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## Article

# Location of dopamine in lipid bilayers and its relevance to neuromodulator function

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ABSTRACT Dopamine (DA) is a neurotransmitter that also acts as a neuromodulator, both functions being essential to brain function. Here we present the first experimental measurement of dopamine location in lipid bilayers using x-ray diffuse scattering (XDS), solid-state deuterium NMR, and electron paramagnetic resonance (EPR). We find that the association of DA with lipid headgroups as seen in electron density profiles leads to an increase of intermembrane repulsion most likely due to electrostatic charging. Dopamine location in the lipid headgroup region also leads to an increase of the cross-sectional area per lipid without affecting the bending rigidity significantly. The order parameters measured by solid-state deuterium NMR decrease in the presence of DA for the acyl chains of PC and PS lipids, consistent with an increase in the area per lipid due to DA. Most importantly, these results support the hypothesis that three-dimensional diffusion of DA to target membranes could be followed by relatively more efficient two-dimensional diffusion to receptors within those membranes.

SIGNIFICANCE

Knowing how dopamine interacts with lipid membranes is relevant to the understanding of transmission and modulation processes. Our experimental results show that dopamine has high affinity for the lipid headgroup region even in the absence of specialized receptors. This suggests that dopamine may first be collected by the target axon membrane and then diffuse along that membrane to its receptors that modulate function.

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## INTRODUCTION

Dopamine (DA) is a neurotransmitter and neuromodulator (1). There are several DA pathways in the brain that play major roles in reward-motivated behavior, motor control, and release of various hormones. DA deficiency and abnormalities in DA signaling can cause life-impairing diseases including Parkinson's, attention deficit hyperactivity disorder, and schizophrenia (2, 3). DA has been extensively studied in biological processes including its role against ferroptosis in cells (4), molecular transport (5, 6), interaction with receptors and transporters (7–9), and ion transfer (10).

As a neuromodulator, dopamine performs its function by diffusing from the release site to G-protein coupled receptors distributed over micrometer lengthscales (1, 11, 12). While aliphatic neurotransmitters such as acetylcholine, GABA, aspartate, glutamate, glycine, and serine might interact directly with their target proteins (13), neurotransmitters that contain aromatic groups such as dopamine, L-dopa, epinephrine, norepinephrine, adenosine, melatonin (14), serotonin (15–17), and histamine have an affinity to lipid headgroups (18) and therefore have a more complex mode of action that involve a broader range of spatial and temporal scales (1).

The conventional understanding is that DA undergoes three dimensional diffusion through aqueous spaces in order to activate both local and distant G protein-coupled receptors (1, 13). Then the membrane and its lipid composition would play no role. An alternative would be that the membrane acts as a collector of DA, concentrating it in the membrane to provide 2D diffusion to receptors that could be more efficient than purely 3D diffusion. In support, phospholipids make a difference in the process of synaptic neurotransmission and neuromodulation (19–21). Our results support this alternative.

Knowledge on the effect of DA on model lipid membranes has accumulated from calorimetry methods (2), solution-state NMR (22), and more recently vibrational sum frequency generation (VSFG) spectroscopy (21, 23). Additionally, it has been shown that DA decreases the main transition temperature of negatively charged lipid membranes (2) and that it breaks the peroxidation chain of methyl linoleate in liposomes assembled from neutral and negatively charged phospholipids (24). The emerging picture of DA interaction with lipid membranes may benefit from a more direct experimental measurement of the location of DA in lipid bilayers and of its effect on membrane structure and interactions. In this work, we use a combination of complementary experimental methods that include x-ray diffuse scattering (XDS), solid-state nuclear

magnetic resonance (NMR), and electron paramagnetic resonance (EPR). From XDS we learn: 1) where DA resides in the membrane, 2) how DA affects mechanical properties of membranes, in particular the bending rigidity $K_C$, and 3) how the bilayer structure is affected. The bending rigidity $K_C$ is a material parameter of lipid membranes that sets the energy scale for membrane shape deformations. Membrane curvature deformations are implicated in the function of membrane receptors and ion channels (25) and affect interactions between membranes which are relevant to cellular processes such as membrane fusion (26–29). In addition to providing information about the effect of DA on the bilayer, XDS provides the compression modulus $B$ that quantifies the interaction between bilayers (30–33). Solid-state $^2$H NMR focuses on how much DA affects the hydrocarbon region of the bilayer by providing order parameter profiles. From EPR measurements we obtain rotational correlation times of paramagnetic probe additives that confer information on the location of DA and on local membrane viscosity.

The interaction and dynamics of dopamine (and related neurotransmitters) are receiving sustained attention from MD simulations (6, 7, 15, 18). Such approaches have the obvious advantage that information is obtained at atomic detail and at time scales ranging from picoseconds to microseconds or more. However, these highly detailed results are subject to uncertainties due to the choice of force fields. Therefore, experimental data in terms of electron density profiles, order parameters, and correlation times as reported in this work can provide a test for MD simulations and guide future developments.

## MATERIALS AND METHODS

### Materials

1,2-dioleoyl-*sn*-glycero-3-phosphocholine (DOPC), 1,2-dilauroyl-*sn*-glycero-3-phosphocholine (DLPC), 1,2-dioleoyl-*sn*-glycero-3-phospho-L-serine (sodium salt) (DOPS), 1-palmitoyl-$d_{31}$-2-oleoyl-*sn*-glycero-3-phosphocholine (POPC-$d_{31}$), 1-palmitoyl-$d_{31}$-2-oleoyl-*sn*-glycero-3-phospho-L-serine (sodium salt) (POPS-$d_{31}$), and N-tempoyl palmitamide (N-TEMPO) were purchased from Avanti Polar Lipids (Alabaster, AL). Dopamine hydrochloride (DA) and 16-doxyl-stearic acid (16-DSA) were purchased from Sigma-Aldrich (St Louis, MO).

### X-ray

#### X-ray sample preparation

DOPC and DLPC lipids were separately dissolved in chloroform to make 20 mg/mL stock solutions. Similarly, a 20 mg/mL solution of DA was prepared in methanol. Appropriate volumes of lipid and DA stock solutions were mixed to obtain a final volume of 200 $\mu$L containing 4 mg of mixture of lipid and DA in molar ratios 0:1, 1:10, and 1:3 (DA:lipid). Samples were spread on flat acid cleaned silicon wafers (30 $\times$ 15 $\times$ 1 $mm^3$) and dried under the fume hood using the rock and roll procedure to make a thin film of oriented multilamellar samples (34, 35). Finally, samples were kept in a vacuum oven for at least 2 hours to remove the last traces of solvent. Dried samples were trimmed to form a 5 mm strip in the center of the wafer, parallel to the 30 mm edge. They were brought to full hydration through the vapor in a thick-walled hydration chamber with a Peltier cooler under the wafer to gently condense water into the sample.

#### X-ray scattering

The x-ray wavelength was 1.5418 Å. The x-ray beam impinges into horizontally held sample while the silicon wafer is rotated constantly between $\theta_{min} = -1.6°$ and $\theta_{max} = 7.0°$ at 20 degrees per second during data collection. Background scattering was collected with the angle $\theta$ set to $-2.4°$. Data were collected using a Rigaku (The Woodlands, TX) Mercury charge-coupled device (CCD) with a 1024 $\times$ 1024 pixel

array. The distance between CCD and sample center was 287 mm. Measurements were carried out at 25 °C.

### X-ray data analysis

X-ray data were analyzed using the NFIT program (36–38). The light background was subtracted and a 2-box subtraction was applied in order to interpolate the lateral background under the actual data. Repeat lattice spacing $D$ was measured using $h = 1, 2$ lamellar peaks. The bending modulus $K_C$ and compression modulus $B$ were calculated using three different fitting boxes, $q_{r2} = q_{r1} + 150$, 200, or 300 for lobes 2 and 3 where $q_{r1} = q_{r0} + 11$ and $q_{r0}$ is the pixel position of the specular center. The molecular volume of DA (246 $Å^3$) has been obtained by first measuring the DA density using a Mettler Toledo DE45 density meter and has been used in electron density profile analysis. Structural analysis was performed using the Scattering Density Profile (SDP) computer program, where form factor data derived from the XDS intensity data and molecular volumes are inputs (39).

### Mean-square fluctuations

The statistical average of out-of-plane excursions of membranes due to shape fluctuations is a function of $K_C$, $B$, and temperature, given by

$$\sigma^2 = \frac{k_B T}{2\pi} \frac{1}{\sqrt{K_C B}}. \tag{1}$$

For completeness, the free energy per unit area is given by

$$F = F_{bare} + \frac{k_B T}{2\pi} \sqrt{\frac{B}{K_C}} = F_{bare} + \left(\frac{k_B T}{2\pi}\right)^2 \frac{1}{K_C \sigma^2}, \tag{2}$$

where $F_{bare}$ is the free energy in the absence of fluctuations and can be thought as the limit $K_C \to \infty$ and $B \to \infty$ with the constraint $B/K_C \to 0$ (30).

## $^2$H NMR

### $^2$H NMR sample preparation

20 mg POPC-$d_{31}$ and 20 mg of POPS-$d_{31}$ were dried separately from chloroform solutions under a stream of nitrogen gas and then kept in the lyophilizer to remove the remaining traces of chloroform. The dry powder was then hydrated to 50 wt % with DA solution in deuterium depleted water in a molar ratio of 1:10 DA to lipid. The samples were vortexed and put through 5 cycles of freezing and thawing. Finally, the resultant suspensions were transferred to a 5 mm NMR tube that was sealed with a Teflon-coated plug. Sealed samples were stored at −80 °C and equilibrated at room temperature before the measurements.

### $^2$H NMR spectroscopy

Solid state $^2$H NMR spectra were recorded at 76.77 MHz on a homebuilt NMR spectrometer (40) reconfigured to operate with a wideline probe constructed by Doty Scientific, Inc. (Columbia, SC) in a 11.75 T superconducting magnet (Oxford Instruments, Osney Mead, UK). Pulse programming was achieved with an in-house assembled programmable generator (41), while signals were collected in quadrature by a dual-channel digital oscilloscope (R1200 M; Rapid Systems, Seattle, WA). A phase-alternated quadrupolar echo sequence ($90^\circ_x$-$\tau$-$90^\circ_y$-acquire-delay) was employed (42). The parameters used were 90° pulse width = 6 $\mu$s; separation between pulses $\tau$ = 50 $\mu$s; delay between pulse sequences = 1 s; sweep width = ± 250 kHz; and number of scans = 4096 or 8192. Temperature was maintained to ± 0.5 °C by a Varian high-stability variable temperature controller.

### $^2$H NMR spectra analysis

$^2$H NMR spectra obtained with lipid samples in the lamellar liquid crystalline phase are a superposition of doublets due to bilayers at all angles relative to the magnetic field ($B$). The splitting of the doublets is given by

$$\Delta\nu(\theta_{NB}) = \frac{3}{2}\left(\frac{e^2 q\, Q}{h}\right)|S_{\mathrm{CD}}|P_2(\cos\theta_{NB}). \tag{3}$$

In this equation $(e^2 q\, Q/h) = 167$ kHz is the quadrupole coupling constant, the angle $\theta_{NB}$ is the orientation of the membrane normal $(N)$ with respect to the magnetic field direction, $P_2(\cos\theta_{NB})$ is the second order Legendre polynomial and $S_{\mathrm{CD}}$ is the CD bond order parameter (43). The splittings for carbon segments $(i = 2-16)$ along a lipid chain were determined from the doublets resolved in de-Paked spectra $(\theta_{NB} = 0°)$ and used to construct profiles of $S_{\mathrm{CD}}^{(i)}$ assuming monotonic variation (44–46).

## EPR

### EPR sample preparation

EPR samples were prepared using N-tempoyl palmitamide (N-TEMPO) to probe the headgroup region or 16-doxyl-stearic acid (16-DSA) to probe the chain region for three different lipids: DOPC, DLPC, and DOPS. First, a total of 20 mg of lipid and EPR probe were mixed in chloroform separately for each lipid. The chloroform was then evaporated under a gentle stream of nitrogen gas. Remaining chloroform traces were removed during lyophilization. The resulting powder was hydrated with DA solutions to a concentration of 5 wt % lipid. The samples were mixed using a vortex mixer and 5 cycles of freezing and thawing. The molar ratio of DA to lipid and N-TEMPO was 50:500:1 and the ratio of DA to lipid and 16-DSA was 10:100:1.

### EPR spectroscopy

EPR spectra were recorded at 9.29 GHz on a Bruker X-band ESP 300 EPR spectrometer (Billerica, MA). Signals were detected as the first derivative of the absorption. The spectral parameters were microwave power, 12.6 mW; field center, 3305 G; sweep width, 100 G; sweep time, 167.77 s; time constant, 655.36 ms; modulation amplitude, 2 G; and dataset, 2048 points. Experiments were run at 25 °C.

### EPR spectra analysis

For probes in quasi-isotropic motion, the EPR spectra can be used to calculate a rotational correlation time $\tau_c$ according to

$$\tau_c = 6.5 \cdot 10^{-10}\, W_0 \left[ \left( \frac{h_0}{h_{-1}} \right)^{1/2} - 1 \right], \tag{4}$$

where $W_0$ is the distance between the central line of two peaks, $h_0$ is the height of the central field line, and $h_{-1}$ is the height of the high field line (see Fig. S3). The prefactor $6.5 \cdot 10^{-10}$ s/G is an averaged parameter that depends on the anisotropic $g$ value, anisotropic nitrogen hyperfine couplings, and the magnetic field strength (47, 48).

## RESULTS

### Lamellar spacing, interaction parameters, and fluctuations

The effect of DA on the $D$-spacing of DOPC and DLPC multilamellar oriented samples is shown in Fig. 2. The figure also shows previous measurements in salt solutions which provide reference swelling curves for these lipids (32). For both lipids, the $D$-spacing increases with added DA similarly to the effect of the monovalent KCl and KBr salts. The figure also shows that the effect of DA on the $D$-spacing is closer to that of KBr than to KCl indicating that the DA effect is due to membrane charging similar to that of $Br^-$ ions (31–33).

The bending modulus $K_C$ and the compression modulus $B$ obtained from the analysis of XDS data are plotted in Fig. 3. While the measured $K_C$ values for DOPC are higher than for DLPC, DA does not have a major effect on $K_C$ values for either lipid. The smaller $K_C$ value for DLPC is consistent with its smaller membrane thickness compared to DOPC (49). As expected, the $B$ parameter is a function of $D$. As mentioned in the Introduction, the $B$ parameter is an effective measure of the combined effect of intermembrane interactions which are known to decrease with increasing distance. However, it is surprising that the $B$ parameter for the two lipids appears to follow the same curve at higher $D$-spacing values.

The interlamellar spacing fluctuations $\sigma$ of DOPC and DLPC as a function of $D$-spacing corresponding to different amounts of DA are presented in Fig. 4. These are calculated from the measured values of $K_C$ and $B$ according to Eq. 1 in Methods. In the absence of DA, a higher value of $\sigma$ is measured for DLPC compared to DOPC due to smaller $K_C$. With increasing DA concentration and consequently $D$-spacing, $\sigma$ increases for both lipids due to the decrease of the compression parameter $B$.

A summary of parameters obtained from x-ray data of DOPC and DLPC for different molar ratios of DA to lipid is given in Table 1. Here, $2D_C$ is the hydrocarbon thickness, and $D_B$ is the overall Luzzati bilayer thickness calculated using molecular volumes and the cross-sectional area per lipid obtained obtained from the SDP program. The thickness of each interfacial headgroup region is about 10 Å (50), so the thickness of the pure interlamellar water region $D'_W$ is $D - 2D_C - 20$ Å.

One noticeable effect of DA on membrane structure is the increase in the area per lipid and this is plotted in Fig. 5. Addition of DA to either lipid at a molar ratio of 1:3 increases the cross-sectional area per lipid by 2.4 $Å^2$. (Extrapolation to 1:1 DA:lipid gives 7.2 $Å^2$ per dopamine molecule.) The increase of

Table 1: Parameters obtained from x-ray data for DOPC and DLPC for different molar ratios of DA:lipid at 25 °C. Measurements for each lipid/DA composition are from single samples.

The error values obtained from the goodness of fit are ±0.5 Å for $2D_C$ and ±1 Å$^2$ for $A$.

| | DA:lipid | $K_C$ ($10^{-13}$ erg) | $B$ ($10^{12}$ erg/cm$^4$) | $D$ (Å) | $2D_C$ (Å) | $D_B$ (Å) | $A$ (Å$^2$) | $D'_W$ (Å) |
|---|---|---|---|---|---|---|---|---|
| DOPC | 0:1 | 8.8 ± 0.1 | 10.9 ± 0.1 | 61.8 | 26.9 | 36.0 | 72.3 | 14.9 |
| | 1:10 | 7.6 ± 0.1 | 7.9 ± 0.2 | 66.7 | 26.6 | 36.3 | 73.0 | 20.1 |
| | 1:3 | 8.4 ± 0.4 | 3.4 ± 0.2 | 70.2 | 26.1 | 36.6 | 74.5 | 24.1 |
| DLPC | 0:1 | 6.4 ± 0.1 | 5.9 ± 0.2 | 59.4 | 21.4 | 32.1 | 61.8 | 18.0 |
| | 1:10 | 6.3 ± 0.1 | 4.8 ± 0.2 | 69.4 | 21.2 | 32.5 | 62.3 | 28.2 |
| | 1:3 | 6.7 ± 0.9 | 1.6 ± 0.9 | 71.3 | 20.6 | 32.8 | 64.2 | 30.7 |

cross-sectional area per lipid due to addition of DA is supported by solid-state $^2$H NMR results that are shown below.

## Electron Density Profiles

Fig. 6 shows electron density profiles (EDPs) obtained from the analysis of XDS data using the SDP program. This analysis provides not only the overall density profiles but also the contribution of various lipid components, water, and DA. In particular, the DA location is indicated by the shaded distributions. Attempts to place DA at different locations, including in the interlamellar water region or in the hydrocarbon region, resulted in larger $\chi^2$ values than the ones shown in Fig. 6.

In Table 2, we show the distance $D_{\text{peaks}}$ between the peaks of the overall EDPs, the average position of DA in the bilayer $z_{\text{DA}}$, and the average position of DA with respect to the EDP peak on the right hand side of the bilayer. We find that DA resides deeper in the headgroup region in the case of DOPC bilayers compared to DLPC, possibly due to the lower lateral density (larger area per lipid) in the case of DOPC. Aside from this minor difference, the major finding is that DA has a high affinity for the interfacial, headgroup region of the lipid bilayer compared to either the hydrocarbon region or, most importantly, to the interlamellar, pure water region. Table 1 shows that the interlamellar thickness $D'_W$ is as large as or larger than the two interfacial thicknesses ($2 \times 10$ Å), so there is ample aqueous volume for the DA to reside in. Our result in Fig. 6 shows that DA has a much higher affinity for the interfacial region. While the undetectability of any DA in the interlamellar space precludes a quantitative determination of the partition coefficient of DA between water and the bilayer, it is clear that it is large. This is supported by surface plasmon resonance experiments as shown in Supplementary Materials. However, our x-ray result is advantageous because it distinguishes between the hydrocarbon and the interfacial regions of the bilayer.

Table 2: $D_{\text{peaks}}$ is the head-to-head distance, $z_{DA}$ is the DA average distance from the bilayer center, and $\Delta z_{\text{DA}} = D_{\text{peaks}}/2 - z_{\text{DA}}$ is the distance between the headgroup peak and DA.

| | DA:lipid | $D_{\text{peaks}}$ (Å) | $z_{\text{DA}}$ (Å) | $\Delta z_{\text{DA}}$ (Å) |
|---|---|---|---|---|
| DOPC | 0:1 | 36.1 | - | - |
| | 1:10 | 37.5 | 15.3 | 3.5 |
| | 1:3 | 37.6 | 14.9 | 3.9 |
| DLPC | 0:1 | 31.0 | - | - |
| | 1:10 | 30.7 | 17.7 | -2.4 |
| | 1:3 | 29.1 | 13.9 | 0.7 |

## $^2$H NMR spectroscopy

For $^2$H NMR spectroscopy we have used the common lipids POPC-$d_{31}$ and POPS-$d_{31}$, which contain a deuterated saturated palmitoyl (16:0) *sn*-1 chain and a monounsaturated oleoyl (18:1) *sn*-2 chain. The measured order parameter profiles with and without DA are shown in Fig. 7. Because the order parameters are highly sensitive to temperature, it is customary to show results over a range of temperatures. Reassuringly, with increasing temperature (from 30 to 45 °C) the order parameters decrease as expected. As commonly seen for saturated lipid chains in lamellar liquid crystalline phases, the order parameters are the highest for carbon segments close to the headgroup region (so-called plateau region) and decrease progressively towards the end of the chain. The order parameters of POPS-$d_{31}$ are higher than those of POPC-$d_{31}$ at all measured temperatures, consistent with literature data (51). As shown in the figure, the presence of DA causes the chains to become more disordered, albeit modestly, in both lipids at all temperatures.

Using a mean-torque model for carbon segment orientations (44), we used the plateau order parameters (carbon 2 to 8) to calculate the cross-sectional area of the palmitoyl (C16:0) chains. These results are shown in Table 3.

Table 3: Average order parameter in the plateau region (carbons 2 to 8) $|\overline{S}_{pl}|$ and cross-sectional area (in units of Å$^2$) per palmitoyl chain $A_{16:0}$ of POPC-$d_{31}$ and POPS-$d_{31}$ in the absence and presence of DA at different temperatures. The molar ratio of DA to lipid is 1:10. Measurements for each lipid/DA composition are from single samples. A reproducibility of ±1% applies to $|\overline{S}_{pl}|$ values.

| Temperature (°C) | POPC-$d_{31}$ | | POPC-$d_{31}$/DA | | POPS-$d_{31}$ | | POPS-$d_{31}$/DA | |
|---|---|---|---|---|---|---|---|---|
| | $\lvert\overline{S}_{pl}\rvert$ | $A_{16:0}$ | $\lvert\overline{S}_{pl}\rvert$ | $A_{16:0}$ | $\lvert\overline{S}_{pl}\rvert$ | $A_{16:0}$ | $\lvert\overline{S}_{pl}\rvert$ | $A_{16:0}$ |
| 30 | 0.201 | 30.74 | 0.195 | 31.11 | 0.229 | 29.16 | 0.222 | 29.53 |
| 35 | 0.191 | 31.55 | 0.188 | 31.75 | 0.219 | 29.86 | 0.214 | 30.14 |
| 40 | 0.187 | 32.00 | 0.182 | 32.35 | 0.211 | 30.49 | 0.205 | 30.84 |
| 45 | 0.181 | 32.61 | 0.177 | 32.92 | 0.202 | 31.22 | 0.197 | 31.53 |

We note that DA increases the cross-sectional area of the 16:0 acyl chain similar to the XDS results shown above. Additional information on the effect of DA on lipid structure and dynamics is obtained by EPR spectroscopy which is shown next.

## EPR spectroscopy

We have acquired the EPR spectra for 16-DSA and N-TEMPO probes incorporated into multilamellar vesicles of DOPC, DLPC, and DOPS lipids in the absence and the presence of DA (see Supplemental Materials). N-TEMPO measures changes near the lipid headgroup while 16-DSA measures changes near the bilayer center. We find that DA produces measurable differences in rotational correlation times $\tau_c$ that are calculated from the spectra (see Eq. 4 in Materials and Methods) and these results are summarized in Table 4.

As opposed to solid-state $^2$H NMR, which gives order parameters and therefore information on chain structure, EPR using N-TEMPO gives us a rotational correlation time that we use to estimate local viscosity which in turn is relevant to the timescale of dopamine diffusion. We included 16-DSA as a probe on the other end of the lipid to illustrate the difference in dynamics between the headgroup region and membrane interior.

The measured 16-DSA spectra are characteristic of high disorder ($S < 0.2$) near the bottom of the chain which is treated as approximately isotropic. The rotational correlation times measured are in the nanosecond range, which is the fast tumbling regime, and are comparable to published work (52). The $\tau_c$ values are larger (corresponding to higher micro-viscosity) in DOPS than in DLPC and DOPC, and are affected by DA in the same manner. For all three lipids, DA increases the probe's rotational correlation times.

Similar to 16-DSA, the N-TEMPO spectrum is also a high-disorder spectrum and is treated as originating from quasi-isotropic motion near the headgroup region. The measured rotational correlation times are in the fast tumbling regime in the nanosecond time scale, analogous to published work (53). The measured N-TEMPO rotational correlation times are larger in DOPS than in DOPC and DLPC (in a different order than for 16-DSA). However, adding DA has the same effect on correlation times: for all three lipids, DA causes the rotational correlation time to increase.

A priori, higher disorder would be expected to be accompanied by a shorter correlation time. The difference in timescale for EPR and NMR, a limitation of the assumption that the label motion is isotropic or a change in depth of the EPR probe in the presence of DA may be responsible for the apparent contradiction posed by our data. That the effect on N-TEMPO is greater indicates, nevertheless, an interfacial interaction

for DA.

Table 4: EPR rotational correlation times of 16-DSA and N-TEMPO obtained from the EPR spectra at 25 °C. The molar ratio of DA to lipid and 16-DSA is 10:100:1 and the molar ratio of DA to lipid and N-TEMPO is 50:500:1. The values for $\tau_c$ are an average of three measurements and the uncertainty is the standard deviation from the mean. For all cases but N-TEMPO with DOPS with and without DA, measurements were performed on single samples and repeated three times. All three measurements were run within 24 hours after making the samples. For N-TEMPO with DOPS with and without DA, three separate samples were measured. The error values indicate standard deviations from the mean.

| Sample | $\tau_c$ (16-DSA)(ns) | $\tau_c$ (N-TEMPO)(ns) |
|---|---|---|
| DOPC | 0.809 ± 0.012 | 1.329 ± 0.014 |
| DOPC/DA | 0.813 ± 0.009 | 1.358 ± 0.004 |
| DLPC | 0.857 ± 0.026 | 1.256 ± 0.036 |
| DLPC/DA | 0.880 ± 0.009 | 1.348 ± 0.027 |
| DOPS | 0.885 ± 0.002 | 1.521 ± 0.040 |
| DOPS/DA | 0.898 ± 0.013 | 1.591 ± 0.011 |

The changes in rotational correlation times ($\Delta\tau_c$) of 16-DSA and N-TEMPO due to the DA for DOPC, DOPS, and DLPC are shown in Fig. 8. The measured $\Delta\tau_c$ values are in the range of 0 to 0.1 ns and are more noticeable for N-TEMPO than for 16-DSA. In the case of N-TEMPO the increase exceeds experimental uncertainty while in the case of 16-DSA the increase is comparable or within experimental uncertainty. For both probes, the changes in rotational correlation times increase from DOPC to DOPS to DLPC.

## DISCUSSION

There are effectively two orthogonal aspects that have evolved in our study. The first and original aspect is the effect of DA on membrane properties. Such effects would support a mechanism by which DA might perform its biological role by modifying the overall membrane lateral pressure profile to activate membrane proteins without close contact with or binding of the DA (54–56). We do find that DA affects membrane properties: it increases the cross-sectional area per lipid corresponding to decreased acyl chain order parameters, it affects membrane-membrane interactions as indicated by changes in lamellar spacing, and it modifies the molecular dynamics in the lipid headgroup region as measured by the rotational correlation times of EPR probes. Surprisingly, despite the above effects, DA does not seem to affect the membrane bending rigidity $K_C$. On the whole, however, these changes are not large, especially when one realizes that the concentrations of DA that we studied are very high. The overall DA concentration in the synaptic region is only of the order of 50 nM (57). Even if all this DA became bound to the target axon membrane, the ratio of DA to lipid would be of order $10^{-6}$ instead of our used ratio of 0.1. Therefore, this putative mechanism does not seem likely to supplant the conventional mechanism of specific binding of DA to a receptor.

The second, more important, aspect of our paper relates to how the membrane could speed up the kinetics of DA signal transduction. Our main result for this aspect is that DA strongly associates with the interfacial region of the membrane. By combining scattering and spectroscopic methods, we have shown that DA has a pronounced affinity to the lipid-water interface. We have shown using XDS that the zwitterionic DA locates in the headgroup region, either near the glycerol-carbonyl region in DOPC, or near the phosphate groups in DLPC. EPR confirmed the headgroup location in DOPC, DLPC, and DOPS, while NMR showed only a slight disordering of the acyl chains in POPC and POPS due to DA. This is consistent with previous measurements by solution-state NMR (22) as well as MD simulation (58) that have indicated the preference of dopamine for the lipid headgroup region. This association of DA with lipid membrane is generally consistent with aromatic moieties having a preference for the lipid headgroup region (32, 59) due to dipole interactions between the aromatic groups and lipid headgroups (60, 61).

Given this preference, it is plausible that DA undergoes 2D diffusion to its target receptor after being collected and concentrated by the membrane (62, 63). Depending upon the appropriate diffusion coefficients,

this could be more efficient than the conventional picture of purely 3D diffusion to the membrane receptor. It is known that the lipid matrix provides a quasi-2D millieu for diffusion of membrane-bound, biological molecules (64–68). These include protein transmembrane domains as well as surface bound G-protein units. It is even more likely that smaller chemical groups, such as DA, located in the membranes would also undergo 2D diffusion within the interfacial headgroup region.

The diffusion of DA in membranes can be estimated based on local viscosity which is obtained from the rotational correlation times of the EPR probes. Membrane local viscosity $\eta$ based on a simplified model is given by

$$\eta = \frac{3k_B T \tau_c}{4\pi r^3}, \tag{5}$$

where $k_B$ is Boltzmann constant, $T$ is temperature, and $r$ is the hydrodynamic radius (69–71). Using a heuristic value of $r = 4$ Å at $T = 25\,^{\circ}$C, the $\eta$ values are on the order of $12 - 14$ mPa·s for 16-DSA and $19 - 24$ mPa·s for N-TEMPO. (Using $r = 3$ Å gives us $29 - 33$ mPa·s for 16-DSA and $46 - 58$ mPa·s for N-TEMPO). To put this range of values in perspective, the dynamic viscosities for water, olive oil, and glycerol at this temperature are $\approx 1$ mPa·s, 100 mPa·s, and 1500 mPa·s, respectively.

Using simple diffusion models (72), we estimate the translational diffusion coefficient by

$$D_t = \frac{k_B T}{6\pi\eta r}. \tag{6}$$

Using $r = 4$ Å for DA's radius (volume = 246 Å$^3$) together with the viscosity of N-TEMPO, the translational diffusion coefficients of DA in the membrane are on order of $2.2 - 2.6 \cdot 10^{-7}$ cm$^2$ s$^{-1}$. That gives an estimated mean-travel distance of 0.2 $\mu$m in 1 ms which is the time scale of dopamine processes in the brain (1, 12). Of course, the effective viscosity experienced by DA is likely to be smaller than for the spin-labeled probe because the latter has a long tail that resides in the more viscous hydrocarbon region. If we use the diffusion coefficient ($8.2 \pm 1.3 \cdot 10^{-7}$ cm$^2$ s$^{-1}$) that has been reported at the cell surface (11), the mean-travel distance increases by about a factor of 2. Also note since DA does not span the membrane, 2D diffusion models for cylindrical transmembrane inclusions might not apply (64).

It is important to realize however that both the cellular membrane and its surroundings are crowded spaces and therefore the viscosity of both environments are expected to be significantly higher than that of

dilute aqueous solutions. Consequently, molecular diffusion in the aqueous space is significantly hindered (73, 74). Moreover, while all molecular species in the membrane diffuse concomitantly, they would do so at different rates (72, 75–78). In particular, a small molecule like DA, residing in the interfacial region composed of a nearly equal concentration of highly mobile lipid headgroups and water, would diffuse laterally much faster than lipids themselves. Furthermore, the dynamics (translation and rotation) of receptors themselves can affect the probability of ligand-receptor encounter. Notably, the question of concomitant diffusion of ligand and receptors is receiving attention in applied mathematical research (79–81).

Moreover, mathematical models of diffusion have shown the marked effect of the number of dimensions in which the molecular motion takes place as well as the influence of the space topology with 2D diffusion being an important case (65, 82). It is conceivable that 2D diffusion in the lipid matrix could play an important role for the encounter of neuromodulators and their membrane receptors (13, 62, 79, 81). Supposing that a quasi-equilibrium is established after initial release of DA from the presynaptic neuron, then the concentration of DA within the target membrane will be much higher than the concentration in water. This provides a reservoir of membrane DA that could be more likely to find target receptors via 2D diffusion than a dilute aqueous concentration of DA undergoing 3D diffusion.

We therefore suggest that the primary pathway for DA signal transduction is diffusion along the lipid membrane headgroup region until it meets its receptor. This hypothesis implies that the lipid composition of the target membrane can affect the time-scale of dopamine action, as has been reported (19–21). Furthermore, although the location of dopamine binding sites on receptors is not entirely clear (18, 83–85), the receptors may have evolved DA binding sites that are themselves buried in the membrane and are therefore less accessible to binding DA from solution. On the other hand, even if the receptor binding site is in the aqueous phase, the off-rate of DA from the headgroup region would still allow the final contact with the reception binding site.

When working with multilamellar samples, there is always the question whether the added molecular species (such as DA in this case) is excluded or not from the interlamellar space. This is important because if DA were excluded into an excess water phase, then the effects we measure would be primarily osmotic as opposed to specific interactions with the lipids (86, 87). One of the best indicators of osmotic effects

is the lamellar repeat spacing: if $D$ decreases with the additive, it strongly indicates that the additive is excluded from the multilamellar structure and acts osmotically within an excess water phase. However, we found that the $D$-spacing increases; that indicates that the added molecular species enters the multilamellar lipid structure where it can either reside in the interlamellar water region or in the membrane, or both.

It should be noted that the choice of lipids in our studies depended on two factors: 1) the limitations of each experimental method, and 2) prior studies. For example, while solid-state $^2$H NMR spectroscopy can in principle be done on any deuterated lipid, the assignment to carbon segments is not easily done for unsaturated chains. For this reason, we opted for deuterated POPC and POPS lipids which have been extensively used in $^2$H NMR spectroscopy. In contrast, measurements of membrane interactions on DLPC and DOPC membranes by other techniques are relatively more common.

Regarding interbilayer interactions, we note that the equilibrium $D$-spacings for DLPC and DOPC in water are very different, as expected based on different interaction parameters, especially $K_C$. Our current $K_C$ values agree well with previous measurements. Previous measurements reported $K_C = 8.0 \cdot 10^{-13}$ erg at 63.3 Å for DOPC (88) and $K_C = 5.5 \cdot 10^{-13}$ erg at 61.1 Å for DLPC (39). Interestingly, when DA is added, the $B$ vs $D$ data tend to follow the same curve at larger values of $D$. One possible explanation is that at these distances, the balance of inter-membrane interactions is primarily between the van der Waals attraction and the electrostatic repulsion caused by the DA molecules associated with the lipid headgroups, and enhanced by the fluctuation term. This particular balance of interlamellar forces leads to swelling curves similar to those measured in the presence of KBr salt. In the case of KBr solutions, it has been shown that the electrostatic repulsion due to $Br^-$ binding to PC headgroups fully explains the observed multilamellar swelling (32, 33). Our results in Fig. 2 indicate that a similar mechanism occurs in the case of DA as well. This swelling of lipid multilayers is accompanied by large changes in the $B$ parameters and a significant effect of DA on the amplitude of membrane shape fluctuations: in the presence of DA, the ratios of $\sigma$ to $D$ and to $D_W$ are $\sigma/D \approx 10\%$ and $\sigma/D_W \approx 18\%$.

Dopamine location and dynamics are also expected to be affected by pH, salt, and lipid membrane composition. Our report using simplified lipid systems provides an experimental baseline for dopamine-lipid membrane interactions which can be used for further development of molecular modeling of dopamine dynamics and its probability of encounter with its receptors.

## CONCLUSIONS

We find that DA is strongly associated with the interfacial lipid headgroup region of lipid bilayers compared to either the hydrocarbon region or the aqueous region. We suggest that DA released in the brain is collected by target membranes in order to provide, via two-dimensional diffusion along the membrane, more efficient encounter with its receptors.

Figure 1: Chemical structure of dopamine hydrochloride (DA) using the standard CPK color codes: carbon (grey), oxygen (red), nitrogen (blue), and hydrogen (white). The chemical structure is drawn using ChemDraw.

Figure 2: $D$-spacing vs. DA:lipid molar ratio for DLPC and DOPC multilayers at 25 °C. Data from DLPC in KCl and KBr salt solutions at corresponding salt:lipid molar ratios are also shown to provide reference swelling curves (32).

Figure 3: Bending and compression moduli obtained from XDS analysis. (a) The bending modulus $K_C$ of DOPC and DLPC, and (b) the corresponding compression modulus $B$ as a function of $D$-spacing for various molar ratios of DA to lipid at 25 °C. Measurements for each lipid/DA composition are from single samples. The average bending modulus $K_C$ and compression modulus $B$ were calculated using the NFIT program (see Materials and Methods) using three different fitting boxes, $q_{r2} = q_{r1} + 150$, 200, or 300 and error bars indicate the standard deviation from the mean. For some data points the standard deviation bars are within the symbols. The $K_C$ and $B$ averages and errors are shown in Table 1.

Figure 4: The interlamellar spacing fluctuations $\sigma$ of DOPC and DLPC as a function of $D$-spacing corresponding to different molar ratios of DA to lipid at 25 °C. The interlamellar spacing fluctuations $\sigma$ were calculated using the average values of $K_C$ and $B$, and errors are calculated using the error propagation analysis based on the errors for $K_C$ and $B$. For some data points the error bars are within the symbols. Numerical results are shown in Table 1.

Figure 5: The cross sectional area per lipid vs. DA:lipid molar ratio at 25 °C obtained using the NFIT program (see Materials and Methods).

Figure 6: Electron density profiles obtained from XDS data at 25 °C showing the overall distributions (black) as well as various contributions: phosphate (Phos, red), carbonyl glycerol (CG, blue), methylene groups (green), methyl groups (pink), water (cyan), and dopamine (DA, shaded grey). The interfacial water region extends to larger distances as given by $D/2$ in Table 1.

Figure 7: Order parameter profiles for POPC-$d_{31}$ and POPS-$d_{31}$ in the absence and presence of DA. Measurement temperatures were 30 °C (a), 35 °C (b), 40 °C (c), and 45 °C (d). The molar ratio of DA to lipid is 1:10. Measurements for each lipid/DA composition are from single samples. A reproducibility of ±1% applies to order parameter values.

Figure 8: The changes in rotational correlation times of 16-DSA and N-TEMPO probes due to the DA for DOPC, DOPS, and DLPC at 25 °C. The molar ratio of DA to lipid and 16-DSA is 10:100:1 and the molar ratio of DA to lipid and N-TEMPO is 50:500:1. For all cases but N-TEMPO with DOPS with and without DA, measurements were performed on single samples and repeated three times. All three measurements were run within 24 hours after making the samples. For N-TEMPO with DOPS with and without DA, three separate samples were measured. The error bars indicate standard deviations from the mean.

## AUTHOR CONTRIBUTIONS

AS prepared samples, performed measurements, analyzed data, wrote manuscript. SM analyzed data, wrote manuscript. SRW analyzed data, wrote manuscript. STN analyzed data, wrote manuscript. JFN performed measurements, wrote manuscript. HIP designed project, analyzed data, wrote manuscript.

## DECLARATION OF INTERESTS

The authors declare no competing interests.

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## Supplemental Materials

### X-ray diffuse scattering

A background-subtracted x-ray diffuse scattering (XDS) image of an oriented and hydrated DLPC sample is shown in Fig. S1. Due to scattering noise, some of the pixel values become negative after background subtraction and those pixels are shown in red. The region of interest for data analysis is in the vicinity of scattering lobes on each side of specular reflection (detector meridian) at $q_r$ = 527 pixels. The scattering on the meridian is due to the lamellar repeat and the peak centers can be used to calculate the lamellar repeat period, ($D$-spacing). For the diffuse part of the spectrum, an example of an analysis window is shown by the blue frame in Fig. S1. Also note that we have used multiple beamstops for different $q_z$ ranges to account for higher overall scattering intensity at lower $q_z$. The blue box that includes the right sections of lobes 2 and 3 contains the data used to calculate the bending modulus $K_C$ and the compression modulus $B$. As mentioned in Materials and Methods, besides the box that is shown in the figure, $K_C$ and $B$ were obtained using two additional fitting boxes with different lateral widths that are not shown.

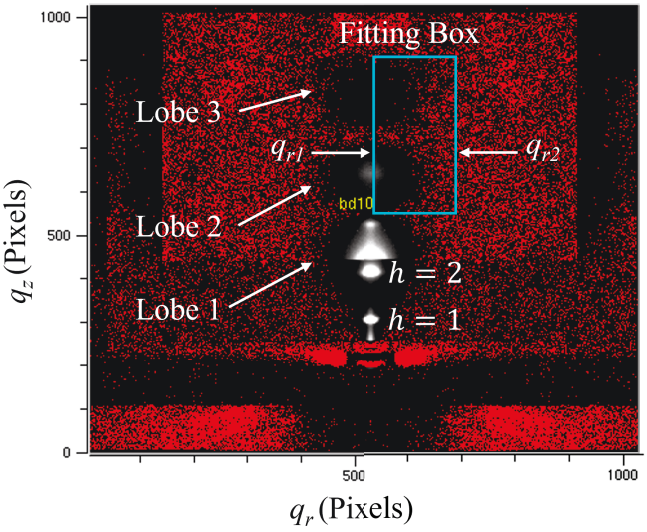


Figure S1: X-ray diffuse scattering of an oriented multilamellar DLPC sample at 25 °C showing an example of a fitting box used to calculate $K_C$ and $B$. 100 pixels correspond to a $q$ range of 1/nm. The $h$ = 1 and $h$ = 2 labels show the lamellar peaks used to calculate the $D$-spacing.

## $^2$H Nuclear Magnetic Resonance

Representative $^2$H NMR de-Paked spectra for POPC-$d_{31}$, POPS-$d_{31}$, and their mixtures with DA at 30 °C are shown in Fig. S2. A series of doublets that can be assigned to individual or groups of segments become resolved. The outer pair of peaks with greatest splitting are a composite of signals from ordered methylene groups in the upper part of the chain (C2-C10), while progressively less ordered methylene groups in the lower part (C10-C15) are responsible for the individual peaks with smaller splitting. The pair of peaks near the center at ± 2.5-3 kHz is due to the highly disordered terminal methyl groups (C16) at the bottom of the chain. The spectrum for POPS-$d_{31}$ is wider than for POPC-$d_{31}$, which means that POPS is more ordered. Adding DA decreases the width of both POPC-$d_{31}$ and POPS-$d_{31}$ which implies lower order.

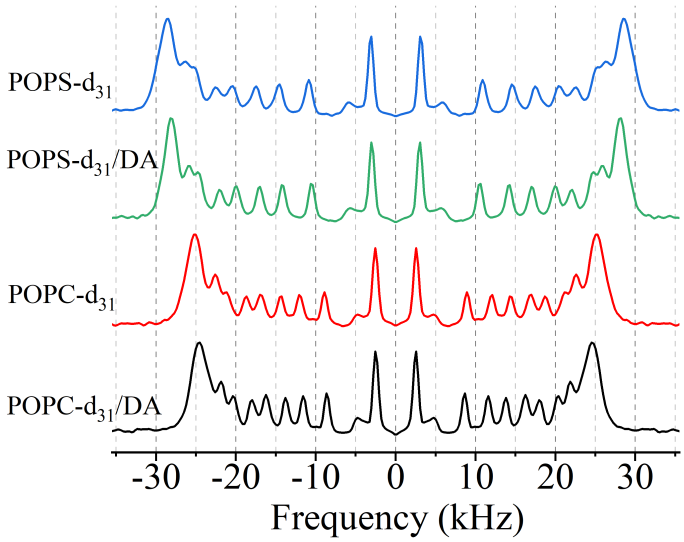


Figure S2: Representative $^2$H NMR de-Paked spectra in the absence and presence of DA at 30 °C. The molar ratio of DA to lipid is 1:10.

**Electron Paramagnetic Resonance**

An example of an EPR spectrum of a 16-DSA paramagnetic probe in DOPC undergoing quasi-isotropic motion is shown in Fig. S3.

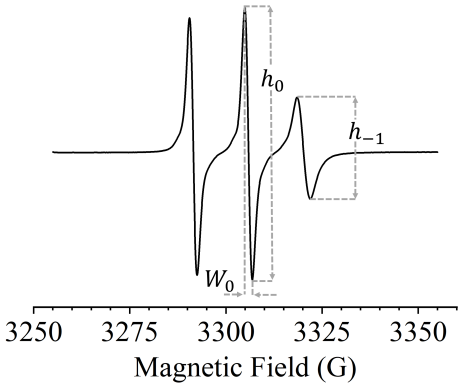


Figure S3: The EPR spectrum of a 16-DSA paramagnetic probe in DOPC at 25 °C. The ratio of lipid to 16-DSA was 100:1.

Fig. S4 shows the EPR spectra for 16-DSA and N-TEMPO probes incorporated into multilamellar vesicles of DOPC, DLPC, and DOPS lipids in the absence and the presence of DA. N-TEMPO measures changes near the lipid headgroup while 16-DSA measures changes near the bilayer center. Panel a shows the spectra of 16-DSA and panel b shows the spectra of N-TEMPO. Because of spectral width, the effect of DA is not easily visible in the figure. However, DA produces measurable differences in rotational correlation times $\tau_c$ that are calculated from the spectra.

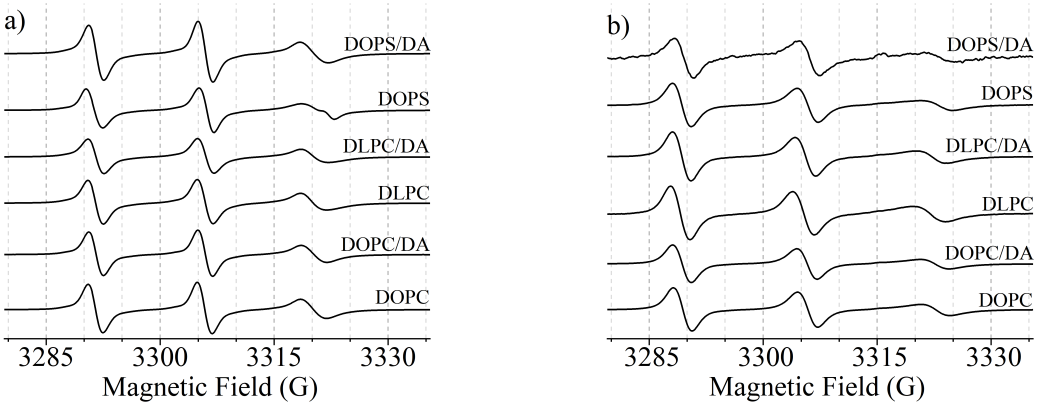


Figure S4: The EPR spectra of 16-DSA-labeled lipids and N-TEMPO-labeled lipids. for DOPC, DLPC, and DOPS in the absence and presence of DA at 25 °C. The molar ratio of DA to lipid and 16-DSA is 10:100:1 and the molar ratio of DA to lipid and N-TEMPO is 50:500:1. Panel (a) shows 16-DSA spectra and panel (b) shows N-TEMPO spectra.

**Surface Plasmon Resonance (SPR)**

**Materials and Methods**: SPR measurements were performed using an OpenSPR instrument (Nicoya, Kitchener, Ontario, CA). In these measurements, dopamine is considered to be the Ligand, and the solvent flowing over it is called the Analyte. Unless otherwise stated, the flow solvent was deionized water. DA was attached to the Sensor Chip using the following steps. Before starting, the chip was examined for bubbles, and the debubbling procedure was performed by flowing 80% isopropanol over the chip. The chip was cleaned with 10 mM HCl and rinsed with water. It was then activated by combining two reagents: 1-ethyl-3-(3-dimethyl aminopropyl) carbodiimide (EDC) and N-hydroxysuccinimide (NHS) (1:1, v:v) that were flowed over the chip. DA was immobilized by adding increasing concentrations, 10, 20 and 40 $\mu g/ml$ in NaAcetate buffer, pH 6.0, by first injecting, and then washing off excess DA. In each case, the Surface Plasmon Resonance response (SR) increased with the injection, then decreased slightly during the washing phase. After DA immobilization, the remainder of the activated sites on the chip were blocked with 1M ethanolamine, and then rinsed with DI water. At this point, unilamellar vesicles (ULVs) of DOPC or DLPC were added as the analyte. The injection phase was 300 seconds, and the wash phase was 900 seconds. The most successful measurements occurred at small lipid concentrations, 0.6 to 0.16 mg/ml. Higher concentrations caused artifacts, and smaller SRs. After measurements with ULVs were performed, a fresh chip was prepared in an identical way, except for the DA immobilization step. Unilamellar vesicles (ULVs) of DOPC and DLPC were flowed over the fresh chip, which served as the control.

**Results**: As shown in Figs. S5 and S6, ULVs of both DOPC and DLPC readily bound onto the DA-coated sensor chip. The control experiment also showed non-specific binding at the higher concentration of DOPC, and at both concentrations of DLPC ULVs. The control experiment was subtracted from the DA experiment in order to calculate $K_D = k_{\text{off}}/k_{\text{on}}$. The initial slope of binding or unbinding for all traces was determined using OriginPro.

For DLPC no unbinding was detected, but rather a continuing binding process after the wash phase, so $K_D$ could not be determined for DLPC. This indicates that the binding of DLPC to DA is stronger than the binding of DOPC to DA. By contrast, when 150 mM PBS pH 7.0 was used as a control analyte there was rapid binding upon injection and rapid unbinding upon washing (data not shown), demonstrating that ULV binding is very different from control.

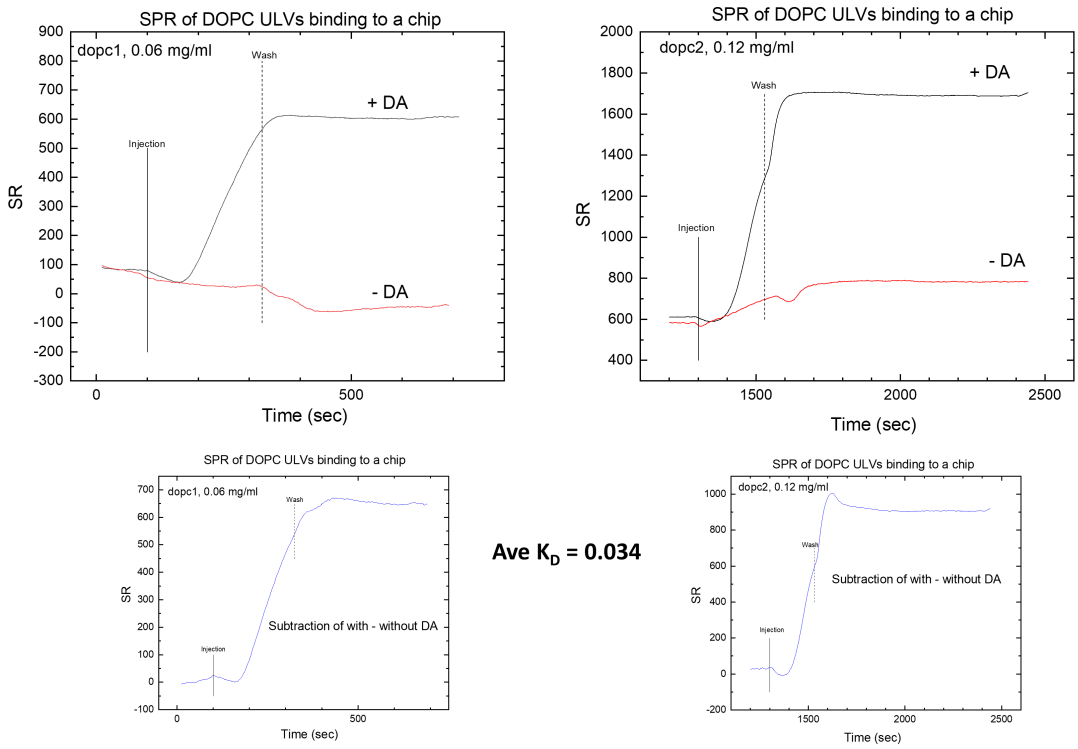


Figure S5: Surface Plasmon Resonance of DA association with DOPC membranes.

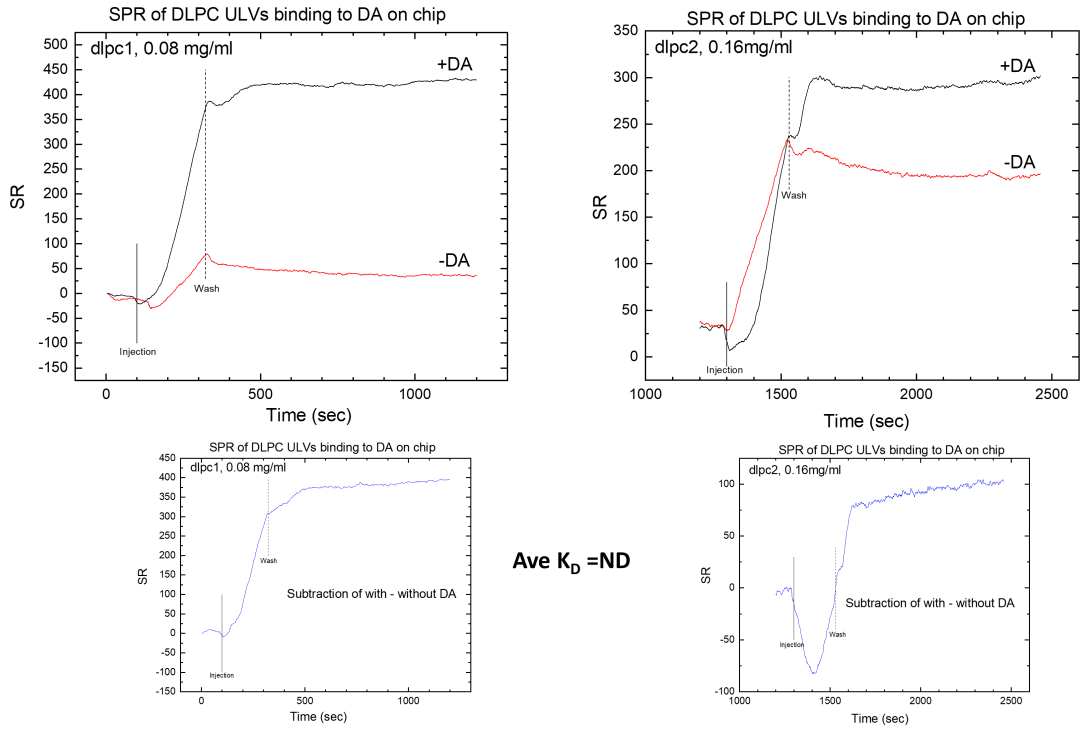


Figure S6: Surface Plasmon Resonance of DA association with DLPC membranes.

**Acknowledgments**

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