Multilocal viruses

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Abstract

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1 Introduction

I learned about very interesting piece of strangeness in biology known already for half a century (see http://tinyurl.com/yyh5s2c8): there are viruses, which can split into segments going into different host cells, replicate and produce proteins there, and self-assemble to original virus after this.

Virus (see http://tinyurl.com/owuwgfk) consist of DNA or RNA, protein coat, and in some cases outside envelope consisting of lipids and analogous to cell membrane. Typically viruses consist of DNA or RNA decomposing to short segments coding for single protein. The reason for this is that RNA replication is prone to errors and for short segments these errors are not so fatal. Also DNA can be segmented but the segments are longer. RNA can be have positive sense in which it can be directly translated to protein or negative sense in which case replication producing positive sense RNA is needed made possible by an enzyme contained by the virus.

The usual thinking about viruses is that virus finds its way to cell and then uses the genetic machinery of the cell to replicate its DNA and RNA and produce also proteins. This does not not occur in the case of multipartite viruses infecting plants. The virus can split into segments infecting host cells separately. The segments of RNA and proteins contained by the virus are thus shared by different cells are replicated and coded to proteins. The outcome of the process is then brought together in some cell which need not contain gene segments in it and self-assembly to full virus can occur. Also fractured viruses can flourish and can infect some other plant.

It has been found that the full complement of most viral segments is missing from most plant cells. Protein required for viral replication present in cells that did not have genome for producing it so that the produced proteins can be transferred from the cell where they are produced to neighboring cells: it is though that so called plasmodesmata connecting cells to a network make this possible.

In standard view assuming that the viral segments are completely independent systems multi-partitioning has high risks. In this view theoretically not more than 4 segments are possible. For instance, 8 has been observed in the examples discussed. Even flu virus decomposes into 8 DNA segments with the cell inside which it replicates. Multi-partitioning produces also problems for spreading. In the case of FBNSV viruses mentioned in the article on the insect - aphid- eating FBNSV spreads the virus to plants. How can it get all 8 parts of virus simultaneously? This is very difficult to understand if the segments are really independent.

This suggests that the view about these viruses somehow wrong. Multi-partitioning happens and standard view does not allow it.

2 TGD based model for multi-local viruses

One can start by asking why the multi-partitioning implying modular reproduction (something analogous to that in industry!)? One good reason is that host cell might not be able to recognize the segments. Also transcription of too large number of RNAs might be too much for the host and kill it. It seems that viruses act as populations.

TGD based model is based on familiar basic notions [L2, L5].

1. The basic mystery of the biology is coherence of organisms. Bio-chemistry alone cannot explain it. In TGD quantum coherence of dark matter identified as $h_{eff} = nh_0$ phases of ordinary matter at magnetic flux tubes of the magnetic body (MB) of the system is quantum coherent in long scales and this quantum coherence forces the coherence of ordinary living matter. Biological self-organization and metabolism reduce in zero energy ontology (ZEO) to dissipation in non-standard direction of space-time [L4].
2. The flux tubes of MB connect cells to larger networks (tensor networks). In particular the segments of virus can be connected to a network in this manner. The segments would be effectively free but their behavior would be correlated. Virus would be multi-local entity at the level of ordinary matter but single connected structure at the level of MB.
3. The TGD based model for bio-catalysis and replication and the model for monopole flux tubes suggests that the phase transition increasing $h_{eff}/h_0 = n$ increases the length of the flux tube. This process requires metabolic energy since quite generally the energy of system increases with n serving as a kind of IQ of the system measuring its algebraic complexity and identifiable as the dimension of extension of rationals assignable to the system. Multi-partitioning requires metabolic energy presumably given by a host cell. The components of multi-partitioned virus are virtually independent but flux tube connections are not lost. There are very many possible multi-partitions and the individual host cell can contain several segments.
4. If the decay of virus to multi-partition corresponds to ordinary state function reduction ("big" state function reduction (BSFR) in zero energy ontology (ZEO) [L6], the arrow of time changes at the level of MB of virus (dark matter). n increases in statistical sense in BSFR so that the multi-partitioned state should have higher IQ and is thus favored by quantum TGD. One might perhaps say that when virus is not active it does not need too much IQ: IQ requires metabolic energy feed and low IQ is the most economical choice in the dormant space. When virus infects the host it become active and and increase of n makes it multi-local at the level of ordinary matter.

   If this view is correct, the self-assembly of the virus would lead back to dormant state with opposite arrow of time. That dormant state of virus would correspond to opposite arrow of time for "virus self" would conform with the general view that observer with opposite arrow of time than conscious entity experiences it as sleeping. One must be of course however very cautious with interpretations.
5. These dormant states would not be specific to viruses. Also folded protein would be dormant. External perturbation would feed metabolic energy feed waking up the dormant protein and protein would un-fold and become active and intelligent.

   Same applies to multi-locality. Also bacterial colony could be seen as single organism multi-local only at the level of ordinary bio-matter. When bacterial colony suffers starvation the bacteria form a single tightly connected structure also at the level of ordinary bio-matter. In the absence of metabolic energy feed the values of n associated with the flux tubes would be reduced and they would shorten causing the phenomenon.

   For cellular organisms the multi-locality at the level of ordinary bio-matter be realized for cell but the distances of cells would be fixed. Also at the level of DNA, RNA, tRNA and amino-acids multi-locality would be realized but the distances would not be fixed. In bio-catalysis the reactants are brought together and here h_{eff} reducing phase transition would take place providing also the energy needed to overcome the potential wall making the reaction extremely slow otherwise. In TGD based model for replication, transcription, and translation this flexible multi-locality is indeed assumed [L5].
6. How sexual reproduction (see `http://tinyurl.com/kuvswc9`) emerged is one of the mysteries of biology. The formation of tightly bound multi-local states of mono-cellulars would have

increased the probability for lateral gene transfer between neighboring cells, and also the replacement of mere replication with a two-step process consisting of replication followed by meiosis and fertilization as its inverse. The reconnection of flux tubes assignable to DNA is a prerequisite of this process in TGD framework so that the formation of states analogous multi-cellulars would have made this process plausible.

It has been found (`http://tinyurl.com/qkzwk5t`, thanks for Nikolina Bendedikovic for a link) that multicellulars have monocellular colonies as predecessors in the sense that the bacteria (monocellulars) form temporarily tight structures resembling multicellular embryos. The transition from loose multi-locality to a more tight one suggets itself. When metabolic energy feed is low bacteria form tightly bound non-multilocal structures analogous to multi-cellulars. The flux tubes are shorten and metabolic energy is liberated, and also the need form metabolic energy is lower when flux tubes have lower values of h_{eff}. Multi-cellulars would be permanently in this configuration and their intelligence coded by distribution of h_{eff}:s would be realized differently.

Multi-cellulars would have been formed when these multi-cellular like bacterial colonies became permanent and began to evolve from embryos to more developed forms [L1, L3]. Hitherto I have assumed that multi-cellulars were formed already before the Cambrian explosion assumed to be induced by a relatively rapid phase transition increasing reducing the local cosmological constant by factor 1/2, and increasing the radius of Earth by a factor 2. This transition would have brought multi-cellulars to the surface from underground oceans giving also rise to the ordinary oceans. I have compared underground oceans to a womb of magnetic Mother Gaia. Ontogeny recapitulates phylogeny principle suggests that the life of the multicellular embryo in womb corresponds to the period of multicellular life in underground oceans.

Second possibility is that the multi-cellulars emerged from underground mono-cellulars during this transition or immediately after it. Could the emergence of bacterial colonies to the surface perhaps providing less metabolic energy feed forced them to form tightly bound colonies forcing the evolution of multi-cellulars?

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