BP 26: Posters: Membranes and Vesicles

Time: Thursday 17:30–19:30 Location: Poster A

BP 26.1 Thu 17:30 Poster A

Describing the motions in phospholipid membranes with concepts from glass physics — •Sebastian Busch[1] and Tobias Unruh[1,2] — [1]Physik-Department E13 and FRM II, Technische Universität München, Garching bei München, Germany — [2]Lehrstuhl für Kristallographie und Strukturphysik, Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany

The diffusion of phospholipid molecules in membranes has been described very successfully by the free volume theory for many decades. This theory had originally been developed in the 1960s for glass physics. Although the *macroscopic* predictions of the theory are very well met, it became clear in recent years that the *microscopic* images of the motions on a molecular scale that are included in the free volume theory cannot be taken very literally.

In this contribution, we give a very short overview over the developments in glass physics since the 1960s and suggest that the microscopic description of the dynamics in phospholipid membranes could profit from an anew loan of their concepts such as soft modes and dynamical heterogeneities.

With these concepts, it is possible to explain the motions of phospholipid molecules on the pico- to nanosecond time scale which occur in transient clusters of molecules that move in a flow-like fashion. It rationalises also the small change of the motions on a 60 ps time scale when crossing the main phase transition.

BP 26.2 Thu 17:30 Poster A

Influence of charge density on bilayer bending rigidity in lipid vesicles: a combined dynamic light scattering and neutron spin-echo study — •Beate-Annette Brüning[1], Ralf Stehle[1,2], Peter Falus[3], and Bela Farago[3] — [1]Helmholtz Zentrum Berlin, Hahn-Meitner Platz 1, 14109 Berlin, Germany — [2]Universität Bayreuth, Postfach 10 12 51, 95440 Bayreuth, Germany — [3]Institut Laue-Langevin, B.P. 156, 6 rue Jules Horowitz, 38042 Grenoble, France

We report a combined dynamic light scattering and neutron spin-echo study on vesicles composed of the uncharged helper lipid DMPC and the cationic lipid DOTAP. Mechanical properties of a model membrane and the corresponding fluctuation dynamics can be tuned by changing composition. We compare the bilayer undulation dynamics in lipid vesicles composed of DMPC/DOTAP to vesicles composed of DMPC and the also uncharged reference lipid DOPC. We find, that on the local scale, lipid headgroup composition and charge change the vesicle fluctuations less than acyl chain packing inhomogenities between the composite lipids. We discuss this result on the basis of domain formation in the lipid mixtures containing charged (DMPC/DOTAP) and uncharged reference lipid (DMPC/DOPC). First, we investigate lipid vesicle size and mass diffusion using dynamic light scattering, then we study collective bilayer undulations and bulk diffusion on two distinct time scales around 25ns and 150ns, using neutron spin-echo spectroscopy. Finally, we estimate bilayer bending rigidities κ_B for the charged and uncharged lipid vesicles.

BP 26.3 Thu 17:30 Poster A

Mathematical modelling of the surface change of erythrocytes due to mechanical influences — •Elisabeth Eckle and Richards Grzhibovskis — Applied Mathematics, Saarland University, Germany

Interactions of erythrocytes with artificial surfaces (e.g. specially prepared glass or a mesh of microfibers) attract a lot of attention from both experimental and modeling communities. Besides rapid changes in the shape of the cell, these phenomena feature forming of contact areas between the cell and the surface in question.

In spite of the overwhelming biochemical complexity of an erythrocyte, simple bilayer membrane models are widely used to gain an insight into a variety of processes it is involved in. We consider the classical Helfrich model of bilayer membranes with additional contact energy terms as well as total volume and surface area constraints. The equilibrium shapes of the cell are obtained numerically through a proper FEM discretization of the weak formulation of the gradient flow for the resulting energy functional. Computations are performed in three space dimensions. We study properties of the model by exploring its results for different physical parameters, discretizations, and configurations of the artificial surfaces.

BP 26.4 Thu 17:30 Poster A

Protein aggregation driven by hydrophobic mismatch — Maxim Manakov[1], Khariton Matveev[1], •Thorsten Auth[2], and Gerhard Gompper[2] — [1]Research-educational Centre "Bionanophysics", Moscow Institute of Physics and Technology, 141700 Dolgoprudniy, Russia — [2]Forschungszentrum Jülich, Institute of Complex Systems and Institute for Advanced Simulation, 52425 Jülich, Germany

The fluid mosaic model for biological membranes proposes a homogeneous distribution of integral proteins in the lipid bilayer. However, cluster formation can be observed if an attractive interaction is taken into account. For asymmetric proteins, bilayer deformation leads to a curvature-mediated interaction. Whereas weakly-curved proteins in a planar membrane repel each other, many-particle interactions can lead to an effective attraction. For symmetric integral proteins, a mismatch of the hydrophobic length of the protein and the thickness of the lipid bilayer induces an interaction that is mediated by monolayer deformation. This system can be modeled using cylindrical inclusions for the proteins and a continuum membrane model for the monolayers; the membrane model is based on the monolayer bending rigidity and the bilayer compressibility. Numerical calculations allow us to obtain pair potentials, many-protein interactions, as well as the interaction of a single protein with a protein cluster. Both membrane-mediated attraction and translational entropy determine the ratios between monomers, dimers, trimers, and bigger aggregates that can be compared with experimental and MD simulation data.

BP 26.5 Thu 17:30 Poster A

Shape as a determinant of membrane protein cluster formation — •Gernot Guigas and Matthias Weiss — Experimental Physics I, University of Bayreuth

Clustering of membrane proteins is a key event in many vital cellular processes, for example during protein sorting or signal transduction. Recent studies have shown that protein clustering can be caused by non-specific attractive interactions between proteins which arise from a hydrophobic mismatch between the membrane and the hydrophobic domain of transmembrane proteins. Here, we show by means of mesoscopic membrane simulations that protein interactions due to a hydrophobic mismatch do not necessarily need to be attractive but can also be repulsive. Key parameter for the character of the interaction is the geometrical shape of the interacting proteins' hydrophobic domains. Attraction of two proteins is observed when they can establish a maximum interfacial contact by adsorbing to each other along the full length of their hydrophobic domains. In contrast, two proteins repell each other when only a pointwise interfacial contact is possible. A geometry-dependent attraction and repulsion hence can fine-tune protein oligomerization events.

BP 26.6 Thu 17:30 Poster A

Modeling vesicular exocytosis in chromaffin cells — •Daungruthai Jarukanont[1], Martin Garcia[1], Imelda Bonifas[2], and Ricardo Femat[2] — [1]Institut für Physik Universität Kassel — [2]División de Matemáticas Aplicadas, IPICyT, San Luis Potosí, Mexico

In cell communications, the transport of vesicles is essential for storage and release of chemical messenger molecules via exocytosis. To understand vesicular exocytosis, current signals induced by transmitter molecules from single cells experiments were measured. Each exocytotic event is characterized by a current spike, and therefore a measurement is represented by a time-series. By performing a series of experiments on chromaffin cells, including cells with pharmacological manipulation of transmitter level with L-DOPA and reserpine, and a careful statistical analysis, we found that the probability for exocytosis events follows a gamma distribution. Combining this with the results from other studies by microscopy method [1], we developed a model for the mechanism of vesicular release and were able to simulate these processes in good agreement with experiment.

[1] Steyer,J. A., Horstmann,H. and Almers,A.,Transport, capture and exocytosis of single synaptic vesicles at active zones, *Nature* 406, 849-854 (2000)

BP 26.7 Thu 17:30 Poster A

Dual emission GFP as highly sensitive fluorophore for the determination of intracellular pH with fluorescence lifetime imaging microscopy (FLIM) — •Franz-Josef Schmitt, Cornelia Junghans, Marco Vitali, and Thomas Friedrich — Biophysical Chemistry, Berlin Institute of Technology, Germany

The determination of the pH in the cell cytoplasm or in intracellular organelles is of high relevance in cell biology. During infection with the influenza virus, cells produce the M2 proton channel, which is encoded by the viral genome and represents a crucial component of the viral reproduction cycle. Influenza treatment utilizes drugs like amantadine, which are targeted against the M2 channel. We present a novel multi-parameter FLIM setup that permits the simultaneous imaging of the fluorescence amplitude ratios and lifetimes of a pH-sensitive dual-emission GFP (deGFP) enabling the determination of the activity of a fusion protein of an membrane intrinsic influenza M2 channel with tagRFP (M2-RFP) monitored by deGFP fluorescence. Both proteins (M2-RFP and deGFP) were expressed in chinese hamster ovary cells (CHO-K1) and monitored with spatial resolution of 500 nm in 2 color channels with time resolution of < 100 ps. It was shown that the presence of M2 leads to an acceleration of proton transfer across the cell membrane that is blocked by amantadine. The time-course of M2-dependent intracellular acidification can be described by a general diffusion equation for the intracellular pH in a buffered medium, thus enabling the determination of transversal proton diffusion coefficients in cell membranes.

BP 26.8 Thu 17:30 Poster A

Membrane Undulations in Ion Channel Systems Undergoing Stochastic Resonance — •Eric Stava[1], Siyoung Choi[2], Minrui Yu[2], Hyuncheol Shin[2], and Robert Blick[1,2] — [1]Universität Hamburg, Hamburg, Deutschland — [2]University of Wisconsin-Madison, Madison, Wisconsin, USA

Stochastic resonance (SR) is the process by which the signal-to-noise ratio of a system is enhanced by an increase in noise. It has been shown that Alamethicin ion channels undergo SR when appropriate levels of voltage noise are applied to them [1,2]. However, changes in the tension of the lipid membrane must also be taken into account. The converse flexoelectric effect enhances the tension in the lipid membrane in the presence of an applied voltage [3]. When voltage noise is applied to the system, this effect causes the lipid membrane to undulate. These membrane undulations enhance the time-averaged membrane area and system capacitance. From the real-time admittance of Alamethicin ion channels undergoing SR, we quantified the effects of voltage noise on the lipid membrane. We find a frequency-dependent enhancement in the system admittance with increasing voltage noise. This increase in admittance correlates with an increase in membrane tension, which enhances the time-averaged ion channel conductance. This results in improved signal transduction over a range of noise intensities.

[1] S. M. Bezrukov and I. Vodyanoy, Nature, 378, 362-364 (1995). [2] E. Stava, et al., submitted for publication. [3] A. T. Todorov, A. G. Petrov, and J. H. Fendler, J. Phys. Chem., 98, 3076-3079 (1994

BP 26.9 Thu 17:30 Poster A

Membrane Adhesion via Lipid-Anchored DNA Oligonucleotides — •Russi Gurov, Reinhard Lipowsky, and Rumiana Dimova — Department of Theory and Bio-Systems, Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

Cells interact via receptor and ligand molecules located at the surface of their membranes. The binding affinities of these molecules are an important characteristic of the membrane-membrane interactions and can be expressed in terms of the dependence of the bound receptor-ligand complexes on the concentrations of unbound receptors and ligands. In the present study, we use fluorescently-labeled complementary DNA oligonucleotides anchored to the membranes of giant unilamelar vesicles to mimic cell adhesion. By measuring the fluorescence intensities in the adhesion and in the non-adhesion regions of the vesicles we estimate the respective concentrations of bound and the unbound receptors and ligands. The obtained results on the binding affinities are compared to predictions of earlier theoretical studies on the law of mass action (Soft Matter, 2009, 5:3354). We also investigate the partitioning of two types of receptor-ligand pairs in the adhesion zone of the vesicles and discuss the implications of the results for T-cell activation.

BP 26.10 Thu 17:30 Poster A

How to tailor giant proteoliposomes — •Susanne F. Fenz[1], Rita Sachse[2], Stefan Kubick[2], and Thomas Schmidt[1] — [1]LION, Leiden University, The Netherlands — [2]Zellulaere Biotechnologie, Fraunhofer IBMT, Potsdam-Golm, Germany

In this project we address the challenge to incorporate transmembrane proteins in the membrane of giant unilamellar vesicles (GUVs). The reconstitution of biologically relevant transmembrane proteins, like receptors or channel proteins, into GUVs makes them easily accessible to further biochemical and physical investigation. Our strategy combines two approaches: in vitro eukaryotic protein expression and electro-swelling. The in vitro protein expression system is based on insect lysates. It provides endoplasmic reticulum (ER)-based vesicles which enable signal-induced translocation and post-translational modification. Starting from these vesicles of approximately 1 mum diameter we applied electro-swelling to achieve giant proteoliposomes. Our recent work showed that the efficiency of this method can be improved substantially by the presence of synthetic lipids in the electro-swelling process. As an example, we introduced the one-transmembrane protein heparin-binding epidermal growth factor-like factor Hb-EGF-eYFP in GUV membranes aided by the lipid DOPC. We applied single-molecule fluorescence microscopy to detect and further characterize the protein. In addition, we introduced biotinylated lipids that enabled us to immobilize the protein-decorated GUVs to streptavidin coated surfaces. We envision this achievement as an important first step toward systematic protein studies on technical surfaces.

BP 26.11 Thu 17:30 Poster A

Translocation of polymer chains through self-assembled lipid bilayers: A Monte Carlo study — •Marco Werner[1,2] and Jens-Uwe Sommer[1,2] — [1]Leibniz-Institut für Polymerforschung Dresden, Germany — [2]Technische Universität Dresden - Institute for Theoretical Physics

Recent experiments have shown that amphiphatic polymers may translocate through phospholipid bilayers using an ATP-independent mechanism [1]. This allows for interesting applications using flexible polymers as gene vectors, drug carriers or in cell imaging techniques. However, the mechanism of translocation is not known. We use a lattice-Monte Carlo model with explicit solvent to study self-assembled lipid bilayers interacting with single polymer chains, where all monomers of a polymer have an effective hydrophobic interaction. Under variation of the polymer hydrophobicity we observe an adsorption transition of the polymer at the surface of the bilayer. Close to the transition point the polymer induces significant perturbations of the orientational order of the lipids and the solvent permeability of the membrane is strongly increased locally. Furthermore, our simulation results indicate that for a critically adsorbed chain there is an additional free energy barrier to translocate through the bilayer's core. For polymer chains with appropiately matched hydrophobicity the bilayer becomes energetically most transparent and we observe a maximum in the translocation frequency.

[1] T. Goda et al., *Biomaterials* 31(8): 2380-2387 (2010)

BP 26.12 Thu 17:30 Poster A

Hydration strongly affects the molecular and electronic structure of phospholipid membranes — Alireza Mashaghi[1], pouya partovi[2], •tayebeh jadidi[2], Nasser Nafari[2], Philipp Maass[2], M. Reza Rahimi Tabar[2], Mischa Bonn[3], and Huib Bakker[1] — [1]FOM Institute AMOLF, Science Park 104, 1098XG Amsterdam, The Netherlands — [2]Fachbereich Physik, Universität Osnabrück, Barbarastraße 7, 49076 Osnabrück, Germany — [3]Max Planck Institute for Polymer Research, Ackermannweg 10, 55128 Mainz, Germany

We investigate the structure and electronic properties of phosphatidylcholine (PC) under different degrees of hydration at the single-molecule and monolayer level by linear scaling ab initio calculations. Upon hydration, the phospholipid undergoes drastic long-range conformational rearrangements which lead to a sickle-like ground-state shape. The structural unit of the gel-phase PC membrane appears to be a water-bridged PC dimer. We find that hydration dramatically alters the surface potential, dipole and quadrupole moments of the lipids and consequently guides the interactions of the membrane with other molecules and the communication between cells.

BP 26.13 Thu 17:30 Poster A

Unpacking the influenza virus at low pH — •Sai Li[1], Frederic Eghiaian[1], Christian Sieben[2], Andreas Herrmann[2], and Iwan Schaap[1] — [1]Drittes Physikalisches Institut, Georg-August-Universität, Göttingen — [2]Institut für Biologie, Humboldt-Universität zu Berlin, Berlin

The genome of the influenza virus is enveloped in a shell made out of a lipid bilayer which inside is covered by a layer of M1 matrix protein. During infection the virus is taken up in the endosomes of the target cell. For the release of the genome the viral composite shell must undergo large conformational changes to allow for membrane fusion with the host-cell endosome. We performed AFM indentation experiments under conditions that mimicked the gradual acidification from early to late endosomes, and we have found that the softening the viral envelope starts as early as at pH 6 and is completed at pH 5.5. We propose that this softening is related to the irreversible destabilization of the M1 layer. In addition, membrane fusion being enhanced after pre-incubation of viruses at pH6, we speculate that stripping the M1 matrix off the lipid envelope during an exposure to this intermediate pH of early endosomes is essential to achieve efficient infection.

BP 26.14 Thu 17:30 Poster A

Measuring particle fluctuations near cell membranes — •Felix Jünger and Alexander Rohrbach — Lab for Bio- and Nano-Photonics, University of Freiburg, Georges-Köhler-Allee 102, 79110 Freiburg, Germany

Thermal fluctuations are omnipresent in the world of living cells and are mainly determined by elastic and viscous forces. It is well known that the viscous drag γ increases when a particle approaches a stiff wall, but is unclear, whether this is still true close to a lipid bilayer or close to a living cell. In our work we investigate how the viscous drag changes when a spherical particle approaches a biological cell and to what extent a cell can vary the bead's temporal thermal fluctuations and the viscous drag γ in its extra-cellular space. We use photonic force microscopy (PFM) to investigate the fluctuations of an optically trapped bead, which is approached to a cell membrane. The motion of the bead is tracked interferometrically in three dimensions with nanometer precision and on a microsecond time scale. The viscous modulus $G''(\omega, d)$, but also the elastic modulus $G'(\omega, d)$ as a function of the particle distance d to the cell surface can be obtained by analyzing the fluctuation data on a broad spectral bandwidth ω. We have measured several bead-cell arrangements and present first results.

BP 26.15 Thu 17:30 Poster A

Clustering of Peripheral Membrane Proteins on Model Membranes — •Tobias Distler, Gernot Guigas, and Matthias Weiss — University of Bayreuth, Bayreuth, Germany

Peripheral membrane proteins (PMP) contribute in various vital cellular functions. In many cases they have to form clusters to accomplish their tasks. Coarse-grained molecular dynamics simulations have predicted PMP cluster formation due to membrane-mediated interactions. Here, we present a measurement setup based on fluorescence correlation spectroscopy (FCS) to probe this prediction. Prior to experiments we have studied the potential measurement signals by means of FCS simulations. These calculations showed that the detection of protein clustering via FCS cross-correlation requires the usage of PMPs with a radius of at least 1.5 nm, and a concentration of 100 Proteins/μm^2. Therefore, we have utilized the fairly large fluorescently labeled cholera toxin subunit B (CTB) bound to the lipid GM1 as a PMP in a free-standing black lipid membrane. Preliminary data indicate that cluster formation of CTB indeed can be detected with this setup.

BP 26.16 Thu 17:30 Poster A

Aggregation of Human Antimicrobial Peptide Fragments at Model Membranes — •Claudia Dannehl[1], Thomas Gutsmann[2], and Gerald Brezesinski[1] — [1]Max Planck Institute of Colloids and Interfaces, Science Park Golm, 14424 Potsdam — [2]Research Center Borstel, Center for Medicine and Biosience, 23845 Borstel

Antimicrobial peptides (AMPs) are short, amphiphilic, proteins and part of the host immune defense. They protect organisms against bacteria, viruses and fungi simply by disrupting their membrane. In our work, we focus on two fragments of the human cathelicidin and lipid monolayers as model membranes to get insight into this peptide-lipid interaction. Both peptides adopt an alpha-helical conformation and lead to a fluidization of a negatively charged DPPG monolayer, indicated by an increased transition pressure from a liquid-like to a liquid-condensed phase (seen by GIXD and IRRAS), but the increase in surface pressure and the change in the amide band upon adsorption is peptide specific. We assume that the stronger peptide-lipid interaction of one peptide is accompanied by a peptide aggregation at the interface, as studied by IRRAS on monolayers and CD spectroscopy with SDS in bulk (above the CMC). No changes in the spectra were recorded with IRRAS for zwitterionic lipids (DPPC, DOPC) and CD for the cationic CTAB , which means that the aggregation of the peptide is dominated by the charge density of the target.

BP 26.17 Thu 17:30 Poster A

elastic model for endocytosis of clathrin plaques — •yu-hsein lin[1], david jasnow[2], and hsuan-yi chen[3] — [1]Graduate Institute of Biophysics, National Central University, Taiwan R.O.C — [2]Department of Physics,University of Pittsburgh, Pittsburgh, USA — [3]Department of Physics, National Central University, Taiwan R.O.C

There are two distinct structures of the clathrin- coated vesicles in the early process of the clathrin-mediated endocytosis, one is spherical pits and the other one is flat plaques. Both of them finally form vesicles and enter the cell.

From the observation of experiments, plaques are only found on the cell membrane which is adherent to the substrates, but pit can be found everywhere on the cell membrane. Experiments show that the actin polymerization is essential for both the formation and the invagination of a plaque. But the details of the process, how a coated membrane is lifted on the cell membrane, remain unknown.

In order to understand the mechanism of the invagination of a plaque, we built a model in which the release of the elastic free energy of the growing actin network lead to the detachment of the membrane domain with clathrin plaque from the substrate. Our study suggests a new role played by the actin network on the subcellular process.

BP 26.18 Thu 17:30 Poster A

Statics and dynamics of stalks studied by minimal coarse-grained models. — Giovanni Marelli, •Yuliya Smirnova, and Marcus Müller — Institut für theoretische Physik, Georg August Universität Göttingen

The stalk is a lipid bridge between two lipid membranes and a fundamental step in the process of membrane fusion. The formation and evolution of the stalk is a collective phenomenon which involves the interaction and change of conformation of many lipids. We use our coarse-grained solvent-free model to simulate a stalk between two opposed membranes. The absence of solvent molecules avoids the non trivial problem of re-equilibrating the number of solvent molecules between the two bilayers present in explicit solvent models. Depending on the type and architecture of lipids we can change the stability and morphology of the stalk. Radial stalks are mostly metastable and we calculate the average density profile and fluctuations of their thickness. Small hydrophobic chains (oil) added in the hydrophobic layer of the membrane preferentially go to the lower and upper ends of the stalk, where the membrane is slightly indented, and relax the total tension. Linear stalks formed by more asymmetric lipids are stable and span the simulation box over the pbc. We calculate their line tension. In case of mixed lipid membranes we observe the segregation of lipids with different spontaneous curvatures to curved and planar portions of the morphology. Finally we compare the thickness profile and the bilayer repulsion with different models and experimental data.

BP 26.19 Thu 17:30 Poster A

STED-FCS on near-critical lipid membranes — •Jens Ehrig, Eugene P. Petrov, and Petra Schwille — Biophysics, BIOTEC, Technische Universität Dresden, Dresden, Germany

Dynamic phase separation in cell membranes is believed to play an important role in many membrane-associated cellular processes. This microheterogeneity is one of the reasons for anomalous diffusion of lipid molecules which is frequently observed in cell membranes. We have recently shown via Monte Carlo simulations that the presence of near-critical fluctuations in a lipid membrane may lead to transient anomalous diffusion of lipid molecules [1]. It is therefore extremely interesting to test whether anomalous diffusion due to critical fluctuations can be observed experimentally in model membranes under appropriate conditions. We report results of our experiments on model lipid membranes exhibiting near-critical fluctuations using STED-FCS [2], an experimental technique which can provide valuable information on diffusion dynamics on spatial scales from a few tens to few hundreds of nanometers on time scales ranging from microseconds to seconds.

[1] J. Ehrig, E. P. Petrov, and P. Schwille, Biophys. J. **100** (2011) 80
[2] L. Kastrup, H. Blom, C. Eggeling, and S.W. Hell, Phys. Rev. Lett. **94** (2005) 178104

BP 26.20 Thu 17:30 Poster A

Testing for domain formation in ER-mimicking and native ER membrane GUV. — •Mária Hanulová, Gernot Guigas, Julia Hoffmann, and Matthias Weiss — Experimentalphysik 1,

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Proteins that are correctly folded are trafficked from the endoplasmic reticulum (ER) to the Golgi apparatus via COPII vesicles. The vesicles bud off from specialized micrometer-sized membrane domains, so-called ER exit sites, after being coated with COPII proteins. Structurally and functionally distinct domains in cellular membranes such as ER exit sites can be based on lipid immiscibility or induced by binding of proteins. Using fluorescence microscopy, we tested for possible lipid-based domain formation in GUV electroformed from ER-mimicking lipid mixtures and native ER membranes. Native ER membranes were isolated from Hela cells by gradient centrifugation. Both types of GUV were homogeneous and the diffusion coefficients measured by FCS were similar to pure liquid-disordered lipid membranes.

BP 26.21 Thu 17:30 Poster A

Influence of charge density on bilayer bending rigidity in lipid vesicles: a combined dynamic light scattering and neutron spin-echo study — •Beate-Annette Brüning[1], Ralf Stehle[1,2], Peter Falus[3], and Bela Farago[3] — [1]Helmholtz Zentrum Berlin, Hahn-Meitner Platz 1, 14109 Berlin, Germany — [2]Universität Bayreuth, Postfach 10 12 51, 95440 Bayreuth, Germany — [3]Institut Laue-Langevin, B.P. 156, 6 rue Jules Horowitz, 38042 Grenoble, France

We report a combined dynamic light scattering and neutron spin-echo study on vesicles composed of the uncharged helper lipid DMPC and the cationic lipid DOTAP. Mechanical properties of a model membrane and the corresponding fluctuation dynamics can be tuned by changing composition. We compare the bilayer undulation dynamics in lipid vesicles composed of DMPC/DOTAP to vesicles composed of DMPC and the also uncharged reference lipid DOPC. We find, that on the local scale, lipid headgroup composition and charge change the vesicle fluctuations less than acyl chain packing inhomogenities between the composite lipids. We discuss this result on the basis of domain formation in the lipid mixtures containing charged (DMPC/DOTAP) and uncharged reference lipid (DMPC/DOPC). First, we investigate lipid vesicle size and mass diffusion using dynamic light scattering, then we study collective bilayer undulations and bulk diffusion on two distinct time scales around 25ns and 150ns, using neutron spin-echo spectroscopy. Finally, we estimate bilayer bending rigidities κ_B for the charged and uncharged lipid vesicles.

BP 26.22 Thu 17:30 Poster A

Simulation of vesicles at surfaces - rupture, fusion and spreading — •Marc Fuhrmans and Marcus Müller — Universität Göttingen, Institut für Theoretische Physik, Göttingen, Deutschland

Adsorption of unilamellar vesicles to an attractive surface is a frequently used way to form supported bilayers. Although this approach is known to produce continuous bilayers, the mechanism of their formation and its dependence on factors like surface roughness, membrane tension, lipid composition and vesicle size is poorly understood. Theoretical considerations based on elastic theory predict rupture of the vesicles caused by adsorption-induced deformation with an exposure of the inner membrane. While some experiments support this mechanism, others result in an exclusive exposure of the outer monolayer or an even exposure of both the inner and outer monolayers. In addition, in some experiments a critical vesicle concentration on the surface is required to initiate the condensation of a supported bilayer, suggesting an involvement of neighboring vesicles in the rupture process.

We have used dissipative particle dynamics simulations to assess the different mechanisms of vesicle spreading on attractive surfaces, placing special emphasis on the initial location and subsequent development of the rupture pore. In addition, we have studied fusion of neighboring adsorbed vesicles and the involvement of free bilayer edges in vesicle rupture and membrane condensation. Making use of the universality of lipid-associated phenomena, we employed a solvent-free coarse-grained model, enabling us to cover the relatively large system sizes and time scales necessary to observe these collective processes.

BP 26.23 Thu 17:30 Poster A

Partitioning of cytochrome c in multicomponent lipid membranes with domains — •Salome Pataraia — Max-Planck-Institute of Colloids and Interfaces Theory & Bio-Systems Potsdam

We characterized the binding of cytochrome c (cyt c), a mitochondrial inner membrane protein, to multicomponent lipid membranes and resolved the role of the bilayer surface charge and lipid composition. As a model system, giant unilamellar vesicles (GUVs) were used. To mimic the membrane composition of the inner mitochondrial membrane we employed lipid mixtures of the charged dioleoyphosphatidylcholine (DOPG), sphingomyelin (SM) and cholesterol. We first characterized the phase behavior of this mixture from confocal microscopy observations on fluorescently labeled GUVs. We localised the region of coexistence of liquid ordered (Lo) and liquid disordered (Ld) phases, mimicking raft-like domains and their environment in cell membranes. We then investigated the change in the phase state of these membranes induced by cyt c at physiological concentrations. Our studies revealed that in the presence of cyt c, the area of the Lo-Ld coexistence region increases on the expense of the single-phase Ld region. By means of fluorescent intensity studies, we also studied the preferential partitioning of cyt c between the Ld and Lo phases. Our results indicate that cyt c strongly prefers the DOPG-rich Ld domains. The specific affinity of the protein to each of the fluid phases are thermodynamically quantified with isothermal titration calorimetry on large unilamellar vesicles with compositions characteristic of either the Lo or the Ld phase.

BP 26.24 Thu 17:30 Poster A

Nonlinear pattern formation in biomimetic membranes — •Chris Händel[1], Bernd Kässemodel[1], Undine Dietrich[1], Sergio Alonso[2], Markus Bär[2], and Josef Käs[1] — [1]Division of Soft Matter Physics, Faculty of Physics and Earth Sciences, University of Leipzig, Linnéstraße 5, 04103 Leipzig , Germany — [2]Physikalisch-Technische Bundesanstalt, Abbestraße 2-12, 10587 Berlin, Germany

The MARCKS (Myristoylated alanine-rich C kinase substrate) protein is an actin filament cross-linking protein which reveals relevant functions in different organisms. It is located at the plasma membrane and interacts via electrostatic forces with the membran lipid PIP2 (1,2- Dipalmitoylphosphatidylinositol 4,5-diphosphate). In a biomimetic membrane, designed by a mixed DPPC/PIP2- monolayer, binding of MARCKS peptide to the membrane increases the lateral pressure, whereas unbinding dynamics modulated by PKC (Protein kinase C) generates a nonlinear reaction-diffusion system. This mechanism leads to oscillations of the lateral pressure which can be correlated to changes in the ratio of ordered and disordered phase in the membrane. Employing a theoretical model, we could calculate the dynamic distribution of acidic lipids in response to cytosolic proteins and regulating enzymes. The present work confirms these theoretical assumptions of this reaction-diffusion system by using model membranes. We obtained oscillations in lateral monolayer pressure which correlate with changes in shape and size of the crystalline lipid domains and the ratio of the area requirement of the liquid and the crystalline phase of the monolayer.