ORDERING OF BICELLES AND PEPTIDE-MEMBRANE INTERACTIONS

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From a biophysical point of view, model membranes are important tools in the study of structural and functional features of the biological systems[1-2]. In our case, we are interested in improving our knowledge about different kind of model membranes, such as bilayered micelles or bicelles. Bicelles are disk-shape structures, in which the flat surface contains the longer chain phospholipid and the edges the shorter one. The magnetic properties of bicelles (ability to orient under a magnetic field) and the absence of surfactant molecules in the composition make them an important tool in the study of membrane proteins and peptides[3-4]. The aim of this experiment is to gain information about bicelles employing SAXS technique for a better characterization of their structural and orientation properties. In parallel, we tried to study the interaction of a more complex system formed by the amyloid peptide Aβ (1-40) (at two different concentrations) involved in the Alzheimer disease, and liposomes formed from a lipid extract of brain (lipid brain, LB) in order to reproduce the physiological conditions. In this case, we have tried to analyze the changes in the liposome structure promoted by Aβ (1-40) peptide in aqueous solution.

The experiments carried out in the BM16 of ESRF consisted in determining the SAXS diffraction patterns of different bicelles, and of two Aβ (1-40) concentrations with LB liposomes, using a distance of 1.4 m from sample to detector. Bicelles were formed by dimiristoyl phosphatidylcholine (DMPC) and dihexanoyl phosphatidylcholine (DHPC) at different lipid concentrations (5, 10, and 15 % lipid (w/v)), and varying the long/short chain lipid molar ratios (q=2, 2.3, and 3.5). LB liposomes (10 mg/ml) were mixed with 25 and 100 μM Aβ (1-40).

The results show that we can obtain information about d-spacing of bicelles (~4 nm very similar for all the compositions) and their orientational properties by the SAXS technique. Thus, we can distinguish a nematic phase in q=3.5 bicelles. LB resulted in non-multilamellar liposomes although the initial population was not homogenized by the common methods (e.g. extrusion). We observed an effect of the Aβ (1-40) on the liposome d-spacing as a function of the peptide concentration (25 and 100 μM).

The SAXS technique is very useful for studying structure and order of bicelles, and also it has allowed us to detect the effect of low concentration of Aβ (1-40) on LB liposomes (similar to the physiological conditions).

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