BP 14: Membranes and Vesicles

Time: Wednesday 9:30–13:00 Location: H 1028

Topical Talk BP 14.1 Wed 9:30 H 1028

Membrane transformations in vesicles enclosing aqueous two-phase polymer solutions — •Rumiana Dimova — Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

The interior of living cells is crowded with macromolecules. In such a concentrated environment, local phase separation may occur, involving local composition differences and microcompartmentation. Recently, giant vesicles loaded with polymer solutions were reported to exhibit spatial compartments formed by phase separation within the vesicle. We employed these artificial cell systems to study various phenomena related to molecular crowding and microcompartmentation in cells. We demonstrate that similarly to the wetting behavior of liquid droplets in contact with surfaces, different polymer aqueous phases in contact with membranes as a substrate can undergo complete to partial wetting transition (J Am Chem Soc, 2008, 130:12252). We find that the degree of wetting is characterized by a hidden material parameter - the intrinsic contact angle, which can be determined from effective contact angles observed by optical microscopy (Phys Rev Lett, 2009, 103:238103). Upon osmotic deflation of vesicles enclosing two aqueous phases that partially wet the membrane, one can observe vesicle budding and/or tube formation (Proc Natl Acad Sci USA, 2011, 108:4731) depending on the competition between the spontaneous curvature of the membrane and the wetting properties of the aqueous phases. Phase separation of aqueous polymer solutions in vesicles can lead to stable and retractable membrane nanotubes, which is relevant for membrane area storing and regulation in cells.

BP 14.2 Wed 10:00 H 1028

In vivo high pressure 1H NMR studies on oocytes of Xenopus laevis — •Joerg Koehler, Sebastian Dietz, Werner Kremer, and Hans Robert Kalbitzer — Institute of Biophysics and Physical Biochemistry, University of Regensburg, 93040 Regensburg, Germany

Oocytes of the African Clawed Frog Xenopus laevis are an excellent candidate for in vivo high pressure Nuclear Magnetic Resonance studies. This is due to their relative good resistance against mechanical stress compared to other living cells and on the other hand their quite large cell size.

We studied the oocytes in the pressure range from ambient pressure to 200 MPa by 1H NMR spectroscopy. The strongest signals come from the lipids contained in the oocytes. The signals of the lipids decrease with increasing pressure where the signals assigned to different groups behave differently. Signals due to protons in unsaturated fatty acids show a smaller pressure effect than signal arising from saturated fatty acids. The T2-values measured by a CPMG sequence are only weakly dependent on pressure. The data can be explained by a pressure dependent phase transition in the lipid droplets. The pressure induced effects observed by NMR spectroscopy are completely reversible up to a pressure of 120 MPa, which agrees well with the vitality measurements on pressure treated cells by patch-clamp experiments on the membrane.

BP 14.3 Wed 10:15 H 1028

Insights into the mechanics and uncoating of influenza virus from atomic force microscopy studies — •Frederic Eghiaian[1], Sai Li[1], Christian Sieben[2], Claudia Veigel[3], Andreas Herrmann[2], and Iwan Schaap[1] — [1]D.P.I, Georg-August-Universität Göttingen — [2]Institut für Biologie, Humboldt Universität, Berlin — [3]Lehrstuhl Zelluläre Physiologie and Centre for Nanosciences, Ludwig-Maximilians-Universität München

During the assembly and budding of the influenza virus, the viral genome is recruited in virions by the matrix proteins. This matrix forms a pseudo-continuous shell that coats the inner layer of the cellular membrane, following which capsule shaped viruses bud out of the cell. After infection this morphology, as well as the membrane-matrix-genome interaction is lost when the virus reaches the acidic endosomes, an essential step for fusion and the release of the viral genome. Using AFM we investigated the contribution of the different building blocks and the effect of pH on the mechanical properties of the virus. Contrary to protein-based capsids, Influenza virions proved highly flexible yet relatively hard to break open, a property that results from the selection of a lipid bilayer as a protective envelope. At the acidic pH of late-endosomes, the stiffness of the viruses decreased irreversibly to a value comparable to that of its lipid envelope alone. Interestingly, at the pH of early endosomes, the virus partially softened, which enhanced its fusion activity. Completed by fusion assays, our AFM study explains how low pH dismantles the flu virions, which has implications for both the viral budding and fusion mechanisms.

BP 14.4 Wed 10:30 H 1028

Local electric recordings of lipid bilayers supported on a microfabricated microporous device — •Theresa Kaufeld[1], Conrad Weichbrodt[2], Claudia Steinem[2], and Christoph F. Schmidt[1] — [1]Drittes Physikalisches Institut — [2]Fakultät für Chemie, Georg-August-Universität Göttingen, Germany

A powerful approach to study membrane proteins is the reconstitution in model membranes. Methods for artificial bilayer formation are e.g. membranes on a solid support, or the classical BLM. We have here focused on the formation of lipid bilayers on porous substrates combining the stability of solid supports and the accessibility of both sides of the bilayer of the classical BLM which is necessary for electrical recordings of membrane channels. Commercially available porous substrates however are typically not suitable for low-noise electrical experiments or for a combination with further manipulation techniques. We therefore designed a microporous substrate meeting several demands: (i) To perform multiple experiments on one chip, we divided the device into arrays of pores with separate electrolyte compartments and integrated electrical connections. (ii) We designed a PDMS sample chamber in a way that allows us to perform electrical and fluorescence recordings at the same time and exchange solutions throughout the experiment. (iii) Large pores (1μm diameter) make it possible to address the bilayer with optically trapped particles. We probed bilayer formation by impedance spectroscopy and fluorescence microscopy. The electrical properties of the substrate and the pores as well as the function of inserted ion channels are measured by current recordings.

BP 14.5 Wed 10:45 H 1028

Rotational diffusion of micrometer-sized solid domains in lipid membranes — •Eugene P. Petrov, Rafayel Petrosyan, and Petra Schwille — Biophysics, BIOTEC, Technische Universität Dresden, Dresden, Germany

The Saffman–Delbrück approximation for translational and rotational diffusion of membrane inclusions [1] is widely used in biophysical studies to relate the inclusion size to the membrane viscosity, but is limited to small inclusion sizes, typically not exceeding 100 nanometers. Although an exact solution of the problem has been derived [2], its computational complexity precludes its practical applications. To overcome this difficulty, we recently developed a simple high-accuracy analytical approximation for the translational diffusion coefficient of a membrane inclusion [3]. Using a similar approach, here we develop a simple and accurate approximation for the rotational diffusion coefficient of a membrane inclusion valid for all combinations of the inclusion size and viscosities of the membrane and surrounding media. We demonstrate the utility of our approximation by using it to analyze our experimental data on rotational diffusion of gel-phase domains on giant unilamellar vesicles showing fluid–gel coexistence.

[1] P. G. Saffman and M. Delbrück, Proc. Natl. Acad. Sci. USA **72** (1975) 3111; P. G. Saffman, J. Fluid Mech. **73** (1976) 593
[2] B. D. Hughes, B. A. Pailthorpe, and L. R. White, J. Fluid Mech. **110** (1981) 349
[3] E. P. Petrov and P. Schwille, Biophys. J. **94** (2008) L41

BP 14.6 Wed 11:00 H 1028

Active membranes - photoswitching of azobenzene cholesterol in host lipid layers — Lars Jørgensen[1], Dordaneh Zargarani[2], Annika Elsen[3], Klaas Loger[3], Benjamin Runge[3], Christian Koops[3], Rainer Herges[2], Bridget Murphy[3], Olaf Magnussen[3], and •Beate Klösgen[1] — [1]University of Southern Denmark, Inst. f. Phys. Chem. and Pharm. - MEMPHYS, Odense, Denmark — [2]CAU Kiel, Otto Diels Inst.f. Org. Chem., Kiel, Germany — [3]CAU Kiel, Inst. for Exp. and Appl. Phys., Kiel, Germany

Phosphocholine (PC) lipid membranes exhibit a sequence of thermotropic lamellar states from solid to gel to liquid ordered (LO) to liquid disordered (LD). The LD membrane conformation is considered to be the biologically relevant phase. The inoculation of guest

molecules into a host lipid layer may locally modify the initial state of the host; e.g., the incorporation of cholesterol passively induces the LO phase into a region that else how is in the LD state. The presence of a protein however may result in an active system fluctuating between the LO and the LD state, depending on the conformational changes of the protein as it conducts its functional work. We here present first results obtained from studies on an active membrane model system that consists of the photoswitchable variety of cholesterol, modified by an azobenzence group (azo-Ch), and a pure POPC host layer. Upon illumination, the azo-Ch can be reversibly switched (365nm * cis / 440 nm * trans). The functionalized cholesterol serves as a mesogen the conformation of which is coupled into the host system that in turn responds by acquiring an adjustment of its (local) structure upon switching.

15 min break

BP 14.7 Wed 11:30 H 1028

Critical and crossover phenomena in the phase separation of a two-component lipid membrane — Jens Ehrig[1], Eugene P. Petrov[1], Petra Schwille[1], and •Chiu Fan Lee[2] — [1]Biophysics, BIOTEC, Technische Universität Dresden, Dresden, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Our recent lattice-based Monte Carlo simulations [1, 2] have shown that two-component lipid membranes are characterized by a non-trivial phase diagram and may show critical behaviour. To better understand our findings, we develop a theoretical description of the system by mapping the two-component membrane onto the Landau-Ginzburg model. This approach qualitatively reproduces the phase diagram obtained in our simulations and allows us to predict the values of the critical exponents. We compare these predictions with results of our simulations and find that, while very close to the critical temperature the system exhibits Ising universality, a crossover behaviour exhibiting non-Ising exponents takes place at higher temperatures. Experimental implications of these results will be discussed.

References: [1] J. Ehrig, E. P. Petrov, and P. Schwille, Biophys. J. **100**, 80 (2011). [2] J. Ehrig, E. P. Petrov, and P. Schwille, New J. Phys. **13**, 045019 (2011).

BP 14.8 Wed 11:45 H 1028

Dynamics of vesicle adhesion mediated by mobile lipid-anchored receptors and ligands — •Susanne F. Fenz[1], Ana-Suncana Smith[2], Rudolf Merkel[3], and Kheya Sengupta[4] — [1]LION, Leiden University, The Netherlands — [2]Institute of Theoretical Physics and Excellence Cluster, Engineering of advanced materials, University Erlangen-Nuernberg, Germany — [3]Institute of Complex Systems 7, Research Centre Juelich, Germany — [4]CNRS UPR 3118, Aix-Marseille Universite, France

Giant unilamellar vesicles (GUVs) adhering to supported lipid bilayers were used as a model system to mimic dynamics of receptor-ligand mediated cell-cell adhesion. We followed the adhesion process in real time by microinterferometry and determined the adhered area, as a function of time. The adhesion process exhibits three phases: nucleation, linear growth and saturation. We find that the onset of adhesion depends critically on the concentration of ligands in the GUV. The growth regime, on the other hand, is quite robust with respect to variations in receptor or ligand concentrations, but is conditioned by the tension in the GUV membrane. GUVs with a larger excess membrane area, exhibit higher fluctuations and form multiple nucleation centers while tense GUVs usually form only one nucleation center. Accordingly, the adhesion zone of tense GUVs grows slower. While the ligand concentration in the GUV membrane sets the timescale for the nucleation, the saturation time till a steady adhesion state is reached, depends on the receptor concentration on the bilayer. We give a qualitative discussion of these experimental results.

BP 14.9 Wed 12:00 H 1028

Effective Monte-Carlo simulations for the domain dynamics in membrane adhesion — •Markus Knoll[1], Timo Bihr[2], Udo Seifert[2], and Ana-Sunčana Smith[1] — [1]Institut für Theoretische Physik and Excellence Cluster: Engineering of Advanced Materials, Universität Erlangen-Nürnberg, Germany — [2]II. Institut für Theoretische Physik, Universität Stuttgart, Germany

The formation of domains in membrane adhesion arises from the competition of the nonspecific interactions with ligand-receptor binding. The latter deform the membrane and induce long-range effects between bonds. The dynamics of this process has been studied previously by Langevin simulations in which the membrane deformations and fluctuations, the diffusion of binders, and the specific ligand-receptor interactions have been treated explicitly as coupled stochastic processes (Reister et al. New J. Phys. 13, 025003, 2011). However, due to the limited system size, these simulations could not provide information on the domain morphology. By using the fact that the membrane shape and fluctuation profile can be calculated explicitly for an arbitrary distribution of bonds, we develop an effective Monte Carlo simulation scheme. Thereby, the membrane is not explicitly simulated but its influence is taken into account through a set of effective rates for the ligand-receptor (un)binding, the latter depending on the temporal local environment of the bond and the free binders. By using these rates we reproduce the equilibrium and the average domain growth dynamics observed in the Langevin simulations and at the same time, find several qualitatively different domain growth regimes.

BP 14.10 Wed 12:15 H 1028

Competing interactions for antimicrobial selectivity based on charge complementarity — Carola von Deuster and •Volker Knecht — Max Planck Institute of Colloids and Interfaces, 14424 Potsdam

An important property of antimicrobial peptides is their ability to discriminate bacterial from eucaryotic cells which is attributed to the difference in lipid composition of the outer leaflet of the plasma membrane between the two types of cells. Whereas eucaryotic cells usually expose zwitterionic lipids, procaryotic cells expose also anionic lipids which bind the cationic antimicrobial peptides electrostatically. An example is the antimicrobial peptide NK-2 which is highly cationic and favors binding to anionic membranes. In the present study, the difference in binding affinity of NK-2 for palmitoyl-oleoyl-phosphatidyl-glycerol (POPG) and palmitoyl-oleoyl-phosphatidyl-choline (POPC) is studied using molecular dynamics simulations in conjunction with a coarse grained model and thermodynamic integration, by computing the change in free energy and its components upon the transfer of NK-2 from POPC to POPG. The transfer is indeed found to be highly favorable. Interestingly, the favorable contribution from the electrostatic interaction between the peptide and the anionic lipids is overcompensated by an unfavorable contribution from the change in lipid-cation interactions due to the release of counterions from the lipids. Overall the interaction between NK-2 and POPG is not determined by a single driving force but a subtle balance of competing interactions.

BP 14.11 Wed 12:30 H 1028

Two-component crystalline shells: invasion by a soft material — •Marc Emanuel, Andrey Cherstvy, and Gerhard Gompper — Institute of Complex Systems, ICS-2/IAS-2, Forschungszentrum Jülich, 52425 Jülich, Germany

We study the pattern formation of the ground state of two-component crystalline shells, with one component considerably softer than the other. Using approximate solutions of this nonlinear elasticity problem, we envisage the picture of invasion of the vesicle surface by the soft material. The energy minimum demands that the soft material occupies the regions of the surface with a maximal density of the elastic energy and stress. These are the 12 vertices and 30 ridges on the icosahedron that are preferred. Our theoretical results can be applicable to description of shape morphologies monitored for two-component elastic shells with very different bending and stretching moduli. From a biological perspective, the analysis can be relevant for formation of viral capsids from different protein capsomer subunits, in particular the shell of giant mimi viruses.

BP 14.12 Wed 12:45 H 1028

Dynamics of multiple vesicles under flow — •Badr Kaoui[1] and Jens Harting[1,2] — [1]Technische Universiteit Eindhoven, Postbus 513, 5600 MB Eindhoven, The Netherlands — [2]Institut für Computerphysik, Universität Stuttgart, Pfaffenwaldring 27, D-70569 Stuttgart, Germany

We study the dynamical behavior under flow of systems consisting of multiple vesicles. We are interested in suspensions of giant unilamellar vesicles (GUVs) and multilamellar vesicles (MLVs). To this purpose we developed a code combining the lattice Boltzmann method and the immersed boundary method. We present simulations of a single GUV under shear flow to validate our method and to investigate the effect of confinement on the GUV's dynamics [Kaoui, Harting and Misbah, PRE 83, 066319 (2011)]. Afterwards we demonstrate that our method is able to capture the physics of multiple vesicles. The effect of poly-

dispersity, the size of the vesicles and the action of gravity on the dynamical response of multiple vesicles subjected to shear flow are investigated