2P236 群れの相互作用の多義性から自己組織化を再考する
Rethinking about the concept of self-organization from the perspective of the interaction multiplicity in collective behavior

Takayuki Niizato (*Tsukuba University*)

The concept of the self-organization is widely known for the emergent phenomena from local simple interactions. Almost of the self-organization's models only consider one aspect of phenomena. However, this attitude may miss the problem of the functional differentiation from a local interaction. Thus, we propose multiplicity of interaction in a simple model constructed from three factors: asynchronous updating, learning site patterns, and agent anticipation. We found that the first two contribute to an efficient searching strategy, and that adding agent anticipation enables sign making in heterogeneous environments. Our model suggests that searching strategies and territorial behavior such as boundary marking emerge from two aspects of our simple interaction rule.

2P237 滑走細菌 *Flavobacterium johnsoniae* の菌表面構造
Cell surface structure of the gliding bacterium *Flavobacterium johnsoniae*

Satoshi Shibata¹, Keiko Sato¹, Yuka Narita¹, Daisuke Nakane², Koji Nakayama¹ (¹*Div. Microbiol./Oral infec., Grad. Sch. Bio/Med Sci., Nagasaki Univ.*, ²*Dept. Phys., Fac. Sci., Gakushuin Univ.*)

Cells of *Flavobacterium johnsoniae* move over surfaces, which is called gliding motility. Gliding motility is unrelated to well-studied motility mechanisms using flagella and type IV pili. In our recent study (Nakane et al., 2013) we proposed a "helical loop track model" for gliding motility, where the SprB molecule is propelled along left-handed helical loop on the cell surface.

Using transmission electron microscopy to characterize the gliding machinery, "Fettuccini pasta-like structures" with 22.1 ± 0.8 nm in width and 8.2 ± 0.2 nm in thickness were observed on the cell surface, and also similar structures were able to be isolated from the cell surface. The structure may play an role in gliding motility. We are in the process of identifying its function.

2P238 *Flavobacterium johnsoniae* におけるコロニースプレッティング
グファクター
Factors influencing colony spreading in *Flavobacterium johnsoniae*

Yuka Narita¹, Keiko Sato¹, Satoshi Shibata¹, Daisuke Nakane², Koji Nakayama¹ (¹*Dept. Mol. Microbiol. Immunol., Grad. Sch. Biomedical Sci., Nagasaki Univ.*, ²*Dept. Physics., Gakushuin Univ.*)

Flavobacterium johnsoniae is an aerobic Gram-negative bacterium, which glides rapidly over solid surfaces at about 2 μ m/s. *F. johnsoniae* shows colony spreading on a poor medium such as PY2 agar, whereas it forms non-spreading colonies on an enriched medium. Size of colony in PY2 agar was decreased by presence of NaCl and glucose in a dose-dependent manner. A number of mutants that showed colony spreading on PY2 agar containing 150 mM NaCl and 10 mM glucose were isolated from a transposon (Tn) mutant library of *F. johnsoniae* ATCC17061. Tn insertion sites in the mutants were determined, which suggested that amino acid biosynthesis, transporter and stress response pathways influence NaCl- and glucose-mediated suppression of colony spreading of *F. johnsoniae*.

2P239 自由エネルギー計算によるハロロドプシンの光駆動イオン輸送メカニズムの解析
Study of the mechanism of the light-driven ion transport in halorhodopsin based on the free energy calculations

Hiroyuki Tamura¹, Shuntaro Chiba¹, Tadaomi Furuta¹, Shun Sakuraba², Nobuyuki Matsubayashi², **Minoru Sakurai**¹ (¹*Tokyo Tech.*, ²*Kyoto Univ.*)

Halorhodopsin (hR) uses the light energy to transport chloride ions from the extracellular side to the cytoplasmic side. The process is thought to be divided into at least the three steps: (i) a chloride ion passively enters the binding site near retinal Schiff base linkage in the protein, (ii) the chloride ion is moved to the cytoplasmic side after the photoisomerization of retinal, and iii) the chloride ion is released to the cytoplasmic medium. The purpose of this work is to reveal the free energy profiles of these processes. The free energies were calculated using the method of energy representation combined with molecular dynamics simulations. Based on these results, we discuss the mechanism of the light-driven ion transport in hR.

2P240 Aureochrome-1 の各ドメインの機能解析
Functional analyses of each domain in Aureochrome-1

Yoichi Nakatani¹, Ken Takeuchi¹, Yosuke Izawa¹, Fumio Takahashi^{2,3}, Hironao Kataoka⁴, Osamu Hisatomi¹ (¹*Grad. Sch. Sci., Osaka Univ.*, ²*Grad. Sch. Life Sci., Ritsumeikan Univ.*, ³*PRESTO, JST.*, ⁴*Botanical Gardens, Tohoku Univ.*)

Aureochrome-1 (AUREO1) found in *Vaucheria frigida* consists of a basic leucine zipper domain (bZip) and a light-oxygen-voltage-sensing (LOV) domain, and is believed to be a blue light-regulated transcription factor¹. We prepared recombinant AUREO1 proteins, containing full coding sequence (FL), bZIP and LOV domains (ZL), and LOV domain. In addition, we made a deletion mutant (dZL) lacking the basic region of ZL. The dZL protein showed a similar spectral change to ZL upon illumination with blue light, but lost the affinity to DNA. Our results suggested that each domain in AUREO1 works as a functional unit and is available to create a new molecular tool.

1. Takahashi, F., et al. *Proc. Natl. Acad. Sci. USA* 104, 19625-19630 (2007)

2P241 Ab initio 電子状態計算における青色光受容体蛋白質の DNA 修復反応の理論的研究
Theoretical Study of DNA Repair Mechanism of Blue Light Photoreceptors by Ab initio Electronic Structure Calculation

Ryuma Sato¹, Tsutomu Kawatsu^{2,3}, Takahisa Yamato¹ (¹*Dept. of Phys., Grad. Sch. Sci., Univ. Nagoya*, ²*CMSI*, ³*Coll. Sci. Engn., Univ. Kanazawa*)

Molecular origin of efficient electron transfer (ET) in DNA photolyase (PHR) was illustrated by the analysis of electron tunneling pathways from FADH- to CPD.

Due to non-local nature and structural sensitivity of the active site electronic states, it is important to select the necessary and sufficient range of the QM region. Therefore, we evaluated the sensitivity of the tunneling matrix element to the perturbation of the Hamiltonian at each amino acid site, and measured the contribution of each site to ET.

We will discuss the role of each amino acid residues in the active site of PHR with respect to (1) explicit contribution to ET and (2) stabilization of the active site structure.