Molecular dynamics simulation study of interaction of cytotixins and nanobio membrane

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This work is a research about the interaction of a family of cytotoxins and nanobio membrane. This process has great importance and is hoped to be used as a novel approach to treat cancers. First nanobio membrane and cytotoxin are introduced then the method is illustrated.

Nanobiomembrane is a very important part of living systems. Alive cells have lipid bilayer nanomembrane in liquid phase. The structure of this nanobiomembrane is based on properties of phospholipids. Each phospholipid has a hydrophilic head and a hydrophobic tail. Lipid bilayers are composed of two monolayers, each monolayer is a line of phospholipids. The hydrophilic heads of outer monolayer are oriented to water solutions outside the cell and those of inner monolayer to water solutions inside the cell. The hydrophobic tails of all phospholipids are oriented to the inner side of bilayer. The average thickness of this bilayer is about 5 nm. The most important function of lipid membrane is to preserve the inner parts of the cell.

Experimental results have shown that some antimicrobial peptides and cytotoxins are able to deform -or in some cases to destroy- the bilayer membrane. The insertion of these peptides and proteins to the outer monolayer of the lipid bilayer, changes the form of the membrane. Sometimes these changes lead to death of the cell. One of the most interesting cytotoxins are Cobra venom cytotoxins (cardiotoxins) that are small basic proteins (60–62 amino acid residues, 4 disulfide bridges) belonging to the large family of three-fingered toxins. A modeled cytotoxin is shown in figure 1. The mechanism of the changes is not clear.

The first step to discover the mechanism of the interaction of cytotoxin with nanobiomembrane is to find the real position of the cytotoxin relative to the nanobiomembrane when meeting it. A suitable tool to find this position is molecular dynamics simulation. The GROMACS package is used to simulate the process of the regarded interaction. The POPC nanobiomembrane, CTX2, CTX3 and CTX4 cytotoxins are selected. Amodeled POPC is shown in figure2. Molecular dynamics simulation is used in several steps and finally the position at which each cytotoxins meets the nanobiomembrane is found. The resulted position of each case is compared with those of the others. The results are compared with experimental results. Finally a relation is found between the relative position of cytotoxins with nanobio membrane and the cytotoxity of different cytotoxins.

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Figures

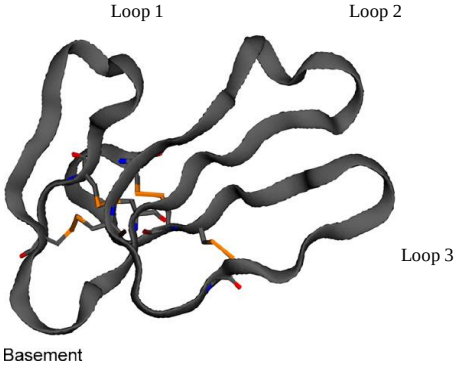

Fig1. A modeled cytotoxin

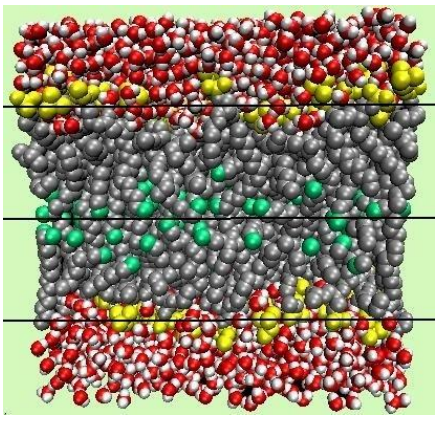

Fig.2. POPC nanobio membrane simulated with VMD to use by GROMACS