Quantitative quality of lipid-cholesterol interactions in atomistic resolution molecular dynamics simulations

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INTRODUCTION

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METHODS

X-ray scattering experiments

This folder contains SAXS data on POPC multilamellar vesicles (MLVs) at various cholesterol concentrations. Data have been obtained at the EMBL BioSAXS beamline (Hamburg) using 20 keV photons, T = 27C. Data were analyzed in terms of the SDP-GAP model described in Heftberger et al., J. Appl. Cryst. 2013 and Heftberger et al. Biophys. J. 2015. Data from MLVs are a convolute of structure factor (the crystalline lattice) and form factor. By fitting the scattered intensity data we obtain both contributions. Here we posted only form factors (ASCII format). For information on the quality of the fit we also give plots of the fitted intensity data. The electron density profile has been modelled in terms of the SDP model (see papers by Kucerka and coworkers), that is volume distribution functions are modelled by individual Gaussians or error functions. Cholesterol is also accounted for by two Gaussians. This model has been proposed by Jianjun Pan (USF, Tampa, FL), but is to the best of our knowledge not published (see also PhD Thesis by Peter Heftberger). Additional figures show the volume distribution functions and the resulting electron density profiles.

Authors to consult and potentially include in publications using this data: Peter Heftberger (peter.heftberger@gmx.at), Georg Pabst (georg.pabst@uni-graz.at)

Molecular dynamics simulations

COMPARISON OF ACYL CHAIN ORDER PARAMETERS BETWEEN EXPERIMENTS AND SIMULATIONS

Order parameters from simulations and experiments for acyl chains of 1-palmitoyl-2-oleoylphosphatidylcholine (POPC) are shown in Fig. 1.

The order parameter changes as a function of cholesterol for each segment are shown in Fig. 2 (currently only sn-1).

COMPARISON OF FORM FACTORS BETWEEN EXPERIMENTS AND SIMULATIONS

The form factors calculated from different simulations with different cholesterol content are shown in Fig. 3.

CONCLUSIONS

TABLE I: Simulated lipid bilayers containing cholesterol. The simulation file data sets marked with * include also part of the trajectory. [a] The number of lipid molecules [b] The number of cholesterol molecules [c] Cholesterol concentration (mol%) [d] The number of water molecules [e] Simulation temperature [f] The total simulation time [g] Time frames used in the analysis [h] Reference link for the downloadable simulation files [i] Reference for the full simulation details

Force field	lipid	[a]N_l	[b]N_{chol}	[c]C_{CHOL}	[d]N_w	[e]T (K)	[f]t_{sim}(ns)	[g]t_{anal} (ns)	[h]Files	[i]Details
Berger-POPC-07 [1]	POPC	128	0	0%	7290	298	270	240	[2]*	[3]
/Höltje-CHOL-13 [4, 5]										
	POPC	120	8	6%	7290	298	100	80	[6]*	[5]
	POPC	110	18	14%	8481	298	100	80	[7]*	[5]
	POPC	84	44	34%	6794	298	100	80	[8]*	[5]
	POPC	64	64	50%	10314	298	100	80	[9]*	[5]
	POPC	50	78	61%	5782	298	100	80	[10]*	[5]
CHARMM36[11, 12]	POPC	128	0	0%	5120	303	150	100	[13]*	[14]
	POPC	100	24	19%	4960	303	200	100	[15]*	[14]
	POPC	80	80	50%	4496	303	200	100	[16]*	[14]
MacRog[17]	POPC	128	0	0%	6400	310	400	200	[18]*	[14]
	POPC	114	14	11%	6400	310	400	200	[18]*	[14]
	POPC	72	56	44%	6400	310	400	200	[18]*	[14]
	POPC	64	64	50%	6400	310	400	200	[18]*	[14]
	POPC	56	72	56%	6400	310	400	200	[18]*	[14]

SUPPLEMENTARY INFORMATION

CHARMM36 results from different simulation packages

The results from CHARMM36 model for lipid bilayers from different simulation packages have been reported to give different results in the literature [19, 20]. The results are mainly dependent on different Lennart-Jones cut–off settings, but all the details are not quite understood. In this work we use the results from Gromacs 5 with settings suggested to be optimal by Gromacs webpage. We also compared the results from Gromacs 5 with these settings to the results simulated with NAMD, OpenMM and literature values. The comparison is shown in Fig. 4

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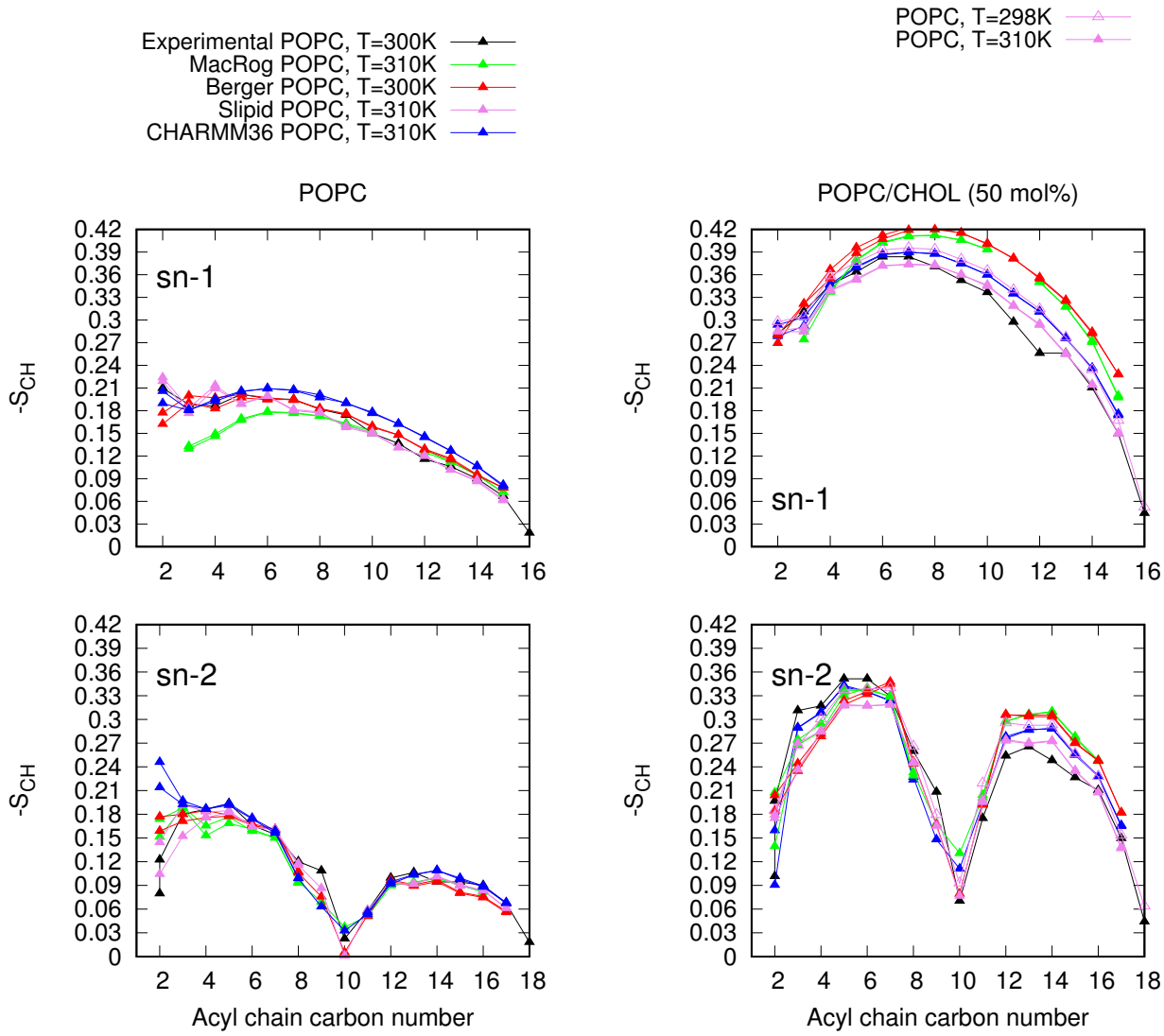

FIG. 1: Order parameters from simulations and experiments for acyl chains of 1-palmitoyl-2-oleoylphosphatidylcholine (POPC).

1.Why are the order parameters of CHARMM36 too large compared to simulations even without cholesterol? Discussion in https://github.com/NMRLipids/NmrLipidsCholXray/issues/4

2.Why there is decrease in order parameters towards beginning of acyl chain in MacRog model without cholesterol?

3.Do the results suggests that condensation effect is too strong in MacRog and Berger models? Discussion in https://github.com/NMRLipids/NmrLipidsCholXray/issues/5

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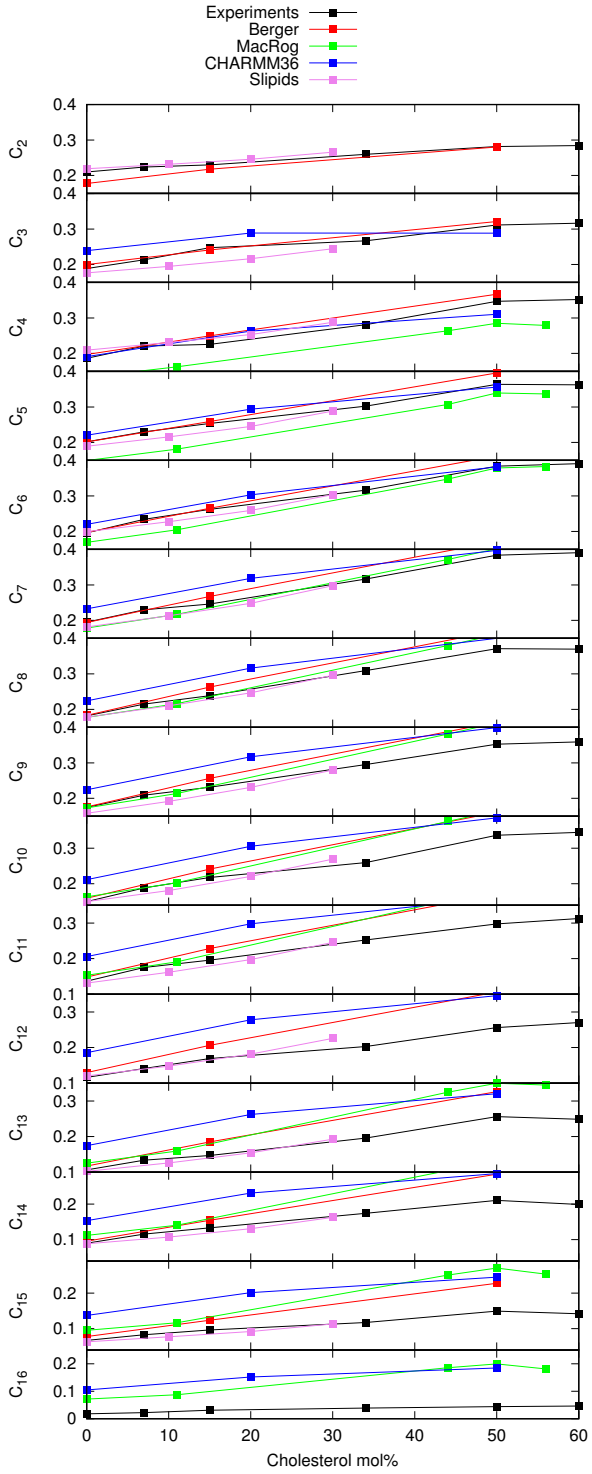
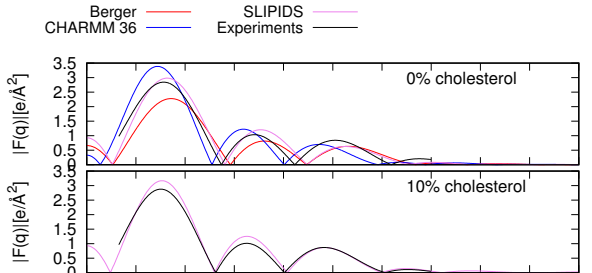


FIG. 2: Order parameter changes from simulations and experiments for each segment in sn-1 chain of 1-palmitoyl-2-oleoylphosphatidylcholine (POPC) as a function of cholesterol concentration.



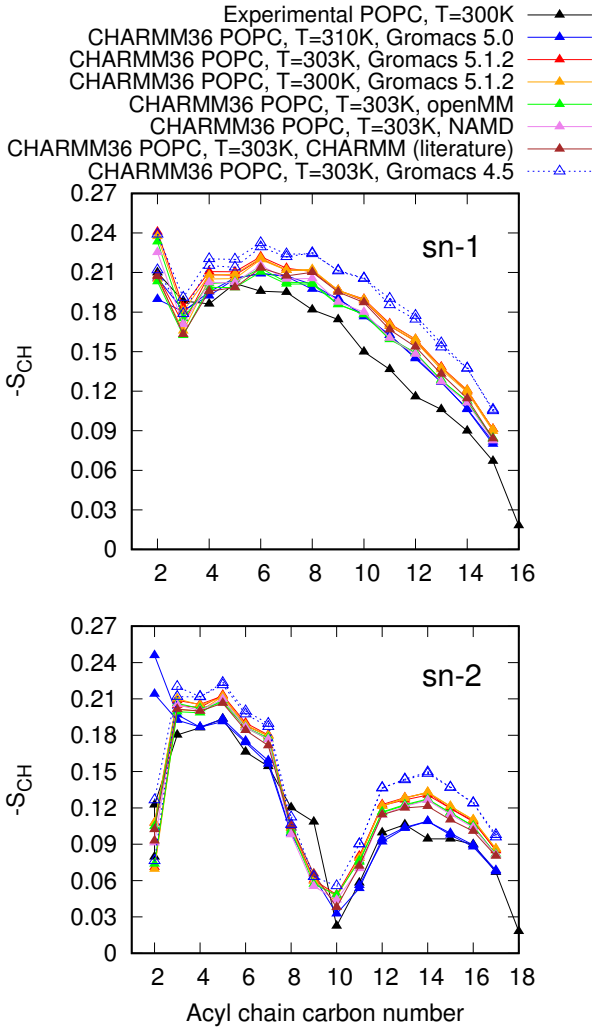


FIG. 4: Results for CHARMM36 model [11] from different simulation packages. Discussion going on at *https://github.com/NMRLipids/NmrLipidsCholXray/issues/4*.