Matinal Membranas

Valencia 19-11-2022

Les membranes, fa cinquanta anys y avui

- Lo que se les puede contar a los niños, y lo que no.
- Fa cinquanta anys
- Modelos científicos
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The Fluid Mosaic Model of the Structure of Cell Membranes

Cell membranes are viewed as two-dimensional solutions of oriented globular proteins and lipids.

S. J. Singer and Garth L. Nicolson

Biological membranes play a crucial role in almost all cellular phenomena, yet our understanding of the molecular organization of membranes is still rudimentary. Experience has taught us, however, that in order to achieve a satisfactory understanding of how any biological system functions, the detailed molecular composition and structure of that system must be known. While we are still a long way from such knowledge about membranes in general, progress at both the theoretical and experimental levels in recent years has brought us to a stage where at least the gross aspects of the organization of the proteins and lipids of membranes can be discerned. There are some investigators, however, who, impressed with the great diversity of membrane compositions and functions, do not think there are any useful generalizations to be made even about the gross structure of cell membranes. We do not share that view. We suggest that an analogy exists between the problems of the structure of membranes and the structure of proteins. The latter are tremendously diverse in composition, function, and *detailed* structure. Each kind of protein molecule is structurally unique. Nevertheless, generalizations about protein structure have been very useful in understanding the properties and functions of protein molecules. Similarly, valid generalizations may exist about the ways in which the proteins and lipids are organized in an intact membrane. The ultimate test of such generalizations, or models, is whether they are useful to explain old experiments and suggest new ones.

Singer (*1*) has recently examined in considerable detail several models of the gross structural organization of membranes, in terms of the thermodynamics of macromolecular systems and in the light of the then available experimental evidence. From this analysis, it was concluded that a mosaic structure of alternating globular proteins and phospholipid bilayer was the only membrane model among those analyzed that was simultaneously consistent with thermodynamic restrictions and with all the experimental data available. Since that article was written, much new evidence has been published that strongly supports and extends this mosaic model. In particular, the mosaic appears to be a fluid or dynamic one and, for many purposes, is best thought of as a two-dimensional oriented viscous solution. In this article, we therefore present and discuss a fluid mosaic model of membrane structure, and propose that it is applicable to most biological membranes, such as plasmalemmal and intracellular membranes, including the membranes of different cell organelles, such as mitochondria and chloroplasts. These membranes are henceforth referred to as functional membranes. There may be some other membrane-like systems, such as myelin, or the lipoprotein membranes of small animal viruses, which we suggest may be rigid, rather than fluid, mosaic structures, but such membrane systems are not a primary concern of this article.

Our objectives are (i) to review briefly some of the thermodynamics of macromolecular, and particularly membrane, systems in an aqueous environment; (ii) to discuss some of the properties of the proteins and lipids of functional membranes; (iii) to describe the fluid mosaic model in detail; (iv) to analyze some of the recent and more direct experimental evidence in terms of the model; and (v) to show that the fluid mosaic model suggests new ways of thinking about membrane functions and membrane phenomena.

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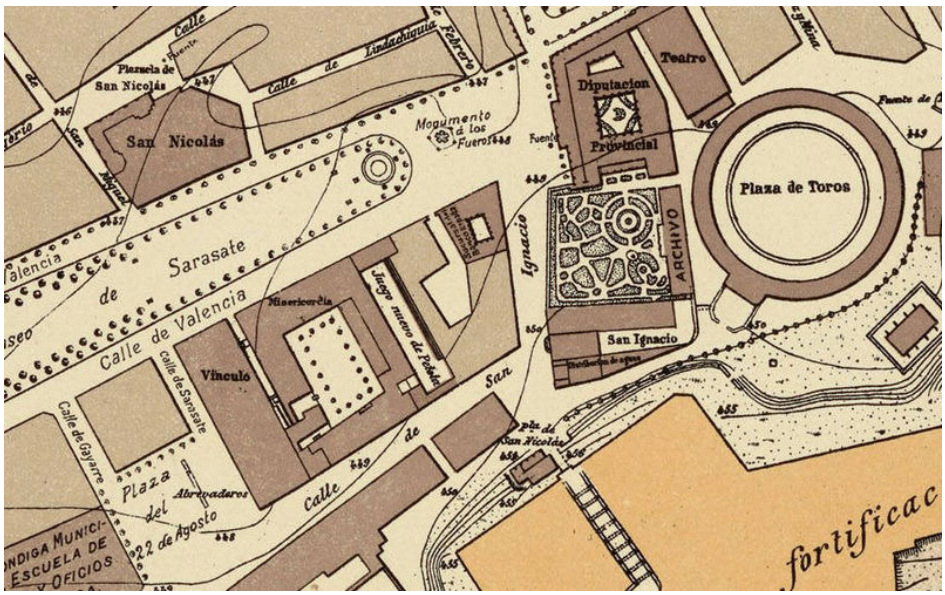
Thermodynamics and Membrane Structure

The fluid mosaic model has evolved by a series of stages from earlier versions (*1–4*). Thermodynamic considerations about membranes and membrane components initiated, and are still central to, these developments. These considerations derived from two decades of intensive studies of protein and nucleic acid structures; the thermodynamic principles involved, however, are perfectly general and apply to any macromolecular system in an aqueous environment. These principles and their application to membrane systems have been examined in detail elsewhere (*1*) and are only summarized here. For our present purposes, two kinds of noncovalent interactions are most important, *hydrophobic* (*5*) and *hydrophilic* (*1*). By hydrophobic interactions is meant a set of thermodynamic factors that are responsible for the sequestering of hydrophobic or nonpolar groups away from water, as, for example, the immiscibility of hydrocarbons and water. To be specific, it requires the expenditure of 2.6 kilocalories of free energy to transfer a mole of methane from a nonpolar medium to water at 25°C (*5*). Free energy contributions of this magnitude, summed over the many nonpolar amino acid residues of soluble proteins, are no doubt of primary importance in determining the conformations that protein molecules adopt in aqueous solution (*6*), in which the nonpolar residues are predominantly sequestered in the interior of the molecules away from contact with water. By hydrophilic interactions is meant a set of thermodynamic factors that are responsible for the preference of ionic and polar groups for an aqueous rather than a nonpolar environment. For example, the free energy required to transfer a mole of zwitterionic glycine from water to acetone is about 6.0 kcal at 25°C, showing that ion pairs strongly prefer to be in water than in a nonpolar medium (*1*). These and related free energy terms no doubt provide the reasons why essentially all the ionic residues of protein molecules are observed to be in contact with water,



PAMPLONA, 1884

J.F. Danielli y H. Davson (1935)
Lipoprotein bilayer model

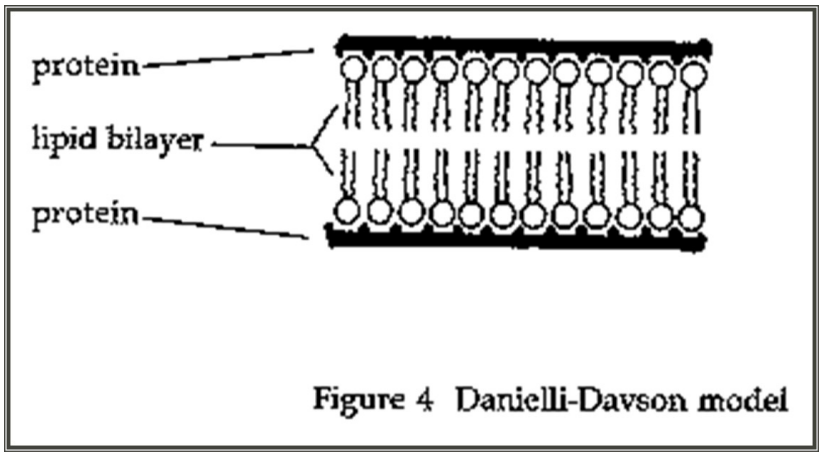
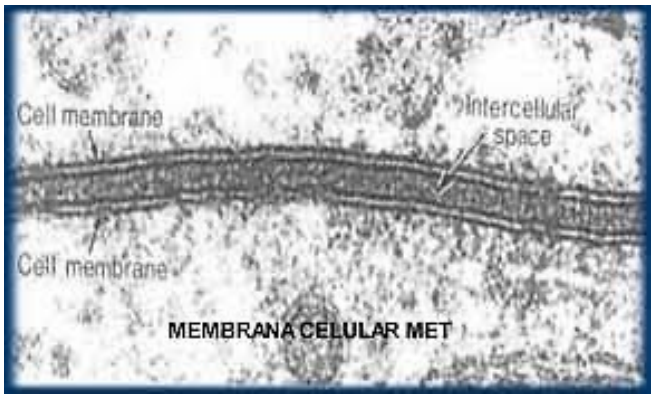
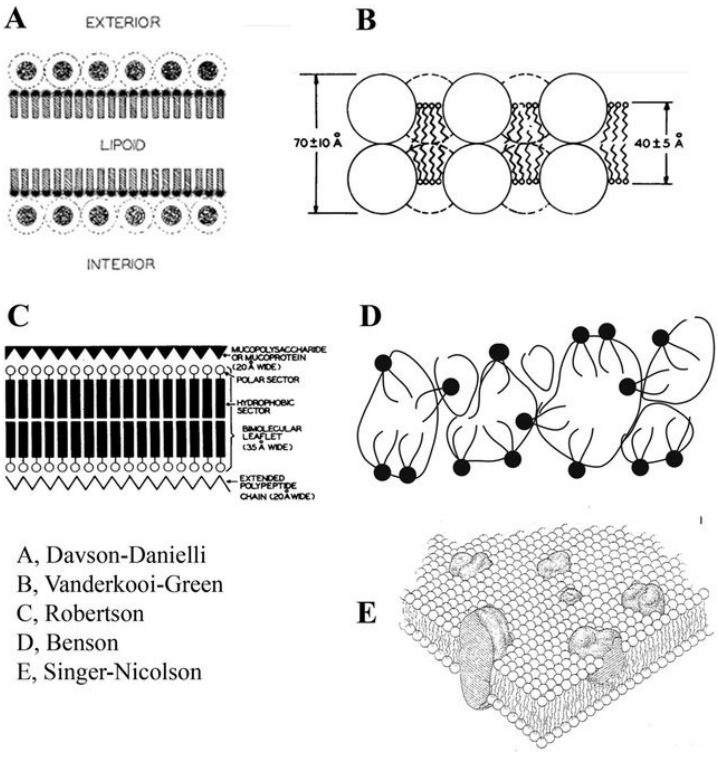


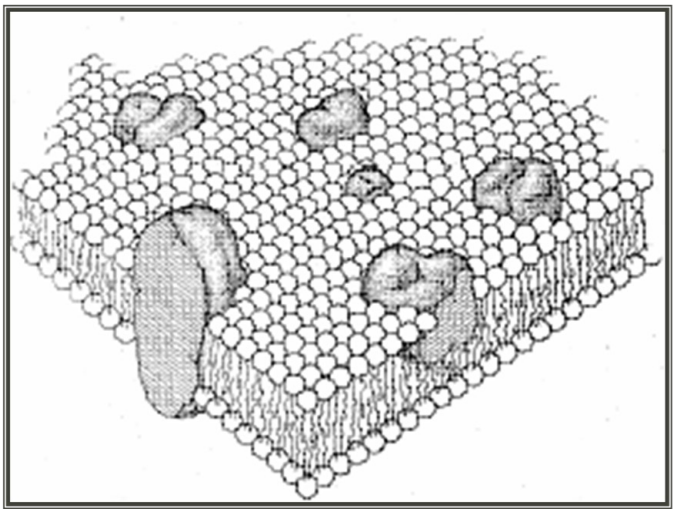
Figure 4 Danielli-Davson model



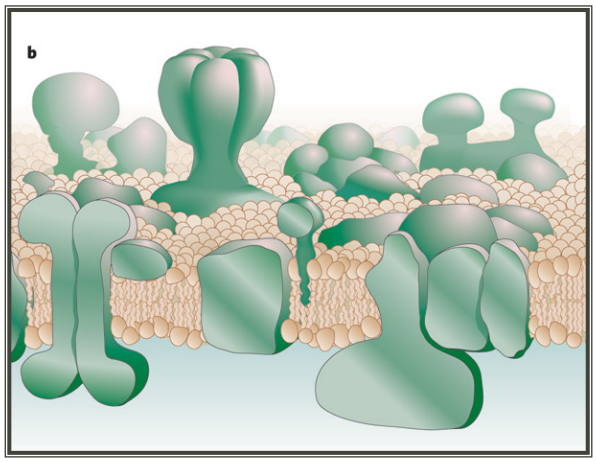


A, Davson-Danielli
B, Vanderkooi-Green
C, Robertson
D, Benson
E, Singer-Nicolson

The Original Fluid Mosaic (Singer-Nicolson) Model of Biomembranes (1972).



1. Transmembrane protein crowding



Engelman (2005) Nature 438, 578.

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Bothorel: Two Years Before Singer-Nicolson

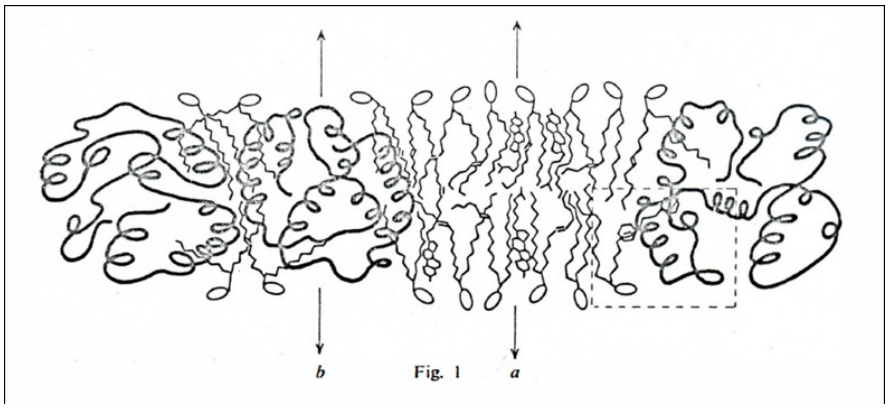

Fig. 1

Pierre Bothorel & Claude Lussan, C. R. Acad. Sc. Paris, t. 271, p. 680-683 (17 août 1970)

Pierre Bothorel

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Ermita de Godella

Óleo de Higinio Pellicer (2010)