BP 38: Membranes and Vesicles II (joint session BP/CPP)

Time: Friday 9:30–12:00 Location: H 2013

BP 38.1 Fri 9:30 H 2013

Change of thermodynamic state of cell membrane during an action potential — •Simon Fabiunke, Christian Fillafer, and Matthias Schneider — Medizinische und Biologische Physik, TU-Dortmund

Nonlinear pulses like action potential are considered to be purely electrical phenomena. However, it has been shown that thermal, mechanical, chemical and optical changes also occur at the excitable membrane. From a thermodynamic perspective such pulses have been described as a propagating state change in the cell membrane.

In the present work, we investigated the emission properties of a commonly used potential-sensitive dye (di-4-ANEPPDHQ) as a function of state in phospholipid vesicles and cell membranes. When the thermodynamic state of vesicles made from di-myristoyl-phosphatidylserine (DMPS) was changed by temperature or pH, the fluorescence intensity and spectrum of the embedded dye underwent characteristic changes. During the transition from the liquid-disordered to the liquid-ordered phase, the fluorescence intensity exhibited a maximum and the emission spectrum shifted to shorter wavelengths (by about 26 nm). Subsequently, the same dye was incorporated into the plasma membrane of an excitable cell (Chara Braunii). When an action potential was triggered the emission spectrum shifted to shorter wavelengths. This indicates that propagation of an action potential is associated with a significant change of state of the excitable cell membrane.

BP 38.2 Fri 9:45 H 2013

Vesicle adhesion and fusion studied by small-angle x-ray scattering — •Karlo Komorowski[1], Annalena Salditt[1], Yihui Xu[1], Halenur Yavuz[2], Martha Brennich[3], Reinhard Jahn[2], and Tim Salditt[1] — [1]Institut für Röntgenphysik, Georg-August-Universität Göttingen, Göttingen, Germany — [2]Department of Neurobiology, Max-Planck-Institute for Biophysical Chemistry, Göttingen, Germany — [3]European Molecular Biology Laboratory, Grenoble, France

Membrane fusion takes place in numerous physiological processes on the cellular and subcellular level as in the case of synaptic neurotransmission. The merger of two membranes generally involves a highly complex interplay on the molecular level among lipids, membrane fusion proteins, ions of the aqueous environment and water molecules. We aim at the structure of intermediate states of a vesicle and membrane fusion pathway. A main emphasis is laid on adhered vesicles. Recent observations indicate that such a docking state, showing two flattened membranes in close proximity, plays a role in vesicle fusion. For this purpose, we have studied adhesion and fusion of lipid vesicles induced by $CaCl_2/MgCl_2$, and show that a stable adhesion state can be induced under certain conditions. The bilayer structure and the inter-bilayer distance between adhered vesicles was analyzed by small-angle x-ray scattering (SAXS). From the obtained structural parameters we aim at an understanding of inter-membrane potentials in adhesion and in fusion. Finally, we have studied structural dynamics of lipid vesicle fusion using time-resolved SAXS techniques, and show that intermediate states can be distinguished over time.

Invited Talk BP 38.3 Fri 10:00 H 2013

The role of dynamin twist in membrane fission — Martina Pannuzzo[1], Zachary A. McDargh[1,2], and •Markus Deserno[1] — [1]Department of Physics, Carnegie Mellon University — [2]Department of Chemical Engineering, Columbia University

The final step of many biological membrane fission events involves the GTPase dynamin, which assembles into a helical filament around the neck of a nascent vesicle and somehow severs this remaining connection. But despite about two decades of research, the actual physical processes that lead to fission are still a matter of debate. Dynamin's action occurs on the scale of a few tens of nanometers over just a few milliseconds, which is too small and fast for many experimental techniques, but too large and slow for atomistic simulations. Here we present coarse-grained simulations that are specifically designed to capture the interplay of geometry and elasticity. We argue that, within reasonable experimental limits, the two widely discussed conformational changes of shrinking the radius or increasing the pitch of a dynamin helix are insufficient to trigger fission. However, a third change, reminiscent of an effective twist of the filament, which accounts for the experimentally observed asymmetric unbinding of dynamin's PH-domains, turns out to efficiently drive the neck into the hemifission state. Following the retraction of the substrate, the remaining dynamin coat can unbind, and the tensile force in the connecting micellar string draws the almost severed membranes together one more time, until bilayer contact catalyzes the scission of the micelle.

BP 38.4 Fri 10:30 H 2013

Appling forces to model cells using microfluidic systems — •Tom Robinson — Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

Biological cells in their natural environment experience a variety of external forces such as fluidic shear stress, osmotic pressures, and mechanical loads. While membrane proteins are a crucial part of the cellular response to external stimuli, in recent years so called *lipid rafts* have been thought to play an important role in the spatial organization of membrane proteins. Synthetic membranes such as giant unilamellar vesicles (GUVs) offer a reduced cell model, whereby individual components can be isolated and studied without interference from the complexity of the natural cell. However, applying specific forces to these delicate objects in a controllable manner is non-trivial. To this end, we report a microfluidic method to capture GUVs and apply a variety of forces. The first device contains micro-patterned electrodes which allows the application of electric fields and observations of the subsequent membrane fusion (Robinson et al. Lab on a chip 2014). The second device uses a valve-based system to apply specific fluidic shear forces to membranes (Sturzenegger et al. Soft Matter 2016). Our latest microfluidic design comprises an integrated micro-stamp which is able to mechanically compress GUVs to study the effects of deformation. We investigate the effects of these forces on the behaviour of lipid domains as a model for lipid rafts in cells.

BP 38.5 Fri 10:45 H 2013

Design of a switchable DNA origami structure for shaping lipid membranes — •Alena Khmelinskaia[1], Megan Engel[2,3], Garima Mishra[3], Jonathan Doye[3], and Petra Schwille[1] — [1]Max Planck Institute of Biochemistry, Planegg, Germany — [2]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford, United Kingdom — [3]Department of Physical and Theoretical Chemistry, University of Oxford, Oxford, United Kingdom

Biological membranes are dynamic cellular barriers that suffer deformation and bending. In recent years, due to its exclusive nanoengineering properties, the DNA origami technology has been vastly used to build synthetic scaffolds that partially recapitulate curvature-inducing mechanisms. Nonetheless, the control over such shaping phenomena is yet scarce. Here, we design a DNA based nanostructure with an integrated conformational switch, with the goal to deform free-standing lipid membranes. Using site-directed single-strand displacement reactions as force elements, DNA nanostructures change their conformation into a bent state. Simulations of the DNA-based nanostructures using the oxDNA coarse-grained model confirm the experimentally observed bending. A complementary approach of nucleotide sequence variation and simulation is used to balance the implemented force elements and consequently optimize the conformational switch. We show that bent DNA-based structures are capable of inducing large scale deformations on free-standing lipid bilayers. Furthermore, our results may confirm theoretical predictions of membrane bending based on the free energy changes of the bound DNA structures.

BP 38.6 Fri 11:00 H 2013

FCS analysis of protein mobility on lipid monolayers — •Jonas Mücksch[1,2], Alena Khmelinskaia[1,2], Franco Conci[1], Grzegorz Chwastek[1], and Petra Schwille[1] — [1]Max Planck Institute of Biochemistry, Am Klopferspitz 18, 82152 Martinsried — [2]authors contributed equally

In vitro membrane model systems are used to study complex biological phenomena under controlled unadulterated conditions. Lipid monolayers are particularly suited to study lipid packing in an unbiased manner. To explore the effect of lipid packing on protein mobility, we used miniaturized chambers instead of conventional Langmuir-Blodgett troughs. This assay requires only minute amounts of protein and is ideally suited to be combined with single molecule sensitive

fluorescence correlation spectroscopy (FCS) to characterize diffusion dynamics. Our results confirm the influence of lipid packing on lipid mobility and validate the use of FCS as an alternative to conventional surface pressure measurements. Furthermore, we study the effect of lipid density on the diffusion of membrane binding biomolecules, ranging from small peptides to large DNA-based nanostructures. We exploit the sensitivity of FCS to characterize protein interactions with the lipid monolayer in a low concentration regime, which is inaccessible to conventional surface pressure measurements. Finally, we relate our measurements to the characteristic hydrodynamic length of the lipid monolayer. Our work provides a detailed strategy for the conduction of point FCS experiments on lipid monolayers, which is the first step towards extensive studies of protein-monolayer interactions.

BP 38.7 Fri 11:15 H 2013

Structure and Conformation of Single and Interacting Bacterial Surfaces — •Ignacio Rodriguez Loureiro[1], Victoria Latza[1], Giovanna Fragneto[2], and Emanuel Schneck[1] — [1]Max Planck Institute of Colloids and Interfaces, Potsdam, Germany — [2]Institut Laue-Langevin, Grenoble, France

The outer surfaces of Gram-negative bacteria are composed of lipopolysaccharide (LPS) molecules exposing oligo- and polysaccharides to the aqueous environment. This unique, structurally complex biological interface is of great scientific interest as it mediates the interaction of bacteria with antimicrobial agents as well as with neighboring bacteria in colonies and biofilms. Structural studies on LPS surfaces, however, have so far dealt almost exclusively with rough mutant LPS of reduced molecular complexity and limited biological relevance. Here, using neutron reflectometry we structurally characterize planar monolayers of wild-type LPS from Escherichia Coli O55:B5 featuring strain-specific O-side chains in the presence and absence of divalent cations and under controlled interaction conditions. For interacting LPS monolayers we establish pressure-distance curves and determine the distance-dependent saccharide conformation.

BP 38.8 Fri 11:30 H 2013

Osmotic instabilities and organelle biogenesis — •Sami Al-Izzi[1,2], George Rowlands[2], Pierre Sens[1], and Matthew Turner[2] — [1]Institut Curie (UMR 168), Paris, France — [2]University of Warwick, Coventry, Uk

We study theoretically a membrane tube with unidirectional ion pumps driving an osmotic pressure difference. A pressure driven peristaltic instability is identified, quantitatively distinct from similar tension-driven Rayleigh type instabilities on membrane tubes. We discuss how this instability could be related to the function and biogenesis of membrane bound organelles, in particular the contractile vacuole complex found in protists. The unusually long natural wavelength of this instability is in close agreement with that observed in cells. We also consider extensions of this result to more complex/realistic systems.

BP 38.9 Fri 11:45 H 2013

Cholesterol effects on lateral structure formation — •Fabian Keller, Davit Hakobyan, and Andreas Heuer — Institut für Physikalische Chemie, Münster, Deutschland

Cholesterol is essential for, e.g. , the domain formation of lipid membrane mixtures and is thus at the heart of many basic properties of lipid membranes.

In recent studies we could show that cholesterol is able to intercalate between DPPC molecules without changing the mean distance of their head groups and, surprisingly, not changing the number of DPPC or DLiPC neighbors. Additionally the presence of cholesterol was found to decrease the lipid-lipid interactions of nearby lipids, indicating the complex interaction mechanisms in cholesterol containing bilayers. Our findings support the observations of cholesterol's condensing capabilities and DPPC-cholesterol interaction to be the driving force for domain formation.

To further understand the underlying mechanisms of cholesterols unique properties it is an essential step to include cholesterol to a formerly introduced Monte Carlo lattice model mapping MD data of DPPC and DUPC bilayers to a lattice [1]. Using this model one will be able to study cholesterol structure formation for decisively greater length and time scales, thereby completely resorting to input from short-time MD data.

[1] D. Hakobyan, A. Heuer, J. Chem. Phys. 146, 064305 (2017)