BP 12: Molecular Motors

Time: Tuesday 9:30–11:45 Location: H43

Invited Talk BP 12.1 Tue 9:30 H43

Motor and Track Systems for Navigating the Cytoskeleton — Joanna Kalita[1,2] and •Ronald Rock[1] — [1]The University of Chicago, Chicago, USA — [2]University of Wrocław, Wrocław, Poland

An emerging paradigm in motility is the notion of "specialized" motors, or motors that are fine-tuned to perform a specific function. Rather than merely traveling anywhere and everywhere, such motors are programmed to select certain tracks, to respond to forces in a defined way, or to actively remodel their tracks. Here, we further develop the ex vivo motility assay to determine how cells remodel their actin tracks and redirect myosin V traffic in response to Rho GTPase signaling. We transfected 3T3 cells with constitutively active or dominant negative forms of Rac1, RhoA, or CDC42, triton extracted the cells to expose the cytoskeletons, and applied labeled myosin V for single molecule tracking. We find that all Rho constructs increase myosin V activity. Remarkably, only a small fraction of actin filaments are used by myosin V, as we find that motors repeatedly travel in limited zones while ignoring nearby regions of high actin density.

BP 12.2 Tue 10:00 H43

Bi-directionality of Single Kinesin-5 Cin8 Molecules is Mediated by the Tail Domains — •André Düselder[1], Christina Thiede[1], Alice Wiesbaum[1], Vladimir Fridman[2], Dieter Klopfenstein[1], Olga Zaitsava[3], Marcel E. Janson[3], Larisa Gheber[2], and Christoph F. Schmidt[1] — [1]Georg-August-Universität, Göttingen, DE — [2]Ben-Gurion University of the Negev, Beer-Sheva, IL — [3]Wageningen University, Wageningen, NL

The tetrameric yeast Kinesin-5 Cin8 can switch from a fast minus-end to a slow plus-end-directed motion. We found evidence that binding between two microtubules switches the motor to plus-end motility. We hypothesized that the tail domains of Cin8 influence the adjacent motor domains, depending on the binding state between microtubules. We designed two different motor constructs to test our hypothesis. To rule out any head-tail-interactions we removed the tail domains of Cin8 (Cin8Δtail). This construct retained its ability to link and slide apart two microtubules. Its motility on single microtubules, however, was under all conditions slow, intermittent, and mostly plus end directed. We also constructed a stably dimeric Cin8/Kinesin-1 chimera (Cin8Kin), consisting of head and neck linker of Cin8 fused to the stalk of Kinesin-1. This chimera showed a similar motility as Cin8Δtail. We therefore conclude that the Cin8 head domains are inherently bidirectional and that the interaction between tail and motor domains of Cin8 are responsible for stably switching the motility to either plus- or minus-end directed motion.

BP 12.3 Tue 10:15 H43

Passive and active cross-linkers can conjointly generate a stable finite overlap between antiparallel polar filaments — Debajit Goswami and •Karsten Kruse — Theoretische Physik, Universität des Saarlandes, Saarbrücken, Germany

During cell division, pairing of sister chromosomes and their segregation is driven by the mitotic spindle. This bipolar structure microtubules consists mostly of microtubules, motor proteins and further associated proteins regulating microtubule dynamics and cross-linking. Through their combined action, a stable structure of overlapping antiparallel microtubules is generated. How this state is maintained is currently unknown. Recently, a possible mechanism based on passive cross-linkers and molecular motors was studied experimentally in vitro. We present a stochastic model for a pair of antiparallel polar filaments that interact via active and passive cross-links. We investigate in detail the dependence of the overlap region's size on parameters. We then apply our system to the specific cases of the active cross-linkers Eg5 and Ncd, respectively, as well as the passive cross-linker Ase1.

BP 12.4 Tue 10:30 H43

Positioning of microtubule organizing centers by cortical pushing and pulling forces — •Nenad Pavin[1,2], Liedewij Laan[3], Rui Ma[1,4], Marileen Dogterom[3], and Frank Jülicher[1] — [1]MPI-PKS, Dresden, Germany — [2]University of Zagreb, Zagreb, Croatia — [3]AMOLF, Amsterdam, The Netherlands — [4]Tsinghua University, Beijing, China

Positioning of microtubule organizing centers (MTOC) with respect to the confining geometry of cells depends on pushing and/or pulling forces generated by MTs that interact with the cell cortex. How, in living cells, these forces lead to proper positioning is still largely an open question. Using in vitro experiments in artificial microchambers it was shown that in a square geometry, MT asters center more reliably by a combination of pulling and pushing forces than by pushing forces alone. Theoretically, we show that pulling and pushing forces acting on the MTOC in different geometries depend on orientations of MTs. We find that these forces can have centering or off-centering behavior in different geometries. Pushing forces center in a one-dimensional and a square geometry, but lead to off-centering in a circle if reorientation is sufficiently pronounced. Pulling forces, however, do not center in a one-dimensional geometry, but improve centering in a circle and a square. In an elongated stadium geometry, positioning along the short axis depends mainly on pulling forces, while positioning along the long axis depends mainly on pushing forces. Our theoretical results suggest that different positioning strategies could be used by different cell types (Laan et al 2012 Cell, Pavin et al NJP 2012).

BP 12.5 Tue 10:45 H43

Theory of Microtubule Length Regulation by Molecular Motors — •Louis Reese[1], Anna Melbinger[2], and Erwin Frey[1] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität München — [2]Institut Pasteur, Paris, France

Important players in microtubule length regulation are depolymerizing motor proteins. The accumulation of kinesin-8 along a microtubule provides sensitive regulation of the microtubule's length [1,2]. However, cellular mechanisms of length regulation are still obscure. This is due to the complicated dynamics of microtubule assembly and disassembly and the presence of a multitude of regulatory proteins. We develop a theoretical framework that allows to address this problem systematically [2]. Employing analytic methods and stochastic simulations, different regimes of motor traffic are identified. With these results at hand it is possible to infer for which parameter regimes depolymerizing motor molecules regulate microtubule length. The resulting microtubule dynamics is analyzed with respect to fluctuations and the microtubule length. We find that particular molecular interactions between kinesin-8 and the microtubule enhance fluctuations such that they are reminiscent of microtubule dynamic instability.

[1] L. Reese, A. Melbinger, E. Frey, Biophys. J. 101 (2011)
[2] A. Melbinger, L. Reese, E. Frey, Phys. Rev. Lett. 108 (2012)

BP 12.6 Tue 11:00 H43

Efficiencies of a molecular motor with application to the F_1-ATPase — •Eva Zimmermann and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart

In experiments, the properties of a molecular motor are often inferred by measuring the stochastic trajectory of an attached probe particle. Recently, Toyabe et al. measured the heat dissipated by the probe particle to investigate the efficiency of the F_1-ATPase and found values for this efficiency close to 1 [1].

We discuss a simple model consisting of two degrees of freedom representing the motor and the probe which are elastically coupled. In this model, the motor protein hydrolyzes (or synthesizes) one ATP molecule per mechanical step which represents tight mechanochemical coupling. We apply the model to the F_1-ATPase and investigate three types of efficiencies both in simulations and in a Gaussian approximation [2]. In particular, we clarify the conditions under which the definition of efficiency used in [1] can become even larger than 1 and should therefore not be interpreted as efficiency in the thermodynamic sense. Overall, we obtain good quantitative agreement with the experimental data.

[1] S. Toyabe et al., Phys. Rev. Lett. 104, 198103 (2010)
[2] E. Zimmermann and U. Seifert, New J. Phys. 14, 103023 (2012)

Invited Talk BP 12.7 Tue 11:15 H43

Molecular Motors from DNA — •Andrew Turberfield — University of Oxford, Department of Physics, Clarendon Laboratory, Parks Road, Oxford OX1 3PU, U.K.

DNA is a wonderful material for nanoscale construction: its self-assembly can be programmed by making use of its information-carrying

capability, and its hybridization or hydrolysis can be used as to provide energy for synthetic molecular machinery. With DNA it is possible to design and build three-dimensional scaffolds, to attach molecular components to them with sub-nanometre precision and then to make them move. I shall describe our work on autonomous, biomimetic molecular motors powered by chemical fuels and the use of synthetic molecular machinery to control covalent chemical synthesis. I shall demonstrate bipedal motors whose operation depends on the coordination of the chemomechanical cycles of two separate catalytic centres and burnt bridges motors that can be programmed to navigate networks of tracks. I shall also discuss the use of kinesin motor proteins to power synthetic devices.