Influence of non-enzymatic template-directed RNA recombination processes on polynucleotides lengths in Monte Carlo simulation model of the RNA World

Dariusz Myszor, Krzysztof A. Cyran

***Abstract*—**RNA World hypothesis assumes that once there was the time when RNA played main role on the field of life. According to this theory RNA strands acted both as catalysers of chemical reactions and information carriers. Despite many evidences that RNA world existed and predated current life based on DNA there is still a lot of unanswered questions and troubles to solve. Main trouble is the length of RNA strands. We conducted series of computer simulations based on modified model of Monte Carlo simulation of the RNA world. Model bases on real chemical processes operating on RNA strands. In our simulations we wanted to check influence of non-enzymatic template-directed RNA recombination process on RNA World. According to many researchers RNA recombination processes might lead to elongation of RNA chains and creation of novel sequences in the solution. These new RNA chains could have catalytic activities and serve as RNA replicase. Outcomes of computer simulations let us assume that RNA recombination processes are important phenomena in the RNA world and might lead to elongation of RNA chains.

***Keywords*—**RNA recombination, RNA replicase, RNA world, Monte Carlo method, computer simulation

I. INTRODUCTION

Since many years scientists have wondered how life emerged. There were many trials of explanation of this process, however up to this time non fully succeeded. Currently researches shed new light on some chemical processes that might play important role during life creation and should be considered in trials of origins' reconstruction. Most popular and consistent theory describing life's beginning is called RNA world[1]. According to this hypothesis there was the time when life based on RNA strands, these strands could store information and act as chemical reaction catalysers [2]–[4]. There are many proofs of this theory visible in current life, for example ribozymes[5]. However there are still many pieces of the puzzle that just do not fit. One of the unfitted piece is the problem with RNA strands lengths. Hypothesis assumes that nucleotides, after emergence in the solution, might join to each other and formulate strands. This RNA molecules binding might be the effect of the process of mineral catalysed synthesis of polynucleotides[6]–[9]. Outcomes of laboratory experiments indicate that there is a possibility to acquire chains up to 50 nucleotides long[10]. Scientists speculates that further elongation of RNA chains might be acquired through RNA recombination processes[11].

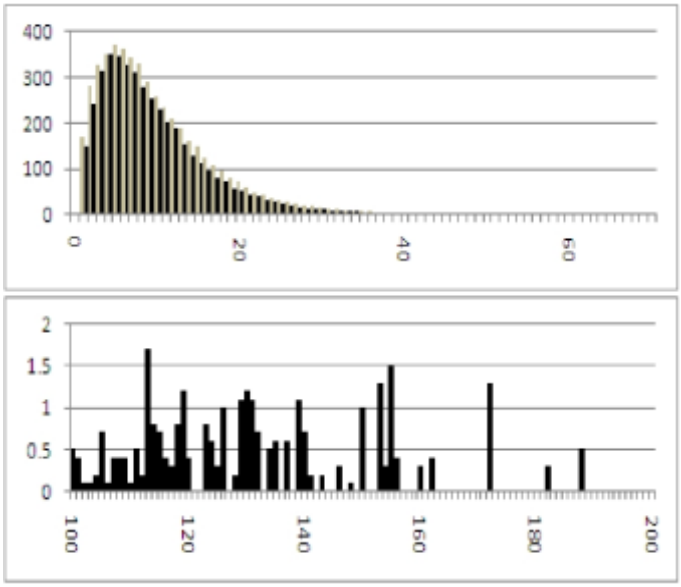

Fig. 1. Histogram of RNA molecules lengths for RNA recombination process turned off (gray) and on (black). N=50 000, P_{NF}=0.0001, P_{ND}=0.001, P_{LMC}=0.0002, P_{BB}=0.0001, P_{AT}=0.01, P_{LT}=0.005, P_{FP}=0.01, P_{SP}=0.9

Manuscript accepted for publication on August 27, 2010.

The scientific work reported in the paper was financed by Ministry of Science and Higher Education in Poland from funds for supporting science in 2008-2010, as a part of research the project number N N519 319035 coordinated by K. A. Cyran. A study was also supported by SUT BK 2010 and SUT BW 2010 activities

D. Myszor is with the Institute of Informatics at Silesian University of Technology, Gliwice, Akademicka 16, 44-100 , Poland (phone: 32-2372843; e-mail: dariusz.myszor@polsl.pl).

K. A. Cyran is with the Institute of Informatics at Silesian University of Technology, Gliwice, Akademicka 16, 44-100 , Poland (e-mail: krzysztof.cyran@polsl.pl).

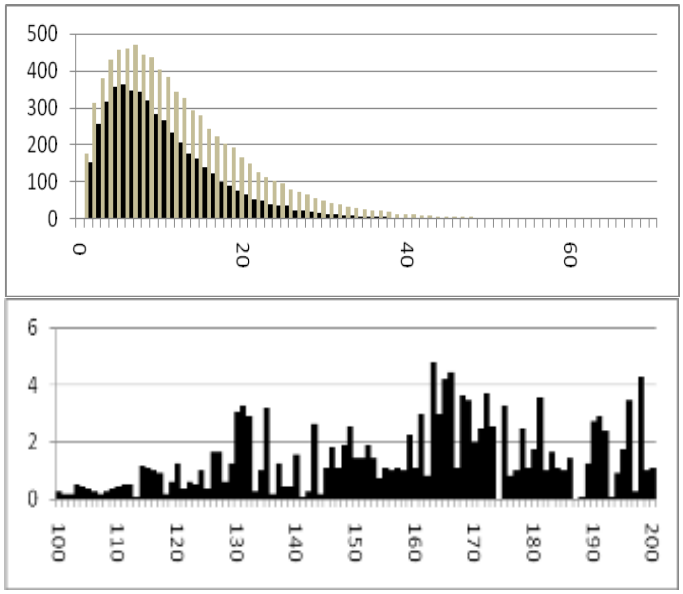

Fig. 2. Histogram of RNA molecules lengths for RNA recombination process turned off (gray) and on (black). N=100 000, P_{NF}=0.0001, P_{ND}=0.001, P_{LMC}=0.0002, P_{BB}=0.0001, P_{AT}=0.01, P_{LT}=0.005, P_{FP}=0.01, P_{SP}=0.9

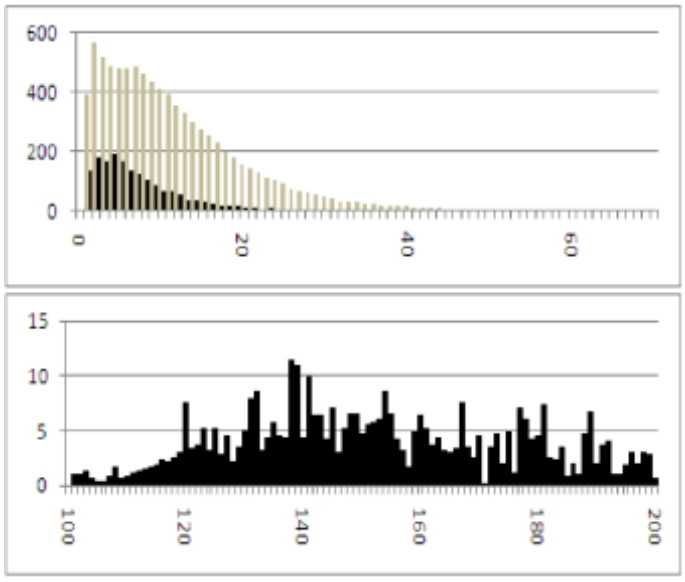

Fig. 3. Histogram of RNA molecules lengths for RNA recombination process turned off (gray) and on (black). N=100 000, P_{NF}=0.0001, P_{ND}=0.001, P_{LMC}=0.0002, P_{BB}=0.0001, P_{AT}=0.1, P_{LT}=0.005, P_{FP}=0.01, P_{SP}=0.9, P_{LT}=0.005, P_{FP}=0.01, P_{SP}=0.9

There are following types of RNA recombination:

- Non-enzymatic recombination: process in which two RNA chains join together with complementary nucleotides. In the next step each strand looses superfluous part in the cleavage reaction and then, through ligation reaction, strands became connected by phosphodiester bond[11] (Fig. 6.).

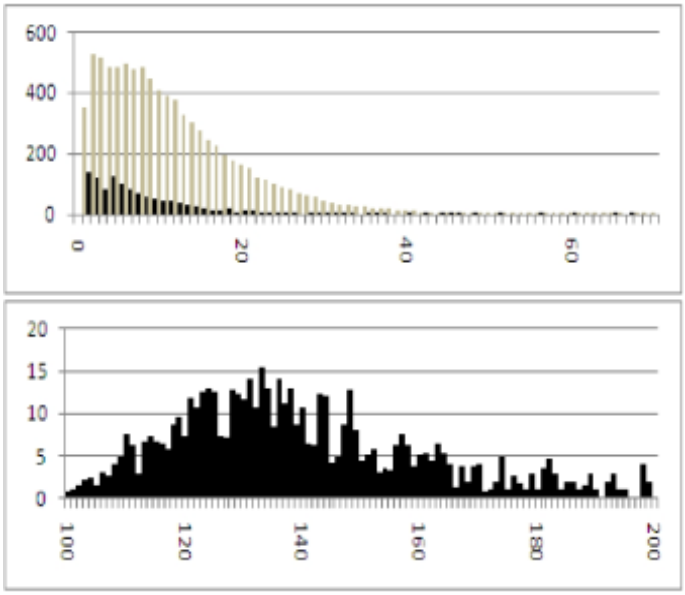

Fig. 4. Histogram of RNA molecules lengths for RNA recombination process turned off (gray) and on (black). N=100 000, P_{NF}=0.0001, P_{ND}=0.001, P_{LMC}=0.0002, P_{BB}=0.0001, P_{AT}=0.1, P_{LT}=0.05, P_{FP}=0.01, P_{SP}=0.9, P_{LT}=0.005, P_{FP}=0.01, P_{SP}=0.9, P_{LT}=0.005, P_{FP}=0.01, P_{SP}=0.9

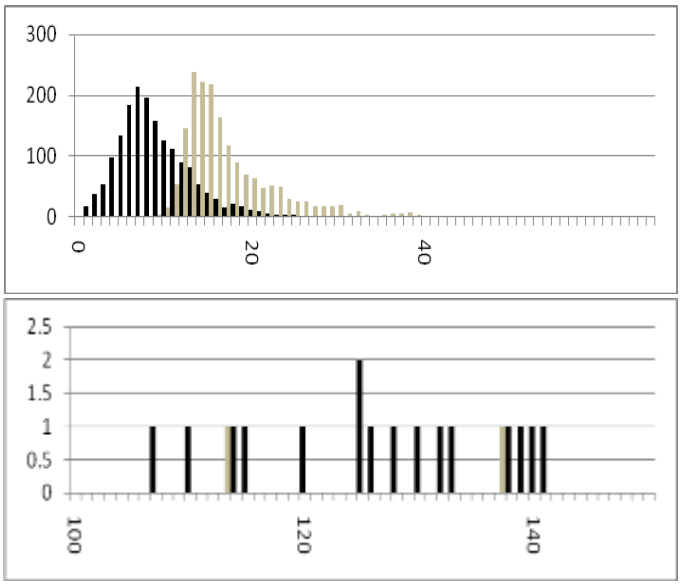

Fig. 5. Histogram of RNA molecules lengths in the presence of replicase sequence (9 nt. long) and RNA recombination. Data from 320 000 generation. RNA chains with replicase sequence or sequence complementary to replicase are gray and non-replicase is black. N=50 000, P_{NF}=0.0001, P_{ND}= 0.001, P_{LMC}=0.0002, P_{BB}=0.0001, P_{AT}=0.01, P_{LT}=0.005, P_{FP}=0.01, P_{SP}=0.9, P_{RB}=0.95, P_{RD}=0.05, P_{ATR}=0.95, P_{LTR}=0.9, P_{LT}=0.05, P_{FP}=0.01, P_{SP}=0.9, P_{LT}=0.005, P_{FP}=0.01, P_{SP}=0.9, P_{LT}=0.005, P_{FP}=0.01, P_{SP}=0.9

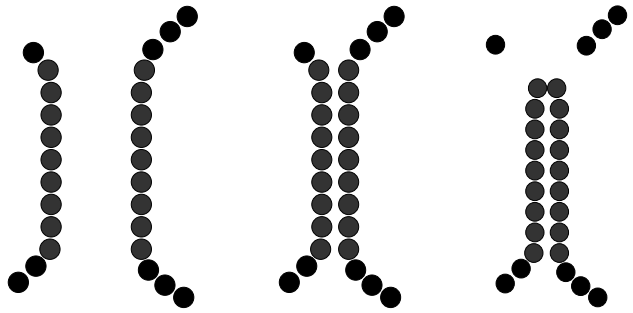

Fig. 6. Two polynucleotides strands with complementary nucleotides (gray), connected in non-enzymatic recombination process. Following steps are presented: polynucleotide approach , complementary parts attraction , cleavage and ligation reaction.

- Non-enzymatic template-directed recombination: there are short templates in the solution – RNA strands - to these RNA molecules other oligonucleotides might be attached with complementary parts. If two attached strands are located close enough to each other, on the template, they might recombine. During the recombination molecules loose superfluous part of chains through cleavage reactions and are joined in ligation reaction. According to laboratory experiments connected strands might tightly cling to the template or different formation might be created around the place of join like 1 or 3 nucleotides bulges, 2-3 internal loops[12] (Fig. 7.).

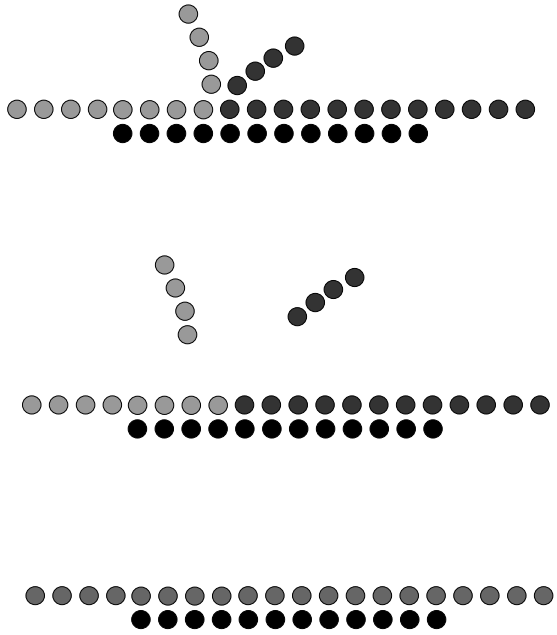

Fig. 7. Non-enzymatic template-directed recombination process. Two RNA strands (light and dark gray) attached to the template (black). Two strands become attached to the template (upper), in cleavage reaction loose superfluous parts (middle) and become connected in ligation reaction (lower).

- RNA directed recombination: there are oligonucleotides with catalytic activity that through binding processes can direct recombination of other strands in the solution[13].

Computer simulations play important role in many fields of science. With rapid rise in computational power constant drop of prices is connected. What is more new versions of software let us easily create more elaborated and sophisticated models. Up-to-date many models of the early life have been proposed, some of them base on mathematical equations ([14] – [16]), other on computer simulations (for example single strand model considered with respect to the complexity threshold [17] or the compartment model proposed by Niesert and modified by Myszor and Cyran [18]). In this paper we applied computer simulations to check influence of non-enzymatic template-direct recombination process on polynucleotides lengths in the RNA World.

II. Simulation Model

In order to conduct computer simulations we implemented and improved model described in W. Ma et al. 2007 (we call it basic model) [19]–[21]. Model bases on real chemical processes operating on RNA strands. Simulated processes take place on a flat two dimensional space divided into rectangular sectors (Fig. 8.). We assume that at the bottom there is a mineral surface that catalyzes polynucleotide formation, above a mixture of chemical substrates. Simulation begins with set of raw material constituents. Model describes phase of RNA world before cells creation. During the simulation of single generation, state of every constituent might be modified only once. The amount of building material in the system is constant (raw material + nucleotides) and is set at the beginning of the simulation. Authors of the model, in order to acquire simulation coefficients, searched for the rate of real chemical reactions. All constituents in the model are activated, we do not consider secondary structure of polynucleotides.

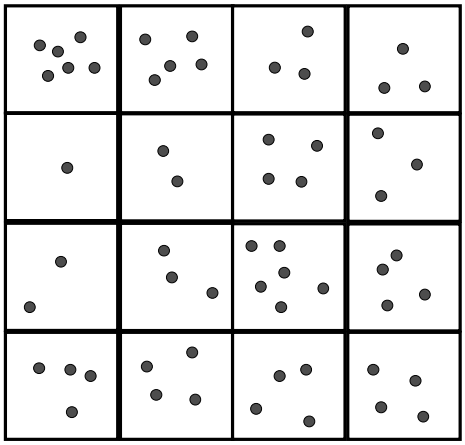

Fig. 8. Two dimensional surface, divided into rectangular sectors. Gray dots are constituents, only constituents in the same sector might react with each other.

A. Constituents types

There are following types of constituents in the system:

- Raw material: constituent that might become nucleotide. Recently experiments point out that nucleotides may be created spontaneously from mixture of substrates presented on early Earth (like 2-aminooxazole, phosphate, part of nucleobases [22]). In order to speed up the simulation process there is only one type of raw material constituent in the system.

- Nucleotide: represents four types of nucleotides (cytosine (C), guanine (G), adenine(A) and uracil (U)). It might become raw material constituent. Nucleotide may join to another nucleotide or polynucleotide in the process of mineral catalyzed synthesis of polynucleotides.

- Polynucleotide: set of nucleotides connected by phosphodiester bonds. It might become longer as an effect of mineral catalysed synthesis of polynucleotide, attach complementary nucleotides and polynucleotides (become the template), split into two chains as an effect of phosphodiester bond break.

- Template: polynucleotide which has a complementary strand attached by hydrogen bonds. It might attach other nucleotides and polynucleotides.

- Attached: RNA chain that is attached to the template. It might be connected with adjacent chain by phosphodiester bond in ligation process. It may be de-attached from the template, longer chains are less likely to be de-attached.

- Replicase: polynucleotide that contains replicase sequence. Replicase sequence is explicitly given at the beginning of the simulation. During simulation we search for replicase sequence in every polynucleotide in the system. Replicase itself has the same properties as other polynucleotides however when binded to other replicase (or strand containing sequence complementary to replicase) initializes and speeds up the process of complementary strand formation (by increase probability of molecule attachment and ligation reaction). It also decrease probability that attached strand drops from the template before formation of whole template's copy [23] – [25].

- Template with replicase binded: RNA chain with replicase polynucleotide binded. It has higher probability of complementary chains attachment, there is also higher probability of ligation of attached strands. If the whole template with binded replicase has a complementary sequence attached and all attached nucleotides are joined by phosphodiester bond with adjacent nucleotides then replicase detach complementary strand and drop from the template.

- Replicase binded: replicase might bind to strand containing replicase sequence or sequence complementary to replicase. Replicase binded to the template directs attachment of complementary strands and ligation of attached strand. Constituent with binded replicase become template with replicase binded. Replicase might drop from the template before complementary strand formation.

B. Simulated processes

We simulate following processes:

- Nucleotide formation: constituent of raw material might become nucleotide with probability P_{NF}. During the creation process we draw a type of nucleobase possessed by nucleotide.

- Nucleotide decay: with probability P_{ND} nucleotide might be broken up into building compounds and become constituent of raw material.

- Mineral catalyzed polynucleotide formation: clay was common mineral on early Earth. It might act as catalyser of polynucleotides formation. Elongation process bases on activated nucleotides and polynucleotides present in the solution. According to the current researches there is a possibility to create short RNA oligonucleotides up to 50 nucleotides long[10]. The probability of reaction is denoted as

$$P_{MCP} = P_{LMC} / L_P \ . \tag{1}$$

Where L_P is polynucleotide length and P_{LMC} is the probability of ligation by mineral catalysis of two nucleotides. Length of joined polynucleotide is incorporated into the equation because in order to be connected RNA strands must be aligned in correct way. Longer polynucleotides are less likely to have correct end to end orientation (Fig. 9.).

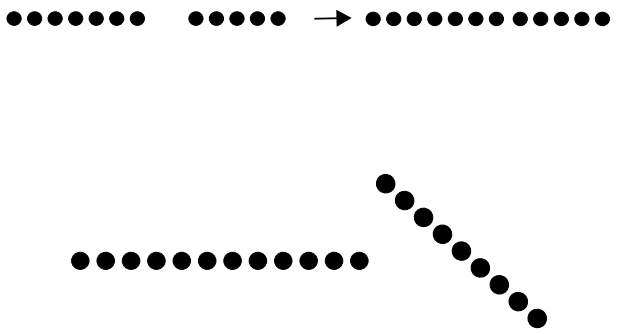

Figure 9. Mineral catalyzed polynucleotide formation. Only polynucleotide that are correctly aligned might react with each other (upper). Example of polynucleotides with incorrect end to end alignment (lower).

- Phosphodiester bond break: degradation process that leads to connection break between nucleotides in the strand. There might be many reasons of phosphodiester bond break as: hydrolysis, high temperature, radiation, chemical substances. Each phosphodiester bond might break with probability P_{BB}.

• Molecule attachment: polynucleotides and templates might attach nucleotides and polynucleotides with probability P_{AT} or P_{ATR} (for template with replicase binded). Whole sequence of attached component must be complementary to some part of the template strand (Fig 10.). There is a possibility of error, with probability P_{FP} nucleotide in attached sequence might not be complementary to respective template's nucleotide and RNA molecule might still be attached (Fig. 10.).

• Molecule de-attachment: at any time a component might be de-attached from the template with the probability

$$P_{DA} = P_{SP} / n. \quad (2)$$

Where n is a number of attached nucleotides and P_{SP} is the probability of the nucleotide separation.

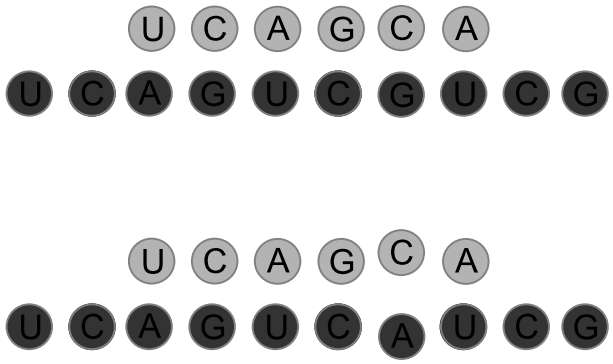

Figure 10. Template (dark gray) with attached polynucleotide (light gray) (upper). Attracted polynucleotide has not complementary nucleotide (lower).

• Ligation: in this process two adjacent strands attached to the template become connected. Ligation took place with probability P_{LT} for molecules attached to the template and with probability P_{LTR} for molecules attached to template with replicase binded.

• Replicase bind: with probability P_{RB} replicase might bind to the chain containing replicase sequence or sequence complementary to replicase.

• Replicase drop: replicase might drop from the template during complementary strand formation with probability P_{RD}. Substrate stays on the template. Template with replicase binded becomes template and acquire default set of probabilities.

• Migration: space is divided into a grid of rectangular sectors, molecules might migrate to adjacent cell with probability

$$P_M = P_{MN} / w^{1/3}. \quad (3)$$

Where w is weight of molecule and P_{MN} is probability of move of constituent with weight equal to 1 (nucleotide and raw material constituent). Target sector must by adjacent by wall to current During the simulation of single generation we mark a component that should be moved to adjacent cells. At the end of generation simulation, after computation of each sector's state, we move the components.

There are two main types of reactions in the system:
• reactions that involve only one constituent (for example nucleotide formation)

• reactions that involve two molecules (for example polynucleotide formation).

During the simulation of each generation (simulation pass) we take each constituent in the system and check whether it takes place in some chemical reaction. If it is true, then depending on the reaction type we modify constituent state (for reactions that involves only one constituent) or search for another molecule to react with (for reactions that involves two constituents). As we said before, during the simulation of each generation, constituent's state might be modified only once, so we mark this second molecule as modified and do not use it any more during this simulation pass. Order in which we check constituents is connected with constituents' location within sectors. For simplicity we use single number to describe this location. In order to make our model closer to the real world, we mix constituents within sectors after each simulation pass. Because we wanted to limit computational impact of this phenomena we change location of only 30% of molecules in the system.
Our simulation are based on stochasticism we used Mersenne Twister pseudo random number generator. It ensure long period and high speed of pseudorandom values generation[26].
Simulation of every sector demands heavy computations. Fortunately during the simulation of every generation there is a time when every sector might be processed independently. In order to achieve results in reasonable time we execute computation of every sector in parallel, so when we run simulation on computer with multi-core processor we get all available computational power.

III. Recombination

RNA recombination processes are new hope on the field of the RNA world theory. There are publications that describe these processes and speculate about possible benefits, however up to this time none of them has incorporated recombination into such exact computer model of the RNA world. In this model we implemented non-enzymatic template-directed recombination. The recombination process in this version is similar to the process of non-enzymatic template-directed replication. At the beginning substrates chains are attached to the template. Contrary to the template direct replication, implemented in the basic model, not whole sequence of attached chain must be complementary to the template sequence. We assume that sequence might be

attached to the template and recombined with adjacent strand if it has at least four complementary nucleotides in a row with the template sequence. In order to be able to compare outcomes returned by model with and without recombination, we took probabilities of component attraction (P_{AT}) and molecules conjunction (P_{LT}) from template directed replication and applied them to recombination processes also, as in the temple direct replication, there is a room for error. If a nucleotide from substrate sequence is not matching respective nucleotide from template sequence it might be accepted with probability P_{FP}. Chains located close enough on the template might recombine. During the recombination dangling ends of recombining chains are being cut through cleavage reaction and attached strands became connected through the ligation reaction. Strands after the connection might closely adjoin to the template, but there is also a possibility for a creation of more complex structures, in the area of recombined strands conjunction like[12] (Fig. 11.) :

- bulge loops, of different size, on attached strand
- symmetric or asymmetric loops on attached strand and on the template

We take into account this phenomena in our simulation and allow for emergence of such constructions. Probabilities of the creation of these structures are based on real experiments.
Simulation of the recombination have a great impact on a computer model performance, in order to recombine two RNA chains there is a need to find complementary parts of chains with the template. In order to speed up the search process we used suffix tree algorithm. It is a time efficient algorithm that let us quickly and easily locate common chains' sequences.

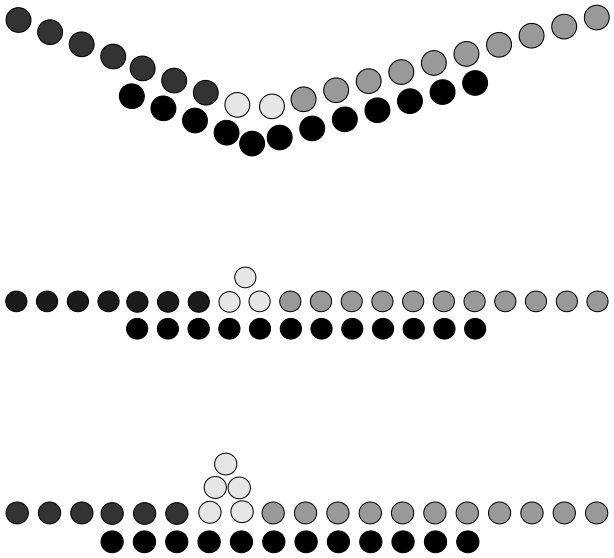

Figure 11. Different formations, around the place of recombined polynucleotides conjunction, after non-enzymatic temple directed RNA recombination process.

IV. Results

At the beginning we simulated model without RNA recombination in order to check whether we can obtain the same results as authors of the basic model. Simulations with RNA recombination begins later. We also checked the influence of RNA recombination on scenario with replicase strands present in the system.
Every simulation starts with set of raw material constituents. In order to achieve trustworthy results first we run simulation for 100 000 generation. Our observations indicate that during this period the outcomes are stabilising. Then we keep running simulation process for 900 000 generations. We collect data from every generation that could be divided by 10 000, for every chain length we save the number of representatives. After the simulation ends for each RNA chain length that occurred during the simulation, we count mean number of representatives (we use data from saved generation). Results are presented in the histogram. Default simulation coefficients are: grid size 10x10, P_{NF}=0.0001, P_{ND}=0.001, P_{LMC}=0.0002, P_{BB}=0.0001, P_{AT}=0.01, P_{LT}=0.005, P_{FP}=0.01, P_{SP}=0.9, P_{RB}=0.95, P_{RD}=0.05 (we used the same probabilities notations and values as in Ma et al., 2007). In order to check the influence of the maximal number of constituents in the system we conducted simulations for different number of constituents in the system N=50 000 and N=100 000. For these coefficients the maximal length of acquired strands is close to 50 nucleotides, so similar to the results obtained in laboratory experiments.

A. Non-enzymatic template-directed ligation

We conducted a set of simulations for default simulation probabilities. For N=50 000 and N=100 000 (Fig. 1, Fig. 2) there is a visible reduction of the number of representatives of shorter oligonucleotides (length < 60 nt.), however significantly longer sequences appear in the solution (length > 100 nt.). It is worth to mention that in the scenario without RNA recombination such long sequences do not occur. This effect might be hard to notice for scenario with lower number of constituents in the system, however when we increase the number of constituents to N=100 000 it is much easier to notice. For scenario with more constituents in the system more long strands are created.
Current researches suggest that life might emerged in a frozen solution[27], [28]. In a proper temperature the rate of ligation reaction is increasing contrary to the rate of phosphodiester bond breaking. What is more, in lower temperatures fewer intermolecular reaction might be required to stabilize RNA complexes. In order to simulate this phenomena we increased P_{AT} to 0.1 (Fig. 3). In the next step we increased P_{LT} to 0.05 (Fig. 4). The results clearly point out that recombination process might be important phenomena in a frozen solution and leads to the formation of much longer nucleotides than in the model without recombination.

B. Replicase in the model with non-enzymatic template-directed ligation

We wanted to examine influence of the RNA recombination on the replicase emergence and spread in the system. We assumed that the replication process of template with replicase binded is directed by replicase and is not subject to recombination processes. We conducted simulation for different lengths of replicase sequence. Outcomes point out that replicase might still emerge and spread in the system (Fig. 5). What is more long sequences created by recombination are also present in the solution, however the influence of recombination is limited. This phenomena might be an effect of the limitation of the number of building constituents in the system. Oligonucleotides containing replicase sequence or sequence complementary to replicase, are created in much more faster and efficient way, than regular polynucleotides. The more replicases sequences in the solution, the faster new replicases are created, thus the number of molecules available for other reactions is limited.

V. Conclusions

The process of non-enzymatic template-directed RNA recombination has an influence on chains lengths in the RNA World. This phenomena limits the number of shorter sequences, however it might lead to the creation of significant longer sequences. These longer RNA chains are very important in the origins of life, because they could have catalytic abilities and in longer perspective lead to further RNA strands elongation. What is more in the presence of RNA recombination process, we were able to obtain replicase of the same length as in model without recombination. Emergence of replicase limits the influence of RNA non-enzymatic template directed recombination process and leads to overtaking of RNA polynucleotides population by oligonucleotides containing replicase pattern or sequence complementary to replicase.

We assume that RNA recombination should be considered by researchers in trials of explanation of life origins and during creation of RNA World models. These processes are especially interesting in frozen solutions – in lower temperatures chains are more stable and probability of oligonucleotide attachment and ligation are rising.

Our researches are not over yet. In the next step we want to incorporate into the model other types of RNA recombination and investigate influence of these processes on model's ability to create long RNA molecules, and polynucleotides containing replicase sequence.

Acknowledgment

The authors would like to thank to Prof. Marek Kimmel from Department of Statistics at Rice University in Houston TX, USA, for long discussions and advices concerning origins of life problems.

References

[1] L. E. Orgel, "Prebiotic chemistry and the origin of the RNA world", Crit. Rev. Biochem. Mol. Biol. vol. 39, 2004, pp. 99–123.

[2] G. F. Joyce , "Evolution in an RNA world", Orig. Life Evol. B vol. 36, 2005, pp. 202–204.

[3] J. C. Cochrane, S. A. Strobel, "Riboswitch effectors as protein enzyme cofactors", RNA vol. 14, 2008, pp. 993-1002.

[4] T. A. Steitz, P. B. Moore, " RNA, the first macromolecular catalyst: the ribosome is a ribozyme", Trends Biochem. Sci. vol. 28, 2003, pp. 411–418.

[5] G. F. Joyce, L. E. Orgel , "Progress toward understanding the origin of the RNA world", in The RNA world, vol. 3, eds. R.F. Gesteland et al, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2006, pp. 23–56.

[6] J. P. Ferris, "Montmorillonite-catalysed formation of RNA oligomers: The possible role of catalysis in the origins of life", Philos. Trans. R. Soc. Lond. B Biol. Sci. vol. 361, 2006, pp. 1777–1786.

[7] J. P. Ferris, " Montmorillonite catalysis of 30–50 mer oligonucleotides: laboratory demonstration of potential steps in the origin of the RNA world", Orig. Life Evol. Biosph. vol. 32, 2002, pp. 311–332.

[8] J. P. Ferris, G. Ertem, "Montmorillonite catalysis of RNA oligomer formation in aqueous solution. A model for the prebiotic formation of RNA", J. Am. Chem. Soc. vol. 115, 1993, pp. 1227012275.

[9] J. P. Ferris, A. R. Hill, R. Liu , L. E. Orgel, "Synthesis of long prebiotic oligomers on mineral surfaces", Nature vol. 381, 1996, pp. 59-61.

[10] W . Huang, J. P. Ferris, "One-step, regioselective synthesis of up to 50-mers of RNA oligomers by montmorillonite catalysis", J. Am. Chem. Soc. vol. 128, 2006, pp. 8914–8919.

[11] A. V. Lutay, M. A. Zenkova, V. V. Vlassov, "Nonenzymatic Recombination of RNA: Possible Mechanism for the Formation of Novel Sequences", Chem. and Biod. vol. 4, 2007, pp. 762 – 767.

[12] S. Y. Nechaev, A. V. Lutay, V. V. Vlassov, M. A. Zenkova, "Non-Enzymatic Template-Directed Recombination of RNAs", Int. J. Mol. Sci. vol. 10, 2009, pp. 1788-1807.

[13] W. E. Draper, E. J. Hayden, N. Lehman, " Mechanisms of covalent self-assembly of the Azoarcus ribozyme from four fragment oligonucleotides", Nucleic Acids Res. vol. 36, 2008, pp. 520-31.

[14] M. A . Nowak, H. Ohtsuki, "Prevolutionary dynamics and the origin of evolution", Proc. Natl Acad. Sci. USA, vol. 105, 2008, pp. 14924-14927.

[15] H. Ohtsuki, M. A. Nowak, "Prelife catalysts and replicators", Proc. R. Soc. B vol. 276, 2009, pp. 3783–3790.

[16] M. Manapat, H. Ohtsuki, R. Bürger, M. A. Nowak, "Originator dynamics", J. Theor. Biol. vol. 256, 2009, pp. 586–595.

[17] K. A. Cyran, " Information amount threshold in self-replicating RNA-protospecies: branching processes approach", Intern. Journal of Math. and Comp. in Sim, vol. 3(1), 2009, pp. 20-29.

[18] D. Myszor , K. A. Cyran, "Estimation of the number of primordial genes in compartment model of RNA World", in Advances in Intelligent and Soft Computing, vol. 59, K. A. Cyran et al. (Eds.), Springer, 2009, pp. 151-161.

[19] W. T. Ma, C. W. Yu, "Intramolecular RNA replicase: Possibly the first self-replicating molecule in the RNA world", Orig. Life Evol. Biosph. vol. 36, 2006, pp. 413–420.

[20] W. Ma, C. Yu, W. Zhang, " Monte Carlo simulation of early molecular evolution in the RNA World", Biosystems vol. 90, 2007, pp. 28-39.

[21] W. Ma, C. Yu, W. Zhang, J. Hu, "Nucleotide synthetase ribozymes may have emerged first in the RNA world", RNA vol. 13, 2007, pp. 2012–2019.

[22] J. W. Szostak, "Systems chemistry on early Earth", Nature vol. 459, 2009, pp. 171-172.

[23] W. K. Johnston, P. J. Unrau, M. S. Lawrence, M. E. Glasner, D. P. Bartel, "RNA-catalyzed RNA polymerization: Accurate and general RNA-template primer extension", Science vol. 292, 2001, pp. 1319–1325.

[24] H. S. Zaher, P. J. Unrau, "Selection of an improved RNA polymerase ribozyme with superior extension and fidelity", RNA vol. 13, 2007, pp. 1017–1026.

[25] P. A. Monnard, J. W. Szostak, "Metal-ion catalyzed polymerization in the eutectic phase in waterice: A possible approach to template directed RNA polymerization", J. In Org. Biochem. vol. 102, 2008, pp. 1104-1111.

[26] M. Matsumoto, T. Nishimuram, "Mersenne twister: a 623-dimensionally equidistributed uniform pseudo-random number generator", ACM TOMACS vol. 8, 1998, pp. 3-30.
[27] S. A. Kazakov, S. V. Balatskaya, B. H. Johnston, " Ligation of the hairpin ribozyme in cis induced by freezing and dehydration", RNA vol. 12, 2006, pp. 446–456.
[28] A. V. Vlassov, B. H. Johnston, L. F. Landweber, S. A. Kazakov, "Ligation activity of fragmented ribozymes in frozen solution", Nucleic Acids Res. vol. 32, 2004, pp. 2966-2974.

Dariusz Myszor was born in Pszczyna, Poland in 1983. He received MSc degree in computer science (2007) from the Silesian University of Technology SUT, Gliwice, Poland.
Currently he is a PhD student at Silesian University of Technology and is involved in scientific and didactic activities of the Institute of Informatics at SUT.
His current research interests are focused in such areas as: artificial neural networks, computational population genetics, computer simulations, early life and bioinformatics.

Krzysztof A. Cyran was born in Cracow, Poland, in 1968. He received MSc degree in computer science (1992) and PhD degree (with honours) in technical sciences with specialty in computer science (2000) from the Silesian University of Technology SUT, Gliwice, Poland. His PhD dissertation addresses the problem of image recognition with the use of computer generated holograms applied as ring-wedge detectors.

He has been an author and co-author of more than 90 technical papers in journals (several of them indexed by Thomson Scientific) and conference proceedings with total number of citations exceeding 140. These include scientific articles like: K. A. Cyran and A. Mrózek, "Rough sets in hybrid methods for pattern recognition," *Int. J. Intel. Syst.*, vol. 16, 2001, pp. 149-168, K. A. Cyran and M. Kimmel, "Interactions of Neanderthals and modern humans: what can be inferred from mitochondrial DNA?" *Math. Biosci. Eng.*, vol. 2, 2005, pp. 487-498, K.A. Cyran and M. Kimmel "Alternatives to the Wright-Fisher model: the robustness of mitochondrial Eve dating" *Theor. Pop. Biol.* 2010 [in press] as well as a monograph: U. Stańczyk, K. Cyran, and B. Pochopień, *Theory of Logic Circuits*, vol 1 and 2, Gliwice: Publishers of the Silesian University of Technology, 2007. Dr. Cyran (in 2003-2004) was a Visiting Scholar in Department of Statistics at Rice University in Houston, US. He is currently the Assistant Professor and the Vice-Head of the Institute of Informatics at Silesian University of Technology, Gliwice, Poland. His current research interests are in image recognition and processing, artificial intelligence, digital circuits, decision support systems, rough sets, aviation and aeronautics, computational population genetics and bioinformatics.

Dr. Cyran has been involved in numerous statutory projects led at the Institute of Informatics and some scientific grants awarded by the State Committee for Scientific Research. He also has received several awards of the Rector of the Silesian University of Technology for his scientific achievements. In 2004-2005 he was a member of International Society for Computational Biology. Currently he is a member of the Editorial Board of Journal of Biological Systems, member of the Scientific Program Committee of WSEAS international conferences in Malta (ECC'08), Rodos (AIC'08, ISCGAV'08, ISTASC'08) and multiconference in Crete (CSCC'08) as well as a reviewer for Studia Informatica and such journals indexed by Thompson Scientific as: Optoelectronic Review, Mathematical Biosciences and Engineering, Journal of Biological Systems, and Neurocomputing.