

Année de publication : 2014

Mijo Simunovic, Patricia Bassereau (2014 Mar 1)

Reshaping biological membranes in endocytosis: crossing the configurational space of membrane-protein interactions.

Biological chemistry : 395 : 275-283 : [DOI : 10.1515/hsz-2013-0242](https://doi.org/10.1515/hsz-2013-0242)

Résumé

Lipid membranes are highly dynamic. Over several decades, physicists and biologists have uncovered a number of ways they can change the shape of membranes or alter their stage behavior. In cells, the intricate work of membrane proteins drives these processes. Considering the highly complex ways proteins interact with biological membranes, molecular mechanisms of membrane remodeling remain still unclear. When studying membrane remodeling phenomena, researchers often observed different results, leading to disparate conclusions on the physiological pace of such processes. Here we show the combination of research methodologies and various experimental requirements contributes to the understanding of the entire phase space of membrane-protein interactions. Using the example of clathrin-mediated endocytosis we try to distinguish the question « how can we remodel the membrane proteins? » from « how do proteins remodel the membrane in the cell? » In particular, we consider how altering physical parameters affect the way a membrane is remodeled. Uncovering the full range of physical requirements under which membrane phenomena take place is key in understanding the way cells take advantage of membrane properties in carrying out their vital tasks.

Sophie Aimon, Andrew Callan-Jones, Alice Berthaud, Mathieu Pinot, Gilman E S Toombes*, Patricia Bassereau* (2014 Jan 27)

Membrane shape modulates transmembrane protein distribution.

Developmental cell : 212-8 : [DOI : 10.1016/j.devcel.2013.12.012](https://doi.org/10.1016/j.devcel.2013.12.012)

Résumé

Although membrane shape varies greatly throughout the cell, the contribution of membrane curvature to transmembrane protein targeting is unknown because of the numerous sorting mechanisms that take place concurrently in cells. To isolate the effect of membrane shape, we used cell-sized giant unilamellar vesicles (GUVs) containing either the potassium channel KvAP or the water channel AQP0 to form membrane nanotubes with controlled radii. Whereas the AQP0 concentrations in flat and curved membranes were indistinguishable, KvAP was enriched in the tubes, with greater enrichment in more highly curved membranes. Fluorescence recovery after photobleaching measurements showed that both proteins could freely diffuse through the neck between the tube and GUV, and the effect of each protein on membrane shape and stiffness was characterized using a thermodynamic sorting model. This study establishes the importance of membrane shape for targeting transmembrane proteins and provides a method for determining the effective shape and flexibility of membrane proteins.

Ludger Johannes, Christian Wunder, Patricia Bassereau (2014 Jan 4)

Bending « on the rocks »-a cocktail of biophysical modules to build endocytic pathways.

Cold Spring Harbor perspectives in biology : [DOI : 10.1101/cshperspect.a016741](https://doi.org/10.1101/cshperspect.a016741)

Résumé

Numerous biological processes Rely on endocytosis. The building is of endocytic pits Achieved by a bewildering complexity of factoring That biochemical function in clathrin-dependent and -independent pathways. In this review, we argue That this complexity can be conceptualized by a deceptively small number of physical principles That Fall into two broad categories: passive Mechanisms, Such As asymmetric transbilayer stress, scaffolding, line voltage, and crowding, and active Mechanisms driven by mechanochemical enzymes and / or cytoskeleton. We Illustrate how the functional identity of biochemical modules depends on system parameters Such As local protein density on membranes, THUS explaining Reviews some of the controversy in the field. Different modules frequently operate in parallel in the Sami Often step and are shared by divergent Apparently uptake processes. The emergence of a novel endocytic classification system THUS May be envisioned in qui functional modules are the elementary bricks.

Année de publication : 2013

Thomas Bornschlögl, Patricia Bassereau (2013 Dec 17)

The sense is in the fingertips: The distal end controls filopodial mechanics and dynamics in response to external stimuli.

Communicative & integrative biology : 6 : e27341 : [DOI : 10.4161/cib.27341](https://doi.org/10.4161/cib.27341)

Résumé

Small hair-like cell protrusions, called filopodia, often establish adhesive contacts with the cellular surroundings with a subsequent build up of retraction force. This process seems to be important for cell migration, embryonic development, wound healing, and pathogenic infection pathways. We have shown that filopodial tips are able to sense adhesive contact and, as a consequence, locally reduce actin polymerization speed. This induces filopodial retraction via forces generated by the cell membrane tension and by the filopodial actin shaft that is constantly pulled rearwards via the retrograde flow of actin at the base. The tip is also the weakest point of actin-based force transduction. Forces higher than 15 pN can disconnect the actin shaft from the membrane, which increases actin polymerization at the tip. Together, this points toward the tip as a mechano-chemical sensing and steering unit for filopodia, and it calls for a better understanding of the molecular mechanisms involved.

Thomas Bornschlögl, Stéphane Romero, Christian L Vestergaard, Jean-François Joanny, Guy Tran Van Nhieu, Patricia Bassereau (2013 Nov 6)

Filopodial retraction force is generated by cortical actin dynamics and controlled by reversible tethering at the tip.

Proceedings of the National Academy of Sciences of the United States of America : 18928-33 :

DOI : [10.1073/pnas.1316572110](https://doi.org/10.1073/pnas.1316572110)

Résumé

Filopodia are dynamic, plasma finger-like membrane protrusions That sense the mechanical and chemical surroundings of the cell. Here, we show in epithelial cells que la filopodial dynamics of extension and retraction are Determined by the difference entre les actin polymerization rate at the tip and the retrograde flow at the base of the filopodium. Adhesion of a bead to the tip filopodial locally Reduces actin polymerization and leads to retraction via retrograde flow, reminiscent of a process used by pathogens to invade cells. Using optical tweezers, we show That filopodial retraction OCCURS at a constant speed contre counteracting force up to 50 pN. Our measurements Point Toward retrograde flow in the cortex together with frictional coupling entre les filopodial and cortical actin networks as the hand retraction force generator for filopodia. The forces exerted by filopodial retraction, HOWEVER, is limited by the connection entre filopodial actin filaments and the membrane at the tip. Upon mechanical breakage of the tip connection, filopodia Exert a passive retraction strength of 15 pN via Their plasma membrane. Transient reconnection at the tip allows filopodia to probe Continuously Their surroundings in a load-and-fail Manner Within a well-defined power range.

Andrew Callan-Jones, Patricia Bassereau (2013 Aug 1)

Curvature-driven membrane lipid and protein distribution.

Current Opinion in Solid State and Materials Science : 17 : 143-150 : DOI :

[10.1016/j.cossms.2013.08.004](https://doi.org/10.1016/j.cossms.2013.08.004)

Résumé

Cellular transport requires that membranes have the ability to recruit specific lipids and proteins to particular positions and at specific times. Here, we review recent work showing that lipids and proteins can be redistributed by spatially varying membrane curvature, without necessarily the need for biochemical targeting signals. We present here an emerging understanding of the various mechanisms by which membrane curvature can sort lipids and proteins, providing the experimental methods in addition to the supporting theoretical concepts.

Winfried Weissenhorn, Emilie Poudevigne, Gregory Effantin, Patricia Bassereau (2013 Apr 16)

How to get out: ssRNA enveloped viruses and membrane fission.

Current opinion in virology : 159-67 : DOI : [10.1016/j.coviro.2013.03.011](https://doi.org/10.1016/j.coviro.2013.03.011)

Résumé

Enveloped viruses ACQUIRE Their membrane from the host cell and accordingly need to separate Their envelope from cellular membranes via membrane fission. ALTHOUGH Reviews some of the enveloped viruses recruit the endosomal sorting complex required for transport (ESCRT) to catalyze the final fission reaction, Many enveloped viruses scem to bud in an ESCRT-independent Manner. Here we describe the principles That Govern membrane fission reactions in general and review progress in the understanding of ESCRT-mediated membrane fission. We ESCRT function relates to budding of single stranded RNA viruses and the Chat alternative ways to mediate membrane fission That May Govern ESCRT-independent budding.

Manuela Dezi, Aurelie Di Cicco, Patricia Bassereau, Daniel Lévy (2013 Apr 15)

Detergent-mediated incorporation of transmembrane proteins in giant unilamellar vesicles with controlled physiological contents.

Proceedings of the National Academy of Sciences of the United States of America : 7276-81 : [DOI : 10.1073/pnas.1303857110](https://doi.org/10.1073/pnas.1303857110)

Résumé

Giant unilamellar vesicles (GUVs) biomimetic systems are convenient size of the Sami have cells That are increasingly used to quantitatively address biophysical and biochemical processes related to cell functions. HOWEVER, current Approaches to Incorporate transmembrane proteins in the membrane of GUVs are limited by the amphiphilic nature of gold proteins. Here, we report a method to Incorporate transmembrane proteins in GUVs, based on concepts Developed for detergent-mediated reconstitution in wide unilamellar vesicles. Reconstitution is Performed Either live by incorporation from purified proteins in detergent micelles or by fusion of native purified vesicles or proteoliposomes in preformed GUVs. Lipid compositions of the membrane and the ionic, protein, or DNA compositions in the internal and external volumes of GUVs can be controlled. Using confocal microscopy and functional assays, we show That unidirectionally proteins are incorporated in the GUVs and keep Their functions on. We-have successfully tested our method with three kinds of transmembrane proteins. Containing GUVs bacteriorhodopsin, a proton pump photoactivable, can generate wide transmembrane potential and pH gradients That are light-switchable and steady for hours. GUVs with FhuA, a bacterial porin, Were used to follow the DNA injection by phage T5 upon binding to receptor transmembrane icts. Incorporating GUVs BMRC / BmrD, a bacterial heterodimeric ATP-binding cassette efflux transport, Were used to Demonstrate the protein-dependent translocation of drugs and Their interactions with encapsulated DNA. Our method shoulds THUS apply to a wide variety of peripheral membrane proteins or for Producing more complex biomimetic GUVs.

Campillo C, Sens P, Köster D, Pontani LL, Lévy D, Bassereau P, Nassoy P, Sykes C. (2013 Mar 19)

Unexpected membrane dynamics unveiled by membrane nanotube extrusion

Biophysical Journal : 104 : 1248-1256 : [DOI : 10.1016/j.bpj.2013.01.051](https://doi.org/10.1016/j.bpj.2013.01.051)

Résumé

In cell mechanics, distinguishing the respective roles of the plasma membrane and of the cytoskeleton is a challenge. The difference in the behavior of cellular lipid membranes and pure is usually attributed to the presence of the cytoskeleton have explored by nanotube membrane extrusion. Here we revisit this prevalent picture by unveiling unexpected strength responses of plasma membrane and cytoskeleton spheres devoid of synthetic liposomes. We show that a tiny variation in the content of synthetic membranes does not affect their static mechanical properties, purpose is enough to reproduce the dynamic behavior of their counterparts cellular. This effect is amplified year attributed to intramembrane friction. Reconstituted actin cortices inside liposomes induce additional year, but not dominant, contribution to the effective friction membrane. Our work underlines the necessity of a careful consideration of the role of membrane proteins on cell membrane rheology in addition to the role of the cytoskeleton.

Emmanuel Lemichez, David Gonzalez-Rodriguez, Patricia Bassereau, Françoise Brochard-Wyart (2013 Feb 27)

Transcellular tunnel dynamics: Control of cellular dewetting by actomyosin contractility and I-BAR proteins.

Biology of the Cell : 105 : 109-117 : [DOI : 10.1111/boc.201200063](https://doi.org/10.1111/boc.201200063)

Résumé

Dewetting is the spontaneous withdrawal of a liquid from the film has non-wettable area by nucleation and growth of dry patches. Two recent reports now offers que la principes of dewetting explain the physical phenomena underpinning the opening of transendothelial cell macroaperture (TEM) tunnels, referred to as cellular dewetting. Reviews This was discovered by studying a group of bacterial toxins endowed with the property of corrupting actomyosin cytoskeleton contractility. For both liquid and cellular dewetting, the growth of holes is-governed by a competition entre area strengths and line voltage. We also how the dynamics of the Chat TEM opening and closure systems to investigate remarkable Represent actin cytoskeleton regulation by sensors of plasma membrane curvature and investigate the impact on membrane voltage and the role of TEM in vascular dysfunctions.

Année de publication : 2012

Stephane Romero, Alessia Quatela, Thomas Bornschlöggl, Stéphanie Guadagnini, Patricia Bassereau, Guy Tran Van Nhieu (2012 Aug 18)

Filopodium retraction is controlled by adhesion to its tip.

Journal of cell science : 4999-5004 : [DOI : 10.1242/jcs.104778](https://doi.org/10.1242/jcs.104778)

Résumé

Filopodia extensions are thin cell sensing the environment. They play an essential role

During cell migration, cell-cell or cell-matrix adhesion, by initiating event contacts and conveying signals to the cell cortex. Pathogenic microorganisms can hijack filopodia to invade cells by inducing their retraction towards the cell body. Because their dynamics depend on a discrete number of actin filaments, filopodia provide a model of choice to study elementary events linked to membership and downstream signaling. HOWEVER, the determinants controlling filopodial sensing are not well characterized. In this study, we used beads functionalized with different ligands that triggered filopodial retraction when in touch with filopodia of epithelial cells. With optical tweezers, we were able to measure strengths stalling the retraction of a single filopodium. We found that the filopodial stall depends on the strength of the coating bead. Stall strengths reach 8 pN for beads coated with the $\beta 1$ integrin ligand Yersinia Invasin, whereas retraction was stopped with a higher strength of 15 pN when beads were functionalized with carboxyl groups. In all cases, stall strength increased in relation to the density of ligands contacting filopodial tips and was independent of the optical trap stiffness. Unexpectedly, a small number of discrete and Shigella-induced type three secretion systems stall force of 10 pN. These results suggest that the number of receptor-ligand interactions at the tip of filopodia determined the maximum retraction forces exerted by filopodia. A discrete number of clustered receptors is sufficient to induce high retraction forces.

Alice Berthaud, John Manzi, Javier Pérez, Stéphanie Mangenot (2012 May 25)

Modeling detergent organization around aquaporin-0 using small-angle X-ray scattering.

Journal of the American Chemical Society : 10080-8 : DOI : [10.1021/ja301667n](https://doi.org/10.1021/ja301667n)

Résumé

Solubilization of integral membrane proteins in aqueous solutions requires the presence of amphiphilic molecules like detergents. The area of the transmembrane proteins is then surrounded by a corona formed by molecules, ensuring a hydrophilic outer surface. The presence of this corona has strongly hampered structural studies of membrane proteins solubilized by small-angle X-ray scattering (SAXS), a technology frequently used to monitor conformational exchange of soluble proteins. Through the online combination of size exclusion chromatography, SAXS, and refractometry, we have determined a precise geometrical model of the n-dodecyl β -d-cyclodextrin surrounding maltopyranoside aquaporin-0, the most abundant membrane protein of the eye lens. The SAXS data were well-fitted by a corona detergent shaped in an elliptical toroid around the crystal structure of the protein, similar to the elliptical shape recently reported for nanodiscs (Skar-Gislinge et al. *J. Am. Chem. Soc.* 2010, 132, 13713-13722). The torus thickness determined from the curve-fitting protocol is in excellent agreement with the thickness of a lipid bilayer, while the number of detergent molecules deduced from the volume of the torus compares well with those therefore obtained on the same sample from refractometry and mass analysis based SAXS forward scattering. For the first time, the partial specific volume of the detergent surrounding a protein was measured. The present protocol is a crucial step toward future conformational studies of membrane proteins in solution.

Patricia Bassereau, Rob Phillips, Petra Schwille³ (2012 May 21)

Focus on the physics of the cell membrane.

New Journal of Physics : 14 : 055021 : [DOI : 10.1088/1367-2630/14/5/055021](https://doi.org/10.1088/1367-2630/14/5/055021)

Résumé

This focus issue on membrane biophysics presents a collection of papers illustrating new developments in modern biophysical research on cell membranes. The work described here addresses questions from a broad range of areas, including cell adhesion, membrane trafficking and activation of cells of the immune system. It also presents recent views on membrane mechanics, the effect of electric fields, as well as on the interplay of mechanics and chemistry and organization at many different scales.

Andrew Callan-Jones, Patricia Bassereau (2012 Apr 21)

Membrane fission: curvature-sensitive proteins cut it both ways.

Developmental cell : 691-2 : [DOI : 10.1016/j.devcel.2012.04.001](https://doi.org/10.1016/j.devcel.2012.04.001)

Résumé

Boucrot et al. (2012) demonstrate a membrane fission mechanism independent of nucleotide hydrolysis that is based on membrane insertion of amphipathic helices. They show that, for N-BAR domain proteins, which promote membrane curvature but also contain amphipathic helices, fission is opposed by the BAR domain that stabilizes tubular membrane structures.

Benoît Sorre, Andrew Callan-Jones, John Manzi, Bruno Goud, Jacques Prost, Patricia Bassereau*, Aurélien Roux* (2012 Jan 3)

Nature of curvature coupling of amphiphysin with membranes depends on its bound density.

Proceedings of the National Academy of Sciences of the United States of America : 109 : 173-178 : [DOI : 10.1073/pnas.1103594108](https://doi.org/10.1073/pnas.1103594108)

Résumé

Cells are populated by a vast array of membrane-binding proteins that execute critical functions. Functions, like signaling and intracellular transport require the abilities to bind to highly curved membranes and membrane deformation to trigger. Among proteins this is Amphiphysin 1 Implicated in clathrin mediated endocytosis. It contains a Bin-Amphiphysin Rvs-membrane-binding domain with an N-terminal amphipathic helix and senses that Generates membrane curvature. However, an understanding of the parameters distinguishing these two functions is missing. By pulling a highly curved nanotube radius of controlled from a giant vesicle in a solution containing Amphiphysin, we observed that the actions of the protein depends on its density on the membrane. At low density of protein on the vesicle nearly flat, the distribution of proteins and the mechanical effects are

induced Described by a model based on spontaneous curvature induction. The tube radius and strength are modified by protein binding but still depends on membrane voltage. In the dilute limit, When Were Practically no proteins present on the vesicle, no mechanical effects Were detected, strong goal protein enrichment proportional to curvature Was seen on the tube. At high densified, the radius is independent of voltage and vesicle protein density, resulting and from the formation of a scaffold around the tube. As a result, the scaling of the power with voltage is modified. For the entire density range, protein enriched Was on the tube as Compared to the vesicle. Our approach shows que le strength of curvature sensing and mechanical effects on the tube depends on the protein density.