

Modeling a primordial, non-enzymatic RNA replication in the early Earth

Carla Alejandre¹, Adrián Aguirre-Tamaral², Carlos Briones¹ and Jacobo Aguirre^{1,3}

¹Centro de Astrobiología, CSIC-INTA, Madrid, Spain

²Centro de Biotecnología y Genómica de Plantas (CBGP), UPM-INIA, Madrid, Spain

³Grupo Interdisciplinar de Sistemas Complejos (GISC), Madrid, Spain

Life appeared on Earth around 3.800 million years ago, not long after our planet became habitable. The hypothesis of the *primordial soup* describes a very young planet in which prebiotic chemistry could have progressively increased the available molecular complexity in several out-of-equilibrium environments such as surface lakes, sea coasts, water-mineral interfaces, oceanic hydrothermal vents, etc. In some of those scenarios, the accumulation of organic compounds and the availability of energetic sources laid the foundations for the emergence of life.

One of the widely accepted hypothesis related to the origin of life, widely supported by experimental data, is the *RNA world*. It suggests that life was originated in an environment in which informational and functional RNA molecules were able to self-replicate (through the activity of RNA ribozymes). Later evolution of these primordial RNA populations would give rise to the decoupling of genotype and phenotype in the RNA/protein and DNA/RNA/protein worlds [1]. However, the sophisticated machinery associated with current RNA polymerase enzymes could not emerge randomly from those initial organic compounds that were available in the stage of prebiotic chemistry. Instead, a step-wise, ligation-based modular evolution of short RNA sequences seems a more plausible pathway for the appearance of the first RNA molecules with enzymatic properties [2]. Nevertheless, even modular evolution of RNA requires the presence of an up-to-now unknown replicative mechanism to guarantee the availability of copies of specific RNA sequences (oligoribonucleotides) in which selection can act.

In this work we describe the development of a computational model to simulate the polymerization of single ribonucleotides and a subsequent non-enzymatic, template-dependent replication mechanism for the primordial RNA molecules. These processes would have arisen in a confined space such as the interphase between an aqueous solution and the interlayers of clay minerals, an environment known

to favor RNA polymerization [3, 4]. In our simulations, two RNA polymerization processes are described: (i) surface-dependent, random polymerization of ribonucleotides, and (ii) template-dependent polymerization thanks to RNA complementary base pairing (RNA replication). This conceptually simple in silico model allows us to test how environmental conditions can affect the length and fidelity of RNA copies, as well as to study how the efficiency of the RNA replicative phenomenology depends on the parameters of the system, such as the amount of available ribonucleotides, size of genetic alphabet, the strength of chemical bonds or environmental fluctuations. Our results point towards oscillatory environments as necessary requirements for the formation of efficient copies of long enough RNA sequences, in agreement with recent works in the field that suggest that fluctuating environments were necessary for life to emerge [5].

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