Magnetic Field effects on Adenosine A2A Receptor: a Molecular Dynamics study

Del Signore F.(1), Marracino P.(2), Cocco D.(1), Setti S.(3), Cadossi R.(3),
Liberti M.(1), Apollonio F.(1)
(1) University of Rome "La Sapienza, DIET, Rome, Italy; e-mail:francesca.apollonio@uniroma1.it
(2) Rise Technology srl, Via Monte Bianco 18, S. Martino di Lupari, Italy; e-mail:paolo.marracino@risetechnology.co
(3) IGEA SpA, Via Parmenide 10/A, Carpi, Italy; e.mail:s.setti@igeamedical.com

The following paper presents the study of an external static magnetic field on adenosine A2A receptor embedded in a phospholipidic bilayer via molecular dynamics simulations. The purpose is to understand specific interactions of the binding site in order to elucidate how magnetic field influences the protein receptor at molecular level.
Several studies have shown how pulsed electromagnetic fields (PEMFs) may have biological effects on different cells function as anti-inflammatory effect [1,2]. To this regard, depending on the intensity of the applied PEMFs experimental data suggest a modulation of adenosine A2A receptor activity, linked to an increase of receptors availability [1]. Nevertheless, the molecular mechanism behind this increase has not been elucidated yet.
Molecular Dynamics (MD) simulations are a perfect tool for studying the behavior of a system at atomistic level and, therefore, understanding how specific conditions change the interactions between atoms and molecules. Gromacs software for MD simulations has been recently modified by the authors in order to introduce a new procedure for the application of a static homogeneous magnetic field, by adding the Lorentz force on all charged particles in the Velocity Verlet algorithm [3]. A preliminary study has been performed on the adenosine A2A receptor in a buffer aqueous environment without the phospholipidic bilayer [4].
Here, the simulation box consisted of an A2A receptor (3PWH) embedded in a phospholipidic bilayer, conceived as a model of a realistic membrane patch. Simulations have been carried out in the NPT (number of particles, pressure and temperature are kept constant) ensemble with SPC water molecules and ions to model intracellular and extracellular media. Several simulations (more than 200 ns each) were carried out, without magnetic field applied and with a 1T static magnetic field B, perpendicular to the membrane surface. Our analysis focused on a specific protein domain involved in the binding process.
Data suggest that the 1 T magnetic field does not produce meaningful structural effects, since protein secondary structures remain essentially stable. On the other hand, a clear effect of the magnetic field has been clearly observed in the dipole moments of specific residues building up the binding site. This results that can be considered extremely localized builds up and gives rise to a more macroscopic effect on the area of the receptor site.
In conclusion, the adenosine A2A receptor embedded in a phospholipidic bilayer subjected to a static magnetic field has been studied through MD simulations. An insight on the binding site has shown interesting effects on some residues. These effects may be tightly related to the protein activity and expression, making possible to understand which is the probable molecular mechanism behind the increasing in density of the A2A receptor protein.

References

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