Towards an Understanding of Cationic Lipid Bilayers from Atomistic Molecular Dynamics Simulations



A. A. Gurtovenko, M. Patra, M. Karttunen, and I. Vattulainen

¹Laboratory of Physics and Helsinki Institute of Physics, Helsinki University of Technology, P.O. Box 1100, FIN-02015 HUT, Finland ²Laboratory of Computational Engineering, Helsinki University of Technology, P.O. Box 9203, FIN-02015 HUT, Finland

e-mail: vattulai@csc.fi

Introduction

- Cationic lipids, being a promising class of nonviral vectors for gene delivery, are able to form compact complexes with DNA and to facilitate transfection of DNA into living cells (see e.g. [1])
- Detailed understanding of a structure of the cationic lipid/DNA complexes is needed for the further development of these delivery vectors. However, due to the complex nature of the problem, the only atomistic computer simulation study of such complexes exists [2].
- As a first step toward detailed atomistic study of complexes of cationic lipids and DNA, in this work we employ molecular dynamics (MD) simulations of cationic lipid bilayers in aqueous solution.
- We study a lipid bilayer consisting of a mixture of zwitterionic lipid dimyristoylphosphatidylcholine (DMPC) and cationic lipid dimyristoyltrimethylammonium propane (DMTAP), see Fig. 1.

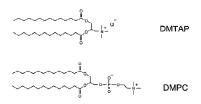


Fig. 1. Structures of DMPC and DMTAP [3], lipids under study

Model and Simulation Details

- System: 128 lipid molecules (64 lipids per monolayer), ~3600 SPC water molecules, and ions Cl[−]. Total: ~17000 atoms.
- United-atom GROMACS force-field modified to describe lipids [4].
- $\bullet \; T = 323 \; K$ and $P = 1 \; Bar$ (Berendsen coupling scheme).
- Electrostatics: Particle Mesh Ewald (PME)
- 11 different concentrations of cationic lipid DMTAP in bilayer are considered:
 0.0 (pure DMPC bilayer), 0.06, 0.16, 0.25, 0.31, 0.39, 0.50, 0.63, 0.75, 0.89, and
 1.0 (pure DMTAP bilayer).
- \bullet Software: GROMACS 3.1.4 [5]

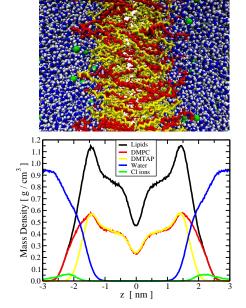


Fig. 2. (Top) Snapshot of final structure for cationic bilayer at $\chi_{TAP}=0.5$ after 30 ns; (Bottom) Mass density profile across the same bilayer (z = 0 corresponds to the bilayer center).

Structural Properties

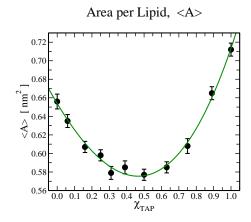


Fig. 3. Average area per lipid $\langle A \rangle$ versus DMTAP fraction χ_{TAP} .

Orientation of PC Head Groups

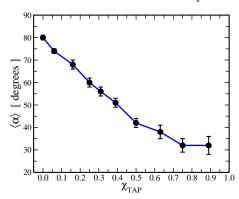


Fig. 4. Average angle $\langle\alpha\rangle$ between the P-N vector of DMPC lipids and the monolayer normal versus DMTAP concentration $\chi_{\rm TAP}$ in bilayer

Deuterium Order Parameter

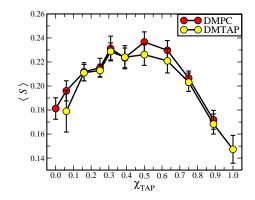


Fig. 5. Plateau order parameter $\langle S \rangle$ calculated by averaging S_{CD} over C2 to C8 hydrocarbons.

Coordination Numbers

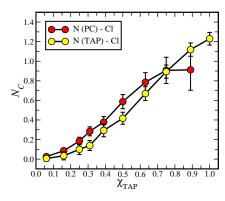
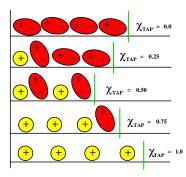


Fig. 6. Coordination numbers N_C of DMPC and DMTAP nitrogens with chloride ions.

Conclusions

- \bullet The average area per lipid has a pronounced non-monotonic dependence on the DMTAP concentration $\chi_{\rm TAP},$ with a minimum around the point of equimolar mixture.
- At low and modest DMTAP concentrations, a considerable compression of the bilayer is observed, see Fig. 3. We address this effect to the re-orientation of dipole moments of DMPC head groups with respect to the bilayer normal, Fig. 4.
- In contrast, at higher DMTAP concentrations (when the re-orientations of PC groups is almost finished) there is a substantial expansion of the bilayer that is mostly driven by electrostatic repulsion between positively charged DMTAP head groups.
- \bullet Deuterium order parameter $|S_{CD}|$ follows closely the change in the area per lipid: The compression of the bilayer is accompanied by the ordering of acyl chains and $vice\ versa.$
- Chloride counter-ions are bound mostly to DMPC nitrogens implying stronger screening of PC heads by Cl ions compared to TAP head groups.
- A proposed schematic picture of the observed change in the area per lipid vs DMTAP concentration χ_{TAP}. Only headgroups of DMPC (red ellipses) and DMTAP (yellow circles) lipids are shown; water (not shown) is above the headgroups.



Publication: A. A. Gurtovenko, M. Patra, M. Karttunen, and I. Vattulainen, Cationic DMPC/DMTAP Lipid Bilayers: Molecular Dynamics Study, Biophysical Journal, 2004, in press.
 Preprint: http://arxiv.org/abs/cond-mat/0312400

Acknowledgments

This work was supported by the Academy of Finland under grant 202598. Computational support from the CSC (Espoo, Finland) and from the SDU Supercluster (Odense, Denmark) is gratefully acknowledged.

References

- W. M. Gelbart et al., Physics Today 53, 38 (2000).
- [2] S. Bandyopadhyay et al., J. Phys. Chem. B ${\bf 103},\,10075$ (1999).
- [3] R. Zantl et al., J. Phys. Chem. B 103, 10300 (1999).
- [4] O. Berger et al., Biophys. J. 72, 2002 (1997).
- [5] E. Lindahl et al., J. Mol. Model. 7, 306 (2001).
- [6] H. I. Petrache et al., Biophys. J. 79, 3172 (2000)
- [7] J. F. Nagle et al., Biophys. J. 70, 1419 (1996).