Supporting Information

Deciphering How Pore Formation Causes Strain-Induced Membrane Lysis of Lipid Vesicles

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Table Caption

Table S1. Size distribution of extruded lipid vesicles measured by dynamic light scattering.

Figure Captions

Figure S1. Δf-ΔD plots for AH peptide-induced degradation of POPC lipid vesicles for representative peptide concentrations.

Figure S2. Rupture time as a function of peptide concentration in solution. For POPC lipid vesicles, the fit was obtained by $t_r = Dc^{-\beta}$, where t_r is the rupture time, c is the peptide concentration in solution, and β and D are fitting parameters. The rupture time was defined as follows: **(a)** Time from initial peptide attachment until there was rupture of the majority of adsorbed vesicles (Δf = -45 Hz, as compared to baseline), with fit showing $\beta = 0.97 \pm 0.20$ (p-value < 0.1, ANOVA). **(b)** Time from initial peptide attachment until the QCM-D inflection point (minimum value of Δf), with fit showing $\beta = 1.41 \pm 0.23$ (p-value is 0.62, ANOVA). **(c)** Time from initial peptide attachment until the ellipsometry inflection point (maximum value of optical mass), with fit showing $\beta = 0.90 \pm 0.20$ (p-value is 0.41, ANOVA). The inflection points define rupture time as the ensemble-averaged onset at which acoustic or optical mass loss, accordingly inferred as vesicle rupture, becomes the predominant event observed in the QCM-D or ellipsometric measurement, respectively. Rupture times based on the inflection point characterizing an ensemble of vesicles do not have a physical meaning on the single-vesicle level, and were more sensitive to variation between individual experiments at each peptide concentration (p-value > 0.1, ANOVA).

Figure S3. Normalized **(a)** Δf, **(b)** ΔD, and **(c)** optical mass shifts for AH peptide-induced degradation of 85 mol% POPC lipid and 15 mol% cholesterol vesicles.

Figure S4. Normalized **(a)** Δf, **(b)** ΔD, and **(c)** optical mass shifts for AH peptide-induced degradation of 70 mol% POPC lipid and 30 mol% cholesterol vesicles.

Figure S5. Normalized **(a)** Δf, **(b)** ΔD, and **(c)** optical mass shifts for AH peptide-induced degradation of 55 mol% POPC lipid and 45 mol% cholesterol vesicles.

Figure S6. Normalized **(a)** Δf, **(b)** ΔD, and **(c)** optical mass shifts for AH peptide-induced degradation of HIV envelope-mimicking vesicles.

Lipid Composition	Diameter (nm)	Polydispersity Index
POPC	56.4	0.078
85% POPC + 15% Cholesterol	56.8	0.074
70% POPC + 30% Cholesterol	59.9	0.093
55% POPC + 45% Cholesterol	99.9	0.240
HIV Envelope Mimic	89.6	0.117

Table S1.

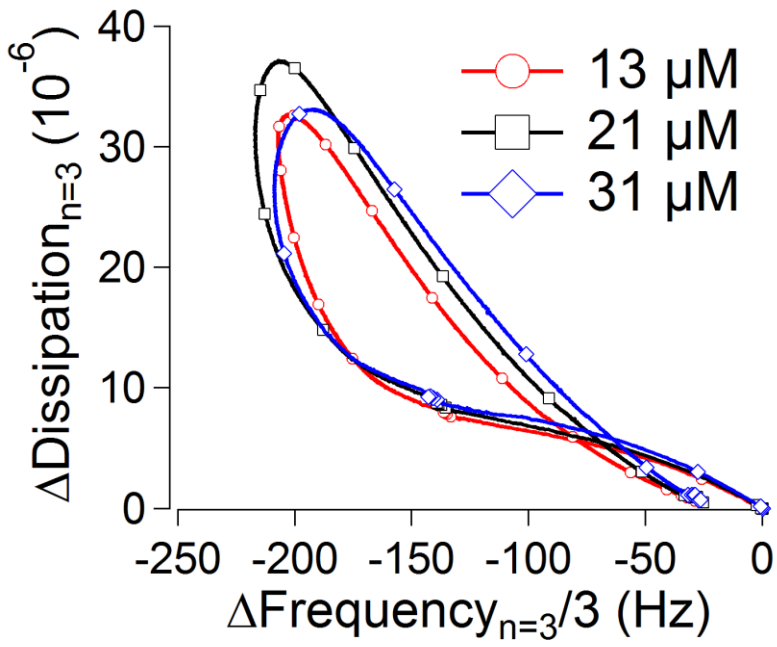
13 μM
21 μM
31 μM
ΔDissipation$_{n=3}$ (10^{-6})
ΔFrequency$_{n=3}$/3 (Hz)
40
30
20
10
0
-250
-200
-150
-100
-50
0

Fig. S1.

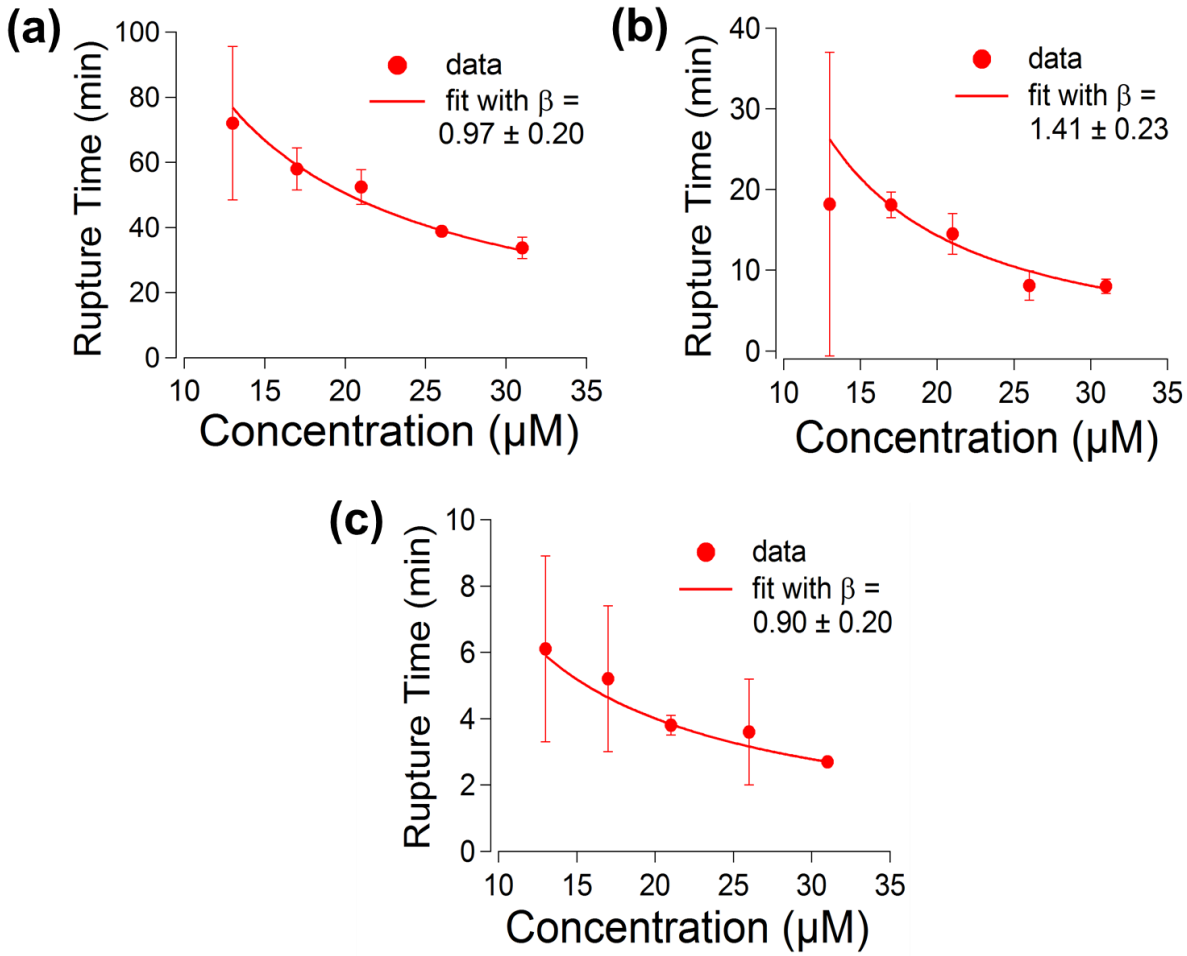
(a)
Rupture Time (min)
Concentration (μM)
data
fit with β =
0.97 ± 0.20
(b)
Rupture Time (min)
Concentration (μM)
data
fit with β =
1.41 ± 0.23
(c)
Rupture Time (min)
Concentration (μM)
data
fit with β =
0.90 ± 0.20

Fig. S2.

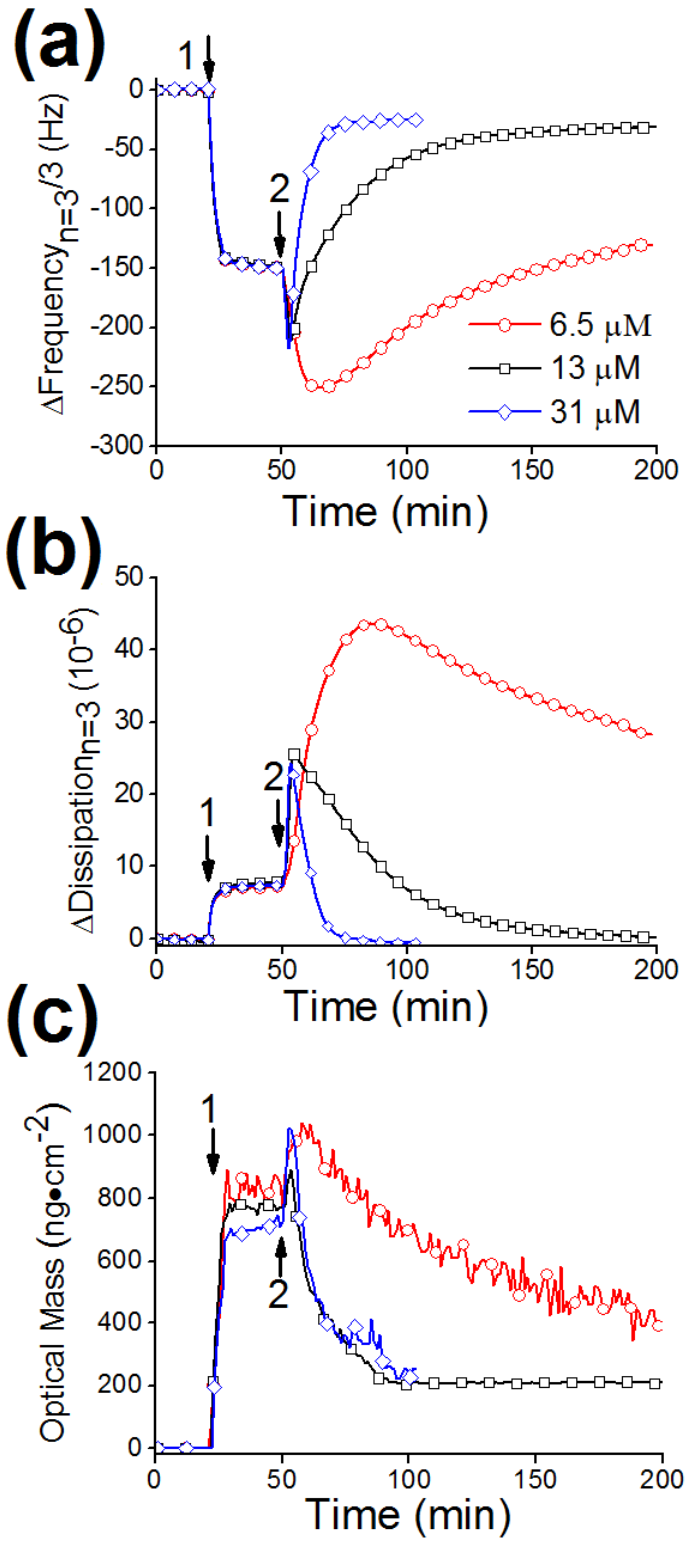
(a)
1
2
0
-50
-100
-150
-200
-250
-300
ΔFrequency n=3/3 (Hz)
6.5 μM
13 μM
31 μM
0
50
100
150
200
Time (min)
(b)
50
40
30
20
10
0
ΔDissipation n=3 (10-6)
1
2
0
50
100
150
200
Time (min)
(c)
1200
1000
800
600
400
200
0
Optical Mass (ng•cm-2)
1
2
0
50
100
150
200
Time (min)

Fig. S3.

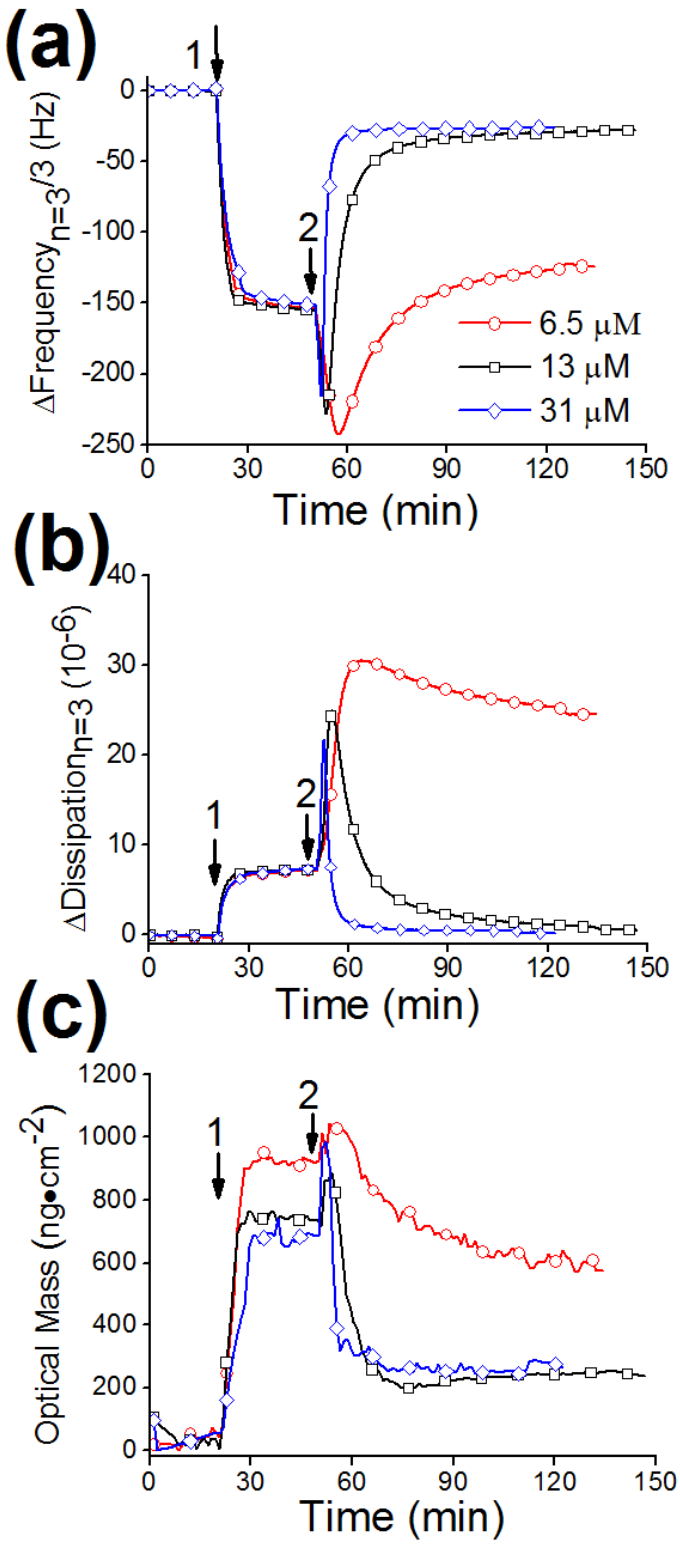
(a)
1
2
0
-50
-100
-150
-200
-250
ΔFrequency n=3/3 (Hz)
6.5 μM
13 μM
31 μM
0
30
60
90
120
150
Time (min)
(b)
40
30
20
10
0
ΔDissipation n=3 (10-6)
1
2
Time (min)
(c)
1200
1000
800
600
400
200
0
Optical Mass (ng•cm-2)
1
2
Time (min)

Fig. S4.

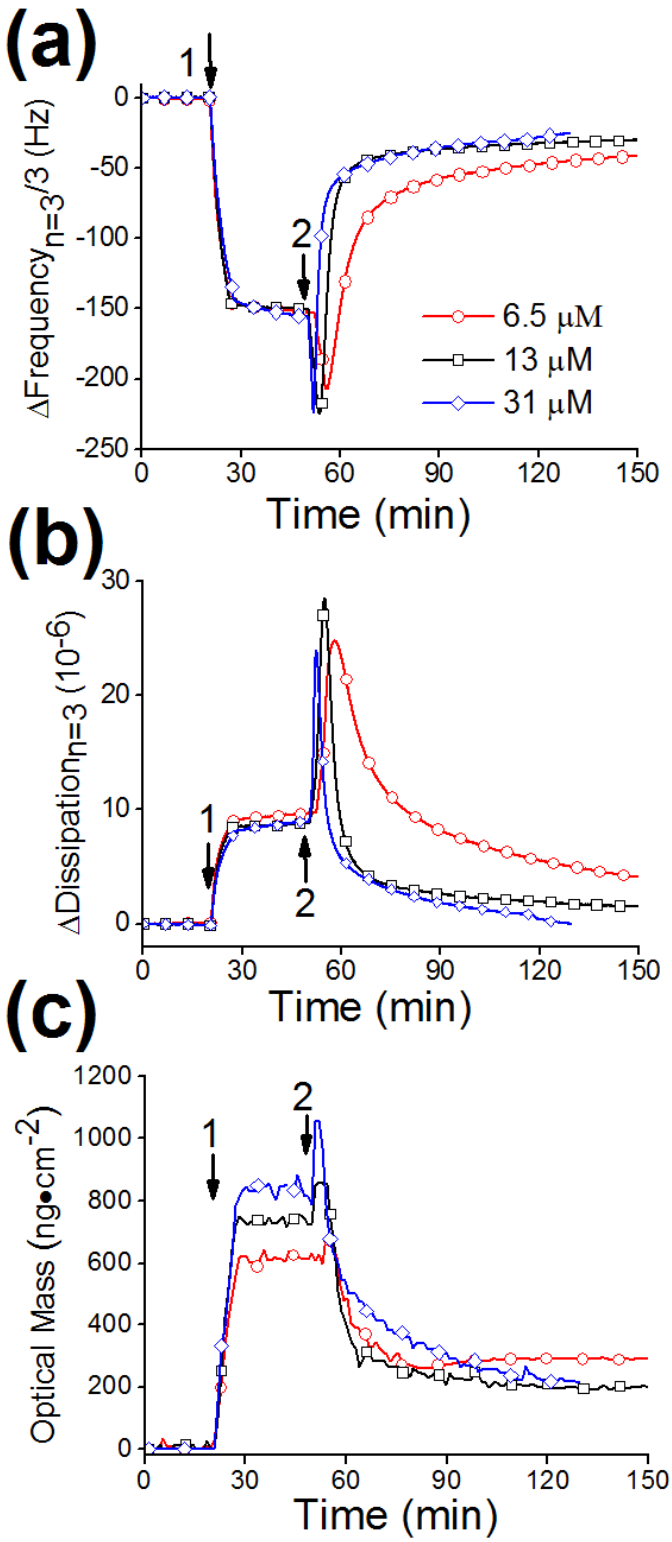
(a)
1
2
0
-50
-100
-150
-200
-250
ΔFrequency n=3/3 (Hz)
6.5 μM
13 μM
31 μM
0
30
60
90
120
150
Time (min)
(b)
30
20
10
0
ΔDissipation n=3 (10-6)
1
2
Time (min)
(c)
1200
1000
800
600
400
200
0
Optical Mass (ng•cm-2)
1
2
Time (min)

Fig. S5.

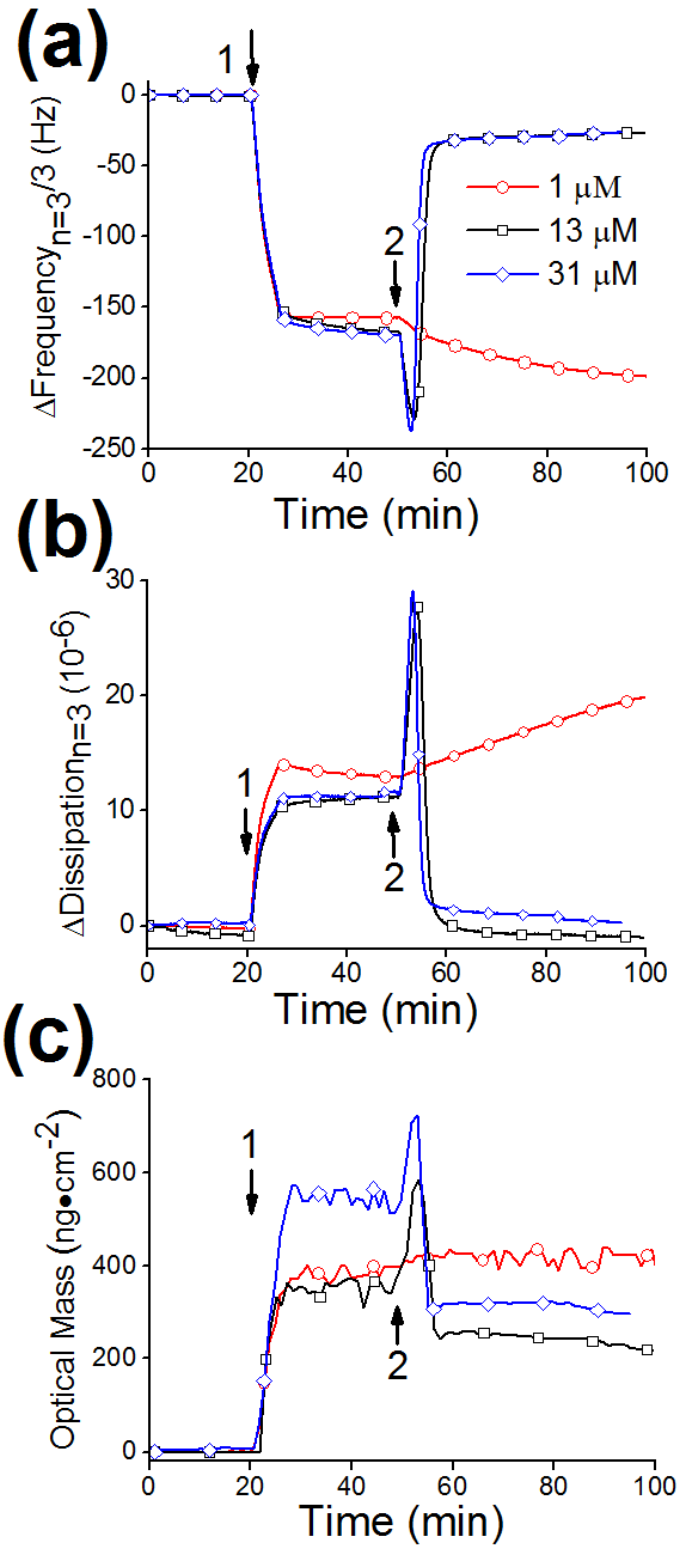
(a)
1
2
0
-50
-100
-150
-200
-250
ΔFrequency n=3/3 (Hz)
1 μM
13 μM
31 μM
0
20
40
60
80
100
Time (min)
(b)
30
20
10
0
ΔDissipation n=3 (10-6)
1
2
Time (min)
(c)
800
600
400
200
0
Optical Mass (ng•cm-2)
1
2
Time (min)

Fig. S6.