INTERACTION BETWEEN PEPTIDES DERIVED FROM DENGUE VIRUS CAPSID PROTEIN AND MODEL MEMBRANES

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Dengue virus is composed by a nucleocapsid surrounded by a lipid bilayer. The nucleocapsid is formed by viral genome complexed with multiple copies of the capsid (C) protein. C protein is a highly basic protein containing four helices (a1 to a4) connected by short loops. In solution, this protein exists as dimers stabilized by the interaction of two pairs of antiparallel helices, a2-a2' and a4-a4'. The a2-a2'interface is formed by part of a conserved hydrophobic region. The a4-a4' forms a coiled-coil structure containing most of basic residues. Based on charge distribution it has been proposed that a4-a4' interacts with the viral RNA whereas the apolar region formed by a2-a2' interacts with the membrane. We evaluated the interaction between phospholipid vesicles and peptides corresponding to C protein segments (residues 45 to 68 – pepM, comprised in the hydrophobic domain, and 74 to 98 – pepR, corresponding to the basic region). Fluorescence studies with pepM showed that increases in the excitation wavelength led to a red-edge effect, suggesting that this peptide aggregates in solution. This hypothesis was confirmed by fluorescence anisotropy experiments. This effect was not observed for pepR. While pepM interacts with neutral, anionic, and cholesterol-enriched membranes, pepR only interacts with anionic phospholipids. Taken together, these data provide insights on the interactions of dengue peptides and specific membranes.
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