Phospholipids undergo hop diffusion in compartmentalized cell membrane

Takahiro Fujiwara,1 Ken Ritchie,1,2 Hideji Murakoshi,2 Ken Jacobson,3 and Akihiro Kusumi1,2

1Kusumi Membrane Organizer Project, Exploratory Research for Advanced Technology Organization (ERATO), Japan Science and Technology Corporation, Nagoya 460-0012, Japan
2Department of Biological Science, Nagoya University, Nagoya 464-8602, Japan
3Department of Cell and Developmental Biology and Lineberger Comprehensive Cancer Center, University of North Carolina, Chapel Hill, NC 27599

The diffusion rate of lipids in the cell membrane is reduced by a factor of 5–100 from that in artificial bilayers. This slowing mechanism has puzzled cell biologists for the last 25 yr. Here we address this issue by studying the movement of unsaturated phospholipids in rat kidney fibroblasts at the single molecule level at the temporal resolution of 25 μs. The cell membrane was found to be compartmentalized: phospholipids are confined within 230-nm-diameter (θ) compartments for 11 ms on average before hopping to adjacent compartments. These 230-nm compartments exist within greater 750-nm-θ compartments where these phospholipids are confined for 0.33 s on average. The diffusion rate within 230-nm compartments is 5.4 μm²/s, which is nearly as fast as that in large unilamellar vesicles, indicating that the diffusion in the cell membrane is reduced not because diffusion per se is slow, but because the cell membrane is compartmentalized with regard to lateral diffusion of phospholipids. Such compartmentalization depends on the actin-based membrane skeleton, but not on the extracellular matrix, extracellular domains of membrane proteins, or cholesterol-enriched rafts. We propose that various transmembrane proteins anchored to the actin-based membrane skeleton meshwork act as rows of pickets that temporarily confine phospholipids.

Introduction

For the past 25 yr, one of the most serious puzzles in the research of membrane dynamics is how the diffusion rate of lipids in the cell membrane is reduced by a factor of 5–100 from that in artificial bilayers (Swaisgood and Schindler, 1989; Lee et al., 1993; Ladha et al., 1996; Sonnleitner et al., 1999). Long-range interactions between lipids and immobilized proteins (Sperotto and Mouritsen, 1991; Almeida et al., 1992; Bussell et al., 1995; Dodd et al., 1995) or interactions with the extracellular matrix (Wier and Edidin, 1986; Lee et al., 1993) may be responsible for such a reduction of lipid diffusion rates. Alternatively, cholesterol-enriched lipid microdomains called "rafts" (for reviews see Simons and Toomre, 2000; Edidin, 2001) may be involved in such a slowing mechanism by inducing partitioning of raft lipids into raft domains or by becoming diffusion obstacles for nonraft lipids.

To address the problem of slowed lipid diffusion and to acquire a better general understanding of the dynamic lipid organization in the cell membrane, we observed the movement of phospholipids at the single molecule level at a very high time resolution (up to 25 μs), which turned out to be absolutely necessary to elucidate such a slowing mechanism. As a test molecule, we used 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (DOPE),* which is a typical nonraft lipid. Such an unsaturated phospholipid is thought to be most difficult to have its diffusion rate reduced in the cell membrane. DOPE diffusion as observed at 25-μs resolution revealed that the cell membrane is compartmentalized with regard to translational diffusion of DOPE. A DOPE molecule is confined within a 230-nm compartment for 11 ms on average before hopping to an adjacent compartment, and by repeating such temporary confinement and intercompartmental hopping, it undergoes macroscopic diffusion over many

*Abbreviations used in this paper: θ, diameter; D_macro, macroscopic diffusion coefficient; D_micro, microscopic diffusion coefficient; DOPE, 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine; LUV, large unilamellar vesicle; MSD, mean square displacement; NRK, normal rat kidney fibroblastic cell; SPT, single particle tracking; TIR, transferrin receptor.
compartments. The DOPE diffusion rate within a 230-nm compartment is 5.4 \( \mu \text{m}^2/\text{s} \), which is nearly as fast as that in large unilamellar vesicles, suggesting that DOPE undergoes free diffusion within 230-nm compartments. In contrast, macroscopic diffusion of DOPE over many compartments is much slower, indicating that the diffusion in the cell membrane is reduced not because diffusion per se is slow in the cell membrane, but because the cell membrane is compartmentalized with regard to the lateral diffusion of phospholipids.

We then investigated how such compartmentalization occurs. The results were quite unexpected: such compartmentalization does not depend on the extracellular matrix, extracellular domains of membrane proteins, or rafts, but on the actin-based membrane skeleton, which is located on the cytoplasmic surface of the cell membrane. It is concluded that the various transmembrane proteins anchored to the actin membrane skeleton meshwork act as rows of pickets due to the effects of both steric hindrance and the circumferential slowing. Circumferential slowing is caused by the increased hydrodynamic friction (in terms of the hydrodynamic theory) (Bussell et al., 1995; Dodd et al., 1995) or by the increased hydrodynamic friction (in terms of the hydrodynamic theory) (Butt, 1995; Dodd et al., 1995). These anchored-protein pickets temporarily confine phospholipids. Such compartmentalization may be necessary for localization of intracellular signals at the point where the extracellular signal has been received.

**Results**

**Both single fluorophore video imaging and single particle tracking of DOPE molecules in a 100-ms time window showed the same diffusion rate of \( \sim 0.5 \mu \text{m}^2/\text{s} \), which is smaller by a factor of \( \sim 20 \) than that in artificial bilayers**

DOPE was tagged with Cy3 in the head group region and was incorporated into the cell membrane of normal rat kidney (NRK) fibroblastic cells, and these Cy3–DOPE molecules were observed individually under an objective lens-type total internal reflection fluorescence microscope at 37°C at the video rate (33-ms resolution; Fig. 1 A; Video 1 available at http://www.jcb.org/cgi/content/full/jcb.200202050/DC1). The diffusion coefficients in a 100-ms time window (obtained for a period of 100 ms; \( D_{100\text{ms}} \)) and in a 3-s time window (\( D_{3\text{s}} \); Fig. 1 B) were 0.41 and 0.42 \( \mu \text{m}^2/\text{s} \) on average, respectively. The predominant freely diffusing behavior of Cy3–DOPE molecules in this time scale is consistent with the single dye tracing results of Cy5–DOPE by Schütz et al. (2000). These values, however, were found to be smaller by a factor of \( \sim 20 \) than those in artificial bilayers (Table I). Such slowing of diffusion suggests the presence of mechanisms for hampering the lipid movement in the cell membrane, mechanisms that cannot be resolved at the video rate.

Because achieving higher time resolutions in single fluorophore observations is difficult due to the problem of low signal-to-noise ratios, we employed a single particle tracking (SPT) technique of binding a 40-nm-diameter (d) colloidal gold particle to a DOPE molecule in the cell membrane (Video 1). SPT provides higher signal intensities that allow high-speed observations, whereas single fluorophore video imaging of Cy3–DOPE has the advantage that a single fluorescent spot represents a single molecule. The movement of DOPE–gold complexes was examined by contrast-enhanced optical microscopy at 37°C recorded by a high-speed video camera with a temporal resolution of 25 µs (a spatial precision of 17 nm at this recording rate). Labeling conditions were optimized by adjusting the concentration of fluorescein–DOPE incubated with the cells and the amount of Fab fragments conjugated with the gold particles, so that the effect of cross-linking by gold particles was minimized while sufficient specificity in binding of the gold particles was maintained.

\( D_{3\text{s}} \) (3-s time window) observed was 0.17 \( \mu \text{m}^2/\text{s} \), which was smaller by a factor of 2.5 than that of single Cy3–DOPE molecules (0.42 \( \mu \text{m}^2/\text{s} \)), suggesting a moderate steric or cross-linking effect of gold particles on long-range diffusion. However, \( D_{100\text{ms}} \) (100-ms time window) under this condition was 0.49 \( \mu \text{m}^2/\text{s} \). This value agrees with that of Cy3–DOPE (0.41 \( \mu \text{m}^2/\text{s} \)), indicating that the labeling with colloidal gold did not affect the movement of DOPE in shorter time windows,
warranting the use of single gold particle tracking to study DOPE movement in a time window of <100 ms.

**Phospholipids undergo hop diffusion**

Fig. 2 A shows two representative trajectories of DOPE at a time resolution of 25 µs obtained for a period of 56 ms. Statistical classification of such trajectories based on the mean square displacement plotted against time (MSD–t plot) was performed for each trajectory (Kusumi et al., 1993). As shown in Table I, 85% of DOPE molecules were found to undergo hop or confined-type diffusion. They were further analyzed based on the theory developed by Powles et al. (1992), which provided hop parameters, compartment size (L), residency time within a compartment, the microscopic

![Image](https://example.com/image.png)

**Table I. Parameters that characterize hop diffusion of DOPE at 25-µs and 2-ms time resolutions**

<table>
<thead>
<tr>
<th>Time resolution</th>
<th>Motional mode</th>
<th>Confinement size (median)</th>
<th>Dmicro</th>
<th>DMACRO</th>
<th>Residency time</th>
<th>N°</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Hop + confined</td>
<td>Diameter</td>
<td>Area</td>
<td>µm²/s</td>
<td>µm²/s</td>
<td>ms</td>
</tr>
<tr>
<td>Cell membrane</td>
<td></td>
<td>%</td>
<td>nm</td>
<td>µm²</td>
<td>4/5</td>
<td>0.99</td>
</tr>
<tr>
<td>25 µs</td>
<td>85</td>
<td>230</td>
<td>0.043</td>
<td>5.4</td>
<td>0.99</td>
<td>11</td>
</tr>
<tr>
<td>2 ms</td>
<td>94</td>
<td>750</td>
<td>0.44</td>
<td>0.16</td>
<td>0.17</td>
<td>650</td>
</tr>
<tr>
<td>LUV</td>
<td></td>
<td>6</td>
<td>NA</td>
<td>NA</td>
<td>9.4</td>
<td>9.5</td>
</tr>
<tr>
<td>25 µs</td>
<td>44</td>
<td>NA</td>
<td>NA</td>
<td>8.8</td>
<td>7.4</td>
<td>NA</td>
</tr>
<tr>
<td>Membrane bleb</td>
<td></td>
<td>10</td>
<td>NA</td>
<td>NA</td>
<td>8.9</td>
<td>9.9</td>
</tr>
<tr>
<td>25 µs</td>
<td>94</td>
<td>260</td>
<td>0.054</td>
<td>5.2</td>
<td>0.31</td>
<td>55</td>
</tr>
<tr>
<td>Membrane bleb + latrunculin-A</td>
<td>85</td>
<td>710</td>
<td>0.4</td>
<td>0.210</td>
<td>0.070</td>
<td>1,800</td>
</tr>
<tr>
<td>Transferrin receptor</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>25 µs</td>
<td>94</td>
<td>260</td>
<td>0.054</td>
<td>5.2</td>
<td>0.31</td>
<td>55</td>
</tr>
<tr>
<td>33 ms</td>
<td>83</td>
<td>710</td>
<td>0.4</td>
<td>0.210</td>
<td>0.070</td>
<td>1,800</td>
</tr>
</tbody>
</table>

Quantitative analysis is based on the method described previously (Powles et al., 1992; Kusumi et al., 1993; Sako and Kusumi, 1994; Tomishige et al., 1998). The diameter (L) of a compartment was determined as \( L = (\pi/4) L_x L_y \) (area of an ellipse whose major and minor axes are \( L_x \) and \( L_y \), respectively). \( D_{\text{micro}} \) represents 100-ms and 20-ms scale diffusion rates (mean), whereas \( D_{\text{MACRO}} \) represents 50-ms (33 ms for LUV and membrane bleb) and 5-s scale diffusion rates (mean) for 25-ms and 2-ms time resolutions, respectively. The mean residency time within each compartment was determined as \( A/4D_{\text{MACRO}} \).

Not applicable or the actual number of particles observed is too small to be statistically significant. In the case of “membrane bleb,” the variations are too large to obtain meaningful mean or median values.

Directions and in a two-dimensional plane, respectively. (C) A typical trajectory of a DOPE molecule in an LUV bilayer, consisting of egg phosphatidylcholine/bovine brain phosphatidylserine/fluorescein–DOPE in a ratio of 500:50:1 by weight, recorded at a time resolution of 25 µs for a period of 33 ms (1,350 frames). A statistical analysis classified this trajectory into a simple Brownian mode. By way of comparison, fake compartments were assigned and indicated by different colors, based on visual examination. The prominent difference in appearance of the trajectories between A and C is that, in the case of real hop diffusion, adjacent compartments tend to be closely apposed and the trajectories are denser within a given compartment (Video 3).
diffusion coefficient within a compartment ($D_{micro}$), and the macroscopic diffusion coefficient over many compartments ($D_{MACRO}$) as listed in Table I. The MSD–t plot for the trajectory on the right in Fig. 2 A and its fit to a theoretical curve for hop-type diffusion (Powles et al., 1992) are shown in Fig. 2 B. Such statistical and quantitative analyses found that the trajectories shown in Fig. 2 A consist of six (left) and four (right) apposing compartments. Individual plausible compartments were identified by software (as well as visual examination) developed to identify these confining compartments and are color coded in Fig. 2 A. Fig. 3 A shows the distribution of the confinement size. Its median value was 230 nm (Table I). The mean residency time within each 230-nm compartment was 11 ms (Table I; Fig. 3 B). Namely, DOPE molecules diffuse rapidly, but are confined within ~230-nm compartments before hopping to adjacent compartments, such hopping occurring once an average of every ~11 ms. In this manner, DOPE undergoes long-range diffusion, a process we call “hop diffusion” (Kusumi et al., 1993; Sako and Kusumi, 1994; Kusumi and Sako, 1996; Tomishige et al., 1998; Tomishige and Kusumi, 1999; Video 2).

As a control, movement of DOPE molecules in the bilayers of large unilamellar vesicles (LUVs) was observed (Fig. 2 C; Video 3). Almost all (94%) the trajectories in LUVs were categorized into the simple Brownian mode. $D_{100\mu s}$ (100-μs time window) in the LUV membrane was 9.4 μm²/s on average (Table I), whereas $D_{100\mu s}$ within 230-nm compartments was 5.4 μm²/s on average (Table I; Fig. 1 B), which is comparable to $D_{100\mu s}$ in the LUV membrane. These results indicate that the diffusion inside a 230-nm compartment in the cell membrane is almost as fast as that of freely diffusing DOPE molecules in LUVs. It is thus concluded that lipid diffusion in the cell membrane is retarded not because the diffusion per se is slow, but dominantly because the cell membrane is compartmentalized with regard to lipid translational diffusion.

As described above, $D_{100\mu s}$ within the compartment (5.4 μm²/s) is 40% smaller than that in LUVs (9.4 μm²/s). This can be explained by the fact that the 100-μs time window is still too long to evaluate the correct diffusion rate within 230-nm compartments. DOPE is estimated to diffuse ~60

Table II. Changes of phospholipid diffusion after trypsin treatment, partial cholesterol depletion, or partial depolymerization/stabilization of f-actin

<table>
<thead>
<tr>
<th>Time resolution</th>
<th>Treatment</th>
<th>Motional mode</th>
<th>Confine size (median)</th>
<th>N*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Hop confined</td>
<td>Diameter (μm)</td>
<td>Area (μm²)</td>
</tr>
<tr>
<td>25 μs</td>
<td>Control</td>
<td>85</td>
<td>230</td>
<td>0.043</td>
</tr>
<tr>
<td></td>
<td>Trypsin</td>
<td>88</td>
<td>250</td>
<td>0.049</td>
</tr>
<tr>
<td></td>
<td>MβCD</td>
<td>96</td>
<td>280</td>
<td>0.061</td>
</tr>
<tr>
<td></td>
<td>Latrunculin-A</td>
<td>97</td>
<td>340</td>
<td>0.093</td>
</tr>
<tr>
<td></td>
<td>Jasplakinolide</td>
<td>96</td>
<td>240</td>
<td>0.044</td>
</tr>
<tr>
<td>2 ms</td>
<td>Control</td>
<td>94</td>
<td>750</td>
<td>0.44</td>
</tr>
<tr>
<td></td>
<td>Trypsin</td>
<td>86</td>
<td>730</td>
<td>0.42</td>
</tr>
<tr>
<td></td>
<td>MβCD</td>
<td>77b</td>
<td>860</td>
<td>0.58</td>
</tr>
<tr>
<td></td>
<td>Latrunculin-A</td>
<td>85</td>
<td>1,100</td>
<td>0.90</td>
</tr>
<tr>
<td></td>
<td>Jasplakinolide</td>
<td>90</td>
<td>670</td>
<td>0.36</td>
</tr>
</tbody>
</table>

Parameters that characterize hop diffusion of DOPE molecules. Cells were treated with trypsin to partially remove the pericellular matrix (61% of the extracellular proteins including extracellular domains of transmembrane proteins and extracellular matrix proteins, and 83% of heparan sulfate glycosaminoglycan), 4 mM methyl-β-cyclodextrin (MβCD) at 37°C for 30 min to partially deplete cholesterol, 50 nM latrunculin-A (f-actin depolymerizing drug), or 400 nM jasplakinolide (f-actin stabilizing drug) at 37°C for 5 min.

N* Number of particles.

bThe apparent low value here is probably due to a combination of a statistical error and the MβCD-induced slight spread of cells, which increased the compartment size by ~15% on average. The latter would make the diffusion of some DOPE molecules look more like simple Brownian.
nm in 100 µs assuming a diffusion rate of 9.4 µm²/s ([4 × 9.4 µm²/s × 10⁻⁴ s]⁻¹), which indicates that even at the highest frame rates, the molecule will frequently rebound from a compartment wall during a frame and hence the displacement will be frequently underestimated.

The actin-based membrane skeleton, rather than the extracellular matrix or rafts, is responsible for compartmentalization of the cell membrane

How are the phospholipid molecules temporarily confined in these compartments? To investigate the possible involvement of extracellular domains of transmembrane proteins and the extracellular matrix due to the interaction with the attached gold particles, the cells were mildly treated with trypsin. Under the conditions in which 61% of the extracellular proteins (including extracellular domains of membrane proteins and extracellular matrix proteins) was cleaved off and 83% of heparan sulfate glycosaminoglycan was removed, the movement of DOPE molecules observed at a 25-µs resolution was not affected (Table II). Taken together with the fact that $D_{100\text{ms}}$ is the same for both Cy3-DOPE and gold-tagged DOPE, it is concluded that the extracellular matrix and the extracellular domains of membrane proteins are not involved in the temporary corraling of phospholipids in 230-nm compartments.

Because DOPE, an unsaturated phospholipid, is excluded from cholesterol-enriched raft domains, the rafts may act as the diffusion obstacles for DOPE in the cell membrane. Therefore, we examined the effect of partial cholesterol depletion on DOPE diffusion (Kilsdonk et al., 1995). The effect of cholesterol depletion was minimal. The diffusion rate in 230-nm compartments was slightly increased (5.4 µm²/s to 7.1 µm²/s), whereas no significant change was observed in other hop parameters (Table II). This result indicates that temporal corraling of DOPE is not caused by the exclusion from cholesterol-enriched raft domains.

After latrunculin-A treatment under conditions that partially depolymerize filamentous actin (Ayscough, 1998), greater compartments appeared for DOPE, the median diameter of 230-nm compartments increasing by a factor of greater compartments appeared for DOPE, the median diameter of 230-nm compartments increasing by a factor of

How are the phospholipid molecules temporarily confined in these compartments? To investigate the possible involvement of extracellular domains of transmembrane proteins and the extracellular matrix due to the interaction with the attached gold particles, the cells were mildly treated with trypsin. Under the conditions in which 61% of the extracellular proteins (including extracellular domains of membrane proteins and extracellular matrix proteins) was cleaved off and 83% of heparan sulfate glycosaminoglycan was removed, the movement of DOPE molecules observed at a 25-µs resolution was not affected (Table II). Taken together with the fact that $D_{100\text{ms}}$ is the same for both Cy3-DOPE and gold-tagged DOPE, it is concluded that the extracellular matrix and the extracellular domains of membrane proteins are not involved in the temporary corraling of phospholipids in 230-nm compartments.

Because DOPE, an unsaturated phospholipid, is excluded from cholesterol-enriched raft domains, the rafts may act as the diffusion obstacles for DOPE in the cell membrane. Therefore, we examined the effect of partial cholesterol depletion on DOPE diffusion (Kilsdonk et al., 1995). The effect of cholesterol depletion was minimal. The diffusion rate in 230-nm compartments was slightly increased (5.4 µm²/s to 7.1 µm²/s), whereas no significant change was observed in other hop parameters (Table II). This result indicates that temporal corraling of DOPE is not caused by the exclusion from cholesterol-enriched raft domains.

After latrunculin-A treatment under conditions that partially depolymerize filamentous actin (Ayscough, 1998), greater compartments appeared for DOPE, the median diameter of 230-nm compartments increasing by a factor of ~1.5 (230 nm to 340 nm), or the area by a factor of ~2 (Table II; Fig. 4, left). Treatment with jasplakinolide, which stabilizes f-actin (Bubb et al., 2000), did not change the confinement size, but it increased the residency time by a factor of ~2 (11 ms to 23 ms) (Table II; Fig. 4, left), indicating that the compartment boundaries were stabilized. These results indicate that the movement of phospholipids in the outer leaf of the membrane, in spite of the lack of direct coupling with the membrane skeleton, can be regulated by the actin-based membrane skeleton fence structure.

Further, we compared DOPE movement with the movement of transferrin receptor (TfR), a transmembrane protein. We have previously shown that the cell membrane of the NRK cell is compartmentalized with regard to lateral diffusion of transmembrane proteins due to the interaction of their cytoplasmic domains with the actin-based membrane skeleton fence structure (Kusumi et al., 1993; Sako and Kusumi, 1994, 1995; Kusumi and Sako, 1996; Tomishige et al., 1998; Tomishige and Kusumi, 1999). As shown in Table I, we found that TRR also undergoes hop diffusion over compartments of 260 nm on average, which is about the same size as the compartments detected by DOPE (230 nm). Sako and Kusumi (1994) previously showed that the movement of TfR was confined in 700-nm compartments as observed at the video rate, a discrepancy we will come back to later in this paper.

As well, the movement of DOPE molecules was observed in membrane blebs, in which the membrane skeleton is partially depleted (Malorni et al., 1991). Approximately 60% (as compared with 15% in the control cell membrane) showed simple Brownian diffusion, and after latrunculin-A treatment, almost all (90%) trajectories observed in blebs were classified into the simple Brownian mode (Table I). Both $D_{100\text{ms}}$ and $D_{33\text{ms}}$ were the same (8.9 µm²/s), consistent with the classification into the simple Brownian mode. In addition, this rate is as fast as that in LUVs (9.4 µm²/s). All these results indicate that the membrane skeleton is responsible for the hop diffusion of DOPE.

**Anchored-protein picket model**

This result is surprising because the phospholipid molecules we observed are localized in the outer leaf of the membrane, whereas the membrane skeleton is located on the cytoplasmic surface of the membrane. Meanwhile, as much as 30% of various kinds of transmembrane protein molecules are immobilized on the membrane skeleton meshwork (Ryan et al., 1988; Saxton, 1996). Furthermore, it has been proposed that immobilized transmembrane proteins significantly reduce the diffusion rate of membrane molecules (Jacobson et al., 1981) due to the circum-
The differential slowing effect referred to as the increased packing near the protein (in terms of the free volume theory) (Sperotto and Mouritsen, 1991; Almeida et al., 1992), or to the increased hydrodynamic friction (in terms of the hydrodynamic theory) (Bussell et al., 1995; Dodd et al., 1995). In light of the proceeding, we propose an anchored membrane-protein picket model (Fig. 5) in which transmembrane proteins anchored to the actin-based membrane skeleton effectively act as pickets along the membrane skeleton fence. Such rows of pickets possibly confine the movement of phospholipids through both steric hindrance (Saxton, 1994) and circumferential slowing. A major characteristic of this model is the coupling of the membrane skeleton to lipids in the outer leaflet of the membrane by means of the membrane skeleton–anchored proteins.

To test this model, a series of Monte Carlo simulations of the diffusion of phospholipids, including the effects of steric hindrance and circumferential slowing caused by proteins anchored to the membrane skeleton, were performed. The free area theory of lipid diffusion gives an expression for the reduction in the diffusion constant that extends radially from the immobilized proteins (Almeida et al., 1992). Fig. 6 A displays typical Monte Carlo trajectories. To reproduce experimental parameters such as the residency time of DOPE within a compartment (11 ms), ~16, 24, and 34% coverage of the compartment boundaries by 1-, 2-, and 3-nm protein obstacles was required, respectively (Fig. 6 B).

The NRK cell membrane is doubly compartmentalized. A representative long-term 2-s trajectory (compared with the short-term 56-ms trajectories displayed in Fig. 2 A) of a DOPE molecule obtained at a 25-μs resolution is shown in Fig. 7 A, left, indicating the presence of compartments greater than the 230-nm compartments. Typical smaller 230-nm compartments present within the greater purple compartment are shown by circles in Fig. 7 A, left (enlarged in Fig. 7 C). Instances of hops between greater compartments at 0.5–1-s intervals are apparent when the locations of gold–DOPE complexes at 81-frame intervals were connected by straight lines (like a time-lapse trajectory at a time resolution of 2 ms) as shown in Fig. 7 A, right. These results clearly indicate the double compartmentalization of the NRK cell membrane (Fig. 8).
Because the quantitative analysis for the doubly compartmentalized movement is overly complicated, recordings at the time resolution of 2 ms (a spatial precision of 6.9 nm at this recording rate) were performed to characterize the greater compartments. The hops among 230-nm compartments, which take place an average of once every 11 ms, are not detected due to the sparsity of points generated at the 2-ms resolution.

Fig. 7 B shows a representative trajectory of a DOPE molecule recorded at a time resolution of 2 ms for a period of 5 s (Video 4). The statistical analysis categorized 94% of DOPE movements into hop or confined-type diffusion (Table I) at this time resolution. The quantitative hop analysis provided the distribution of the confinement size (Fig. 3 A), its median value being 750 nm. The mean residency time within each 750-nm compartment was 0.65 s (Table I). Plausible compartments in the trajectory in Fig. 7 B were identified by a computer program developed here (the same as used for Fig. 2 A) and are shown in different colors. Long-range diffusion occurs by successive hops among 750-nm compartments.

The residency time of DOPE in 750-nm compartments can be estimated from $D_{ph}$ for Cy3–DOPE (0.42 μm$^2$/s) and the average compartment size determined with gold-tagged DOPE (750 nm). The $D_{ph}$ for Cy3–DOPE is likely to give more correct $D_{ph}$ than that for gold-tagged DOPE because the $D_{ph}$ obtained with gold probes is smaller than $D_{ph}$ for Cy3–DOPE by a factor of 2.5, as stated in the beginning of the Results, possibly due to moderate steric or cross-linking effects of gold particles on long-range diffusion. Meanwhile, the compartment size could only be determined with gold-tagged DOPE, and the size is likely to be the same for both Cy3–DOPE and gold-tagged DOPE. Therefore, the residency time of Cy3–DOPE in 750-nm compartments is estimated to be 0.33 s ([0.75 μm$^2$/s]$^2$[4 × 0.42 μm$^2$/s]) on average.

The diffusion rate inside 750-nm compartments ($D_{20ms}$) is 1.6 μm$^2$/s (Table I), which coincides with the diffusion rate expected from a series of intercompartmental hops over 230-nm compartments once every 11 ms ([0.23 μm$^2$/s]$^2$[4 × 11 ms] = 1.2 μm$^2$/s) (see the model in Fig. 8). In addition to the reduction of the diffusion rate from 5.4 μm$^2$/s to 1.6 μm$^2$/s due to the confinement by 230-nm compartments, the further reduction in the diffusion rate by a factor of 4 to 0.42 μm$^2$/s ($D_{ph}$ for Cy3–DOPE) is consistent with the presence of barriers every 750 nm. These results support the model in which the NRK cell membrane is compartmentalized into 750-nm and then into 230-nm compartments with regard to the lateral diffusion of DOPE molecules (Fig. 8).

The presence of such double compartments is not likely to be an artifact of observing 230-nm compartments at lower time resolutions, because the distinct 230- and 750-nm com-

Figure 7. NRK cell membrane is doubly compartmentalized with regard to translational diffusion of phospholipids. (A, left) A typical long-term trajectory of DOPE recorded at 25-μs resolution for a period of 5 s (81,000 frames). (A, right) A trajectory that sampled the coordinates of the left trajectory at 81-frame intervals, giving a time-lapse trajectory at a time resolution of 2 ms. Plausible compartments greater than 230-nm compartments were identified, and are shown in different colors with residency times: purple, 0.9 s; blue, 0.5 s; green, 0.5 s; orange, 0.1 s. The instances of intercompartmental hops are shown in dark green. (B) A representative trajectory of a DOPE molecule observed at a 2-ms time resolution for a period of 5 s (2,500 frames). The particle started from the purple compartment at the left-bottom, and after it reached the orange compartment, it hopped to the red compartment and came back to the orange compartment (shown in purple), which appeared to have shifted slightly toward the right. Finally, the molecule hopped to the blue compartment. The instances of intercompartmental hops are shown in dark green. (Video 4). (C) Intercompartmental hops among 230-nm subcompartments for a period of 120 ms. Individual compartments are color coded and numbered sequentially. The circles coincide with those in the purple (750 nm) compartment in A (left). Note that compartments 5, 7, and 12 (also 6 and 8; 4 and 13) match with those in the orange (750 nm) compartment in A (left). The median compartment size determined with gold-tagged DOPE, and the size is likely to be the same for both Cy3–DOPE and gold-tagged DOPE. Therefore, the residency time of DOPE in 750-nm compartments is estimated to be 0.33 s ([0.75 μm$^2$/s]$^2$[4 × 0.42 μm$^2$/s]) on average.

The diffusion rate inside 750-nm compartments ($D_{20ms}$) is 1.6 μm$^2$/s (Table I), which coincides with the diffusion rate expected from a series of intercompartmental hops over 230-nm compartments once every 11 ms ([0.23 μm$^2$/s]$^2$[4 × 11 ms] = 1.2 μm$^2$/s) (see the model in Fig. 8). In addition to the reduction of the diffusion rate from 5.4 μm$^2$/s to 1.6 μm$^2$/s due to the confinement by 230-nm compartments, the further reduction in the diffusion rate by a factor of 4 to 0.42 μm$^2$/s ($D_{ph}$ for Cy3–DOPE) is consistent with the presence of barriers every 750 nm. These results support the model in which the NRK cell membrane is compartmentalized into 750-nm and then into 230-nm compartments with regard to the lateral diffusion of DOPE molecules (Fig. 8).

The presence of such double compartments is not likely to be an artifact of observing 230-nm compartments at lower time resolutions, because the distinct 230- and 750-nm com-

Figure 8. A model of double compartmentalization for DOPE diffusion. A DOPE molecule undergoes free diffusion inside a 230-nm compartment for an average of 11 ms, and then hops to an adjacent compartment. It also experiences confinement in the greater 750-nm compartments. The diffusion rate within a 750-nm compartment is 1.6 μm$^2$/s due to the confinement by 230-nm compartments, the further reduction in the diffusion rate by a factor of 4 to 0.42 μm$^2$/s ($D_{ph}$ for Cy3–DOPE) is consistent with the presence of barriers every 750 nm. These results support the model in which the NRK cell membrane is compartmentalized into 750-nm and then into 230-nm compartments with regard to the lateral diffusion of DOPE molecules (Fig. 8).
Double compartmentalization for TfR diffusion in the NRK cell membrane

As shown in Table I, TfR diffusion was also found to be doubly compartmentalized into 710-nm compartments and then into 260-nm compartments. This is consistent with double compartmentalization of DOPE molecules into 750- and 230-nm compartments, suggesting the involvement of the membrane skeleton for the greater compartment.

Previously, Sako and Kusumi (1994, 1995) demonstrated the existence of 700-nm compartments with regard to the diffusion of TfR in NRK cells. However, in these previous studies performed at a video rate time resolution (33 ms), the smaller 260-nm compartments were not observed. Because TfR hops among 260-nm compartments an average of once every 55 ms (Table I), there was no way of detecting the smaller compartments at this frame rate of every 33 ms. The problem of the unexpectedly slow diffusion rate within 700-nm compartments found previously (~0.1 μm²/s) (Kusumi et al., 1993; Sako and Kusumi, 1994) is clarified in the present investigation: namely, TfR diffusion in 700-nm compartments is slowed due to the presence of smaller 260-nm compartments within them.

The next question, then, is whether there are yet smaller compartments within 260-nm compartments (i.e., triple compartmentalization). We think it very unlikely because the diffusion rate of TfR within a 260-nm compartment is almost as great as that of DOPE in LUVs or in bleb membranes (reduction by ~40%) can be explained by the reflection of TfR molecules at the boundary and the lack of time resolution for its visualization, the same argument used to explain the reduction of DDOPE for gold-tagged DOPE). The hop rate for TfR over 700-nm compartments is once every 1.8 s on average, which is ~10 times faster than that reported previously (Sako and Kusumi, 1994). This is probably due to better control of preparation of gold probes to avoid cross-linking in this study.

The agreement of sizes of both greater and smaller compartments for DOPE and TfR again suggests that the membrane skeleton is involved in the formation of compartments of both sizes.

Anchored-protein pickets also form the boundaries of greater compartments

We examined again the involvement of the extracellular matrix, extracellular domains of membrane proteins, cholesterol-enriched rafts, and actin-based membrane skeleton in DOPE hop diffusion over 750-nm compartments observed at a 2-ms time resolution, as was done for 230-nm compartments. Neither trypsin treatment nor cholesterol depletion caused any significant change in DOPE’s hop movement over 750-nm compartments (Table II, bottom part indicated by “2 ms,” but see footnote b). However, partial depolymerization of f-actin with latrunculin-A increased the median diameter of 750-nm compartments by a factor of ~1.5 (750 nm to 1,100 nm), or the area by a factor of ~2. Meanwhile, stabilization with jasplakinolide increased the residency time by a factor of ~2 (650 ms to 1,100 ms) (Table II, bottom; Fig. 4, right; Video 5). These results indicate that pickets located along the actin membrane skeleton fence are again responsible for the corraling of DOPE molecules inside 750-nm compartments.

Discussion

We have shown, for the first time, that the cell membrane is compartmentalized with regard to lateral diffusion of phospholipids, and thus their long-range diffusion is largely limited by the hop rate across the compartment boundaries. Three types of experimental results indicated that the actin-based membrane skeleton is involved in such compartmentalization. (1) The boundaries are not dependent on the extracellular matrix, extracellular domains of the membrane proteins, or cholesterol content in the membrane, but are modulated by modification of the actin-based membrane skeleton. (2) DOPE undergoes rapid simple Brownian diffusion, rather than hop diffusion, in membrane blebs in which the membrane skeleton is largely depleted. (3) The compartment size for phospholipids is almost identical to that found for TfR, whose compartment size is largely determined by the membrane skeleton fence. Based on these results, together with the previous findings of membrane skeleton fences for transmembrane proteins (Kusumi et al., 1993; Sako and Kusumi, 1994, 1995; Kusumi and Sako, 1996; Tomishige et al., 1998; Tomishige and Kusumi, 1999), we propose here an “anchored membrane-protein picket model.” In this model, transmembrane proteins anchored to the membrane skeleton are called “pickets,” as they act as posts along the membrane skeleton fence. These rows of pickets act as effective diffusion barriers due to steric hindrance as well as circumferential slowing (packing and frictional) effects even for phospholipids in the outer leaf of the membrane.

These immobilized picket proteins are likely to include various transmembrane proteins, rather than limited protein species, as we have found that almost all transmembrane proteins we have studied so far exhibited various amounts of immobilized populations (even after excluding the populations in the process of internalization; Kusumi and Sako, 1996). In addition, transmembrane proteins transiently associated with the membrane skeleton also act as diffusion barriers if they are immobilized longer than the period in which phospholipids are within the boundary regions (estimated to be ~100 μs, assuming that the boundary region is ~20 nm wide and the effective diffusion coefficient of phospholipid is decreased to 1 μm²/s in this region; [0.02 μm²/4 × 1 μm²/s] = 100 μs).

Our earlier work on transmembrane protein diffusion led us to propose the membrane skeleton fence model, in which the cytoplasmic domains of transmembrane proteins collide with the membrane skeleton, which induces temporary confinement (corraling). A transmembrane protein could hop from a compartment to an adjacent one when the membrane skeleton fluctuates to allow space between itself and the membrane, when the membrane skeleton is transiently dissociated, or
when the transmembrane protein has reached the boundary while possessing sufficient kinetic energy to surmount the barrier potential. The anchored-protein pickets found in the present study would provide another diffusion barrier for transmembrane proteins in the cell membrane. Because the picket barriers would act on all membrane molecules, both the membrane skeleton fence and the anchored-protein pickets would limit movement of transmembrane proteins. Because these interactions are found in all cell types (such as CHO, PtK2, COS1, and ECV304) we have observed so far (unpublished data), they are likely to be universal in the reduction of the diffusion rates. Double compartmentalization has been found only in NRK cells among the cells we have studied thus far. The compartment sizes of the NRK cell membrane (230 and 750 nm for DOPE; 260 and 710 nm for TIR) are substantially greater than others (unpublished data), which we suspect might make it necessary for NRK cells to possess a more stable membrane skeleton every ~700 nm on average.

There is growing interest in the size of rafts that may range from a scale of several tens to several hundreds of nanometers (for reviews see Jacobson and Dietrich, 1999; Eddin, 2001). Pralle et al (2000) and Varma and Mayor (1998) found that the size might make it necessary for NRK cells to possess a more stable membrane skeleton every ~700 nm on average.

Lipid probe incorporation

DOPE was purchased from Avanti Polar Lipids, Inc., Cy3 from Amersham Pharmacia Biotech, and FITC (isomer I) from Molecular Probes Inc. For single fluorophore imaging, DOPE conjugated with Cy3 in the head group region (Cy3–DOPE) was dissolved in 10 µM of methanol (10 µg/ml), which was then diluted to 1 ml with HBSS buffered with 2 mM Pipes, pH 7.2, (HP) while vortexing vigorously. It was further diluted to 0.4 ng/ml for the appropriate incorporation into cells at 37°C. Individual Cy3–DOPE molecules were observed on the dorsal cell membrane at the video rate using an objective-type total internal reflection microscope (Sako et al., 2000; Iino et al., 2001). For high-speed video imaging, DOPE conjugated with fluorescein in the head group region was diluted with the HP medium in the same way as Cy3–DOPE except that the final concentration of fluorescein–DOPE was 2 µg/ml.

Gold probe preparation and labeling

40-nm-ϕ colloidal gold particles (BBInternational) conjugated with Fab fragments of antifluorescein antibodies (Molecular Probes Inc.) were prepared by mixing 50 µl of 13.2 µg/ml Fab on 2 mM phosphate buffer, pH 7.2, and 500 µl of colloidal gold suspension (1.2 µg/ml of Fab in the mixture) (Tomishige et al., 1998). After incubating for 1 h at room temperature, the Fab–gold complex was further stabilized with 0.05% Carbocowx 20 M (Sigma-Aldrich). After two washes by centrifugation and resuspension in 0.05% Carbocowx 2 mM phosphate buffer, pH 7.2, the conjugates were resuspended in 0.05% Carbocowx 20/40 HBSS buffered with 2 mM Pipes, pH 7.2 (HPM). The gold probe suspension (~0.12 nM of gold particles) was added to cells that had been incubated with fluorescein–DOPE.

The amount of Fab fragments mixed with the gold particles was varied to minimize the effect of lipid cross-linking by the gold probe. As the Fab concentration was reduced (when it was mixed with gold particles), the diffusion rate of the gold–DOPE complex determined at the video rate (D(2000)) was increased, and it reached a plateau value of 0.49 µm²/s when 1.2 µg/ml of Fab was used. At this concentration, the ratio of particles bound specifically versus nonspecifically (without incorporation of fluorescein–DOPE) was 7.3 to 1 (13.2 vs. 1.8 particles/cell on average).

Colloidal gold particles conjugated with bovine holo transferrin (Wako) were prepared according to Sako and Kusumi (1994) while minimizing the effect of cross-linking by reducing the transferrin concentration mixed with the gold particles.

LUVs, as large as 10 µm in diameter, were prepared essentially according to Akashi et al. (1996) and attached to poly-L-lysine–coated coverslips. Membrane blebs, up to 20 µm in diameter, were formed by incubating the cells with 1 mM menadione (Sigma-Aldrich) in the HP medium at 37°C for 1 h (Malorni et al., 1991). When further removal of the membrane skeleton was desired, the cells were then treated with latrunculin-A in the same way as described below.

High-speed video microscopy

High-speed video microscopy was performed as described previously (Tomishige et al., 1998). The precision of the position determination was estimated from the standard deviation of the coordinates of 40-nm-ϕ particles fixed in a 10% poly-L-lysine–coated coverslip, and was 17 nm and 6.9 nm at time resolutions of 25 µs and 2 ms, respectively. On the cell membrane, the positions correspond to the probability distribution peaks of the diffusing gold particles during each exposure time. The quantitative analysis of lipid movement was performed based on the MSD methods described previously (Powles et al., 1992; Kusumi et al., 1993; Sako and Kusumi, 1994; Tomishige et al., 1998). For every trajectory of a particle, MSD, \( < \Delta t^2 > \), for every time interval was calculated according to the formula:

\[
MSD(n\delta t) = 1 \sum_{j=1}^{N} [(x(j+\delta t)-x(j))^2 + (y(j+\delta t)-y(j))^2]
\]

(Qian et al., 1991; Kusumi et al., 1993), where δt is the time resolution and \( (x(j+\delta t), y(j+\delta t)) \) describes the particle position after a time interval \( \Delta t = n \delta t \) after starting at position \( (x(j), y(j)) \). N is the total number of frames in the sequence, n and j are positive integers, and \( \delta t \) determines the time increment.

Materials and methods

Cell culture

NRK fibroblastic cells were grown in Ham’s F12 medium supplemented with antibiotics and 10% FBS. Cells were plated on 12-mm-ϕ coverslips (for single fluorophore imaging) or 18-mm × 18-mm coverslips (for high-speed video imaging) and used 2 d later.

Phospholipids undergo hop diffusion | Fujitake et al. 1079
Tilting and reorientation of lipids are not likely to seriously affect the measurement of the lateral diffusion rate even at a 25-μs resolution because $D_{\text{theo}}$ of DOPE in LUVs (9.4 μm²/s) is almost the same as $D_{\text{theo}}$ (9.5 μm²/s).

**Treatment of cells with trypsin and drugs**

To partially remove the extracellular domains of membrane proteins and the extracellular matrix, cells were treated with 25 μg/ml trypsin (Dilco Laboratories) in the HP medium at 37°C for 10 min. To monitor the extent of cleavage, extracellular surface proteins were first tagged with sulfosucinimidyl biotin (Sigma-Aldrich) and visualized by fluorescein–streptavidin (Molecular Probes Inc.) before and after trypsin digestion. Heparan sulfate glycosaminoglycan was detected by indirect immunofluorescence method using HepS-1 antiheparan sulfate (Seikagaku Corp.) and fluorescein–goat anti–mouse antibody (Zymed Laboratories). Epifluorescence images of cells were quantitated by MetaView software (Universal Imaging Corp.). For cholesterol depletion (Kisdonk et al., 1995), cells were incubated in the HP medium containing 4 mM methyl-β-cyclodextrin (Sigma-Aldrich) at 37°C for 30 min. Latrunculin-A and jasplakinolide were provided by G. Marriott (University of Wisconsin, Madison, WI). Cells were incubated in the HP-CW medium containing 50 nM latrunculin-A (Ayscough, 1998) or 400 nM jasplakinolide (Bubb et al., 2000) on the microscope stage at 37°C for 5 min. Microscopic observations were completed within 30 min after addition of drugs, before large morphological changes of the cells took place. Longer observations or higher concentrations of latrunculin-A and jasplakinolide caused the collapse and aggregation of the actin-based membrane skeleton, which results in the immobilization of gold probes, and hence were avoided.

**Computer simulation**

The two-dimensional, Brownian Monte Carlo algorithm employed here (Rossky et al., 1978) takes steps that are predicated on the Langevin equation, and hence allows the inclusion of the circumferential slowing effect. Extensions were made to include a spatially variable diffusivity as in Evans and Ritchie (1997). The variation in the diffusion coefficient away from the protein obstacles was taken from free area theory using the parameters of Almeida et al. (1992) (a coherence length of 15 Å for the free area disturbance, 0.25 for the relative critical free area next to an obstacle with respect to the bulk free area and a 0.25 for the relative critical free area for diffusion with respect to the bulk free area).

**Online supplemental materials**

Included in the online supplemental materials (available at http://www.jcb.org/cgi/content/full/jcb.200202050/DC1) are the quantitative analysis (Fig. S1) to confirm double compartmentalization of the NRK cell membrane, and the videos (Videos 1–5) showing movement of single DOPE molecules in the cell membrane, recorded by single fluorophore imaging and high-speed single particle imaging techniques. Video 1 shows the movement of single Cy3–DOPE molecules and a gold-tagged DOPE molecule on the NRK cell surface recorded at the video rate. Arrowheads in the first sequence indicate some of the DOPE molecules (with its fluorescence signal lasting longer than the average). Fluorescent spots are photobleached in single steps, indicating that these represent single Cy3–DOPE molecules. Video 2 shows the hop diffusion of gold-tagged DOPE over 230-nm compartments observed at a 25-μs resolution for 62 ms (×270 slowed). In the second sequence, their trajectories are superimposed. In the trajectories, plausible compartments are shown in different colors, based on quantitative analysis. 750-nm compartments cannot be detected in the 62-ms period. Video 3 shows the movement of gold-tagged DOPE (×270 slowed) diffusing freely on a large unilamellar vesicle, observed at a 25-μs resolution. In the second sequence, its trajectory is superimposed. Video 4 shows the hop diffusion of gold-tagged DOPE over 750-nm compartments, observed at a 2 ms resolution (×3.3 slowed). At this time resolution, the 230-nm compartments, where DOPE stays for 11 ms on average, cannot be identified due to the sparsity of points. Video 5 shows the effects of f-actin depolymerizing/stabilizing drugs on the movement of DOPE at a 2-ms resolution. Partial depolymerization of the actin-based membrane skeleton by latrunculin-A treatment increased the compartment size by a factor of ~2 in area, whereas stabilization by jasplakinolide increased the residency time by a factor of ~2.

We would like to thank G. Marriott for providing latrunculin-A and jasplakinolide, K. Metz-Honda (ERATO) for synthesizing Cy3–DOPE, R. lino (ERATO) for building the total internal reflection microscope, and K. Suzuki (ERATO) and C. Dietrich (University of North Carolina, Chapel Hill, NC) for their helpful advice and discussion.

**References**


Phospholipids undergo hop diffusion | Fujiwara et al. 1081


Double compartmentalization is further confirmed by quantitative anomaly analysis

To further confirm double compartmentalization of the NRK cell membrane, we performed another quantitative analysis using the MSD (see the Materials and methods), i.e., the mean log(MSD/time) for gold-tagged DOPE is plotted as a function of log(time) based on the data obtained at time resolutions of 25 μs, 0.22 ms, 2 ms, and 33 ms (Fig. S1). The slope in this display is sensitive to anomaly of diffusion: due to the relationship of log(MSD/time) = (α – 1) log(time) (0 ≤ α ≤ 1), α parametrizes the level of anomaly (Saxton, M.J. 1994. *Biophys. J.* 66:394–401; Saxton, M.J. 1996. *Biophys. J.* 70:1250–1262; Feder, T.J., I. Brust-Mascher, J.P. Slattery, B. Baird, and W.W. Webb. 1996. *Biophys. J.* 70:2767–2773). In the case of simple Brownian diffusion, the plot becomes flat (α – 1 = 0) and α = 1. When the diffusion is anomalous, α becomes <1, giving a negative slope (α – 1 < 0) to the plot. For DOPE molecules undergoing free Brownian diffusion in LUVs (Fig. S1), the plot is almost flat between 100 μs and 10 ms when observed at a 25-μs resolution. The best fit for the plot yields an α of 0.97 (~1), which indicates that DOPE in LUVs is undergoing simple Brownian diffusion. On the other hand, the plot for the cell membrane exhibits multiple negative slopes depending on the observation time intervals. The plot can be fitted with three lines with αs of 0.74 (<12 ms), 0.55 (12–590 ms), and 0.79 (>590 ms). The transitions were found to occur at 12 ms and 0.59 s, comparable to the residency times within 230-nm (11 ms) and 750-nm (0.65 s) compartments for DOPE hop diffusion, respectively. Therefore, we interpret this time dependence as a result of (a) DOPE being corralled inside 230-nm compartments for an average of 11 ms while undergoing free diffusion inside the compartment, (b) DOPE being corralled inside 750-nm compartments for an average of 0.65 s while undergoing hop movement among 230-nm compartments (because we are using the data for gold-tagged DOPE, the hop rate among 750-nm compartments is 0.65 s rather than the 0.33 s estimated for Cy3–DOPE), and (c) DOPE undergoing hop movement among 750-nm compartments once every 0.65 s. Although anomalous diffusion in the cell membrane could be caused by various kinds of obstacles and binding sites (Saxton, 1994, 1996), the good agreement of these transition times in Fig. S1 with the residency times (11 ms and 0.65 s) supports the predominant involvement of double compartmentalization (into 230- and 750-nm compartments) in limiting the macroscopic diffusion rate of DOPE.

![Figure S1. Plots of log(MSD/time) against log(time) provide useful information on the changes of diffusion characteristics that depend on the observation time intervals. MSD of the trajectories was estimated using data obtained at the time resolutions of 25 μs (5,000 frames; purple), 0.22 ms (5,000 frames; blue), 2 ms (2,500 frames; green), and 33 ms (500 frames; orange) for the time windows where theoretically expected statistical errors in MSD are <40% (Qian et al., 1991). Then the mean log(MSD/time) values (circles) and their standard deviations (curves) for each time resolution were plotted as a function of log(time). The shorter (log(time) < ~1.5) and the longer (~1.5 < log(time)) periods contain 1,113 and 1,388 time points, respectively, which would give rather uniform weight over the entire time window when least square fitting is performed for these points as described below. Normal (simple Brownian) and anomalous diffusion can be distinguished in this display as having no time dependence (slope ~ 0) and having negative slopes, respectively (Saxton, 1994, 1996; Feder et al., 1996). The best fit on the data obtained for the cell membrane using the continuous three linear segments (red solid line, representing three anomalous exponents) gives transitions at 12 ms and 0.59 s. These three segments are consistent with (a) the confinement of freely diffusing DOPE within a 230-nm compartment for an average of 11 ms, (b) the confinement of DOPE undergoing consecutive hops over 230-nm compartments within a 750-nm compartment for an average of 0.65 s, and (c) consecutive hop movement of DOPE over many 750-nm compartments. The slope in the experimental data is shallower at the high time resolution end (left end) because at these time intervals, DOPE molecules that are not located near the compartment boundaries are undergoing simple Brownian diffusion. In addition, if we had employed lower resolution or longer time intervals of observation, the slope at the right end would have become shallower because DOPE molecules would have looked as if they were undergoing simple diffusion by hopping from one (750 nm) compartment to another. For comparison, the plot for the trajectories in LUVs (2,250 frames; n = 17) and the best regression result (red line, α = 0.97) are also shown.](http://www.jcb.org/cgi/doi/10.1083/jcb.200202050)