3P145 Control of microtubule trajectory within an electric field by altering surface charge density

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A challenge for using microtubules (MTs) driven by kinesin motors in functional nanosystems is to control their direction of movement. A method was developed to guide kinesin-propelled MTs in multiple directions under an electric field by designing a charged surface of MT minus ends labeled with dsDNA via a streptavidin-biotin interaction. Experimental trajectories were in good agreement with values predicted from measured electrophoretic mobilities. As the effective charge of labeled DNA molecules matches to that of freely dispersed DNA molecules, MT trajectory can be estimated even by selecting labeling molecules with known charges. Our molecular design and prediction methodology demonstrate the feasibility of using molecular sorters driven by motor proteins.

3P146 キネシンとダイニンによる Tug-of-war 分子系の再構築および多分子ダイニンの発生力計測

Tug-of-war molecular system between dynein- and kinesin-coated regions and force measurement of multiple dyneins

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A large number of microtubule-based motor proteins, such as kinesin and dynein, are involved in mitosis. It is believed that chromosome oscillations in mitosis arise from tug-of-war between two opposite-polarity motors. However, the behavior of multiple motors as a team is poorly understood. Here, to contribute for understanding of multiple motor behavior in mitosis, we adopted microtubules motility assay on dynein- and kinesin-coated substrate. First, we measured force generated by multiple dyneins using optical tweezers. Dyneins exerted ~60 pN against optical trap to a bead attached to the tail of a microtubule. Moreover, we designed a tug-of-war molecular system between dynein and kinesin by photolithographically patterning motors in two different regions.

3P147 べん毛モーター解析のための長時間リアルタイム観察・刺激システムの構築

Development of the real-long-time observation and local stimulation system for flagellar motor analysis

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Recently, in cell analysis, local environment control technology for single cell analysis is being established. In this study, we try to develop a real-long-time observation and cultivation system that can changing and keeping local environment condition stably and apply this system for analyze the bacteria flagella motor. We have implemented "fast response measurement" and "solution spouting by micropipette" for this system. And then we confirm the performance of this system by measuring the rotational speed of bacteria flagellar motor for long-time with stable condition and controlling the rotational speed of flagellar motor diametrically.

3P148 Visualization of functional components of the bacterial flagellar motor

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The bacterial flagellar motor is a reversible rotary nano-machine embedded in the cell envelope. The motor consists of a rotor ~45 nm in diameter surrounded by ~10 independent stator units functioning as ion-channels and the torque is generated by interaction between the rotor and stator. To understand how the motor works, direct observation of motor movements at the site of torque generation is required. For this purpose, we have been developing the assay to detect motor dynamics by fluorescent microscopy at single-molecule level. In this study, we tried to track the movement of stator units MotB labeled with tetramethylrhodamine of rotating tethered cell.

3P149 Molecular dynamics simulations of the β subunit in F₁-ATPase: Relation between the large-scale structural change and common motifs

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The F₁-ATPase is rotated by the structural changes of the catalytically active β subunits which have two driving forces; the ATP binding and ATP hydrolysis. The former is elucidated in our previous MD simulations (Y. Ito, *et al.* JACS, 2011). Therefore, in this study, we simulated the latter, which contains important issues; 1) the timing of the Pi release, 2) the unsolved half-closed form, and 3) the ADP releasing mechanism. The simulation solved all these issues. Also, we found that conserved residues among the ATPase family, induced the large (open-closed) structural change. This leverage like relationship was also observed in our previous study (the structural change by the ATP binding), suggesting that the obtained mechanism may be shared with other ATPase proteins.

3P150 Slow axonemal dynein e facilitates the motility of faster dynein c

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We highly purified the Chlamydomonas flagellar inner-arm dynein "e" and "c." EM observations and single particle analysis showed that the head domains of these two dyneins were morphologically similar. The ATPase activities of dynein e were lower than those of dynein c. Dynein e was expected to be a processive motor judged from microtubule landing rate assays. From in vitro motility assays, microtubule translocation by dynein e was found to be slow ($V = 1.2 \pm 0.1 \mu\text{m/s}$), whereas that by dynein c was very fast ($V_{\text{max}} = 15.8 \pm 1.5 \mu\text{m/s}$). The microtubule translocation of the "fast" dynein c became even faster in the presence of the "slow" dynein e. In flagella, dynein e would act as a "facilitator" by holding adjacent microtubules to aid dynein c's power stroke.