The Genetic code: Section III

Tranformations between number–base systems

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

Bases - totals of ams − 5 x ES- numbers − Generative production of the 12-groups

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

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

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

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

	nb-10		nb-8	24 ams R
G	151	⟶	227	
C	111	⟶	157... sum **384** *, x 2 = 768 ~ **770**	
U	112	⟶	160	
A	135	⟶	207... sum **367**, x 2	= **734**
	509		= 751	= 1504
	↓			
x 2 =	**1018**	⟶	**1772 = 24 B-chains unbound**	

* G + C transformed together = 386 in nb-8.

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

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

<u>nb-10</u> <u>nb-6</u>
768 —> **3276** 24 ams R + B, unbound (rewritten from 3320)

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

<u>nb-10</u> <u>nb-6</u>
752 —> **2848** 24 ams R + B. bound (rewritten from 3050)

Fig 17-2. *From 752 as sum of ES-numbers 5', 4' and 3' to 2848 in nb-6:*

5' 292_{10} —> 1204_6, - 244 = **960** U+A
4' 252_{10} > 1100_6, + 244 = **1344**, 24 B-chains bound
3' 208_{10} —> 544_6 = **544** G C
↑ = **2848**
1' 100_{10} —> 244_6 —

2848 = 24 ams R + B bound

1.2 Some general annotations:

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

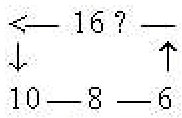
All derived numbers shall naturally be regarded as nb-10-numbers, hence transformations as nb-10 →> nb-8 may be repeated, illustrated for instance in the carbon-nitrogen cycle in the sun, from ^{12}C to ^{14}N to ^{16}O, intermediate steps showing one way to perform such transformations.

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

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

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

Fig Ti-1



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

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

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

C16H32O2: 256-**10** → 1104-6 = **3 x 368**
C18H36O2: 284-**10** → 1152-**6** = **3 x 384**, (Note: 1152 = 752 rewritten)

Cf. the hexagonal pattern in Table 0: fatty acids as a third way to read such a pattern.

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

384 x ½ = 192-**10** → 300-**8** / 300-**10** → 454-**8** = 2 x 227 = 2 G-**8**
368 x ½ = 184-**10** → 268-**8** / 268-**10** → 414-**8** = 2 x 207 = 2 A-**8**

1.4 . Bases → totals:

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

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

G1 + U1 = C2 + A2 = **1468**
C1 + A1 = G2 + U2 = **1808**... Sums of coded amino acids (R + B)

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

Fig. 17-3

	10-base		8-base
4 G-bases = 4 x 151 =	604	—>	1134
4 C-bases = 4 x 111 =	444	—>	674...sum **1808**
1 A-base =	135	—>	207, x 4 = 828
1 U-base =	112	—>	160, x 4 = 640... sum **1468**

In nb-10 we have groups of ams paired in keto-/amino types:
Here G- and A-bases have exchanged partners and bases A and U must be multiplied with 4 after transformation.

Fig. 17-4

	10-base	8-base		
4 G	= 604 —>	1134		
1 U	= 112	160,	x 4 =	640, + 1134 = **1774** ~ B-chains +2
4 C	= 444 —>	674		
1 A	= 135	207,	x 4 =	828, + 674 = **1502** ~ R-chains - 2

Rewriting 640 to 638 and 828 to 830 gives the right sums B 1772 and R 1504.

1.4.2 Two sets of bases from ES-numbers 5', 4' and 3':

Fig. 17-5

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

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

2. The bases in the ES-chain:

Fig. 17-6

10-base		8-base						
G 151	—>	227	(denotation here G_8 etc.)					
U 112	—>	160						
C 111	—>	157....sum	**544**					
					10-base		8-base	
A 135	—>	207... sum	**208 -1**		A_8 **207**	—>	**317** = U_8 + C_8	**(2 x158,5)**

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

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

$5^{2/3}$ $4^{2/3}$ $3^{2/3}$ $2^{2/3}$ $1^{2/3}$ $x10^2$

292 252 208 159/158 100 0 → *ES-chain*

\ / **207 A_8** \ /

544 <— ^ ——> **317 = U_8 + C_8** (159 = U_8 -1, 158 = C_8 +1)

diff. **227 G_8**

[207_{10} = 317_8]

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

3. 5 times ES-numbers:

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

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

	nb-10		nb-8	
C1 + U1 =	**816**	<——>	1460 = **5 x 292**	
G1 + A1 =	**688**	<——>	1260 = **5 x 252**	- 10 x 544
G1 + C1 =	**544**	<——>	1040 = **5 x 208**	
U1 + A1 =	**960**	<——>	1680 = **5 x 336** (544 - 208)	
816 -				
	1776	<——>	3360 = **10 x 336**	
	↓ 24 B-chains à 74 A			
	2848	<——>	5440 = **10 x 544** ◄	
	↓ **24 ams R+B bound**			

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

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

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

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

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

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

There is also the feature that divisions stepwise as polarizations of numbers 816 in U1 + C1, separately transformed to nb-8 give 1260, next lower level, and this back to nb-10 and divided G1 and A1 gives 1040 in nb-8:

Fig 17-10. *Stepwise polarization giving next number x5 in Es-chain:*

Steps of "polarisations" "5" —> "4" —> "3":

Steps:	Ams	nb-10		nb-8		ES-numbers
"5"	C1 + U1:	**816**	<—	**1460**		= 5 x 292
	C1:	↓ 353	—>	541		
	U1:	463		717....1258 ~ **1260**		= 5 x 252
				↓		
"4"	G1 + A1:	**688**	<—	**1260**	<—— 1260	
	G1:	↓ 191	—>	277		
	A1:	497		761....1038 ~ **1040**		= 5 x 208
				↓		
"3"	G1 + C1:	**544**	<—	**1040**	<—— 1040	

3.2 About the interval 84 = 292 →> 208 in the ES-chain we have that n x 84 (n = 1, 2, 4) times 10 (1040 ~ 840, 1680 and 3360) in nb-8 gives the groups 544, 960 and 1776 in nb-10:.

Fig 17-11. *n x interval 84:*

84 = interval 292 – 208:

	nb-10		nb-8	ES-series
24 B-chains à 74 A:	1776	<—	336 x 10	= **4 x 84**. x 10 (292 - 208)
A+U-coded ams R:	960	<—	168 x 10	= **2 x 84** "
G+C-coded ams R:	544	<—	84 x 10	= **1 x 84** "

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

Fig. 17-12 *5 x interval in the ES-chain:*

Ams	10-base		8-base	Intervals in the exponent series:
G1+1	**192**	<—	300 = 5 x interval 60	= 292 - 352 = "5" — ("4 + 1")
A1 -1:	**496**		760 = 5 x interval 152	= 252 - 100 = "4" — "1"
U1+1	**464**		720 = 5 x interval 144	= 352 - 208 = ("4 + 1") — "3"
C1 - 1	**352**		540 = 5 x interval 108	= 208 - 100 = "3 — "1"

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

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

Fig..**17-13** *5 times ES-numbers in nb-6 to 396-564.*

	10-base		6-base	
396	396	<——	1460 = 5 x 292	a)
	324	<——	1260 = 5 x 252	
564 <			>	b)
	240	<——	1040 = 5 x 208	
	960		**752 x 5**	
↓	= A + U			

396	=	**292** + **104**	**396** + 101 = 497 = A1	a)
564	=	**460** + **104**	**564** - 101 = 463 = U1	b)
Σ:		752 +208		

:

3.5 The parts above of 960 in nb-16 gives the total mass of bound ams in nb-8:

Fig 17-14

	16-base	10-base	8-base	
G1,A1 - G2, A2	396	918	1626	
G1,A1 - C2, U2	292	658	1222	
	688		**2848** —>	**2848 = 24 ams bound**
But 2 x	344	———>	**1504** x 2 = 2 x 24 ams R	

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

nb-8
816 ~ 1016
688 ~ 710 ... Sum 1726-8./ 1726-10 → **3276**-8

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

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

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

```
      544 <— 177  —> 367              367 x 2 = 734
     /    \        /     \
292 — 252 —— 208 —|— 159 —— 100 —— 0
                  49
 |<———————|———————>|
       385 , x 2 = 770
```

Cf Table 2,3 in file 02.

Numbers 770 and 734 generated from 177 and 208:
- From **177** we get 385 in two steps nb-10 to nb-8:
- From 208 we get 734 in three such steps:

Fig. 17-15b

```
nb-10 → 8   nb-10 → 8
177 ——> 261 ——> 385        → x 2 = 770
|<——— 208 ———>|

nb-10 → 8              nb-10 → 8   nb-10 → 8
208 ——> 320 ~ 318* —|—> 476 —|—> 734
                  |   158        258   |
                  |<——— 416 ———>|
```

* 318 = 2 z 2', 159, from there only two steps:

Fig 17-15c:

```
                 10→8-base   10→8-base
2 x 159:         318   →    476   →    734   → RNA+Pair-coded ams
```

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

Fig 17-15-d*:*

```
                         10→8-base  10→8-base
                         208  →  320  →  500
                          |               |
                          |<—— 292 ——>|            575

                         10→8-base   10→8-base
Interval 208-159:         49   →   61   →  75         → Meth, R 75
                          |               |
                          |<——— 26 ———>|
```

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

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

Fig 17-15e:

```
257 ——> 381 ——> 575
|                 |
|<——— 318 ———>|
```

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

75 → 113 → **159** (161 rewritten)

4.2 A- and T-bases give the sum 575 of ams with non-mixed codons:

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

Fig. 17-16: *A+T*

	10-base		8-base/10-base			8-base	10-base
A:	135	—	207	207	—>	317, +3 = **320** = AA-AU-coded ams R	
T:	126		176	176	—>	258, - 3 = **255** = UU-UA-coded ams R	
					=	**575**	

The Exponent series: **317** = 2 x 158,5., ~ 2 x "2" . **258** = 158 + 100, ~"2 + 1".

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

4.3 770-group from 4':

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

2 x 4' (252) = **504-10 →770-8**

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

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

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

Cross-coded = **418** = 2 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:	292 - 252	-	208 - 159 - 100
	544		467
10-base:	x ½ = 272		x ½ =234. (round number)
↓	↓		↓
8-base:	418		352
=	**2 x 209**		**2 x 176**

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

Fig. 17-18:

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

	10-base		8-base	
384 - **G_{10}** 151 =	233	—>	**351**	= **N-number in 770-group**
384 - C_{10} 111 =	273	—>	421 ~ **419**	= **Z-number in 770-group**
768	2x 253	—>	772 - **770 ~ 768**	

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

	10-base		8-base	
367 - U_{10} 112 =	255	—>	*377*	
377 - 112 =	265	—>	411 ~ **409**	= **Z-number in 734-group**
367 - A_{10} 135 =	232	—>	*350* ~*348*	
348 - 135 =	213	—>	**325**	= **N-number in 734-group**
734			**734**	

18. More on totals and other notable transformations

CCC − Why 24 ams? - H-atoms - N-numbers - C-atoms in R - B-chains - 1st to-2nd base

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

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

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

nb-16   nb-10
CCC —> **3276 = 24 ams R+B unbound**
↓
12.12.12*

nb-10   nb-8
CC —> **204** ——> 314 ($\sim \pi \times 10^2$)
= Trp, R+B,
the heaviest amino acid.

2 x 314 ——————> **2848 = 24 ams R+B bound**

(2 π x 100: the bound 24 ams as a closed circle!)

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

2. Why 24 ams?

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

20-**10** → 24-**8**

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

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

292 — 252 —208 —— 159 — 100 — 0
————|<-44-><|——108——>|

This interval is divided 4'-3' = 44 and 3'-1' = 108: Transformed from nb-16 to nb-6 they give total Z-numbers of R-chains and N-numbers separately:

Fig 18-2: *H-atoms:*

44_{16} —> $\mathbf{152_6}$ = **H** in R-chains

152 <   > 828 = **total Z** in R-chains

108_{16} —> $\mathbf{676_6}$ – **N** in R-chains

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

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

Fig. 18-3: *Neutron numbers to totals*

	10-base		8-base	
G1: N	86	—>	126	
C1: N	158		236	
U1: N	213		325	
A1: N	219		333	...Σ 1020, ~ **1018 = 2 x 4 code bases** in 10-base system ↓
↓—>	1018	—>	**1772**	**= 1772 = 24 B-chains**
G2: N	187	—>	273	
C2: N	58		72	
U2: N	190		276	
A2: N	241		361	...Σ 982 = 2 x 491 ↓
↓—>	491	—>	**753, x 2**	**= 1506 = 24 R-chains +2H***
* 2 x 491:	**982**	—>	1726 ↓	
↓→	1726	—>	**3276**	**= 3276 = 24 ams R + B**

- 491_8 ~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.)

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

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

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

Fig. 18-4a: *Transformations along the ES-chain as a nxC-chain:*

C7
/ \
C4 C3 + C0 C2 C1 + C9 = *Trp*

584 **198** **306** **162** **124** **+130**
584 **504** **286**

2 x 544 2 x 208
1088 **416**

584 = 1088 = 584 + 198 + 306
10-base —> 8-base

198 = 306
10-base —> 8-base

306 ~ **286** (re-written)
8-base 8-base

286 = 436 = 306 + 130 (Trp)
10-base —> 8-base
↓
C2 162 = 242
C1 124 = + 174 = **416**
10-base —> 8-base |
= **286 + 130 (Trp)**

174 —> 256 = 124 + 130 + 2H
10-base --> 8-base

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

/ C7 \
C4 | C3 + C0 C2 C1 + C9
584 198 306 162 124 +130 (Trp)
| *790 ~ C1 + U2* | *(C here for ams groups)*
| |
714 ~ G1 + A2

Fig. 18-4c: *nxC-atoms - three more details:*

The Exponent series:

"5" "4" "3" "2" "1"
292 252 208 159/158 100

544 <—— **286** ——> 258(+1)
= **C2 + C1**

467 (208 + 259)
= **C3 + C2** ——> = **305** + **162**

Different intervals in transformations through re-writings:

10-base 8-base
584 —> 1088 ~|~ 890

C7 = **198** out of re-writing

584 <——|——> 890
306 = C3 + C0

Trp:

Interval: 504 <——|——> 416

88 ——> **130** Trp
10-base 8-base

6. B-chains:

6.1 Number 752, sum of first 3 numbers in the ES-chain:

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

292-16 → 658-**10**
252-16 → 594-**10**
208-16 → 520-**10**... sum **1772**, 24 B-chains unbound

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

Fig. 18-5:

nb-16 nb-10
½ x 752: **376** —> **886**, x 2 = **1772, 24 unbound B-chains**

6.2 A single, unbound B-chain = 74:

Two sets of the 4 RNA-bases, sum 1018, gave in nb-8 the sum of 24 B-chains unbound = 1772. A single unbound B-chain à 74 gives the sum of 2 bound B-chains.

Fig 18-6: *From one unbound B-chain to two bound ones:*

nb-10		nb-8	
74	—>	**112**	**= 2 x 56** = 2 B-chains bound

Cf. **U-base = 112 A** and exchange T to U in mRNA for synthesis.

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

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

	nb-10		nb-8
2 x 292:	**584**	—>	1088 ~ **888**. x 2 = **1776 = 24 B-chains à 74 A**
	292	—>	**444** = 6 B-chains à 74 A
292, x ½:	**146**	>	**222 = 3 B-chains unbound à 74 A**
	↓		↓
	222	—>	**336 = 6 B-chains bound à** 56 A

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

Fig. 18-8:

	10-base		8-base		
4 G	604	—>	1134		
4 C	444		674...sum 1808 ~1810		
				>	**3544 = 2 x 1772,** B-chains
4 U	448		700		
4 A	540		1034...sum	1734	

6.5 Total of bound B-chains = 1344 from the bases:

Fig. 18-9:

10-base		8-base		
194	<——	302	2 x G	2 x RNA-bases read as 8-base numbers
184	<——	270	2 x A	
146	<——	222	2 x C	
+ 148	<——	224	2 x U	
672	——————————>			x 2 = **1344**, = **24 B-chains bound**

388	<——	604	4 x G	
+ **352**	<——	540	4 x A	
= **740**	——>	**1344**		= **24 B-chains bound**

10-base		8-base	6-base	
352	<——	540 4 x A-base		
↓				
352	——————————>		**1344**	= **24 B-chains bound**

	16-base		10-base	
4 x A:	540	——>	**1344**	= **24 B-chains bound**

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

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

Fig. 18-10:

10-base - 8-base
136 → 208

10-base - **8-base**	10-base - 8-base	10-base - 8-base	10-base - 8-base
208 → 320	320 → 500 ~ 480	480 → 740	740 → **1344**

10-base - **6-base**	10-base - 8-base	10-base - 8-base	10-base - 8-base
136 → 344	344 → 530 ~528	528 → 1020 ~ 1018	1018 → **1772***

*Note that without rewritings 530 ~ 528 and 1020 ~ 1018 we get 1776 (24 x 74 A).

7. Displacements between 1st and 2nd base order: Numbers 220 - 26:

7.1 Relations between displacements 220 and 26:

Fig. 18-11:

Ams groups R:
G1 + A1 ——— +246 ———> G2 + A2
C1 + U1 ——— - 246 ———> C2 + U2
G1 —> G2 = 220, C1 —> C2 = - 220 G+C-coded ams = 544.
A1 —> A2 = 26, U1 —> U2 = - 26 A+U-coded ams = 544 + 2 x 208

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.

Fig 18-12:

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

G+C-group, N 100 to 220:	10-base		8-base / 10-base		8-base:
	100	——>	144 144	——>	**220**

|→ displacement = Z-number **120** ←—|.

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

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

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

	10-base	8-base		
144	64	100 N		**100 N** = N: **C1 — C2**, +1 = G2—G1 (101)
	l-1	|—— **23** N		**23 N** = N: **U1 — U2**, - 1 = A1—A2 (22)
	63	77		
	80	120 Z		**120 Z** = Z: **C1 — C2**; -1 = G2—G1 (119)
	l-1	|—— **3** Z		**3 Z** = Z: **U1 — U2**; +1 = A1—A2 (4)
	79	117 Z		

A1 - A2: N 22, Z 4: 10-base 8-base
N 22 <——|——> 26 N+Z
4

Fig. 18-14:

HPO_2 = **64**, PO_2~ = **63**, $HPO3^{-}$~ = **80**, PO_3~ = **79**.

64 + 80 = 144 = 220 in nb-8. 77 + 117 = number **194**. 220 - 194 = **-26**.

7.2 The number 220 in displacements in group G+C:

Fig. 18-15:

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

16-base 10-base 6-base
220 <—> **544** = 292+252 1040 = **5 x 208**

292
|—— **84** ——> **220** = **5 x 44**, the interval 252 — 208.
208 ——————> 544

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

544 + 220 = 764 = C1 + G2 = 353 + 411, difference 58
544 - 220 = 324 = G1 + C2 = 191 + 133, - " - 58

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

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

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

10-base 8-base
101 ——|——> 145
44

G1 = **292** - 101 **336** - 145 = 191 = **G1**
C1 = **252** + 101 **208** +145 = 353 = **C1**

Number 220 as a nb-6 number: 6-base
220 ~ **176**: G1 = **367** - 176 = 191
re-writing C1 = **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:
("5 + 4") - ("3 + 2") = **177**, - 44 = **133** = C2.
("3 + 2") = **367**, + 44 = **411** = G2 (?)

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

The sum of R-chains of the 4 ams with two different codons are "also" 246, i.e., the sum of displacements 220 and 26 above.
All 4 may become 37 in different nb-systems.

Fig. 18-16:

10-base 8-base
Arg AG **101** ——> **145** = Ser 31 + Leu 57 + Ile 57

10-base 8-base 10-base 6-base
Arg AG 37 <— 101 ~ 57
Ser AG 31 <——> 37 37 <——> ~ 57 = Leu2, Ile2 in nb-10

19- P- phosphorous groups - Coenzymes - Nucleotides - Met AUG

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

Fig 19-1*: P-groups:*

a. $H_2PO_4^-$ ~group, 97 A, $PO3^{2-}$ ~group, 79 A, HPO_3^- ~group = 80 A

	10-base		8-base	
HPO_3^- ~group	**80**	<——>	**98** ~120	= H_3PO_4 98 A
			↓	= HPO_3^- ~ + H_2O = H_3PO_4
H_2O	18	<——>	22, difference	

	10-base		8-base	
PO_3^{2-} ~group, 79 A:	**79**	——>	**97** ~ 117	(79 + 117 = 2 x 98 = 2 H_3PO_4)
	↓		↓	
HPO_3^- ~group, 80 A:	80	——>	120, + 117	
	↓		↓	
2 P-groups	79 + 80 = 159	——>	237	= **3 P-groups** à 79

(Energy storing in the bindings.)

8-base
79 ~ 81 = + 2 H

b. Coenzyme groups:

	16-base		6-base		
H_3PO_4 =	**98**	—>	**372** = ribose-P-P-P in coenzymes of bases		**(-TP)**
HPO_3^-~ =	**80**	—>	**292** = ribose-P-P	- " -	**(-DP)**
	10-base				
$HPO3^-$	**80**	—>	**212** = ribose-P	- " -	**(-MP)**

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

	16-base		6-base		
H_3PO_4:	98	—>	**372** ~	**412**	
	I-18		+	+	< difference 80 ~ HPO_3^-~
HPO_3^-~:	80	—>	**292** ~	**332.**	
			= **664**	**744**	
			= **NAD**	**NADP**	in nb-10 system

	16-base		10-base		8-base
NADP	**744**	—>	1860	—>	3504
	= 2 x 372		**= 5 x 372**		**12 x 292**
			372 = P~P~P -ribose,		292 = P~P-ribose

d. The exponent series:	10-base		6-base
interval "3 - 2" =	**49**	—>	**81** = H_2PO_3~

A form of life was found some years ago, said to use arsenic instead of phosphorus (P), i. e. next higher element in the phosphorus group of elements in the periodic system. If so, it could of course lead to the conclusion that all such transformations between masses including phosphorus are irrelevant and in any case no necessary condition for life as an eventual part of a reference system.

Yet, phosphorus could have had a decisive role at the very creation of the genetic code, while this not excludes further evolution?

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

2.1 Tables of masses of the coenzymes

Fig. 19-2: *Survey*

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

4 - 5 code bases, mass numbers, including +1 for bond to ribose:
G 151, A 135, U 112, C 111...Σ **509**, +T 126...Σ **635**

Sum of 2 x 24 bases, 1st and 2nd in the codons:
15 A + 13 U + 11 G + 9 C= **6141**

Coenzymes of the code bases:

-TP		-DP		-MP	
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**

2.2 From 4 bases to their mass as coenzymes

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

4 RNA-bases	10-base	8-base	6-base	
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)

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

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

Fig. 19-4: *From the bases to coenzymes -MP, -DP, -TP*

-MP:

	10-base		8-base /	10-base		8-base
4 RNA-bases:	**509**	—>	751	751	—>	**1357**
- separately transformed to 751						= 4 RNA-bases as coenzymes -MP

|<—— **4 x 212** ——>|
212 = P~ribose

-DP

	10-base		8-base /	10-base		8-base
2 x 4 RNA-bases:	**1018**	—>	1772	1772	—>	3354 = **2 x 1677** [1)]
	= 2 x 4 RNA-bases					= 2 x 4 RNA-bases as coenzymes -DP

|<—— **8 x 292** ——>|
292 = P~P ~ribose

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

(1772 = 24 ams B-chains)

-TP:

	10-base		8-base		10-base		8-base	6-base
G_8+C_8:	384 (386)	—>	601 (-/+1)					1997
A_8+U_8:	367	—>	557.... Sum		**1158 ~ 1160**	**—>**	**2188**	

↓

2188 —> 3994 = **2 x 1997**

↓

= 2 x 4 RNA-bases as coenzymes -TP

4 bases nb-10:
509 <—— **4 x 372** ——> 1997
372 = P ~P ~ P-ribose

2.4 5 bases to 5 coenzymes -TP:

Fig. 19-5:

	10-base		8-base		6-base	
5 bases with T-base	635	—>	1173, ~ 973	—>	**2495** =	**5 bases as coenzymes -TP**

|<—— **5 x 372** ——>|
= 5 x P~P~P-ribose

[2495_6 ~ 2535 = 5 x 507. 507 = ATP_{10}]

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

Fig. 19-6:

	10-base		8-base		8-base		6-base	
G+C:	**262**	—>	386					
			>753 /		**753**	—>	**2095**	—> = **5 bases as coenzymes -DP**
A+U:	**247**	—>	367				↓	
							~ 1695	—> = **5 bases as coenzymes -MP**

Re-writing gives - 5 x 80, ~ 5 P-groups (HPO_3)

**2.6 From 751, the sum of 4 bases in nb-8,
to 5 bases as coenzymes -TP and to 6141, the sum of 48 codon bases:**

Fig. 19-7:

10-base → 8-base
751 ——> **1357** = **4 coenzymes -MP (G, A, U, C)**

1357 ——> **2495** = **5 bases as coenzymes -TP (including TTP)**

6-base
1357 ——> **6141 = 48 code bases, 1st and 2nd, for 24 ams**

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

3. Nucleotides:

3.1 Survey of nucleotides in chain binding:

Fig 19-8:

Nucleotides in chain binding:

RNA: G 345, A 329, U 306, C 305...Σ **1285**, ionized -1 in P-groups = **1281**
cGMP = 345, cAMP = 329
DNA: G 329, A 313, T 304, C 289...Σ **1235**, ionized -1 in P-groups = **1231**

3,2 Two sets of the nucleotides from 2 sets of the bases *(from file 17)*:

The four RNA-nucleotides in chain-binding and uncharged = 345, 329, 306 and 305 =**1285**.
The four DNA-nucleotides (= 1285 - 4 x 16 + 14 in T-base) = **1235**.

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

2G + 2C = **768** in nb-8:
768-10→> 1400-**8**/ 1400-**10** →> 2570-**8** = **2 x 1285** ~ RNA-nucleotides

2U + 2A = **734** in nb-8:
734-10 →> 1336-**8** / 1336-**10** →> 2470-**8**= **2 x 1235 ~** DNA-nucleotides

3.3 ES-number 752 gives in two steps the sum of 4 nucleotides in DNA and RNA:

Fig 19-9:

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

	10-base		8-base	
4 bses in nb-8: 751/753	**752**	——>	**1360**	(5 x 272 from the exponent series)
	↓ **1360**	——>	**2520**	= **1285 + 1235**

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

Fig. 19-10:

4 RNA-bases bound = 16-base **505** <—|—> 10-base **1285** = 4 RNA-nucleotides, not ionized

↓

780 = **4 x 195:**

↓

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

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

Fig. 19-11: *cGMP - cAMP:*

	10-base		8-base		
	167	<——	247	A+U	
	178		262	G+C	
	345		**509**		**345 = cGMP = G-nucleotide**
< 674*					
	329	<——	509		**329 = cAMP = A-nucleotide**
	10-base		6-base		
*Base pair:	**262**	——>	**674** = 2/3 x 1011, sum of exponent series.		

(674 also the number of atoms in 2 x 24 codon bases, 1st and 2nd, in the codons.)

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

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

Fig 19-12: *AUG, codon for Meth:*

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

16-base — 8-base

149 = Meth, R+B —>= **509** = 4 RNA-bases in base-10 system

16-base — 10-base

149 —> **329** = **cAMP**, also = A-nucleotide

The exponent series:

16-base — 10-base

"5" = 292 —> 658 = **2 x 329** (~ cAMP)

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

	10-base		8-base	The "triplet series" 543-432-321-210:
Nucleotides:	**329** A	—>	511 ~ **509** (4 RNA-bases)	
	306 U		462............Σ. **973**	= 543 + 432 - 2
	345 G		531............... **531**	= 321 + 210
	= **1504**		= **24 ams R**	

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

10-base:		8-base:	
93	<—	135: A	
74	<—	112: U	
+ 105	<—	151: G	
= **272**	<—	398	**272** = ½ x **544**, "5" + "4" in the exponent series

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

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

Fig 19-13: *tRNA-ends ACC:*

c. ACC-ends of tRNAs:

		nb-10		nb-8		ES-series	
A+C+C-bases:		**357**	—>	**544 + 1**			
	A	135	—>	207	=	208 -1	
or ACC: <							> **544 -1**
	2 C	222	—>	336	=	544 - 208	

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

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

20. Additions to files 17 - 18

1. Rewritings

1.1 Rewriting G - C:

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

Fig. 20-1:

```
     544      460     367      259
   /     \  /     \  /     \    /     \
292      252      208      159/158    100      0

            10-base        6-base
G-base      151       =    411* ~ 367   = "3 + 2"  re-written  (367 = A8 + U8)
                           I-108
C-base      111       =    303* ~ 259   = "2 + 1"  re-written
```

*411 = sum of G2-coded ams.

Cf. 44 = the interval 252 - 208 = 4' - 3'. G1 + C1 = 544 divided <u>177 + 367</u>:
C2 = 177 - 44 = 133
G2 = 367 + 44 = 411

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

Fig. 20-2:

```
292 - 101 = 191 = G1-coded ams R
252 + 101 = 353 = C1-coded ams R
 |
 |         16-base          10-base        8-base                         6-base
 |           65     ---->    101
 v  ---->                     65    ---->   101 ~ 81 re-written*  ->  145
                                                                        ↓
  292 - 65 = 227 = G8            272, - 65 = 207 = A8.          (207 + 2 x 145 = A1)
+ 252 + 65 = 317 = C8+U8       + 272 + 65 = 337 = (U+C)8        (317 + 145 = U1 -1
= 544                            544                             317 = U8 + C8

*Cf. ams-groups:   272 - 81 = 191 = G1.   544 - 81 = 463 = U1.
                   272 + 81 = 353 = C1.   416 + 81 = 497 = A1.
```

[U 112 and C 111 = 223, transformed together = 337-8.
Further transformed to nb-6 = 1011= total sum of the ES-chain in nb-10..]

1.3 Simple rewriting of 2 x 5', 4', 3' in the ES-chain, taken as nb-8 numbers:

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

2 x 292-10: = 584. 584-8 ~ 604 = G1 + G2 +2; → 604 + 416 = 1020 = A1 + A2
2 x 252-10 = 504, 504-8 ~ 484 = C1 + C2 - 2; → 484 + 416 = 900 = U1 + U2

Fig. 20-3:

	8-base		8-base	Ams-groups R-chains in base-10 system	
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)

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

Fig. 20-4:

	10-base		8-base	10-base		8-base	
A-base:	**135**	—>	207, ~ 187 re-written	187	—>	**273**	x 12 = 3276

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

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

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

Fig. 20-5:

292 —	252 —	208	"5-4-3" in the exponent series
├──>	+ 156 —>	+ 136	Orotate and Inosine added
Sums:	**408**	**344**	
x 2 =	816	688	
=	C1+U1	G1+A1	

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

	10-base		8-base	6-base		Mixed nb-10 + nb-8 numbers:
Inosine	136	—>	208 —>	344	→	136 + 208 = 344, x 2 = **688** = **G1+A1**
Orotate	156	—>	234 —>	416,	→	156 + 234 = 390, = 408 read as nb-8, x 2 = **816** = **C1+U1**

3. Number 888 in different appearances:

Fig. 20-7:

888 in nb-10 = **543** + **345**, numbers of the **triplet series** = 12 x B-chains à 74 A

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

888 in nb-6 = **344** in nb-10 = ***888* - 544**. 344 **x 2** = ***688*** = **ams-groups G1 + A1**.

344 in nb-6 = 136 (= **Inosine**) in nb-10 (1/4 x 544).

888 in nb-16 = **2184**$_{10}$ = 4 x 546, 8 x 273 (the mean value of 2 **ams R+B** = 273)

4. Difference of bases in nb-10 and nb-8, read in nb-16, gives 2 x 272 = 544;

Fig. 20-8:

nb-8		nb-10	16-base		10-base	8-base	
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)

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

Fig. 20-9:

10-base (left), 8-base (right)

4 DNA-bases: 523 <—— 490 ——> 1013

523 ↓ 490 ; 1013 |—> **261** = base pair $\mathbf{A_{10}+T_{10}}$

490 <—— 262 ——> 752

262 ↓ base pair $\mathbf{G_{10}+C_{10}}$

6. Sum of the whole ES-chain 1011:

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

Fig. 20-10:

10-base	**292**	**252**	**208**	**159**	**100**	Sum = 1011
↓	↓	↓	↓	↓	↓	|- 508~510, 509 = 4 bases
8-base	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

Cf. sum 3282 and sum of triplet series in

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

Fig. 20-11:

	10-base		6-base	
	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.

7. Totals, two mere operations

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

Fig. 20-12:

	16-base		10-base		8-base	
"5":			**292**	—>	**444**	444 x 4 = 24 B-chains à 74 A.
	↓ (444)					
	444	—>	**1092**		—>	1092 x 3 = **3276** = 24 ams R+B
	888	—>	2184 = 4 x 546, x 3/2 = 3276			

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

Fig. 20-13:

		10-base		8-base	
Base pair	G+C	**262**	—>	386	
		↓ **386**			
		x 4 = 1544	—>	3008	**3008 = 2 x 1504**, R-chains

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

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

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

Fig 20-14:

```
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

   10->8        10->8     6->10       6->10        6->10   6 -->10
49 --->    59, ~ 61 --->  75<---->  47  <---->  31  <--> 19<--->15
|          Asp            Meth      Cys         Ser              Ala
|           |- 10-->8                |            | 10->8   10->6
|          73 Glu / Lys              |           31 --->  37 --->  101 (~ 61, ~ 57)
| 10->6                              |           Ser               Arg
49 --->    81                        |            |
|          His                       |            | 10->8   10->8    10->6
|           |                        |           31 --->  37 --->  45 --->  73
|           |                        |           Ser               Thr      Glu
|           | 8-base                 |                                      Lys
|          81 ~ 101                  | 10->8   10->8      10->8
|              Arg                  47 --->  57 --->  71 --->  107
| 10->16                              Ileu / Leu       |        Tyr
49 ---> 31 = Ser                                       | 6->10
                                                      71   --->  43 = Val
        8 --> 10    8->10     8 ->10
 101 (Arg) ---> 65   --->   53 --->   43 Pro before ring binding.
100   ---------> 64    --->   52 --->   42 Pro

  8-base           6 ---> 10                6 --> 10    8 --> 10
108   ~  110   110   --->   42             84 --->   52 --->  42
                            Pro                               Pro
 8-base  10 --> 8
108 ~   88   ----> 130                      10->8  10->8  8 --> 8      6 --> 6
                   Trp                     59 --> 73 --> 111 ~ 91     111 ~ 107
                                                             Phe          Tyr
   8->10    8->10      8->10
133   ---> 91    --->   73 --->   59
           Phe      Glu/Lys    Asp             8->10          8->10     8->10
                                            93*   -->   75    159   --->113 --> 75
   6->10      10->8    10->8                            Meth                  Meth
133   --->   57 --->   71 --->   107                                 10--->8
           Leu/Ileu              Tyr                           *  93 --> 135  A-base

  10-->6    6-base        8-base    10->8                Only some of these steps
44 --->   112 ~   108    108   ~  88  --->  130           would possibly have
                                            Trp           chemical correlations.
```

21. I. Triplet series — II. An alternative series 151-111

I. The triplet series

I. Triplet series; intervals outwards - inwards:

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

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

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

Fig. 21-1:

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

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

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

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

Fig. 21-2: *Number 982:*

10-base		8-base	
355	<——	543	
282		432	
209		321	
136.....982		210	
982	——>	1726	= 1506 + 220

↓ (from 1726)

1726 ————> **3276, total sum 24 ams R+B, unbound**

1.2 Codon bases read as nb-8-numbers give sums triplets in nb-10:

Fig. 21-3:

4 DNA-bases

	10-base		8-base
G	105	<—	151
C	73		111
T	86		126
A	93		135
Sum:	**357**		**523**

4 RNA-bases:

	10-base		8-base:
G	105	<—	151
C	73		111
U	74		112
A	93		135
	345		**509**

Triplet series "inwards"

4 RNA-bases → **345** = **345**, + 012 = 357 → DNA
4 DNA-bases → **357** = -| **234** |
| **123** |
012——|

2. Sums 1506 - 714 and intervals 792:

Fig. 21-4:

The Triplet chain "outwards" – "inwards":

543	345
432...975	234
321	123
210...531	012
1506 <——+——>	**714**

792

10-base		8-base	
792	—>	1428	= **2 x 714**

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

	10-base		8-base
2 G	302	—>	456
2 C	222		336... **792**
2 x U	112 x 2	—>	160 x 2 = 320, ~318
2 x A	135 x 2		207 x 2 = 414, ~394...sum **714**, ... **712**

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

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

	nb-**16**		nb-10
C-base:	**111**	—>	**273**

The triplet chain with intervals **111**: 543 - 432 - 321 - 210:

210-10 → 546-6 = 2 x 273.

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

Fig. 21-6:

	16-base		10-base		
	975	——>	2421		
1506 <	I- **444**		⊢——	**1092, x 3**	= **3276** = 24 ams R+B
	531	——>	1329		
Compare:	**666**	——>	**1638**	**x 2 = 3276.**	= 24 ams R+B

4. The triplet series and number 1875:

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

Fig 21-7*: Number 1875:*

$543_{16} \to 1347_{10}$
$432_{16} \to 1074_{10}$
753 < **>1875**
$321_{16} \to 801_{10}$
$210_{16} \to 528_{10}$

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

The sums (pair wise added) reminds of the second spectral line of hydrogen from Balmer series, mentioned in *Introduction:* Formula $\mathbf{1/2^2 - 1/4^2 = 0{,}1875}$. Cf. 210 and spectral line 0,21 (!).

Two other operations give relations between sums and intervals:

$^{10}\mathbf{log\ 1{,}875} \approx 0{,}\underline{273}\ 00...$

$\mathbf{187{,}5^{2/3}} \times 100 = 3275{,}93 \approx \underline{3276}$, total of 24 ams R+B

[1/4 × ES-chain numbers = 73 – 63 – 52 – 39.75 – 25,
with exponent <u>3/2</u> = 623.7. – 375. – 500 .- 250.6. – 125: sum ~1875 (1874.32.)

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

15/8 = <u>5 × 3 × 1</u> / <u>4 × 2</u> = 1.875

24 ams R+B = 3276. = <u>409</u> × **8**.01.

48 codon bases (1st nd 2nd) = 6141 = <u>409</u> × **15**.01.

II. An alternative numeral series

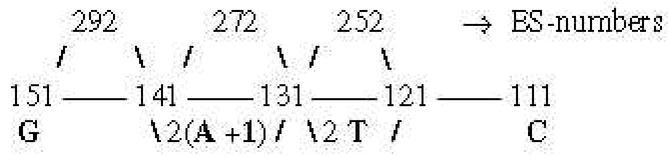
Another series, from G- to C-base:

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

151 - 141 - 131 - 121 - **111**

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

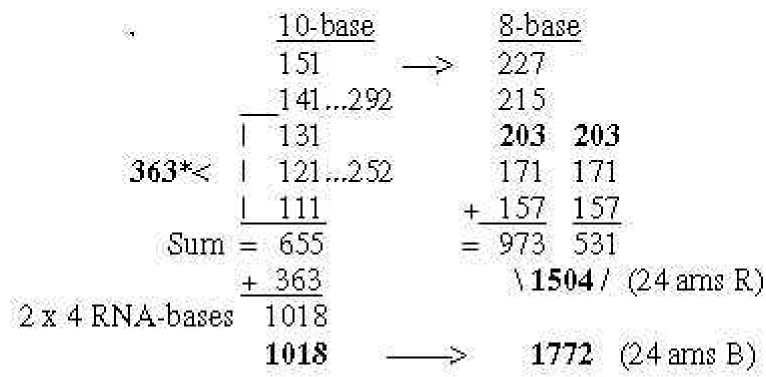
Fig 21-8: *An alternative series G - to C:*



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

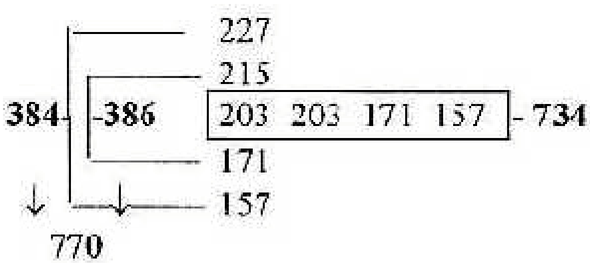
All these numbers transformed to nb-8 give the triplet sums 975 (543 + 432) - 2 and 531 (321 + 210), sum 1504, 24 ams R:

Fig. 21-9:



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

Fig 21-10:



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

973 - 157 = **816** = U1 + C1
531 + 157 = **688** = G1 + A1.

Some other paired groups of ams R from this alternative series:

Fig. 21-11:

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

10-base		8-base
101	—>	**145**

973 - 145 = ***828*** = **Z** total 24 ams R
531 + 145 = **676** = **N** total 24 ams R

973 - 157, + 145 = **961** = **A+U +1**
531 +157, - 145 = **543** = **G+C -1**

Fig. 21-12:

***848* -- 656 division:**

	10-base		8-base
	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....sum **792**	= 2 x 292 + 208
227 + 171 = 398	
157 + 157 = 314....sum **712**	= 2 x 252 + 208

The doubled last steps re-written:

203 ~ 183 = -20
171 ~ 169 = - 2
157 ....sum **531 - 22** = **509** = sum of 4 codon bases RNA
157 ....sum **531 - 22** = **509** = sum of 4 codon bases RNA

22. Other substances

Fats — Sugar — Na-Cl, Na-K-pump

Some annotations about other substances:

1. Fatty acids

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

Fig. 22-1: *Two comon fatty acids*

	10-base	6-base	Cf. codon type groups of ams:
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 = $G_8 + C_8$
368 - 1 x 2 = RNA- plus Pair-coded ams R. 367 = $A_8 + U_8$

6-base 1152 ~ 752 re-written = ½ x 24 ams R.

2. Carbohydrates:

Carbohydrates, some examples, transformations nb-16 → 10 → 8 or → 6:
- ^{12}C → H2O → HCOH = 12-**16** → 18-**10** → 30-**6**, the building stone of sugar.

- O2 16 A → H2CO3 62 A (built into ribose): 32-**16** → 50-**10** → 62-**8** = + 18, H2O, + 12, C.

- Hexoses 180 in nb-10: In nb-16 180 = 384-**10** (= 2 citrate à 192 or e.g. G-**8** + C-**8**).
- A fructose in P-P-bonds = 178: 178-**16** = 376-**10**= ½ x 752 in the ES-chain.

- Ribose 150 as a number in nb-16 = 336 in nb-10, 544 - 208 in ES-chain.

- A disaccharide 342 or two hexoses 180 from ES-numbers as *intervals* in transformation steps:

252-**16** → 594-**10** = + 342, a disaccharide.
146-**16** → 326-**10** → 506-**8** (ATP charged -1) = + 180, + 180.

Fig. 2-2: *Sugar synthesis*

Sugar synthesis:

16-base		10-base		6-base	
12		**18**		**30**	
C	——>	H_2O	—>	H-C-OH	~1/6 x hexose

16-base 10-base 8-base

32 = O_2 —|—> 50 —|—> **62** = H_2CO_3 (62 also = NO_3^-)

+18 (| H_2O) +12 (| C); ↓ incorporated at the sugar synthesis ionized

18 ——> 24 ——> **30**

H_2O (2 C, Mg ?) H-C-OH ~ 1/6 of hexose

Sugar synthesis - the summation formula with following relations:

6 CO2 + 6 H2O ——> 6 HCOH + 6 O2;

372 372 → Cf. P-group 98 nb-16 to nb-6.

	16-base		10-base			8-base
6 H2O:	**108**	**——>**	**264**	**= 6 x CO2**		
			180	**= 6 H-C-OH**	<—	**264 = 6 CO2**
	6 O2:		**192**		—>	**300** ↓

		10-base	46	8-base		6-base
1a)	6 H2O	**108** —>	v —>	154	—>	**300** (- 108 = 192)
	372 <		**146**		Sum of intervals 46 + 146 = 192	
2a)	6 CO2	**264** ——	v ——	410		
			= **192**		→**192** = **6 O2**, in nb-10	
		↙		> 300		
			108		→**108 = 6 H2O**	
1b)	6 O2	**192** ——	v ——	**300**		
	372 <		**84**		Sum of intervals 108 + 84 = 192	
2b)	6 HCOH	**180** ——	v ——	**264**	→ **264** = **6 CO2** in base-10 = 6 HCOH in base-8 number	

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.:

16-base 10-base 16-base 10-base 8-base

252 —|—> 594 146 —|—> 326 —|—> 506 (~ ATP^-)

342 ~ disaccharide 180 180 ~ fructose/glucose

3. Na-Cl and the Na-K-pump:

Na-Cl and Na-K-pump in the nervous system:
Na 11 Z→Cl 17 Z→K 19 Z: Na 11-**16** →Cl 17-**10** →K 19-**8**
Na 23 A, Cl 35 A (most common isotope): Na 23-**16**→> Cl 35-**10**

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

Fig. 22-3:

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 —> Z-numbers <—> A-numbers:

		16-base		10-base		8-base	
Na	Z	11	——>	17	Cl, Z		
Cl	Z			17	——>	19	K Z
K	Z			19	——>	23	Na A

A —> Z:

		10-base	8-base		16-base
K	A		39 ~ 41	—>	21

↓

Z 17 <— 21 —> 11
Cl, Z ~ 19, K: Z Na Z

A:

		10-base	8-base	16-base	
K	A	39	——————>	27	$(27_{10} = 39_6)$

↓

Na A 23 <—— 27
Cl A 35 ——————> 23 Na: A

e-numbers:			10-base	8-base	
	Na^+	e	10	12	= + 2
	K^+	e	18	22	= + 4......... ~ H-wanderings - ? -
	Cl^-	e	18	22	" through cell membrane
	H_2O	A	18	22	"

*

Discussion

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

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

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

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

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

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

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

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

It's shown too that not only mass distribution on codon groups of ams correlates with the ES-chain but also other bases for mass division, for instance with main groups of atom kinds and the not codon-dependant B-chains as well as with several features in the origin of ams from stations in glycolysis - citrate cycle. This suggests an interpretation where the same principle scheme is developed on different levels or as representing different axes in a coordinate system when the genetic code emerged.
The single fact that the mass division on C-skeleton and other atoms (960 and 544) is the same as between main codon groups (U+A, 960 and G+C, 544) supports in itself the general suggestion that the code is built on a numeral series.

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

Then about mass again, rejected as irrelevant for codon assignments: In addition to arguments in the *Introduction* it's reasonable to ask for instance why precisely these ams have been selected for coding, not other ones? The selection seems rather random. Why just this number of ams with oxygen as end groups, that number of ams with nitrogen? (Besides that both types and polar and non-polar ams surely have been necessary.)
Further, when much research in this field has been focusing on the "most stable" configuration of the coding system, one could naturally ask what the background is for this stability? One aspect is of course that the most common isotopes have shown up to be most stable. (When calculating with common mix of isotopes today, atomic weights should change the sum of R- plus B-chains of ams from 3276 →> 3280 abbreviated, R-chains from 1504 →> 1506, no more than the deviations of single units (u) in this analysis.) In addition, the analysis here mostly concerns groups of ams, i. e. sums were an individual deviation in mass might have a rather small influence.
The fact that Ileu sometimes gets mixed with Leu by tRNAs could also be mentioned, differing in structure but having the same mass and atoms.

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

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

If proposals in this paper are accepted as hypotheses, they will naturally raise many new questions and lead to secondary hypotheses, which in their turn could be possible to test. The dimensional aspects, mostly omitted here, should reasonably, if elaborated further, have implications for protein structures and their different functions in cells.

Whatever to believe about the arithmetic, something of that kind resembles life - in being very simple and very productive - and naturally multidimensional.

*

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