2P133 マイクロドロップアレイを用いた一分子 DNA からの無細胞タンパク質合成

Cell free protein synthesis from single DNA in microdrop array

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Protein plays a very important role in cells. It is known that number of proteins in each cell is heterogeneous because regulation of gene expression takes place at a single DNA locus within a cell. On the other hand, cell-free protein synthesis system was developed. However, it is unknown whether heterogeneity of protein expression in vivo and that of proteins synthesized with reconstituted protein synthesis system are same or not. Then it is necessary to examine fluctuation of synthetic quantity of proteins from single DNA with reconstituted protein synthesis system such as PURE system. In this study, precise quantification of protein synthesis from single DNA is implemented with microdroplet array. At present, kinetic analysis of protein synthesis is attempted.

2P134 転写制御ダイナミクスの in vitro 1 分子計測

In vitro single molecule assay for the dynamics of transcriptional regulation

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Stochastic gene expression is generally explained by a two-state model of gene regulation, where a gene stochastically fluctuates between on and off states. The on state is explained by a molecular mechanism where RNA polymerase binds to the promoter, initiates transcription, and mRNA is produced at a constant rate. Comparatively little is known, however, about the off state.

In this study, we reconstructed prokaryote transcription and transcriptional regulation in vitro, and visualized mRNA production at the single molecule level by using fastFISH. Our data suggest that our experimental system is capable of clarifying the transcription kinetics, especially the transcription initiation step. We are applying this method to investigate the off state.

2P135 アポトーシスに伴う上皮恒常性維持への機械的力の寄与 Maintenance of tissue integrity by intrinsic and extrinsic forces during apoptosis in Drosophila epithelial tissue morphogenesis

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How tissue integrity is preserved during apoptosis in epithelia is largely unknown. We studied tissue replacement process known as histoblast expansion during Drosophila metamorphosis and revealed 1) the apoptotic cell is squeezed out from the tissue by the contraction of actomyosin cables formed within the dying cell and within the neighboring non-apoptotic cells formed upon apoptosis and 2) the cell adhesion between dying and non-dying cells is well regulated, for instance, E-Cadherin is dissociated from the plasma membrane during the apical constriction. Our results provide new mechanical and molecular insights of the maintenance of tissue integrity during apoptosis and the mechanical contribution of apoptosis in epithelial tissue morphogenesis.

2P136 枯葉にそっくりな蝶の翅の模様はどのように進化してきたのか？

Gradual and contingent evolutionary emergence of leaf wing patterns

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How leaf mimicry evolved has fascinated many biologists, but it remains unclear. Here we show evolutionary origin and process of leaf wing patterns of butterflies (*Kallima*). First, comparative morphological analyses indicated that *Kallima* leaf patterns are decomposed into the same pattern elements as 31 closely related species share, suggesting that the pattern elements have been inherited across species. Next, we used Bayesian phylogenetic methods to estimate the past wing patterns, and revealed that the leaf pattern has evolved through several intermediate patterns from a non-mimetic ancestor. Finally, we estimated the temporal order of state evolution in the pattern elements. In summary, our study provides the first evidence for gradual evolution of leaf mimicry.

2P137 多細胞の形態形成における力学機構を明らかにするための三次元バーテックスモデル

3D vertex model for revealing mechanics in multicellular morphogenesis

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In biological development, global deformations of multicellular tissues emerge from dynamics of subcellular structures such as cytoskeletons. One fundamental challenge is to understand how subcellular mechanical behaviors can be orchestrated into global tissue deformations on the regulatory background. To elucidate such physical phenomena in multi-component systems, in this study, we have developed a novel 3D vertex model. The proposed vertex model has been succeeded expressing changes in cell configurations, cell divisions, and 3D dynamic deformation processes. In this presentation, we would like to demonstrate the applicability of the proposed model for revealing mechanics in tissue morphogenesis.

2P138 細胞性粘菌由来ミオシン II の SH1 ヘリックス上の変異が運動活性に与える影響

Mutations in SH1 helix affect the motile activity of Dictyostelium myosin II

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Mutations at the SH1 helix region of the myosin II motor domain have been reported to link to some autosomal-dominant diseases. The SH1 helix region acts as a linker for transmitting the structural changes of ATP-binding site in the catalysis domain to the lever arm. To investigate the effects on the motile activity, we introduced each of three mutations (E683K and R686C) into the SH1 helix in Dictyostelium myosin II. The mutation resulted in a decrease in the actin-myosin sliding velocity and the thermal stability, and the thermal aggregation of the myosin, which might be implicated in the disease process.