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A model for the lateral diffusion of "stiff" chains in a lipid bilayer

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Abstract. We present random walk models for the diffusive motion of lipid probe molecules in a lipid bilayer and calculate the diffusion constants for probes spanning the entire bilayer and for probes extending through one lipid layer only. The "stiffness" of such molecules can explain the observed value of 2/3 for the ratio of these diffusion constants.

Key words: Lipid diffusion, random walk, multistate random walk, master equations, two dimensions

Introduction

Recently, Vaz et al. have observed the translational diffusion of lipid probes in the liquid crystalline phase of lipid bilayers (Vaz et al. 1985). The lipid probes investigated were chosen either to extend only through *one* layer or to span *both* layers of the host membrane. The measurements revealed diffusion coefficients, D_1, for single layer penetrating probes which were independent of the actual chain length of the probe molecule (Vaz et al. 1985). However, for probes endowed with polar head groups at both ends of the chain, which span both layers of the membrane, an unexpectedly large diffusion coefficient, D_2, was observed, equal to about 2/3 of the monolayer probe diffusion coefficient D_1, independent of temperature (Vaz et al. 1985). In this paper we will present a simple model which relates the D_2/D_1 ratio to the mechanisms of microscopic diffusive displacements and to the structure of the lipid probe. Our model yields the observed D_2/D_1 ratio for a plausible choice of molecular properties.

Diffusion in lipid bilayers is 2-dimensional. We will consider here neither those features of diffusion in membranes which are due to the hydrodynamic difficulty of defining stationary, strictly 2-dimensional diffusion nor will we be concerned with the effects of the viscosity of the surrounding 3-dimensional medium (for a recent review see: Clegg and Vaz 1984). We assume that these aspects of membrane diffusion do not contribute significantly to the D_2/D_1 ratio. Rather, we imagine that the D_2/D_1 ratio is mainly influenced by the "stiffness" of those probe molecules which extend through both layers of the lipid membrane since their stiffness may lead to certain couplings between the microscopic diffusive displacements in the two liquid crystalline layers. Hence, a comparison between the results of model calculations on probe molecule diffusion in lipid monolayers and bilayers with the observed D_2/D_1 ratio may provide information on the microscopic events within the host lipid matrix which are connected with the translational mobility.

In our model the lipid membrane is represented by two parallel, planar, discrete lattices which have been chosen to be hexagonal because of the hexagonal structure of the liquid crystalline phase. The lattice spacing, a, may be taken to be the diameter of the host lipids. The diffusion of the probe molecule is restricted to the lattice points. Hence, the monolayer diffusion of the lipid probes is described as a simple random walk on one lattice only, whereas the translational motion of the probes spanning both layers is modelled as a coupled random walk on the two parallel lattices. The latter model bears some resemblance to multistate random walk models which have been used, for instance, to describe the motion of atomic clusters on surfaces (see Weiss 1983 and references therein). However, whereas these models were formulated as continous time random walks, we describe the diffusive process in a simpler way by a master equation (see e.g. Haken 1977, chap. 4). This description corresponds to a continous time random walk with a single exponential waiting time distribution (see Weiss 1983, chap. II.A.3).

Before presenting the 2-dimensional model and its solution in Sect. 3 we will first investigate, in Sect. 2, the monolayer and bilayer diffusion processes in one

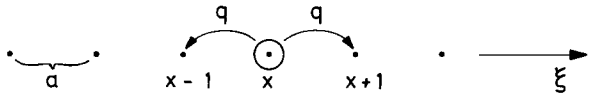

Fig. 1. Free diffusion in a 1-dimensional monolayer; q is the probability that the probe molecule at lattice site x jumps to $x-1$ or to $x+1$ within the time r

dimension, since the 1-dimensional problem furnishes a simple introduction to the theory and its assumptions. Section 4 discusses the results and the microscopic mechanisms which have to be invoked by our model to account for the observed D_2/D_1 ratio.

Diffusion models in one dimension

Monolayer diffusion

To introduce our treatment of lipid probe diffusion in a lipid membrane we first describe the case of 1-dimensional monolayer diffusion. In this case the diffusion is modelled as a random walk on a lattice with positions $\xi = ax$, $x = 0, \pm 1, \pm 2, \ldots$ (see Fig. 1). Our picture of the physical events which cause microscopic diffusive displacements is that these displacements are preceded by the appearance of a free volume proximate to the probe. Let r be the average time within which such a free volume, generated by random density fluctuations in the host lipid matrix, appears at a lattice site in the neighbourhood of the probe. The probability that the free volume appears at a particular site in the immediate neighbourhood of the probe is then $1/z$, where z is the number of nearest neighbour lattice points.[1] In the 1-dimensional case considered here the coordination number z is 2, of course. The free volume may then be occupied either by the probe or by one of the host lipids next to the free volume. If the probability of either event is the same, i.e. again $1/z$, one obtains for the total probability, q, that the probe is displaced within the time, r, to a particular neighbouring lattice point

$$q = \frac{1}{z^2} \tag{1}$$

and the rate constant for a diffuse displacement to a neighbouring lattice site is q/r. If we exclude memory effects, i.e. if we assume that the free volume left behind the displaced probe molecule at its original position is immediately filled up by the host lipids and that the probe has to wait at its new position, again an average time r, for the appearance of a random free volume at a neighbouring site, then we can describe the probe diffusion by a master equation. Denoting the probability of finding the probe at time t, at the position $\xi = ax$, by $p(x,t)$ this rate equation assumes, for the process depicted in Fig. 1, the form

$$r\frac{\partial}{\partial t}p(x,t) = q[p(x-1,t) - 2p(x,t) + p(x+1,t)] . \tag{2}$$

The diffusion constant is measured by the long time behaviour of the mean square displacement of a probe starting at $\xi = 0$ and, according to continuum diffusion theory in d dimensions, is defined as

$$D = \frac{1}{2d}\lim_{t\to\infty}\frac{d}{dt}\langle\xi^2(t)\rangle . \tag{3}$$

Although the evaluation of D from Eq. (2) is trivial we include it as an illustration of the mathematical method:

$$\begin{aligned}\frac{d}{dt}\langle\xi^2(t)\rangle &= \sum_x a^2x^2\frac{\partial}{\partial t}p(x,t)\\ &= \frac{a^2q}{r}\sum_x x^2[p(x-1,t) - 2p(x,t)\\ &\quad + p(x+1,t)]\\ &= \frac{a^2q}{r}\sum_x [(x+1)^2 - 2x^2\\ &\quad + (x-1)^2]p(x,t)\\ &= 2\frac{a^2q}{r}\sum_x p(x,t) .\end{aligned} \tag{4}$$

Since the conservation of probability holds, i.e.

$$\sum_x p(x,t) = 1 , \tag{5}$$

Equation (4) identifies the single layer diffusion constant to be ($z = 2$, $d = 1$):

$$D_1 = \frac{z}{2d}\frac{a^2q}{r} . \tag{6}$$

Bilayer diffusion

For the description of the diffusive motion of a probe molecule which has two polar head groups, one at each end of the hydrocarbon chain, and extends across

1 In general r may depend on z. However, such a dependence is immaterial since we will consider only the ratio of diffusion coefficients D_2/D_1, which is independent of r

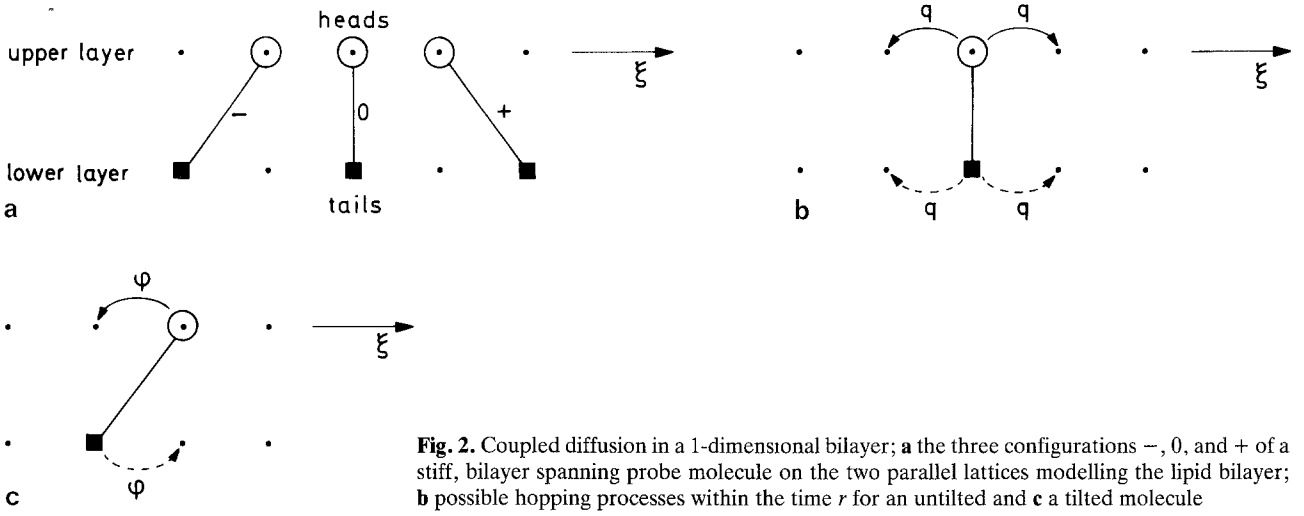

Fig. 2. Coupled diffusion in a 1-dimensional bilayer; **a** the three configurations −, 0, and + of a stiff, bilayer spanning probe molecule on the two parallel lattices modelling the lipid bilayer; **b** possible hopping processes within the time r for an untilted and **c** a tilted molecule

both layers of the membrane, we call one of these groups the "head" and the other the "tail" of the probe and the corresponding layers of the membrane the "upper layer" and the "lower layer". To simulate a certain degree of "stiffness" in the probe we assume that it can only exist in three possible configurations: the tail may be either directly below the head or in two tilted positions, i.e. either one lattice spacing to the left or one to the right (cf. Fig. 2a). We denote these configurations with the indices 0, − and +. Head and tail displacements of the probe are assumed to be statistically independent processes and are assumed to be produced by the same stochastic free volume mechanism as in the case of single layer diffusion. Thus, on the *average,* one free volume appears within the time, r, in each layer proximate to the head *and* to the tail. Statistical independence of the density fluctuations in the two layers requires that head – head, tail – head, head – tail and tail – tail consecutive displacements within r are equally probable. Then the probability is $1/z$ that a free volume appearing in the upper (lower) layer is created at a particular lattice site proximate to the head (tail). The probability that the head (tail) of a probe molecule in the upright configuration, 0, hops into this free volume is taken to be $1/z$, which amounts to the assumption that the free volume becomes occupied with equal probabilities either by the head (tail) of the probe or by one of the surrounding host lipids. Hence the rate at which a probe in the upright configuration, 0, jumps into a tilted configuration by head *or* tail displacement is q/r, where q is the single layer hopping probability given by Eq. (1) (see Fig. 2b). For tilted probes, we also assume that free volumes arrive at either side of the probes head and tail at the rate $1/r$. Denoting by φ/r the rate of displacement which untilts the probe (see Fig. 2c) and by a the probability that a tilted probe uses a particular neighbouring free volume for untilting we have:

$$\varphi = \frac{a}{z} . \tag{7a}$$

In this definition of the untilting probability, φ, we have assumed that the processes of free volume generation at a particular site and of untilting the probe are statistically independent such that φ is the product of the corresponding probabilities $1/z$ and a.[2] The untilting rate φ/r is assumed to be larger than the tilting rate q/r, i.e.

$$a \geq \frac{1}{z} . \tag{7b}$$

The parameter a describes a tendency of the probe to regain its untilted form by winning the competition for the appropriate free volume against the host lipids. Consequently, a can be considered as a measure of a force restoring the upright configuration. If one denotes the probability of finding the head of the probe in configuration i at time t at position $\xi = ax$ by $p_i(x, t)$, where i characterizes the configurations 0, + or −, one can derive the master equations for coupled bilayer diffusion:

$$\begin{aligned} r\frac{\partial}{\partial t} p_0(x) &= -4qp_0(x) + \varphi[p_+(x) + p_+(x-1) \\ &\quad + p_-(x) + p_-(x+1)] \\ r\frac{\partial}{\partial t} p_\pm(x) &= -2\varphi p_\pm(x) + q[p_0(x) + p_0(x \pm 1)] , \end{aligned} \tag{8}$$

2 If this condition of statistical independence is not fulfilled then Eq. (7a) represents only a formal separation of a factor $1/z$ from the untilting rate φ/r and a cannot be considered a probability anymore

where we have dropped the explicit time dependence of the probability distributions for notational convenience. Owing to the equivalence of the two layers, one obtains for a molecule starting at $\xi = 0$ in configuration 0 the symmetry relation

$$p_-(x+1) = p_+(x) \,. \tag{9}$$

Using Eqs. (8) and (9) we can calculate the time derivative of the mean square displacement

$$\frac{d}{dt}\langle \xi^2(t)\rangle = \sum_x a^2 x^2 \frac{\partial}{\partial t}\left[p_-(x) + p_0(x) + p_+(x)\right] \tag{10}$$

of the heads quite analogously to the calculation in Eq. (4) and find:

$$\frac{d}{dt}\langle \xi^2(t)\rangle = 2\frac{a^2 q}{r}\sum_x p_0(x) \,. \tag{11}$$

Denoting by p_i the probability that the probe at time t is in configuration i

$$p_i = \sum_x p_i(x) \,, \quad i = -, 0, + \tag{12}$$

we obtain from Eq. (8), by summation over all points x of the lattice, a relaxation equation for these probabilities:

$$r\frac{\partial}{\partial t}p_0 = -4qp_0 + 2\varphi(p_+ + p_-)$$

$$r\frac{\partial}{\partial t}p_\pm = -2\varphi p_\pm + 2qp_0 \,. \tag{13}$$

A simple analysis of Eq. (13) shows that the probabilities, p_i, relax on a time scale of the order of r to the equilibrium values. Denoting these stationary solutions of Eq. (13) by $\bar{p}_i$ and using Eq. (9) gives for the long time behaviour of Eq. (11):

$$\lim_{t\to\infty}\frac{d}{dt}\langle \xi^2(t)\rangle = 2D_1\bar{p}_0 \,. \tag{14}$$

Evaluation of $\bar{p}_0$ from Eq. (13) finally yields the ratio of the diffusion constants in terms of the rates

$$\frac{D_2}{D_1} = \left(1 + \frac{2q}{\varphi}\right)^{-1} \tag{15a}$$

or with Eqs. (1) and (7) in terms of the coordination number $z = 2$ and of the parameter α measuring the restoring force:

$$\frac{D_2}{D_1} = \left(1 + \frac{1}{\alpha}\right)^{-1} \tag{15b}$$

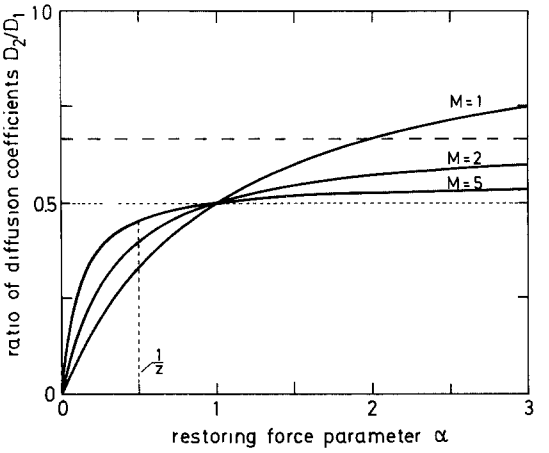

Fig. 3. Results of 1-dimensional model calculations on the ratio D_2/D_1 as a function of the variable, a, which measures the force restoring the untilted configuration; the curves are labeled by the stiffness parameter, M, which determines the number $2M + 1$ of allowed configurations (for discussion, see text)

Figure 3 shows a plot of Eq. (15b) (this is the curve labelled by the parameter $M = 1$; see below). The curve demonstrates the main aspects of our model: A lipid probe extending across the whole bilayer has a reduced diffusion constant. The reduction depends on the force, α, restoring the untilted configuration. The reduction decreases as α increases and reaches the observed value of 2/3 for $\alpha = 2$. In terms of our original interpretation of α as a probability, a value of $\alpha > 1$ seems to be unreasonable. However, if the assumption that the generation of free volumes and the untilting of the probe are statistically independent processes is dropped, α can assume values larger than 1 (see above). For instance, the value $\alpha = 2$ implies that a tilted probe is certain to use all free volumes appearing in its neighbourhood for regaining its upright configuration even if the free volume appears at the wrong proximate lattice site. Thus, the result suggests that a tilted probe molecule, in order to untilt itself, generates a free volume at the proper place by pushing neighbouring host molecules away. For such a process the existence of a second dimension is a prerequisite and so we cannot account for it properly in this simple 1-dimensional model.

There are, however, a couple of further conclusions which can be drawn from considerations in one dimension. The three configuration model for a *stiff* probe discussed above allows a straightforward generalization to an $2M + 1$ configuration model for a rather *flexible* probe molecule. Here the configurations i ($i = 0, \pm 1, \ldots, \pm M$) are characterized by a shift of the tail compared with the head by i lattice sites. Assuming the hopping rates for head and to be q/r in all configurations $|i| \leq M - 1$ and to be φ/r for the transitions $M \to M - 1$ and $-M \to -M + 1$ one finds

$$\frac{D_2}{D_1} = \frac{M}{2M - 1 + \dfrac{1}{\alpha}} \tag{16}$$

which tends to 1/2 for large M, independently of α. Only for very stiff probe molecules ($M = 1$) is the observed experimental ratio, $D_2/D_1 = 2/3$, reached at finite values of α (see Fig. 3). Therefore, for very flexible lipid probes extending through both layers the predicted diffusion is much slower than that observed.

Diffusion in 2-dimensional bilayers

For the description of the 2-dimensional diffusion of a lipid probe in a lipid membrane we have chosen a hexagonal lattice as shown in Fig. 4a. As in the 1-dimensional case the displacement of a probe molecule moving in only one of the two layers is considered to be affected by the random appearance of a free volume in the matrix of the host lipids within an average time r at one of the $z = 6$ neighbouring lattice sites. The calculation of the diffusion constant, D_1, follows exactly the same lines as the treatment presented in Eqs. (1)–(6) of the 1-dimensional case and yields the same result. Thus, D_1, is given by Eq. (6) with $z = 6$ and $d = 2$; furthermore a is the lattice constant of the hexagonal lattice and q/r the rate at which the probe is displaced to a neighbouring lattice site.

A stiff probe molecule spanning both layers of the host membrane is considered to exhibit seven possible configurations in the two parallel lattices representing the lipid bilayer: an untilted configuration denoted by 0 and six tilted configurations in which the tail is shifted by one lattice spacing in the directions $\pm\xi$, $\pm\eta$, $\pm\xi\eta$, as shown in Fig. 4b. The corresponding configurations will be labeled by the indices i:

$$i \in I_0 = \{0, \pm x, \pm y, \pm xy\} . \tag{17}$$

The rates q/r and φ/r for the tilting and untilting processes, respectively, are chosen as in the 1-dimensional problem (compare Figs. 2b and 2c). As an additional process we assume that a tilted molecule can rotate at a rate $\tilde{q}/r$ around its head if a free volume is generated at an appropriate position next to the tail and vice versa (see Fig. 4c). Denoting the probability of finding the head of a probe molecule in configuration i at position $(\xi, \eta) = (ax, ay)$, $x, y = 0, \pm 1, \pm 2, \ldots$, at time t by $p_i(x, y)$ the master equation for bilayer diffusion assumes the form:

$$\begin{aligned} r\frac{\partial}{\partial t} p_0(x, y) = &-12q p_0(x, y) + \varphi[p_x(x, y) \\ &+ p_x(x - 1, y) + p_{-x}(x, y) \\ &+ p_{-x}(x + 1, y) + p_y(x, y) \\ &+ p_y(x, y - 1) + p_{-y}(x, y) \\ &+ p_{-y}(x, y + 1) + p_{xy}(x, y) \\ &+ p_{xy}(x - 1, y - 1) + p_{-xy}(x, y) \\ &+ p_{-xy}(x + 1, y + 1)] \end{aligned}$$

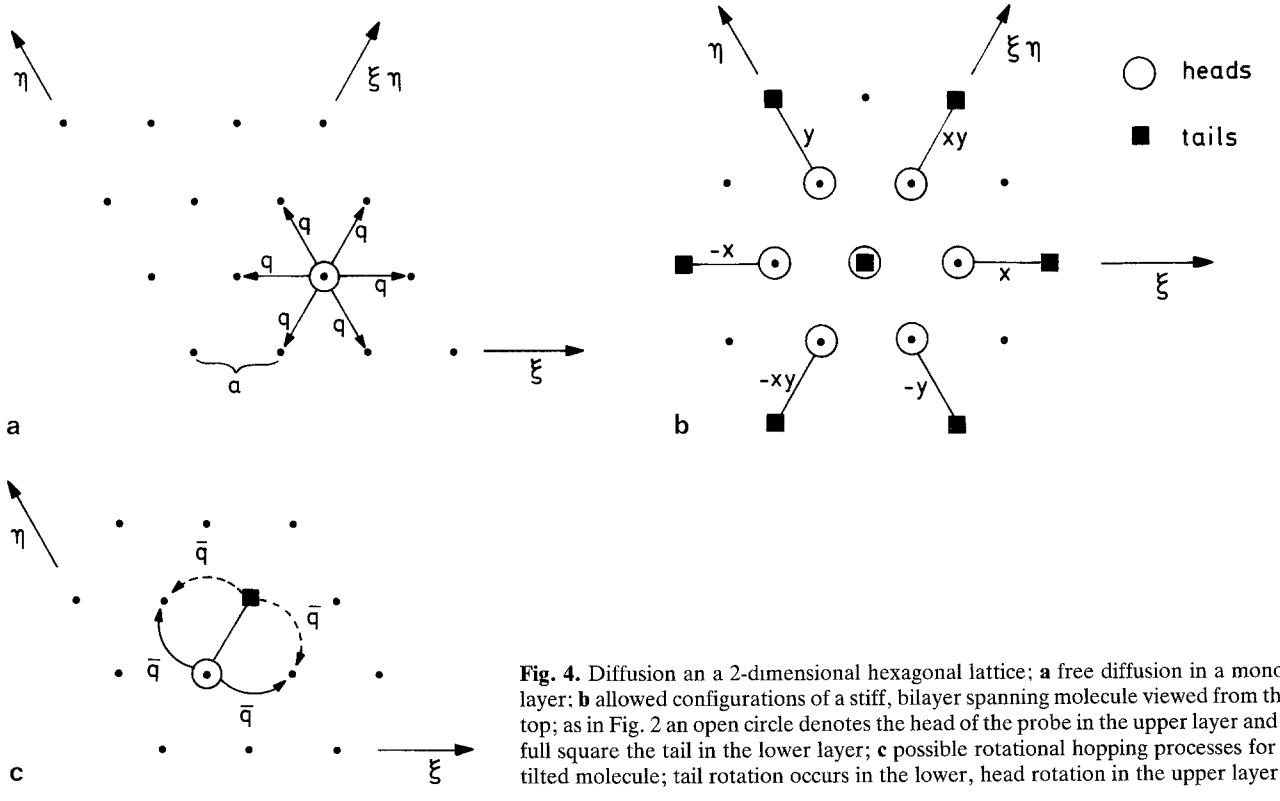

Fig. 4. Diffusion an a 2-dimensional hexagonal lattice; **a** free diffusion in a monolayer; **b** allowed configurations of a stiff, bilayer spanning molecule viewed from the top; as in Fig. 2 an open circle denotes the head of the probe in the upper layer and a full square the tail in the lower layer; **c** possible rotational hopping processes for a tilted molecule; tail rotation occurs in the lower, head rotation in the upper layer

$$r\frac{\partial}{\partial t}p_{\pm x}(x,y) = -2\varphi p_{\pm x}(x,y) + q[p_0(x,y) + p_0(x\pm 1,y)] - 4\bar{q}p_{\pm x}(x,y) + \bar{q}[p_{\mp y}(x,y) + p_{\mp y}(x\pm 1, y\pm 1) + p_{\pm xy}(x,y) + p_{\pm xy}(x, y\mp 1)]$$

$$r\frac{\partial}{\partial t}p_{\pm y}(x,y) = -2\varphi p_{\pm y}(x,y) + q[p_0(x,y) + p_0(x, y\pm 1)] - 4\bar{q}p_{\pm y}(x,y) + \bar{q}[p_{\mp x}(x,y) + p_{\mp x}(x\pm 1, y\pm 1) + p_{\pm xy}(x,y) + p_{\pm xy}(x\mp 1, y)]$$

$$r\frac{\partial}{\partial t}p_{\pm xy}(x,y) = -2\varphi p_{\pm xy}(x,y) + q[p_0(x,y) + p_0(x\pm 1, y\pm 1)] - 4\bar{q}p_{\pm xy}(x,y) + \bar{q}[p_{\pm x}(x,y) + p_{\pm x}(x, y\pm 1) + p_{\pm y}(x,y) + p_{\pm y}(x\pm 1, y)] \quad (18)$$

Since the upper and the lower layer are equivalent, analogously to Eq. (9) for a probe molecule starting at $\boldsymbol{r} = (\xi, \eta) = (0, 0)$ in the upright configuration, the following symmetry relations hold:

$$\begin{aligned} p_{-x}(x+1,y) &= p_x(x,y) \\ p_{-y}(x,y+1) &= p_y(x,y) \\ p_{-xy}(x+1,y+1) &= p_{xy}(x,y)\,. \end{aligned} \quad (19)$$

Using Eq. (19), the time derivative of the mean square displacement

$$\frac{d}{dt}\langle \boldsymbol{r}^2(t)\rangle = a^2 \sum_{x,y}(x^2+y^2-xy)\sum_{i\in I_0}\frac{\partial}{\partial t}p_i(x,y) \quad (20)$$

can be evaluated in a straightforward calculation. One obtains:

$$\frac{d}{dt}\langle \boldsymbol{r}^2(t)\rangle = 2dD_1\left(p_0 + \frac{\bar{q}}{zq}\sum_{i\in I} p_i\right), \quad (21)$$

Where I is the set (Eq. (17)) of configurations excluding the upright configuration 0 and p_i is the probability that the probe is in configuration i at time t:

$$p_i = \sum_{x,y} p_i(x,y)\,, \qquad i \in I_0\,. \quad (22)$$

As in the 1-dimensional case a relaxation equation follows from Eqs. (18) and (22) for the p_i:

$$r\frac{\partial}{\partial t}p_0 = -12qp_0 + 2\varphi\sum_{i\in I} p_i$$

$$r\frac{\partial}{\partial t}p_{\pm x} = -(2\varphi + 4\bar{q})p_{\pm x} + 2qp_0 + 2\bar{q}(p_{\mp y} + p_{\pm xy})$$

$$r\frac{\partial}{\partial t}p_{\pm y} = -(2\varphi + 4\bar{q})p_{\pm y} + 2qp_0 + 2\bar{q}(p_{\mp x} + p_{\pm xy})$$

$$r\frac{\partial}{\partial t}p_{\pm xy} = -(2\varphi + 4\bar{q})p_{\pm xy} + 2qp_0 + 2\bar{q}(p_{\pm x} + p_{\pm y}) \quad (23)$$

Denoting the stationary solutions of Eq. (23) by $\bar{p}_i$, the long time behaviour of Eq. (21) results in:

$$\lim_{t\to\infty}\frac{d}{dt}\langle \boldsymbol{r}^2(t)\rangle = 2dD_1\left(\bar{p}_0 + \frac{\bar{q}}{zq}\sum_{i\in I}\bar{p}_i\right). \quad (24)$$

Evaluation of the equilibrium probabilities $\bar{p}_i$ from Eq. (23) and use of Eq. (3) yields the final result:

$$\frac{D_2}{D_1} = \frac{1 + (\bar{q}/\varphi)}{1 + (zq/\varphi)}\,. \quad (25)$$

We would like to note that a treatment of our model on a square lattice ($z = 4$) yields the identical result. In addition, a comparison with Eq. (15a) reveals that Eq. (25) reduces to the one dimensional result ($z = 2$) if the rotation rate $\bar{q}/r$ is set to zero. Consequently, it is seen that the additional degree of freedom created by rotations of tilted probes speeds up the diffusive motion.

Discussion

If one assumes for the rotation rate, $\bar{q}/r$, of the tilted lipid probes extending through the whole membrane the same microscopic free diffusion mechanism as for the tilting displacements ($\bar{q} = q$) then using Eqs. (1) and (7) the ratio D_2/D_1 given in Eq. (25) can be

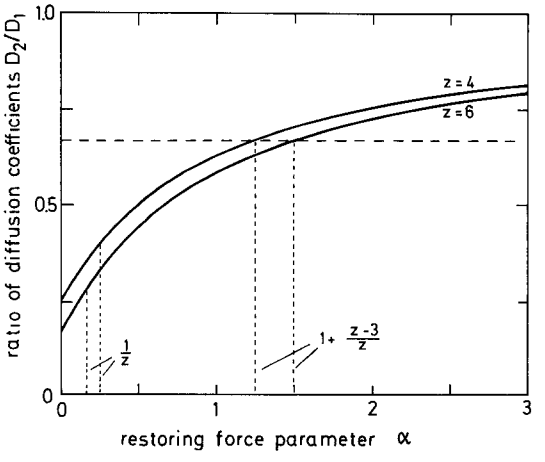

Fig. 5. The ratio D_2/D_1 for 2-dimensional diffusion on a square ($z = 4$) and on a hexagonal ($z = 6$) lattice as a function of the restoring force parameter, α; also indicated are the values of α at which there is no restoring force ($\alpha = 1/z$) and at which D_2/D_1 reaches the experimental value [$\alpha = 1 + (z-3)/z$] (for discussion, see text)

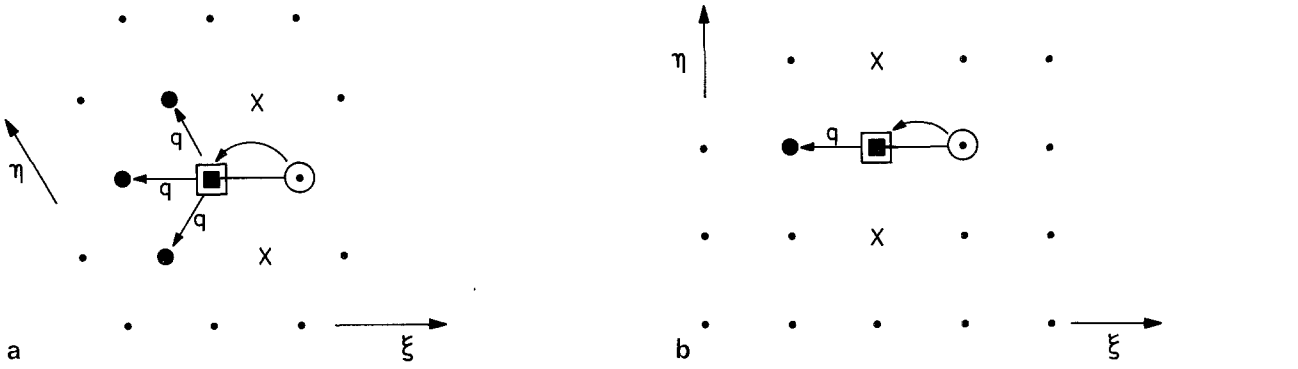

Fig. 6. Creation of free volumes (denoted by open squares) for untilting in the upper layer of **a** a hexagonal and **b** a square lattice; it is assumed that the head can force a host lipid molecule to jump with the monolayer diffusive hopping rate q/r ($q = z^{-2}$) into one of the free volumes appearing at the $z - 3$ next nearest neighbour positions (indicated by full circles) and can use the created free volume to untilt immediately; the nearest neighbour positions accesible for head rotations (denoted by the crosses) have been excluded from this process for consistency

rewritten in terms of the coordination number, z, and the untilting parameter, α, as

$$\frac{D_2}{D_1} = \frac{1 + (1/z\alpha)}{1 + (1/\alpha)} . \tag{26}$$

Figure 5 shows the graphs of the D_2/D_1 ratio for the square and the hexagonal lattice as a function of the variable α. In terms of microscopic events, α has been defined as the probability that a tilted probe uses a particular free volume to regain its upright configuration if such a vacancy has appeared at the proper position. According to this interpretation the value of α is $1/z$ if there is no preference for the untilting process as compared to the process of tilting. The respective D_2/D_1 ratios

$$\frac{D_2}{D_1} = \begin{cases} 2/5 = 0.40 , & z = 4 \\ 2/7 \approx 0.29 , & z = 6 \end{cases} \tag{27}$$

are much smaller than the observed value of 2/3, indicating that there must be a preference for the untilting process. The value of α is 1 if a tilted molecule is certain to win the competition for the free volume against the surrounding molecules of the host lipid matrix. However, the corresponding ratios

$$\frac{D_2}{D_1} = \begin{cases} 5/8 \approx 0.63 , & z = 4 \\ 7/12 \approx 0.58 , & z = 6 \end{cases} \tag{28}$$

are still slightly too small to explain the experimental result. To obtain larger D_2/D_1 ratios one must assume, in addition, that a tilted molecule, by exerting a force on the host lipid molecules, can create a free volume at the proper place. If, for instance, random free volumes appearing within r at the $z - 3$ positions, which are indicated in Fig. 6 and are not accessible by rotations of the probe, are used by host molecules with the free hopping probability $1/z$ to give room for the untilting of the probe, i.e.

$$\alpha = 1 + \frac{z - 3}{z} , \tag{29}$$

then one obtains, for both lattice, the experimental value

$$\frac{D_2}{D_1} = \frac{2}{3} , \quad z = 4, 6 . \tag{30}$$

In view of the result of the 1-dimensional $2M + 1$ state model for very flexible probes stating that the D_2/D_1 ratio decreases with increasing flexibility one may summarize now that the large observed D_2/D_1 ratio should be due to a force which restores "stiff" probe molecules to their upright configuration.

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