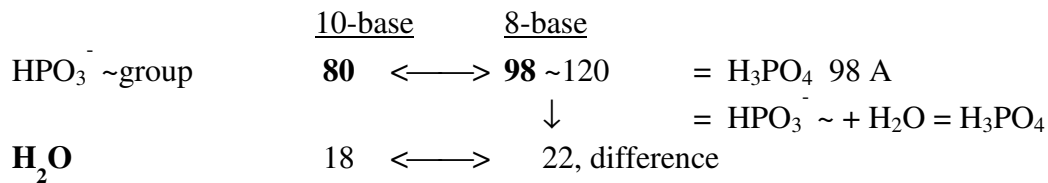
¹⁾ Note:

$$\begin{array}{rcccl}
 & \underline{10\text{-base}} & & \underline{8\text{-base}} & & \underline{10\text{-base}} & & \underline{8\text{-base}} \\
 & 291 & \longrightarrow & 443 & & 1157 & \longrightarrow & 2185 = 2188 -3. \\
 751 & < & & >1157 & & & & \\
 & 460 & \longrightarrow & 714. & & & & | \\
 & & & & & & & | \\
 509 & \longleftarrow & 1677 -1 & \longrightarrow & & & & \\
 & & 4 \text{ RNA-bases as coenzymes -DP, -1} & & & & &
 \end{array}$$

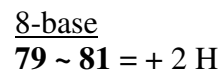
6. P-groups:

Here it's shown that P-groups generates - or defines - to themselves the additional H₂O-molecules both through transformation nb-10 to nb-8 and through re-writing. It's also shown (point b.) that the P-P-(P)-ribose-groups in the coenzymes of codon bases are directly given from single P-groups in nb-16 to nb-6. So are the masses of NAD and NADP:

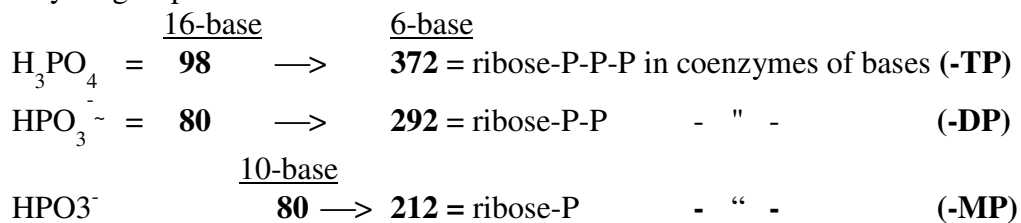
a. H₂PO₄⁻ ~group, 97 A, PO₃²⁻ ~group, 79 A, HPO₃⁻ ~group = 80 A



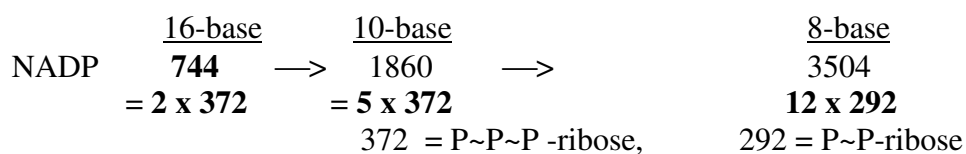
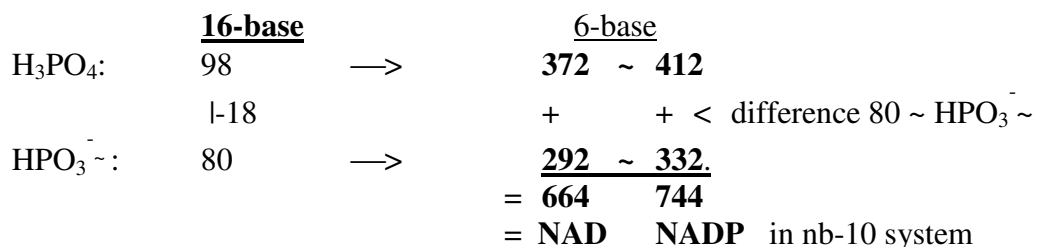
(Energy storing in the bindings.)



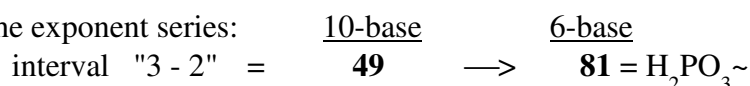
b. Coenzyme groups:



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



d. The exponent series:



7. Five times numbers in the exponent series in nb-8 generating main ams groups:

These examples seem to point out the significance of number 5. They could also support the idea of polarisation steps in the background 5-dimensional model.

a. 5 x numbers "5-4-3" in the exponent series as base-8 numbers give main codon groups of amino acids:

It's of course possible to read the transformation in the opposite direction, but the exponent series has a broader application.

<u>Ams-groups</u>	<u>10-base</u>		<u>8-base</u>		<u>The Exponent series x 5</u>
C1+U1:	816	←	1460 =		5 x 292 "5"
G1+A1:	688		1260 =		5 x 252 "4" *
G+C:	544		1040 =		5 x 208 "3"
A+U:	960	←	1680		5 x 336 = 5 x [544 - 208] = "5+4 - 3"
	816 —				
	1776	←	3360		10 x 336 ¹⁾
	↓				
	24 B-chains à 74 A				

*["4", 1260 ~1258 = 20 ams without double-coded ams = 688 +1 Z, 570 -1 N.]

b. Steps of "polarisations" "5" → "4" → "3":

<u>Steps:</u>	<u>Ams</u>		<u>10-base</u>		<u>8-base</u>		<u>The Exponent series:</u>
"5"	<u>C1 + U1:</u>	816	←	1460			= 5 x 292
	C1:	↓ 353		541			> 544
	U1:	↓ 463	→	717....1258 ~ 1260			= 5 x 252
"4"	<u>G1 + A1:</u>	688	←	1260	←	1260	↓ 336
	G1:	↓ 191		277			
	A1:	↓ 497	→	761....1038 ~ 1040			= 5 x 208 > 208
"3"	<u>G1 + C1:</u>	544	←	1040	←	1040	↓
		544 = 292+252					= return to "5 - 4"
	A1 + U1:	960	←	1680..	←	1680	= 5 x 336 ←
							↓
		416	→	640			> quotient 2/1
							↓
		544	←	1040	~	840	= 5 x 168

¹⁾ 5 x ½ x 752 = 1880 (= 10 x 336 - 5 x 292):

	<u>10-base</u>		<u>8-base</u>
G+C, x 2 = 544 x 2:	1088	←	1880 = 3360 - 1460 = 5 x 376
G1+A1 R:	688	→	1260, 5 x 252
	1776	←	3360

c. **10 times the sum 544 gives the sum of 24 ams in peptide ring binding:**

$$24 \text{ ams, bound, R+B: } \quad \begin{array}{ccc} \text{10-base} & & \text{8-base} \\ \mathbf{2848} & \leftarrow & \mathbf{5440} \end{array} \quad 10 \times (292 + 252)$$

d. **5 x intervals in the exponent series in nb-8 give separate code base groups -/+1:**

<u>Ams</u>	<u>10-base</u>	<u>8-base</u>	<u>Intervals in the exponent series:</u>
G1+1	192	$\leftarrow 300 = 5 \times \text{interval } 60 = 292 - 352 = \text{"5"} - \text{"4 + 1"}$	
A1 -1:	496	$760 = 5 \times \text{interval } 152 = 252 - 100 = \text{"4"} - \text{"1"}$	
U1+1	464	$720 = 5 \times \text{interval } 144 = 352 - 208 = \text{"4 + 1"} - \text{"3"}$	
C1- 1	352	$540 = 5 \times \text{interval } 108 = 208 - 100 = \text{"3"} - \text{"1"}$	

e. **84 = interval 292 - 208:**

	<u>10-base</u>	<u>8-base</u>	<u>Exponent series</u>
24 B-chains à 74 A:	1776	$\leftarrow 336 \times 10$	$= 4 \times 84, \times 10 (292 - 208)$
A+U-coded ams R:	960	$\leftarrow 168 \times 10$	$= 2 \times 84$ "
G+C-coded ams R:	544	$\leftarrow 84 \times 10$	$= 1 \times 84$ "

f. **5 x intervals "5" to "3" and "3" to "1":**

	<u>10-base</u>	<u>8-base</u>	<u>Interval</u>
$544 / 2 <$	128	$\leftarrow 200 = 5 \times 40$	(292-252)
	<u>144</u>	<u>$\leftarrow 220 = 5 \times 44$</u>	<u>(252-208)</u>
$=$	272	$\leftarrow 420 = 5 \times 84$	
	+		
"4 + 1"	<u>352</u>	<u>$\leftarrow 540 = 5 \times 108$</u>	(208-100)
$=$	3 x 208	960 = 5 x 192	(292-100)

g. **5 x numbers of exponent series in base-6:**

	<u>10-base</u>	<u>6-base</u>	
396	396	$\leftarrow 1460 = 5 \times 292$	a)
	324	$\leftarrow 1260 = 5 \times 252$	
564			> b)
	<u>240</u>	<u>$\leftarrow 1040 = 5 \times 208$</u>	
	960	752 x 5	

↓ = A + U

$$396 = \mathbf{292 + 104} \quad \mathbf{396 + 101 = 497 = A1} \quad \text{a)}$$

$$564 = \mathbf{460 + 104} \quad \mathbf{564 - 101 = 463 = U1} \quad \text{b)}$$

$$\Sigma: \quad 752 + 208$$

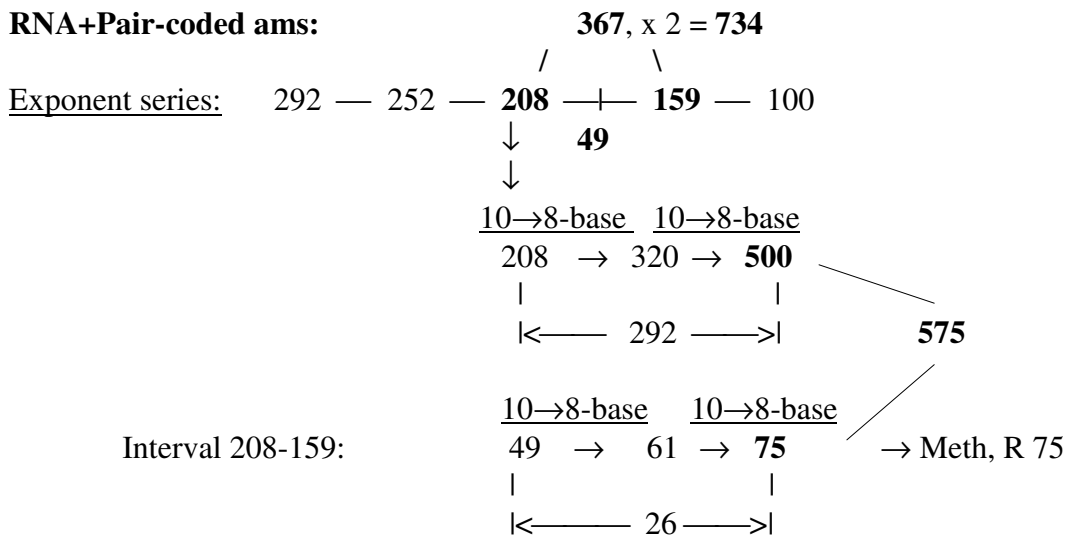
(Cf. page 11..)

h. **10 x 104 as nb-8 number = 544 in nb-10:**

<u>10-base</u>		<u>8-base</u> / <u>10-base</u>	<u>8-base</u>
544	\longrightarrow	1040	
		$\sim 838 \longrightarrow 838 \longrightarrow$	1506 , 24 ams R + 2H

8. Generative production of partial sums of amino acids in codon type groups:

Here it's shown that transformation of numbers and intervals in the exponent series in 2 steps generates these codon type groups and main divisions within them. Meth from the interval 49 in the middle step "3 — 2":



575 = sum of A+U-coded ams, R, in the **RNA- and Pair group** out of transformations of numbers 208 + 49 in two steps:

500 = AU-, AA-, UU- plus UA-coded ams without Meth: **AUG = 75**.

159 = G+C-group of ams in this codon type group.

Sum of displacements above: **292** ~ "5", + **26** = **318** = **2 x 159** ("2").

318 is also = number 320 above re-written, received from 208_{10} in a first step:

$$\begin{array}{ccccccc}
 & & & \underline{10 \rightarrow 8\text{-base}} & \underline{10 \rightarrow 8\text{-base}} & & \\
 2 \times 159: & & \mathbf{318} & \rightarrow & 476 & \rightarrow & \mathbf{734} \rightarrow \text{RNA+Pair-coded ams} \\
 & & | & & & & | \\
 & & \leftarrow & 416 & \rightarrow & &
 \end{array}$$

734 = 2×367 = sum of RNA- plus Pair-coded groups of ams.

Sum of displacement = **416** = 2×208 ("3"), in steps 158 + 258.

Cross- and Form-coded ams = 2×385 $385 = 544 - 159$, ~ "5" + "4" - "2"

$$\begin{array}{cccc}
 \text{AG} & \text{UG} & \text{CA} & \text{GA} \\
 \text{AG} & \text{UG} & \text{CA} & \text{GA} \\
 + \text{AC} & + \text{UC} & + \text{CU} & + \text{GU} \\
 \hline
 177 & 208 & 210 & 175 \\
 \backslash & / & \backslash & / \\
 \Sigma & 385 & & 385
 \end{array}$$

$544 - 367 = 177$ ("5" + 4") - ("3" + "2") in the "exponent chain".

$$\begin{array}{ccccccc}
 & & & \underline{10 \rightarrow 8\text{-base}} & \underline{10 \rightarrow 8\text{-base}} & & \\
 \mathbf{177} & \rightarrow & 261 & \rightarrow & \mathbf{385} & & (261 = \text{A+T-bases in nb-10, } 262 = \text{G+C-bases.}) \\
 & & | & & | & & \\
 & & \leftarrow & \mathbf{208} & \rightarrow & & \text{Displacement sum = number 208.}
 \end{array}$$

9. More transformations related the exponent series:

It was noted that transformation of the codon bases nb-10 to nb-8 gave the sum 752 +/- 1, the same sum as the first three numbers in the exponent series. Here the focus is on this series and number base relations are examined 1) to the codon bases, 2)) to groups of amino acids.

$$= \overset{2/3}{5} \quad \overset{2/3}{4} \quad \overset{2/3}{3} \quad \overset{2/3}{2} \quad \overset{2/3}{1} \quad \times 100$$

$$= \underline{292} \cdot - \underline{252} \cdot - \underline{208} \cdot \text{---} \underline{159/158} - 100$$

Relations to codon bases:

a. Grouping of the codon bases in nb-8: G + U + C = 544, A = 208 -1:

<u>10-base</u>	→	<u>8-base</u>	
G 151		227	(denotation here G ₈ etc.)
U 112		160	
C 111		157...sum	544
A 135		207... sum	208 -1
		<u>10-base</u>	<u>8-base</u>
		A ₈ 207	→ 317 = U₈ + C₈ (2 x158,5)

b. From numbers of the exponent series to codon bases, steps "5 - 4 - 3":

"5":	<u>10-base</u>	→	<u>8-base</u>	
	292		444	
				> 818, ~ 1018 = 2 x 4 RNA-bases 509
"4"	252	→	374	in base-10 system
2 x "3"	<u>16-base</u>	→	<u>10-base</u>	
	416		1046	1046 = 2 x 4 DNA-bases 523
				in base-10 system

RNA-bases presumably first in the development?

A transformation from nb-16 to nb-10 for receiving the number for DNA-bases reminds of the aspect on groups of amino acids with "bridges" back from "3" to "5" (page 19) - and a suggestion that it could involve some kind of feed back mechanism. The inward direction from "3" to "5" in the chain has a correlation in the inward directed T-base and DNA in relation to RNA. It could support the interpretation of nb-16 as a sum, bridging over to nb-10 from nb-6.

$$\begin{array}{c} \hline 16 \quad ? \\ \hline | \quad \quad \quad | \\ 5 \text{ --- } 4 \text{ --- } 3 \\ \text{nb-10} \quad \text{nb-8} \quad \text{nb-6} \end{array}$$

c. 4 DNA-bases as a sum defines in transformation gaps base-pairs of DNA as intervals:

4 DNA-bases:	<u>10-base</u>	←	490	→	<u>8-base</u>	
	523				1013	
	↓					→ 261 = base pair A₁₀+T₁₀
	490	←	262	→	752	
			↓			base pair G₁₀+C₁₀

d. The 4 DNA-bases read as base-6 numbers give the sum of $U_{10} + C_{10}$:

<u>10-base</u>		<u>6-base</u>	
67	←	151	G-base
43	←	111	C-base
59	←	135	A-base
+ 54	←	126	T-base
= 223		523	
223	—————→	1011	= the sum of the whole exponent series.
223 = C 111 + U 112.			

e. Transformation gaps between bases in nb-10 and nb-8 read as nb-16:
(Difference in nb-10 74 +/-2 for G and A, 47 +/-1 for C and U.)

<u>nb-8</u>	<u>nb-10</u>	<u>16-base</u>	<u>10-base</u>	<u>8-base</u>
G: 227	- 151 = 76	76	—→ 118	166
C: 157	- 111 = 46	46	70	106....sum 272
U: 160	- 112 = 48	48	72	110
A: 207	- 135 = 72	72	114	162....sum 272
			374	544 = ams G+C (R)

The Exponent series and groups of amino acid (cf. page 36):

f. 24 B-chains out of the exponent series "5 - 4 - 3" = 12 R-chains:

	<u>16-base</u>	<u>10-base</u>	
"5"	292	—→ 658	
"4"	252	594	
"3"	+ 208	+ 520.	
½ x 24 R-chains:	752	= 1772	1772 = 24 B-chains unbound

g. The sum 752 for 12 ams R gives also divided the sum of 24 bound ams in nb-6:

	<u>10-base</u>	<u>6-base</u>	
"5"	292	—→ 1204	
"4"	252	1100...Σ 4 x 24 ²	
"3"	208..Σ 752	544 ...Σ	= 2848 = 24 ams bound
"2"	159	—→ 423	↓
"1"	100	—→ 244	
		$292_6 - 100_6 = 1204 - 244 = 960 = A + U, R\text{-chains}$	
		$252_6 + 100_6 = 1100 + 244 = 1344 = 24 B\text{-chains bound}$	
		544 = 544 = G + C, R-chains	

h. Ams-groups G1 + A1 (~ "00-bases") alone read as nb-16, "defines" the same sum in nb-8:

<u>Codons</u>	<u>16-base</u>	<u>10-base</u>	<u>8-base</u>
00-00:	396	918	1626
00-0:	292	658	1222
	688	2848	—→ 2848 = 24 ams bound
But	2 x 344	—————→	1504 x 2 = 2 x 24 ams R

- i. **First two numbers in the exponent series with +1 in number "4",**
(cf. page 19 where N-Z-differences G1 — G2 gave 292, C1 — C2 number 253):

$$\begin{array}{l} \text{10-base} \quad \text{8-base} \\ \text{G-base} \quad 292 \longrightarrow 444, \times 4 = \mathbf{1776}, - 4H = \text{B-chains } 24 \text{ ams} \\ \text{C-base} \quad 253 \longrightarrow \underline{375}, \times 4 = \mathbf{1500}, +4H = \text{R-chains } 24 \text{ ams} \\ \quad \quad \quad = \mathbf{819}, \times 4 = \mathbf{3276}, 24 \text{ ams R+B} \end{array}$$

(Cf. page 48: the transformation to 2 x RNA-bases: $444 + 374 = 818 \sim 1018$.)

- j. **From "5" in the exponent series to B-chains to the total R+B-chains:**

$$\begin{array}{l} \text{16-base} \quad \text{10-base} \quad \text{8-base} \\ \text{"5":} \quad \quad \quad \mathbf{292} \longrightarrow \mathbf{444} \quad 444 \times 4 = 24 \text{ B-chains } \grave{\text{a}} 74 \text{ A.} \\ \quad \quad \quad \downarrow \quad \quad \quad \downarrow \\ \mathbf{444} \longrightarrow \mathbf{1092} \quad \quad \quad \longrightarrow \underline{1092 \times 3 = \mathbf{3276}} = 24 \text{ ams R+B} \\ \mathbf{888} \longrightarrow \mathbf{2184} = 4 \times 546, \times 3/2 = 3276 \end{array}$$

- k. **A note about number 888:**

888 in nb-10 = $\mathbf{543} + \mathbf{345}$, numbers of the **triplet series** = 12 x B-chains $\grave{\text{a}}$ 74 A

888 in nb-8 = $\mathbf{1110}_8 = \mathbf{584}$ in nb-10 = 2 x 292 in **the exponent series**.

888 in nb-6 = $\mathbf{344}$ in nb-10 = $\mathbf{888} - \mathbf{544}$. $344 \times 2 = \mathbf{688} = \text{ams-groups G1 + A1}$.

344 in nb-6 = 136 (= **Inosine**) in nb-10 ($1/4 \times 544$). Inosine - Orotate, see below.

888 in nb-16 = $\mathbf{2184} = 4 \times 546, 8 \times 273$ (the mean value of 2 **ams R+B** = 273)

- l. **Re-writing sums C1 + U1, G1 + A1 (R), as nb-8-numbers, and these transformed again 10 \rightarrow 8, generates 24 ams R+B:**

$$\begin{array}{l} \text{10-base} \quad \quad \quad \text{8-base} \\ 526 \longleftarrow \quad \quad \quad \mathbf{816} \sim 1016 \quad 816 = \text{C1+U1-coded ams R} \\ + 456 \longleftarrow \quad \quad \quad \mathbf{688} \sim 710 \quad \underline{688} = \text{G1+A1-coded ams R} \\ \mathbf{982} \quad \quad \quad \xrightarrow{744} \mathbf{1726} \quad (1504) \\ \quad \quad \quad \downarrow \\ \mathbf{1726} \quad \quad \quad \xrightarrow{\quad} \mathbf{3276} \quad \quad \quad \mathbf{3276} = 24 \text{ ams R + B} \end{array}$$

Transformation gap 744 above \sim NADP 744 A in nb-10.

- m. **20 ams R, without 4 double-coded ams = 1258: Two sets derived from 4 bases in nb-8, 752:**

$$\begin{array}{l} \text{10-base} \quad \quad \quad \text{8-base} \\ \frac{1}{2} \times 24 \text{ ams R} \quad \mathbf{752} \longrightarrow 1358 \sim 1360 \\ \quad \quad \quad \downarrow \\ \mathbf{1358} \longrightarrow \mathbf{2516} = 2 \times 1258 = 2 \times 20 \text{ ams R} \end{array}$$

12. Three special number relations:

- a. The sum of ams-groups in 1st and 2nd base ordering, as counting with two sets of ams, give in nb-8 through re-writing the simple scheme from the exponent series below (cf. page 13):

	<u>8-base</u>	→	<u>8-base</u>		<u>Ams-groups R-chains in base-10 system</u>
2 x 292:	584	~	604 =		G1 + G2 +2 (191 + 411)
2 x 252:	504	~	484 =		C1 + C2 - 2 (353 + 133)
2 x 208:	416	+	604 = 1020 =	A1 + A2	(497 + 523)
	416	+	484 = 900 =	U1 + U2	(463 + 437)

Number 59: 604 - 484 = 118 = 2 x 59:

(604 - 2) - (484 + 2) = 2 x 58. 58 = G1 — C2, C1 — G2.

1020 - 900 = 2 x 60. 60 = A1 — U2, U1 — A2.

- b. Codon types: The division of Cross- and Form-coded ams (770) in groups 209 / 176 +/- 1 (cf. page 52):

Cross-coded = **418** = 2 x 209: CA+CA+CU = 210, UG+UG+UC = 208,
Form-coded = **352** = 2 x 176: GA+GA+GU = 175, AG+AG+AC = 177.

The exponent series: $\frac{292 - 252}{544} - \frac{208 - 159 - 100}{467}$

<u>10-base:</u>	x ½ = 272	x ½ = 234. (round number)
↓	↓	↓
<u>8-base:</u>	418	352
=	2 x 209	2 x 176

- c. Division between ams with U in 1st or 2nd position of the codon and the rest of ams in the two groups of codon types (cf. page 24):

	<u>U in codons</u>	→	<u>The Rest</u>	<u>Exponent series</u>
Cross- +Form-coded 770:	308	→	462	(460 +2 = "4 + 3", +2)
	↓		↑	
RNA- + Pair-coded: 734	444	←	290	(292 - 2 = "5" , - 2)
	<u>10-base</u>		<u>8-base</u>	
	307	→	463	Sum 770
	291	→	443	Sum 734

The exponent series:

292	>	<u>544, - 100 = 444</u> , U in codons		The rest 292 -2
252	>	<u>208, +100 = 308</u> , U in codons		" 252+208, +2

All ams with U-contenting codons derivable from glycolysis, the rest from citrate cycle. Thus, the transformations above seem like illustrating opposite directions to and from mitochondria - and a mix of nb-10 and dependent nb-8 numbers.

13. B-chains:

Some first annotations:

It may perhaps seem odd treating the B-chains separate from R-chains of ams. Yet, in peptide binding they form their own zigzag co-ordinate axis - the forming of which seems to be the main aim for unbound B-chains too. And they are the common part for transportation of the ams to t-RNA by the A-base as coenzyme (ATP).

Besides the main theme here it could be worth mentioning the inverse number relations between the A-base and free B-chains:

A-base 135 \wedge 740740740740...(x10^x). B-chains unbound normally 74 A.

In numbers of the triplet series: 543 + 345 = 888 = 12 x 74, ~ 12 B-chains.
543 + 210 = 753, mean value ~ 12 R-chains + 1.

Difference: 888 - 753 = 135, the A-base, but also the starting ams Meth when its end-group CH₂ is deducted at the beginning of the protein synthesis [1].

As said in part I: the number 370 = 5 x 74 (+/-1) appears also in codon grouped R-chains: UU + UG + GG + GU = 370 - 1, AA + AC + CC + CA = 370 + 1.

Number 370 may be generated from steps in an elementary "5-dimensional chain":

$$\frac{1 \times 54}{54} + \frac{2 \times 43}{86} + \frac{3 \times 32}{96} + \frac{4 \times 21}{84} + \frac{5 \times 10}{50} = 370$$

$$\sqrt{54.86.96.84.50} = \underline{740740740}... \times 10^x, \text{ the inverted number of the A-base.}$$

The exponent series (part I) gave the sums of 6 unbound and 6 bound B-chains as intervals:

$$\begin{aligned} \text{"5+4" - "1":} & \quad 544 - 100 = \mathbf{444} = 6 \times 74 \\ \text{"5+4" - "3":} & \quad 544 - 208 = \mathbf{336} = 6 \times 56 \quad \text{"3 - 1" = 108} \sim 6 \text{ H}_2\text{O}. \end{aligned}$$

Transformations in number base systems:

a. One B-chain unbound = 74 A gives two B-chains à 56 A in peptide binding:

$$\text{B-chain in free ams } \underline{74} \xrightarrow{\substack{10\text{-base} \\ 8\text{-base}}} \mathbf{112} = 2 \times \mathbf{56} = 2 \text{ B-chains in peptides.}$$

The code base U = **112 A**, same number. Compare the exchange of T to U in m-RNA.

b. 3 H₂PO₄⁻ = 3 x 97 A = 291 A (for the P-group bonds of nucleosides triplets ?)

$$\text{"5" - 1} = \frac{10\text{-base}}{\mathbf{291}} \quad \frac{8\text{-base}}{\mathbf{443}}, \quad \times 4 = \mathbf{1772} = 24 \text{ B-chains unbound}$$

c. Number 292 in the exponent series:

$$\begin{aligned} & \frac{10\text{-base}}{292} \quad \frac{8\text{-base}}{\mathbf{444}} = 6 \text{ B-chains à } 74 \text{ A} \\ 2 \times 292 = \mathbf{584} & \xrightarrow{\quad} 1088 \sim \mathbf{888} \cdot \times 2 = \mathbf{1776} = 24 \text{ B-chains à } 74 \text{ A}. \end{aligned}$$

d. From R-chains to B-chains:

$$\begin{array}{r} \text{16-base} \\ \underline{376} \\ 376 = 1/4 \times 1504, 24 \text{ ams R} \end{array} \quad \begin{array}{r} \text{10-base} \\ \underline{886,} \\ \times 2 \end{array} = 1772, \text{ 24 unbound B-chains} \\ \text{(-1 H in Arg1,2, Lys, Pro)}$$

e. From α -ketoglutarate (or Glu charged) = 146 to unbound to bound B-chains (cf. the role of Glu in amination of the B-chains):

$$\begin{array}{r} 292, \times 1/2: = 2 \times 73: \\ \text{146} = \alpha\text{-ketoglutarate} \\ = \text{Glu charged, R} = 73. \end{array} \quad \begin{array}{r} \text{10-base} \\ \underline{146} \\ \downarrow \\ \underline{222} \end{array} \quad \begin{array}{r} \text{8-base} \\ \underline{222} \\ \downarrow \\ \underline{336} \end{array} \quad \begin{array}{l} \longrightarrow \\ \longrightarrow \\ \longrightarrow \end{array} \quad \begin{array}{l} = 3 \text{ B-chains unbound à } 74 \\ = 6 \text{ B-chains bound à } 56 \end{array}$$

f. From bases to 24 B-chains bound, 1344 A:

$$\begin{array}{r} f1. \quad \begin{array}{r} \text{10-base} \\ 194 \\ 184 \\ 146 \\ + 148 \\ \hline 672 \end{array} \quad \begin{array}{r} \text{8-base} \\ 302 \\ 270 \\ 222 \\ 224 \end{array} \quad \begin{array}{l} 2 \times \text{G} \\ 2 \times \text{A} \\ 2 \times \text{C} \\ 2 \times \text{U} \end{array} \quad \begin{array}{l} 2 \times \text{RNA-bases read as 8-base numbers} \\ \\ \\ \\ \end{array} \\ \longrightarrow \times 2 = 1344, = 24 \text{ B-chains bound} \end{array}$$

$$\begin{array}{r} f2. \quad \begin{array}{r} 388 \\ + 352 \\ \hline = 740 \end{array} \quad \begin{array}{r} \text{8-base} \\ 604 \\ 540 \end{array} \quad \begin{array}{l} 4 \times \text{G} \\ 4 \times \text{A} \end{array} \\ \longrightarrow 1344 = 24 \text{ B-chains bound} \end{array}$$

$$\begin{array}{r} f3. \quad \begin{array}{r} \text{10-base} \\ 352 \\ \downarrow \\ 352 \end{array} \quad \begin{array}{r} \text{8-base} \\ 540 \end{array} \quad \begin{array}{l} 4 \times \text{A-base} \\ \\ \end{array} \\ \longrightarrow 1344 = 24 \text{ B-chains bound} \end{array}$$

$$\begin{array}{r} f4. \quad \begin{array}{r} \text{16-base} \\ 540 \end{array} \quad \begin{array}{r} \text{10-base} \\ \underline{1344} \end{array} \\ \longrightarrow 1344 = 24 \text{ B-chains bound} \end{array}$$

g. From Inosine 136 through 5 transformations to 24 B-chains, bound 1344 and unbound 1772:

$$\begin{array}{r} \text{10-base - 8-base} \\ 136 \rightarrow 208 \end{array}$$

$$\begin{array}{r} \text{10-base - 8-base} / \text{10-base - 8-base} / \text{10-base - 8-base} / \text{10-base - 8-base} \\ 208 \rightarrow 320 \quad 320 \rightarrow 500 \sim 480 \quad 480 \rightarrow 740 \quad 740 \rightarrow 1344 \end{array}$$

$$\begin{array}{r} \text{10-base - 6-base} / \text{10-base - 8-base} / \text{10-base - 8-base} / \text{10-base - 8-base} \\ 136 \rightarrow 344 \quad 344 \rightarrow 530 \sim 528 \quad 528 \rightarrow 1020 \sim 1018 \quad 1018 \rightarrow 1772^* \end{array}$$

*Without re-writings the last sum is 1776, 24 B-chains à 74.
Transformation gap 136 to 1772 + 2 (as for one re-writing?) = 1638, x 2 = total sum of 24 unbound ams R+B 3276. 1018 in last step = 2 x 4 codon bases.

14. Neutrons and N-Z-divisions:

It's curious that the number of neutrons - or Z-numbers without H-atoms - in R-chains of codon base groups give the total numbers of R- and B-chains through transformations in 2 (or 3) steps.

In 1st base order also the sum of 2 x 4 codon bases in nb-8 (cf. page 48).

a. Neutron sums in code base groups giving the total sum of 24 ams unbound:

	<u>10-base</u>	<u>8-base</u>	
G1: N	86	126	
C1: N	158	236	
U1: N	213	325	
A1: N	<u>219</u>	<u>333...Σ 1020, ~ 1018</u>	= 2 x 4 code bases in 10-base system
	↓		
	↓ → 1018	→ 1772	= 1772 = 24 B-chains

G2: N	187	273	
C2: N	58	72	> 3276 + 2H
U2: N	190	276	
A2: N	<u>241</u>	<u>361...Σ 982 = 2 x 491</u>	
	↓		
	↓ → 491	→ 753, x 2	= 1506 = 24 R-chains + 2H*

* 2 x 491: 982	→	1726	
	↓		
	↓ → 1726	→ 3276	= 3276 = 24 ams R + B

- 491₈ ~511 ~509 re-written, sum of 4 RNA-bases.
- (982 re-written = 1202, + 1018 = 2220 (nb-8). = 490 in nb-16.
- 490 in nb-16 = 1168 in nb-10 = 4 x 292 in the exponent series, = 4 x Inosine + 4 x Orotate, = the sum of ams with 3rd base A/G (A or G) or U/C +1.)

b. Total sum R-chains: N = 676, H = 152, Z = 828:

	<u>16-base</u>	<u>6-base</u>	
	108	→ 1120 ~ 676 = N	
152 <			> 828 = Z
	44	→ 152 = H	
	← 108 →		

c. The whole exponent series transformed separately and whole give N- and Z-numbers of 24 ams + 3, the sum 3282 of the expanded triplet series (see below):

<u>10-base</u>	292	252	208	159	100	Sum = 1011
↓	↓	↓	↓	↓	↓	508~510, 509 = 4 bases
<u>8-base</u>	444	374	320	237	144	Sum = 1519 = N + 3
						> 3282*
10- to 8-base, whole sum				1011	→	= 1763 = Z + 3
				752		
				1/2 x 24 ams R		

*The triplet series expanded: $\underline{987 + 876 + 765 + 654 + 543 + 432 + 321 + 210}$

$$= \begin{array}{ccc} 3282 & \leftarrow \text{---} | \text{---} \rightarrow & 1506 \\ \text{interval:} & & 1776 \\ & & 24 \times 74 \end{array}$$

Compare how 2 x 4 separate codon bases transformed gave R-chains of ams, the sum of them transformed gave the B-chains (page 36):

Whole sums and divided ones: such differences could eventually be seen in terms of polarisations to other d-degrees where the co-ordinate axes define different complementary properties... ?

c. N-Z-numbers in the codon type groups 770 / 734: out of differences between code bases in nb-8 and nb-10:

G+C-group: $G_8 + C_8 = 384$, difference transformed in 1 step:

$$\begin{array}{l} \begin{array}{ccc} & \underline{10\text{-base}} & \underline{8\text{-base}} \\ 384 - G_{10} 151 = 233 & \longrightarrow & \mathbf{351} & = \mathbf{N\text{-number in 770-group}} \end{array} \\ \begin{array}{ccc} \underline{384 - C_{10} 111} = \underline{273} & \longrightarrow & \underline{421 \sim 419} & = \mathbf{Z\text{-number in 770-group}} \\ 768 & 2 \times 253 & \longrightarrow & 772 - \mathbf{770 \sim 768} \end{array} \end{array}$$

A+U-group: $A_8 + U_8 = 367$: difference transformed in 2 steps:

$$\begin{array}{l} \begin{array}{ccc} & \underline{10\text{-base}} & \underline{8\text{-base}} \\ 367 - U_{10} 112 = 255 & \longrightarrow & \underline{377} \\ 377 - 112 = 265 & \longrightarrow & 411 \sim \mathbf{409} & = \mathbf{Z\text{-number in 734-group}} \end{array} \\ \begin{array}{ccc} 367 - A_{10} 135 = 232 & \longrightarrow & \underline{350 \sim 348} \\ \underline{348 - 135} = 213 & \longrightarrow & \underline{\mathbf{325}} & = \mathbf{N\text{-number in 734-group}} \\ \mathbf{734} & & \mathbf{734} \end{array} \end{array}$$

Subtracting steps with C-U-bases 111, 112 give Z-numbers.
Subtracting steps with G-A-bases 151, 135 give N-numbers.

15. Cn: amino acids grouped according to number of C-atoms in R-chains:

With reference to page 21:

Interpreting the positions of Phe, Tyr and Trp + Gly as on page 21, it gave the first three numbers of the exponent series "5 → 4 → 3" doubled in the order 584 - 504 - 416. They seem connected through transformations in number-base systems:

(N.B.! C in this special context indicates C-atoms.)

$$\begin{array}{rcc}
 & \text{C7} & \\
 \text{C4} & / \quad \backslash & \\
 & \text{C3 + C0} & \\
 \hline
 \text{C2} & & \text{C1} & + \text{C9} = \text{Trp} \\
 \hline
 \underline{584} & \underline{198} & \underline{306} & & \underline{162} & \underline{124} & \underline{+130} \\
 \underline{584} & & \underline{504} & & \underline{286} & & \\
 \hline
 2 \times 544 & & & & 2 \times 208 & & \\
 \underline{1088} & & & & \underline{416} & &
 \end{array}$$

$$\underline{584} = \underline{1088} = \underline{584 + 198 + 306}$$

10-base → 8-base

$$\underline{198} = \underline{306}$$

10-base → 8-base

$$\underline{306} \sim \underline{286} \text{ (re-written)}$$

8-base 8-base

$$\underline{286} = 436 = 306 + 130 \text{ (Trp)}$$

10-base → 8-base

↓

$$\text{C2} \quad 162 = \quad 242$$

$$\text{C1} \quad \underline{124} = + \quad \underline{174} = \underline{416}$$

10-base → 8-base

$$= \underline{286} + \underline{130} \text{ (Trp)}$$

$$\underline{174} \rightarrow \underline{256} = \underline{124} + \underline{130} + 2\text{H}$$

10-base → 8-base

Repeating it here:

Why connection of Trp to the group with one C-atom: Ala - Ser1 - Ser2 - Cys ?

Trp is constructed from 3C + 4C plus and minus more C-atoms, as if it represented "the other way around" in the number chain:

- Ser contributes in the synthesis of Trp.
- Trp can break down to Ala...
- Trp shares the UG-code with Cys, which originates from Ser.

(Gly, 0 C, connected with Pro, 3 C, in collagen. As 1 H from the ring formation of Pro??)

The Exponent series:

$$\begin{array}{cccccc}
 \text{"5"} & \text{"4"} & \text{"3"} & \text{"2"} & & \text{"1"} \\
 292 & 252 & 208 & 159/158 & & 100 \\
 | & & & & & | \\
 544 & \leftarrow & \text{286} & \rightarrow & 258(+1) & \\
 & & = C2 + C1 & & & \\
 & & | & & & | \\
 & & \text{467 (208 + 259)} & & & \\
 & & = C3 + C2 & \rightarrow & = \underline{305} + 162 &
 \end{array}$$

Cn, two details:

a. Different intervals in transformations through re-writings:

$$\begin{array}{ccc}
 \text{10-base} & \text{8-base} & \\
 584 \rightarrow 1088 \sim | \sim 890 & & | \\
 | & & \\
 C7 = \mathbf{198} & \text{out of re-writing} & \\
 \\
 584 & \leftarrow \text{---} | \text{---} \rightarrow & 890 \\
 & \mathbf{306} = C3 + C0 &
 \end{array}$$

b. Trp:

$$\begin{array}{ccc}
 \text{Interval:} & 504 & \leftarrow \text{---} | \text{---} \rightarrow & 416 \\
 & & | & \\
 & & \underline{\mathbf{88}} & \rightarrow \underline{\mathbf{130}} \text{ Trp} \\
 & & \text{10-base} & \text{8-base}
 \end{array}$$

Division of the sum 1504 of 24 ams R in $714 \leftarrow \text{---} \rightarrow 792, -2$, sums from the Triplet chain:

$$714 \text{ inwards: } 012 + 123 + 234 + 345.$$

$$792 \text{ as interval outwards - inwards} \\ = 4 \times 198 (= 543 - 345, 432 - 234, 321 - 123, 210 - 012):$$

$$\begin{array}{cccccc}
 / & C7 & \backslash & & & \\
 C4 & | & C3 + C0 & C2 & C1 & + C9 \\
 584 & \underline{198} & \underline{306} & 162 & 124 & \underline{+130 \text{ (Trp)}} \\
 | & & \text{790} \sim C1+U2 & & & | \text{ (C here for ams groups)} \\
 | & & \text{714} \sim G1 + A2 & & & |
 \end{array}$$

16. The Triplet series in transformations:

Here is a closer look on this triplet series, approximating sums of 24 ams, which was suggested as an eventual, more elementary mathematical level steering the genetic code.

The Triplet chain “outwards” – “inwards”:

$$\begin{array}{r}
 543 \qquad \qquad \qquad 345 \\
 432\dots975 \qquad \qquad 234 \\
 321 \qquad \qquad \qquad 123 \\
 \underline{210\dots531} \qquad \qquad 012 \\
 1506 \leftarrow \text{---|---} \rightarrow 714 \\
 \qquad \qquad \qquad \qquad \qquad \qquad 792
 \end{array}$$

a. 2 times the inward chain in nb-8 out of the interval 792:

$$\begin{array}{r}
 \underline{10\text{-base}} \qquad \qquad \underline{8\text{-base}} \\
 792 \quad \longrightarrow \quad 1428 \quad = 2 \times 714
 \end{array}$$

(What should a duplication in inward direction imply? An association goes to the relation between a single RNA-string and the double DNA-spiral.)

A1+U1-groups of ams (R) without the 4 double-coded = 714.
 Ams groups of 24 ams, mixed: G1 + A2 = 714, C1 + U2 = 790

b. Codon bases x 2 giving the sum of 24 ams R, divided 792 — 714 -2:

$$\begin{array}{r}
 \qquad \qquad \underline{10\text{-base}} \qquad \qquad \underline{8\text{-base}} \\
 2 \text{ G} \quad 302 \quad \longrightarrow \quad 456 \\
 2 \text{ C} \quad 222 \qquad \qquad \quad 336\dots 792 \\
 \\
 2 \times \text{U} \quad 112 \times 2 \quad \longrightarrow \quad 160 \times 2 = \quad 320, \sim 318 \\
 2 \times \text{A} \quad 135 \times 2 \qquad \quad 207 \times 2 = 414, \sim 394\dots\text{sum } 714, \dots 712
 \end{array}$$

c. Nb-16: interval in each step of the triplet series = 111:

$$\begin{array}{r}
 \underline{16\text{-base}} \qquad \qquad \underline{10\text{-base}} \\
 111 \quad \longrightarrow \quad 273 \qquad \qquad \times 12 \quad = 3276, 24 \text{ ams R+B} \\
 273 = \text{mean value of } 2 \text{ ams R+B}
 \end{array}$$

d. Nb-16, interval between sums 975 - 531:

$$\begin{array}{r}
 \underline{16\text{-base}} \qquad \qquad \underline{10\text{-base}} \\
 975 \quad \longrightarrow \quad 2421 \\
 1506 < \text{---|---} 444 \qquad \qquad \text{---|---} \qquad \qquad \qquad 1092, \times 3 \quad = 3276 = 24 \text{ ams R+B} \\
 \underline{\qquad \qquad \qquad 531} \quad \longrightarrow \quad \underline{\qquad \qquad \qquad 1329}
 \end{array}$$

Compare: $666 \longrightarrow 1638 \times 2 = 3276.$

- e. From the triplet chain "outwards" as nb-8 numbers to nb-10 gives the number 982, which in 2 steps gives 3276:

<u>10-base</u>		<u>8-base</u>	
355	←	543	
282		432	
209		321	
<u>136....982</u>		<u>210</u>	
982	→	1726	= 1506 + 220
		↓	
↓			
1726	→	3276, total sum 24 ams R+B, unbound	

- f. Triplets "outwards" + "inwards" as base-8-numbers transformed to base-10:

<u>8-base</u>		<u>10-base</u>		Sums		<u>10-base</u>		<u>8-base</u>
345	→	229	→	4 x 146	←	355	←	543
234		156	→	3 x 146	←	282		432
123		<u>83</u>	→	2 x 146	←	<u>209</u>		321
<u>012</u>		<u>10</u>	→	1 x 146	←	<u>136</u>		<u>210</u>
714		478				982		1506

Sum **1460 = 5 x 292**, the number "5" of the Exponent series. (Cf. page 45.)

Intervals 229 – 355, 156 – 282 etc. = **126, x 4 = 504 = 2 x "4"** in the Exponent series.

(Cf. number 146 in connection with Histones, said to bind 146 base pairs in chromosomes [4].)

- g. Transforming the 4 codon bases DNA and RNA separately from nb-8 to nb-10 gives triplet sums:

	4 DNA-bases				4 RNA-bases:		
	<u>10-base</u>	←	<u>8-base</u>		<u>10-base</u>	←	<u>8-base:</u>
G	105		151	G	105		151
C	73		111	C	73		111
T	86		126	U	74		112
<u>A</u>	<u>93</u>		<u>135</u>	<u>A</u>	<u>93</u>		<u>135</u>
Sum:	357		523		345		509

	<u>Triplet series "inwards"</u>			
4 RNA-bases →	345	=	345 ,	+ <u>012</u> = 357 → DNA
4 DNA-bases →	357	= -	234	
			123	
			012	

Difference 012 = 14 in base-8 numbers = + CH₂ in U-base to T-base in DNA:

	<u>10-base</u>		<u>8-base</u>	
Cf.	345	→	531	= 321 + 210 outwards
	357	→	545	= 543 + 2. " "

17. Another kind of "5-dimensional" chain - in another context?

The number chain below could be seen as a special variation of the transformation between codon bases and groups of amino acids, as if it were developed between G- and C-bases and with A-base (or Inosine) and T-base doubled. And last three steps have to be doubled to give the sum of ams in nb-8. It may be observed that pairs of numbers give the first to numbers "5" + "4" of the exponent series, which add to the sum of G+C-coded ams.

How to look on such a variation? If accepting the hypothesis of some underlying 5-dimensional scheme behind the genetic code, could it be reasonable to count with such variations of number growth in different parts of the protein processes, as for instance this chain with DNA-bases in connection with t-RNA...?

a. Mass numbers of 2 x codon bases DNA:

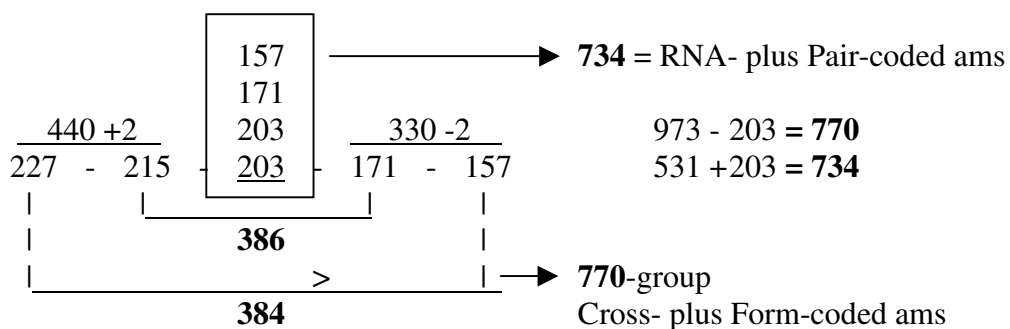
$$\begin{array}{rll}
 & & \mathbf{151} & \longrightarrow \text{G-base} \\
 2 \times \text{G-base } \underline{-10}: & \mathbf{292} < & \mathbf{141} & \\
 & & > \mathbf{272} = 2 \times \text{A-base} + 1 \text{ (~ Inosine)} \\
 & & \mathbf{131} & \\
 2 \times \text{T-base (126 A)} & \mathbf{252} < & \mathbf{121} & \\
 & & > \mathbf{232} = 2 \times \text{C-base} + \underline{10} \\
 \hline
 \text{Sum} & \mathbf{1048} & \mathbf{111} & \longrightarrow \text{C-base} \\
 & & \text{2 x 524 (4 bases DNA = 523)} &
 \end{array}$$

This chain with *last 3 steps doubled* (cf. point f. below):

	<u>10-base</u>		<u>8-base</u>
	151	→	227
	— 141...292		215
	131		203 203
363* <	121...252		171 171
	111		+ <u>157 157</u>
Sum =	655		= 973 531
	+ <u>363</u>		\ 1504 / (24 ams R)
2 x 4 RNA-bases	1018		
	1018	→	1772 (24 ams B)

The division 973 - 531 is the same as in 3rd base grouping: A/G-coded + "2-base-coded" ams = 638 + 335 = 973, U/C-coded 531.

b. Codon type groups, here the RNA+Pair-groups in the middle of the chain, as in the exponent series:



c. Some other paired groups of ams R from chain 227 - 215 - 203 - 171 - 157:

$$973 - 157 = \mathbf{816} = \mathbf{C1+U1}$$
-coded ams

$$531 + 157 = \mathbf{688} = \mathbf{G1+A1}$$
-coded ams

848 -- 656 division:

	<u>10-base</u>		<u>8-base</u>	
	151		227	
	141		215	
2 x	131	2 x	203 = 406.....	Sum 848 = G2 + U2

2 x	121	2 x	171 = 342	
2 x	111	2 x	157 = 314.....	Sum 656 = C2 + A2

792-712:

Exponent series:

$$215 + 171 = 386$$

$$203 + 203 = 406....\text{sum } \mathbf{792} = 2 \times 292 + 208$$

$$227 + 171 = 398$$

$$157 + 157 = 314....\text{sum } \mathbf{712} = 2 \times 252 + 208$$

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

<u>10-base</u>	→	<u>8-base</u>
101		145

$$973 - 145 = \mathbf{828} = \mathbf{Z}$$
 total 24 ams R

$$531 + 145 = \mathbf{676} = \mathbf{N}$$
 total 24 ams R

$$973 - 157, + 145 = \mathbf{961} = \mathbf{A+U} + \mathbf{1}$$

$$531 + 157, - 145 = \mathbf{543} = \mathbf{G+C} - \mathbf{1}$$

e. The doubled last steps re-written:

$$203 \sim 183 = -20$$

$$171 \sim 169 = -2$$

$$\underline{157} \dots\dots\dots \text{sum } \mathbf{531} - \mathbf{22} = \mathbf{509} = \text{sum of 4 codon bases RNA}$$

f. Transformations with the 3 middle steps doubled:

<u>10-base</u>		<u>8-base</u>	
151		227	
141	2 x	215	215 ~195
131	2 x	→	203 ~183, ~183
121	2 x	171	171
+ 111		+ 157	2 x 183 = 366
= 655		770	734 -2
+ 393		\	/
= 1048		1502	(Sum of 24 ams R -2)

with the re-writings

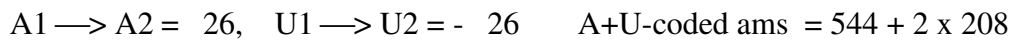
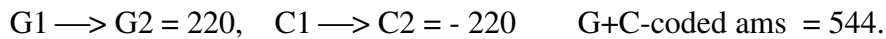
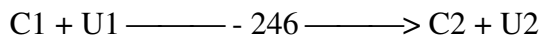
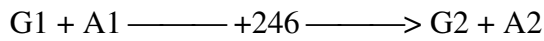
18. Number 246:

This number 246 appears as the sum of differences or “displacements” between ams-groups in 1st and 2nd base order, and also as the sum of the 4 double-coded ams.

The aim here was to see if these numbers reveal some interesting connection with others in an eventual scheme of transformations. (Cf. page 19.)

a. The displacements between ams in 1st and 2nd base order and number 194:

Ams groups R:



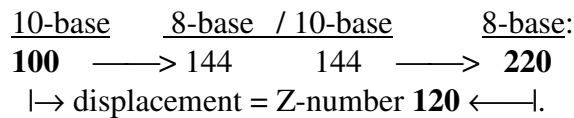
220 - 26 = 194, the difference +/-2 in the division of number **416** in the exponent series, (A+U) - (G+C): $(A1-G1) - (U1-C1) = 194 - 2 = 306 - 110$.

$$(A2-G2) - (U2-C2) = 194 - 2 = -112 + 304.$$

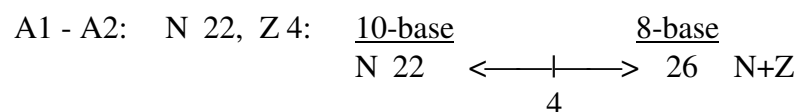
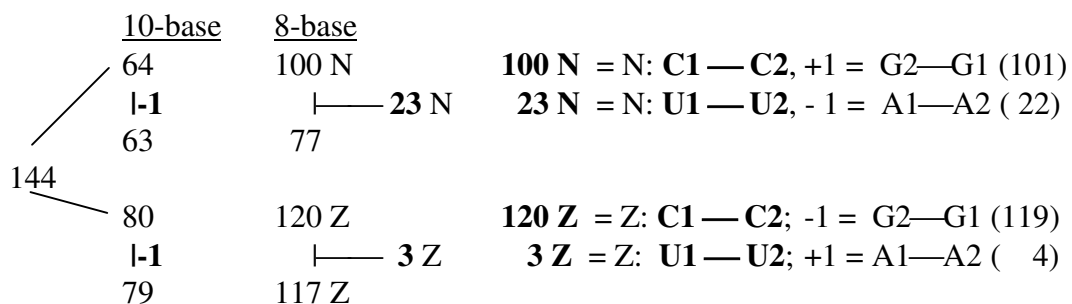
194 = 2 x 97: an H₂PO₄⁻-group. **194** also a charged ribose-P-group in nucleotides.

b. From N-displacement to N+Z-displacement:

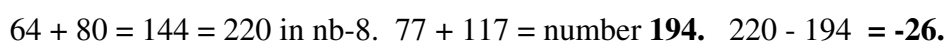
Number 220 divided N = 100 (101), Z = 120 (119) in G-C-group
 N = 23 (22), Z = 3 (4) in A-U-group.

b1. In G+C-groups:**b2. In the A-U-group?**

Numbers 23 and 3 as out of -1 at a 10- to 8-base transformation? Example:



A single change of one H-atom, chemically, could result in such big changes in a transformation process. Compare perhaps P-groups in nucleotides, uncharged and charged:



d. Number 220: = G1 → G2, C1 ← C2, connected with the sum of ams G+C 544:
In relation to numbers of the exponent series:

$$\begin{array}{ccc} \text{16-base} & \text{10-base} & \text{6-base} \\ \mathbf{220} & \longleftrightarrow \mathbf{544} = 292+252 & 1040 = \mathbf{5} \times \mathbf{208} \end{array}$$

$$\begin{array}{ccc} & \mathbf{292} & \\ & | \text{---} \mathbf{84} \text{ ---} & \mathbf{220} = \mathbf{5} \times \mathbf{44}, \text{ the interval } 252 \text{ --- } 208. \\ \mathbf{208} & \text{---} & \mathbf{544} \end{array}$$

d1) 220 in nb-16: a transition version or reference for the G+C-guided groups 544 between 1st and 2nd base order?

$$\begin{array}{l} \underline{544 + 220} = 764 = C1 + G2 = 353 + 411, \text{ difference } 58 \\ \underline{544 - 220} = 324 = G1 + C2 = 191 + 133, \text{ - " - } 58 \end{array}$$

d2) 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:

$$\begin{array}{l} 544 \text{ divided } 292 \text{ --- } 252 = \text{"5"---"4"} \\ 544 \text{ - " - } 336 \text{ --- } 208 = (\text{"5 + 4 - 3"}) \text{ --- "3"} \\ 544 \text{ - " - } 177 \text{ --- } 367 = (\text{"5 + 4"}) \text{ - ("3 + 2")} \text{ --- ("3 + 2")} \end{array}$$

$$\begin{array}{ccc} \text{10-base} & & \text{8-base} \\ 101 & \text{---|---} & 145 \\ & \mathbf{44} & \\ \mathbf{G1} = \mathbf{292} - 101 & & \mathbf{336} - 145 = 191 = \mathbf{G1} \\ \mathbf{C1} = \mathbf{252} + 101 & & \mathbf{208} + 145 = 353 = \mathbf{C1} \end{array}$$

Number 220 as a nb-6 number: 6-base
 $\mathbf{220} \sim \mathbf{176}$: G1 = $\mathbf{367} - 176 = 191$
re-writing C1 = $\mathbf{177} + 176 = 353$

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

$$\begin{array}{l} (\text{"5 + 4"}) \text{ - ("3 + 2")} = \mathbf{177}, \text{ - } 44 = \mathbf{133} = \mathbf{C2}. \\ (\text{"3 + 2"}) = \mathbf{367}, \text{ + } 44 = \mathbf{411} = \mathbf{G2} \quad (?) \end{array}$$

e. The double-coded ams, Arg, Ser, Leu, Ile = 246 (R):

The transformation of number 101 = Arg2 to nb-8 gives 145, which is the sum of the three other double-coded ams. There are some number relations below but it's very doubtful if they could contribute to an explanation of why just these ams are double-coded.

$$\text{Arg AG } \mathbf{101} \xrightarrow{\text{10-base}} \mathbf{145} \xrightarrow{\text{8-base}} = \text{Ser } 31 + \text{Leu } 57 + \text{Ile } 57$$

$$\begin{array}{l} \text{Arg AG} \quad \text{10-base} \quad \text{8-base} \quad \text{10-base} \quad \text{6-base} \\ \quad \quad \quad 37 \quad \leftarrow 101 \sim 57 \\ \text{Ser AG} \quad 31 \leftarrow \quad 37 \quad \leftrightarrow \quad 37 \quad \leftarrow \sim 57 = \text{Leu2, Ile2 in nb-10} \end{array}$$

19. Separate ams, R-chains, as transformed into one another:

Could all *separate* R-chains of ams be derived from the exponent series? Here examples including an unlimited use of transfers between different number base systems.

292 --|-- 252 --|-- 208 --|-- 159/158 ---|--- 100 --|-- 0
 40 44 49 59/58 100
 |<-----133----->| - intervals as starting
 |<-----93----->| numbers:
 |<-----84----->||<-----108----->|

R-chains:

10-->8

59 --> 73 Asp --> Glu / Lys

58 --> 72 Asn --> Gln

<u>10->8</u>	<u>10->8</u>	<u>6->10</u>	<u>6->10</u>	<u>6->10</u>	<u>6->10</u>	<u>6->10</u>
49 --->	59, ~ 61 --->	75 <--->	47 <--->	31 <--->	19 <--->	15
	Asp	Meth	Cys	Ser		Ala
	<u>10->8</u>			<u>10->8</u>	<u>10->6</u>	
	73 Glu / Lys			31 --->	37 --->	101 (~ 61, ~ 57)
<u>10->6</u>				Ser		Arg
49 --->	81					
	His			<u>10->8</u>	<u>10->8</u>	<u>10->6</u>
				31 --->	37 --->	45 ---> 73
				Ser		Thr
	<u>8-base</u>					Glu
	81 ~ 101	<u>10->8</u>	<u>10->8</u>	<u>10->8</u>		Lys
	Arg	47 --->	57 --->	71 --->	107	
<u>10->16</u>		Ileu / Leu			Tyr	
49 --->	31 = Ser			<u>6->10</u>		
				71 --->	43 = Val	

<u>8 --> 10</u>	<u>8->10</u>	<u>8->10</u>
101 (Arg) --->	65 --->	53 --->
	43 Pro before ring binding.	
100 ----->	64 --->	52 --->
	42 Pro	

<u>8-base</u>	<u>6 ---> 10</u>	<u>6 --> 10</u>	<u>8 --> 10</u>
108 ~ 110	110 --->	42	
	Pro		Pro

<u>8-base</u>	<u>10 --> 8</u>	<u>10->8</u>	<u>10->8</u>	<u>8 --> 8</u>	<u>6 --> 6</u>
108 ~ 88	---->	130			
	Trp				
		<u>10->8</u>	<u>10->8</u>	<u>8 --> 8</u>	<u>6 --> 6</u>
		59 -->	73 -->	111 ~ 91	111 ~ 107
				Phe	Tyr

<u>8->10</u>	<u>8->10</u>	<u>8->10</u>
133 --->	91 --->	73 --->
	Phe	Glu/Lys
		Asp

<u>8->10</u>	<u>8->10</u>	<u>8->10</u>
93* -->	75	159 --->
	Meth	113 -->
		75
		Meth

<u>6->10</u>	<u>10->8</u>	<u>10->8</u>
133 --->	57 --->	71 --->
	Leu/Ileu	107
		Tyr

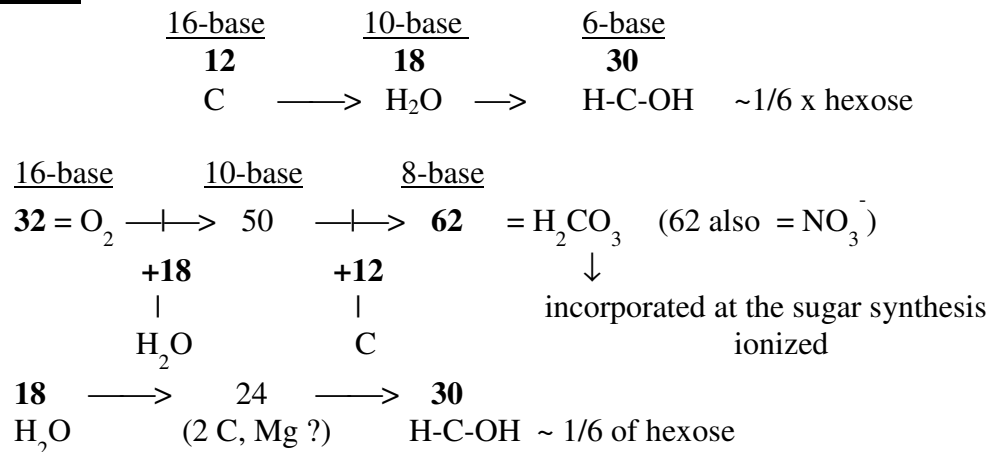
10--->8
 * 93 --> 135 A-base

<u>10-->6</u>	<u>6-base</u>	<u>8-base</u>	<u>10->8</u>
44 --->	112 ~ 108	108 ~ 88	---->
			130
			Trp

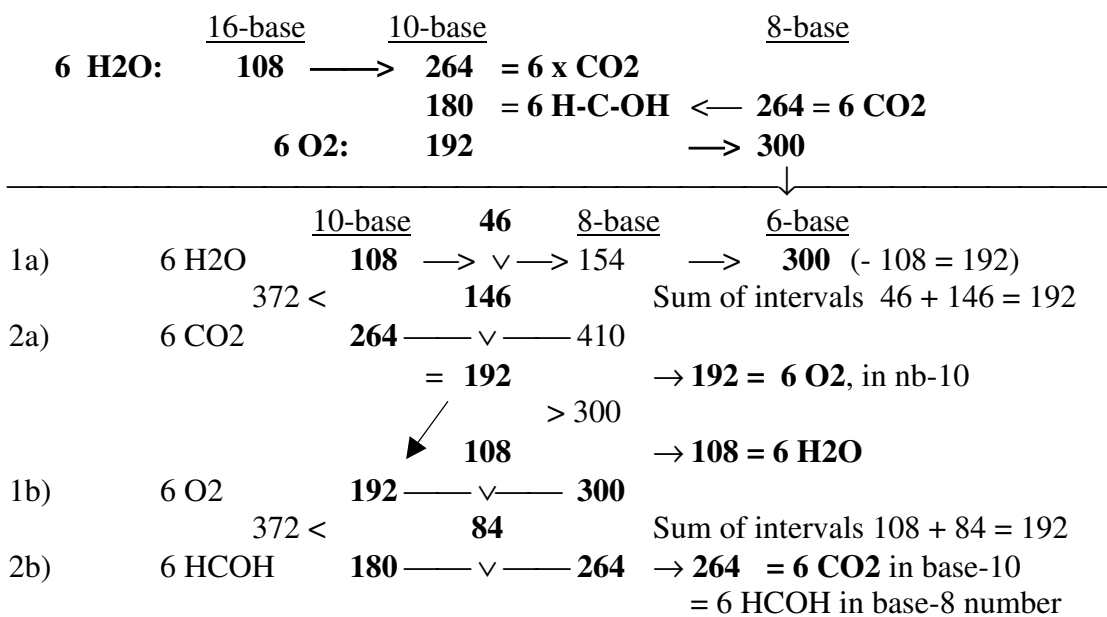
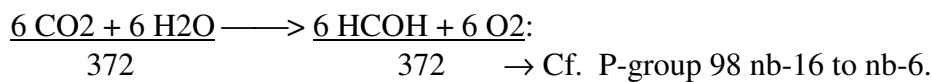
Only some of these steps
 would possibly have
 chemical correlations.

20. Transformational operations applied to some other molecules and atoms:

Sugar synthesis:



Sugar synthesis - the summation formula with following relations:



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

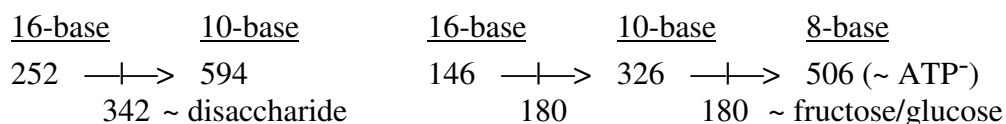
A simultaneous fixation of nitrogen occurs during which **Molybdenum** take part: Mo 42 Z, 96 A.

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

NO₃⁻ = 62 A, x 6 = **372 = 108 + 264** or **180 + 192**.

62 = 108 - 46, 146 - 84, intervals above. **NO₃⁻ + NO₂⁻ = 62 + 46 = 108**.
 α -ketoglutarate, aminating amino acids = 146.

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



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

Na	11 Z, 23 A	
Cl	17 Z, 35 A	(or. 37 A, mean value 35,4 A in nature)
K	19 Z, 39 A	(or. 41 A, 0,0018 %)

Z-numbers \longrightarrow Z-numbers \longleftarrow A-numbers:

		<u>16-base</u>		<u>10-base</u>		<u>8-base</u>
Na	Z	11	\longrightarrow	17	Cl, Z	
Cl	Z			17	\longrightarrow	19 K Z
K	Z			19	\longrightarrow	23 Na A

A \longrightarrow Z:

		<u>10-base</u>		<u>8-base</u>		<u>16-base</u>
K	A			39 ~ 41	\longrightarrow	21
				↓		
	Z	17	\longleftarrow	21	\longrightarrow	11
		Cl, Z		~ 19, K: Z		Na Z

A:

		<u>10-base</u>		<u>8-base</u>		<u>16-base</u>	
K	A	39	\longrightarrow			27	($27_{10} = 39_6$)
				↓			
Na	A	23	\longleftarrow	27			
Cl	A	35	\longrightarrow			23	Na: A

e-numbers:

		<u>10-base</u>		<u>8-base</u>	
Na ⁺	e	10		12 = + 2	
K ⁺	e	18		22 = + 4..... ~ H-wanderings - ? -	
Cl ⁻	e	18		22 "	through cell membrane
H ₂ O	A	18		22 "	

A little addition:

Fatty acids, 2 of the common ones: with OH-groups:

	<u>10-base</u>	<u>6-base</u>	<u>Cf. codon type groups of ams:</u>
C18	284	1152	= 3 x 384
			> 3 x 752 = 3/2 x 24 ams R
C16	256	1104	= 3 x 368

384 + 1 x 2 = Cross- plus Form-coded ams R. 384 = G₈ + C₈
 368 - 1 x 2 = RNA- plus Pair-coded ams R. 367 = A₈ + U₈

6-base 1152 ~ 752 re-written = 1/2 x 24 ams R.

Summary and discussion:

The background for this research was an elementary 5-dimensional conceptual structure, suggested by the author for interpretations in physics. The hypothesis was that such a model, if valid, should appear in some form on superposed levels too, not least in the nearly universal genetic code.

The research started from a table of 24 codons for 20 plus 4 double-coded amino acids, where codons differing in 1st and/or 2nd base, or *type* of base (pyrine or pyrimidine) in 3rd position (only Ile), was regarded as doubled codons.

It has been shown in Part I that an elementary number chain 5 - 4 - 3 - 2 - 1 - 0 with exponent $2/3 \times 100$, giving the abbreviated chain 292 - 252 - 208 - 159 - 100 - 0, surprisingly correlates with mass sums of *codon* grouped R-chains of amino acids: differentiations within main groups often through simple mathematical operations as plus/minus lower numbers and intervals in the chain. It gives for instance

- codon type groups, base pair groups in 1st and 2nd base ordering of different polarities as G+A versus C+U, G+C versus A+U,
- single base groups in 1st and 2nd base order, main 3rd base groups and
- groups of the similar B-chains, bound and unbound.

The number chain correlates in the same way also with

- mass division of atoms in side chains of amino acids,
- side chains grouped according to kind of atoms, groupings according to number of C-atoms in R-chains, in N -Z-division etc.

These findings contradict the view that the genetic code is a “frozen hazard” and suggests that it could be governed by an underlying pattern, however dynamic and intricate.

With the vague idea of a connection between different dimension degrees and different number base systems, transformations of mass numbers between number base systems were tested, first on the numbers of the codon bases. Very surprisingly a double set of bases generated the mass sums of the codon type groups of amino acids and transformed together the sum of their 24 B-chains. This led to the further investigations in part II.

It has been shown that transformations between number base systems nb-10 - nb-8, - nb-6 and nb-16 connect many essential mass numbers of the genetic code and amino acids as

- codon bases giving the mentioned mass sums of the amino acids,
- partial sums in codon type groups,
- the bases generating their appearances as coenzymes -TP-DP-MP,
- P-groups generating P~P~P-ribose-groups,
- AUG-bases as nucleotides (the starting codon) generating the sum of 24 amino acids etc. etc.

There is also shown that such transformations have many connections with the *exponent series* in generating mass sums from the genetic code and amino acids, as for instance five times numbers in the exponent series in base-8 giving main codon grouped amino acids in base-10, just to mention one example.

Discussion:

The simple arithmetical facts are presented as such, speculations avoided. Only some hints of possible aspects are given, without pretending any ability to explain *why* the exponent series or the number-base transformations give such results. Nor has the ambition so far included efforts to systematise transformation rules or the like. That would demand much more data and must be left to eventually interested scientists in bioinformatics and related fields.

Yet, accepting in a first step the hypothesis that the results reflect a real, organising

pattern behind the genetic code, there are of course a lot of things to discuss, not possible to do here. Only a few features and implications could be pointed out:

The fact that the results mainly concern groups of amino acids indicates a view where “the whole” is given before differentiation and aggregating of amino acids. It seems to contradict an interpretation in terms of stepwise synthesis, where the most stable, error-reducing configurations of codons survive. But is it necessarily a contradiction (?) if the assumed underlying pattern is regarded as a drawing for a construction or expression for *laws* in relation to the practical execution?

Two more elementary chains, the “triplet chain” 543 - 432- etc. and 151 - 141... etc. were also touched upon in the text and it was shown that mass sums of some main codon grouped amino acids could be deduced, approximately or exactly, from these chains too. Those facts and others, as the number of amino acids, could support the general hypothesis behind this research that some form of a 5-dimensional structuring principle lies behind the genetic code. (The concept “dimension” maybe re-defined.)

As touched upon in the text the fact that the same number divisions appears within different properties as for instance within codon groups and kind of atoms, without mutual connection, seem to suggest the view that numbers reign and that “the whole” is polarised along separate co-ordinate axes for different properties. The deriving of codon groups etc. from the exponent series, which implied operations as plus/minus lower numbers and/or intervals in the chain - and halvings, could suggest such an interpretation in terms of a multidimensional co-ordinate system with signs +/- for directions.

One implication of the results could eventually be that the codons in themselves tell more about the functions of proteins than the composition of the amino acids?

About transformations between number-base systems, the suggestion here has been to see them as steps between dimension degrees, operating as a factor in “affinities” and internal connections in the processes, an “operator” for growth - and reduction. A problem is the extensive amount of possible number generations if not limiting rules are found.

Testing possibilities?

This is of course the first question. Mass numbers of ordinary isotopes for the formation of bases and amino acids is an elementary condition for the hypotheses. A simple very first biochemical test could be to use only other isotopes of for instance H or C in liquids used to precipitate amino acids: Should such experiments change the results?

(Dropping the exponent series into the liquid (!) to see if it eventually works as some kind of activator or matrix, is of obvious reasons not possible, but what about a chain of molecules constructed with mass numbers of the series - if doable?)

The essential part of “testing” has certainly to be done in the theoretical field and include the composition of many other related substances as histones, r-RNA (as a mix of bases and proteins), t-RNAs etc., just to mention a few.

The arithmetic patterns here, if of significance, should be expected to have deep roots in multidimensional physics and quantum mechanics and would be a field for investigations in applied physics and mathematics too. (Probably also related to findings in chaos research.)

In spite of mentioning the “5-dimensional” background model for this research, any effort to make a dimensional analysis of codon-grouped amino acids and other relations has been avoided. Yet, if suggestions here are elaborated further, dimensional interpretations could naturally have implications for protein structures and different functions in cells, however intricate they may be.

Whatever to believe about the arithmetic here, something of that kind resembles life - in being very simple and very intricate, very productive - and multidimensional.

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Table 3: Separate ams with exponent 2/3, R-chains:

GG	Gly	1	1,000
GC	Ala	15	6,082
GU	Val	43	12,274
GA	Asp	59	15,155
GA	Glu	73	17,467
		191	51,978
CC	Pro	42	12,083
CU	Leu1	57	14,811
CA	Gln	72	17,307
CA	His	81	18,721
CG	Arg	101	21,688
		353	84,61
UC	Ser	31	9,868
UG	Cys	47	13,024
UU	Leu2	57	14,811
UU	Phe	91	20,231
UA	Tyr	107	22,538
UGG	Trp	130	25,662
		463	106,134
AG	Ser2	31	9,868
AC	Thr	45	12,651
AU	Ileu1	57	14,811
AUA	Ileu2	57	14,811
AA	Asn	58	14,984
AA	Lys	73	17,467
AUG	Meth	75	17,784
AG	Arg2	101	21,688
		497	124,064

Sum with exponent 2/3 = numbers from 1 til 25,66 = **366,787**.

Table 4: Separate ams with exponent 2/3, with B-chains in peptide binding

GG	Gly	57	14,811
GC	Ala	71	17,146
GU	Val	99	21,400
GA	Asp	115	23,648
GA	Glu	129	25,531
		471	102,536
CC	Pro	98	21,256
CU	Leu2	113	23,373
CA	Gln	128	25,398
CA	His	137	26,575
CG	Arg	157	29,103
		633	125,705
UC	Ser	87	19,634
UG	Cys	103	21,973
UU	Leu	113	23,373
UU	Phe	147	27,853
UA	Tyr	163	29,840
UGG	Trp	186	32,584
		799	155,257
AG	Ser2	87	19,634
AC	Thr	101	21,688
AU	Ileu	113	23,373
AUA	Ileu2	113	23,373
AA	Asn	114	23,511
AA	Lys	129	25,531
AUG	Meth	131	25,794
AG	Arg2	157	29,103
		945	192,007

Sum with exponent 2/3 = numbers from 14,8 to 32,6. = **575,5**.

= circa 24^2 , 576.