

The Molecular Structure of the Liquid Ordered Phase of Lipid Bilayers

Alexander J. Sodt, Michael Logan Sandar, Klaus Gawrisch, Richard W. Pastor and Edward Lyman

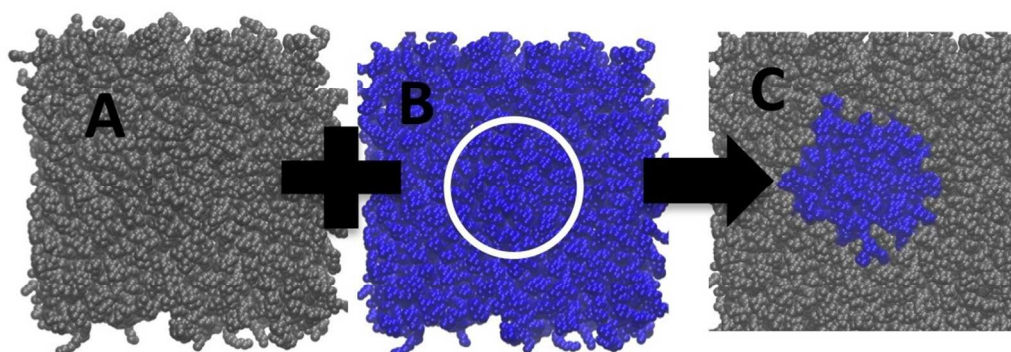


Fig. S1. Building an L_0 domain. A bilayer with the composition of the L_d phase (panel A) and another with the composition of the L_0 phase were relaxed until the areas equilibrated. (All three components are rendered in the same color.) A 5 nm diameter region from the relaxed L_0 system was embedded in the L_d system to build the initial configuration for the $T < T_m$ L_0/L_d system.

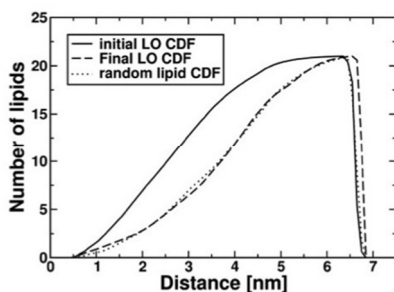


Figure S2. The cumulative distribution function of the lipids initially in the L_0 region (blue in **Fig. 1**) confirms that by the end of the 10 μ sec simulation (dashed line) these lipids are indistinguishable from the same number of randomly chosen lipids (dotted line).

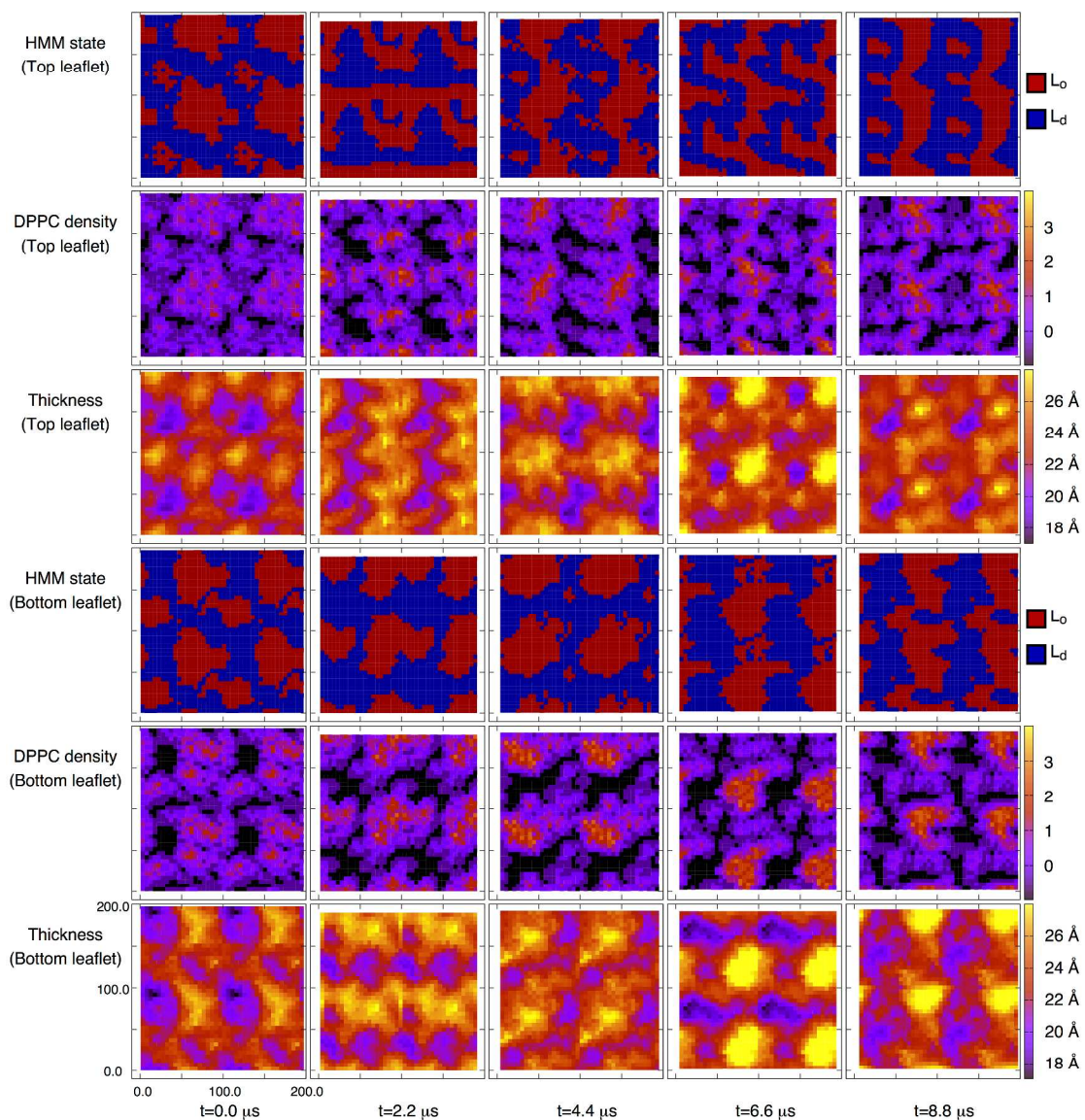


Fig. S3. Comparison of HMM state assignment to the local density of DPPC and the membrane thickness for $T < T_m$ (298 K). In addition to the simulation cell, three periodic replicas are shown.

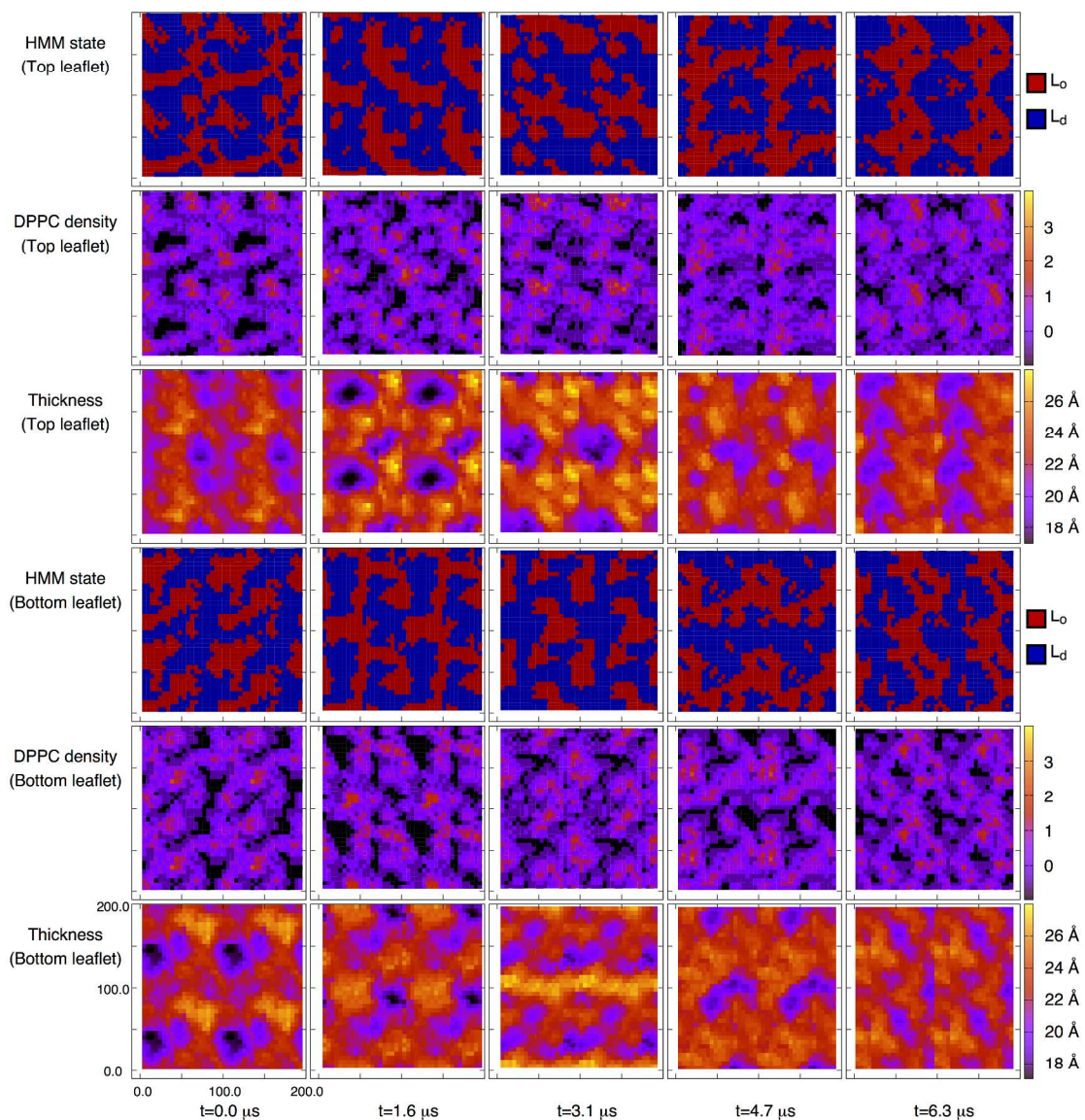


Fig. S4. Comparison of HMM state assignment to the local density of DPPC and the membrane thickness for 328 K ($T > T_m$). In addition to the simulation cell, three periodic replicas are shown.

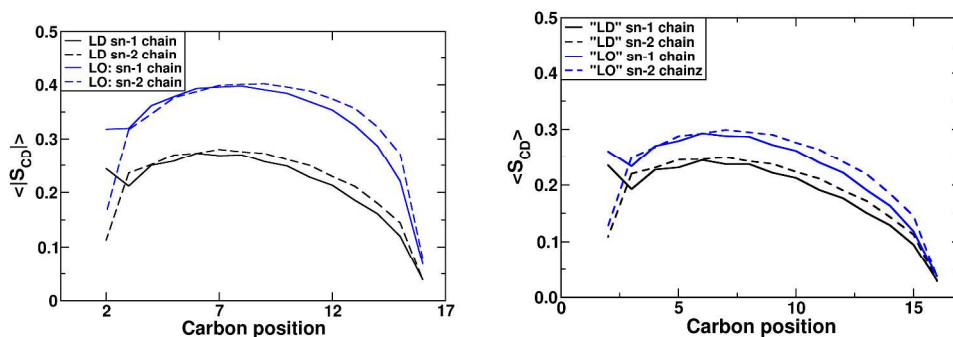


Figure S5. Carbon deuterium order parameters computed from simulation data. The left panel shows the order parameters for the L_0 and L_d phases (as identified by the HMM) below T_m , the right panel for $T > T_m$.

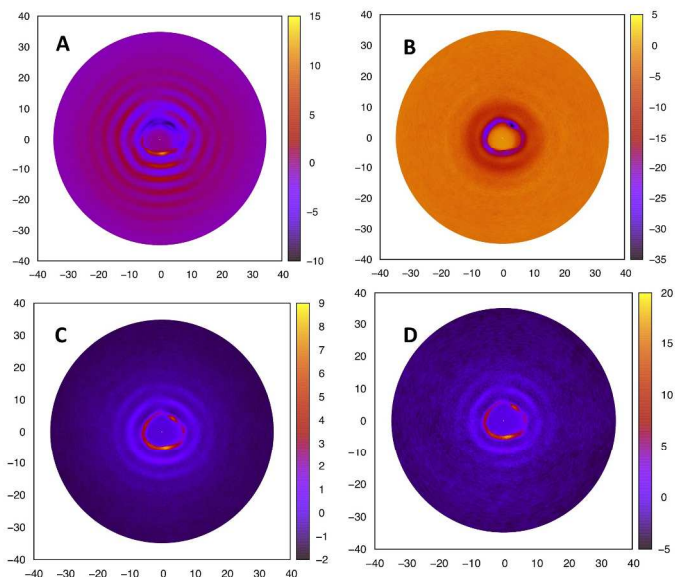


Figure S6. Orientational distributions of acyl chains around cholesterol in liquid ordered and liquid disordered phases. Shown is the difference between DPPC chain density and DOPC chain density, so that positive values are enhanced DPPC density and negative values are depleted DPPC relative to DOPC. At low T in the L_0 phase (Figure S6 Panel A), there is a clear preference for saturated chains to pack along the α face (oriented downward) and unsaturated chains to pack along the β face, with the preference for the α face extending out to at least three coordination shells. The hydrocarbon chain distribution in the L_d phase (Figure S6 panel B) is much more homogeneous, and lacks the clear structure of the coordination shells seen in the L_0 phase. The exception is a localized area of depleted saturated chain density, which breaks the “left-right” symmetry of the β face. These results are consistent with previous simulations of binary mixtures, though in this case we can directly observe the relative preference for the two chains. For $T > T_m$, the orientational structure is similar in the two local

environments identified by the HMM as “L_o like” (Figure S6 panel C) and “L_d like” (Figure S3 panel D), supporting the assertion that despite *compositional* fluctuations similar in structure to the low T data, the high T data do not contain bona fide L_o phase. In both cases above T_m, DPPC prefers the α face, but the preferences are overall much weaker than below T_m.