BP 26: From Single-Molecule to Tissue Dynamics

Time: Thursday 14:00–17:15 Location: H43

Invited Talk BP 26.1 Thu 14:00 H43

Molecular misfolding investigated by mechanically unzipping nucleic acids — •Felix Ritort — Departament de Fisica Fonamental, Facultat de Fisica, Universitat de Barcelona, Diagonal 647, 08028 Barcelona (Spain) — CIBER-BBN of Bioengeneering, Biomaterials and Nanomedicine, ISCIII, Madrid (Spain)

Recent developments in micro and nano technologies allow for the controlled manipulation of individual molecules by exerting and detecting forces in the piconewton range. The possibility to detect such tiny forces together with the ability of measuring extensions with nanometer resolution allows scientists to monitor molecular reactions in real time (e.g. molecular folding) and characterize thermodynamics and kinetics of individual molecules (e.g. nucleic acids and proteins) with unprecedented energy accuracy within tenths of a kcal/mol.

Single molecule manipulation make possible to disrupt molecular bonds that hold native structures in nucleic acids and proteins. In this talk I will show experimental results on irreversibility and dissipation in nucleic acid hairpins that are mechanically unzipped using optical tweezers. Our aim is to explore complex molecular free energy landscapes and nonequilibrium behavior in small systems . For this we have designed DNA hairpins of specific sequences that exhibit molecular misfolding to investigate the role of irreversibility and dissipation during the folding process. Our results suggest the existence of a universal mechanism used by chaperones to assist molecular folding of RNAs and proteins.

BP 26.2 Thu 14:30 H43

Import of DNA by *Helicobacter pylori* is reversible by application of external force — •Stephanie Müller[1,2], Kerstin Stingl[1,2], Gerda Scheidgen-Kleyboldt[2], Martin Clausen[2], and Berenike Maier[2] — [1]equal contribution — [2]Westfälische Wilhelms-Universität, Biological Department, 48149 Münster, Germany

Many bacterial species are capable of taking up and incorporating exogenous DNA in their genome. For the transport of DNA across the outer and inner membrane, the gram-negative gastric pathogen *Helicobacter pylori* uses a reverse type-IV-secretion-system, termed ComB. Besides this secretion-system related mechanism, further proteins are also involved in DNA uptake, among them the inner membrane channel ComEC. DNA-uptake experiments revealed that *H. pylori* cells posses multiple polar DNA-uptake complexes. In addition, knockout mutants in two motor proteins, ComB4 (an ATPase) and ComB6 (an inner membrane protein), and in the inner membrane channel ComEC were characterized revealing that the ComB-system and the inner membrane channel act at different steps of DNA uptake. The physical properties of the uptake motor were characterized in laser-trap experiments: Upon application of external force, previously imported DNA was extracted, revealing reversibility of the motor at 23pN external force. The average DNA import velocity was 2,2 kbp/sec. Taken all data together, a temporally uncoupled mechanism of DNA uptake is proposed: First the fast and reversible uptake across the outer membrane mediated by the ComB-system, and secondly the ComEC-dependent inner-membrane transport.

BP 26.3 Thu 14:45 H43

Monitoring a single F_oF_1-ATP synthase in an anti-Brownian electrokinetic (ABEL) trap — •Karin Seyfert, Torsten Rendler, Andrea Zappe, Stefan Ernst, Nawid Zarrabi, and Michael Börsch — 3. Physikalisches Institut, Pfaffenwaldring 57, 70569 Stuttgart

ATP (adenosine triphosphate) is the energy currency of every cell. It is produced by the F_oF_1-ATP synthase. This membrane-embedded enzyme consists of two rotary motors. To analyze the functioning of this enzyme, we measure FRET (Fluorescence Resonance Energy Transer) with single, freely diffusing F_oF_1-ATP synthases in a confocal microscope. The disadvantage of this method is the limited observation time up to 300 ms due to Brownian motion [1]. We aim to trap the enzyme inside the confocal volume. The ABEL (Anti Brownian Electrokinetic) trap is a microfluidic system invented by A.E. Cohen (Harvard) and W.E. Moerner (Stanford) [2]. Fluorescent lipid vesicles containing a single FRET-labeled ATP synthase are monitored by an EMCCD camera and the image is used for the electrokinetic feedback in real time to bring the vesicle back to a set point. Thereby, extended FRET measurements on a single enzyme in solution are possible.

[1] M.G. Duser, N. Zarrabi, D.J. Cipriano, S. Ernst, G.D. Glick, S.D. Dunn, and M. Borsch: 36 degrees step size of proton-driven c-ring rotation in FoF1-ATP synthase, Embo Journal 28, 2689 (2009). [2] A.E. Cohen and W.E. Moerner: Suppressing Brownian motion of individual biomolecules in solution, Proc Natl Acad Sci U S A 103, 4362 (2006).

BP 26.4 Thu 15:00 H43

Cooperative binding of kinesin motors on microtubules studied with atomic force microscopy — •Karen Hollenberg, Iwan A. T. Schaap, and Christoph F. Schmidt — Drittes Physikalisches Institut, Fakultät für Physik, Georg-August-Universität Göttingen

Kinesin motor proteins move actively along microtubules and drive intracellular transport of vesicles and organelles in cells. Since most transport processes involve smaller or larger ensembles of motors, it is an interesting question if and how motors communicate and coordinate their activity in such ensembles. One possibility is direct head-to-head interaction. An intriguing alternative is interaction via the substrate, the microtubule lattice.

We have here used atomic force microscopy in buffer to search for axial and lateral cooperativity in the binding of motors. The results show that kinesin-1 dimers and monomers cluster when immobilized on the track by AMP-PNP. For monomers this effect is less pronounced.

BP 26.5 Thu 15:15 H43

Nuclear centering in fission yeast mediated by kinesin-8 motor proteins — •nicola maghelli[1], vladimir krstić[2], nenad pavin[2], frank jülicher[2], and iva tolić-nørrelykke[1] — [1]MPI-CBG, Dresden, GERMANY — [2]MPI-PKS, Dresden, GERMANY

In the fission yeast *Schizosaccharomyces pombe*, the nucleus is positioned at the cell center. Since the nucleus determines the cell division site, keeping the nucleus at the center is crucial for ensuring symmetrical cell division (1). Microtubules push against the cell ends and exert force on the nucleus (2), but how the cell regulates these forces in order to center the nucleus remains unknown. Here we tackle this problem by using a combination of live cell imaging, cell manipulations by laser ablation and optical tweezers, and a theoretical model. We show that microtubule pushing forces can center the nucleus because of a larger number of contacts between the microtubules and the proximal cell end than the distal one. Moreover, kinesin-8 motors (Klp5/6) increase the rate of microtubule catastrophe (transition from growth to shrinkage) in a microtubule length- and contact time-dependent manner. Thus, the motor behavior results in a longer contact between a microtubule and the proximal than the distal cell end. Taken together, our experimental and theoretical results provide a novel centering mechanism, where kinesin-8 motors increase the efficiency of nuclear centering.

1. I. Tolić-Nørrelykke, L. Sacconi, C. Stringari, I. Raabe, F. S. Pavone, Curr Biol 15, 1212 (Jun 30, 2005).
2. P. T. Tran, L. Marsh, V. Doye, S. Inoue, F. Chang, J Cell Biol 153, 397 (Apr 16, 2001).

BP 26.6 Thu 15:30 H43

Cargo transport by molecular motors against shear flow — •Fridtjof Kowald[1,2], Christian Korn[3], and Ulrich Schwarz[2,3] — [1]Karlsruhe Institute of Technology, Theoretical Biophysics Group — [2]University of Heidelberg, Institute for Theoretical Physics — [3]University of Heidelberg, Bioquant

Processive molecular motors like kinesins transport cellular cargo like vesicles, organelles, nuclei or viruses along cytoskeletal tracks like microtubules. In a physiological context, the motors usually work in groups. This allows them to stay attached to the filament for a long time and to produce high levels of force. There are several sources for opposing forces which disrupt cargo transport, including viscous forces on the moving cargo, forces from motors pulling in other directions, forces from the interaction of the cargo with other cellular structures, and shear forces due to hydrodynamic flow in the environment. Here we address the latter case using computer simulations for adhesive motor dynamics. Our Langevin equation includes hydrodynamic interactions of the spherical cargo with the wall and the shear flow, rupture and rebinding of the motor connections to the filament, and motor stepping with a linear force-velocity relation. Our main result is the distribution of unbinding times as a function of motor number

and shear rate. This allows us to predict how the critical shear flow for non-productive transport increases as a function of motor number. We comment on possible applications of our results to cellular systems and in nanobiotechnology.

15 min. break

BP 26.7 Thu 16:00 H43

Origin and Spatial Distribution of Forces in Motile Cells — Claudia Brunner[1], Michael Gögler[1], Allen Ehrlicher[1], Daniel Koch[1], Thomas Fuhs[1], Charles Wolgemuth[2], and •Josef A. Käs[1] — [1]Division of Soft Matter Physics, Department of Physics, University of Leipzig — [2]Department of Cell Biology and the Center for Cell Analysis and Modeling, University of Connecticut Health Center

Inspired by ambivalent data of individual cellular forces we provide a first complete and consistent set of forces that act in a moving cell measured by a novel SFM technique. Besides contributions from blebbing and hydrodynamics flows it was generally believed that the protrusion of a migrating cell*s leading edge is driven by actin polymerization. Our force measurements modulated by various cytoskeletal drugs show that hydrodynamics flows are negligible and solely actin polymerization drives the advancement of the central lamellipodium. Moreover, we measure the retrograde forces in the midst of the lamellipodium, the central missing link to understand how forces are balanced in motile cells. While the motions in the central lamellipodium, i.e. protrusion and retrograde flow, are solely driven by polymerization and depolymerization forces, the lamellipodial wings and the forces that pull the cell body along rely heavily on contractile actin-myosin interactions. The traction forces in the wings significantly contribute to the local retrograde flow and are the origin of strong forces that advance the cell body.

BP 26.8 Thu 16:15 H43

Theoretical modelling of bacterial motor dynamics — •Eva Baresel and Rudolf Friedrich — Institute for Theoretical Physics, WWU Münster, Wilhelm-Klemm-Str. 9, 48149 Münster, Germany

The motion of self-propelled flagellated bacteria consists of two different modalities: "running" if all flagella rotate counter-clockwise or "tumbling" if at least one flagellum rotates clockwise. As a model for these bacterial motors we consider the dynamics of an ensemble of swimming objects which are composed of two rigidly connected point vortices. The single objects are able to show translation or rotation depending on the circulations of the single point vortices. We discuss the collective behaviour for several of these objects and the resulting velocity fields by means of numerical calculations.

BP 26.9 Thu 16:30 H43

Transition to clustering in bacterial colonies: myxobacteria mutants as self-propelled rods — •Fernando Peruani[1], Joern Starruss[2], Markus Baer[3], Andreas Deutsch[2], Vladimir Jakovlievic[4], and Lotte Sogaard-Andersen[4] — [1]Service de Physique de l Etat Condense, CEA Saclay, 91191 Gif-sur-Yvette, France — [2]ZIH, Technische Universitaet Dresden, Zellescher Weg 12, 01069, Dresden, Germany — [3]Physikalisch-Technische Bundesanstalt, Abbestr. 2-12, 10587 Berlin, Germany — [4]Max Planck Institute for Terrestrial Microbiology, Karl-von-Frisch Str. 35043 Marburg, Germany

Myxobacteria, as many other bacteria, exhibit a transition from unicellularity to multicellularity when the level of nutrients is low. This fascinating process starts with the onset of clustering and collective motion. In contrast to Dictyostelium discoideum and other microorganisms, myxobacteria aggregate and coordinate their motion, in this early stage, without making use of diffusing chemical signals. We show through experiments with the mutant A+S-Frz- of M. xanthus, as well as through theoretical models, that is the active motion of the cells plus their rod-like shape what presumably allows cells to exhibit such collective effects. Provided the cell density is above a given threshold, a transition to clustering occurs. The cluster size statistics from experimental data can be reproduced by a simple models for self-propelled rods.

BP 26.10 Thu 16:45 H43

Compartment boundaries in developing epithelia — •Maryam Aliee[1], Katharina Landsberg[2], Jonas Ranft[1], Christian Dahmann[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physcis of Complex Systems, 01187 Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, 01307 Dresden, Germany

During the development of tissues distinct cellular compartments are established. Straight and sharp interfaces between these compartments are maintained during development, so called compartment boundaries. A fundamental question is to identify the mechanisms by which boundaries form and remain stable. An important model system to study compartments is the wing development of the fruit fly Drosophila.Two different compartment boundaries are established during the development of the wing imaginal disc, the Anterior-Posterior boundary and the Dorsal-Ventral boundary. To study the role of cell mechanics and cell division we use a vertex model. We consider two dividing populations of cells and analyze the effect of local changes of cell bond tension and cell proliferation on the morphology of compartment boundaries. We find that a straight interface is maintained between two compartments if the proliferation rate of cells near the boundary is reduced. Increased bond tension at interface also leads to sharp boundaries. We quantify cell packing properties and interface roughness and study the interfacial tension associated with the compartment boundary using the stress profile in the system.

BP 26.11 Thu 17:00 H43

Antisymmetric stress and the role of angular momentum conservation in complex fluids. — •Sebastian Fürthauer, Stephan Grill, and Frank Jülicher — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Str. 38, 01187 Dresden, Germany

The stress tensor of a Newtonian fluid is symmetric in the hydrodynamic limit. However, in complex fluids, such as nematic liquid crystals, the director field can exert a torque if it is locally rotated away from its undistorted configuration. This produces a reactive antisymmetric contribution to the stress tensor. Here, we provide the derivation of a hydrodynamic theory for a complex fluid based on identifying the entropy production rate from the rate of change of the free energy. Analyzing the angular momentum balance, reveals that an additional dissipative contribution to the antisymmetric stress exists. We obtain an expression for the antisymmetric dissipative stress by expanding thermodynamic fluxes in terms of thermodynamic forces, which is crucial in understanding the non-equilibrium dynamics of chiral complex fluids, such as the acto-myosin cytoskeleton or a fluid driven by beating cilia.