Supporting Information: NMRlipids IV: Headgroup & glycerol backbone structures, and cation binding in bilayers with PE and PG lipids

O. H. Samuli Ollila*,†

†*Institute of Organic Chemistry and Biochemistry, Academy of Sciences of the Czech Republic, Prague 6, Czech Republic*

‡*Institute of Biotechnology, University of Helsinki*

E-mail: samuli.ollila@helsinki.fi

S1 Simulated systems

S1.1 CHARMM36

POPE Simulation details by M. Javanainen.

POPE with additional NaCl Simulation details by A. Peon.

POPG Simulation details by Ollila.

POPG with additional NaCl Simulation details by A. Peon.

POPC:POPE mixtures Data is available at.[1,2] 300 K with v-rescale (tau=0.1 ps), 1 bar with PR semiisotropic (tau=4 ps, compressibility=4.5e-5 bar^{-1}), PME order 4 and space 0.12, rcoulomb and rvdw 1.0, 128 lipids per leaflet, no ion Full simulation details by Fuchs et al.

POPC:POPG mixture with additional calcium Simulation details by J. Madsen.

POPC:POPG mixture with additional NaCl Simulation details by A. Peon.

S1.2 CHARMM36ua

POPE Data is available at.[3] Simulation details by T. Piggot.

S1.3 Slipids

POPE Data is available at.[4] Simulation details by T. Piggot.

POPE with additional NaCl Simulation details by A. Peon.

DPPE Data is available at.[5] Simulation details by F. Favela.

POPG Data is available at.[6] Simulation details by F. Favela.

POPG with additional NaCl Simulation details by A. Peon.

DPPG Data in 298 K is available at[7] and in 314 K at.[8] Simulation details by F. Favela.

POPC:POPG mixture with additional NaCl Simulation details by A. Peon.

S1.4 Berger

POPE Data is available at.[9,10] Simulation details by T. Piggot.

DOPE Data is available at.[11,12] Simulation details by T. Piggot.

POPC:POPE, POPC:DOPE and DOPC:DOPE mixtures Data is available at.[13,14] 300 K with v-rescale (tau=0.1 ps), 1 bar with PR semiisotropic (tau=4 ps, compressibility=4.5e-5 bar^{-1}), PME order 4 and space 0.12, rcoulomb and rvdw 1.0, 128 lipids per leaflet, no ion Simulation details by Fuchs et al.

S1.5 GROMOS 43A1-S3

POPE Data is available at.[15] Simulation details by T. Piggot.

S1.6 OPLS-UA

POPE Data is available at.[16] Simulation details by T. Piggot.

POPE with vdW interaction in H Data is available at.[17] Simulation details by T. Piggot.

S1.7 GROMOS-CKP and GROMOS-CKPM

POPE Data is available at.[18] Simulation details by T. Piggot.

DOPE Data is available at.[19] Simulation details by T. Piggot.

DPPE Data is available at.[20] Simulation details by T. Piggot.

S2 R-PDLF and SDROSS experiments

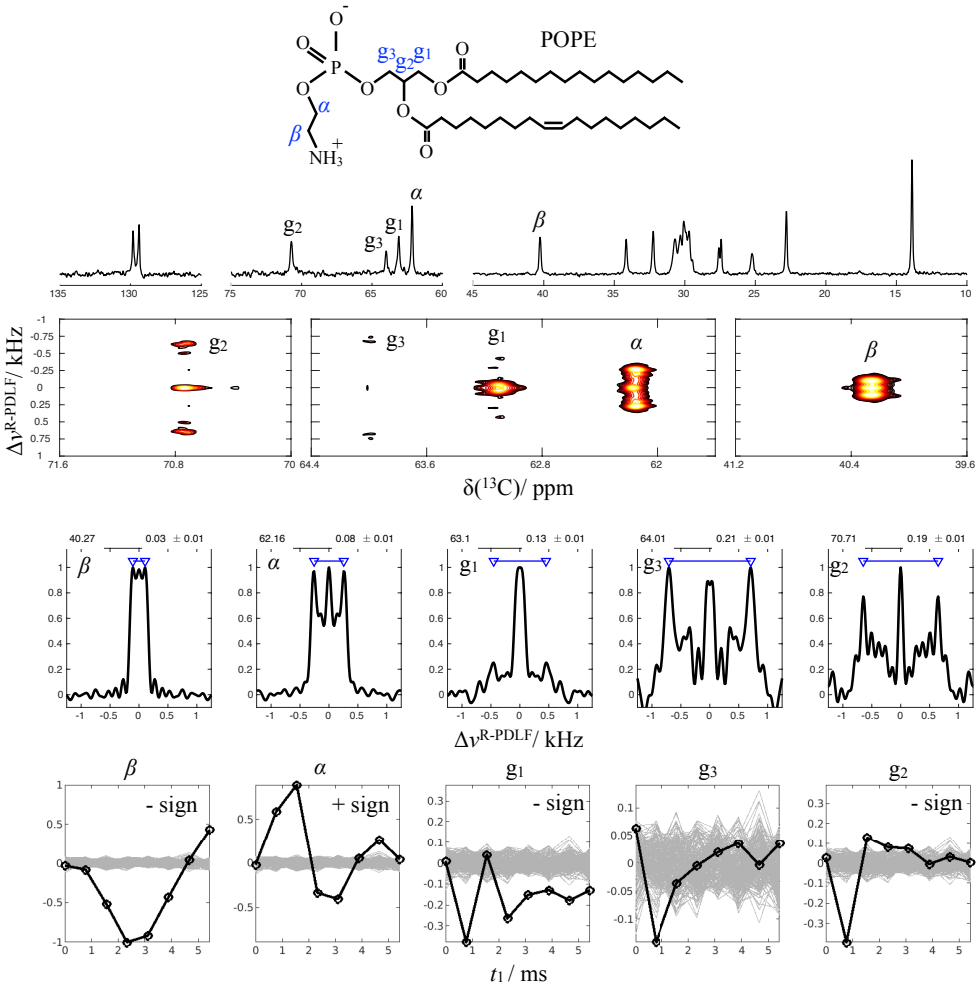

Figure S1: (A) Chemical structure of POPE with the labeling of headgroup and glycerol backbone carbons. (B) INEPT spectra from POPE sample with the headgroup and glycerol backbone peaks labeled. (C) 2D R-PDLF spectra (D) Dipolar sliced from the 2D R-PDLF spectra with the resulting order parameters on top of figures. (E) Experimetal S-DROSS curves giving signs of the order parameters.

A, B etc. labels to be put in the figure.

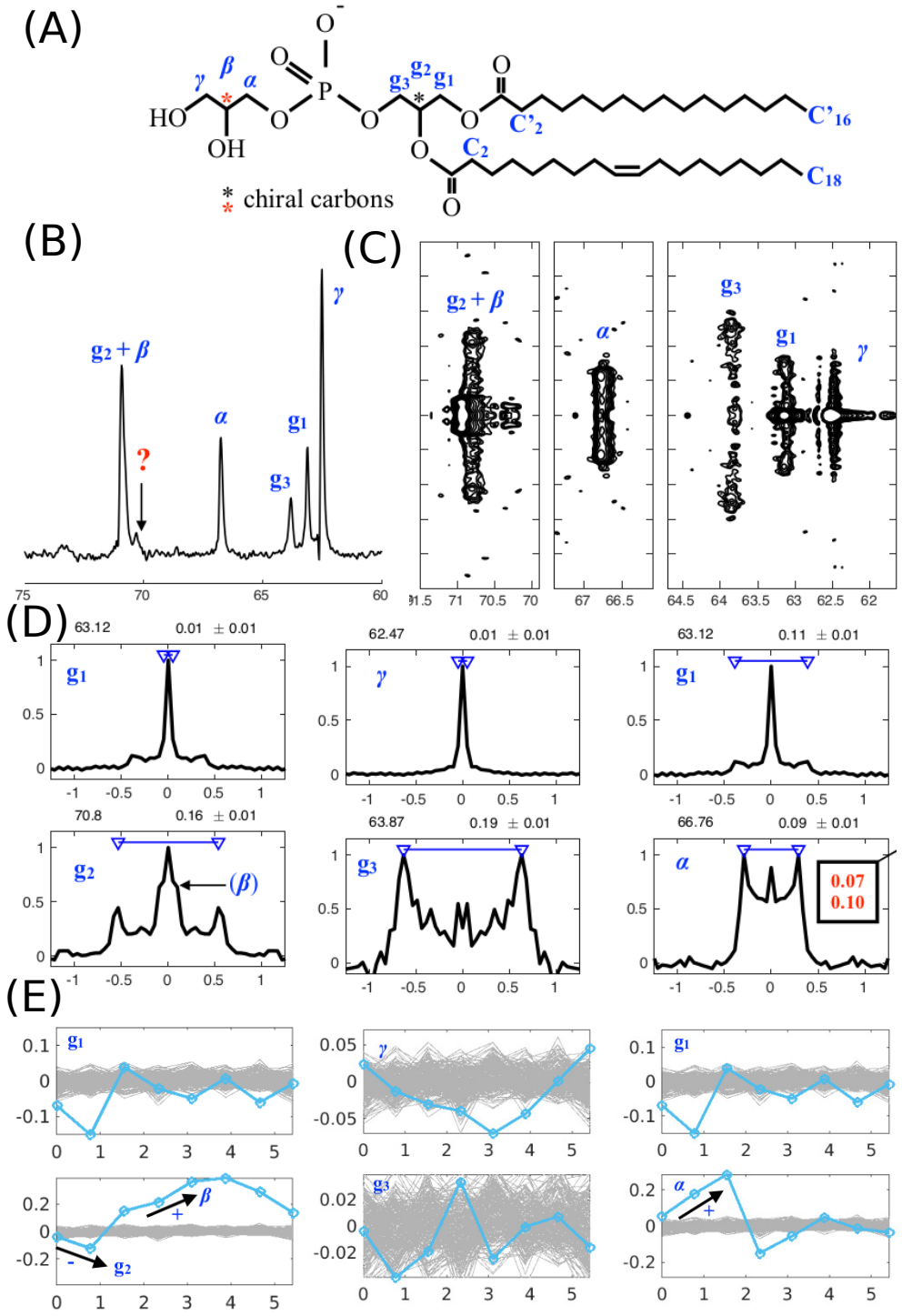

Figure S2: (A) Chemical structure of POPG with the labeling of headgroup and glycerol backbone carbons. (B) INEPT spectra from POPG sample with the headgroup and glycerol backbone peaks labeled. (C) 2D R-PDLF spectra (D) Dipolar sliced from the 2D R-PDLF spectra with the resulting order parameters on top of figures. (E) Experimetal S-DROSS curves giving signs of the order parameters.

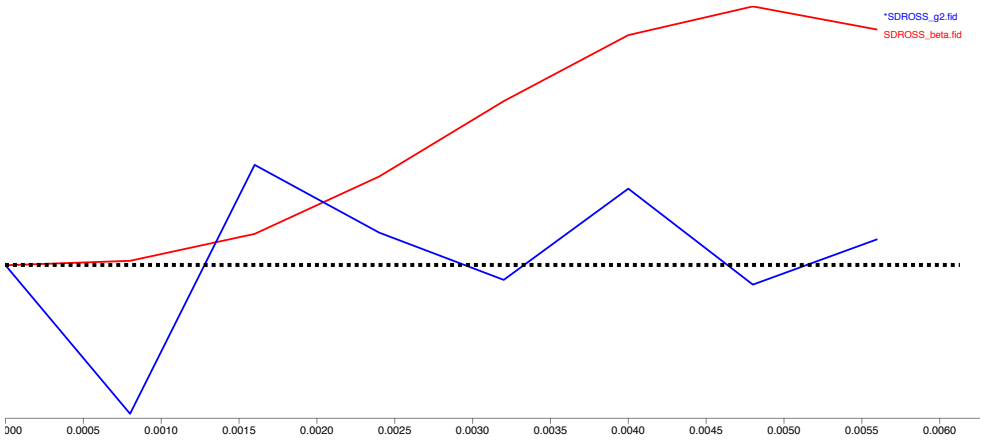

Figure S3: Simpson simulaton of S-DROSS curve of β-carbon of POPG.

S3 Changes of PG headroup order parameters upon addition of PC

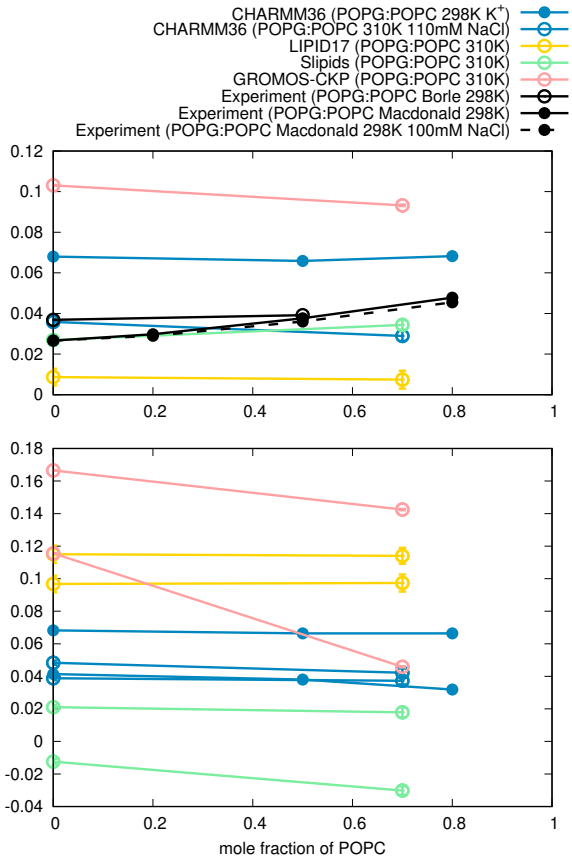

Figure S4: Modulation of PG lipid headgroup order parameters with the increasing amount of PC in lipid bilayer from experiments[21,22] and simulations with different force fields.

S4 Sodium binding to POPC simulations

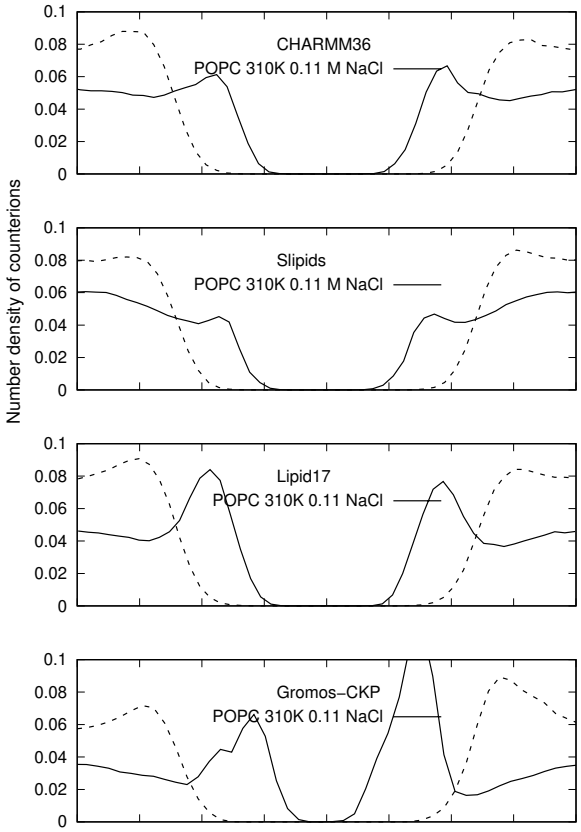

Figure S5: Sodium (solid line) and choride ion density profiles along membrane normal from different simulations with PC lipids.
Discussion about differences to the NMRlipids II to be discussed once we have the details on ions models.

References

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(6) Favela-Rosales, F. MD simulation trajectory of a fully hydrated POPG bilayer: SLIPIDS, Gromacs 5.0.4. 2017. 2017; https://doi.org/10.5281/zenodo.546133.

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