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Editorial

The Hexagonal Lipid Phase's Role in Biological Membrane Organization

Peter Vedsted*

Editorial Office, Neurology and Neurorehabilitation, Germany

Introduction

All biological membranes include lipids that prefer to exist in a non-bilayer phase. Recent findings imply that membrane proteins in the thylakoid membrane urge all lipids to create a bilayer structure, and that non-bilayer-forming lipids in the thylakoid membrane help to drive the creation of membrane stacks. Lateral heterogeneities in biomembranes are important in a variety of cellular physiological activities. Demixing of lipid components and the creation of different liquid domains in the membrane are the result of such heterogeneities. To discover liquid-liquid phase coexistence in model membranes, we investigate lateral heterogeneities in terms of topological rearrangements of lipids. We describe the liquid-ordered and liquid-disordered areas in model lipid bilayers by calculating the degree of nonaffine deformation associated with individual lipids using principles from amorphous system and glass physics. This approach is used to investigate all-atom and coarse-grained lipid bilayer motions.

One of the most pressing issues in biophysics today is the self-assembly of membrane components, particularly lipids and proteins. Many membrane lipids spontaneously create a bilayer when combined with water, which has long been known . Recently, it was shown that even membrane proteins may create a bilayer shape). The Singer and Nicolson (1972) model of a biomembrane is based on the premise that lipids create a bilayer matrix into which proteins are inserted and can diffuse more or less freely in two dimensions.

If the main role of the lipids is to generate this fluid matrix, why does a biological membrane frequently include more than 100 distinct lipid species? In addition, many lipids do not form bilayers with water on their own.

Even the primary lipid in a membrane, such as monogalactosyldiglyceride in chloroplasts, may not always form a bilayer.However, the membrane lipids and proteins combine to produce a stable, functional membrane with the traits required for a live cell, i.e., to act as both a barrier and a communicator with its environment. As a result, the Singer and Nicolson model predicts that the membrane lipids do not function only as a fluid matrix. They are most likely structurally significant in biological membranes. This approach is useful for establishing the instantaneous domain boundaries in complicated multicomponent bilayer systems with many components. The characterisation also highlights the influence of line-active compounds on phase boundaries and domain mixing. Overall, we present a paradigm for investigating the molecular origins of spatial and dynamical heterogeneity in biomembrane systems that can be used in both computer simulations and experiments.

The plasma membrane is a complicated self-assembly of various lipids, sterols, and proteins. Differential molecular interactions between these various elements result in spatial and dynamic membrane structural heterogeneities . Such heterogeneities cause membrane constituents to phase separate, resulting in discrete domains that may be distinguished by their specific lengths and timelines. The domains are essential for cell signalling, membrane trafficking, protein complex building, pathogen uptake, and vesicle trafficking . Because of domain budding, plasma membrane domain development has also been linked to membrane remodelling mechanisms. The phospholipids of biological membranes exist in a bilayer structure, with integral membrane proteins attached to the bilayer by hydrophobic forces .

Pure or mixed systems of natural or manufactured lipids, including phospholipids, may adopt different shapes in addition to a bilayer arrangement under variable temperature or hydration conditions .

It has been proposed that nonbilayer lipid structures play a crucial role in modulating various membrane activities, including fusion The majority of these biological activities have been linked to a kind of lipid domain known as "rafts." Over the years, the concept (and definition) of "raft" in membrane biophysics has evolved. In vivo, "rafts" are currently viewed as dynamic nanoscale-ordered regions rich in cholesterol, sphingolipids, inositol-based phospholipids, and glycoproteins. The lipid and fatty acid composition of membranes is distinct for each kind of membrane and, to a large degree, species independent, implying that various lipids or certain combinations of lipids play a specialised role.the lipid makeup of several mammalian membranes. It is now well acknowledged that plasma membranes have a high concentration of cholesterol and glycolipids (mainly sphingolipids in animals), whereas intracellular membranes contain a low concentration of these two components. After the zwitterionic lipids, PC and SM, PE is the most abundant phospholipid in all membranes, although it is greatest in mitochondria. Only mitochondria, particularly the inner membrane, contain a large amount of CL. Many authors have written about amphiphile self-aggregation over the years. Israelachvili et al. have attempted to quantify the aggregation

Correspondence to: Peter Vedsted. Editorial office, Neurology and Neurorehabilitation, Germany; E-mail: nneurorehabilitation@gmail.com

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process and explain the production of distinct types of aggregate morphologies (1976, 1980). Their theoretical model reveals a fairly basic concept: the geometry of the amphiphilic molecules in the system controls the form of the lipid aggregation. Although oversimplified, it is a valuable tool for anticipating, for example, the modulation of membrane lipid content in live organisms . Phase coexistence in lipid membranes has traditionally been studied in two and three component membrane systems. They were the first to theoretically characterise the lateral heterogeneities in this two-component lipid system using the experimental phase diagram of the dipalmitoyl phosphatidyl choline (DPPC) and cholesterol combination. They proposed the occurrence of two demixed liquid phases and labelled them "liquid-ordered" and "liquid-disordered." Based on a theoretical framework, eventually attributed the molecular origins of this demixing to cholesterol's "decoupling nature." The phase, which is mostly composed of saturated lipids, displays strong structural order (similar to the gel phase) as well as translational chaos (similar to liquid crystalline phase).

The phase is indicated by the absence of long-range intermolecular conformational order. Despite the fact that the average diffusion coefficients of the two types of lipids in the membrane are of comparable orders of magnitude, the lipids in the ordered domains exhibit unique subdiffusive behaviour in comparison to those in the disordered phase . In model membrane systems including two or three types of lipids and cholesterol, nano- to microscale domains emerge depending on the nature of the lipid components. Although seeing tiny domains in pure lipid systems has become simpler, defining nanoscale domains remains difficult.