Controlling the Morphology of Lipid Bicelles

V Urban[1]

[1]Oak Ridge National Lab

urbanvs@ornl.gov

Authors: Wellington Leite(1), Yuqi Wu(2), Sai Venkatesh Pingali(1), Raquel L. Lieberman(2), Volker S. Urban(1)

Affiliations:

(1) Neutron Scattering Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee

(2) School of Chemistry and Biochemistry, Georgia Institute of Technology, Atlanta, Georgia

Lipid bicelles provide an interesting, versatile nanostructured fluid environment that can be used as a model system and platform for studies of integral membrane proteins. They represent a middle ground between the simpler surfactant micelle structures and the highly complex environments of the protein decorated, lipid bilayer membranes that are encountered in the biological membranes that serve both as the boundary of external cells membrane as well as for providing compartmentalization within cells. Nature furthermore has evolved ways to structure its lipid bilayers and to organize them into extended continuous systems that facilitate transport and control processes of metabolism. Examples are the endoplasmic reticulum, Golgi apparatus, as well as thylakoid and mitochondrial membranes. On the other hand, human designed self-assembly systems are still a far cry from such intricately controlled organized fluid structures. It may however be speculated that by careful selection of lipid and cosurfactant molecules, similarly sophisticated bilayer structures could be generated and their morphology may be controlled by selection of co-surfactants and lipids or control of temperature and other environmental factors. Moreover, identifying physicochemical driving forces that connect miscibility and co-organization in mixed lipid/surfactant systems to the morphology or architecture of the resulting bilayer assemblies, could contribute to our understanding of the physiology and pathophysiology of the outer and internal cell membranes.

In this contribution we will present new data on the DMPC/CHAPSO bicelle system (DMPC = 1,2-dimyristoyl-sn-glycero-3-phosphocholine, CHAPSO = 3-((3-cholamidopropyl)dimethylammonio)-2-hydroxy-1-propanesulfonate). We have studied the influence of temperature and of added co-surfactant n-Dodecyl β-D-maltoside (DDM) on the the DMPC/CHAPSO assembly. Small-angle neutron scattering (SANS) data, measured on a series of different isotope contrast scenarios provide a detailed picture about the distribution of the different molecules in different domains of the bicelle system. Our data suggests that increased temperature and added co-surfactant may increase mixing of the primary bilayer constituents and thereby can alter the nanoscale dimensions of bicelle membrane channels as well as drive larger scale assembly into an extended worm-like bicelle system.

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