BP 31: Cell adhesion, mechanics and migration II

Time: Wednesday 17:00–18:30 Location: ZEU 250

Topical Talk BP 31.1 Wed 17:00 ZEU 250

Active torque generation by the actomyosin cortex — •Stephan Grill — BIOTEC, TU Dresden, Germany — MPI-PKS Dresden, Germany — MPI-CBG Dresden, Germany

Many developmental processes break left/right symmetry with a consistent handedness, which requires cellular processes that are chirally asymmetric. Here we describe a novel process of active torque-generation in the actomyosin cortex. We present evidence that active torques drive chiral counter-rotating cortical flow in the polarizing Caenorhabditis elegans zygote, depend on myosin activity, and can be specifically altered through changes in cortical structure and dynamics. Notably, genes that affect the establishment of the C. elegans left/right body axis also control active torques. Our work suggests that actomyosin-based cell chirality provides a fundamental mechanism for chiral morphogenesis in development.

BP 31.2 Wed 17:30 ZEU 250

Keratocyte-like movement of the slime mold *Physarum polycephalum* — •Christina Oettmeier, Jonghyun Lee, Erik Bernitt, and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen, 28359 Bremen

We report on a particular motility pattern in *P. polycephalum*, which closely resembles the forward movement of fish keratocytes. When microplasmodia are plated upon an agar surface, they will fuse and form a network in a percolation transition [1]. However, under certain environmental conditions, the microplasmodia fuse into wedge-shaped structures ("satellites") and start to move outwards for several hours. The satellites are laterally elongated, with one large, curved growth front along the front arc. They move unidirectionally for several cm and maintain a half-moon shape. This behaviour has not been described in *P. polycephalum* locomotion before, but is characteristic for, e.g., fish keratocytes. One mutant *Dictyostelium* cell line, however, was shown to exhibit this movement as well [2]. We characterize the morphology and different phases of development of the satellites, using light microscopy, fluorescence imaging and electron microscopy. The fact that both *Dictyostelium* amoebae and vertebrate cells are relatively small whereas *P. polycephalum* is huge and multinucleate, makes the discovery of a seemingly common movement pattern significant for further investigation of universal modes of motility. [1] Fessel, Oettmeier, Bernitt, Gauthier, Döbereiner, *PRL* **109** (2012) [2] Asano, Mizuno, Kon, Nagasaki, Sutoh, Uyeda, *Cell Motility and the Cytoskeleton* **59** (2004)

BP 31.3 Wed 17:45 ZEU 250

Actin-MT interactions result in mutual sensing and remodeling — •Florian Huber[1], Magdalena Preciado López[1], Michel O. Steinmetz[2], Anna Akhmanova[3], Gijsje Koenderink[1], and Marileen Dogterom[1] — [1]FOM Institute AMOLF, Amsterdam, The Netherlands — [2]Laboratory of Biomolecular Research, Paul Scherrer Institut, Switzerland — [3]Division of Cell Biology, Utrecht University, The Netherlands

The cooperative functioning of actin and microtubules (MTs) is increasingly regarded as a central element for many cellular key processes including cell division, cell migration, and adhesion. Several specific actin-MT linker molecules have been discovered, but a detailed understanding of their effects on actin-MT co-organization remains elusive. For a more profound and quantitative understanding of actin-MT crosstalk we developed a simple yet realistic reconstituted model system. To account for the diversity of cytoskeleton architectures we confront dynamic MTs with loose actin networks or rigid bundles. Coupling between the two cytoskeleton components is introduced in form of transient binding of growing MT plus ends to actin filaments using a physiologically relevant actin-MT linker (MACF). We find that MACF allows growing microtubules to steer actin bundle formation and to transport actin filaments. In return, existing actin bundles can reliably capture and guide growing microtubules. Facing a wide spectrum of different geometrical and mechanical settings, the same dynamic actin-MT cross-linker can hence lead to a rich repertoire of co-organizational effects, independent of biochemical regulation.

BP 31.4 Wed 18:00 ZEU 250

Speed and nuclear deformations during cancer cell migration through narrow pores — •Christoph Kämmerer[1], Lena Lautscham[1], Sebastian Lachner[1], Amy Rowat[2], Carolin Gluth[1], and Ben Fabry[1] — [1]Department of Physics, Biophysics Group, University of Erlangen-Nuremberg, Germany — [2]Department of Integrative Biology and Physiology, UCLA, USA

To metastasize, cancer cells migrate through the narrow pores of the extracellular matrix. To study cell migration and nuclear deformations in narrow pores, we use soft lithography to fabricate a series of channel segments ($18\mu m$ length, $3.7\mu m$ height, decreasing width from $10.5 - 1.7\mu m$), each separated by a $20x20\mu m$ chamber so that cells can spread and relax between channel crossings. We compare highly invasive HT1080 fibrosarcoma cells with less invasive MDA-MB-231 breast carcinoma cells. Cells are stained with Hoechst 33342 dye to track the speed and shape of the nucleus. For channels $> 7\mu m$, cell migration is largely unimpeded. When encountering smaller channels, the cell nucleus stalls while the cell body migrates through the channel. Eventually, the nucleus elongates and enters the channel. Once fully elongated, the nucleus glides through and exits the channel with higher speed. Highly invasive HT1080 cells migrate faster through narrow channels compared to MDA-MB-231 cells. These data show that the nucleus is the principal source of resistance against migration through narrow channels. The stalling of the nucleus when entering a channel, and the speed-up of the nucleus when exiting a channel indicate that cells need to build up traction forces to pull the nucleus along.

BP 31.5 Wed 18:15 ZEU 250

Real-time and high-throughput mechanical phenotyping of suspended cells — •Oliver Otto[1], Philipp Rosendahl[1], Stefan Golfier[1], Alexander Mietke[1], Salvatore Girardo[1], Stefano Pagliara[2], Ulrich Felix Keyser[2], and Jochen Guck[1,2] — [1]Biotechnology Center, TU Dresden, Tatzberg 47/49, 01307 Dresden, Germany — [2]Cavendish Laboratory, University of Cambridge, JJ Thomson Avenue, Cambridge, CB3 0HE, UK

The mechanical properties of cells have been emerging as label-free, inherent marker of biological function and disease. Concerted utilization has so far been hampered by the availability of a convenient and robust measurement technique. We report the development and characterization of a microfluidic system for mechanical single cell classification in real-time with analysis rates of several hundred cells per second.

A cell suspension is driven through the constriction zone of a microfluidic chip resulting in cell deformation due to hydrodynamic interactions only. Our custom-built image processing software is capable of performing image acquisition, image analysis and data storage on the fly allowing for mechanical phenotyping of several hundred cells per second in real-time.

The ensuing deformations can be described by an analytical hydrodynamic model. Initial experiments based on our novel technology with different cell types are in agreement with results obtained with atomic force microscopy and optical stretcher. Our method allows continuous mechanical phenotyping of large cell populations with a throughput previously only known from flow cytometry.