EFFECTS OF LIPID-MEDIATED INTERACTIONS ON PROTEIN PAIR DISTRIBUTION FUNCTIONS

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Membrane proteins can perturb the lipid bilayer and produce a lipid-mediated inter-protein interaction. We have treated this problem by expanding the free energy density as a Taylor series expansion in terms of the gradient of some scalar membrane parameter and its deviation from an equilibrium (i.e., particle-free) value.[1] Minimization of total membrane energy yields a field equation

$$\left(\frac{\Delta^2}{\eta^2} - 1\right)\phi(r) + \phi_0 = 0, \qquad (1)$$

where $\phi(r)$ is the membrane parameter, ϕ_0 is its particle free value, and η^{-1} is a correlation length characteristic of the membrane.

Solution of Eq. 1 for one, two, and many particles, using suitable approximations, gives an expression for the effective interaction energy between two particles in terms of the correlation length, effective particle radius r_0, and particle density ρ. The pairwise interaction between particles changes with increasing particle density because of changes in the mean value of ϕ_0 in the presence of particles.

Fig. 1 shows a plot of $V(\eta r)/E_1$ against ηr for ρ=0 for a number of values of ηr_0, where $V(\eta r)$ is the inter particle potential energy and E_1 is the self-energy of one particle.

RESULTS AND DISCUSSION

It is of interest to know how this lipid-mediated potential energy affects the interparticle pair distribution function (PDF). To this end we are carrying out calculations of the PDF based on the recently published algorithm of Lado (1968) for solving the Ornstein-Zernike (OZ) relation in two dimensions using the Percus-Yevick (PY) closure,

$$c(r) = \{1 - \exp[V(r)/kT]\}g(r) \qquad (2)$$

where $c(r)$ is the direct correlation function defined in the OZ relation

$$h(r) = g(r) - 1 = c(r) + \rho \int c(|r - s|)h(s)d^2s. \qquad (3)$$

$h(r)$ is calculated from its Fourier transform,

$$\hat{h}(k) = \frac{\hat{c}(k)}{1 - \rho\hat{c}(k)}, \qquad (4)$$

where in general,

$$\hat{f}(k) = \int_0^\infty f(r)J_0(kr)\, rdr. \qquad (5)$$

In Fig. 2 we show PDFs calculated from Eqs. 2 and 4 for r_0 = 4 nm, η^{-1} = 3, 5, 8 and 10 nm, with E_1 = $1.7kT$ and $1.5kT$, respectively, and ρ = 0.003 nm^{-2}. These are comparable to PDFs measured from freeze-fracture pictures of *Acholeplasma laidlawii* membranes shown in Fig. 3 (Edelman, 1978; James and Branton, 1973).

It is apparent that to this level of approximation the calculated PDF does not reproduce the "noise" of the measured functions. However, the qualitative characteristics of the decay of the PDF from its peak to 1.0 are reproduced if the noise of the measured function is averaged. It is proposed that accurate calculations of the PDF

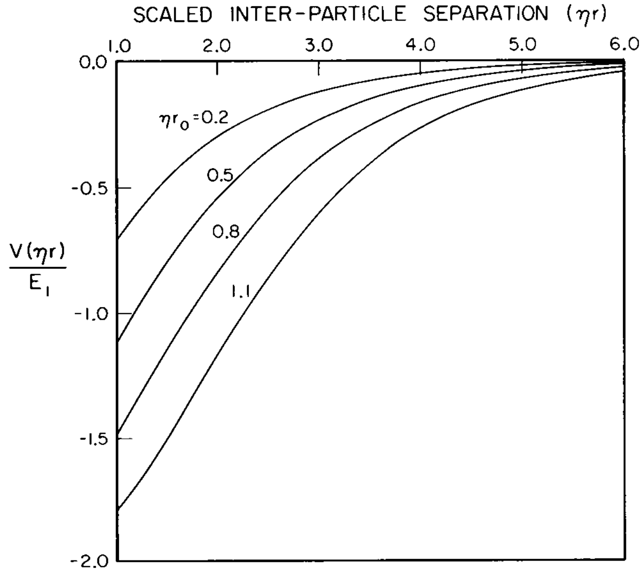

FIGURE 1 $V(\eta r)$ against ηr for ηr_0 = 0.2, 0.5, 0.8, and 1.1.

[1]Edelman, J., T. Pearson, and S. I. Chan. Statistical mechanics of lipid membranes. I. Protein aggregation and lipid ordering. Submitted for publication.

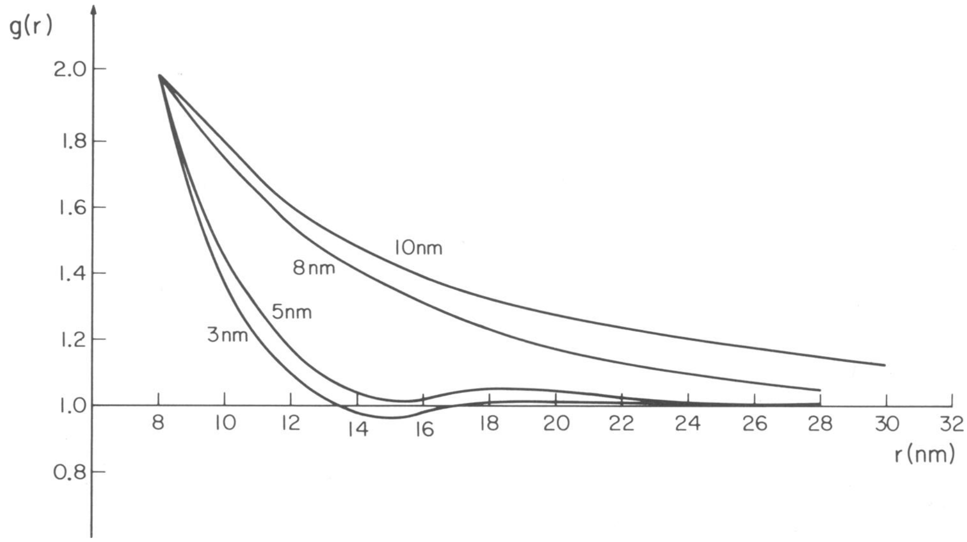

FIGURE 2 Calculated functions for $r_0 = 4.0$, $\eta^{-1} = 3, 5, 8$ and 10 nm.

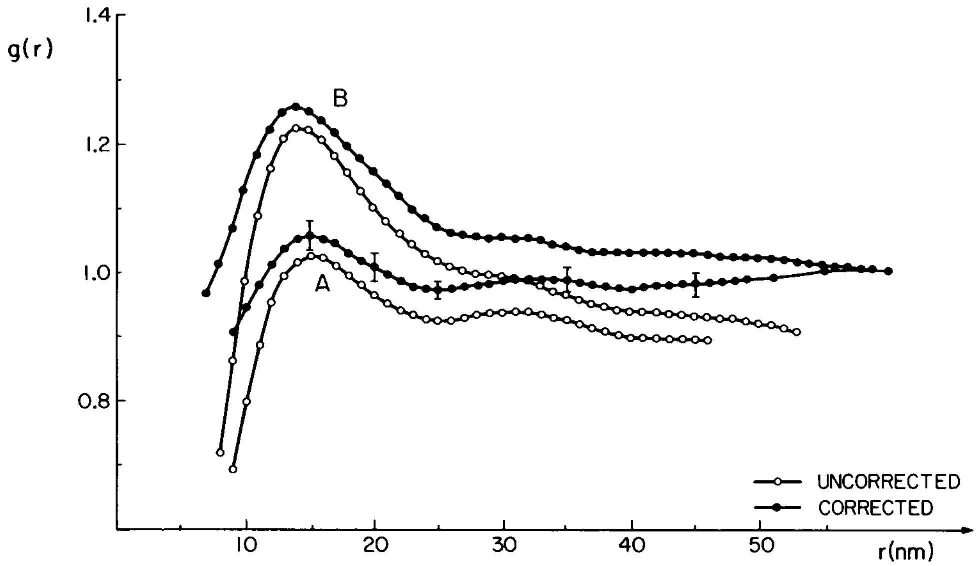

FIGURE 3 Measured functions from Fig. 1 *A* and *B* of James and Branton (1973).

with measured PDFs from well-defined model membrane systems will yield accurate values of membrane correlation lengths and quantitative measures of protein lipid interactions through values of E_1 which on the basis of present results appears to be of the order of 1–$2kT$, with η^{-1} of the order of a few nanometers from the protein-lipid boundary.

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