Supplementary Material

Configurational entropies of lipids in pure and mixed bilayers from atomic-level and coarse-grained molecular dynamics simulations

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Supplementary Tables

Table s 1 Summary of the simulation trajectories considered in the present work. For each case the resolution of the model, the system, the source, the simulation length, and the reference temperature are specified.

run	model	system	source	time period [ns]	*T* [K]
1	AL	2×64 DPPC lipids	ref. 66	25	323
2	AL	2×64 DOPC lipids	ref. 44	40	303
3	AL	2×64 DOPE lipids	ref. 44	30	303
4	AL	$2\times(48/16)$ DOPC/DOPE 3:1	ref. 44	40	303
5	AL	$2\times(32/32)$ DOPC/DOPE 1:1	ref. 44	40	303
6	AL	$2\times(16/48)$ DOPC/DOPE 1:3	ref. 44	40	303
7	CG	2×64 DPPC lipids	this work	1000	323
8	CG	2×256 DOPC lipids	this work	1000	323
9	AL	128 C16 molecules	ref. 90	200	323
10	AL	128 C18:c9 molecules	ref. 90	200	303
11	CG	256 C16 molecules	ref. 90	1000	323
12	CG	512 C18:c9 molecules	ref. 90	1000	303

Table s 2 Single-fragment configurational entropies of lipid chains in a bilayer of pure DPPC and DOPC from MD simulations using the AL model. For fragments (*fc*) nomenclature we refer to Figure 1. See Table 1 for definition of entropy codes and Methods section for configurational entropy nomenclature.

System[a]	*fc*	$S^{i}_{sn1}(sn1)$	$S^{ip}_{sn1}(sn1)$	$S^{ir}_{sn1+2}(sn1)$	$S^{irp}_{sn1+2}(sn1)$	$S^{i}_{sn2}(sn2)$	$S^{ip}_{sn2}(sn2)$	$S^{ir}_{sn1+2}(sn2)$	$S^{irp}_{sn1+2}(sn2)$
		$\left[J \cdot K^{-1} \cdot mol^{-1}\right]$							
DPPC[b] (pure)	A	241	60	278	69	249	61	279	69
	B	240	60	301	75	242	60	301	75
	C	242	60	316	79	241	60	314	78
	D	260	65	333	83	260	65	331	83
DOPC[c] (pure)	A	246	61	270	67	254	61	271	68
	B	239	60	293	73	241	60	292	73
	C	113	56	160	80	113	56	159	79
	D	242	60	314	78	242	60	312	78
	E	267	67	333	83	268	67	331	83
DOPE[d] (pure)	A	224	56	251	63	234	59	257	64
	B	211	53	245	61	216	54	252	63
	C	105	52	129	64	107	53	133	66
	D	216	54	254	64	217	54	256	64
	E	255	64	297	74	253	63	297	74

[a] Results are averages over entropies for all 128 lipids forming a bilayer. Standard deviation from the average (over all molecules) are smaller than 0.5 $J \cdot K^{-1} \cdot mol^{-1}$ (not reported).

[b] From 25 ns MD simulation at 323 K. 500 trajectory configurations are used for the entropy calculation.

[c] From 40 ns MD simulation at 303 K. 800 trajectory configurations are used for the entropy calculation.

[d] From 30 ns MD simulation at 303 K. 600 trajectory configurations are used for the entropy calculation.

Table s 3 Single-fragment configurational entropies of lipid tails in DOPC:DOPE bilayers of different composition from MD simulations using the AL model. The composition of each lipid mixture is given together with the number of lipids of each component per layer.[a] For fragments (*fc*) nomenclature we refer to Figure 1. See Table 1 for definition of entropy reference codes and Methods section for configurational entropy nomenclature.

system[b]	*fc*[c]	$S^{i}_{sn1}(sn1)$	$S^{ip}_{sn1}(sn1)$	$S^{ir}_{sn1+2}(sn1)$	$S^{irp}_{sn1+2}(sn1)$	$S^{i}_{sn2}(sn2)$	$S^{ip}_{sn2}(sn2)$	$S^{ir}_{sn1+2}(sn2)$	$S^{irp}_{sn1+2}(sn2)$
3:1 (48:16)				$\left[\mathrm{J\cdot K^{-1}\cdot mol^{-1}}\right]$				$\left[\mathrm{J\cdot K^{-1}\cdot mol^{-1}}\right]$	
DOPC	A	243	61	266	66	252	63	266	66
	B	235	59	287	72	239	60	287	72
	C	112	56	157	78	113	56	156	78
	D	240	60	309	77	240	60	307	77
	E	265	66	329	82	266	66	328	82
DOPE	A	239 ± 1	60	260 ± 1	65	249 ± 1	62	260 ± 1	65
	B	234 ± 1	58	285 ± 1	71	237 ± 1	59	284 ± 1	71
	C	112	56	156 ± 1	78	113	56	156 ± 1	78
	D	239 ± 1	60	309 ± 1	77	240 ± 1	60	308 ± 1	77
	E	264 ± 1	66	329 ± 1	82	267 ± 1	67	329 ± 1	82
1:1 (32:32)									
DOPC	A	237	59	266	66	252	63	267	67
	B	231	58	285	71	237	59	288	72
	C	111	55	155	77	113	56	156	78
	D	237	59	306	76	239	60	305	76
	E	264	66	327	82	266	66	325	81
DOPE	A	236	59	264	66	250	62	267	67
	B	231	58	285	71	236	59	287	72
	C	111	55	156	78	112	56	156	78
	D	237	59	307	77	239	60	306	76
	E	263	66	328	82	264	66	327	82

Table s 3 (Continued)

1:3 (16:48)									
DOPC	A	230 ± 1	57	251 ± 1	63	244 ± 1	57	251 ± 1	63
	B	218 ± 1	54	270 ± 1	67	230 ± 1	54	274 ± 1	68
	C	106	53	146 ± 1	73	110	51	148 ± 1	74
	D	233 ± 1	58	295 ± 1	74	234 ± 1	55	293 ± 1	73
	E	260 ± 1	65	319 ± 1	80	263 ± 1	62	317 ± 1	79
DOPE	A	231	58	250	62	244	61	249	62
	B	227	57	271	68	233	58	273	68
	C	110	55	148	74	110	55	148	74
	D	235	59	297	74	235	59	295	74
	E	263	66	321	80	261	65	319	80

[a] Results are averages over entropies for all the lipid chains of a particular component. Standard deviations around the average are not reported unless larger than 0.5 $J \cdot K^{-1} \cdot mol^{-1}$. All results are from 40 ns MD simulation at 303 K. 800 trajectory configurations are used for the entropy calculations.

[b] Each mixture is composed of a total number of 128 lipids. The corresponding composition per layer is reported between parentheses.

[c] Note: fragment C includes only 2 united atoms.

Supplementary Figures

Figure s 1 Comparison between single-fragment entropies $S_{ch}^{type}(fc)$ of *cis*-9-octadecene chains in the liquid phase and DOPC lipid tails in a bilayer obtained from MD simulations at 323 K with the AL and CG models. Internal configurational entropies $S_{ch}^{i}(fc)$ (upper panel), internal plus rotational configurational entropies $S_{ch}^{ir}(fc)$ (middle panel) for the AL model, and internal plus rotational configurational entropies $S_{ch}^{ir}(fc)$ for the CG model (lower panel) are shown for consecutive fragments along the chain. Results for sn1 (▼) and sn2 (▲) chains are given separately. Standard deviations around the average are smaller than 0.5 $J \cdot K^{-1} \cdot mol^{-1}$ in all cases. The lines are meant to guide the eye.

Figure s 2 Configurational internal plus rotational entropies $S_{sn1+2}^{ir}(sn1+2)$ as a function of simulation time. The average values for (thick line) and the corresponding error bars (dashed lines) are shown as calculated from (a) 25 ns of simulation for 128 lipids in a DPPC bilayer and (b) 40 ns of simulation for 128 lipids in a DOPC bilayer. The final values are reported in Table 3. See Table 1 for definition of entropy reference codes and Methods section for configurational entropy nomenclature.

Figure s 3 Normalized probability distributions of pseudo-bond angles around the double bond moiety from simulations (AL: 40 ns; CG: 1 μs) of DOPC lipids (averaged over sn1 and sn2 tails), based on mapped beads (MAP; gray lines) or beads (CG; black lines). Mapped beads refer to the centers of mass of the AL fragments. Alternative mapping procedures (424 or 343; the codes refer to the numbers of AL particles being mapped to each fragment/bead) are employed to describe the central double-bond moiety. The distributions for liquid C18:c9 given in ref. 90 were obtained using the 424 mapping scheme.

Figure s 1

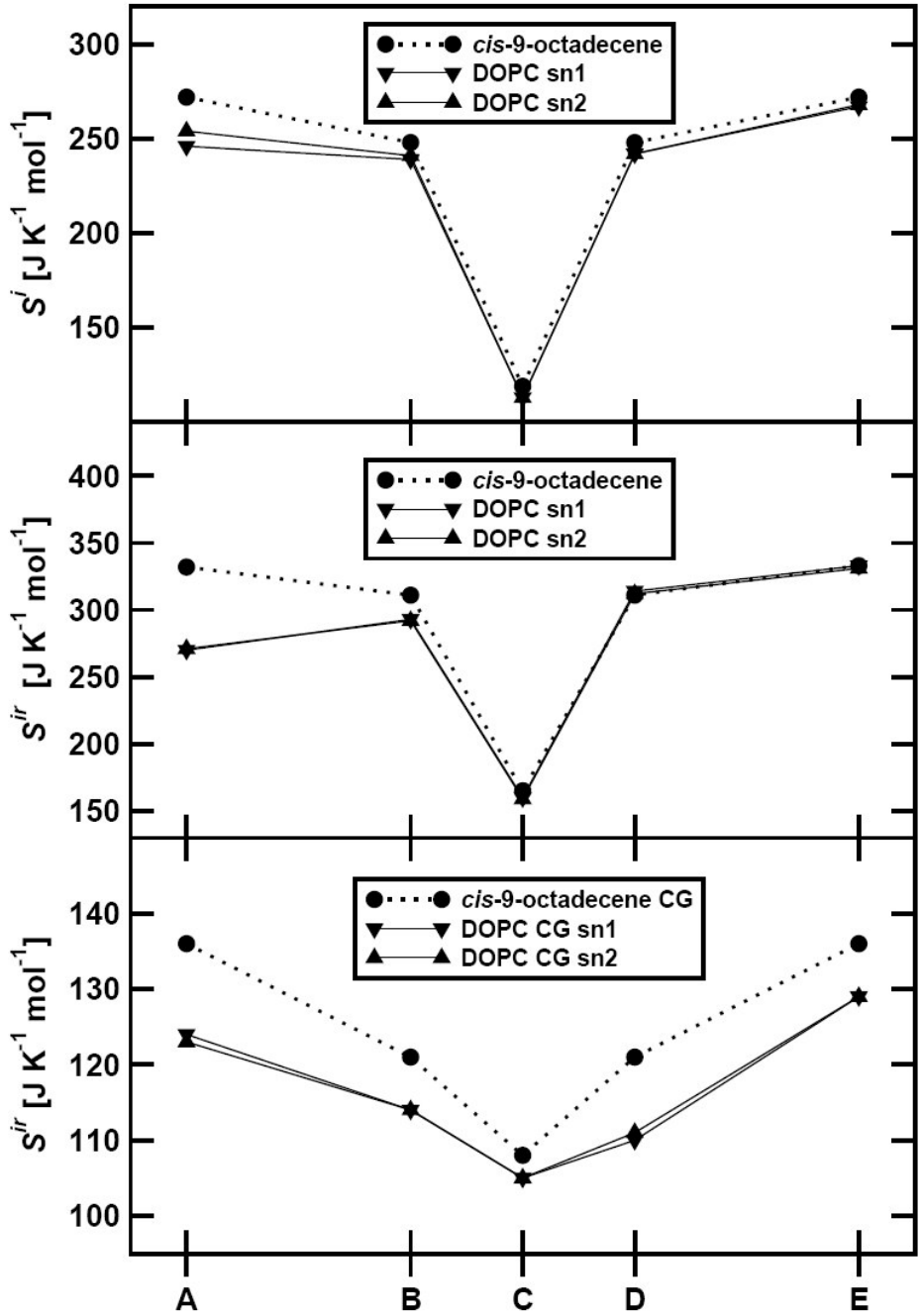

cis-9-octadecene
DOPC sn1
DOPC sn2
S^{i} [J K^{-1} mol^{-1}]
300
250
200
150
cis-9-octadecene
DOPC sn1
DOPC sn2
S^{ir} [J K^{-1} mol^{-1}]
400
350
300
250
200
150
cis-9-octadecene CG
DOPC CG sn1
DOPC CG sn2
S^{ir} [J K^{-1} mol^{-1}]
140
130
120
110
100
A
B
C
D
E

Figure s 2

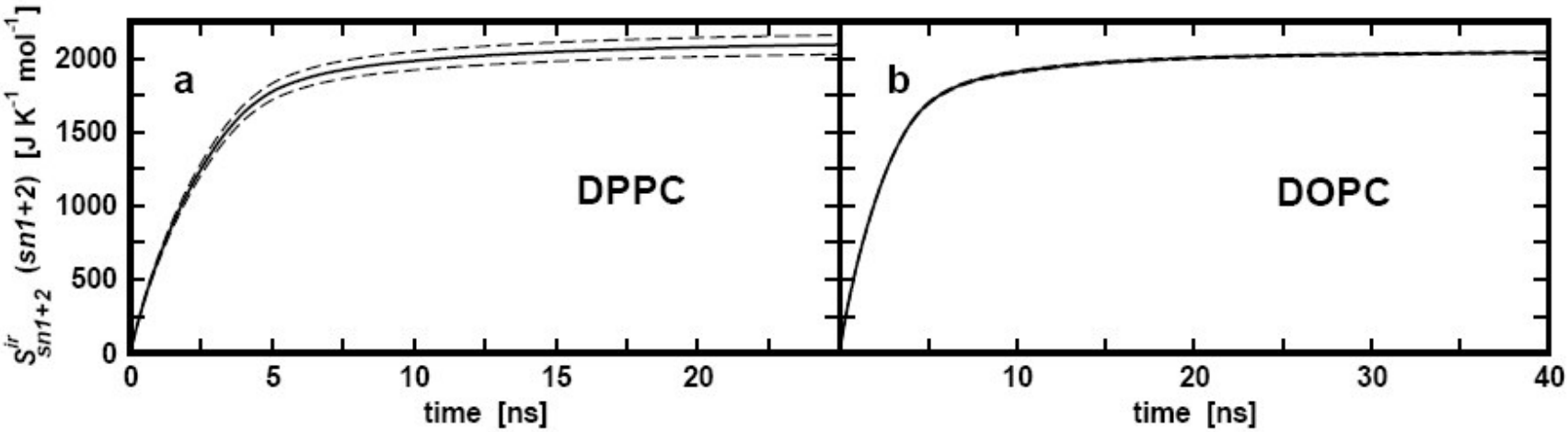
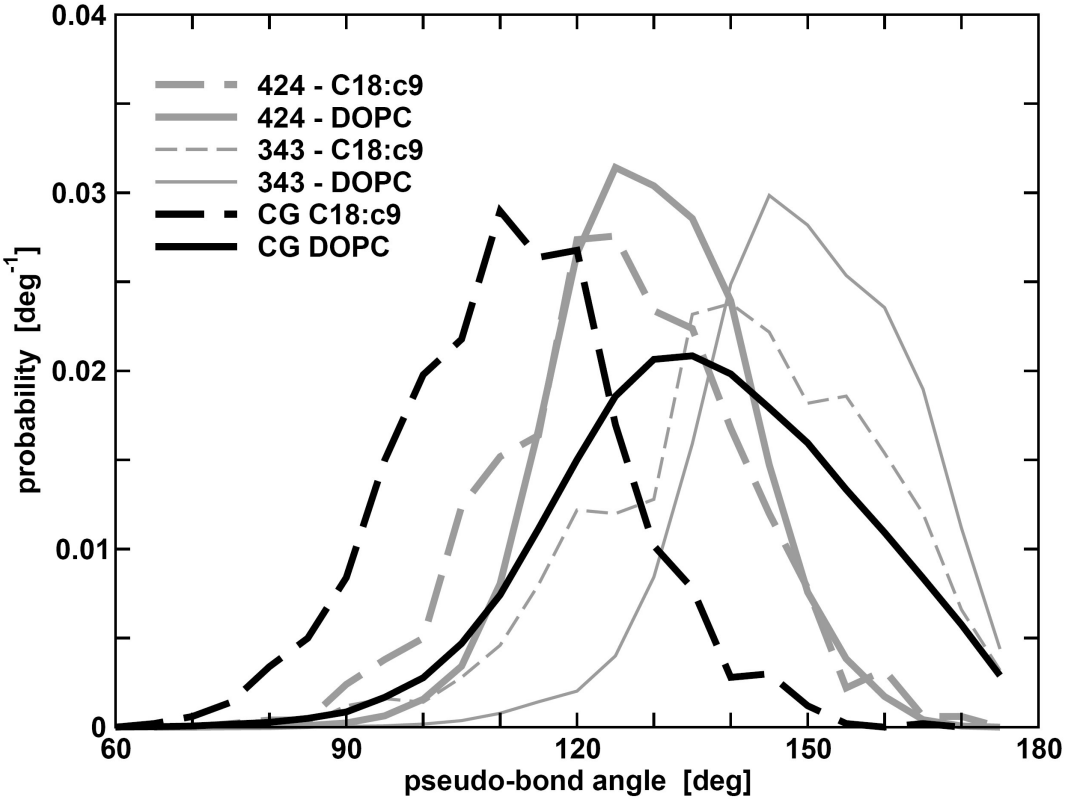

a
b
DPPC
DOPC
S^{ir}_{sn1+2} (sn1+2) [J K^{-1} mol^{-1}]
0
500
1000
1500
2000
0
5
10
15
20
10
20
30
40
time [ns]
time [ns]

Figure s 3


0.04
0.03
0.02
0.01
0
probability [deg^{-1}]
60
90
120
150
180
pseudo-bond angle [deg]
424 - C18:c9
424 - DOPC
343 - C18:c9
343 - DOPC
CG C18:c9
CG DOPC