BP 65: Membranes and Vesicles II

Time: Thursday 15:00–16:15 Location: H43

Invited Talk BP 65.1 Thu 15:00 H43

Design features of a membrane-assisted protein oscillator — •Petra Schwille — Max Planck Institute of Biochemistry, Martinsried

The MinCDE protein machinery, which orchestrates the positioning of the division ring in E.coli bacteria, shows a distinct oscillation of protein concentrations between the two cell poles, which are based on self-organization through reaction-diffusion. We have been able to reconstitute these self-organized oscillations of purified proteins in artificial cell-shaped compartments, as well as the faithful downstream positioning of protofilaments of the Z division ring. This could be the first step towards autonomous division of an artificial cell system which we aim to establish in a bottom-up synthetic biology approach. In my talk, I will discuss the design features of this very simple and archetypical kind of a biological oscillator and particularly highlight the role of the membrane, acting as a heterogenous catalyst and providing spatial cues in two and three dimensions.

BP 65.2 Thu 15:30 H43

Electrostatically driven formation of double lipid membranes studied by evanescent light scattering microscopy — Björn Agnarsson[1], Hannah Wayment-Steele[2], Sofia Svedhme[1], Fredrik Höök[1], and •Angelika Kunze[3] — [1]Dept. of Applied Physics, Chalmers Univ. of Technology, Göteborg, Sweden — [2]Dept. of Chemistry, Pomona College, CA, USA — [3]Inst. of Physical Chemistry, Univ. of Göttingen, Göttingen, Germany

Since their introduction, solid-supported lipid membranes (SLMs) have been widely and successfully applied as platforms to study membrane-related processes and interactions. Remaining challenges when it comes to model studies involving SLMs are to ensure the formation of defect-free membranes and to minimize side effects of the underlying substrate. As a consequence, great efforts have been devoted to the development of surface sensitive techniques allowing for the characterization of SLM formation as well as to the development of highly mobile membranes or multiple membranes. Here, the formation of a highly fluid SLM and a double lipid membrane is demonstrated and monitored using label-free evanescence light scattering microscopy (EvSM) in combination with acoustic sensing and fluorescence microscopy. The dominating driving force for the formation of both lipid structures is electrostatic interaction. We propose this demonstrated approach to be a promising tool for the preparation of highly fluid lipid membranes and double membranes for the study of membrane processes. Furthermore, is EvSM shown to be and an excellent tool for probing membrane related interactions with a single vesicle resolution.

BP 65.3 Thu 15:45 H43

A new free energy-based lattice model of lipid membranes — •Andreas Heuer and Davit Hakobyan — Institute f. Phys. Chemistry, WWU Münster

The thermodynamic properties of lipid mixtures in membranes are, on the one hand, strongly influenced by the specific enthalpic interactions among lipids and, on the other hand, by the entropic degrees of freedom of the hydrocarbon chains [1]. We suggest the formulation of a lattice model, each site corresponding to one lipid, where the enthalpic and the entropic effects are taken into account in a quantitative way. The chain entropy is reflected by an appropriately chosen order parameter distribution. All properties of the lattice model are extracted from atomistic molecular dynamics simulations of saturated and unsaturated lipids, respectively.

We can show via kinetic Monte Carlo simulations that the lattice model displays on a quantitative level the same temperature effects as the atomistic system. Specifically, we discuss gel formation for the pure saturated lipid and phase separation for a mixed system upon cooling. This agreement reflects the fact that the different free energy contributions of the atomistic system are contained in the lattice model.

[1] D.Hakobyan, A. Heuer, PLoS ONE 9/2, e87369 (2014).

BP 65.4 Thu 16:00 H43

An entropic attraction mediates vesicle tethering in early endosomes — •Marcus Jahnel[1,2], David Murray[1], Marino Zerial[1], and Stephan Grill[1,2] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [2]Biotechnology Center, TU Dresden, Dresden, Germany

Vesicle tethering is mediated by long, rather rigid coiled-coil membrane proteins that can bind Rab GTPases at their free end. Yet it is still unclear how these large fibrous proteins help to decrease the initial separation between two membranes for downstream docking and fusion. Which mechanism brings the two ends together?

Here, we address this question with a minimal tethering system consisting of the small GTPase Rab5 and the coiled-coil tethering protein early endosome antigen 1 (EEA1). Importantly, we show through a combination of high-resolution optical tweezer and EM experiments that EEA1 undergoes a global conformational change upon binding to Rab5 in the presence of GTP.

In the unbound (free) state EEA1 is rather rigid with a persistence length larger than its contour length of around 220 nm. However, in the bound state, the EEA1 dimer adopts a more flexible configuration with a persistence length of < 30 nm. This sudden, over 10-fold reduction in persistence length upon binding gives rise to an elegant physical mechanism for vesicle capture and tethering: an entropic collapse force — the result of an extended rigid structure suddenly becoming more flexible — pulls the membranes together to potentially initiate docking and fusion.