BP 27: Membrane Morphology and Adhesion

Time: Friday 10:15–12:45 Location: C 243

Invited Talk BP 27.1 Fri 10:15 C 243

Secretion of protein-coated vesicles — •Pierre Sens — CNRS, PhysicoChimie Théorique - ESPCI, Paris

Cellular trafficking generally involves spherical or tubular membrane vesicles, the formation of which often rely on the aggregation of membrane proteins (COPI, COPII, Clathrin and Caveolae). I will review some of the theoretical models that have been developed to describe this phenomenon, with particular emphasis on systems driven out of equilibrium by the expenditure of energy through the activity of GT-Pases proteins. I will show how vesicle secretion and traffic can be very efficiently regulated by the alteration of the GTP hydrolysis cycle, which is known to be affected, for instance, by the presence of cargo.

BP 27.2 Fri 10:45 C 243

Fluctuations of red blood cell membranes — •Thorsten Auth[1,2], Nir S. Gov[1], and Samuel A. Safran[1] — [1]Weizmann Institute of Science, Rehovot 76100, Israel — [2]Forschungszentrum Jülich, IFF, 52425 Jülich, Germany

We model the red blood cell membrane by a lipid bilayer that is coupled to a polymerized membrane. Using experimental fluctuation spectra, this model allows us to determine the elastic constants and to quantify the active, ATP-driven fluctuations. The extensive experimental studies on and the easy availability of red blood cells make them especially attractive for setting up and testing theoretical models to quantitatively explain the experimental results. However, using a simple fluid-polymerized membrane model, several basic aspects regarding the mechanical properties of the cell membrane are not completely understood. On the one hand, static deformation experiments indicate that the cell is very stiff with a high shear modulus of the order of $10^{-3} - 10^{-2}\,\mathrm{k_B T\,nm^{-2}}$. On the other hand, the relatively large fluctuation amplitudes, observed in light scattering/video microscopy spectra at wavevectors, $q \approx 0.010\,\mathrm{nm^{-1}}$, indicate that the shear modulus is small. Furthermore, experiments that measure the fluctuation amplitude as a function of the position on the cell are — within the continuum theory — compatible only with a vanishing shear modulus. We have performed simulations of inhomogeneous membranes and find that localized fluctuations, due to irregularities of the cytoskeleton, are capable to explain both riddles.

BP 27.3 Fri 11:00 C 243

Adhesion dynamics of fluctuating membranes — •Ellen Reister-Gottfried and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, 70550 Stuttgart, Germany

We study a system consisting of a fluctuating membrane close to a flat substrate that may adhere to the substrate via receptor-ligand bonds that we model as springs with a certain stiffness. We keep the position of the ligands on the substrate fixed and assume such a high abundance of receptors in the membrane that lateral diffusion has no influence on the adhesion process. While the energy of the membrane and the bonds combined with an appropriate Onsager coefficient determine the equation of motion for the membrane, the binding and unbinding of receptor-ligand pairs is expressed with Kramers rates, that depend on the local distance between membrane and substrate. Applying stochastic simulations we study the adhesion process of an initially unbound membrane as a function of binding energy, spring stiffness, and bending rigidity of the membrane. We analyse two limiting cases: the average distance between the membrane and substrate is *i)* either fixed or *ii)* variable allowing center of mass movement of the membrane. For *i)* we find that membrane fluctuations together with the height dependent reaction rates increase the number of bonds compared to a flat membrane. Furthermore, strong spatial correlations between the bonds are observed. In situation *ii)* equilibrium calculations for a flat membrane reveal a bimodal binding probability for certain binding energies. Our simulations show that membrane fluctuations break this bimodality. Additionally, spatial correlations are reduced compared to *i)*.

BP 27.4 Fri 11:15 C 243

Large scale organization in crowded membranes — •Stefan Semrau[1], Timon Idema[2], Cornelis Storm[2], and Thomas Schmidt[1] — [1]Physics of Life Processes, Leiden University, The Netherlands — [2]Lorentz Institute for Theoretical Physics, Leiden University, The Netherlands

Over the past years, the classical fluid mosaic model - in which membrane proteins have ample space to explore the entire membrane - has undergone some serious revision. In actuality, the membrane environment is highly crowded and heterogeneous. Crowding has profound implications for the dynamical behavior of the proteins, and is therefore a determining factor for the mechanisms of cell signaling. Only very recently the importance of membrane mediated interactions in such processes was recognized. Here we use two-phase GUVs (giant unilamellar vesicles) with multiple budded, liquid ordered domains to model this class of interactions. Such budded domains repel as our recent analytical model of completely phase separated GUVs (Semrau, Idema et al.) suggests. Here we measure the strength of the repulsion by analysis of domain diffusion and find that it gives rise to a preferred domain size. Furthermore, we observe that the interaction strength has peaks at distinct domain sizes. These sizes correspond to the addition of a domain to a shell of domains surrounding a central, pinned domain. This implies that in a crowded system governed by membrane mediated interactions clustering of proteins of similar size or interaction strength is promoted.

15 min. break

BP 27.5 Fri 11:45 C 243

Coarse-grained simulation studies of peptide-induced pore formation in lipid membranes — Gregoria Illya[1,2] and •Markus Deserno[2,3] — [1]Institut für Anorganische und Physikalische Chemie, TU Darmstadt, Petersenstraße 20, 64287 Darmstadt — [2]MPI für Polymerforschung, Ackermannweg 10, 55128 Mainz — [3]Department of Physics, Carnegie Mellon University, 5000 Forbes Ave, Pittsburgh PA 15213, USA

We investigate generic aspects of the impact of antimicrobial peptides on lipid membranes using a solvent-free coarse-grained simulation technique. Lipids are modeled as strings of four beads, peptides as bead-composed cylinders with hydrophilic caps and a transmembrane hydrophobic region with possibly small hydrophilic strips. As a function of hydrophobic peptide-lipid attraction the preferred state of the peptide changes from desorbed to adsorbed to inserted, and peptides can mutually catalyze their own insertion. In the presence of hydrophilic strips along the transmembrane region peptides aggregate to form pores in the bilayer, whose size and morphology depends on the generic interaction parameters. For instance, whether pores appear as "toroidal" or "barrel stave" is triggered by the strength of an additional hydrophobic peptide-peptide cohesion beyond the hydrophilicity-driven pore formation.

BP 27.6 Fri 12:00 C 243

Phase Separation in Membranes on Corrugated Substrates — •Bartosz Rozycki, Thomas R. Weikl, and Reinhard Lipowsky — Max Planck Institute of Colloids and Interfaces, Science Park Golm, 14424 Potsdam, Germany

We study separation of two liquid phases in lipid membranes that strongly adhere to a corrugated solid substrate. Both mean field theory and Monte Carlo simulations show that the spatial distribution of the two liquid phases are governed by membrane curvature. [1] For small curvature amplitudes, the membrane undergoes complete separation of the two liquid phases. For larger membrane curvature amplitudes, the two phases form patterns which follow the membrane curvature contour lines. These theoretical results are in agreement with recent experiments [2,3] and explain a possible control mechanism of domain arrangement in biological membranes.

[1] Bartosz Rozycki, Thomas R. Weikl, Reinhard Lipowsky (in preparation). [2] Tae-Young Yoon et. al, Nature Matherials 5, 281 (2006). [3] Raghuveer Parthasarathy, Cheng-han Yu, and Jay T. Groves, Langmuir 22, 5095 (2006).

BP 27.7 Fri 12:15 C 243

Curvature induced interaction between a membrane protein and a fluctuating model membrane: the influence on membrane dynamics and protein diffusion — •Stefan Leitenberger, Ellen Reister-Gottfried, and Udo Seifert — II. Institut für The-

oretische Physik, Universität Stuttgart

In our work the influence of an interaction between a curved protein and a fluctuating membrane whose energy is given by the Helfrich Hamiltonian on the dynamics of the system is analyzed. We derive coupled equations of motion for the membrane dynamics and the lateral protein diffusion. In a first step, the influence of the protein on the membrane dynamics is neglected. Within this approximation we calculate the curvature-coupled diffusion coefficient, which is enhanced compared to free diffusion. This increase is caused by the additional force acting on the protein. To probe our results and overcome other approximations of the calculations, we set up simulations that also neglect the changed membrane dynamics. Comparing the results we find qualitative agreement, however, the diffusion coefficients achieved in the simulations are smaller since the particle tries to follow energetically favorable positions. Correlations between protein position and local membrane shape are not accounted for correctly in the analytical calculations. In a second step, the influence of the curvature-coupling on the membrane dynamics is taken into account. Using an extension of our simulation scheme we study the changed height correlations of the membrane and the effect on the lateral protein diffusion as a function of the protein's spontaneous curvature and bending rigidity.

BP 27.8 Fri 12:30 C 243

Contact lines for fluid surface adhesion — •Martin Michael Müller[1,2], Markus Deserno[1,3] und Jemal Guven[4] — [1]Max Planck Institute for Polymer Research, D-55128 Mainz, Germany — [2]Laboratoire de Physique Statistique, ENS, F-75231 Paris Cedex 05, France — [3]Department of Physics, Carnegie Mellon University, Pittsburgh, PA 15213, USA — [4]Instituto de Ciencias Nucleares, UNAM, Apdo. Postal 70-543, 04510 México D.F., Mexico

When a fluid membrane or a similar surface adheres to a substrate, the location of the contact line adjusts in order to minimize the overall energy. This implies boundary conditions which depend on the characteristic surface deformation energies. In this talk a general geometrical framework is presented within which these conditions can be derived in a completely systematic way [1,2]. Both adhesion to a rigid substrate as well as adhesion between two fluid surfaces will be treated and illustrated for several important Hamiltonians involving both curvature and curvature gradients.

[1] M. Deserno, M. M. Müller, and J. Guven, Phys. Rev. E **76**, 011605 (2007). [2] M. M. Müller, Phd thesis, available at http://www.geomnat.com/veroeff_en.php