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Commentary

Characterization of Lipid Protein Interactions through Molecular Stimulation

Mary Alice*

Department of Biomolecules, University of Warsaw, Warsaw, Poland

DESCRIPTION

Membrane lipids interact with proteins in a variety of ways for providing a stable membrane environment for proteins to encapsulation and detailed roles in complex and well-controlled protein functions. Experimental and computational advances have converged on the rapidly expanding field in study of lipid-protein interactions. Experimentally a database of high-resolution membrane protein structures is growing, identifying complex lipid compositions of various membranes, scrutinizing difficult time and length scales of lipid-protein interactions. There are more opportunities to link protein interactions to proteins it works with a variety of proteins. Computational, more accurate membrane models provide a detailed view of lipid-protein interactions, increasing duplication of simulation and experimental observations for experimental validation and co-interpretation.

The cell membrane that encloses both the internal organelle and the entire cell is an essential structural element in all life. They are composed of a complex mixture of lipids and proteins, with lateral structures that have not yet been elucidated in detail, depending on cell type and membrane location. Cell membranes allow tight control of the flow of energy, information, nutrients and metabolites. Although these roles have historically been attributed primarily to membrane proteins, there is increasing evidence that lipid-protein interactions are important determinants of the membrane binding process. As a direct result membrane proteins are an important drug target and the lipid component of the growing body, the evidence membrane. The cell membrane is composed of two lipids, outer and inner, and is arranged from tail to tail. Lipids often fall into three major classes include glycerophospholipids, sphingolipids and sterols. Lipid-protein interactions are far from highly specific interactions between specific lipids that directly affect the selective binding sites of proteins, with changes in the physical properties of the membrane that change the membrane structure on a microscopic scale. It is classified as a range up to general interactions in length such as dimerization of two membrane proteins.

The structural properties of the lipid binding site can be realized by X-ray crystal structure analysis. In X-ray crystallography high resolution structures can be obtained by extracting membrane proteins from the lipid bilayer using detergents for solubilization. Due to the use of detergents in the purification and crystallization of proteins, naturally related lipids associated with proteins are often lost or if they are purified and crystallized together. It may not be clearly identifiable due to its structure. However, despite the many challenges encountered when dealing with membrane proteins, tightly bound lipids that survived the solubilization and purification steps have been identified by X-ray crystallography for some proteins. Heat treatment can affect protein-lipid interactions with respect to free radical formation altered emulsifying capacity and altered conjugated lipoprotein structures. Lipid-protein free radicals can be formed when free radicals produced by the oxidation of unsaturated lipids react with proteins. High temperatures significantly increase the rate of oxidation of sulfur containing amino acids through reaction with lipid oxides.

Quantitative analysis and identification of natural lipid species closely related to membrane proteins can be achieved through Mass Spectrometry (MS) studies. In this study the membrane protein complex was solubilized in a non-ionic detergent to provide resistance to the electrospray ionization step and gas phase. This technique has been applied to several transporters and other membrane proteins to provide information on lipid selectivity, binding stoichiometry, and the role that lipids may play in protein mechanisms. Native MS technology allows us to study the thermodynamics of lipid binding to membrane proteins and shed light on the mechanisms of molecular recognition between lipids and proteins.

Correspondence to: Mary Alice, Department of Biomolecules, University of Warsaw, Warsaw, Poland, E-mail: alice@gmail.com

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