1P211 ラフト中でのアミロイド前駆体タンパク質の膜貫通部位の二量化にコレステロールが与える影響**Cholesterols affect to the association of the transmembrane region of Amyloid Precursor Protein in the raft**

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The bio-membrane often forms nano-domains, rafts, and provides a special environment to a membrane protein. Amyloid precursor protein (APP) produces an Amyloid beta peptide, which is the source of senile plaque in a brain. The APP forms dimer or monomer conformations in the bio-membrane. Recent experiments have suggested that the cholesterols attach to the Gly-xxx-Gly motif in the raft-like environments. However, the Gly-xxx-Gly motif is the important interface of the dimerization of APP too. We investigated how the cholesterols compete with the dimerization of APP, using Martini Coarse Grained (CG) model simulations. The cholesterols, of course, favored the dimer interface. Our results suggested that the cholesterols assist to the association of APP too.

**1P212 リソソーム内膜タンパク質合成が誘起する脂質膜の形態変化
Morphological changes of the lipid membrane induced by in-liposome membrane protein synthesis**

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Letm1, one of the mitochondrial inner membrane proteins, is assumed to be involved in the morphological changes of mitochondria. In vivo, it has been found that Letm1 dysfunction induced by knockdown or knockout experiments resulting morphological abnormalities of mitochondria. However, the exact role of Letm1 on the membrane morphology remains unclear. We, thus, aimed to elucidate it by the bottom-up approach. We synthesized Letm1 using a reconstituted in vitro transcription-translation system (the PURE system) inside a cell-size liposome, thereby investigating the role of the membrane protein on the dynamics of the cellular membrane. We observed clear morphological changes of the lipid membrane by synthesizing Letm1 inside the liposome.

1P213 光応答 DNA と細胞サイズリボソームの融合による人工細胞型分子ロボット**Artificial cell-based molecular robots by fusion of light responsive DNA and cell-sized liposomes**

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Molecular robotics has attracted much attention as a novel engineering concept of self-assembled biological systems. Although nano-sized molecular robots based on the DNA/RNA molecules have been reported, micro-sized molecular robots have never been developed yet. Here, we proposed an artificial cell-based molecular robots as an integrated system of designed DNA/RNA molecules and cell-sized liposomes. In this system, we designed that RNA transcription starts by light stimulation, and the RNA and proteins autonomously self-assembles into a RNA-protein complex. We will report the more complex functions within interaction between RNA-protein complex and liposome.

1P214 チューブリン封入ジャイアントリボソームの温度・静水圧変化による可逆的形態制御**Reversible morphological control of tubulin-encapsulated giant-liposomes induced by change of hydrostatic pressure and temperature**

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We examined the effect of hydrostatic pressure and temperature on the tubulin-encapsulated giant-liposomes. Many of the liposomes kept a bipolar shape with a central sphere and two tubular protrusions that aligned in a straight line at room temperature and ambient pressure as reported previously (Kaneko et.al., 1998). Immediately after the application of high pressure (80 MPa) or low temperature (4°C), the protrusions shrunk within several tens of seconds. This process was reversible; after the pressure was released or the temperature increased to 25°C, the protrusions regenerated within several minutes. Our results demonstrate that the shape of giant liposomes is controllable using the polymerization and depolymerization process of microtubules.

**1P215 粘弾性流体を内包したリボソームの膜変形
Effects of viscoelastic cytoplasm in liposome on the shape deformation**

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Liposomes have been used as a model of living cells. Under a hypotonic condition, the liposomes deform their shapes to minimize the bending energy. We investigated how the existence of macromolecules inside affects the liposomal deformation. We prepared liposomes containing 80 mg/ml macromolecules of BSA or a protein mixture extracted from *Escherichia coli*. The macromolecules were concentrated up to the physiological concentration, i.e. 300 mg/ml. Consequently, the condensation process and the shape deformation differed between BSA- and Cell Extract-containing liposomes. These results strongly suggested that the crowded environment in cells is different from that found in typical single-component systems.

[1] K. Fujiwara and M. Yanagisawa, ACS Synth. Biol., in press.

1P216 表面張カレプリカ交換分子動力学法の開発と生体膜系への応用**Surface-tension replica-exchange molecular dynamics simulations of biological membrane systems**

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Conformational sampling is fundamentally important for simulating complex bio-molecular systems. Here, we propose a new enhanced simulation method for membrane systems, which we call the surface-tension replica-exchange molecular dynamics method. We tested the method on two biological membrane systems: DPPC lipid bilayers and WALP23-POPC membranes. During these simulations, large-scale lateral deformation of the membranes took place, and there was accelerated lateral diffusion of DPPC lipid molecules compared with conventional MD simulation. We succeeded to predict the optimal orientation of WALP23 based on the free-energy calculation. Our method could be applicable to a wide variety of biological membrane systems.