ness landscape of promoter sequences, our result suggested a following image of the landscape: a high sharp peak (corresponding to the final survivor) and a not-so-high but very broad hill, although we need further study to confirm this image. We also report about the competition experiment between the optimal promoter obtained and the natural &p;# 2.5 promoter.

1P284
数値計算を持つ環境応答ダイナミクス: エタノールストレス環境下での大腸菌人工進化実験における網羅的表現型/遺伝子型解析

Environmental adaptation over multiple time scales: comprehensive expression/mutation analysis of evolved E. coli under ethanol stress

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Advances of technologies for comprehensive analysis now make it possible to reveal the phenotypic and genetic changes responsible for the adaptive evolution. Such detailed information of evolutionary traits provides a basis for understanding intra-cellular dynamics with multiple time-scales, including environmental response, adaptation, and evolution. In this study, we performed parallel evolution experiments of Escherichia coli under 5% ethanol stress condition. After cultivation of more than 1000 generations (2500 hours), we obtained 6 ethanol-tolerant strains independently, which exhibited about 2 folds increase in specific growth rates compared to the parent strain. We performed comprehensive gene expression analysis of these tolerant strains to analyze phenotypic changes occurring during the adaptive evolution, and found that several gene functions were significantly up- or down-regulated. Furthermore, single-nucleotide substitutions in the tolerant strain’s genome fixed during the adaptive evolution were analyzed by microarray-based resequencing experiments, and we found that the number of fixed mutations were less than 10 in some tolerant strains, suggesting that the phenotype of ethanol tolerance was not caused by genomic mutations, instead it was due to environmental adaptation having long-time-cale occurred without genomic mutations. Based on these comprehensive phenotypic/genetic data, the relationship between adaptive dynamics over different time scales will be discussed.

1P285
遺伝子型-表現型型応対戦略から見た初期開発系の起源へのアプローチ

An approach towards the origin of primitive translation system from the viewpoint of genoype-phenotype linking strategy

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As one of the post-genome era problems, an artificial minimum cell has been investigated in recent years, and the first trial was reported. The minimalization problem has had an ambiguity about the setup of the “ecological” environment, especially when one treated a heterotrophic cell. And this ambiguity will become inaccessible in the study of the origins of life. For example, how the translation system was emerged in a cell on the Earth? Eigen’s hypercycle theory was a plausible answer to this question [1]. We found that there is an alternative way to introduce the Darwinian evolution into the hypercycle theory from a point of view of genotype-phenotype linking strategy [2]. In order to link DNA or RNA (genotype) to protein (phenotype), there is the virus-type strategy in addition to the cell-type one. In evolutionary molecular engineering, the virus-type strategy (e.g. phage display) is more powerful than the cell-type in the selection of single function of a protein. Thus, we tried to examine which strategy is more efficient in the evolution of a primitive translational activity, using a stochastic mathematical model for a simple virus-like molecule like “in vitro virus” [3] and a proto-cell model. We found that the virus-like molecule of which protein binds to its genomic RNA can accelerate the translational activity smoothly in comparison with the proto-cell of which division occurs randomly.


1P286
進化する選択情報の自己複製システムの構築

Construction of an evolvable self-replication system of genetic information

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Evolutionality is one of the central characteristics of life. This ability allows a living system to diversify into a vast number of species. Non-living entity does not have evolvability. How can such ability emerge from non-living molecules? If a system obtains evolvability, does it evolve as an extent life? These questions have not been experimentally investigated. We addressed these questions by constructing an evolvable system. We used a self-replication system of genetic information that was previously constructed in vitro. This system is composed of two template RNA (the genetic information) encoding RNA replicase (Q6 replicase) and a cell-free translation system. We encapsulated the system into microsized compartments to link the genotype with phenotype. In addition, we amplified the self-replicated RNA through reverse-transcription, PCR, and in vitro transcription. Cycles of these successive reactions enabled the continuous self-replication process. As model experiment, mixture of two template RNAs that have slightly different self-replication activities were subjected into the self-replication-amplification cycles. The result shows that one of the RNA with 1.3 fold higher self-replication activity dominates the population after four rounds of the cycle. This result implies that a mutant RNA with slightly higher self-replication activity can dominate the population after several round of the cycle, that means the RNA is evolvable in the cycle. We are now repeating the cycle to evolve the RNA spontaneously.

1P287
生命の始原系における原始タンパク質のアミノ酸配列についての仮説

Investigation on the repetitive amino-acid sequences of native proteins and a hypothesis of the earliest proteins

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Periodic proteins, which have the region composed of repetitive amino-acid sequences, are very interesting proteins from the viewpoint of molecular evolution. All repetitive amino-acid sequences were extracted from currently available databases. It is shown that the repetitive sequences generally contain Pro or Gly residue, and it is well known that Pro and Gly residues are characteristic among 20 naturally occurring amino-acid residues from the viewpoint of the conformational role of each amino-acid residue stabilizing the three-dimensional structure of proteins. Taking into account these points and going back the process of molecular evolution of proteins in the history of life, a new hypothesis can be derived on the question which has not been solved yet, that is, the earliest proteins had started their long evolution process from what kind of amino-acid sequence. An outline of the proposed hypothesis is as follows. The earliest proteins would be constructed by the repetitive amino-acid sequences.

1P288
対掌性の異なるアミノ酸の双極子モーメントに関する理論研究

Theoretical study on dipole moments of amino acids with different chirality

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Each amino acid except glycine has an asymmetric center at the alpha carbon: as a result, an amino acid can have either L- or D-type chirality. However, forms of most naturally-occurring amino acids are only of the L-form. Though various hypotheses have been proposed for the reason why amino acids have homochirality, there is still no conclusive explanation. We focus on dipole moments of amino acids. The dipole-dipole interaction plays a significant role in predicting the reactivity or the stability between biological macromolecules such as proteins and DNA. Although the theoretical values of the dipole moments of all standard amino acids are available, dipole moments of amino acid residues in peptides have not been reported to our knowledge. Here, we calculate the dipole moments of all standard L- and D-amino acids with taking into account of polarization by main-chain of peptide. The term “dipole moment of amino acid” here indicates the dipole moment of an amino acid residue in a protein.

We find that the dipole moments of L-type enantiomer is larger dipole than that of D-type for most of amino acids. Larger dipole moment of an amino acid induces the larger stabilization effect by dipole-dipole interaction with other biological macromolecules. Thus, L-type enantiomer can induce larger dipole-dipole interaction than D-type. Therefore, most naturally-occurring amino acids have L-type chirality; in other words, the difference in the dipole moments between L- and D-type enantiomers may cause the homochirality.

1P289
モデル代謝系から構築される“生態系”の変動する環境に対する応答

Evolution of ecological network of ideal metabolic networks under fluctuating environment

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