Molecular Dynamics of Adenosine Triphosphate Interacting with Phosphatidylcholine Lipid Bilayers

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Adenosine triphosphate (ATP) provides the chemical energy needed in most biological processes from metabolic reactions to cellular mechanics. ATP consists of an adenine ring, a ribose sugar, and a chain of three phosphate groups. Hydrolysis of ATP that cleaves phosphate bonds is the mechanism by which energy is released to the environment, resulting in lower energy derivative form of ATP as adenosine diphosphate (ADP) and adenosine monophosphate (AMP). Within biological cells, this chemical reaction often takes place in the vicinity of lipid membranes. Biophysical experiments by x-ray scattering and NMR spectroscopy have indicated that ATP binds to lipid membranes primarily through the adenine ring, leaving the phosphate chains available for hydrolysis. However, the exact dynamics of ATP, and in particular the possible cooperativity between bound ATP molecules is still unknown. To address these important questions, I have used molecular dynamics simulations at atomic level using the CHARMM force field. Twelve different ATP systems in the presence of lipid bilayers were run for 0.5 microseconds each. In addition, four different simulations containing either ADP or AMP were performed for comparison. Each of these systems contained 100 phosphatidylcholine lipid molecules and an appropriate amount of water. Simulations reveal that ATP, ADP, and AMP bind to lipid headgroups cooperatively and this behavior generates significant electrostatic charging of membranes even at low concentrations that are typical in biological cells. The important finding is that ATP is directly involved in the electrostatic charging of membranes and this mechanism can affect the transmission of the action potential in neurons.

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