THEORY: EVOLUTION OF PROTOMETABOLIC SYSTEMS

The Divergence and Natural Selection of Autocatalytic Primordial Metabolic Systems

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Abstract The diversity of the central metabolism of modern organisms is caused by the existence of a few metabolic modules, combination of which produces multiple metabolic pathways. This paper analyzes biomimetically reconstructed coupled autocatalytic cycles as the basis of ancestral metabolic systems. The mechanism for natural selection and evolution in autocatalytic chemical systems may be affected by natural homeostatic parameters such as ambient chemical potentials, temperature, and pressure. Competition between separate parts of an autocatalytic network with positive-plus-negative feedback resulted in the formation of primordial autotrophic, mixotrophic, and heterotrophic metabolic systems. This work examined the last common ancestor of a set of coupled metabolic cycles in a population of protocells. Physical-chemical properties of these cycles determined the main principles of natural selection for the ancestral Bacteria and Archaea taxa.

Keywords Autocatalytic network \cdot Feedback \cdot Chemical potentials \cdot Phase diagrams \cdot Natural selection \cdot Ancestral metabolism \cdot Last common bacterial (archaeal) ancestor

Introduction

The metabolism of living systems parallels the biochemical homeostatic networks organized by negative-plus-positive feedback. In these networks, the primary metabolism corresponds with a minimal feedback system (Tsokolov 2010). The organization of biological feedback loops has been previously described (Eigen and Schuster 1979; Kauffman 1993), and they are believed to be the common denominator for all subsequent forms of life following their appearance (Lahav et al. 2001). Theoretical models of ancestral biochemical autocatalytic systems have been developed for more than 30 years (e.g. Eigen 1971; King 1978; Dyson

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