2P259 Target analysis of the photosystem II-enriched membrane: The effect of oxidizing agent on fluorescence quenching in PSII

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We studied picosecond time-resolved fluorescence spectra of photosystem II (PSII)-enriched membrane at 77 K by a streak-camera system to reveal its light-harvesting dynamics. We globally fitted data by using the target analysis to build up a new compartment model for PSII, which is consistent with a microscopic model based on the structure [Shibata, Y., et al. (2013), JACS]. Excitation was made at 430 nm and 460 nm with different powers to populate different antenna components.

Though there were several studies on the fluorescence quenching in PSII induced by oxidizing chlorophyll Z (ChlZ⁺) or carotenoids, its mechanism has not been well clarified so far. We will use our compartment model to shed light on the mechanism of the oxidant-induced quenching in PSII.

2P260 超音波に誘発されるケージ化合物の活性化 Ultrasound-induced activation of caged compounds

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Caged compounds are widely used as tracers and activators of biological reactions and their activities can be temporarily masked using a photosensitive moiety. However, photoradiation is not always successful in clinical applications. Therefore, we attempted to activate caged compounds using ultrasound rather than light. To determine the mechanism of ultrasound-induced activation of CMNB-caged fluorescein, an irradiated product was analyzed by fluorospectrometry and HPLC. As a result, fluorescent unmasked molecules were detected in an ultrasound-irradiated caged compound solution. However, the fluorospectrometric and HPLC profiles of its degradation products were not identical to photoirradiated caged fluorescein.

2P261 ノロウイルス RNA 複製酵素を用いた試験管内 RNA 淘汰実験から、新奇な dsRNA 複製機構が示唆された A novel dsRNA replication mode was suggested from the *in vitro* RNA selection using Norovirus RNA replicase

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We had confirmed that Norovirus RNA replicase (NV3D^{pol}) amplified dsRNA isothermally. In order to identify the optimal 3'-terminal sequence of the RNA template for NV3D^{pol}, an *in vitro* selection using the serial transfer was performed for a random library (3'-terminal 4 nts). The population landscape on the 4-dimensional sequence space of the 17th round of transfer gave a main peak around the CAAC. In the batch amplification, the C-stretch was much more effective than the CAAC, but in the serial transfer condition in which the CAAC was sustained stably, the C-stretch was washed out. Based on these results we proposed the existence of the "shuttle mode" replication of dsRNA. We also proposed the optimal terminal sequences of RNA for *in vitro* evolution with NV3D^{pol}.

2P262 phi29DNA 複製酵素を使った自己複製系の確立 Establishment of a self-replication system using phi29 DNA polymerase

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Living organisms have replication systems of their genetic information, in which genomic DNA is replicated by its encoded proteins. This self-replication of the genetic information is essential for living system to evolve. To understand how life can evolve, we are attempting to construct a self-replication system in which a DNA encoded polymerase is replicated through translation of the protein. This system was assembled by a circular DNA encoding phi29 DNA polymerase and a cell-free translation system reconstituted from purified proteins. We found phi29 DNA polymerase is translated from the genomic DNA and replicate it. If we add a recursivity to this system, it would be possible to observe the evolution of DNA self-replication system.

2P263 分子動力学計算を用いたβ2 アドレナリン受容体と G タンパク質間の相互作用解析 Structural analysis of interaction between β2 adrenergic receptor and G-protein using molecular dynamics simulation

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The study of the interaction between G-protein coupled receptor (GPCR) and G-protein (Ga) is important to understand the feature of Ga binding selectivity, which cause different downstream phenomenon of GPCR.

Based on the 3D structure (PDB ID: 3sn6) of β₂ adrenergic receptor (β₂AR) with G_s, we made several mutated complexes (β₂AR with G_{i10}, G_{q11} or G_{12/13}), by comparative modeling, and evaluated behaviors of native or mutated complexes, by using molecular dynamics simulations in vacuum or in implicit water solvent with AMBER99 force field.

It was suggested that the native β₂AR - G_s complex is the most stable through 12 ns simulation. This stability was caused by attractive interaction of key residues on C terminal of Ga, on DRY motif of TM3 and on ICL2 of β₂AR.

2P264 Global clustering of whole organisms enabled by the GP method

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In this study, we demonstrate genome profiling (GP)-based global clustering by taking an example of a case with 48 samples from five classes of animalia. The resultant cluster showed well-discriminated clustering of five classes of kingdom animalia. In addition, this cluster showed correspondence to the phenotype-based classification. Furthermore, we constructed a genome sequence space where these 48 samples were separated by their corresponding genome distance with high correlation to Euclidean distance. The results support the effectiveness and universality of genome distance-based approach which does not require a priori knowledge of sequence for analysis and can be ubiquitously applied. To our knowledge, this is the first trial and success of this kind.