Interaction of L-alanine and L-valine Aminoacid Molecules with Phospholipid Bilayer. Molecular Dynamics Simulation

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ABSTRACT
It is well known the importance of investigations of interactions between proteins and biological membranes. We decided to give a deeper sight to this problem by the determination of ways of interactions between main structural elements of of ptoteins and membranes: aminoacid molecules and phospholipid bilayers correspondingly, using computer simulation methods. By means of simulation, remarkable progress is being made in the understanding of lipid bilayer behavior influence on the peptide-lipid interaction.

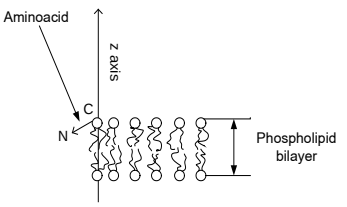
Keywords
Molecular dynamics simulation, phospholipid bilayer, aminoacids.

1. INTRODUCTION
Particularly for these simulations the method of molecular dynamics was used. There were investigated localization of the molecules of L-alanine, and L-valine on phospholipid bilayer and their influence on the physical properties of bilayer. The phospholipids bilayer is consisting of from 128 Dipalmitoylphosphatidylcholine (DPPC) and 3655 water molecules, which corresponds to fully hydrated state of phospholipid bilayer.

2. METHODS
The molecular dynamics simulations were carried out using GROMACS simulation package (version 3.2.1) [1-3].The VMD package [4] was used for visualization and molecular graphics. The starting configurations of DPPC bilayers, force fields and topologies [5] were taken from Tieleman's group website http://moose.bio.ucalgary.ca. Simulations were made at same conditions. The long-ranged Coulomb interactions were cut off to 2.5nm and the short-range van der Waals interactions were cut off to 1.4nm. Simulations were done under NPT ensemble with constant temperature (303K) and pressure (1 bar). After energy minimization molecular dynamics simulations were done with duration of 15 ns each.

3. RESULTS
For the description of bilayer properties there were measured average area per lipid molecule on the surface of bilayer and bilayer thickness. From the real physical experiment area per lipid was received as 0.62 nm^2 [6]. During the simulation time this value (measured on the aminoacid neighboring part of bilayer) is decreasing to approximately 0.4 nm^2. This means that lipid molecules are getting closer to each other after aminoacid addition. The bilayer thickness, measured as a distance between aminoacid neighboring lipid molecule headgroup`s phosphorus atoms of upper and lower layers, which from real experiment is equal to 3.7 nm, but during simulations this value is decreasing to ~3.5 nm. It was measured also the penetration of aminoacid molecules inside the bilayer to the phosphorus atom (7.5 ns) and then even go deeper then phosphors atom. Furthermore at the end of simulation (15 ns), starting from 12 ns, L-valine penetrates deeper then L-alanine, which can be explained by L-valine's more hydrophobicity compared with L-alanine.

For the determination of aminoacid molecules orientation in bilayer there were measured and compared



aminoacid's nitrogen atoms and carboxyl group's carbon distances from neighboring upper layer phosphors. In both cases carboxyl group's carbon atoms placed upper in the bilayer than nitrogen. Also it was calculated the angle between bilayer normal z axis and aminoacid carboxyl carbon-nitrogen vector. This angle is blunt during simulation time. From these data we can present the possible orientation of aminocids in the bilayer (see the Fig.).

4. CONCLUSIONS
In conclusion we can point out some essential results that we have received. At first we have modeled for the first time the interactions between aminoacids and phospholipid bilayer. We have got that area per lipid and bilayer thickness for the aminoacid neighboring part of bilayer are decreasing. Aminoacids center of masses are penetrating into the bilayer deeper then lipids average phosphorus for 0.3 nm, furthermore L-valine is penetrating deeper than L-alanine. And finally we have suggested the possible orientation of aminoacids in the bilayer.

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