

Accepted Manuscript

Title: Crucial steps to life: From chemical reactions to code using agents

Author: Guenther Witzany

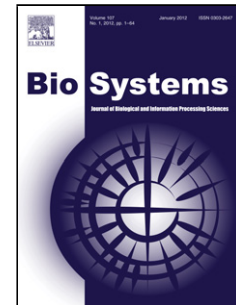
PII: S0303-2647(15)00206-3
DOI: <http://dx.doi.org/doi:10.1016/j.biosystems.2015.12.007>
Reference: BIO 3627

To appear in: *BioSystems*

Received date: 18-11-2015
Revised date: 5-12-2015
Accepted date: 7-12-2015

Please cite this article as: Witzany, G., Crucial steps to life: From chemical reactions to code using agents, *BioSystems* (2015), <http://dx.doi.org/10.1016/j.biosystems.2015.12.007>

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



Crucial steps to life: From chemical reactions to code using agents

Guenther Witzany

Telos-Philosophische Praxis, Vogelsangstr. 18c, 5111-Buermoos, Austria

Tel./Fax:+43 6274

Email: witzany@sbg.at

Abstract

The concepts of the origin of the genetic code and the definitions of life changed dramatically after the RNA world hypothesis. Main narratives in molecular biology and genetics such as the “central dogma”, “one gene one protein” and “non-coding DNA is junk” were falsified meanwhile. RNA moved from the transition intermediate molecule into center stage. Additionally the abundance of empirical data concerning non-random genetic change operators such as the variety of mobile genetic elements, persistent viruses and defectives do not fit with the dominant narrative of error replication events (mutations) as being the main driving forces creating genetic novelty and diversity. The reductionistic and mechanistic views on physico-chemical properties of the genetic code are no longer convincing as appropriate descriptions of the abundance of non-random genetic content operators which are active in natural genetic engineering and natural genome editing.

Keywords: non-coding RNAs, repeat sequences, genetic parasites, natural code users

1. Introduction

While the RNA world hypothesis is strongly supported by an abundance of detailed results in RNA biology and virology the origin of biological selection in contrast to prebiotic chemistry remains unknown. Although several promising approaches investigate this borderline between life and non-life empirically and theoretically, i.e. coherent and essential use of nucleic acid codes for genetic information generation, storage and heredity, a breakthrough with convincing explanatory power is lacking (Lehman 2015). The complementary features of genetic phenomena that are clearly absent in prebiotics, such as usage of (i) combinatorial rules of nucleotide syntax (ii) the context dependent (pragmatic) transcription that lead to (iii) the final function (semantics) of the transcription products are not part of quantitative analyses in molecular biology and genetics. Therefore it is less helpful to simply ignore these features and to propose a gradual emergence out of prebiotic chemistry into biology (Eigen and Schuster 1982; Szathmary and Maynard Smith 1997; Mayr 2004; Goldenfeld and Woese 2011, Koonin 2011, Yarus 2011, Waechtershauser 2015). This review will therefore look at essential features of natural codes that may lead to a new definition of life.

2. Deficits of the old main narratives in molecular biology and genetics

For decades it was assumed that if the genetic code represents a context-free universal grammar determined exclusively by natural laws, copying events can form only identical copies of the wild type. If there is any change in such copies it is correct to term them as replication errors. Error replications (mutations) are a key element in explanatory models of the evolutionary origin of genetic diversity, being the ultimate resource for biological selection.

More detailed, error-prone RNAs are a resource for generating genetic diversity followed by selection out of cumulative series of error replications. If the error rate is too high, then genetic content gets lost, followed by quasi-species collapse. Thus the genetic code looks like an emergent property of self-organizing matter and information that underlies

Download English Version:

<https://daneshyari.com/en/article/8406891>

Download Persian Version:

<https://daneshyari.com/article/8406891>

[Daneshyari.com](https://daneshyari.com)