

Molecular dynamics in conformational analysis of *Pseudomonas aeruginosa* lipopolysaccharides.

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Lipopolysaccharides (LPS) are molecules in the membrane of gram-negative bacteria. They are stimulators of innate immune responses and play a key role in the pathogenesis of infections in both plants and animals. In most bacterial LPS there are three domains: lipid A, oligosaccharide core (OS), and O-antigen, which structure widely varies and determines bacterial serotype.

It is important to study the conformational mobility of the O-antigen and LPS in general, because due to their high variability there is currently not enough experimental data describing their conformation.

Aim: Analysis of the conformational mobility of *Pseudomonas aeruginosa* A- and B-forms LPS molecules using molecular modeling methods.

Topologies for all-atom LPS models were generated with the online service charmm-gui in the force field CHARMM36. Calculations were carried out using GROMACS software package. Visualization was carried out using the PyMOL. A single LPS molecule of *Pseudomonas aeruginosa* serotype O5a (B-form), with five repeating fragments, was placed in a reaction volume filled with water. The simulation was conducted for 450 ns. A single polyrhamnose LPS molecule of *Pseudomonas aeruginosa* (A-form), with five repeating fragments of O-antigen, was placed in a reaction volume filled with water. The simulation was carried out for 150 ns.

Intermediate results: All-atom models of *Pseudomonas aeruginosa* LPS molecules A-form and B-form were generated. Molecular dynamics simulation was carried out and confirmed by further analysis of their conformation with the distributions of dihedral angles around the selective O-glycosidic bonds in O-antigens.

Final results: The computation results showed differences in the conformational mobility of the A- and B- forms of the O antigen. The B-form molecule underwent strong changes, folding along the O-glycosidic bond between the core and the O-antigen, whereas the deviations of the A-shape from the initial conformation were insignificant. The computational data was confirmed by the analysis of dihedral angles.

References.

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