

- 3P268 プロテノイド・マイクロソフィアが存在する熱水環境下でのアミノ酸の重合  
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 Prebiotic oligomerization of amino acids in protenoid maicrosphere in hydrothermal environments  
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We have already attempted an experimental model simulating seawater circulation in the vicinity of hydrothermal vents in the primitive ocean. We found that the oligomeric yields from glycine increased in the presence of three different kinds of lipid vesicles made of unsaturated fatty acids, saturated fatty acids and phospholipids. In this experiment we used a flow reactor constructed to simulate the pressure and temperature conditions of circulating water in a hydrothermal environment, and to examine the role protenoid maicrosphere might have played in the synthesis of oligopeptides from amino acids. Protенoid maicrosphere was constructed from thermal heterocopolymers of L-aspartic acid and L-proline. We heated a mixture of 50 mmol L-aspartic acid and L-proline without water at 180 degree for 6hr in a 50ml Teflon inner vessel covered with a stainless steel outer vessel and the suspension of thermal heterocopolymers was made by adding distilled water 50mL. Identification of the oligomeric products was subjected to an HPLC analysis. We observed that a yield of diglycine in the presence of protенoid maicrosphere was increased. However, enhancement of oligomerization of glycine was relatively low compered with in the presence of three kinds of lipid vesicles.

- 3P270 抽象原始多細胞系における代数方程式を用いた最大多様性パターンの解析  
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- 2aB13 Analysis of (a)periodic pattern with the highest cell-type diversity in the primitive multicells by algebraic equations  
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The development of a multicellular organism is a dynamic process. Starting with one or a few cells, the organism develops into different types of cells with distinct functions. We have constructed a simple model by considering the cell number increase and the cell-type order conservation, and have assessed conditions for cell-type diversity. This model is based on a stochastic Lindenmayer system with *cockroach-leg* cell-to-cell interactions for three types of cells. In the present model, we have successfully derived complex but rigorous algebraic relations between the proliferation and transition rates for high cell-type diversity by using algebraic methods such as quantifier elimination (QE). In virtue of the rigorous equations, it has been revealed that the pattern with the highest cell-type diversity is usually aperiodic and is periodic only under specific conditions. Such aperiodic pattern has self-similarity, which seems to be related to self-reproduction. These facts may shed some lights on emergency of primitive multicells.

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- 3P269 配列空間における構造自由エネルギー地形の描像  
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 Conformational Free Energy Landscapes in Sequence Space for a Certain Protein Conformation  
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Functional proteins, that possess enzymatic activity or receptor-binding ability, evolved toward acquiring not only the activity inherent in a molecule but also the emergence frequency at equilibrium and folding ability. Therefore, the molecular fitness landscapes should be considered in two aspects: one is the landscape of molecular activity and the other is the landscape of the emergence frequency or folding ability. We focused on the fraction  $f$  of a given reference conformation in an ensemble of polypeptide conformations at equilibrium and examined statistical properties of a "conformational free energy landscape", which is defined by assigning values of the natural logarithm of  $f$  ( $\ln f$  corresponds to the conformational free energy for the reference conformation) into the amino acid sequence space. The free energy landscape was analyzed in the theoretical framework of Kauffman's NK landscape model, in which a parameter  $k$  governs the degree of the ruggedness on the landscape. For a given landscape, we introduced the "apparent  $k$ -value",  $k_{app}$ , which is determined by exploring local fitness distributions and fitting theoretical equations onto those fitness data. Our conclusion is as follows: if the energy function for polypeptides is given by a  $(1+k)$ -body potential, the free energy landscape takes  $k_{app}=k$ . This theoretical prediction was confirmed numerically by computer experiments by using a diamond lattice model.

- 3P271 リボソーム内自己複製系の構築  
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 RNA-protein self-replicating system in liposome  
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In all living systems, the genome is replicated by proteins encoded within the genome itself. We constructed a simplified self-replicating system in cell-size liposomes, which can conduct this universal reaction within a microcompartment bounded by a lipid bilayer. The self-replicating system was assembled using one template RNA sequence as an information molecule and an in vitro translation system reconstructed from purified translation factors as the machinery for decoding the information. In the in vitro translation system, the catalytic subunit ( $\beta$  subunit) of Q $\beta$  replicase, an RNA-dependent RNA polymerase, is synthesized from template RNA encoding the protein. The replicase thus produced in turn replicates the template RNA used for its production. We designated this as RNA-protein self-replication reaction. First, we show the kinetic behavior of the self-replication reaction in vitro. Then, we show expandability, where a new functional gene is incorporated into the RNA sequence to allow the self-replicating system to exhibit additional phenotypes (functions). Finally, we show that the self-replication reaction can be encapsulated and performed in cell-size liposomes. This in liposome RNA-protein self-replicating system is one of the simplest such systems available, consisting of only 144 gene products, where the information and the function for its replication are encoded on different molecules and are compartmentalized into the microenvironment for evolvability.