BP 2: Membranes and vesicles I (joint session BP/CPP)

Time: Monday 9:30–12:30 Location: H10

BP 2.1 Mon 9:30 H10

Soft Thermal Treatment Stabilizes Vacuum-deposited Phospholipid Layers for Sensor Applications — Sebastian Molina[1], Marcelo Cisternas[1], Maria J. Retamal[2], Nicolas Moraga[1], Hugo Zelada[1], •Jonas Fortmann[1,3], Tomas P. Corrales[4], Patrick Huber[5], Marco Soto-Arriaza[2], and Ulrich G. Volkmann[1] — [1]Institute of Physics and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [2]Faculty of Chemistry and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [3]TU Clausthal, Germany — [4]Department of Physics, UTFSM, Valparaiso, Chile — [5]TUHH, Hamburg, Germany

Artificial membranes allow one to study of the behavior of biological membranes, which are the base of the cell membrane structure. The cell membrane is composed of different lipids and proteins that change their behavior when they are stimulated physically and/or chemically. Besides traditional methods we use a solvent free, dry method for phospholipid deposition in high vacuum onto residue-free silicon substrates. The cleanness of the substrate and the precise thickness of the DPPC layer on the substrate is controlled in-situ using Very High Resolution Ellipsometry. In this work we show the enhancement of phospholipid bilayer self-assembling and stability due to a soft thermal treatment. The behavior of the artificial membranes is studied in air and immersed in aqueous medium, which mimics the natural environment of the biological membrane. Acknowledgements: FONDECYT Nos. 3160803 (MJR), 1180939 (UGV) 1171047 (MSA) and 11160664 (TPC), CONICYT Fellowship (MC) and CONICYT-PIA ACT 1409.

BP 2.2 Mon 9:45 H10

Prolonged Phospholipid Bilayer Stability due to Hydration on Porous Silicon: Pore Diameter and Porosity Optimization — Nicolas Moraga[1], Marcelo Cisternas[1], Diego Diaz[1], Rodrigo Catalan[1], Maria J. Retamal[2], Tomas P. Corrales[3], Mark Busch[4], Patrick Huber[4], Marco Soto-Arriaza[2], and •Ulrich G. Volkmann[1] — [1]Institute of Physics and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [2]Faculty of Chemistry and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [3]Department of Physics, UTFSM, Valparaiso, Chile — [4]TUHH, Hamburg, Germany

Study of artificial membranes has become an important way to gain insight into the physical behavior of cell membranes. In this work, porous silicon substrates (pSi) were prepared with different pore diameters and porosities. The substrates were characterized with Field Emission Electron Microscopy. The phospholipid (DPPC) was deposited in high vacuum from the gas phase on the pSi. Film thickness was controlled in-situ using Very High Resolution Ellipsometry (VHRE). Samples were hydrated in air with ultrapure water to assemble the bilayer. Phase transitions were measured with VHRE and Stray Light Intensity during temperature cycles. AFM was used to study morphological changes of bilayers as a function of temperature. Our results show that specific pore diameters and porosities of nanoporous substrates prolong phospholipid bilayer stability due to hydration with water stored in the pores. Acknowledgement: FONDECYT Nos. 3160803 (MJR), 1180939 (UGV), 1171047 (MSA) and 11160664 (TPC), CONICYT Fellowship (MC) and CONICYT-PIA ACT 1409.

BP 2.3 Mon 10:00 H10

Mechanisms of Interactions between Lipid Membranes in the Presence of Biological Cosolutes — •Amanuel Wolde-Kidan[1], Quoc Dat Pham[2], Alexander Schlaich[3], Emma Sparr[2], and Roland Netz[4] — [1]Freie Universität, Berlin, Germany — [2]Lund University, Lund, Sweden — [3]Laboratoire Interdisciplinaire de Physique, Grenoble, France — [4]Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

Lipid membranes form the diffusional barrier of eukaryotic cells and determine processes when cells come into close contact, for example during cell fusion or vesicle formation. We analyze the effects of three cosolutes on membrane interactions, which are all abundantly found in biological systems, namely urea, TMAO and sodium chloride. The effect of the polar solutes urea and TMAO on protein stability has been studied extensively, but their influence on lipid bilayers has only recently started to be investigated. Using atomistic molecular dynamics simulations and theoretical modeling we analyze different mechanisms of lipid-solute and lipid-lipid interactions. By means of solution thermodynamics we model the effect of the cosolutes on the hydration repulsion between lipid bilayers. Results from our simulations compare well to experimental calorimetric measurements. We find that the osmotic pressure due to the added solute has the most important influence on the hydration repulsion. Furthermore, we find that the interaction mechanism of sodium chloride with lipid bilayers is dominated by the ion-membrane potentials of mean force. Other factors such as the dielectric response seem to be of less importance.

BP 2.4 Mon 10:15 H10

Glycolipids as zippers between phospholipid membranes — •Victoria Latza[1], Bruno Demé[2], and Emanuel Schneck[1] — [1]Max-Planck Institut für Kolloid und Grenzflächenforschung, Potsdam, Germany — [2]Institut Laue-Langevin, Grenoble, France

Essential mechanisms in biological cells, such as molecular transport and cell division, involve the spatiotemporal reorganization of membranes in terms of membrane adhesion or vesicle release. These processes are largely determined by membrane-membrane interactions and thus highly sensitive to the membranes* surface chemistry. It is known that certain membrane-bound saccharide motifs, such as the LewisX trisaccharide, promote membrane adhesion. These cases, however, have been viewed as exceptions. Here, with the help of small-angle x-ray scattering, we investigate the interaction between membranes composed of ternary lipid mixtures of (i) uncharged phospholipids as matrix, (ii) negatively charged phospholipids to induce electrostatic repulsion, and (iii) glycolipids featuring various mono- and oligosaccharide headgroups. We find that a large fraction of saccharide types are able to induce membrane adhesion through the formation of weak inter-membrane bonds. These bonds are resistant to electrostatic repulsion at levels that lead to the complete unbinding of pure phospholipid membranes. Our results strongly indicate that glycolipid-induced membrane-binding is not an exceptional feature of few saccharide types but a highly abundant phenomenon of great relevance for membrane biophysics.

Invited Talk BP 2.5 Mon 10:30 H10

Lessons learned from complex mimics of biological membranes — •Georg Pabst — University of Graz, Institute of Molecular Biociences, NAWI Graz, 8010 Graz, Austria

Lipid-only mimics of biological membranes serve as valuable platforms for studying the functional role of membrane lipids under chemically and experimentally well-defined conditions. Of recent, we have focused on complex mimics of mammalian and bacterial plasma membranes with either lateral or transbilayer inhomogeneities. In particular, we have developed protocols for fabricating and analyzing asymmetric lipid vesicles, which are sufficiently stable and which are amenable for biophysical studies using diverse techniques. We have specialized on small-angle X-ray/neutron scattering combined with complimentary techniques to address leaflet specific structure and transbilayer coupling mechanisms. Complementary, we are currently developing tools for reliable estimates for intrinsic lipid curvatures, which are known to play a pivotal role in coupling to protein function. I will present recent research highlights resulting from these efforts and discuss some applications to membrane-active drugs, such as antimicrobial peptides, or the partitioning of transmembrane proteins function.

30 minutes break.

BP 2.6 Mon 11:30 H10

The interaction of viral fusion peptides with model lipid membranes at high hydrostatic pressure — Göran Surmeier[1], Michael Paulus[1], Susanne Dogan[1], Yury Forov[1], Mirko Elbers[1], Simon Egger[2] und •Julia Nase[1] — [1]Fakultät Physik/DELTA, TU Dortmund, 44221 Dortmund — [2]Physikalische Chemie, TU Dortmund, 44221 Dortmund

When a virus enters a host cell, the insertion of viral fusion peptides (FPs) into the target membrane catalyzes the membrane fusion reaction. We investigated the interaction of different FPs with model membranes in X-ray reflectivity measurements at the interface between monoolein/water mixtures and a silicon substrate. In addition, the bulk and interfacial structures were investigated with small angle X-ray scattering in transmission and in grazing incidence. Monoole-

in/water mixtures have a very rich pressure-dependent phase diagram. Notably, the inverse bicontinuous cubic phases exhibit structural analogies to the hemifusion intermediates. We found that pressurization triggers formation of ordered lamellar monoolein multilayers close to the interface even in a pressure range where the bulk material is in the cubic phase. Previous studies demonstrated the effect of FPs on the pressure-dependent phase boundaries [1]. We resolved the vertical membrane structure of some multilayers and monitored the penetration of FPs into the membrane. Experiments were performed in a custom-made high hydrostatic pressure cell [2] at beamlines ID31 of the ESRF and BL9 of DELTA. [1] A. Levin et al, J Phys Chem B 121 (2017) [2] F.J. Wirkert et al, J. Synchr. Radiat. 21 (2014)

BP 2.7 Mon 11:45 H10

Lipid membrane fusion in proteoliposomes and multilamellar stacks studied by X-ray scattering — •Kilian Frank[1], Karlo Komorowski[1], Veronica Chappa[2], Max Scheu[1], Marcus Müller[2], and Tim Salditt[1] — [1]Georg-August-Universität, Institute for X-ray Physics, Friedrich-Hund-Platz 1, 37077 Göttingen — [2]Georg-August-Universität, Institute for Theoretical Physics, Friedrich-Hund-Platz 1, 37077 Göttingen

Intermediate structures of membrane fusion, e.g. during release of neurotransmitter at the synapse, are difficult to resolve at the molecular level, especially in the close-to-physiological regime with SNARE fusion proteins. To provide structural information, we combine two X-ray scattering approaches: First, SAXS on proteoliposomes (PL) with reconstituted SNAREs serves to identify changes in PL size and radial density profile upon fusion in a hydrated environment. We present a simulation framework based on 3D-FFT to estimate how well size and shape changes (homogeneous swelling of an ensemble, thermal fluctuations, and strong equilibrium defomations) are detected in PL-SAXS. Second, GISAXS on solid-supported multilamellar membrane stacks at controlled humidity and salt concentration allows to characterize the energy of fusion stalk formation, prior to crystallization to a stalk phase with rhombohedral symmetry. Here we find that CaCl2, in contrast to other salts, facilitates stalk phase formation, also cooperatively in fusiogenic lipid mixtures. By combining both methods, we lay the foundation for a quantitative X-ray analysis of the membrane fusion process with natural proteins or artificial peptides.

BP 2.8 Mon 12:00 H10

Structural changes in biomimetic myelin membranes induced by Myelin Basic Protein — •Benjamin Krugmann[1,2], Andreas Stadler[1], Aurel Radulescu[2], Alexandros Koutsioumpas[2], and Stephan Förster[1,2] — [1]Forschungszentrum Jülich JCNS-1, 52428 Jülich, Germany — [2]Forschungszentrum Jülich JCNS-MLZ, 85748 Garching, Germany

The myelin sheath plays an important role in nerve signal conduction. It acts as an insulating layer which enables fast signal transport by reducing conduction losses. In demyelinating diseases like multiple sclerosis, this membrane is damaged, which leads to severe problems in nerve conduction. In literature different values for the lipid composition of healthy and modified membranes have been found. Based on these results, we investigate the membrane structure for the respective compositions. As next step we add Myelin Basic Protein (MBP) to the membrane and investigate the induced structural change. Small angle neutron scattering (SANS) and cryo-transmission electron microscopy data show the structure of vesicles with healthy and modified membrane composition and the strong structure change induced by MBP. Neutron Reflectometry (NR) data indicates that MBP interacts differently with healthy and modified myelin membranes.

BP 2.9 Mon 12:15 H10

Influenza A matrix protein (M1) multimerization is the main driving force for membrane bending and tubulation. — •Ismail Dahmani — Cell Membrane Biophysics Group / Universität Potsdam Karl-Liebknecht-Str. 24-25, Haus 25, B/1.04 14476 Potsdam-Golm Deutschland

The matrix protein of the Influenza A virus (M1) forms a shell underlying the viral lipid envelope and controls the geometry of the virus capsid. In infected cells, M1 orchestrates the process of new virion formation by binding to the inner leaflet of the plasma membrane (PM), which finally results in bending of the lipid bilayer and virus release . The exact role of M1 polymerization in inducing membrane deformation and budding is not clear. Here, to model virus egress through the PM, we analyzed M1 binding to giant unilamellar vesicles (GUVs). Our results show that M1 and a construct consisting of its Nterminal domain (NM1) bind to negatively charged lipids causing unidirectional deformation by imposing an inward curvature and membrane tabulation . Detergent-mediated solubilization of the lipid bilayer after M1 binding leaves the three-dimensional organization of the protein intact, indicating that M1 forms a very stable network adjacent and independent from the lipid membrane. Our data also indicate that the C-terminal domain of M1 is not needed for the establishment of protein-protein interactions and membrane deformation. Finally in acidic conditions (pH=5) M1 irreversibly loses its ability to multimerize and induce curvature, thus confirming that M1 multimerization is the molecular mechanism responsible for membrane deformation.