Electronic Supplementary Information (ESI) Physical properties of mixed bilayers containing lamellar and nonlamellar lipids: insights from coarse-grain molecular dynamics simulations

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1 Shifted-force dipolar interaction

Considering two point dipoles \vec{p}_i and \vec{p}_j , the shifted-force pair potential energy is:

$$E_{ij} = \left[1 - 4\left(\frac{r}{r_c}\right)^3 + 3\left(\frac{r}{r_c}\right)^4\right] \left[\frac{1}{r^3}(\vec{p}_i \cdot \vec{p}_j) - \frac{3}{r^5}(\vec{p}_i \cdot \vec{r})(\vec{p}_j \cdot \vec{r})\right]$$

where \vec{r} and r are the pair distance vector and its magnitude, respectively, and r_c is the cutoff distance. Note that we use the convention $\vec{r} = \vec{r}_i - \vec{r}_j$. Forces and torques were derived following Appendix C.3 in Allen and Tildesley.¹ In particular, the pair forces are:

$$\vec{F}_{ij} = -\vec{F}_{ji} = \frac{3}{r^5} \left\{ \left[1 - \left(\frac{r}{r_c}\right)^4 \right] \left[(\vec{p}_i \cdot \vec{p}_j) - \frac{3}{r^2} (\vec{p}_i \cdot \vec{r}) (\vec{p}_j \cdot \vec{r}) \right] \vec{r} + \left[1 - 4 \left(\frac{r}{r_c}\right)^3 + 3 \left(\frac{r}{r_c}\right)^4 \right] \left[(\vec{p}_j \cdot \vec{r}) \vec{p}_i + (\vec{p}_i \cdot \vec{r}) \vec{p}_j - \frac{2}{r^2} (\vec{p}_i \cdot \vec{r}) (\vec{p}_j \cdot \vec{r}) \vec{r} \right] \right\}$$

The pair torque \vec{T}_{ij} is:

$$\vec{T}_{ij} = -\frac{1}{r^3} \left[1 - 4\left(\frac{r}{r_c}\right)^3 + 3\left(\frac{r}{r_c}\right)^4 \right] (\vec{p}_i \times \vec{p}_j) + \frac{3}{r^5} \left[1 - 4\left(\frac{r}{r_c}\right)^3 + 3\left(\frac{r}{r_c}\right)^4 \right] (\vec{p}_j \cdot \vec{r}) (\vec{p}_i \times \vec{r})$$

The pair torque \vec{T}_{ii} is:

$$\vec{T}_{ji} = -\frac{1}{r^3} \left[1 - 4\left(\frac{r}{r_c}\right)^3 + 3\left(\frac{r}{r_c}\right)^4 \right] (\vec{p}_j \times \vec{p}_i) + \frac{3}{r^5} \left[1 - 4\left(\frac{r}{r_c}\right)^3 + 3\left(\frac{r}{r_c}\right)^4 \right] (\vec{p}_i \cdot \vec{r}) (\vec{p}_j \times \vec{r})$$

These expressions were implemented in the pair_dipole_sf.cpp module of the program LAMMPS.^{2,3}

2 Force field parameters

Table 1 reports the parameter set for the *elba-1.1* force field. For convenience, the parameters are reported using different conventions. The "BRAHMS units" column reports the parameters in the units used by the program BRAHMS;⁴ this highlights the hydrogen-bonding scale factors. The "LAMMPS units" column report the parameters in the format required by the LAMMPS program;^{2,3} corresponding input files are available online.⁵

3 Tangential pressure profile for 2-body interactions: equivalence of "perparticle" and Harasima formulations

The "per-particle" pressure for the 2-body virial term in the main body of the paper can be rewritten in terms of the interparticle distance $r_{ijx} = r_{ix} - r_{jx}$:

$$V_{s}P_{xx}(z_{s}) = \frac{1}{2} \left\langle \sum_{\substack{i=1\\i\in V_{s}}}^{N} \sum_{\substack{j=1\\j\neq i}}^{N} \left(r_{i_{x}}f_{ij_{x}} + r_{j_{x}}f_{ji_{x}} \right) \right\rangle = \frac{1}{2} \left\langle \sum_{\substack{i=1\\i\in V_{s}}}^{N} \sum_{\substack{j=1\\j\neq i}}^{N} r_{ij_{x}}f_{ij_{x}} \right\rangle = \left\langle \sum_{\substack{i=1\\i\in V_{s}}}^{N-1} \sum_{\substack{j>i\\i\in V_{s}}}^{N} \frac{r_{ij_{x}}^{2}}{r_{ij}} \frac{\partial v(r_{ij})}{\partial r_{ij}} \right\rangle$$

$$(1)$$

where we have used $f_{ij_x} = -f_{ji_x}$ (Newton's third law), and:¹

$$\mathbf{f}_{ij} = -\nabla_{\mathbf{r}_{ij}} v(r_{ij}) = -\frac{\partial v(r_{ij})}{\partial r_{ij}} \nabla_{\mathbf{r}_{ij}} r_{ij} = -\frac{\partial v(r_{ij})}{\partial r_{ij}} \frac{\mathbf{r}_{ij}}{r_{ij}} \Rightarrow f_{ij_x} = -\frac{\partial v(r_{ij})}{\partial r_{ij}} \frac{r_{ij_x}}{r_{ij}}$$

with $v(r_{ij})$ the interaction potential.

The $P_{yy}(z_s)$ term can be obtained trivially by simply replacing x with y in equation 1. The tangential pressure $P_T(z_s)$ can then be written as:

$$P_{T}(z_{s}) = \frac{1}{2} \left[P_{xx}(z_{s}) + P_{yy}(z_{s}) \right] = -\frac{1}{4V_{s}} \left\langle \sum_{\substack{i=1\\i \in V_{s}}}^{N} \sum_{\substack{j=1\\j \neq i}}^{N} \frac{r_{ijx}^{2} + r_{ijy}^{2}}{r_{ij}} \frac{\partial v(r_{ij})}{\partial r_{ij}} \right\rangle = -\frac{1}{2V_{s}} \left\langle \sum_{\substack{i=1\\i \in V_{s}}}^{N} \sum_{\substack{j>i\\j > i}}^{N} \frac{r_{ijx}^{2} + r_{ijy}^{2}}{r_{ij}} \frac{\partial v(r_{ij})}{\partial r_{ij}} \right\rangle$$
(2)

which is the expression first developed by Harasima⁶ and later reported in several publications.^{7–12}

4 Mean square displacements and diffusion coefficients

The mean square displacement (MSD) in the plane of the bilayer was calculated with:

$$MSD = \frac{1}{N} \sum_{i=1}^{N} [\mathbf{r}_i(t) - \mathbf{r}_i(0)]^2$$
(3)

with *N* the number of lipids, *t* the time, and \mathbf{r}_i is the 2-dimensional vector defining the position of lipid *i* in the *xy*-plane (parallel to the bilayer plane by construction). In practice, we make the (reasonable) assumption that the position of a lipid corresponds with the position of its glycerol CG particle, so \mathbf{r}_i in Eq. 3 is really the position of the glycerol particle of lipid *i*. The lateral diffusion coefficient *D* was obtained through:

$$D = \frac{MSD}{4t} \tag{4}$$

where *MSD* is defined in Eq. 3 and $t = 1 \mu s$ is the simulation time.

Fig. 1 reports the *MSDs* calculated for the mixed bilayer systems simulated. The plot shows that the lipids in all the systems studied diffuse laterally in a similar way, showing no apparent sensitivity to composition. Diffusion coefficients computed using Eq. 4 are reported in Table 2, together with corresponding literature data from atomistic simulation and experiment.

Symbol	BRAHMS units	LAMMPS units	Other units
σ_{CC}	0.54 nm	5.4 Å	
σ_{PP}	0.52 nm	5.2 Å	
σ_{GG}, σ_{EE}	0.46 nm	4.6 Å	
σ_{AA}, σ_{TT}	0.45 nm	4.5 Å	
σ_{WW}	0.305 nm	3.05 Å	
$\epsilon_{CC}, \epsilon_{PP}$	6.0 kJ/mol	1.434 kcal/mol	
$\epsilon_{GG}, \epsilon_{EE}$	4.0 kJ/mol	0.956 kcal/mol	
$\epsilon_{AA}, \epsilon_{TT}$	3.5 kJ/mol	0.837 kcal/mol	
ϵ_{WW}	1.534 kJ/mol	0.367 kcal/mol	
ϵ_{WW}^{tot}	$1.5 \varepsilon_{WW}$	0.550 kcal/mol	
ϵ_{WP}	$1.3\sqrt{\epsilon_{WW}\epsilon_{PP}}$	0.943 kcal/mol	
ϵ_{WG}	$1.1\sqrt{\epsilon_{WW}\epsilon_{GG}}$	0.651 kcal/mol	
ϵ_{WE}	$1.2\sqrt{\epsilon_{WW}\epsilon_{EE}}$	0.710 kcal/mol	
ϵ_{AW}	$1.1\sqrt{\epsilon_{AA}\epsilon_{WW}}$	0.609 kcal/mol	
ϵ_{AP}	$1.3\sqrt{\epsilon_{AA}\epsilon_{PP}}$	1.424 kcal/mol	
ϵ_{AG}	$1.1\sqrt{\epsilon_{AA}\epsilon_{GG}}$	0.984 kcal/mol	
ϵ_{AE}	$1.3\sqrt{\epsilon_{AA}\epsilon_{EE}}$	1.163 kcal/mol	
Q_C, Q_A	$+0.7 \mathrm{e}$	$+0.7 \mathrm{e}$	$1.12 \times 10^{-19} \mathrm{C}$
Q_P	$-0.7 \mathrm{e}$	$-0.7 \mathrm{e}$	$-1.12 \times 10^{-19} \mathrm{C}$
μ_G	1.6 D	0.333 e Å	
μ_E	2 D	0.416 e Å	
μ_W	2.6 D	0.541 e Å	
k	$1260 \text{kJ/(mol nm}^2)$	$2*1.506 \text{ kcal/(mol Å}^2)$	
W	30 kJ/mol	2*3.585 kcal/mol	
С	10 kJ/mol	2*1.195 kcal/mol	
$\alpha_{0_{CPG}}, \alpha_{0_{APG}}$	115°	115°	2.01 rad
$\alpha_{0_{PGE}}$	90°	90°	1.57 rad
$\alpha_{0_{GET}}, \alpha_{0_{ETT}}, \alpha_{0_{TTT}}^{saturated}$	180°	180°	3.14 rad
$\alpha_{0_{TTT}}^{cis-unsaturated}$	120°	120°	2.09 rad
m_C, m_P	90 amu	90 g/mol	$14.9 \times 10^{-23} \text{ g}$
m_G, m_E	62 amu	62 g/mol	10.3×10^{-23} g
m_T, m_A	42 amu	42 g/mol	$7.0 \times 10^{-23} \text{ g}$
m_W	40 amu	40 g/mol	$6.6 \times 10^{-23} \text{ g}$
$I_{G,E}$	$10 \mathrm{amu}\mathrm{nm}^2$	$1000 \text{ g} \text{ Å}^2/\text{mol}$	-
I_W	$1 \text{ amu } \text{nm}^2$	$100 \text{ g} \text{ Å}^2/\text{mol}$	

 Table 1 Elba-1.1 force field

Subscripts *C*, *A*, *P*, *G*, *E*, *T* and *W* stand for the site types *choline*, *amine*, *phosphate*, *glycerol*, *ester*, *tail* and *water*, respectively. Lennard-Jones cross-terms are calculated by the standard Lorentz-Berthelot rule except for increased ε terms representing hydrogen bonding; in particular, ε_{WP} , ε_{WG} , ε_{WE} , ε_{AW} , ε_{AP} , ε_{AG} , ε_{AE} are set as reported in the table. Charges and dipoles are identified by *Q* and μ ; cross terms are obtained via standard electrostatic formulae. Within the same lipid molecule, nonbonded interactions between bonded pairs are zero (1-2 LJ and electrostatic interactions are excluded). The rigidity of the Hooke harmonic potential is identified by *k*; reference lengths are set to $0.9 \sigma_{ij}$. The rigidity of the angle potential is identified by *w*. The rigidity of the dipole orientation-restraining potential is *c*. Masses and principal moments of inertia are identified by *m* and *I*, respectively.



Figure 1 Mean square displacements, in the *xy*-plane, for mixed lipid bilayers at different PC:PE fractions (see main body of the paper for details).

Table 2 Lateral diffusion coefficients in units of $nm^2/\mu s$

System	CG (this work)	Atomistic	Experiment
PC-only	8 ± 2	$2 - 12^{13}$	9.5, ¹⁴ 11.5, ¹⁵ 12 ¹⁶
3_{PC} : 1_{PE}	17 ± 7		
1_{PC} : 1_{PE}	8 ± 3		
$1_{PC}:3_{PE}$	8 ± 2		
PE-only	9 ± 3		

5 Kinetic energy pressure term from velocity vs. number density

The kinetic energy contribution to the tangential pressure $P_{xx}^{\text{KE}}(z_s)$ can be obtained in two different yet equivalent ways. The first approach involves the use of the particles' velocities through:

$$P_{xx}^{\text{KE}}(z_s) = \frac{1}{V_s} \left\langle \sum_{\substack{i=1\\i \in V_s}}^N m_i v_{i_x} v_{i_x} \right\rangle$$
(5)

where m_i and v_i represent the mass and velocity of particle *i*, V_s is the slab volume, and *N* is the total number of particles. The pressure profiles obtained using Eq. 5 are displayed in Fig. 2. Alternatively, the following expression can be used:

$$P_{xx}^{\text{KE}}(z_s) = k_B T \langle \rho(z_s) \rangle \tag{6}$$

where $\rho(z_s)$ is the number density, k_B is Boltzmann's constant, and T is the temperature. The pressure profiles obtained using Eq. 6 are displayed in Fig. 3.

6 Composition of self-assembled mixed bilayers

Table 3 reports the number of PC/PE lipids per monolayer in the bilayers formed through self-assembly.



Figure 2 Tangential pressure. Kinetic energy contribution obtained from particles' velocities.



Figure 3 Tangential pressure. Kinetic energy contribution obtained from number density profiles.

Table 3 Composition of mixed DOPC/DOPE bilayers after self-assembly from random solution

System	N _{lipids} layer1 / layer2	N _{DOPC} layer1 / layer2	N _{DOPE} layer1 / layer2
PC-only	63/65	63/65	0/0
3_{PC} : 1_{PE}	63/65	45/51	18/14
1_{PC} : 1_{PE}	64/64	27/37	37/27
$1_{PC}:3_{PE}$	62/66	12/20	50/46
PE-only	66/62	0/0	66/62

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