Was ribosome the first self-replicator?

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Abstract

M. Root-Berstein and R. Root-Berstein have made a fascinating proposal that ribosome defining the basic translation machinery was the first self-replicator. They have demonstrated that in the case of E. Coli bacterium the predictions deriving from this hypothesis are true. This could mean the identification of one important missing link in evolution. In this article this identification is considered in TGD framework, where the emergence of life corresponds to the emergence of dark matter with basic bio-polymers having dark proton sequences defining dark nuclei as their counterparts with biochemistry induced from the dynamics of the dark proton strings acting as masters.

1 Introduction

In the group Thinking Allowed Original there as a link to a popular article describing a highly interesting work [I1] by M. Root-Bernstein and R. Root-Bernstein (daughter and father). The title of the popular article "Forget the selfish gene: Evolution of life is driven by the selfish ribosome, research suggests". As a matter of fact, the article itself is not selling anything of type "selfish X", a dogma which to my opinion is more or less dead: synergy and quantum coherence are much more promising notions relevant to biomatter. "Selfish X" is a paradigm, which suits much better to the description of cancer. The title of the article "The ribosome as a missing link in the evolution of life" would have been much more appropriate also for the popular article.

First a summary of motivations by authors. The basic problem relates to the emergence of life and there are many theories. The models can be divided to "genetics first" and "metabolism first" type models.

1. RNA world is basic example of "genetics first" models. The problem of the "genetics first models" is that it is difficult to understand how prebiotic life could have coped before the complex molecular machinery of metabolism. The second problem of RNA world is that polynucleotides and proteins almost certainly co-evolved. So called compositional replication models start from this assumption but have difficulties in explain replication schemes. Both approaches fail to explain how complex cells emerged from molecular evolution. It is however known that lipid layers of cell membrane are emergent structures not coded by genes (soap films).

2. Second class of models try to proceed from complexity to simplicity by assuming the first replicator (pro-cell typically) but are not able to answer the question "What before this?". The natural assumption is that simple bio-molecules gradually evolved to polymers and polymer aggregates and eventually cell membrane emerged.

According to authors, the challenge is to bridge the gap between self-replicating polymers and fully functional cell by identifying intermediate structures able to replicate, restore and replicate information, capture metabolic components and energy, and transform all these into biochemical networks.

2 Trying to catch the idea

The basic idea of the authors is simple and brilliant. Ribosome is the transcription machinery transforming DNA to proteins. Also the first replicator must have contained the transcription machinery. Perhaps the first replicator was minimal and contained just this machinery! Perhaps ribosome or its predecessor ("pre-ribosome") indeed was the first self-replicator. One would have beautiful self-reference: ribosome would be the recipe for making a copy about the recipe! Brings in mind Gödel-Escher-Bach!

This assumption is highly non-trivial. In the following I try to sketch for myself what this could mean. In the following I drop "pre"or notational convenience with understanding that ribosome, RNA, amino-acid etc. means "pre-ribosome", "pre-RNA", "pre-amino-acid", "pre-tRNA" etc.. In TGD framework pre-ribosome could be of non-biochemical nature and realized at the level of dark matter.

1. It seems natural to assume that the basic raw material consisted of RNA and amino-acid molecules in the environment. Ribosome could use them to build copies of itself. The question how these were generated will not be considered now.

2. Ribosome consists of rRNA and proteins and uses tRNA to associated to mRNA sequence amino-acid sequence. If ribosome was the first replicator realizing genetic code as mRNA-amino-acid correspondence it had to use its own rRNA as a template for the translation to a corresponding protein.

   If nothing has changed after the emergence of the recent replication mechanisms, the testable prediction is that ribosome amino-acids are images of rRNA sequences under genetic code. One of course expects that the stricture of ribosome has not conserved in precise sense so that this prediction could be too strong.

3. tRNA is a molecule of form RNA-X-amino-acid and rRNA should have contained the genetic information allowing to transcribe and translate the RNA and amino-acid polymers appearing in tRNA.

According to [I1] these predictions are indeed tested in the work considered for Escheria Coli bacterium and it is found that the findings are consistent with the hypothesis.

On basis of these observations one can try to imagine how the ribosome or its predecessor "pre-ribosome" might have replicated.

1. Both the basic units of RNA sequences and corresponding amino-acid polymers of rRNA had to replicate. The most economic assumption is that this occurred simultaneously.

2. One can imagine that rRNA "gene" and the protein coded by it arranged themselves so that they were parallel. The amino-acid coded by rRNA codon acted as a catalyzer for the attachment of a conjugate of rRNA codon to the growing rRNA sequence just as in DNA replication promoter catalyzes the replication. rRNA codon in turm acted as a catalyzer for the addition of new amino-acid to the growing protein. tRNA molecules of form RNA-X-amino-acid from the environment provided the needed RNA codon and amino-acid.

   Remark: I have already earlier considered an RNA world scenario in which amino-acids of tRNA catalyzed the replication of RNA sequences [K1]. When DNA emerged, the roles would have changed and amino-acid sequence was formed instead of the replication of RNA.

This replication differs from ordinary transcription. In transcription incoming mRNA sequences produce amino-acid sequences as tRNAs attach to the mRNA codons of mRNA attached to the ribosome. tRNA looses its amino-acid but keeps RNA. Now tRNA loses both amino-acid and RNA codon and only the unit X in tRNA? RNA-X-amino-acid remains.

At some step of evolution the replication of rRNA would have ceased to occur and tRNA would have kept its RNA in the double translation process. Is this possibly biologically?

3. Concerning tRNA there are many possibilities. One can imagine that ribosome and Xs could have served as co-replicators. The reaction $X \rightarrow RNA - X - amino - acid$ and its inverse could have occurred spontaneously. The resulting complex would have attached to the end of RNA-amino-acid sequence associated with some portion of mRNA just as it does in ordinary translation . In the replication or ribosome RNA-X-amino-acid would have attached to ribosome and X:s would have been produced in the replication of X forming a part of ribosome. In the environment the attachment of RNA and corresponding amino-acid to X would have taken place.

A possible objection is based on ontogenesis-recapitulates-phylogeny vision (ORP). The replicating pre-ribosomes should be still there but they are not. There should be some very simple mechanism preventing the replication but still one can ask whether the ribosomal replication could not occur in special circumstances.

3 How the pre-ribosome as first replicator relates to TGD approach?

TGD framework predicts that replication as a splitting of 3-surfaces to two copies is a fundamental mechanism of quantum TGD analogous to the $1 \rightarrow 2$ decay of elementary particle and the replication of DNA, cells, etc... should reduce to a hierarchy of replications starting from long length scales and proceeding as replications at shorter length scales with master slave relationship between the subsequent levels of the scale hierarchy.

This identification of replication as a mere splitting of 3-surfaces saying nothing about what happens for the quantum states associated with them is too general to allow to talk about unique primary replicator. If one however restricts the consideration to systems consisting of RNA and amino-acid sequences the idea about ribosome as primary replicator becomes highly non-trivial.

In TGD framework it is possible that pre-biopolymers were not bio-polymers but their dark counterparts formed from dark protons sequences at magnetic flux tubes with states of dark proton in 1-1 corresponds with DNA ,RNA, amino-acids and tRNA. If so pre-ribosome was realized at the level of dark matter as dark ribosome - a complex formed by dark analogs of bio-polymers.

If so, then pre-ribosome consisting of dark matter at flux quanta could be the primary replicator and the formation of its bio-molecular counterpart would be induced from that of dark pre-ribosome like the dynamics of slave in master slave hierarchy.

This raises questions. How does this replication proceed? Does ribosome still replicate as all other biological structures do and induce replication of low ever level structures in the dark matter hierarchy? Does the ordinary biomatter induced at the lowest level of hierarchy would only make visible this replication?

In the following I briefly summarize the basic TGD based notions involved in attempt to answer these questions.

3.1 4-D self-organization and magnetic body

One class of questions concerns the roles of self-organization and genetices. Even the definition of the notion of self-organization is poorly defined. In TGD zero energy ontology (ZEO) forms the basic framework of both quantum TGD proper and its applications to consciousness and biology. In zero energy ontology (ZEO) self-organization is replaced with self-organization by quantum jump sequence leading to the emergence of not only 3-D spatial patters but also of 4-D behavioral patterns: one can say that living system is 4-dimensional and also its geometric past changes in quantum jumps (Libet's findings).

1. Various motor actions of magnetic body appear as basic processes of the quantum self-organization. This includes braiding and knotting, h_{eff} changing phase transitions changing the lengths fo flux tubes, reconnections allowing to build connections between different system consisting of flux tube pairs, and also replication. Also signalling by dark photons is an essential part of the picture and the general hypothesis is that dark photons have same universal energy spectrum as bio-photons and thus in the energy range of molecular transition energies.

2. Replication in TGD framework occurs at the fundamental level as a replications of 3-surface and is completely analogous to $1 \to 2$ decay for point elementary particle. This replication could take place for the magnetic flux quanta representing various biopolymers and higher level structures and induced the replication at the level of visible matter. As noticed, this replication is not enough in biology and must be accompanied by the replication of the quantum states associated with 3-surfaces.

3. One key question is how the bio-molecular processes arranged into a functional network. Here the hypothesis that magnetic flux tubes form a 3-D grid analogous to coordinate grid with points of grid at intersections of 3 flux tubes and flux tubes as coordinate lines is very attractive. This Indra's web would be behind the gel like structure of cellular water and make it single coherent unit. Behavioral modes would be time evolutions of this grid: motor actions of the magnetic body - or hierarchy of them.

3.2 Does dark matter induced the dynamics of visible biomatter?

The idea that dark matter induces the dynamics of biomatter is extremely attractive since the enormous complexity of biochemistry would be only adaptation to the dynamics of the much simple almost topological dynamics of the master represented as flux tubes carrying dark matter.

1. In TGD framework there are good reasons to believe that water contained the prebiotic life forms as dark analogs of various biomolecules consisting of dark proton sequences at magnetic flux tubes with the states of dark proton in 1-1 correspondence with various bio-polymers (DNA,RNA, amino-acids, tRNA). These string like objects would be dark nuclei but with a large value of Planck $h_{eff} = n \times h$ constant and with same size scale as biopolymers. The proposal is that they are present also in living matter and that is interaction between various levels based on dark photons which give bio-photons as decay products.

2. All the basic processes such as transcription, translation, and replication would be realized already at this level. The analogs of these processes assigning to dark analogs of biopolymers the biopolymers themselves would have evolved later. (ORP) suggests that ordinary biopolymers are accompanied by parallel flux tubes carrying dark protons sequences representing them. Ordinary manner would condense around dark matter.

   The strongest assumption is that dark processes induce their bio-chemical counterparts as biomolecules attach to the magnetic flux tubes for which they form images at the level of visible matter. This might explain why strong dehydration leads to denaturation of biomolecules and why denatured biomolecules are not biologically active. Dark DNA would represent the "soul" of DNA not present in denatured DNA! Same of course would apply to other biopolymers: the loss of dark matter would induce the in vivo $\to$ in vitro transformation.

   I have proposed the identification of dark counterparts of RNAs and amino-acids as complex braided and knotted structures with braiding carrying information making possible topological quantum computation like processes and topological realization of memory. DNA would provide a symbolic representation coding also the braiding characteristics of the dark amino-acid sequence. Dark amino-acid sequence would represent the braiding physically ad dark DNA as a sequence of symbols.

   Cyclotron frequencies are crucial for communication and the strength of magnetic field on flux tubes emanating transversally from dark amino-acid sequence would be determined by the state of dark proton. The correspondence between dark RNA and amino-acid would be determined by the condition that cyclotron frequencies are identical for the corresponding

dark proton states (DNA and mRNA, RNA and amino-acid) so that resonant interaction is possible.

3. This picture conforms with the chemical properties of DNA, RNA and proteins.

   (a) RNA does not appear as double strands and in unfolded form is much less stable than DNA. This conforms with the fact that DNA serves as an information storage providing symbolic representation of RNA and amino-acids including their folding or at least braiding. RNA in turn would provide the concrete representation for braiding and folding.

   (b) DNA double strand is stable against hydrolysis but only inside cell - this could be due to the fact that the phase of water is ordered and ice-like so that it cannot induce hydrolysis by providing water molecules - perhaps the fourth phase of water discovered by Pollack and leading to the formation of dark proton sequences in TGD framework is in question.

   (c) The braiding structure of DNA is repetitive and carries no information. This conforms with the idea that DNA and its dark variant provide a purely symbolic representations in terms of genetic code for the corresponding amino-acid- and RNA polymers including also their braiding.

4. One can invent objections against the hypothesis that the dynamics of biopolymers is induced from that for their dark variants.

   (a) RNA is not stable against hydrolysis but it can gain stability by folding. Thus the shape of RNA molecule would not be determined by its dark variant in conflict with induction hypothesis. One can however consider the much weaker possibility that dark sector determines only topological dynamics. Only the braiding of the fold RNA molecules would determined by the braiding of dark variant.

   (b) DNA double strand is stable and braided in repetitive and very simple manner. If chemistry determines the stability of the DNA double strand then DNA double strand would induce the braiding of dark DNA strand rather than vice versa. Now one can argue that if dark DNA appears as double strand this forces the repetitive braiding.

To how high level can one continue this parallelism. For instance, does it make sense to talk about dark variants of cell and cell membrane? Can one tell whether it was pro-cell or bio-molecules that emerged first? It seems that all these structures could have emerged simultaneously. What emerged was dark matter and its emergence involved the emergence of all the others. Hens and eggs emerged simultaneously.

1. Here the findings of Pollack about the generation of exclusion zones, which are negatively charged regions of water obeying exotic stoichiometry $H_{1.5}O$, are suggestive. The TGD based model assumes that a phase transition generating dark protons sequences at flux tubes of magnetic body outside the EZ takes place. The self-organization at the level of ordinary matter would generate dark matter at quantum criticality - a basic aspect of self-organization process leading to higher hierarchy levels taking the role of master. Dark matter would be the master or rather - there would be entire hierarchy of masters labelled by the values of h_{eff}. I have also considered the possibility that the generation of large h_{eff} phases happens at criticality quite universally so that life would be universal phenomenon rather than random thermodynamical fluctuation.

2. EZs with sizes about 200 microns (size of cell) could have been the prebiotic cells. There is also evidence that EZs consist of structures with size of order micron called coherent regions (CDs to be not confused with Causal Diamonds!). Could they have been the predecessors of the cell nuclei inside which dark DNA would be stable? The TGD model for the formation of EZs assumes that they are formed from CDs under irradiation.

   This picture leads also to a view about metabolism predict that UV radiation with energies about 12.6 eV must play a key role in metabolism. The proposal is that this radiation arrives

as dark photons along magnetic flux tubes of the magnetic body and excites water molecules inside CDs so that they are energetically at distance of about .5 eV from the splitting of OH bond. The excitation of water molecules inside CDs by metabolic energy quantum of nominal value .5 eV transforms this phase to EZs of Pollack.

3.3 Emergence of life as emergence of dark matter?

Many basic questions of biology seem to be hen-egg questions such as "genetics or metabolism?", "cell membrane or biomolecules?", "DNA or RNA?", "RNA or amino-acids?", etc.. This suggests that there exists a deeper level and emergence at this level induced the emergence at the level of biochemistry and cell biology.

In TGD the emergence of living systems would reduce to the emergence of dark matter as large h_{eff} phases of ordinary matter taking place at quantum critical and perhaps even critical systems [K3].

1. The question whether genetics or metabolism emerged first ceases to be relevant in this framework, where basic physics provides candidates for the fundamental mechanisms of metabolism (for instance liberation of zero point kinetic energy when the p-adic length scale of space-time sheet (magnetic flux tube) increases).

   Also genetic code would have been realized already before biochemistry if dark proton sequences provided the counterparts for the fundamental biomolecules. The dark biology as dark nuclear physics would make itself visible via biochemistry induced by it. We would see directly the dynamics of dark matter just by looking living systems!

2. If one takes this picture seriously, then also pre-RNA and various other pre-biopolymers could have been realized in terms dark proton sequences associated with dark magnetic flux tubes. The dark replication process could have been the arrangement of RNA and amino-acid flux tube portions in parallel and replication of the dark proton sequences with the help of the analog of tRNA attaching to the corresponding amino-acid. In this framework the notion of dark ribosome makes sense. It would however replicate only in cell replication.

3. In the biochemical scenarios also the emergence of DNA looks like mystery. In TGD framework dark DNA could have emerged at the same time as dark RNA and dark amino-acids as CDs and EZs emerged and make the stable presence of also ordinary DNA inside CDs and EZs. All basic biomolecules and prebiotic cell and metabolism would have accompanied the emergence of CDs and EZs under the irradiation of water feeding metabolic energy and giving rise to prebiotic photosynthesis (note that the negative net charge of DNAs could be due to the fact that part of protons is at dark flux tubes). Dark DNA could be interpreted as an information storage representing the braiding patterns of dark RNA and dark amino-acids symbolically.

4. In this framework the basic step of the replication is the generation of flux tube parallel to the flux tube from which one forms copy or map (say in DNA replication and and transcription). How this happens?

   A possible answer to the question relies on the earlier proposal that living system involves kind of coordinate grid formed from magnetic flux tubes serving as coordinate lines and meeting each other at the points of the grid [K2]. The replication process would involved translation of nearby flux parallel flux tube of the grid near to a given flux tube assignable to say DNA strand as a first step - maybe by h_{eff} reducing phase transition for flux tubes orthogonal the flux tube. After this the building bricks of the new biomolecule would be brought along either of the remaining locally orthogonal flux tubes - perhaps by h_{eff} reducing phase transition. The basic structure would be this Indras web containing visible matter at its nodes with dynamics consisting of magnetic motor actions.

This vision involves of course considerable challenges. One should model the dark ribosome counterparts of the replication process for dark DNA, transcription of dark DNA to dark mRNA, translation of dark mRNA to dark amino-acids, and also possible self-replication of dark ribosome.

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