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Dancing along microtubules: Molecular mechanism of one-dimensional diffusive motion of proteins along microtubules

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In a cellular environment, two kinds of motion exist: diffusion and directed transport. While diffusion (a passive process driven by thermal energy) is effective on short distances, directed motion (driven by motor proteins that convert chemical energy into directed motion) is effective over large distances. Diffusion is of interest because a number of recent studies reports examples where motor proteins and microtubule associated proteins use diffusive motion in one dimension along microtubules (MTs) for physiologically essential cell functions, such as: to search for binding sites (e.g. MCAK/ kinesin-13 [1] targeting MT ends for MT depolymerization), or to directionally slide MTs against each other (e.g. Ncd/kinesin-14 [2] and Ase1/ MAP65 [3] stabilizing the mitotic spindle during the cell division). Despite the fact that the diffusive motion along MTs is crucial for a whole variety of vital cell functions, the biophysical properties and precise molecular mechanism of such motion are remaining largely unexplored. Here, we (i) present a method for the quantitative characterization of the dynamic properties of the diffusive motion of molecules along MTs; (ii) discuss what would be an optimal way to describe the diffusive motion of molecules over MTs in single molecule experiments; and (iii) use the presented method to report on the dependence of the diffusive motion of Ase1 and Ncd on the ionic strength of the surrounding solution. It is well accepted that the diffusive motion of proteins along charged filaments occurs via two modes of motion: sliding, whereby protein remains in continuous contact with the filament, and microscopic hopping events [4]. In hopping, the protein dissociates from the filament, diffuses in solution and almost immediately reassociates in direct proximity to the dissociation point on the same filament. Here, to our knowledge for the first time, we discuss the diffusive motion of proteins along MTs in terms of hopping and sliding.

This work was supported by the DFG (FOR 877).

References

[1] J . Helenius, G . Brouhard, Y. Kalaidzidis, S . Diez, J. Howard: *The depolymerizing kinesin MCAK uses lattice diffusion to rapidly target microtubule ends*. Nature **441**, 115–119 (2006)

[2] G. Fink, L. Hajdo, K.J. Skowronek, C. Reuther, A.A. Kasprzak, S. Diez: *The mitotic kinesin-14 Ncd drives directional microtubule-microtubule sliding*. Nat. Cell. Biol. **6**, 717–723 (2009)

[3] M. Braun, Z. Lansky, G. Fink, F. Ruhnow, S. Diez, M.E. Janson: *Adaptive braking by Ase1 prevents overlapping microtubules from sliding completely apart*. Nat. Cell. Biol. **13**, 1259–1264 (2011)

[4] P.H. von Hippel, O.G. Berg: *Facilitated target location in biological systems*. J. Biol. Chem. **264**, 675–678 (1989)