Canadian Association of Physicists
Association canadienne des physiciens et physiciennes

Contribution ID: **4615** Type: **Poster (Non-Student) / Affiche (Non-étudiant(e))**

(POS-43) Molecular Dynamics Simulation of Lung Surfactant Protein SP-B fragments in model bilayers

Tuesday 28 May 2024 18:31 (2 minutes)

In lungs, a lipid-protein surfactant layer enables breathing by reducing surface tension at the air-water interface. Lung surfactant function requires cycling of material between bilayer reservoirs and an active surfactant layer, presumably involving transient formation of highly curved lipid structures. Surfactant protein SP-B, a 79-residue protein that forms homodimers, is essential for lung function. To study how lipid-SP-B interactions might contribute to implied lipid assembly reorganization, GROMACS molecular dynamics simulations were used to study conformation and orientation of SP-B fragments SP-B_{1-9} and SP-B_{1-25} in DPPC/POPG (7:3) model lipid bilayers. SP-B_{1-9} includes SP-B's initial 7-residue insertion sequence. SP-B_{1-25} also includes the first of SP-B's four amphipathic helices. To obtain averages and test for protein-induced bilayer perturbation, each simulation involved multiple copies of each fragment (18 SP-B1 − 9 or 9 SP-B_{1-25} copies per bilayer leaflet). Simulations were also run with no peptide and with only one copy of SP-B_{1-9} per leaflet. The simulation with multiple copies of SP-B_{1-9} started with randomly oriented peptides inserted in the lipid bilayer and ran for 450 ns. SP-B1-25 simulations started with (i) randomly oriented peptides, (ii) peptides oriented along the bilayer surfaces, and (iii) peptides inserted across the bilayer (trans). On average, SP-B_{1-9} was found to tilt only slightly into the bilayer with its N-terminal phenylalanine staying within about 0.75 nm of the bilayer phosphate layer. Comprising the insertion sequence plus first SP-B helix, SP-B_{1-25}, tended to remain in the trans-bilayer orientation when started in that orientation. If started roughly parallel to the bilayer surface, SP-B_{1-25} tended to settle into non-trans orientations but with excursions toward the trans configuration. When starting from random peptide orientations, SP-B_{1-25} largely settled into a mixture of trans and surface orientations. SP-B_{1-25} is nearly the first third of the SP-B monomer. Its capacity to be accommodated in both trans-bilayer and single-leaflet environments may reflect SP-B's role in promoting lipid assembly reorganization implied by the cycling between bilayer reservoir and surface-active layer structures.
Supported by NSERC, ACENet, and Digital Research Alliance of Canada.

Keyword-1

Lipid-protein interaction

Keyword-2

Lung surfactant

Keyword-3

Molecular Dynamics Simulation

Author: MORROW, Michael

Co-authors: SHEIGANI, Vahid (Memorial University of Newfoundland); ZHAO, Yimiao (Memorial University of Newfoundland); JYOTHINI, Abinu (Memorial University of Newfoundland); SAIKA-VOIVOD, Ivan (Memorial University of Newfoundland)

Presenter: MORROW, Michael

Session Classification: DPMB Poster Session & Student Poster Competition (28) | Session d'affiches DPMB et concours d'affiches étudiantes (28)

Track Classification: Technical Sessions / Sessions techniques: Physics in Medicine and Biology / Physique en médecine et en biologie (DPMB-DPMB)