BP 15: Motor Proteins

Time: Wednesday 14:30–15:45 Location: ZEU 260

BP 15.1 Wed 14:30 ZEU 260

Diffusion of yeast kinesin-8 on the microtubule lattice is a random walk with 8-nm steps — •Volker Bormuth[1], Vladimir Varga[1], Jonathon Howard[1], and Erik Schäffer[2] — [1]MPI of Molecular Cell Biology and Genetics, Pfotenhauerstraße 108, 01307 Dresden, Germany — [2]Biotechnology Center, TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany

The yeast kinesin-8 (Kip3p) walks highly processive towards the plus-end of microtubules in the presence of ATP. In contrast, we found that in the presence of ADP Kip3p diffuses in a one-dimensional manner on the microtubule lattice. Using single molecule fluorescence we measured that the diffusion coefficient was $5400\pm1500\,\mathrm{nm}^2/\mathrm{s}$ with an average lifetime on the microtubule lattice of 8 s. The diffusion did not require the highly charged C-termini of tubulin, unlike kinesin-13. We biased the diffusion using optical tweezers and analyzed the time-traces of biased diffusion by means of a fluctuation analysis. We found that Kip3p diffusion is a multi-step process with a physical step size of 8 nm and an average dwell time of 6 ms per step. The step size was supported by the direct observation of 8 nm motions and a non-linear force-velocity relationship. At high forces the biased diffusion appeared like a one-step process indicating the presence of only one force-dependent step. Our results compared well with Monte Carlo simulations and suggest that Kip3p diffusion is a undirected, hand-over-hand, random walk along the microtubule lattice.

BP 15.2 Wed 14:45 ZEU 260

The Motility of Monomeric and Dimeric Variants of Eg5 studied in the Presence of the Kinesin-5-specific Inhibitor Monastrol — Stefan Lakämper, •Christina Thiede, Stefanie Reiter, Kerstin v. Roden, and Christoph Schmidt — 3. Physikalisches Institut, Georg-August-Universität, 37077 Göttingen

The homo-tetrameric motor-protein Eg5 from Xenopus laevis drives relative sliding of anti-parallel microtubules, most likely by the processive action of its two sets of dimeric motor domains at each end. As recently shown by Kwok et al. (NCB 2006) and Kapitein et al. (JCB 2008), tetrameric motors move on a single microtubule in a fashion including diffusional and directional episodes, while motors moving between anti-parallel microtubules act in a highly directional and processive fashion. We have studied the processive behavior of a dimeric chimera (Eg5Kin) carrying the Eg5-motor and neck-linker and the Kinesin-1 neck and stalk. While Eg5Kin displays essentially the same motile properties as a truncated Eg5 (Eg5-513 his, Krysziak et al., JBC 2006, Valentine et al., NCB, 2006) its processivity is 40x increased to about 240 consecutive 8nm-steps on average, at a velocity of 95 nm/s. With increasing monastrol concentrations we find a dose-dependent and cooperative reduction in run length, but not in speed, indicating that two monastrol molecules are required to terminate a processive run. To further study the allosteric effect of monastrol on the motility of Eg5-motors, we generated monomeric and dimeric Eg5-constructs and compared their surface gliding-velocities in the presence of increasing concentrations monastrol.

BP 15.3 Wed 15:00 ZEU 260

Buckling of semiflexible filaments under action of molecular motors — •Krzysztof Baczyński[1], Melanie Müller[1], Reinhard Lipowsky[1], and Jan Kierfeld[1,2] — [1]Max Planck Institute of Colloids and Interfaces, Department of Theory & Bio - Systems, Science Park Golm — [2]TU Dortmund University, Faculty of Physics, D - 44221 Dortmund

In this work we present a model for the buckling of semiflexible filaments under the action of molecular motors. We investigate a system in which a group of motors moves along a clamped filament carrying a second filament as a cargo. The cargo-filament is pushed against the wall and eventually buckles. Depending on boundary conditions we observe different buckling behaviors. For a long cargo-filament the critical Euler force for buckling is much smaller than the stall force of a single molecular motor, which leads to buckling of the cargo-filament. We use an analytical linear approximation of the resulting force-extension relation of the buckled filament [1]. Using Bell-theory for unbinding of a motor and a linear velocity-force relation we obtain a stochastic equation for probability pn(t) that n motors link both filaments at time t. Finally, we calculate the mean first passage time needed for unbinding of linking motors which corresponds also to the transition between buckled and unbuckled state of cargo-filament. Our results show that for sufficiently long filaments the movement of kinesin motors is not affected by the load force generated by the cargo filament. Our numerical solution is confirmed by computer simulations.

1) K. Baczyński, R. Lipowsky, J. Kierfeld, PRE 76, 061914, 2007

BP 15.4 Wed 15:15 ZEU 260

Stochastic simulations of cargo transport by several processive motors — •Christian Korn[1], Stefan Klumpp[2], Reinhard Lipowsky[3], and Ulrich S. Schwarz[1,4] — [1]University of Heidelberg, Bioquant 0013, Im Neuenheimer Feld 267, 69120 Heidelberg, Germany — [2]Center for Theoretical Biological Physics, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0374, USA — [3]Max Planck Institute of Colloids and Interfaces, Science Park Golm, 14424 Potsdam, Germany — [4]University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany

We use stochastic computer simulations to study the transport of a spherical cargo particle along a microtubule-like track by several kinesin-like processive motors. Our adhesive motor dynamics algorithm combines the numerical integration of a Langevin equation for the motion of a sphere with rules for the reaction kinetics of molecular motors. The Langevin part includes diffusive motion, the action of the pulling motors, and hydrodynamic interactions with the planar substrate. The kinetic rules for the motor reactions model binding and unbinding to the filament as well as active motor steps. As a first validation of our model, we show that the simulated mean transport length increases exponentially with the number of bound motors, in good agreement with earlier results. For a fixed number of motors attached to the cargo, the distribution of the number of motors in binding range to the motor track is found to be Poissonian in most cases. We also find that load is equally shared due to a corresponding spatial arrangement of the motors only for unusually long-lived bonds.

BP 15.5 Wed 15:30 ZEU 260

Diffusion of cooperative molecular motors displaying bidirectional motion — •Ernesto M. Nicola and Benjamin Lindner — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

The movement of motor proteins along filaments forming part of the cytoskeleton is usually directional. However, recently it has been observed experimentally that collections of certain motor proteins can move bidirectionally [1]. This bidirectional motion can be described, as proposed by Badoual et al. [2], by a two-state model with many particles attached to a rigid backbone. We contrast this model with a even simpler description based on an active Brownian particle dynamics. This simple description is shown to capture the main features of the more complex ratchet model. In particular, we predict that there should exist a critical force for which the effective diffusion coefficient jumps from very large values to small ones [3]. This critical force applied to the backbone separates a region of giant diffusion from a regime of reliable directed transport.

[1] Endow and Higuchi, Nature **406**, 913 (2000).
[2] Badoual, Jülicher and Prost, Proc. Natl. Acad. Sci. **99** (2002).
[3] Lindner and Nicola, Phys. Rev. Lett. **101**, 190603 (2008).