

ON THE EMERGENCE OF FUNCTIONS IN THE ORIGIN OF LIFE**Clas Blomberg****Dept. of Theoretical Physics, Royal Institute of Technology,
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There are still a number of unresolved questions that concern the development of the variety of functions needed for the first functioning organisms. This is directly related to the proper understanding of various stages and their relationships in the origin of life. These questions are not really amenable to experimental research. Thus, they are considered as 'speculative', and this is clearly a reason that they are not much studied although the questions are essential for a proper understanding of the emergence of life. Still, the rules of the game are known, and one can reach important conclusions by theoretical methods. With common sense, one may use mathematical models or simulation methods and also make analogies to similar problems in biological evolution. The aim is here to present such considerations.

Stages that were achieved in the path to life comprise: 1) The RNA-world with free genes that were self-replicative and with capacity to catalyse this reproduction and appropriate molecule processing. 2) A DNA-directed synthesis of RNA-genes. 3) Gene-directed protein synthesis via the genetic code, and 4) Cell organisation. There are many ideas about the relationships of these stages, but rather little is known about what was required to go from one state to another. It is important to remember that these stages had to make use of new controlling, catalysing agents, which were of no use in the RNA world. So how could they arise? The problems are of a conceptual character, and there are probably no chemical problems for these transitions (as there are for the onset of the RNA world). It may also have been possible for spontaneously formed peptides and/or other agents to have played an active role stage at an early stage as independent catalysts, e.g. in the RNA world.

An RNA-world is undeniably a very relevant state with the essential features of a real living system (Joyce, 1989). It might have been able to evolve into a complex system by developing further function possibilities. It is related to the abstract 'hypercycle system' presented by Eigen and Schuster (1979). However, most considerations, also experimental and analogies to biological evolution, suggest that such a system is not prone to evolve any diversity. It certainly has the potentials of evolution and may well have achieved a state of high evolution pressure, but most knowledge

about such systems tells that they would develop to something rather simple with a minimum of necessary functions. Further, even an efficient RNA-world (described as a hypercycle system) is vulnerable to mutations that produce inactive components or components that can deteriorate the efficiency. (Blomberg, 1995, also Maynard Smith and Szathmary, 1995)

A spatial (cell) organisation is proposed as a remedy to such vulnerability. It certainly improves the situation in some respects, but does not completely solve the problems. It is still not clear how a diversity could be reached. Further, although the RNA-world certainly to a large extent is life-like, most of its information would be lost in the transition to a protein world and probably also to the incorporation of DNA. In that respect, new stages had to make new starts.

A main message here will be that although they would chemically be functioning, there was no need for a high efficiency in the first stages. It may even have been a drawback. At a final stage there should be an association between oligonucleotides and amino acids that gave rise to a nucleic-acid directed protein synthesis. This may at the onset have been unsystematic, giving rise to an immense variety of proteins and protein functions. We will stress that the only way to get a stabilized genetic code is by feedback mechanisms: A code produced proteins that recognized and controlled that association between amino acids and anticodons which gave just that code and produced these proteins. Also, enzymes that controlled the accuracy could be produced. There may have been preferred associations between amino acids and nucleotides that biased the code, but essentially this leads to a 'frozen accident' code established by its results.

In this picture, a large manifold of proteins would emerge at one stage. Up to about 10^9 or even more different types are not unrealistic, and in that a great variety of functions were certainly possible. Once relevant feedback loops were established, one stabilized system could grow and become dominant. First at this stage, real life was being approached.

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