2SCA-02 Visualizing stator-protein distributions of bacterial flagellar motors
Chien-Jung Lo 1,2, Tsaishun Lin 2−3 (Dept. of Phys., National Central Univ., 2Inst. Biophys., National Central Univ.)

The bacterial flagellar motor is a natural electrical rotary molecular machine. The stator-unit consists of MotA/B proteins couples ion-flux to motor rotations. More than 10 stator-units in a motor turn over dynamically in response to the cellular energetical conditions and external loads. However, spatial features and temporal dynamics of stator-units have never been studied thoroughly. We have built a super-resolution fluorescent microscope with 10 nm resolution to study stator-units dynamics using dual color labeling on rotor- and stator- proteins. We will present protein counting, spatial distribution and dynamical properties of stator proteins. We thank Seiji Kojima, Hajime Fukuoka, Akihiko Ishijima and Michio Homma for the bacterial strains.

2SCA-03 塩貴ヘモトモーターの回転方向変換制御に関わる構造 Structure of the bacterial flagellar motor involved in the directional switching mechanism
Tomoko Miyata1, Takayuki Kato1, Yusuke V. Morimoto1−2,3, Syuichi Nakamura4, Hideyuki Matsunami1, Keiichi Namba1,2 (1Grad. Sch. Frontier Biosci., Osaka Univ., 2QBiC, RIKEN, 3Grad. Sch. Sci., Osaka Univ., 4School of Engineering, Tohoku Univ., 5Trans-Membrane Trafficking Unit, OIST)

Many bacteria swim by reversibly rotating flagella. The three switch proteins, FlIG, FlIM and FlIN, form the C-ring on the cytoplasmic face of the MS ring spanning the membrane and control counterclockwise-clockwise (CCW/CW) switching of the motor rotation. CheY is a response regulator in bacterial chemotaxis, and phosphorylated CheYP (CheY-P) binds to FlIM and changes the rotational direction from CCW to CW. We previously reported the C ring structures locked in CCW (che deletion strain) and CW (FlIG ΔPAA strain). Comparison of the two strucutres showed differences in the position of the C ring and the subunit arrangement in its outer wall. In this meeting, we will report the structure of the CheYP bound C ring and discuss the switching mechanism of flagellar rotation.

2SCA-04 Conformational Spread as a Mechanism for Cooperativity in the Bacterial Flagellar Switch
Fan Bai (Sch. Life Sci., Peking Univ.)

The Bacterial Flagellar Motor is a molecular machine which rotates the helical filaments that propel swimming bacteria. In our previous work, we used high-resolution optical microscopy to observe switching of single motors and uncover the stochastic multistate nature of the switch. Our observations are in quantitative agreement with a general model of allosteric cooperativity that exhibits conformational spread. On the basis of this model, we constructed a unified mathematical model describing both BFM torque generation and switching mechanism. Our model framework minimized free adjustable parameters and successfully reproduced the load-switching dynamics of the BFM reported in recent experiments and made predictions on the stator dependence in motor switching dynamics.

2SCA-05 Coordination and control in the ring-shaped molecular motors
Jin Yu (Beijing Computational Science Research Center)
The ring-shaped NTPase motor consists of multiple subunits that form a ring-like structure. The molecular motors use chemical free energy to move along nucleic acid or protein substrate in a directional manner. To achieve this function, inter-subunit coordination is required to ensure cooperative or sequential activities among the motor subunits. We will first show our previous modeling work on a viral DNA packaging motor, based on single molecule measurements. The focus is on how multiple subunits coordinate to achieve sequential ATP binding, hydrolysis, and ADP release around the ring, as well as on push-and-roll of DNA through the ring. Then I will introduce our preliminary work on gamma-less F1-ATPase, focusing on biased mechanistic correlation among chemical sites.

2SCA-06 高速原子間力顕微鏡によるリング状 ATPase の協同的構造変化の観察 Cooperative Conformational Change of Ring-Shape ATPase Observed by High-Speed AFM

Cooperativity among subunits in oligomeric proteins is often indispensable for their functions. Oligomeric proteins generally undergo concerted or sequential conformational transitions due to changes in intersubunit interactions upon the ligand binding/dissociation to/from proteins. Although static structures have been available for many oligomeric proteins, there have been no ways to directly observe cooperative conformational changes of subunits in the complex. Here we applied high-speed AFM, which is one of promising tools to visualize conformation of each subunit simultaneously, to ring-shaped ATPase such as F1-ATPase. In the presentation, we will demonstrate HS-AFM movies and discuss how the catalytic and conformational states are cooperatively regulated.

2SDA-01 クロマチン動構造とヒストンバリアント Structural basis of chromatin dynamics regulated by histone variants
Hitoshi Kurumizaka (Waseda University, Faculty of Science and Engineering)

Chromatin dynamics function to regulate replication, recombination, and transcription of genomic DNA. Histones H2A, H2B, H3, and H4 are major nuclear proteins that form the core structure of the nucleosome. In many species, H2A, H2B, and H3 have isoforms (variants). Incorporation of specific histone variants into nucleosomes results in versatile structure and dynamics. These structural and physical characters of nucleosome isoforms containing histone variants play essential roles in genomic DNA regulation. In this symposium, I will discuss about the structural basis of chromatin dynamics based on the crystal structures of the nucleosomes containing histone variants.