Reversible binding and rapid diffusion of proteins in complex with inositol lipids serves to coordinate free movement with spatial information

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Polyphosphoinositols convey spatial information partly by their interactions with cellular proteins within defined domains. However, these interactions are prevented when the lipids’ head groups are masked by the recruitment of cytosolic effector proteins, whereas these effectors must also have sufficient mobility to maximize functional interactions. To investigate quantitatively how these conflicting functional needs are optimized, we used different fluorescence recovery after photobleaching techniques to investigate inositol lipid-effector protein kinetics in terms of the real-time dissociation from, and diffusion within, the plasma membrane. We find that the protein-lipid complexes retain a relatively rapid (~0.1–1 μm²/s) diffusion coefficient in the membrane, likely dominated by protein–protein interactions, but the limited time scale (seconds) of these complexes, dictated principally by lipid–protein interactions, limits their range of action to a few microns. Moreover, our data reveal that GAP1IP4BP, a protein that binds PtdIns(4,5)P₂ and PtdIns(3,4,5)P₃ in vitro with similar affinity, is able to “read” PtdIns(3,4,5)P₃ signals in terms of an elongated residence time at the membrane.

Introduction

The inositol lipids regulate a wide range of cellular functions, from signal transduction to lipid transport (Balla, 2006; Di Paolo and De Camillii, 2006). As rare constituents on the cytosolic face of membranes, one of the principle means by which these lipids exert their function is through the recruitment of cytosolic proteins that contain lipid-binding motifs (Cho and Stahelin, 2005; Lemmon, 2008). Once restricted to the two-dimensional membrane surface, the increased local concentration of these proteins facilitates their interaction with binding partners and substrates.

Many interacting motifs bind specifically to a particular inositol lipid with high affinity, whereas others are more promiscuous, with a lower affinity that requires a secondary interaction for recruitment (Carlton and Cullen, 2005; Lemmon, 2008). The most abundant inositol lipid-binding motif in eukaryotic genomes is the pleckstrin homology (PH) domain (Yu et al., 2004; Lemmon, 2008). Many high-affinity PH domains bind to the d-3 phosphorylated inositol lipids phosphatidylinositol 3,4,5-trisphosphate (PtdIns(3,4,5)P₃) and phosphatidylinositol (3,4)-bisphosphate (PtdIns(3,4)P₂), whose synthesis is driven by activated cell surface receptors (Park et al., 2008); this causes recruitment of the PH domain-containing proteins to the plasma membrane, where they participate in the subsequent signal transduction cascade. However, the majority of PH domains bind with little selectivity and with lower affinity to inositol lipids (Yu et al., 2004; Lemmon, 2008). Examples include the cytohesin family of ARF guanine nucleotide exchange factors: in these, the 3G splice variants bind with low affinity and selectivity to phosphatidylinositol 4,5-bisphosphate (PtdIns(4,5)P₂) and PtdIns(3,4,5)P₃ (Klarlund et al., 2000), and their plasma membrane recruitment is assisted by an interaction with ARF-like GTPases (Cohen et al., 2007; Hofmann et al., 2007; Li et al., 2007).

Because the inositol lipids may be quite sparsely distributed on the cytosolic face of membranes, binding proteins must retain sufficient mobility to meet their interacting partners. Recent estimates place the lateral diffusion coefficients of PtdIns(4,5)P₂ and PtdIns(3,4,5)P₃ at 0.5–1 μm²/s (Haugh et al., 2000; Balla, 2006).
Yaradanakul and Hilgemann, 2007; Golebiewska et al., 2008). Measurements in model membranes and the outer leaflet of plasma membranes yield a value threefold higher, which suggests that endogenous PtdIns(4,5)P_2 is spending two thirds of its time in complex with slow or immobile membrane components (Golebiewska et al., 2008). Furthermore, previous work has shown that several proteins maintain a comparable mobility when bound to inositol lipid as when free in the cytosol (Brough et al., 2005).

The picture is further complicated by the ability of inositol lipids to act at a more local level within a given membrane (Haugh et al., 2000). For example, localized synthesis of PtdIns(3,4,5)P_3 at the leading edge of motile cells (coupled to its degradation toward the sides and rear) is required for efficient cell motility (see Discussion for further examples; Kolsch et al., 2008). Therefore, as well as maintaining sufficient mobility to form interactions, inositol lipid effector proteins must be constrained from diffusing too far from the site of lipid synthesis, because if they do, as long as they “mask” the inositol lipid head group, they will protect it from metabolism, and so “smear out” the lipid gradient.

So, how can free mobility be reconciled with a constrained localization in the same membrane? One possibility is that an inositol lipid-bound protein retains lateral mobility but is correlated into specific membrane subdomains, such as cholesterol-enriched “rafts” (Pike and Miller, 1998) or actin-based “picket fences” (Morone et al., 2006). Alternatively, the protein may rapidly exchange between the bound and free states, which, coupled to rapid diffusion through the cytosol, leads to repeated sampling of the target membrane (Teruel and Meyer, 2000; Matsuoaka et al., 2006).

In this study, we assess quantitatively the mechanisms governing spatial and temporal recruitment of PH-domain containing proteins to the membrane. Specifically, we concentrate on proteins with high-affinity PH domains, targeted to the plasma membrane via their interaction with PtdIns(4,5)P_2 and/or PtdIns (3,4,5)P_3. FRAP techniques are used that can discriminate lateral diffusion on the membrane versus exchange between bound and unbound molecules. Our results suggest that, whereas the protein–lipid complexes retain free lateral diffusion (~0.1–1 μm^2/s), they are constrained by the short-lived (seconds) time scale of this interaction.

**Results**

**FRAP of proteins in complex with inositol lipids using total internal reflection fluorescence (TIRF)**

The central aim of this paper was to distinguish lateral diffusion of inositol lipid-bound proteins from their interaction with an unbound, cytosolic pool. Therefore, we conceived a FRAP experiment whereby the entire basal membrane could be bleached selectively by TIRF microscopy, a technique that allows the imaging of the plasma membrane adherent to a glass coverslip (Axelrod, 2001). Fig. A shows HEK cells expressing GFP fused to the isolated PH domain from phospholipase Cδ1 (PLCδ1) and the PH domain-containing protein GAP1^IRBP, both of which are targeted to the plasma membrane by interaction with PtdIns(4,5)P_2 (Várnai and Balla, 1998; Cozier et al., 2000). Also shown (Fig. 1 A, top) is YFP targeted to the plasma membrane by the palmitoylation and myristoylation sequence from Lyn kinase (PM-YFP). Epifluorescence images of the adhesion plane, or “footprint,” show the uniform haze from the basal plasma membrane, along with a ring of lateral membrane. Conversely, only uniform fluorescence in the footprint is seen.
To achieve substantial photobleaching of fluorescence (≤50%) in the cellular footprint, we found it necessary to bleach for 8 s. To highlight the recovering fluorescence, residual fluorescence immediately after bleaching was subtracted from subsequent images, and the contrast was rescaled (this procedure is described in Fig. S1, available at http://www.jcb.org/cgi/content/full/jcb.200809073/DC1). Representative images from such experiments are presented in Fig. 1 C and Videos 1–3; as expected, PM-YFP (with its integral lipid anchors) recovered its fluorescence from the cell periphery, which is consistent with lateral diffusion in the plane of the membrane.

We reasoned that the recovery of fluorescence in the footprint after photobleaching by TIRF would then proceed via two mechanisms: lateral diffusion through the membrane, which would approach from the border of the footprint where the basal membrane is continuous with the apical surfaces, and exchange with the overlying cytosolic pool, which would occur uniformly throughout the footprint (Fig. 1 B).

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by TIRF when the evanescent field decays with a length constant of ~100 nm (Fig. 1 A). Consistent with a previous paper (van Rheenen et al., 2005), we saw no local enrichment of these PtdIns(4,5)P₂-binding proteins in the adhesion plane.

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proteins, however, showed a uniform recovery of fluorescence across the footprint, which suggests recovery via exchange with the overlying cytosol.

Together, these experiments suggest that over the scale of a cellular footprint (~10 μm) and a time period of several seconds, exchange between bound and unbound molecules dominates recovery. However, because an extended time period was required for bleaching relative to the recovery time, we cannot determine quantitatively (a) the time course of this exchange and (b) whether there is lateral diffusion of the bound molecules.

**Spot bleaching to measure lateral diffusion and membrane dissociation**

To quantify lateral diffusion and membrane dissociation, we turned to a simpler bleaching paradigm (Fig. 2 A) developed by Oancea et al. (1998) to quantify lateral diffusion and dissociation of diacylglycerol-binding C1 domains. Here, a laser-scanning microscope is used, and bleaching is achieved via a brief (10 ms) pulse of light centered on the plasma membrane (Fig. 2 B). Because the laser beam has a Gaussian intensity profile, a Gaussian distribution can be fit to the bleach profile (Fig. 2 A, i), as long as the cellular fluorescence is not completely photo-bleached toward the center of the beam. Experiments with fixed cells confirmed these criteria, and Gaussian fits to the bleach profile showed the maximum extent of bleaching in the center of the profile to be $83 \pm 1.4\%$ ($n=6$; unpublished data). Lateral diffusion of bleached molecules along the membrane causes a widening of this profile while conserving the area under the curve; the rate of change of the square of the Gaussian radius with time is proportional to the apparent lateral diffusion coefficient $D$ (Fig. 2 A, ii; Fig. 2 D; and Materials and methods). Conversely, dissociation of bleached molecules from the membrane and their replacement with unbleached protein causes a decrease in the area of this Gaussian profile, without a change in the radius. Assuming the majority of bleached material is the protein bound to the membrane, and there is little change in the total cellular levels of unbleached protein, it has previously been shown that the dissociation rate constant governs fluorescence recovery (Buliniski et al., 2001). Thus, a membrane dissociation time constant $\tau$ can be found that should be the reciprocal of the dissociation rate constant (Fig. 2 A, iii; and Fig. 2 E; see Discussion). A simple relationship (Oancea et al., 1998) has been shown to account for simultaneous lateral diffusion $D$ and dissociation $\tau$, and can assign values to each parameter (Fig. 2 C and Materials and methods).

The bleaching and subsequent imaging were performed with the pinhole on the confocal laser scanning microscope (CLSM) fully open in order to produce an extended bleach region above and below the plane of focus. Thus, recovery of fluorescence from the $z$ axis (which could occur by diffusion but not change the Gaussian radius) should be excluded. To test whether this assumption was correct, we used PM-YFP, which, being integral to the inner leaflet of the plasma membrane, should recover solely by lateral diffusion. As expected, this protein displayed lateral diffusion (Fig. 2 D) and usually showed no apparent displacement from the membrane (Fig. 2 E). Considering all
the cells imaged \((n = 43)\), a range of dissociation time constants \(\tau\) were found, from 9.6 s to \(\sim 10^{22}\) s; the lower value suggests that in certain cases, diffusion from above and below the focal plane was contributing to recovery. However, the range of values collectively produces a mean value for \(\tau\) that is essentially infinite (Table I), which led us to conclude that the model accurately assigns lateral diffusion verses dissociation across a sufficient sample size.

To further verify our approach, we considered a protein whose lateral diffusion coefficient had already been determined by single particle tracking (SPT), namely the three tandem PH domains from myosin X. Spot bleaching yielded an estimated \(D\) of \(\sim 0.07\) \(\mu\)m\(^2\)/s (Table I), which is in excellent agreement with measurements by SPT in fibroblasts of 0.06–0.1 \(\mu\)m\(^2\)/s (Mashanov and Molloy, 2007). The protein also displayed an apparent \(\tau\) of \(\sim 7\) s (Table I); note that this is longer than the time for which a single protein can be tracked (because of bleaching), which is why this parameter could not be determined by SPT (Mashanov and Molloy, 2007).

This model also assumes that lateral diffusion in the cytoplasm is rapid and thus does not affect the plasma membrane profile. To test this assumption, we also determined cytoplasmic diffusion coefficients, again from spot bleaching and the subsequent rate of increase of a Gaussian radius (Fig. 3), as described in Seiffert and Oppermann (2005). Cytosolic diffusion of GFP was estimated as \(\sim 31\) \(\mu\)m\(^2\)/s (Table I), which is consistent with previous estimates; e.g., Braeckmans et al. (2007) and Brouch et al. (2005).

Studies of the PtdIns(4,5)P\(_2\)-binding PH domain form PLC\(_{\delta}^1\)

The PH domain from PLC\(_{\delta}^1\) binds with high affinity and specificity to PtdIns(4,5)P\(_2\) both in vitro (Garcia et al., 1995; Lemmon et al., 1995) and in cells (Várnai and Balla, 1998), where it is localized to the plasma membrane (Fig. 4 A). Lateral diffusion of this probe on the membrane was rapid, \(\sim 1.2\) \(\mu\)m\(^2\)/s (Fig. 4 B and Table I; see Fig. 2 D for an example), a speed similar to that of its PtdIns(4,5)P\(_2\) ligand (Golebiewska et al., 2008), which suggests that the lipid limits diffusion. Consistent with this, we used a point mutation of arginine 40, which renders the domain incapable of high affinity PtdIns(4,5)P\(_2\) binding (Várnai and Balla, 1998), leading to a cytosolic localization (Fig. 4 A). The cytosolic protein is very much more mobile than the membrane-bound wild type, with a \(D\) of \(\sim 21\) \(\mu\)m\(^2\)/s (Fig. 4 B and Table I; see Fig. 3 for an example).

The apparent membrane dissociation time for PH-PLC\(_{\delta}^1\) at the plasma membrane was 2.4 s (Fig. 4 C and Table I; see Fig. 2 E for an example). We reasoned that if this time constant reflects the time a typical molecule spends bound to a lipid (i.e., the inverse of the off-rate constant), then fusing two such PH domains in tandem should cause greater avidity and thus a longer \(\tau\). Fig. 4 C shows that such a tandem dimer, tagged at the N or C terminus, exhibited an apparent \(\tau\) approximately fourfold longer than that of a single domain. That this reflects increased membrane affinity was further indicated by the cellular localization: whereas the single domains showed mainly membrane fluorescence with a weaker haze of unbound protein in the cytosol, the tandem dimers showed much less fluorescence in the cytoplasm (Fig. 4 A).

Unexpectedly, the tandem dimers also displayed a diffusion coefficient approximately fourfold lower than for the single domains (Fig. 4 B). We were concerned that this may indicate a more complex interpretation of our parameters. In particular, we could envisage a scenario whereby random walks of the proteins diffusing in the cytosol adjacent to the plasma membrane could lead to multiple collisions with the surface, and thus repeated incidences of lipid binding. Our membrane diffusion coefficient would thus represent cytosolic diffusion interrupted by occasional binding to relatively slow lipid molecules. Because the tandem PH domain would have to release two lipid molecules before it could undergo a period of rapid cytosolic diffusion, this would happen less often and the protein would thus appear to diffuse much slower.

We addressed this issue with two approaches. First, we rendered the first domain of a tandem dimer incapable of binding PtdIns(4,5)P\(_2\) by mutation of arginine 40. As expected, this protein appeared similarly distributed to the single domain (Fig. 4 A) and yielded a similar \(\tau\) (Fig. 4 C). Yet, its apparent diffusion coefficient was unchanged and identical to the wild-type tandem domains (Fig. 4 B and Table I). This indicates that \(D\) is not determined primarily by lipid binding, as posited in the preceding paragraph, but is rather caused by some other property of the protein, most likely transient binding to other, less-mobile
We observed (a) that the value of membrane dissociation time \( \tau \) in response to PLC activation or by bleaching was significantly longer for the tandem dimer than the isolated domains and that, (b) importantly, for each protein, \( \tau \) was not significantly different when comparing the values derived from the two methods (Fig. 5 C). Therefore, we conclude that the membrane dissociation time \( \tau \) does indeed represent the time for individual protein–lipid complexes to dissociate; i.e., it is the reciprocal of the dissociation rate constant (and so is related to affinity).

Studies of the RAS GTPase-activating proteins GAP1 and GAP1 IP4BP:

GAP1 contains a PH domain with high affinity for PtdIns(3,4,5)P3, and so translocates to the plasma membrane in response to PI 3-kinase activation (Lockyer et al., 1999). HEK cells transfected with GFP-GAP1 and incubated in serum-free medium and a PI 3-kinase inhibitor (to ensure no production of PtdIns(3,4,5)P3) showed cytosolic fluorescence (Fig. 6 A) and a rapid diffusion coefficient of \( \sim 4 \) \( \mu \)m2/s (Fig. 6 B) and a \( \tau \) of \( \sim 3.4 \) s (Table I). This confirms that when bound to membranes, GFP-GAP1 retains a high mobility (Brough et al., 2005), though that earlier study overestimated the \( \tau \) by not taking dissociation into account, thus missing the detectable decrease in \( \tau \) value caused by membrane binding (Table I).
accompanied by a nearly twofold increase in the dissociation time (Fig. 7C). This result was unexpected because even at the height of PI 3-kinase activation, plasma membrane PtdIns(3,4,5)P$_3$ levels reach only a fraction (<10%) of PtdIns(4,5)P$_2$ levels (Stephens et al., 1993), but it does suggest that GAP1 IP4BP can recognize receptor-generated PtdIns(3,4,5)P$_3$, and this in turn points to the possibility that it might be a PtdIns(3,4,5)P$_3$ effector.

GAP1 IP4BP can be displaced from the membrane by high concentrations of wortmannin, most likely because of inhibition of PI 4-kinase activity and depletion of PtdIns(4,5)P$_2$ (Cozier et al., 2000). Incubation of cells with 10 μM wortmannin led to cytosolic localization of the protein, where it diffused much faster at 4.6 μm$^2$/s (Table I), which is very similar to GAP1 m (as seen also by Brough et al., 2005).

The PH domain of GAP1 IP4BP was shown to be necessary for its inositol lipid-dependent targeting to the plasma membrane (Lockyer et al., 1997). To investigate if it was also sufficient to explain the protein’s slower lateral mobility and dissociation compared with GAP1 m, we produced two truncations. First, we removed the two N-terminal C2 domains (C2), as these are known to contribute to membrane targeting in other proteins (Cho and Stahelin, 2005; Lemmon, 2008). Second, we produced the isolated PH domain (Fig. 7A).

The highly homologous GAP1 IP4BP makes an interesting contrast with GAP1 m because in addition to binding PtdIns(3,4,5)P$_3$, GAP1 IP4BP protein also binds with high affinity to PtdIns(4,5)P$_2$ (Cozier et al., 2000). As a result, this protein is constitutively targeted to the plasma membrane (Fig. 7A). Under conditions of no PtdIns(3,4,5)P$_3$ production, there is a slight cytosolic haze of unbound protein (Fig. 7A), but the majority is bound to the plasma membrane, where it binds with an apparent τ of ~3.5 s and moves with a lateral diffusion coefficient somewhat slower than GAP1 m at ~0.3 μm$^2$/s (see also Brough et al., 2005). Activation of PtdIns(3,4,5)P$_3$ synthesis in the cells leads to a minor effect on the lateral diffusion coefficient (Fig. 7B and Table II). However, it causes an increase in the ratio of plasma membrane to cytosolic fluorescence (Fig. 7A), as the cytosolic haze is no longer discernable in most cells. This was

**Table II. Differences between diffusion coefficients of GAP1 IP4BP truncations**

<table>
<thead>
<tr>
<th></th>
<th>ΔC2</th>
<th>PH</th>
</tr>
</thead>
<tbody>
<tr>
<td>5 μM LY294002</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Full length</td>
<td>NS</td>
<td>P &lt; 0.01</td>
</tr>
<tr>
<td>ΔC2</td>
<td>NA</td>
<td></td>
</tr>
<tr>
<td>100 nM insulin</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Full length</td>
<td>P &lt; 0.001</td>
<td>P &lt; 0.001</td>
</tr>
<tr>
<td>ΔC2</td>
<td>NA</td>
<td>P &lt; 0.05</td>
</tr>
</tbody>
</table>

Results are from a Kruskal-Wallis test with a post hoc Dunn’s multiple comparison test, and are considered significant at P < 0.05. NA, not applicable; NS, not significant.
although we cannot reach a definitive conclusion from these data as to whether the C2 domains influence this lateral mobility.

Discussion

Our results show that the PH domain–containing proteins studied here spend seconds bound to the membrane but, during this short interaction, are able to undergo appreciable lateral diffusion of $\sim 1 \, \text{μm}^2/\text{s}$. Using these values, the mean distance proteins will travel on the membrane before a defined fraction dissociates can be estimated as $\sqrt{2 \times D \times \tau}$ (Teruel and Meyer, 2000); these estimated values are also presented in Table I as “Range” of a protein before either 63% or 90% dissociation.

<table>
<thead>
<tr>
<th>GAP1IP4BP</th>
<th>Ratio ($F_{PM}/F_{Cyt}$)</th>
<th>$D$ (μm$^2$/s)</th>
<th>$\tau$ (s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Full length</td>
<td>$P &lt; 0.0001$</td>
<td>$0.0633$</td>
<td>$0.0006$</td>
</tr>
<tr>
<td>ΔC2</td>
<td>$P &lt; 0.0001$</td>
<td>$0.2077$</td>
<td>$0.001$</td>
</tr>
<tr>
<td>PH</td>
<td>$P &lt; 0.0001$</td>
<td>$0.0373$</td>
<td>$0.001$</td>
</tr>
</tbody>
</table>

Results from a Mann-Whitney test. Results are considered significant at $P < 0.05$. No difference between full length, ΔC2, or PH was observed for the values of $\tau$ after either insulin or LY294002 treatment (Kruskal-Wallis test with a post hoc Dunn’s multiple comparison test, $P > 0.05$).
95% dissociates. What is clear is that, despite appreciable mobility on the membrane, the inositol lipid-bound proteins studied here do not travel farther than a distance of ~1–3 μm from where they bind. This range is a little farther than that described for the Dictyostelium discoideum CRAC protein, which binds PtdIns(3,4,5)P$_3$ with an estimated τ of 0.12 s and diffuses at 0.14 μm$^2$/s (Matsuoka et al., 2006), giving an estimated range of ~0.2 μm.

Our estimates are consistent with the qualitative data obtained by TIR bleaching (Fig. 1). Consider a typical HEK cell with a footprint 16 μm in diameter: it might take a single molecule of PH-PLCβ1 ~40 s to diffuse from the periphery to the center of the cell, but it dissociates with a τ of ~2.4 s (Table I). Indeed, during the 8-s bleaching period, the majority of PH-PLCβ1 and GAP1$^{IP4BP}$ molecules will have dissociated from the membrane, explaining why mobility on the scale of a cellular footprint (~10 μm) is dominated by dissociation from the membrane, as opposed to lateral diffusion.

This limited diffusion of inositol lipid-binding proteins has important functional implications. Free diffusion of the inositol lipids themselves, coupled to subcellular distributions of the enzymes that modify their head groups, can lead to the generation of local inositol lipid signals: many studies highlight the importance of PtdIns(3,4,5)P$_3$ generated at the leading edge of cells for efficient cell motility (Kolsch et al., 2008), and local PtdIns(3,4,5)P$_3$ signals are also required for epithelial cell polarity (Gassama-Diagne et al., 2006). Other examples include local generation of PtdIns(4,5)P$_2$ at the cleavage furrow during cytokinesis (Emoto et al., 2005; Field et al., 2005) and at regions of endocytosis and actin dynamics in adipocytes (Huang et al., 2004). Notably, all these locally produced inositol lipid signals have dimensions of micrometers. Hence, the limited diffusion of effector proteins described here (Table I) show that once recruited to these regions, the rapid diffusion of the proteins will allow them to thoroughly explore the locality of the signal and make functional interactions, whereas their dissociation ensures the lipid–effector complexes do not stray too far from the locally directed lipid synthesis. This provides a mechanism for inositol–lipid-mediated recruitment of proteins to specific regions of the plasma membrane.

The upper limit of the diffusion coefficients for the proteins described herein (Table I) are in good agreement with those described for the lipids themselves (Haugh et al., 2000; Yaradanakul and Hilgemann, 2007; Golebiowska et al., 2008) at ~1 μm$^2$/s; this makes sense given that the higher viscosity of the lipid bilayer produces a greater hindrance to lateral diffusion than the aqueous cytosol (Saffman and Delbrück, 1975). However, we are left with the curious observation that lateral diffusion on the membrane varies over an order of magnitude for the different proteins, irrespective of their membrane dissociation times (see Table I). Short-lived interactions or retention in membrane corals that hinder free diffusion manifest as a slower diffusion coefficient when they occur over a much faster time scale than the measurements performed in this study (Ritchie et al., 2005). A similar suggestion has been made for PtdIns(4,5)P$_2$, which exhibits slower diffusion in cells than in vitro, suggesting that the major fraction is transiently bound by immobile membrane components (Golebiowska et al., 2008). SPT has shown that full-length PLCβ1 shows anomalous diffusion that is consistent with trapping in 0.7-μm membrane partitions (Mashanov and Molloy, 2007). A popular idea is that such partitions might consist of viscous, cholesterol-enriched microdomains (“rafts”). However, the inositol lipids contain polyunsaturated fatty acid tails, and so they have been shown to partition into cholesterol-enriched fractions only through electrostatic interactions between the head group and polybasic proteins such as NAP-22 (Epand et al., 2004). PH domains bind inositol lipids via a deep canonical binding pocket (Lemmon, 2008), effectively screening the head group. This would exclude head group–assisted partitioning, and so we would expect PH domain–lipid complexes to be excluded from any such localization.

The membrane dissociation times described here vary between 2 and 7 s (Table I). As discussed in the results, these times most likely reflect the dissociation rate constants ($k_{off}$) for the lipid–protein complexes, and are therefore a determinant of affinity between a PH domain and its ligand, given by $K_D = k_{off}/k_{on}$. This leads to interesting implications for the kinetics and affinities of PH domain–inositol lipid interactions. Dissociation constants ($K_D$) for high-affinity PH domain interactions of the type studied here are in the micromolar range (Garcia et al., 1995; Lemmon et al., 1995; Cozier et al., 2000); so, assuming that these estimates apply in vivo, our measured dissociation times in turn lead to $k_{off}$ values for binding of the order of 10$^6$ M$^{-1}$s$^{-1}$, significantly slower than a diffusion-limited binding (which would be nearer to 10$^7$ M$^{-1}$s$^{-1}$; Shoup et al., 1981; Laufenburger and Linderman, 1996). A similarly low value was estimated from in vitro binding experiments with several PH domains (Manna et al., 2007) and suggests that formation of an inositol lipid–PH domain complex follows more complex, reaction-limited kinetics. Such kinetic parameters can include accessory interactions with other anionic lipids within the membrane (Garcia et al., 1995; Corbin et al., 2004) or possible hydrophobic interactions between the bound PH domain and the membrane (Flesch et al., 2005; Manna et al., 2007). Nonetheless, an on-rate constant of 10$^7$ M$^{-1}$s$^{-1}$ predicts translocation of proteins in the nanomolar-to-micromolar concentration range to inositol lipid signals with micromolar concentration (Stephens et al., 1993) within seconds, which is consistent with experimental measurements for translocation of PH domains to newly generated inositol lipids; e.g., Haugh et al. (2000) and Várnai and Balla (1998).

Materials and methods

DNA constructs

PH-PLCβ1-GFP wild type and R40L mutant (Várnai and Balla, 1998), and the GFP. PH-PLCβ1 $×$ 2 (van Rheenen et al., 2005) were gifts of T. Balla (National Institute of Child Health and Human Development, Bethesda MD) and K. Jalink (the Netherlands Cancer Institute, Amsterdam, Netherlands). The tandem PH-PH-GFP and PH(R40L)-PH-GFP from PLCβ1 were made by insertion of a second, wild-type domain in-frame into the respective PH-PLCβ1-GFP constructs at BamH1 sites, as described previously (van Rheenen et al., 2005). PH123-MyoX (Mashanov et al., 2004) was a gift of M. Peckham (University of Leeds, Leeds, England, UK). GFP-GAP$^{IP4}$ and GFP-GAP$^{IP4}$RFP were as described previously (Lockyer et al., 1997). The isolated PH domain of GAP1$^{IP4}$ was amplified from the full-length construct via PCR using the primers 5′-CCGAATTCGTCCTAGAAGAAGGGTTCC-3′ (forward) and 5′-GTCGGCCTGCACGTGTAAGATACCC3′.
(reverse), and cloned into pEGFP-C1 (Clontech Laboratories, Inc.) at EcoRI-BamHI sites (underlined). The ΔC2 domain truncation was amplified using 5'-GCGGAGCTCCGGTAAAGCGAGAGAC-3' (forward) and 5'-CCCTCACTATCCAAAGGTACCGG-3' (reverse), and cloned into pEGFP-C1 at SacI-Kpn1 sites (underlined). PM-YFP is the palmitoylated/myristoylated N-terminal 11 residues of human lyn kinase (MGC15526-KDS) cloned into pEYFP-N1 (Clontech Laboratories, Inc.) at EcoRI-BamHI sites. PM-YFP was a gift of T. Meyer (Stanford University, Stanford, CA). Isolated GFP was expressed from the pEGFP-N1 vector (Clontech Laboratories, Inc.). All constructs were subject to deoxy sequencing.

Cell culture and transfection
CHO cells expressing the M1 receptor (CHO-M1) were a gift from M. Edvardsson (University of Cambridge, Cambridge, England, UK). CHO-M1 and HEK293 cells were maintained in DMEM supplemented with 10% FCS, 100 μg/ml penicillin, 100 units/ml streptomycin. 1 d before transfection, 50,000–100,000 cells were seeded in the central 12-mm glass-bottomed well of a 35-mm dish (Nunc I wsells), which had been coated with poly-L-lysine. Cells were transfected with 2 μg DNA using 6 μl Lipofectamine 2000 (Invitrogen) in Opti-MEM (Invitrogen) according to the manufacturer’s instructions. After 24 h, cells were rinsed and then imaged in DME without phenol red (Invitrogen) containing 25 mM Hepes, and supplemented with 10% FCS. 100 nM insulin (Sigma-Aldrich) was included where indicated, and the cells were preincubated for 1 h at 37°C before imaging. When cells were treated with 5 μM LY294002 (Sigma-Aldrich), 10% FCS was omitted and cells were preincubated for 1 h at 37°C before imaging.

TIRF microscopy
A custom-built “through-the-lens” TIRF microscope was used as described previously (Holtr et al., 2004); essentially, this consisted of a modified inverted microscope (Axiovert S100TV; Carl Zeiss, Inc.) fitted with a 60 × plan apo objective (1.45 NA oil immersion objective (Olympus)). Images were acquired at ~5 frames/s on a Pentamex cooled charge-coupled device camera (Pinnova Instruments) controlled by IPLab software (version 3.9; BD). Excitation was with the 488-nm line of an Argon ion laser (100 mW, Melles Griot), power was set to 80%, and the beam was attenuated by 99% via a neutral density filter. Photobleaching within the evanescent field was achieved by removal of the neutral density filter for 8–20 frames were acquired before bleaching, and postbleach images were acquired until fluorescence recovery was complete. Experiments were performed at room temperature. Image stacks were exported from the IPLab software as TIFF files. These were opened with ImageJ (version 1.38: http://rsb.info.nih.gov/ij/) and converted to 8 bit. The “image calculator” function was used to subtract the first postbleach image intensity from the other images in the stack to highlight the fluorescence recovery. Contrast was then adjusted to show only the first 100 gray levels (see Fig. S1).

Spot bleaching experiments
Experiments were conducted on a laser scanning confocal microscope (SP5 TCS; Leica) attached to a DMi6000 inverted microscope equipped with a 63 ×  plan-apochromatic 1.4 NA oil immersion objective (Leica). Images were acquired from the principle behind this technique, see Results.

Image stacks from spot bleach experiments in the Leica image file (iff format) were imported into ImageJ using the LCO biosformat import tool (http://www.loci.wisc.edu/ome/formats.html). Stacks were subject to 3 × 3 smoothing, and the 10 prebleach frames were averaged to form a prebleach baseline, to which all subsequent frames were normalized. Next, the segmented line tool was used to trace a line along the plasma membrane across the bleached spot; the fluorescence intensity profile along this line was then recorded for several postbleach frames in the normalized image stack, using the built-in “record profile” macro. These data were then copied into an Excel spreadsheet (Microsoft) and normalized to the total cellular fluorescence (relative to the first frame) at each time point to correct for photobleaching during acquisition.

Corrected intensity profiles were then copied into Prism 4 (GraphPad Software) and fit independently with the following Gaussian function:

$$F(x) = 1 - B \times e^{-\frac{(x-c)^2}{2w^2}}$$  

where $F$ is the normalized fluorescence intensity, $c$ represents the center of the bleach profile (in distance x, in μm), $B$ represents the depth of the Gaussian profile, and $r$ is the Gaussian radius at e^{-1}. Fitted to these three parameters from the first time point were then used to define $B_c$, $n_0$, and $c$ for the following function (Oancea et al., 1998):

$$F(x,t) = 1 - B_0 \times \left(1 - \frac{r_0}{\sqrt{4Dt + r_0^2}}\right) \times e^{-\frac{(x-c)^2}{2w^2}}$$  

where $D$ is the apparent lateral diffusion coefficient (in μm²/s) and $r$ is the apparent membrane dissociation time (in seconds). Thus, this Gaussian function finds a single value of $D$ and $r$ for the change in shape of all the profiles with time caused by lateral diffusion and membrane dissociation, respectively.

A semi-independent check was then performed for the fitted values from Eq. 2. First, the values of $r^2$ were calculated from those values fitted from Eq. 1; these were plotted against time, and a line on the graph was defined in terms of the value of $D$ obtained from Eq. 2 using:

$$r^2 = 4Dt + t^2$$

Second, the relative area under the curves was estimated as $\sqrt{2\pi}Br$, normalized to the first postbleach frame, and plotted against time. Again, a curve was plotted using Eq. 2’s fitted value of $r$: relative area = $e^{-\sqrt{2\pi}B}$. This allowed the goodness of fit for the defined curves from Eq. 2 to be inspected, relative to the independent values of $r$ and $B$ fitted using Eq. 1.

Estimating the cytosolic diffusion coefficient of soluble proteins
This technique estimates the diffusion coefficient from the rate of expansion of a Gaussian bleach profile with time, as described by Seiffert and Oppermann (2005). Image stacks were normalized as described earlier for membrane proteins, and a straight line through the bleach spot was recorded from several time points. These profiles were bleach-corrected as for membrane proteins, and fit in Prism 4 using the following Gaussian function:

$$F(x) = 1 - B \times e^{-\frac{(x-c)^2}{2w^2}}$$  

where $F$ is the normalized fluorescence intensity, $B$ is the depth of bleaching at the center of the spot, $c$ is the full width at half maximum of the Gaussian profile. Fitted values of $w^2$ were then plotted against their respective time $t$, and the diffusion coefficient fit from:

$$w^2 = 2Dt + w^0$$
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Online supplemental material

Fig. S1 provides an outline of the normalization process used to present data from TIRF experiments. Videos 1–3 show real-time videos of the cells presented in Fig. 1C after such normalization. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200809073/DC1.

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Figure S1. **Normalization of TIRF data.** (A, left) Images show the raw data acquired at the indicated times. (A, right) The resulting image after subtracting the first postbleach frame. (B) After subtracting, contrast was adjusted to highlight the first 100 gray levels of the 8-bit images. A mask of the outline of the cell was then produced using the autothreshold function in ImageJ, using the original prebleach image; this was used to exclude noise from outside the cellular footprint. Bar, 10 µm.
Video 1. **TIR bleaching of PM-YFP.** Images were acquired and are displayed at 5 frames/s, and residual fluorescence after photobleaching has been subtracted. For details, see the legend to Fig. 1.

Video 2. **TIR bleaching of PH-PLCδ1-GFP.** Images were acquired and are displayed at 5 frames/s, and residual fluorescence after photobleaching has been subtracted. For details, see the legend to Fig. 1.

Video 3. **TIR bleaching of GFP-GAP1p45R.** Images were acquired and are displayed at 5 frames/s, and residual fluorescence after photobleaching has been subtracted. For details, see the legend to Fig. 1.