

Genetics does not hold an argument for the existence of panspermia for explaining the origin of life on Earth

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INTRODUCTION

In their article *Genetics indicates extra-terrestrial origins for life: the first gene*, Joseph and Wickramasinghe (2011) once more draw attention to panspermia, the possibility of life having originated elsewhere in the universe. Life could thus have reached and seeded the Earth from outside. This is not the first time the authors have written on this subject; in fact this article comprises work of several decades and covers information from a long list of references. In their article, the authors concentrate, again not for the first time, on genetic data. These data could indicate an early, extraterrestrial origin of life of no less than 10 billion years ago instead of the ca. 4 billion years of Earthly existence and evolution, as commonly held in the literature. This is obviously an important conclusion concerning a problem which is significant both within and outside the scientific community.

Joseph and Wickramasinghe's (2011) paper is very open in giving the successive arguments leading to their conclusion concerning the occurrence of panspermia of life in the universe. Because it is so open, it invites comment. I shall concentrate on a few of the

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steps they take as arguments, arguing why I hesitate to accept their conclusions of both the occurrence of panspermia, as well as of the great age of life within the universe.

Because this contribution is meant to be a commentary on their paper, I have chosen not to consult the various books and articles published earlier by these authors. I also accept the graphs, tables, and references they give in their text as correct; because of their openness in their argumentation, I have no reason for doubt.

THEIR FIGURE 1

I want to concentrate on their Figure 1 taken from Lynch (2007), as this graph takes a central position in their analysis. This graph shows a positive, and tightly linear relationship between the logarithm of the amount of coding DNA on the y-axis against the logarithm of the total amount of DNA in an organism on the x-axis. This relationship applies to prokaryotes, unicellulars, bacteriophages, and eukaryote viruses. In contrast to the general increase in coding DNA in all these microbes, however, the amount of coding DNA for both land plants as well as animals does not follow the general positive trend but remains constant after a certain value has been reached. Therefore, these multicellular taxa deviate from the general statistical expectation of an increase in coding DNA with an increasing complexity of organization. This is the more striking because, as taxonomic Kingdoms, these taxa are genetically independent. This mutual deviation is obviously due to their specific genetic organization.

WHY MULTICELLULARS DEVIATE

The organization of the operation of the genome in multicellulars does indeed differ significantly from that in the other taxa. Possibly due to the complex ontogenetic development of individuals, a simple, relatively direct sequence of transcription and translation of the genome of unicellular organisms into their structure and dynamic was replaced by a highly complex and abstract organization of genome expression. Egg cells, namely, can impossibly code for the enormous complexity of the complete multicellular organism as well as for the intricate pathway leading to it. Therefore, they only code for the first step to be taken, this step coding for the second step, and so on. During this process, individual genes are repeatedly switched on and off hundreds of times, obtaining different functions in different, subsequent biochemical environments. Egg cells therefore contain only a fraction of the information of the total amount expressed by the mature organism; they solely contain the information of the initial step in an information-generating program. This is similar to our brain, or our Blackberry, i-pod, or MP-3 player which do not contain all the information you need either, but use a program for obtaining and generating this information. This difference in organization of their genetic material can, as a biological adaptation, explain why plants and animals deviate in their Figure 1.

SYSTEMS STABILIZATION

Similarly, there is no guarantee that the same relationship can be extrapolated to the lower end of the graph, that is to the earliest evolutionary forms of life. Biological processes different from present-day ones will have occurred during and immediately after life originated, when those forms were still relatively simple. In general, the

organization of early life forms will have been less stable than later ones: before enzymes were available, for example, molecules in the biochemical cycles had to be built up and fall apart relatively easily, implying that they consisted of weakly electronegative atoms (e.g. Hengeveld, 2012). Only later, more stable and reliable molecules could be formed from more strongly electronegative atoms, constituting increasingly more complex systems. Initially, coenzymes and a multitude of forms of RNA were derived from, for example, ATP. This stage, known as the RNA world is supposed to have occurred prior to the world based on the chemically more stable form of RNA, DNA. RNA, moreover, can replicate itself (Cech, 2000). Thus, there seems to have been a general trend from unstable molecular and biochemical structures towards more stable ones, culminating in a stage in which the strongly electronegative atoms of carbon, nitrogen and oxygen dominate a reliably regulated system, but in which the early biochemical processes based on RNA are still operating.

Initially, when the biochemical system was relatively simple, no centralized, stable reference or steering system with discrete genes will have become necessary, the network of chemical interactions keeping the system stable and operating. Replication by partitioning the many redundant and self-replicating molecules and processes will still have been sufficient. Only when the system grew in complexity, was a centralized genome as a stable reference and steering molecule necessary. Simple life forms will therefore have operated differently than the later, more complex microbial ones did and still do. Exclusively relying on genes as we know them today as essential cell constituents is unnecessary for early life forms.

The consequence of a less stable, early beginning of life is that not only is a search for the earliest gene unjustified, but also that endosymbiosis resulting in horizontal information transfer, even horizontal gene transfer, was more easily obtained during those early stages. Thus, a highly complex Central Metabolic Pathway could have been built up from several systems that had evolved independently (Kooijman and Hengeveld, 2005). This will have sped up the evolution of complex life considerably. This means that a simple extrapolation of the statistical relationship, that keeps the same rate of evolution towards the lower end of the range, is unwarranted. This means, in turn, that an extrapolation of the straight line in Figure 1 down to the point where it crosses the x-axis at about 10 billion years ago is biologically indefensible.

PROBLEMATIC DEFINITIONS

Here, a deeper problem shows up: our desire to define life prior to its analysis. Although this is common practice in biogenetic research and astrobiology, it is a faulty methodology: it prevents us from analyzing the first evolutionary stages (Hengeveld, 2010). Typically, Joseph and Wickramasinghe repeatedly use the cautionary expression “life as we know it,” although the initial life processes will have followed pathways “as we don’t know them.” By defining life in terms of properties of present-day organisms like genes, the authors fall into the trap they have set themselves. By assuming the existence and operation of such complex, replicating macromolecules like genes right from the beginning, they cannot possibly see a biogenetic state in which genes could not have existed, let alone could have operated. Genes themselves require an exceedingly complex peripheral organization, unavoidably linked as they are with mechanisms for duplication, transcription, translation,

replication, and repair, etc. They also require a biochemically complex system in which they can function. Typically, horizontal gene transfer concerns operational rather than informational genes (Jain et al., 1999); they form a large and fine-tuned complex of interdependent mechanisms. A tightly organized steering and replicating complex of genes on which such mechanisms depend, also operating within a biochemically functioning system could impossibly have existed *ab initio*. A DNA-based genetic replication system only becomes necessary and feasible after a certain level of organizational complexity had been reached as a means of fine tuning and stabilizing the dynamic processes within organisms. Talking about “first genes” simplifies a set of complex interactive mechanisms to the extreme.

In fact, a trend towards fine tuning and stabilization, culminating in a genetic system, expresses a general tendency towards stabilization, both in the external environment, as well as within the (proto-)cells. As easily available protons and electrons ran out, trends occurred in the environment from reducing to more oxidizing conditions, and towards stronger covalent binding. Gradually, more strongly electronegative atoms took over from weaker ones. Internally, an increasing complexity, partly to meet the greater electronegative pull of the environment and partly as an inherent tendency of biological evolution towards complexification, required the use of atoms with more stable bonds and, hence, a more complex, stable organization. To keep order, an organizing genetic system together with its peripheral equipment will have developed out of functional necessity from a phase of organization that lacked genes. Negating the evolutionary phase prior to one of greatly increased complexity is negating the very process of biogenesis.

CONCLUSION

Any statistical pattern expresses a physical process, in this case one of biological evolution. But all processes operate only over a certain range beyond which other processes take over. We can never extrapolate the operation of any process indefinitely. The evolution of biological complexity too has its limits: at two points it changes character, firstly when it becomes necessary and feasible to become handled by a central standardizing mechanism, and secondly when it becomes too complex to be handled by such a mechanism. Simply extrapolating a statistical trend beyond those points without allowing for the operation of the biological system is clearly unwarranted for multicellulars as shown by Joseph and Wickramasinghe's (2011) Figure 1. It seems equally unwarranted for the lower end of variation of complexity. Life forms must have existed before an intricate genetic system could function within the dynamic of the biochemical system as a whole. Immediately after life's origin, there was no need for a complex system for coordinating the operation of a few simple reactions. At that time, due to the lack of a coordinating system for stabilizing a great number of processes, evolution could be speeded up considerably by horizontal transfer of operational – metabolic – functions *sensu* Jain et al. (1999). Such a speeding up of evolutionary rates destroys the relationship on which Joseph and Wickramasinghe's (2011) timing of the biogenetic process and its inherent panspermia depends. The extrapolation of this relationship beyond the range of present-day microbes is no basis for presuming that panspermia exists. From this genetic perspective, panspermia can impossibly explain life's existence on Earth.

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