

RECYCLING OF EARLY FUNCTIONAL BIOPOLYMERS AND IMPLICATIONS FOR THE EMERGENCE OF LIFE. S.I. Walker^{1,2,3}, ¹School of Earth and Space Exploration, Arizona State University; ²Beyond Center for Fundamental Concepts in Science, Arizona State University; ³Blue Marble Space Institute of Science, Seattle WA.

The availability of prebiotic molecular building blocks was likely limited on the early Earth. Feasible prebiotic pathways to synthesize biologically relevant precursor molecules were impeded both by mixtures of products formed and by product yields [1]. The large variety of molecules and meager amounts of the right products have led some to argue it would make it improbable for any reproducing system to arise spontaneously in a prebiotic soup, and thus that more favorable conditions would have been possible in a recycling chemical system capable of a recurrent use of organic compounds, fed by an external energy supply [2]. Accordingly, herein I consider the evolutionary potential of systems with a finite pool of monomers that must be recycled through polymer degradation to replenish resources available for polymer assembly, and assess the potential for such systems as candidate chemistries for the origin of life. Our previous results have shown that recycling can both enhance the search rate for functional sequences [3], and enable selection of functional biopolymers [4]. Here, I specifically report results on two distinct classes of models, based on replicators and catalytic networks respectively, where recycling is necessary to mediate the transition to more life-like states of chemical organization and compare and contrast their properties.

Recycling and the Emergence of Replicators. The emergence of replicators is considered to be a critical step in the emergence of life. I discuss the results of a kinetic Monte Carlo model demonstrating the spontaneous emergence of functionally fit replicators [5]. In the model, the fitness of replicators is determined by two factors: (1) a functional trade-off between stability and replicative efficiency and (2) resource availability. I show that recycling via degradation of polymers is essential to the transition to selection for function, where recycling enables both a rapid search rate for functional biopolymers (Fig. 1) and the restructuring of the distribution of resources in the system to accommodate their selection.

Recycling and the Emergence of Catalytic Networks. In a second model, also implemented with a kinetic Monte Carlo algorithm, I demonstrate that the spontaneous emergence of catalytic networks, based on ligation and cleavage of sequences, is similarly-dependent on degradative recycling in systems with a finite sup-

ply of resources. The transition to catalytic selection demonstrates analogous features to that for selection for replication, including a transition rate dictated by the rate of recycling and the existence of an abrupt transition to catalytic selection, which is mediated by a restructuring of the distribution of resources.

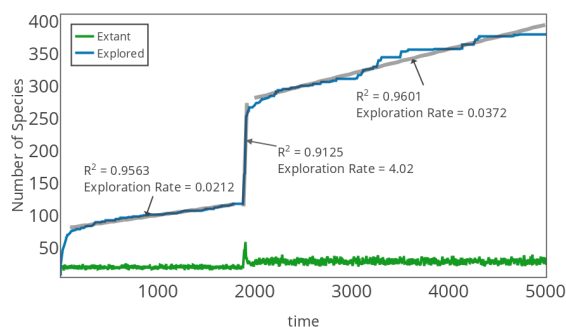


Fig. 1: Time evolution of the exploration of novel diversity in a model demonstrating the spontaneous emergence of replicators. Exploration rate is dependent on the sequence-degradation rate and is highest during the transient regime where replicators first emerge and restructure the system (here at $t \sim 2000$). Adopted from [5].

Conclusions. The results indicate that for systems with a finite supply of resources, both the emergence of functional replicators and of catalytic networks are strongly dependent on the rate of degradative recycling of the relevant biopolymers. Since recycling rates are in turn dependent on both the chemical properties of early biopolymers (e.g., liability of backbone linkages [1]) and the environment, the results place new constraints on the relevant prebiotic chemistries. I thus discuss these implications for identifying and characterizing the chemistries that may have first given rise to life.

References: [1] Engelhart, A.E., and Hud, N.V. (2010). Cold Spring Harb. Perspect. Biol. 2, a002196. [2] King, G.A. (1982). Biosystems 15, 89–97. [3] Vaidya, N., Walker, S.I. and Lehman, N. (2013) Chem. Biol. 20, 241. [4] Walker, S.I., Grover, M. and Hud, N.V. *PLoS One* 7, e34166. [5] Mathis, C., Bhattacharya, T. and Walker, S.I., *submitted*.