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Supporting Material

Hydrophobic Surfactant Proteins Strongly Induce Negative Curvature

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SUPPORTING INFORMATION

Additive curvature: Our analysis requires an expression for the variation of curvature, c, in response to changes in the concentration of total added protein, SP_t. Based on studies with different lipids,

$$c = \sum_i c_i \cdot X_i$$

where the c_i are the intrinsic curvatures for each component of a mixture, and X_i are their mol fractions. For the binary mixture of lipids combined with the proteins, because the tetradecane fits between the cylindrical monolayers and has no effect on curvature (48),

$$c = c_{PE} \cdot X_{PE} + c_{PC} \cdot X_{PC} + c_{sp} \cdot X_{sp}^{b}.$$

The sub- and superscripts b, f and t refer to bound, free and total moieties, respectively.

For the lipids alone,

$$c_0 \equiv c_{PE} \cdot X_{PE} + c_{PC} \cdot X_{PC}$$

For the small X_{sp} used here, the X_i for the lipids are approximately the same with and without the proteins. The change in curvature induced by the proteins, Δc, is given by

$$\Delta c \equiv c - c_0 \approx c_{sp} \cdot X_{sp}^{b}.$$

$X_{sp}^{b} = \frac{SP_b}{SP_b + PL_t}$ for concentrations of bound protein, SP_b, and total phospholipid, PL_t.

Particularly for molar concentrations, $SP_b \ll PL_t$.

$$\therefore X_{sp}^{b} \approx \frac{SP_b}{PL_t}$$

and $$\Delta c = c_{sp} \cdot \frac{SP_b}{PL_t}$$

Langmuir model: The Langmuir model of binding by the proteins to a limited concentration of discrete sites, S, provides access to SP_b. Because $SP_b = S_b$, Δc can be expressed in terms of the fraction of occupied sites, $\theta \equiv \frac{S_b}{S_t}$:

$$\Delta c = c_{sp} \cdot \frac{SP_b}{S_t} \cdot \frac{S_t}{PL_t} = c_{sp} \cdot \theta \cdot \frac{SP_b^m}{PL_t} \qquad [1]$$

where SP_b^m is the maximum possible concentration of bound protein. The association constant, K_a, is given by

$$K_a = \frac{SP_b}{SP_f \cdot S_f} = \frac{S_b}{(SP_t - S_b)\cdot(S_t - S_b)}$$

$$S_b^2 - S_b \cdot \left(S_t + SP_t + \frac{1}{K_a}\right) + SP_t \cdot S_t = 0$$

Solving the quadratic,

$$S_b = \frac{1}{2}\left(S_t + SP_t + \frac{1}{K_a}\right) \cdot \left[1 \pm \left(1 - \frac{4 \cdot SP_t \cdot S_t}{\left(S_t + SP_t + \frac{1}{K_a}\right)^2}\right)^{\frac{1}{2}}\right]$$

A series expansion for $(1-x)^{\frac{1}{2}}$ provides the square root. If the ratio, $x = \frac{4 \cdot SP_t \cdot S_t}{\left(S_t + SP_t + \frac{1}{K_a}\right)^2}$, is small, the first term of the expansion reasonably approximates the full expression. For x to be small, $\left(S_t + SP_t + \frac{1}{K_a}\right)^2 > 4 \cdot SP_t \cdot S_t$, which requires that the difference between the two terms must be positive.

$$\left(S_t + SP_t + \frac{1}{K_a}\right)^2 - 4 \cdot SP_t \cdot S_t = (S_t + SP_t)^2 + \frac{2(S_t + SP_t)}{K_a} + \frac{1}{K_a}^2 - 4 \cdot SP_t \cdot S_t$$

$$= (S_t - SP_t)^2 + \frac{2(S_t - SP_t)}{K_a} + \frac{4\,SP_t}{K_a} + \frac{1}{K_a}$$

$$= \left(S_t - SP_t + \frac{1}{K_a}\right)^2 + \frac{4\,SP_t}{K_a}$$

Because both $\left(S_t - SP_t + \frac{1}{K_a}\right)^2$ and $\frac{4\,SP_t}{K_a}$ are positive,

$$\left(S_t + SP_t + \frac{1}{K_a}\right)^2 - (4 \cdot SP_t \cdot S_t) > 0$$

$$\left(S_t + SP_t + \frac{1}{K_a}\right)^2 > (4 \cdot SP_t \cdot S_t)$$

$$\therefore x = \frac{4 \cdot SP_t \cdot S_t}{\left(S_t + SP_t + \frac{1}{K_a}\right)^2} < 1.$$

For $S_t \gg SP_t$, $x \ll 1$.

Using the expansion $(1-x)^{\frac{1}{2}} = 1 - \frac{x}{2}$,

$$S_b = \frac{1}{2} \cdot \left(S_t + SP_t + \frac{1}{K_a}\right)\left[1 \pm \left(1 - \frac{2 \cdot SP_t \cdot S_t}{\left(S_t + SP_t + \frac{1}{K_a}\right)^2}\right)\right]$$

$$= \frac{SP_t \cdot S_t}{S_t + SP_t + \frac{1}{K_a}} \qquad \text{for the root with the negative sign}$$

$$= \frac{\epsilon \cdot SP_t}{1 + \epsilon \cdot SP_t} \cdot S_t \qquad \text{for } \epsilon = \frac{K_a}{1 + K_a S_t}$$

$$\theta = \frac{S_b}{S_t} = \frac{\epsilon \cdot SP_t}{1 + \epsilon \cdot SP_t}$$

For the conditions of our experiments, where $S_t \gg SP_t$, the expression for θ has the same form as the exact expression of the Langmuir equation, $\theta = \frac{K_a \cdot SP_f}{1 + K_a \cdot SP_f}$, but in terms of the concentration of total protein, SP_t, rather than free, unbound protein, SP_f, and with ϵ replacing K_a. Note that because ϵ depends on SP_b^m as well as K_a, changes in the binding capacity as well as the binding affinity would affect how θ depends on SP_t.

From equation [1], these relationships indicate that

$$\Delta c = c_{sp} \cdot \frac{\epsilon \cdot SP_t}{1 + \epsilon \cdot SP_t} \cdot \frac{SP_b^m}{PL_t}$$

For our data, $\Delta c = \alpha_1 \cdot SP_t \cdot X_{PC}$.

$$\therefore \Delta c = \frac{a_1 \cdot SP_t}{1 + a_2 \cdot SP_t} \cdot X_{PC}$$

where $a_1 \cdot X_{PC} = c_{sp} \cdot \epsilon \cdot \frac{SP_b^m}{PL_t}$,

$a_2 = \epsilon$,

and $\frac{a_1 \cdot X_{PC}}{a_2} = c_{sp} \cdot \frac{SP_b^m}{PL_t}$