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IMAGE OF THE MAIN MECHANISM IN THE WORK OF THE ORGANISM OF A LIVING CELL

ANNOTATION

This work is a continuation of **2012.0112** , in terms of the construction of carbohydrate compounds , from the main **1701.0488** with the extension **2009.0160** .

In it, for the first time, a model of the mechanism that performs a set of actions for the translation of Proteins , RNA , DNA and organelles - the "Ribosome" of a living cell, will be built and described.

Its cyclic image A ⇄ B is shown on pages 5-6.

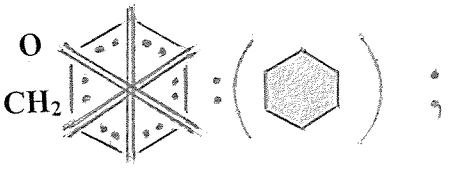
DESCRIPTION

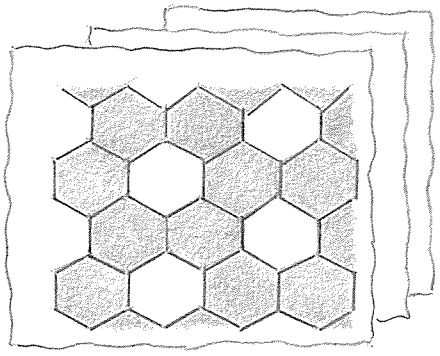
Absorption by a living cell of a substance from the environment : photosynthesis through chloroplasts or chromatophores and chemosynthesis through the Golgi apparatus , provides it with the necessary building material based on glucose.

This happens on the thylakoids in chloroplasts, the inner membranes of mitochondria and the endoplasmic reticulum of the cell.

Her image was obtained in a previous work :

$C_6H_{12}O_6$:



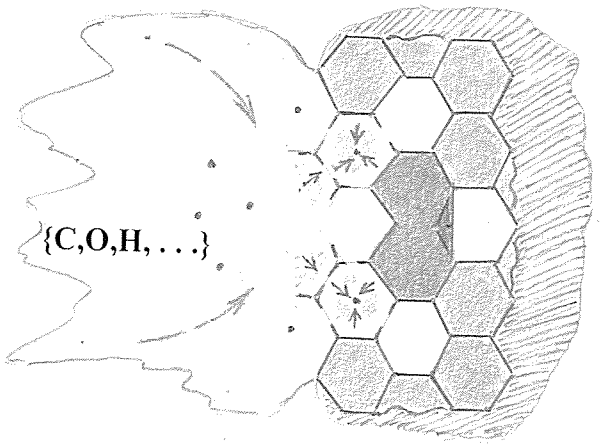


$\{C_6H_{12}O_6\}$

To obtain it, a "figurative" effect on the excited source of formation is necessary: during photosynthesis it will be a set of $\{CO_2, H_2O, H\}$ with their previously presented geometric images $\{\Delta, \square, \circ\}$.

The exciter of the source will be the action of light or the result of chemical reactions , and the "figurative" action will be the reaction from the subsequent deformable image from $\{C_6H_{12}O_6\}$ as a result of which ribose is formed → deoxyribose with a phosphorus residue.

Figuratively speaking, the assembly-puzzle $\{C_6H_{12}O_6\}$ is carried out from its source to the active deformable form under the action of a light or chemical exciter through a series of transformations:

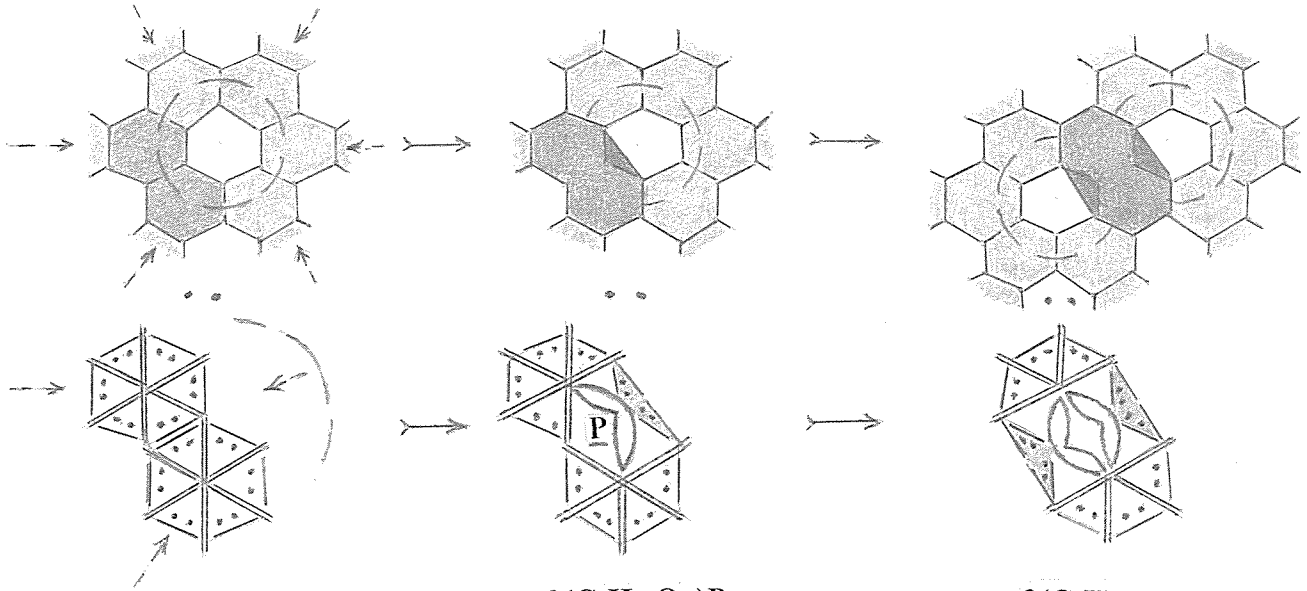


$2(C_5H_{10}O_5)P + \{C_6H_{12}O_6\}$

Let us dwell on the deformable images $\{C_6H_{12}O_6\}$.

The set $\{C_6H_{12}O_6\}$ is a ring image of bonds of its elements $C_6H_{12}O_6$: from $6(C_6H_{12}O_6)$. with six compounds in its continuation.

And the result from the pressure arising in them leads to a pair connection of their components with deformation from the inside of this ring image :



$2(C_6H_{12}O_6)$ $2(C_5H_{10}O_5)P$ $2(C_5H_{10}O_4P)$

$...+2CH_2$

These species are formed similarly to the formation of starch from glucose described earlier, with some additions.

In particular, there is a transition, by joining, of two interacting oxygen atoms **2O** into a bonding phosphorus atom **P** : **2O → P** , from their increased pressure.

This will happen at the moment when the distance of their interaction and the distance of interaction of elements **8LΛS** in **O** will become equal .

Here, one "extra" element **LΛS** from **2O** gives the phosphorus atom **P** an "excessive" mass - **30.97376**, ceasing to produce an electron, forming the glow of the atom itself.

This has also been described in previous papers.

The rationale for this, as well as the subsequent formation of nitrogen **N**, will be the absence of these constantly demanded elements in the source of photosynthesis in plants, prokaryotes, etc ..

So, we get nucleotides - ribose and deoxyribose in a compound through a phosphorus residue.

And if we take into account oxygen-phosphorus compounds in them together with hydrogen. then we will get a built-in image of phosphoric acid, which translates these nucleotides into **RNA** and **DNA** elements, without a nitrogenous base.

Unlike paired - $\mathbf{2(C_6H_{12}O_6)}$, the resulting nucleotides have carbon - hydrogen "wings" with phosphorus interaction and their "range" will depend on the state of the latter.

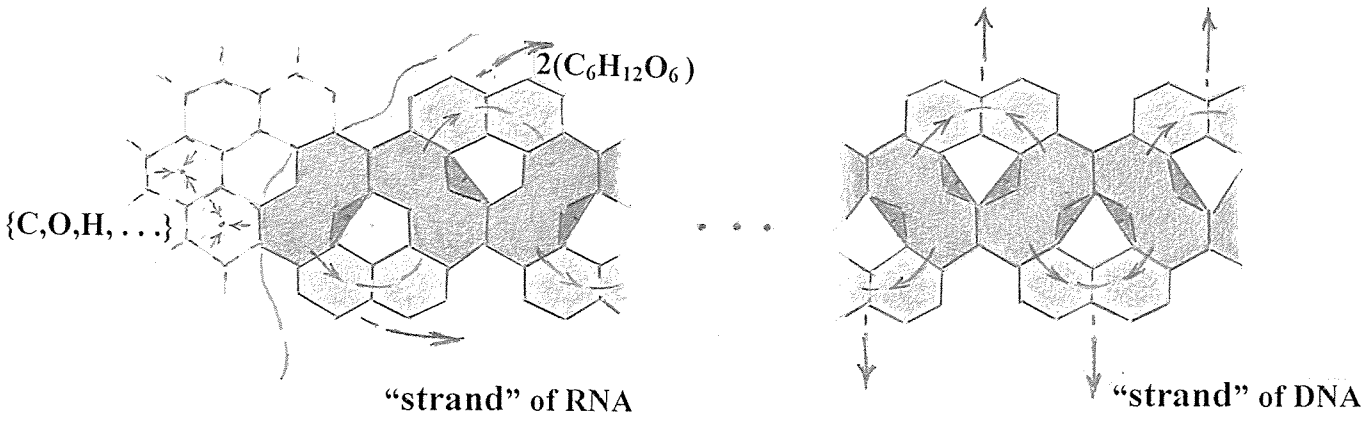
We get that the nucleotides have an image of a variable " **state** " from $\mathbf{2(C_6H_{12}O_6)}$ to the " **limit** " : in a mutually horizontal arrangement of "wings" from the maximum reaction of their action.

Thus, the figure of nucleotides will be deformed by its " **state** " causing, and perceiving, pressure in the immersed set $\mathbf{\{C_6H_{12}O_6\}}$, from its side ring structure $\mathbf{6(C_6H_1\,O_6)}$, in the direction of their "wings".

Moreover, the direction of pressure forces on $\mathbf{\{C_6H_{12}O_6\}}$ from the side of ribose will be directed along the thread of its compounds, and deoxyribose - across the thread of its compounds.

As a result, the pressure in the immersed set $\mathbf{\{C_6H_{12}O_6\}}$ from the action of the strand of the nucleotide form of ribose leads it to the form of deoxyribose.

This is how we get the formation of a " **chain** " of nucleotides: ribose → deoxyribose, as a result of their "accumulation", with a change in free structures $\mathbf{2(C_6H_{12}O_6)}$ in their ring patterns $\mathbf{6(C_6H_{12}O_6)}$:

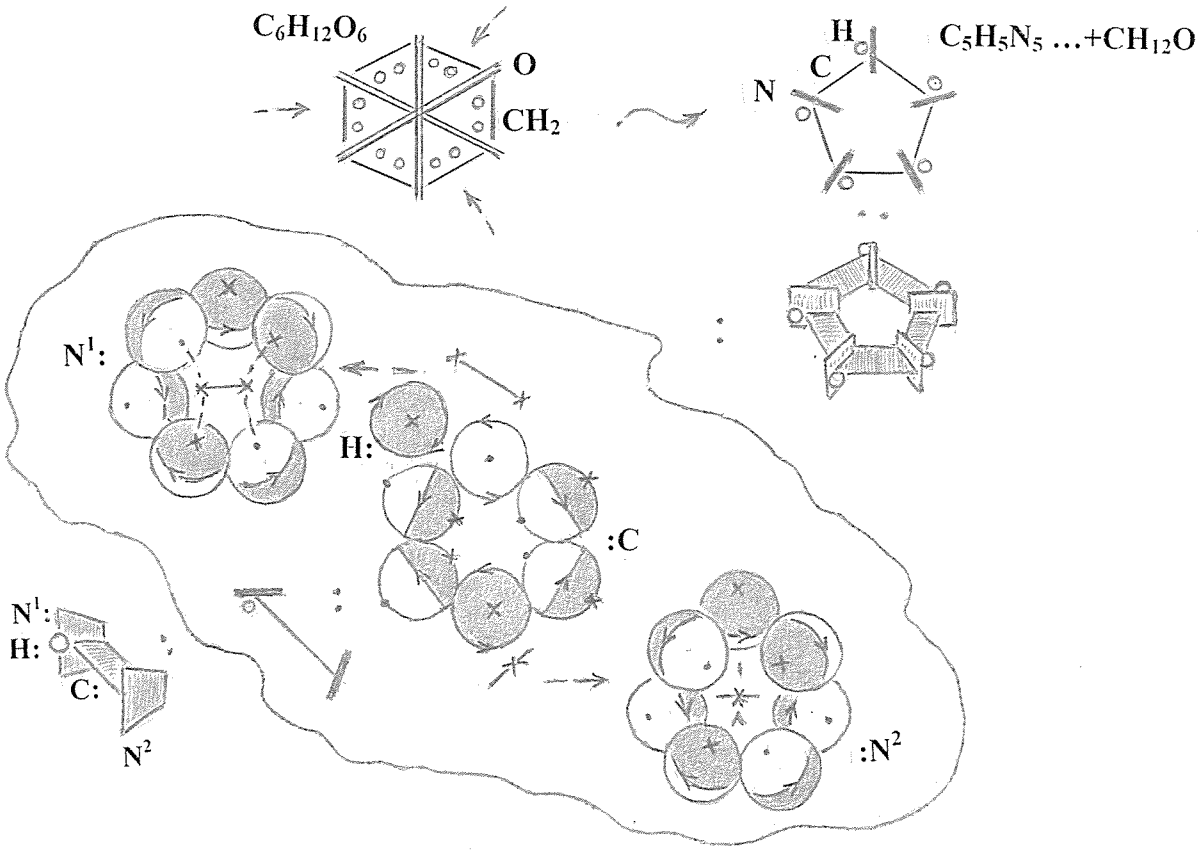


The pressure in those $\mathbf{2(C_6H_{12}O_6)}$, through oxygen compounds from the action of nucleotides, forms nitrogen **N** : **O** → **N + H**, converting these carbohydrates into nitrogenous bases.

The shape and content of these nitrogenous bases depend on the " **states** " of their parent nucleotides.

Their shape does not correspond to the forms of carbohydrates depicted in the figures. it only reflects a holistic image of the whole picture.

For their clarity, we present the formed "free" image of adenine $\mathbf{(C_5H_5N_5)}$:



Now, having collected everything described, we will present the image of the operation of the cyclic "**mechanism**", with its explanation, from the result of the action of the formed nucleotide " **chain** ", in the immersed set $\{C_6H_{12}O_6\}$, under the influence of photosynthesis or chemosynthesis and an active nucleotide pathogen :

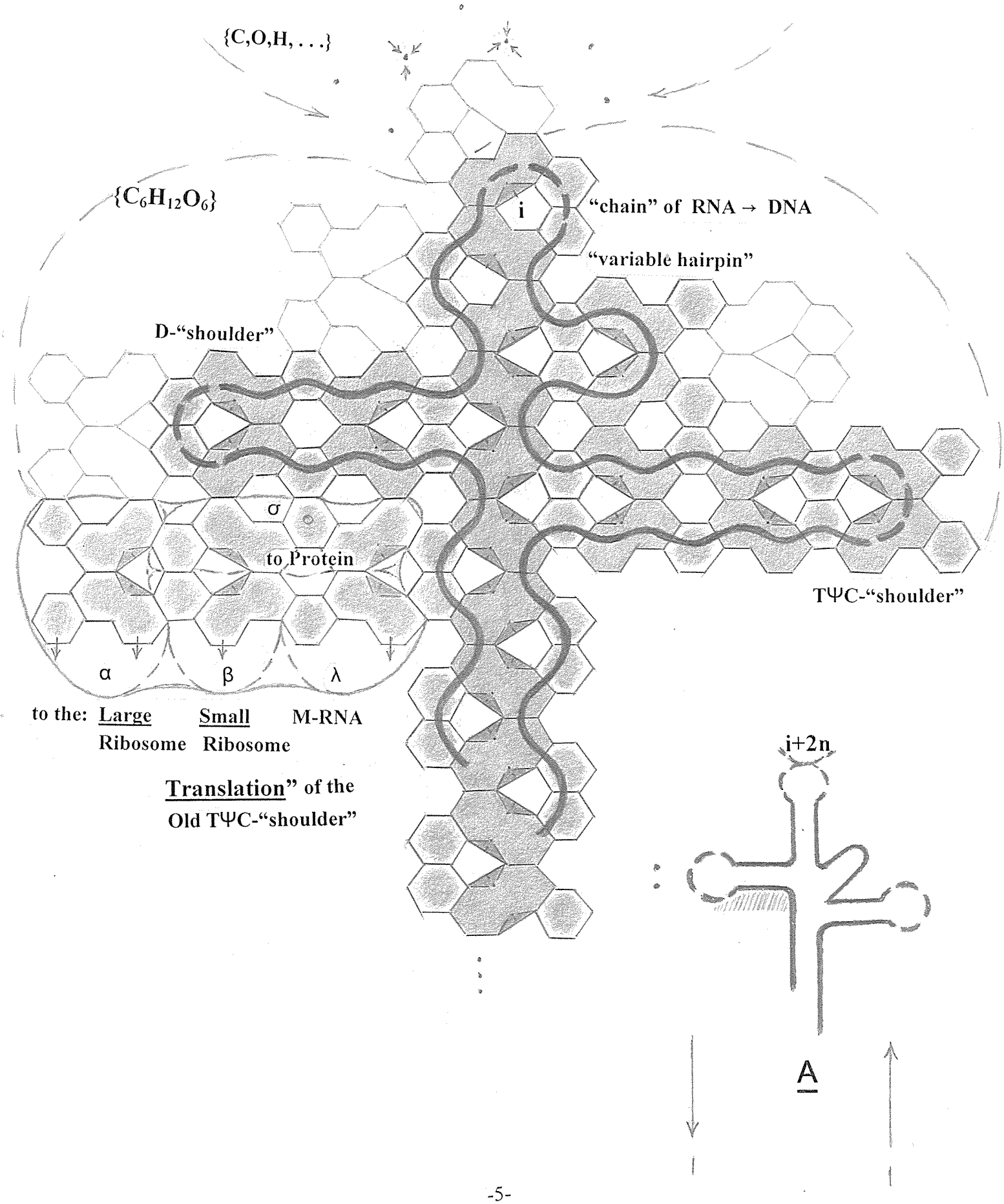
Picture A : step i+2n , A → B

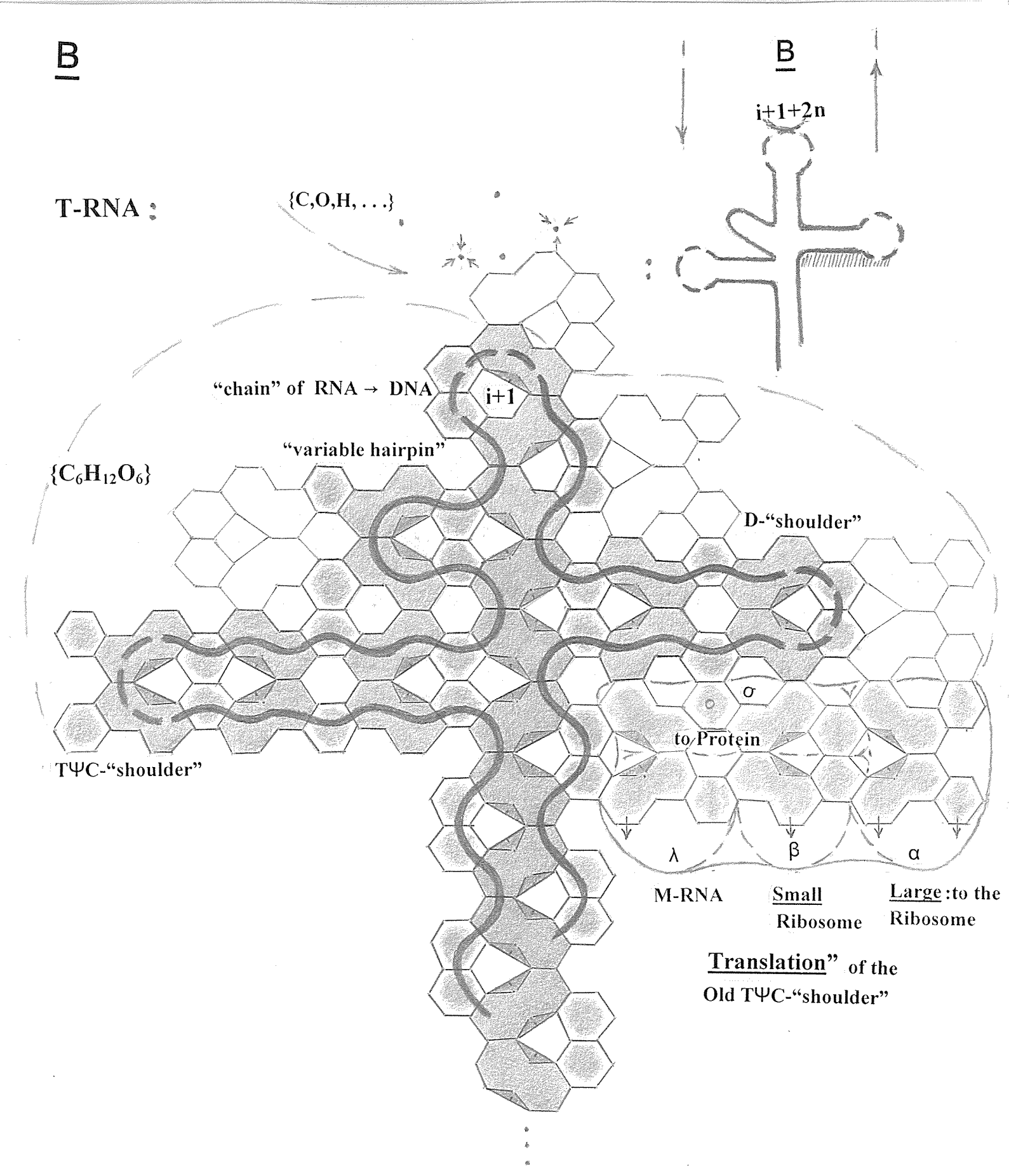
Picture B : step i+1+2n , B → A

$$A \rightleftarrows B$$

A

T-RNA :


{C,O,H, . . .}
{C6H12O6}
i
"chain" of RNA → DNA
"variable hairpin"
D-"shoulder"
σ
to Protein
TΨC-"shoulder"
α
β
λ
to the: Large Ribosome
Small Ribosome
M-RNA
"Translation" of the Old TΨC-"shoulder"
i+2n
A


B
B
i+1+2n
T-RNA :
{C,O,H, . . .}
"chain" of RNA → DNA
i+1
"variable hairpin"
{C6H12O6}
D-"shoulder"
σ
to Protein
TΨC-"shoulder"
λ
β
α
M-RNA
Small
Ribosome
Large :to the
Ribosome
Translation" of the
Old TΨC-"shoulder"

Description of the model.

Her image: **T-RNA** .

This is a nucleotide " **web** " with nitrogenous bases, formed by their reaction under the action of the forces of the " **state** " of the nucleotide " **chain** " (**RNA → DNA**) from the structure of the immersed set $\{C_6H_{12}O_6\}$.

During the passage of the nucleotide " **chain** " (**RNA → DNA**), the action of the forces of its " **state** " on the structure of the immersed set $\{C_6H_{12}O_6\}$ leads to the formation of a "**web**" there, followed by its decay along with this set .

We get that the "building up" of the nucleotide " **chain** " leads to a figurative change in its " **web** " – a movement in the direction of its "growth" .

This creates the illusion of multiple **T-RNAs** .

These changes are displayed in the model as unshaded additions to the current images with their "development" in the next step .

So, we get the image of the " **web** " - **T-RNA** :

a) left side for A and right side for B :

- **D** -shoulder ;

b) right side for A and left side for B :

- "variable hairpin" ;
- **TΨC** -shoulder .

This form is formed from the direction of action of the forces of the attached nucleotide to the " **chain** " – its angle in the ring form of carbohydrate **6**($C_6H_{12}O_6$) towards the structure $\{C_6H_{12}O_6\}$.

A "fold" is formed there in the form of: a growing hairpin with an elongation **TΨC** - shoulder .

And the subsequent attachment of a nucleotide to the " **chain** " reverses this angle and leads to the following change-addition of the current image of the " **web** " :

a) left side for A and right side for B :

- a "variable hairpin" is formed ;
- **D** -shoulder goes into **TΨC** -shoulder ;

b) right side for A and left side for B :

- "variable hairpin" goes into **the D** -shoulder ;
- **TΨC** -shoulder peeling off passes to a fragmented " **translation** " .

Thus, we get the turn of the " **web** " .

And the next step - adding a nucleotide to the "**chain**" - will lead to the same result.

This is reflected in the model as a cyclic process : A ⇄ B .

So we get the " **mechanism** " : cyclically changing - by turning, the image of **T-RNA** in the process of "growth" of the nucleotide " **chain** " **RNA → DNA** from the formed set $\{C_6H_{12}O_6\}$.

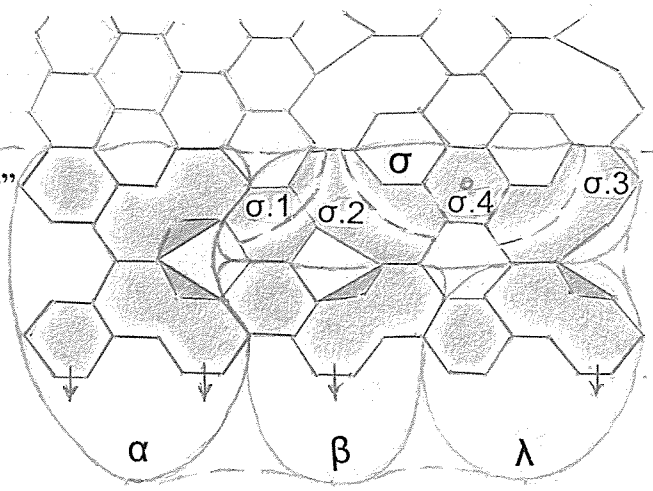
The final stage of each step of the cycle is " **translation** " .

This is a fragmentary decay of the "old" **TΨC** -arm of **T-RNA** , formed by the previous step of the cycle, with the continuation of its subsequent formation.

Let's imagine it :

"Translation":

Old TΨC-"shoulder"



α÷ R-RNA+σ.1–amino acid, to the Large ribosome ;

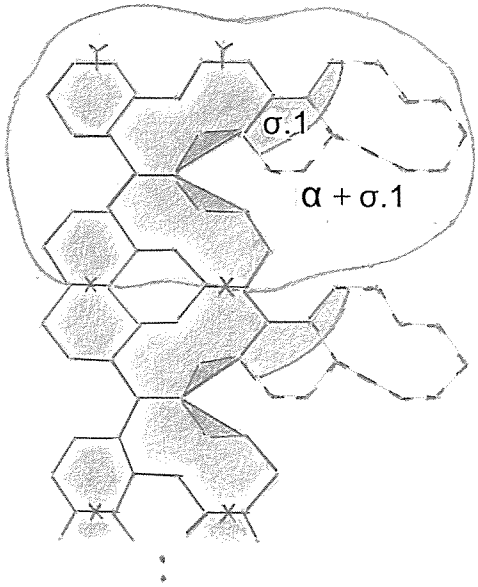
β÷ R-RNA+σ.2–amino acid, to the Large ribosome ;

λ÷ -RNA+σ.3-nucleotide part. to the M-RNA ;

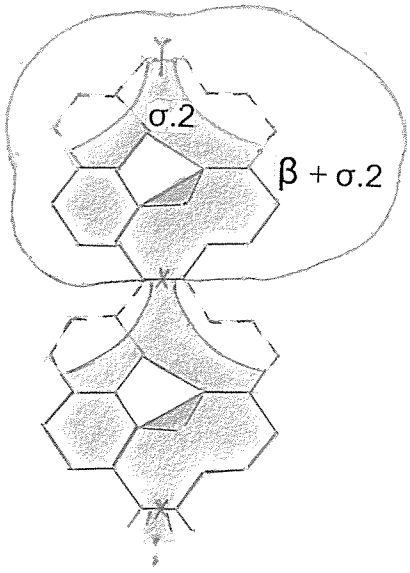
σ.4 ÷ α/amino acid , to Protein ;

A. "Large Ribosome", "Small Ribosome", "M-RNA"

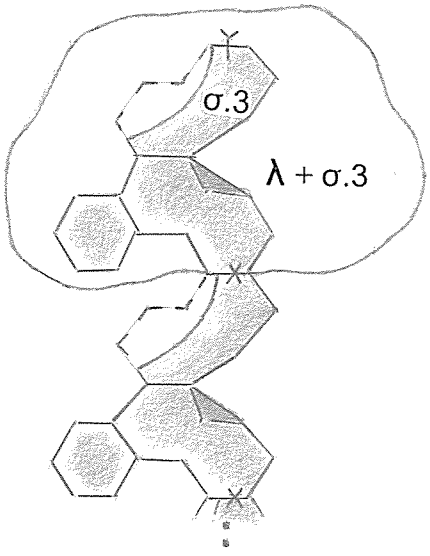
Large Ribosome {α + σ.1}:



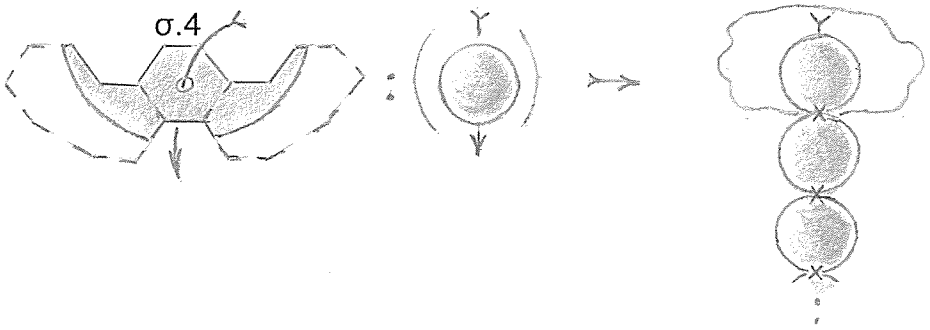
Small Ribosome {β + σ.2}:



M-RNA {λ + σ.3}:



B. "Protein" {σ.4}



Fragmental decay of the "old" **TΨC** -arm of **T-RNA** passes through the sites of "step-by-step gluing" of its nucleotides in cycles, taking into account the changes that have taken place in them.

It has six nucleotide-nitrogenous bases and consists of five areas : α; β; λ; σ .

Of these, α; β; λ externally - open, and allow their nucleotide - nitrogenous bases to figurative deformation from the action of their " **states** " .

σ - is closed by these areas and will be "destroyed" by them into fragments: **σ.1**; **σ.2**; **σ.3**; **σ.4** .

This is the source of amino acids and other chemical compounds .

Each of the "culprits" : α; β; λ , will carry its part of the "fragment" σ :

- α ÷ **σ.1** - amino acid ;
- β ÷ **σ.2** - amino acid ;
- λ ÷ **σ.3** -nucleotide part .

, and **σ .4** will be an independent unit : A/amino acid, and represent a fragment of the formed Protein .

σ.1 and **σ.2** are formed under the action of a triangular structure from α; β : $\{CH_2O_2\}$. with their further weakening in the "decay" : $+\{CH_2\}$, with the addition of {N} from a nitrogenous base that is in the way of their action.

The absence of nitrogenous bases in the "path" of action of λ gives - **σ .3**, the form of the nucleotide part .

And **σ .4** will be formed according to the "residual" principle .

The figure shows only route images **σ.1**; **σ.2**; **σ.3**; **σ .4** in their derivation from actions α; β; λ .

"Peeling off" α; β; λ from the " **cobweb** " and $\{C_6H_{12}O_6\}$ occurs during their connective accumulation through active nucleotide-nitrogen sites, forming organelles:

- Large ribosome : { α + **σ.1**} ;
- Small ribosome : { β + **σ.2**} ;
- mRNA : { λ + **σ.3**} .

Ligamentous accumulation of **σ .4** in the Protein - {**σ.4**} , will occur in the direction - up / down, to the indicated organelles and according to the same principle .

In this case, the following actions can take place :

a)_ The presented organelles and the Protein in their subsequent connection perform their own axial turn in their growing tertiary structure. In this case, **T-RNA** will have on each side the result of its " **translation** ": two each - Large ribosomes ; Small ribosomes ; M-RNA and Protein . True, the last two: M-RNA and Protein , may have one copy of themselves, due to the proximity of their location to the nucleotide " **strand** ".

b)_ These formations in their subsequent connection perform spatial - axial movement along the acceptor arm of **T-RNA** . In this case, **T-RNA** will have only one copy of the result of its " **translation** ": one for the Large ribosome ; Small ribosome ; M-RNA and Protein .

It is possible that the result may be mixed.

In the first case, the resulting build-up formations will be inextricably linked with the subsequent elements of their build-up, which gives "reliability" to the ongoing process and gives an advantage to this option .

Detailing the structure of protein formation is beyond the scope of this work .

In the presented " **mechanism** ", the Protein is one of the results of its action and its further functions , apparently, will be associated with the responsibility for the implementation of photosynthesis and chemosynthesis for this "mechanism".

And in conclusion, we note that the described " **mechanism** " introduces a certain "ENGINEERING" into the functioning of a living cell.
