Hydrodynamic Interprotein Interaction in a Biomembrane

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Abstract. A membrane of the lipid bilayer is regarded as a two-dimensional viscous and incompressible fluid coupled to the surrounding water. A long-range interaction arises between protein molecules moving in this two-dimensional fluid in a weak coupling limit.

1. Introduction

A biomembrane may be treated as a two-dimensional viscous and incompressible fluid. The lateral diffusion of protein molecules in the biomembrane is investigated. Here a protein molecule is represented by a hard disk.

The biomembrane layer is sandwiched by semi-infinite regions of water and the momentum of lipid molecules may leak into the surrounding water system. From this point of view, Saffman and Delbrück first obtained the mobility of the disk by taking into account both the thickness of the membrane and the viscosity of the outer water[1,2]. They predicted that the mobility of a protein inserted in the membrane depends very weakly on its size. The size dependence is only logarithmic. We stress that this result suggests the presence of a long-range interaction among membrane proteins.

In this report, we consider a simplified version[3] of the Saffman-Delbrück model, which is free from the Stokes paradox. The diffusion coefficient of protein molecules is obtained through the Einstein relation. Then we calculate the interprotein forces arising from the hydrodynamical origin.

2. Hydrodynamic Model with Momentum Decay

Let us start with the hydrodynamical equation

$$-\frac{1}{\rho}\text{grad } P + \nu\nabla^2\vec{v} - \frac{1}{\tau}\vec{v} = 0, \qquad \text{div } \vec{v} = 0, \tag{1}$$

where $\vec{v}$ is the velocity field of the two-dimensional fluid, ρ is the two-dimensional density, ν is the kinematical viscosity, grad, ∇^2 and div are the two-dimensional operators, P is the hydrostatic pressure, and τ is the relaxation time of the momentum of the lipid assembly.

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Consider a disk A with radius a moving with a constant velocity $-\vec{U}$. We take the Cartesian coordinates (x, y) with the origin fixed at the center of the disk and the x-axis along the direction $\vec{U} = (U, 0)$. The polar coordinates will be (r, θ). In this reference frame we write $\vec{v} = \vec{U} + \vec{u}$ and replace $-\vec{v}/\tau$ by $-\vec{u}/\tau$ in (1). The boundary conditions are $\vec{u} = 0$ for $r \to \infty$ and $\vec{v} = 0$ at $r = a$. An important parameter turns out to be $\kappa \equiv 1/\sqrt{\nu\tau}$.

In the weak coupling limit ($\kappa a \ll 1$), the diffusion coefficient is obtained by the Einstein relation as

$$D = \frac{k_B T}{4\mu\pi} \log \frac{1}{\kappa a}, \tag{2}$$

where $\mu = \rho\nu$. This agrees with Saffman-Delbrück's result. The pressure field around the disk is

$$P = \frac{\mu U}{\log \kappa a} \frac{\cos\theta}{r}. \tag{3}$$

Consider next two disks A and B, moving with velocities U and U', respectively. Let A be at the origin (0,0) and B be at $(x, y) = (r\cos\theta, r\sin\theta)$. For $\kappa r \gg 1$, the force acting on B is obtained as

$$F_x^{(B)} = C\pi a \frac{\cos 2\theta}{r^2}, \qquad F_y^{(B)} = C\pi a \frac{\sin 2\theta}{r^2}, \tag{4}$$

where $C = 2\mu U / \log \kappa a$. This is our main result. The hydrodynamic interaction is rather long-ranged. Details of the calculation will be published elsewhere.

3. Conclusion

It is remarkable that even in the presence of a momentum dissipation mechanism, the interprotein interaction is long-ranged as seen from (4). In the many protein system in the membrane, each protein does not move independently. The system exhibits collective motions leading to certain patterns.

References

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