From RNA world to RNA-tRNA world to RNA-DNA-tRNA world to DNA-RNA-protein world: how it went?

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Abstract

A concrete model for prebiotic evolution as a sequence of 4 worlds: RNA world → RNA-tRNA world → RNA-DNA-tRNA world → DNA-RNA-protein world is proposed. The h_{eff} increasing phase transition in which tRNAs originally catalyzing addition of RNA to growing RNA sequences starts to catalyze an addition of amino-adic to growing amino-acid sequence would lead from RNA-DNA-tRNA world to DNA-RNA-protein world.

1 Introduction

I encountered a highly interesting work [I1] (see http://tinyurl.com/y9ps2efz) related to the emergence of RNA world and I warmly recommend it to the reader (for a popular article see).

First a summary of basic terms for the possible reader of the article. There are three key enzymes involved in the process which is believed to lead to a formation of longer RNA sequences able to replicate.

1. Ribozyme is a piece of RNA acting as catalyst. In RNA world RNA had to serve also as a catalyst. In DNA world proteins took this task but their production requires DNA and transcription-translation machinery.

2. RNA ligase promotes a fusion of RNA fragments to a longer one in presence of ATP transforming to AMP and diphospate and giving metabolic energy presumably going to the fusion. In TGD fUniverse this would involve generation of an atom (presumably hydrogen) with non-standard value of $h_{eff} = n \times h$ having smaller binding energy scales so that ATP is needed. These dark bonds would be involved with all bio-catalytic processes.

3. RNA polymerase promotes a polymerization of RNA from building bricks. It looks to me like a special kind of ligase adding only single nucleotide to an existing sequence. In TGD Universe $h_{eff} = n \times h$ atoms would be involved as also magnetic flux tubes carrying dark analog of DNA with codons replaced with dark proton triplets.

4. RNA recombinase promotes RNA strands to exchange pieces of same length. Topologically this corresponds to two reconnections occurring at points defining the ends of piece. In TGD Universe these reconnections would occur for magnetic flux tubes containing dark variant of DNA and induce the chemical processes at the level of chemistry.

Self ligation should take place. RNA strands would serve as ligases for the generation of longer RNA strands. The smallest RNA sequences exhibiting self-ligation activity was found to be 40-nucleotide RNA and shorter than expected. It had lowest efficiency but highest functional flexibility to ligate substrates to itself. R18 - established RNA polymerase model - had highest efficiency and highest selectivity. What I can say about the results is that they give support for the notion of RNA world.

The work is related to the vision about RNA world proposed to precede DNA-RNA-protein world. Why I found it so interesting is that it relates to on particular TGD inspired glimpse to what happened in primordial biology.

2 TGD based view about the sequence of worlds

In TGD Universe it is natural to imagine 3 or even 4 worlds.There are two scenarios: RNA world, RNA-tRNA world, and DNA-RNA-protein world and RNA world, RNA-tRNA world, DNA-RNA-tRNA world and DNA-RNA-tRNA-protein world.

Years ago I developed a rather detailed version of the idea about transition from RNA world to DNA-RNA-protein world [K1] but I did not realize the tRNA-RNA world as intermediate step (see `http://tinyurl.com/y8ho27rq`).

1. RNA world would contain only RNA. Protein enzymes would not be present in RNA world and RNA itself should catalyze the processes needed to for polymerization, replication, and recombination of RNA. Ribozymes are the RNA counterparts of enzymes. In the beginning RNA would itself act as ribozymes catalyzing these processes.

2. One can also try to imagine RNA-tRNA world. The predecessors of tRNA molecules containing just single amino-acid could have catalyzed the fusion of RNA nucleotide to a growing RNA sequence in accordance with the genetic code. The function of tRNA would thus been different: since the roles of RNA codon and amino-acid would have been changed from the usual. Amino-acid sequences would not have been present at this stage since there would be no machinery for their polymerisation.

3. One can consider a transition from this world to DNA-RNA-tRNA world. This would storage of genetic information to DNA from which it would have been transcribed by using polymerase consisting of RNA. This phase would have required the presence of cell membrane like structure since DNA is stabilized inside membranes or at them. Transition to this world should have involved reverse transcription catalyzed by RNA based reverse-transcriptase. Being a big evolutionary step, this transition should involve a phase transition increasing the value of $h_{eff} = n \times h$.

4. My earlier proposal has been that a transition from RNA world to DNA-RNA-protein world took place. The transition could have also taken place from DNA-RNA-tRNA world to world containing also amino-acid sequences and have led to rapid evolution of catalysis based on amino-acid sequences.

   The amino-acid sequences originating from tRNA originally catalyzing RNA replication stole the place of RNA sequences as the end products from RNA replication. The ribosome started to function as a translator of RNA sequences to amino-acid sequences rather than replication of them to RNAs! The roles of protein and RNA changed! Instead of RNA in tRNA the amino-acid in tRNA joined to the sequence! The existing machinery started to produce amino-acid sequences!

   Presumably the modification of ribosome or tRNA involved addition of protein parts to ribosome, which led to a quantum critical situation in which the roles of proteins and RNA polymers could change temporarily. When protein production became possible even temporarily, the produced proteins began to modify ribosome further to become even more favorable for the production of proteins.

   But how to produce the RNA sequences? The RNA replication machinery was stolen in the revolution. DNA had to do that via transcription to mRNA! DNA had to emerge before the revolution or at the same time and make possible the production of RNA via transcription of DNA to mRNA. The most natural options corresponds to "before", that is DNA-RNA-tRNA world. DNA could have emerged during RNA-tRNA era together with reverse transcription of RNA to DNA with RNA sequences defining ribozymes acting as reverse transcriptase. This would have become possible after the emergence of predecessor of cell membrane. After that step DNA sequences and amino-acid sequences would have been able to make the revolution together so that RNA as the master of the world was forced to become a mere servant!

   The really science fictive option would be the identification of the reverse transcription as time reversal of transcription. In zero energy ontology (ZEO) this option can be considered at least at the level of dark DNA and RNA providing the template of dynamics for ordinary matter.

How the copying of RNA strand to its conjugate strand catalysed by amino-acid of tRNA could have transformed to translation of RNA to amino-acid sequence? Something certainly changed.

1. The change must have occurred most naturally to tRNA or - less plausibly - to the predecessor of the ribosome machinery. The change in the chemical structure of tRNA is not a plausible option. Something more than chemistry is required and in TGD Universe dark matter localized at magnetic flux tubes is the natural candidate.

2. Evolution corresponds in TGD Universe gradual increase of $h_{eff} = n \times h$. A dramatic evolutionary step indeed took place. The increase of the value of $h_{eff} = n \times h$ for some structural element of tRNA could have occurred so that the catalysis for amino-acid sequence instead of that for RNA sequence started to occur.

3. The general model for bio-catalysis in TGD Universe involves a contraction of magnetic flux tubes by a reduction of h_{eff} and bringing together the reacting molecules associated with flux tubes: this explains the magic looking ability of biomolecules to find each other in the dense molecular soup. The reduction of h_{eff} for some dark atom(s) of some reacting molecules(s) to a smaller value liberates temporarily energy allowing to kick the reactants over a potential wall so that the reaction can occur (atomic binding energies scale as $1/h_{eff}^2$). After than the liberated energy is absorbed and ordinary atom transforms back to dark atom.

   In the recent case h_{eff} associated with a dark atom (or atoms) of tRNA could have increased so that the binding energy liberated would have increased and allowed to overcome a higher potential wall than before. If the potential wall needed to overcome in the fusion of additional amino-acid to a growing protein is higher than that in the fusion of additional RNA to a growing RNA sequence, this model could work.

4. The activation energy for the addition of amino-acid should be larger than that for RNA nucleotide. A calculated estimate for the activation energy for the addition of amino-acid is 63.2 eV (see `http://tinyurl.com/yab6dmrm`). An estimate for the activation energy for the addition of RNA nucleotide at the temperature range 37-13 C is in the range 35.6 - 70.2 eV (see `http://tinyurl.com/y8xwpvvg`). An estimate for the activation energy for the addition of DNA nucleotide is 58.7 eV (see ://tinyurl.com/yc8nr4kh). The value in the case RNA would be considerably smaller than that in the case of amino-acids at physiological temperature. For DNA and amino-acid the activation energy would be somewhat smaller than for amino-acid. This is consistent with the proposed scenario. I am not able to decide how reliable these estimates are.

The natural first guess is that the dark atoms are hydrogen atoms. It is however not at all clear whether "ordinary" hydrogen atoms correspond to $n = h_{eff}/h = n = 1$.

1. Randell Mills [D1] has proposed his notion of hydrino atom to explain anomalous energy production and EUV radiation in 10-20 nm range taking place in certain electrolytic system and having no chemical explanation. The proposal of Mills is that hydrogen atom can make in presence of a catalyst a transition to a lower energy state with a reduced size. I have already earlier considered some TGD inspired models for hydrino. The resemblance with the claimed cold fusion suggests that the energy production involved in the two cases might involve the same mechanism.

   I have considered two models for the findings [L1]. The first model is a variant of cold fusion model that might explain the energy production and the observed radiation at EUV energy range. Second model is a variant of hydrino atom assuming that ordinary hydrogen atom corresponds to $h_{eff}/h = n_H > 1$ and that catalyst containing hydrogen atoms with lower value of $n_h < n_H$ could induce a phase transition transforming hydrogen atoms to hydrinos with binding energy spectrum scaled up by scaling factor $(n_H/n_h)^2$ and radii scaled down by $(n_h/n_H)^2$. The findings of Mills favour the value $n_H = 6$.

2. Suppose the transition corresponds to a transition analogous to photon emission so that it occurs between $\Delta J = 1$ transitions of hydrogen atom. There are two simple options: either the direction of electron spin change but orbital angular momentum remains unaffected or the angular momentum of electron changes by $\Delta L = 1$ but spin direction does not change.

(n_{Hi}, n_i)	(n_{Hf}, n_f)	$\Delta E/eV$
$(3,1)$	$(1,2)$	17.0
$(4,1)$	$(1,2)$	40.8
$(4,1)$	$(2,2)$	0.0
$(5,1)$	$(1,2)$	71.4
$(5,1)$	$(2,2)$	7.7
$(6,1)$	$(1,2)$	109.0
$(6,1)$	$(2,2)$	17.0

Table 1: The liberated energy in transition $(n_{Hi}, n_i = 1) \to (n_{Hf}, n_f = 2)$ in some cases.

The simplest assumption is that the principal quantum numbers in the initial and final state are $n_i = 1$ and $n_f \geq n_i$. Assume first that initial state with $(n_{Hi}, n_i = 1)$ having $L_i = 0$ and final state with $(n_{Hf}, n_f \geq n_i)$.

3. The energy difference between the initial state with $(n_{Hi}, n_i = 1)$ and final state with (n_{Hf}, n_f). The initial binding energy is the ordinary binding of thought-to-be hydrogen atom in the ground state: $E_i = E_f(n_{Hf}/n_{Hi})^2 \simeq 13.6$ eV. Here E_f denotes the final ground state binding energy. The final state binding energy is $E_{fn_f} = E_f/n_f^2$.

   The liberated energy defining the order of magnitude for the activation energy (thermodynamical quantity) is given by

$$\Delta E \quad = \quad E_{fn_f} - E_i = \frac{E_f}{n_f^2} - E_f(\frac{n_{Hf}}{n_{Hi}})^2 = E_i \left[(\frac{n_{Hi}}{n_{Hf}})^2 n_f^{-2} - 1 \right] \quad . \tag{2.1}$$

   The condition $\Delta E > 0$ gives

$$\frac{n_{Hi}}{n_{Hf}} > n_f \quad .$$

   For $n_{Hi}/n_{Hf} = n_f$ one has $\Delta E = 0$. For instance, this occurs for $(n_{Hi}, n_{Hf}) \in \{(2,1), (6,3), (6,2)\}$ $\Delta E > 0$ condition gives $n_{Hi} > 2$.

4. Consider first $n_i = n_f = 1$ for which the spin direction of electron changes if the transition is analogous to photon emission. By putting $n_f = 1$ in Eq. 2.1 one obtains a formula for the transition energy in this case. For instance, $(n_{Hi}, n_i) = (6,1) \to (n_{Hf}, n_f) = (3,1)$ would correspond to $\Delta E = 40.8$ eV perhaps assignable to RNA polymerization and the transition $(n_{Hi}, n_i) = (7,1) \to (n_{Hf}, n_f) = (3,1)$ to $\Delta E = 60.4$ eV perhaps assignable to amino-acid polymerization and DNA polymerization. Note that $n_H = 6$ is supported by the findings of Mills.

5. Table 1 gives the liberated energies ΔE for transitions with $(n_i, n_f) = (1,2)$ in some cases.

   The transitions $(4,1) \to (1,2)$ resp. $(5,1) \to (1,2)$ might give rise to the activation energies associated with RNA resp. amino-acid polymerization.

6. If ordinary hydrogen atom and atoms in general correspond to $h_{eff}/h = n = 1$, the liberated energies would be below the ground state energy $E_0 = 13.6$ eV of hydrogen atom and considerably below the above estimates. For heavier atoms the binding energy scale would be Z^2-fold and already for carbon with $Z = 6$ by a factor 36 higher. It is difficult to obtain ΔE in the scale suggested by the estimates for the activation energies.

One could try to test whether tRNA could be modified to a state in which RNA is translates to RNA sequences rather than proteins. This would require a reduction of $h_{eff} = n \times h$ for the dark atom in question.

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