2P260 次世代シーケンサーを用いた人工細胞モデルにおけるゲノムRNAの進化プロセスの解析
Analysis of the evolutionary process of the RNA genome in an artificial cell-like system using next generation sequencing technology

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Evolution is a key function of living things that produce present-day living world. However, the detailed process of evolution is still obscure due to the lack of sufficiently simple experimental model. Recently, we have constructed a simple cell-like system which contains a single-stranded RNA genome and has the ability of evolution through the continuous fusion-division cycle of cell-like compartment. Here, we investigated the evolutionary process in detail by using the next-generation sequencing technology. The analysis revealed the existence of clonal interference and positive epistasis throughout the evolutionary process. The method used in this study and the obtained result would contribute to the deeper understanding of evolutionary process.

2P261 Q β レプリカースによる RNA 複製反応中の二本鎖 RNA 形成の理解
Double-stranded RNA formation during Q β long RNA replication

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Q β replicase is an RNA-dependent RNA polymerase of coliphage Q β , which synthesizes the complementary RNA using a single-stranded RNA as a template. The formation of non-replicable double-stranded RNA (dsRNA) by hybridization between newly synthesized RNA and the template RNA hinders the broader application of Q β replicase. Here, we developed a kinetic model of Q β RNA replication consisting of two reaction pathways of dsRNA formation, which quantitatively explains the dynamics of dsRNA formation of three template RNAs. We also found that part of the Q β phage genomic RNA sequence including the central hairpin loop significantly decreases the rate of dsRNA formation and revealed that the secondary structure of RNA affects the dsRNA formation during Q β RNA replication.

2P262 人工自己複製モデルと寄生体が生み出す振動ダイナミクス
Oscillation dynamics of Host-Parasite population in an artificial cell-like system

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The appearance of parasite is one of the biggest hurdles for primitive self-replicators in prebiotic evolution. It casts a question: how has the primitive self-replication been established under threats of parasites? To understand this question, we are attempted to construct the artificial host-parasite interacting self-replication system derived from RNA phage Q-beta.

We found that this artificial host-parasite system long-term lasting in water-in-oil emulsion with the populations of the host and the parasite oscillating. Moreover, the host genomic RNA acquired frequent changes of the genetic sequence during the oscillation. It might suggest that this parasite-driven oscillation dynamics facilitates the evolution of the host RNA.

2P263 Directed evolution of a self-encoding system

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We have constructed a simplified system, in which the genetic information is replicated by self-encoded replicase in liposomes. Here we demonstrate the directed evolution of the self-encoding system. Cell-sized giant liposome was used as a micro reactor, and fluorescence-activated cell sorter (FACS) was used to analyze and sort the liposomes. The antisense of the beta-galactosidase gene was used as a reporter gene. Fluorescent liposomes with higher active replicase gene were sorted by FACS. The DNA templates for next selection round were amplified from the selected RNA in a test tube. After 69 rounds of selection, the self-replication activity of the selected mutants was evaluated in liposomes, and the mutants were higher active than wild-type replicase.

2P264 出芽酵母における染色体の構造変化と転写制御との関連について
Relationship between conformational change of chromosomes and transcriptional control in budding yeast

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Recently, 3-dimensional eukaryotic genome structures have been inferred from next-generation sequencing combined with chromosome conformation capture (Tanizawa et al., 2012). However, it has not been clarified how the 3-dimensional genome structure affects transcriptional regulation. For example, Taddei et al., *Genome Res.* (2009) showed that the expression pattern of many genes in budding yeast is changed when mutation is introduced to prevent telomeres from being anchored to the nuclear periphery, but the mechanism of this misregulation is elusive. In this talk, we will discuss the reason why genes are misregulated in the mutant by using a dynamical structural model of chromosomes (Tokuda et al., 2012) and microarray gene-expression data.

2P265 天然変性タンパク質データベース IDEAL の機能拡張 —PPI ネットワーク
New IDEAL: availability of PPI networks involving intrinsically disordered proteins

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The IDEAL database (<http://www.ideal.force.cs.is.nagoya-u.ac.jp/IDEAL/>) has been constructed to collect the knowledge of intrinsically disordered proteins (IDPs). Because it is quite important to understand IDPs in the context of a biological system and/or a protein-protein interaction (PPI) network, IDEAL has been improved to show the PPI networks. We regarded a protein in IDEAL as a NODE, and an interaction of two proteins as an EDGE, preparing NODE pages as well as EDGE pages. Users can easily walk around a PPI network by clicking the link bottoms which connect the NODE and the EDGE pages each other. The birds-eye view of the PPI network is also provided. We will demonstrate the features of new IDEAL with some examples.