Membrane deformation by lipid-protein interactions

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Eukaryotic cells are compartmentalized into membrane-bounded organelles, such as nucleus, endoplasmic reticulum, Golgi apparatus, endosomes and lysosomes. Each organelle shows characteristic morphology and contains unique set of proteins to facilitate its specific functions. Proteins must be properly delivered to each organelle by membrane traffic. Membrane traffic is a sequential process of membrane deformation: cargo-containing vesicle budding and fission from the donor organelle followed by vesicle fusion with the acceptor organelle. Cellular membranes also dynamically change their morphology during cytokinesis and organelle biogenesis.

“Membrane-sculpting proteins” play central roles in membrane deformation. BAR domain superfamily proteins are typical membrane sculpting proteins which form curved banana-shaped homodimers. Using its positively charged concave surface, BAR domain can sense and induce curvature of acidic membrane surface. Overexpression of several BAR domains is known to induce membrane tubules in cells. It has been demonstrated that BAR domain proteins can deform liposomes into tubules *in vitro*. BAR domains are supposed to oligomerize into scaffold lattices by lateral tip-to-tip interactions and also longitudinal interactions along the cylindrical membrane tubules.

We are incorporating *in vitro* assay systems using giant unilamellar vesicles (GUVs) to study dynamics of lipid membrane deformation by BAR domain proteins. GUVs are composed of single lipid bilayers up to several tens of microns in diameter, nearly close to the cell size. GUVs are readily formed by swelling dried lipid films. They are easily visualized by fluorescence microscopy and also would be subjected to time-resolved analysis using future light sources.