Final Report

2016. 12. 1. - 2019. 11. 30.

Összefoglaló

A pályázatban két korai evolúciós modell elkészítését tűztem ki célul. Az 1. téma az MCRS modell keretében felület kötött metabolitok tulajdonságainak hatását vizsgáltuk a replikátorok együttélésére. A 2. témában egy vezikula populációban kerestük arra a választ, hogy a metabolikus folyamat és vezikulumok membránja milyen módon tud kölcsönhatni egymással, és hogyan tudják egymás evolúcióját elősegíteni. A támogatott időszakban egy rövid tanulmány úton vettem részt Olaszországban, ahol segítséget kaptam a 2. téma kidolgozásához. Továbbá több konferencián is részt vettem, ahol az eredményeimet előadások és poszterek formájában is bemutattam. A támogatott időszakban két cikk került publikálásra, és további két cikk kéziratán dolgozunk még.

Summary

In this application I proposed to develop two early evolutionary models. In *project 1* I investigated the effects of the features of metabolites on coexistence of replicators in the MCRS model-frame. In *project 2* I developed a model to investigate interactions and co-evolution of metabolic process and membrane in a vesicle population. I took part in a short study tour in Italy in 2017 where I received assistance for *project 2*. I have taken part in international conferences to present my results both in oral and in poster presentation forms. During the supported period two articles were published, and another two ones have been being prepared.

Report

Project 1

In this project my aim was to investigate the effect of explicit metabolic reaction network on the coexistence of replicators within the MCRS model-frame on cellular automatons. In all MCRS model the metabolism have been treated implicitly, so far: all essential metabolic intermediate molecules and monomers (hereafter *metabolites*) had to be present in a local grid area (*metabolic neighbourhoods*) to support the monomer production and the replication of replicators. Additionally, our previous models focused on replicators ignoring any complications with metabolites and reaction networks. Thus the structure of neighbourhood fitted to replicator-centric approach: each grid site occupied by only one replicator or empty, and the metabolic efficiency was calculated as a function of the number of replicators within the neighbourhood of the focal replicator assuming all essential metabolites were available within it. My aim was in this project to change the original implicitly implemented metabolic process step-by-step. At first (*project 1*), I developed a model where only one metabolite type (practicably *monomers*) was implemented: metabolites attached to surfaces reversibly additionally I ignored reaction network topologies and the presence of other metabolites from the system. Therefore, the focus of the model was shifted towards metabolites and it demanded a new neighbourhood structure: each grid site could be occupied by more replicators and more metabolites and the metabolic activity was localized only one grid site that depended on the number of replicators (original *metabolic connection*) and the replication depended on the number of monomers that were present at the grid site explicitly. I assumed that the intensity of limited diffusion of monomers on mineral surfaces as well as consumption and production rates of monomers affect on the coexistence of replicators. I would have implemented the diffusion of monomers by the discretized form of Fick's Diffusion Law but it resulted in several technical complications that is way I replaced it with a simple random walk algorithm. In the last

year I made some fine tuning of parameter setting of the model and now “harvest the fruits” of the first results: *Figure 1* shows that the coexistence of replicators depends on the intensity of the random walk of monomer and the consumption of monomers during replication: the system survives (black) or collapses (white) and the other parameters represent moderate parameter setting.

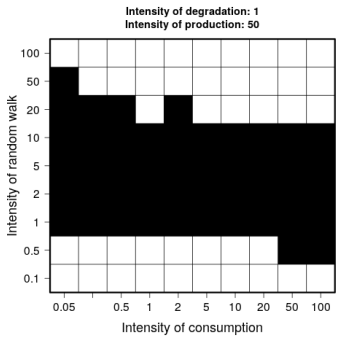

Figure 1

Project 2

The aim of this project was to investigate the interaction and co-evolution of prebiotic membrane and metabolism. We hypothesize that metabolic reaction networks within prebiotic vesicles and their membrane may have co-evolved at the dawn of life: lipid composition of vesicle membranes affects the metabolism, and *vice versa*. To verify this hypothesis we initialized an international collaboration within the frame of the COST Action CM1304 with Prof. Fabio Mavelli (Universita delgi Studi di Bari Aldo Moro, Italy) and Prof. Ruiz-Mirazo (University of the Basque Country, Spain) in which we would develop a new model with Prof. Mavelli's ENVIRONMENT platform in order to reveal the relationship between prebiotic metabolism and membrane. I visited Prof Fabio Mavelli in his department to work on our common project in October 2017. During this study tour I developed a simple vesicle in which I tried to implement the MCRS concept: the vesicle had a metabolic process that produced both monomers for the replications of replicators and lipids for membrane, and all reaction of the reaction-network were catalyzed by replicators. After the study tour I realized that the ENVIRONMENT platform was not capable of working properly as I had expected before. The ENVIRONMENT platform is a very complex program thus it is very sensitive and vulnerable for parameter settings. I have tried to fine-tuning the parameters in our new model version but I failed it. In addition, I have realized the ENVIRONMENT platform was not able to manage huge vesicle populations that necessary in general, for the studies of evolutionary processes. Thus I should develop a new and much simper model and that is more adequate to my original question. In this model each vesicle is capable of growing and proliferating because their volumes change continuously due to the active metabolism and to the membrane permeability of the vesicle. Membrane consists of several lipid molecules that is produced by a metabolic process. Membrane producing reaction is able to evolve and produces new lipid types with new features thus the permeability property of membrane/vesicle change affecting on the metabolic process, as well. I have developed the model but the fine tuning of parameters will be done after the supported period, thus some research articles will be published in the next year, not from this project but the *project 1* as well.

Publications

Published research articles

1. A Szilágyi, I Zachar, I Scheuring, Á Kun, **B Könnyű** & T Czárán: *Ecology and evolution in the RNA World. Dynamics and stability of prebiotic replicator systems.* Life 7: 48, 2017. doi: 10.3390/life70400048.

2. A Szilágy, **B Könnyű**, & T Czárán: *Dynamics and stability in prebiotic information integration: an RNA World model from first principle* . (*accepted in Scientific Reports, doi: 10.1038/s41598-019-56986-8*)

Research articles in preparation

3. D. Vörös, **B. Könnyű** & T. Czárán: *Information integration before membrane compartmentalization by catalytic promiscuity* (*in prep.*)

4. **B. Könnyű** & A. Kun: *Surfaces, the missing link in the origins of life* (*in prep*)

Conference lecture

5. T. Czárán, **B. Könnyű** & E. Szathmáry: *Metabolically Coupled Replicator System (MCRS), overview of an RNA-world model concept of prebiotic evolution on mineral surfaces*. XVIIIth ISSOL Conference 16-21 July, 2017, San Diego, California, USA. Conference publication: https://www.hou.usra.edu/meetings/issol2017/pdf/sess603.pdf.

6. **B. Könnyű**: *Prebiotic evolution of RNA molecules on mineral surface*. 1st EvolBiolDay 28. March 2018, Eötvös Loránd University, Budapest, Hungary.

7. D. Vörös, **B. Könnyű** & T. Czárán: *The role of catalytic promiscuity in the evolution of prebiotic replicators*. Interdisciplinary Origin of Life (IOoL) Meeting, 22-24 October 2018, Düsseldorf, Germany (https://www.origins-center.nl/category/events/).

8. D. Vörös, **B. Könnyű** & T. Czárán: *The role of catalytic promiscuity in the evolution of prebiotic replicators*. 2nd EvolBiolDay, 18. April 2019, Szeged, Hungary

Conference posters

9. **B. Könnyű**, A. Szilágyi & T. Czárán: *The role of enzymatic promiscuity in the evolution of RNA molecules*. Science of Early Life Conference 24-27 June, 2018, Hamilton, Canada. Conference publication p. 11.

10. D. Vörös, **B. Könnyű** & T. Czárán: *The role of catalytic promiscuity in prebiotic evolution*. Evolution Montpellier 2018, 18-22 August 2018, Montpellier, France. Conference publication (p-0171) p. 69.

MSc thesis

11. Vörös Dániel: *A katalitikus promiszkuitás szerepe a prebiotikus evolúcióban. (Title: The role of catalytic promiscuity during prebiotic evolution)*

Budapest, 30th November 2019.

Balázs Könnyű