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Authors
Strahl, Thomas
Hama, Hiroko
DeWald, Daryll B
et al.

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Yeast phosphatidylinositol 4-kinase, Pik1, has essential roles at the Golgi and in the nucleus

Thomas Strahl,1 Hiroko Hama,2 Daryll B. DeWald,2 and Jeremy Thorner1

1Department of Molecular and Cell Biology, University of California, Berkeley, Berkeley, CA 94720
2Department of Biology, Utah State University, Logan, UT 84322

Introduction

Phosphatidylinositol (PtdIns) and derived molecules have crucial functions in eukaryotes, including yeast (Michell et al., 2003). PtdIns can be phosphorylated on certain hydroxyls in its head group by specific lipid kinases; phosphoinositides (PIPs) so generated can be hydrolyzed by various lipid phosphatases. PIPs, especially PtdIns4,5P2, can be cleaved by PLC, producing DAG and water-soluble inositol-1,4,5-P3 (IP3). IP3 can be acted on by other kinases and phosphatases to generate other inositol-phosphate species (IPx). Thus, different membrane PIPs and soluble IPx's are well suited to serve as spatial and temporal regulators of diverse cellular processes.

The Saccharomyces cerevisiae genome encodes three PtdIns 4-kinase (P14K) isoforms that generate PtdIns4P: Pik1 (Flanagan et al., 1993), Stt4 (Yoshida et al., 1994), and Lsb6 (Han et al., 2002; Shelton et al., 2003). All are conserved from yeast to humans (for review see Heilmeyer et al., 2003). The mammalian Pik1 orthologue is PI4KIIIβ (Kapp-Barnea et al., 2003). Pik1 (120 kD) is soluble in cell extracts (Flanagan and Thorner, 1992) and Stt4 (215 kD) is localized in the plasma membrane (PM; Audhya and Emr, 2002). Each is essential for cell viability (Flanagan et al., 1993; Yoshida et al., 1994), indicating they serve nonoverlapping roles. Lsb6 (70 kD) is membrane associated, but dispensable, and is purported to function in endosome motility (Chang et al., 2005).

The first sst4 mutants were identified because they were hypersensitive to staurosporine, which is an inhibitor somewhat specific for PKC-related protein kinases (Yoshida et al., 1994). This phenotype is now understood. Pkc1 is essential for cell viability (Levin et al., 1990) and activated by the small GTPase, Rho1 (Camada et al., 1996). Rho1 activation depends on the recruitment of its cognate guanine nucleotide exchange factor (GEF) Rom2, which contains a PtdIns4,5P2-specific pleckstrin homology (PH) domain (Audhya and Emr, 2002). Stt4 generates the pool of PtdIns4P at the PM that is converted to PtdIns4,5P2 by the PtdIns4P 5-kinase, Mss4 (Desrivieres et al., 1998; Audhya and Emr, 2003). Thus, PtdIns4P serves as an intermediate in the generation of PtdIns4,5P2 and, in many eukaryotes (but not S. cerevisiae), PtdIns3,4,5P3, which each have been ascribed roles in actin dynamics, receptor-tyrosine kinase signaling, and endocytosis (Martin, 1998). However, compelling cumulative evidence, obtained first in yeast, shows that PtdIns4P itself has an important function in the Golgi (Hama et al., 1999; Walch-Solimena and Novick, 1999; Levine and Munro, 2002; Wang et al., 2003).
Genetic evidence implicates Pik1 in the synthesis of the Golgi pool of PtdIns4P. However, there is conflicting data concerning subcellular localization of Pik1. In cell lysates, the enzyme fractionates mainly like a soluble protein (Flanagan and Thorner, 1992; Huttner et al., 2003). Nevertheless, when examined by indirect immunofluorescence, epitope-tagged Pik1 localized to prominent cytosolic bodies, only some of which seemed congruent with a marker (Chs5) of the late Golgi (Schnieders, 1996; Walch-Solimena and Novick, 1999). In some cells, the nucleus was prominently stained (but it could not be discerned whether staining was inside or decorating the nuclear envelope). Yet another study that used an antibody of uncertain provenance and questionable utility for specific detection of Pik1, localized the protein exclusively to the nucleus upon subcellular fractionation (Garcia-Bustos et al., 1994). In contrast, a recent global analysis of yeast proteins using COOH-terminal GFP fusions concluded that Pik1 is localized uniformly in the cytosol (Huh et al., 2003). To further complicate matters, Pik1 binds and is positively regulated by the small, N-myristoylated, Ca\(^{2+}\)/H11001-binding protein, Frq1 (frequenin/neuronal calcium sensor-1; Hendricks et al., 1999; Ames et al., 2000); however, the role of Frq1 in subcellular localization of Pik1 has not been explored.

Given the evidence that PIP-derived products have roles in the nucleus in both yeast (Odom et al., 2000) and animal cells (Irvine, 2003), the potential duality in Pik1 localization was intriguing, suggesting that, the essential functions of this enzyme may involve generation of PtdIns4P pools both at the Golgi and in the nucleus. To this end, and to better understand the mechanisms that control its subcellular localization, we first examined the intracellular distribution and dynamics of Pik1 in vivo using a fully functional GFP-Pik1 fusion, which revealed that Pik1 undergoes nucleocytoplasmic shuttling. We then used genetic approaches to discern the requirements for nuclear import and export of Pik1. Moreover, using appropriate mutants, we also analyzed the contributions that Frq1 makes to intracellular localization of Pik1. Finally, using strategies to restrict Pik1 to either the cytosolic or nuclear compartments, we investigated whether Pik1 serves essential physiological functions at the Golgi and in the nucleus and whether its PI4K activity is required in either organelle.
Results

Pik1 localizes to both the Golgi and the nucleus

Prior work (Hama et al., 1999; Walch-Solimena and Novick, 1999; Audhya et al., 2000) indicated that Pik1 function is needed for the Golgi-to-PM stage of secretion. At a restrictive temperature, pik1\textsuperscript{ts} mutants (but not isogenic PIK1/\textsuperscript{H}11001 cells) accumulate aberrant membranous structures (Fig. S1 A, available at http://www.jcb.org/cgi/content/full/jcb.200504104/DC1) that are similar in the EM to those accumulated by sec mutants blocked in Golgi-to-PM transport (Esmon et al., 1981; Fig. S1 B). The hypertrophied sacs that accumulate represent Golgi cisternae because they contain bona fide Golgi marker proteins, but not marker proteins of other compartments (Fig. S1 C). However, where Pik1 itself resides had not been resolved.

To examine subcellular localization in real time in live cells, GFP fusions were constructed. An NH\textsubscript{2}-terminal fusion (GFP-Pik1) was functional, as judged, first, by its stable expression that was determined by immunoblotting (unpublished data) and, second, by its ability to fully restore viability to pik1\textsuperscript{ts} cells (unpublished data). A COOH-terminal fusion (Pik1-GFP) was stable, but not functional. When expressed from the native PIK1 promoter on a low-copy (CEN) plasmid in a wild-type strain, GFP-Pik1 decorated numerous cytoplasmic puncta in the majority of cells (Fig. 1 A). To demonstrate that this compartment represents the Golgi, we exploited the properties of a chimera between a diagnostic marker for the late Golgi cisternae, Sec7 (Franzusoff et al., 1991), and Discosoma spp. red fluorescent protein (DsRed). Because DsRed tetramerizes, normally dispersed Golgi cisternae that contain Sec7-DsRed tend to clump into larger aggregates (Reinke et al., 2004). When GFP-Pik1 and Sec7-DsRed were coexpressed, GFP-Pik1 also clumped into a few large aggregates (Fig. 1 B, top left), just like Sec7-DsRed (Fig. 1 B, top right); and, both proteins colocalized in the majority of these clusters (Fig. 1 B, top left). Hence, the cytosolic puncta decorated by GFP-Pik1 are the Golgi itself.

However, we noted consistently that, even when expressed at a near-endogenous level, GFP-Pik1 was found in the nucleus in 2–13% of the cells (depending on the strain examined; Fig. 2 A). No correlation between bud morphology and Pik1 distribution was seen, suggesting localization is not regulated by the cell cycle. When expression of GFP-Pik1 was elevated (Fig. 2 B), all cells displayed a very bright fluorescence that was congruent with the nucleus (stained with a vital DNA dye) and the cytosolic puncta were obscured by the general increase in cellular fluorescence.

Pik1 undergoes nucleocytoplasmic shuttling

The preceding results suggested that GFP-Pik1 is imported into the nucleus and, when overexpressed, accumulates there because its rate of entry exceeds its rate of export. Given its size, this nuclear import of GFP-Pik1 should require one (or more) of the known karyopherins (Strum and Weis, 2001). Therefore, we expressed GFP-Pik1 in strains carrying null mutations or temperature-sensitive alleles in all of the known importins. Nuclear accumulation of GFP-Pik1 was not impeded in mutants lacking any of the nonessential importins: Kap104, Sxm1, Mtr10, Kap114, Nmd5, Lph2, Pse1, Pdr6, and Yrb4 (unpublished data).

Kap60/Srp1/importin-\(\alpha\) and Kap95/Rsl1/importin-\(\beta\) are each essential for viability. Typically, cargo proteins that use these karyopherins to enter the nucleus bind (via their NLS) to

![Figure 3](http://www.jcb.org/cgi/content/full/jcb.200504104/DC1)
Kap60, which, in turn, binds to Kap95 (Enenkel et al., 1995). If Pik1 has an essential role in the nucleus, then these karyopherins may mediate its entry. In a \textit{kap60}ts mutant (Loeb et al., 1995), GFP-Pik1 still localized to the nucleus, even after a prolonged incubation at a restrictive temperature, which was no different from \textit{KAP60}/H11001 cells at the same high temperature (Fig. 3 A).

In contrast, nuclear accumulation of GFP-Pik1 was largely abolished in a \textit{kap95}ts mutant (Iovine and Wente, 1997), even at permissive temperature, whereas robust nuclear accumulation of GFP-Pik1 was seen in otherwise isogenic \textit{KAP95}/H11001 cells even at restrictive temperature (Fig. 3 B). Thus, although not unprecedented (Nikolaev et al., 2003), Pik1 is among the rare cargo whose nuclear import is mediated by Kap95 directly.

Consistent with this conclusion, mutagenesis of the only close match in Pik1 to the classical NLS recognized by Kap60 (\textit{284KLPKRKPK} to \textit{284KLPKLLLK}) did not prevent its nuclear import or otherwise alter its intracellular distribution (unpublished data).

For confirmation, the ability of Pik1 to associate directly with Kap95 was examined in vitro. Empty nickel agarose beads or beads coated with purified Kap95-His\textsubscript{6} were incubated with the soluble fraction of extracts from yeast cells carrying an empty vector or expressing NH\textsubscript{2}-terminally c-Myc epitope–tagged Pik1 or a truncation, Pik1(\textit{793-1066}), lacking its catalytic domain. Bound proteins were analyzed by SDS-PAGE and immunoblotting. No species cross-reactive with the anti-c-Myc mAb was detected in extracts from cells carrying vector alone (Fig. S2, top, lanes 2 and 5; bottom, lane 2). In contrast, \~80% of the input mycPik1 bound to the Kap95-His\textsubscript{6}-coated beads, whereas \~5% of the input mycPik1 bound to empty beads (Fig. S2, top panel, compare lane 1 with lane 4). Although expressed at a lower level (Fig. S2, bottom, compare lane 3 with lane 1), \~80% of the input mycPik1(\textit{793-1066}) bound to the Kap95-His\textsubscript{6} beads, whereas no detectable binding to empty beads was observed (Fig. S2, top, compare lane 3 with lane 6). Thus, Pik1 binds to Kap95 via an interaction site within its NH\textsubscript{2}-terminal regulatory domain.

**Role of Frq1 in subcellular localization of Pik1**

The NH\textsubscript{2}-terminal regulatory domain of Pik1 also contains a high-affinity binding site for Frq1, and Frq1 is required for optimal activity of Pik1 and for normal Pik1 function in vivo (Hendricks et al., 1999; Ames et al., 2000; Huttner et al., 2003).
Based on its fractionation properties and its tight binding to Pik1, Frq1 might promote membrane interaction of Pik1, which lacks any known membrane-targeting motifs or domains. To determine whether Frq1 plays any role in subcellular localization of Pik1, we first examined a small deletion mutant, Pik1Δ152-191, that retains considerable catalytic function (~80% of wild-type Pik1), but lacks nearly all Frq1-binding activity (Huttner et al., 2003). Compared with GFP-Pik1, which displayed the expected distribution between the Golgi puncta and the nucleus (Fig. 4 A, left), GFP-Pik1Δ152-191 showed a somewhat enhanced nuclear accumulation, diffuse cytoplasmic distribution, and never any detectable cytoplasmic puncta, even in cells expressing it at a low level (Fig. 4 A, right). As independent confirmation, we took advantage of the fact that inviability of frq1Δ cells can be rescued when Pik1 is highly overexpressed. Although overexpression tends to obscure visualization of the Golgi puncta, such bodies are still seen in a fraction of FRQ1Δ cells where GFP-Pik1 is produced from the GAL1 promoter (not depicted), but never observed in frq1Δ cells (Fig. 4 B).

If Frq1 is required for Golgi recruitment of Pik1, then Frq1 itself should localize to the Golgi. Hence, Frq1 was tagged at its COOH terminus with GFP (because its NH2-terminal myristoyl group is important for its function) and was fully functional (unpublished data). Frq1-GFP displayed prominent cytoplasmic puncta, congruent with Sec7-DsRed (Fig. 5). As in pik1Δ mutants at restrictive temperature, secretion of invertase (Suc2) is largely blocked in frq1Δ mutants (even at permissive temperatures; Fig. S3 A, available at http://www.jcb.org/cgi/content/full/jcb.200504104/DC1) and aberrant Golgi-like structures are seen in frq1Δ cells at the restrictive temperature (Fig. S3 B). Thus, Frq1 plays a critical role in secretion because it is necessary for recruitment of Pik1 to the Golgi, but not for its nuclear import or export.

**Nuclear export of Pik1 is dependent on Msn5**

A hallmark of proteins that undergo continuous nucleocytoplasmic shuttling (as opposed to those bound and sequestered in the nucleus) is that they accumulate dramatically in the nucleus if the karyopherin responsible for their active export is removed. To demonstrate that Pik1 cycles between the nucleus and the cytosol and to identify the exportin responsible, we expressed GFP-Pik1 in strains that carry temperature-sensitive or null mutations in the exportin genes indicated (see Table II), and their otherwise isogenic parental strains, were transformed with either pTS6 or pTS8, as necessary, and inspected by fluorescence microscopy. Pronounced nuclear accumulation occurred only in the msn5Δ mutant, but cytosolic puncta were also present (arrows).

**Retention of Pik1 in the cytosol**

To test whether nuclear entry is essential for its function, we devised means to restrain Pik1 in the cytosol. There is no known consensus sequence for Kap60-independent, Kap95-dependent import. Hence, we exploited the COOH-terminal CCAAX motif of S. cerevisiae Ras2, which is S-prenylated, S-palmitoylated and carboxymethylated (Hancock, 2003) and serves as a constitutive membrane anchor (Pryciak and Hntress, 1998) that traffics proteins from the ER to the Golgi and then to the PM (Hancock, 2003). The five COOH-terminal residues of Pik1 (QGYIS-COOH) were replaced with the five COOH-terminal residues of Ras2 (CCHIS-COOH), designated Pik1-CCAAX. When expressed briefly from the GAL1 promoter on a CEN plasmid in normal cells, both GFP-Pik1 and GFP-Pik1-CCAAX decorated the Golgi puncta (although the latter was expressed at a somewhat lower level; Fig. 7 A), but GFP-Pik1-CCAAX was never observed in the nucleus, even upon prolonged expression from the GAL1 promoter (not depicted). When expressed in the same way in msn5Δ cells, GFP-Pik1 accumulated detectably in the nucleus, whereas GFP-Pik1-CCAAX did not (Fig. 7 B), confirming that GFP-
Pik1-CCAAX does not enter the nucleus. Thus, attachment of the Ras2 CCAAX motif to the Pik1 COOH terminus did not interfere with Golgi localization, but prevented nuclear import.

Retention of Pik1 in the nucleus

A 28-residue site (147–172) in Pik1 is necessary and sufficient for Frq1 binding (Huttner et al., 2003; Strahl et al., 2003), as judged by deletion mutants that remove these residues. To determine how such mutations affect subcellular localization, we examined Pik1 derivatives tagged with an NH₂-terminal c-Myc epitope by indirect immunofluorescence. Generally, localization in fixed cells observed using the epitope-tagged constructs gave the same result as for GFP-Pik1 fusions in live cells, for example, GFP-Pik1-CCAAX (Fig. 7) and mycPik1-CCAAX, as indicated, grown to mid-exponential phase, induced with galactose for 45 min, returned to glucose medium to repress further expression, and were viewed in the fluorescence microscope (left) or under Nomarski optics (right) after 1 h.

Pik1-CCAAX does not enter the nucleus. Thus, attachment of the Ras2 CCAAX motif to the Pik1 COOH terminus did not interfere with Golgi localization, but prevented nuclear import.

No consensus for cargo recognition by Msn5 is known, yet Pik1(DΔ10-192) must lack not only its Frq1-binding site, but also some sequence required for its Msn5-dependent export, confining it in the nucleus.

Pik1 has essential functions inside and outside of the nucleus

Pik1-CCAAX does not enter the nucleus, whereas Pik1(DΔ10-192) accumulates in the nucleus. Hence, we examined whether Pik1 restricted to these compartments can provide its essential function, when present as the sole source of this enzyme. Each variant was expressed from the GAL1 promoter on a TRP1-marked CEN plasmid in a heterozygous pik1::KanMX4/pik1::KanMX4 diploid. The resulting transformants were sporulated, and the tetrads were dissected on Gal medium at 26°C. If a Pik1 variant is functional, it permits growth of the otherwise inviable pik1::KanMX4 spores. Expression of mycPik1 rescued inviability of the pik1::KanMX4 spores because most tetrads yielded three or four viable colonies (Fig. 9, C) and many of the spore clones were both G418-resistant and Trp⁺ (not depicted). Neither mycPik1-CCAAX nor mycPik1(DΔ10-192) supported growth of the pik1::KanMX4 spores because only two viable spores were produced from every tetrad (Fig. 9 A and B) and both spores were always G418-sensitive (not depicted).

Failure to rescue pik1::KanMX4 spore viability could arise if Pik1-CCAAX and Pik1(DΔ10-192) were expressed at a much lower level than normal Pik1; yet, immunoblotting indicated that mycPik1, mycPik1(DΔ10-192), and mycPik1-CCAAX were produced at similar levels (Fig. S4, bottom; available at http://

Figure 7. GFP-Pik1-CCAAX is restrained in the cytosol. A wild-type (MSN5+/MSN5⁺) diploid (BY4743) (A) and a homozygous msn5Δ/msn5Δ derivative (YTS002) (B) were transformed with pTS9 (GFP-Pik1) or pTS11 (GFP-Pik1-CCAAX), as indicated, grown to mid-exponential phase, induced with galactose for 45 min, returned to glucose medium to repress further expression, and were viewed in the fluorescence microscope (left) or under Nomarski optics (right) after 1 h.

Figure 8. Pik1(DΔ10-192) accumulates in the nucleus. Diploid strain (BYB67) expressing from pK5314(GAL-mycPik1), pTS2 and pTS3, respectively, mycPik1 (top), mycPik1(DΔ10-192) (middle) or mycPik1-CCAAX (bottom) were fixed and examined by indirect immunofluorescence using α-Myc mAb 9E10 (left), after counterstaining with DAPI to reveal the nucleus (right).
www.jcb.org/cgi/content/full/jcb.200504104/DC1). Another explanation could be that the modifications in Pik1-CCAAX or Pik1(Δ10-192) severely compromised catalytic activity. To examine this possibility, epitope-tagged proteins were recovered from extracts by immunoprecipitation and used as the enzyme source in in vitro PI4K assays. For cells expressing mycPik1, robust PtdIns4P production was found (Fig. S4, top, lane 1). A trace of PtdIns4P was generated when untagged Pik1 was overexpressed (Fig. S4, top, lane 2), presumably because, when a Myc-tagged protein is absent, some of the abundant untagged Pik1 binds nonspecifically to the c-Myc mAb-coated beads. This background disappeared when a Myc-tagged protein was present and Pik1 was at its endogenous level. For example, immunoprecipitation of a known catalytically inactive derivative, mycPik1(Δ302-785), produced no PtdIns4P (Fig. S4, top, lane 3).

By contrast, mycPik1-CCAAX exhibited a specific activity indistinguishable from mycPik1 (Fig. S4, top, lane 5), whereas mycPik1(Δ10-192) displayed a specific activity about ~10% of mycPik1 (Fig. S4, top, lane 4). Thus, the inability of Pik1(Δ10-192) to complement a pik1Δ mutation might be caused by its lower catalytic potency. However, several observations suggest that this is not the case. First, very low expression of normal Pik1, for example, from the GAL1 promoter under repressing conditions (i.e., on glucose medium) is sufficient to support the growth of pik1Δ cells (Schniders, 1996). Second, expression of Pik1(Δ10-192) from the strong GAL1 promoter on a CEN plasmid is still unable to rescue the inviability of pik1Δ cells (Fig. 9).

As a further test that the inability of Pik1(Δ10-192) to complement is caused by its restricted compartmentalization and not its lower specific activity, mycPik1(Δ10-192) and mycPik1-CCAAX were coexpressed from the GAL1 promoter on differentially marked plasmids in the pik1Δ::KanMX4/PIK1+ diploid. GAL1-expressed mycPik1-CCAAX was introduced into the diploid on the two differentially marked plasmids as a control for the effect of elevated Pik1 level because of its expression from two separate plasmids. When nuclearly localized mycPik1(Δ10-192) was coexpressed with cytoplasmically localized mycPik1-CCAAX, the pik1Δ spores were able to survive, as judged by recovery of tetrads with three or four viable spores (Fig. 10 A), and Trp+ Leu+ KanR spores were recovered at a reasonable frequency (not depicted). As judged by immunoblotting, the viable Trp+ Leu+ KanR spores produced both mycPik1-CCAAX and mycPik1(Δ10-192), albeit sometimes not in equal proportions, and did so in a galactose-dependent manner (Fig. 10 B). Despite the fact that Pik1-CCAAX has a catalytic activity indistinguishable from wild-type Pik1, expression of this derivative alone from two different plasmids did not rescue inviability of the pik1Δ spores because only two viable (and both G418 sensitive) spore colonies were recovered in every tetrad (Fig. 10 A). Because only those pik1Δ spores that expressed Pik1 in both the nucleus and the cytosol survived, it suggests that discrete PtdIns4P pools must be generated for nuclear functions and for secretory transport. The data presented here demonstrate that this is normally achieved by nuclearcytoplasmic shuttling of Pik1 and its Fpq1-dependent tethering to the Golgi.

To determine whether the PI4K activity of Pik1 is required for its function at the Golgi and in the nucleus, we mutated a residue (D918A) that is invariant in all PI4Ks (and PI3Ks). The crystal structure of a type IIβ PtdIns-phosphate kinase shows the equivalent position makes contact with both ATP and the substrate (Rao et al., 1998). The corresponding mycPik1(D918A), mycPik1(D918A)-CCAAX and mycPik1(Δ10-192 D918A) proteins were stably expressed (not depicted) and upon immunoprecipitation (Fig. S5 A, bottom, available at http://www.jcb.org/cgi/content/full/jcb.200504104/DC1) none of them displayed detectable PI4K activity, whereas mycPik1 displayed robust activity under the same conditions (Fig. S5 A, top). In addition, neither mycPik1(D918A) nor GFP-Pik1(D918A) was able to complement the inviability of pik1Δ spores (Fig. S5 B). Moreover, the mutation did not cause mislocalization because GFP-Pik1(D918A) was readily detectable both at Golgi puncta and in the nucleus (Fig. S5 C).

Finally, to determine whether Pik1 catalytic activity is needed for its essential functions in either compartment, either mycPik1-CCAAX and mycPik1(Δ10-192 D918A) or mycPik1(D918A)-CCAAX and mycPik1(Δ10-192) were coexpressed on differentially marked plasmids in the pik1Δ::KanMX4/PIK1+ diploid, which was subjected to tetrad analysis.
For the former combination, only two viable (and G418-sensitive) spores were recovered from every tetrad (Fig. 10 C, left panel), indicating that the kinase activity of Pik1 is essential for its nuclear function. For the latter combination, the vast majority of the tetrads (90 total) also yielded only two viable (and G418-sensitive) spores; however, in each of three tetrads, one of the pik1/H9004 (KanR) spores was recovered and carried both plasmid markers (Leu/H11001 and Trp/H11001). Nonetheless, when subsequently propagated, these cells grew very slowly (especially on glucose, where wild-type Pik1 expressed from the GAL1 promoter supports a normal growth rate, even when repressed), appeared grossly enlarged, were highly vacuolated and/or accumulated apparent vesicular material in the cytosol (data not shown). Clearly, therefore, the kinase activity of Pik1 is also important for its function at the Golgi.

**Discussion**

This is the first comprehensive study of Pik1 localization in live cells. Our findings confirm our own prior observations (Schnieders, 1996; Hama et al., 1999) and those of others (Walch-Solimena and Novick, 1999; Sciorra et al., 2005), but significantly extend those conclusions and provide new insights about the factors that regulate subcellular localization of this PI4K. In particular, we demonstrated that Pik1 enters the nucleus and undergoes active nucleocytoplasmic shuttling. Moreover, we showed that a primary role of its tightly bound regulatory subunit, Frq1, is to assist with targeting of Pik1 to the cytoplasmic face of the Golgi. By preventing cycling of Pik1 between the nucleus and the cytosol and, conversely, by coexpressing Pik1 derivatives restricted to each of those compartments, we found that execution of the cellular functions of Pik1 requires its presence in catalytically active form both in the nucleus and at the Golgi.

Pik1 and Stt4 catalyze the same biochemical reaction, but play nonoverlapping roles, as deletion of either gene is lethal and overexpression of each gene cannot compensate for the loss of the other. This lack of redundancy is now explained by localization of each essential PI4K to distinct compartments: Stt4 to the PM (Audhya and Emr, 2002) and Pik1 at the Golgi and in the nucleus. Dual localization of Pik1 is not an artifact of overexpression because it was observed when cells expressed GFP-Pik1 from its own promoter on a low-copy-number vector. Moreover, nuclear entry of Pik1 was blocked by the loss of a specific importin (Kap95), and nuclear exit was blocked by the loss of a specific exportin (Msn5). But, we cannot exclude the possibility that other karyopherins may make minor contributions to nucleocytoplasmic transport of Pik1.

Cytosolic Pik1 localizes to the Golgi. Residence of Pik1 on this compartment is in accord with prior evidence that Pik1-generated PtdIns4P is important for efficient formation of Golgi-derived secretory vesicles destined for exocytosis at the PM (Hama et al., 1999; Walch-Solimena and Novick, 1999; Audhya et al., 2000). The Pik1-containing cytosolic puncta
were identified as Golgi via colocalization with an Arf-GEF, Sec7, a well-accepted marker for this organelle in yeast (Franzusoff et al., 1991). Reportedly, Arf itself has a role in recruitment of PI4KIIIβ to the Golgi in tissue culture cells (Godi et al., 1999). Treatment of yeast cells with brefeldin A, which inhibits Sec7 GEF activity in vitro (Sata et al., 1998), causes aberrant Golgi to accumulate and blocks secretory transport (Chang et al., 2004), closely resembling the abnormal structures accumulated and the marked reduction in protein secretion seen in temperature-sensitive pik1 mutants at the restrictive temperature. However, we have no direct evidence that any yeast Arf involved in anterograde secretory transport is required for Pik1 function (unpublished data). Rather, as shown here, its regulatory subunit, Frq1, is targeted to the Golgi and is required for recruitment of Pik1 to the Golgi. Indeed, after our discovery of Frq1 as a permanently bound positive regulator of Pik1 in yeast (Hendricks et al., 1999), evidence has accumulated that its mammalian orthologue plays a similar role in localizing PI4KIIIβ at the Golgi (Bourne et al., 2001; Kapp-Barnea et al., 2003; Haynes et al., 2005).

PtdIns4P generated by Pik1 at the Golgi is not efficiently converted to PtdIns4,5P2 presumably because the PtdIns4P 5-kinase, Mss4, localizes to the PM and to the nucleus, but not to the Golgi (Desrivieres et al., 1998; Audhya and Emr, 2003). In addition, Inp53/Sj3, a PIP 5-phosphatase that operates at the Golgi (Ha et al., 2003), may prevent inadvertant or premature conversion of PtdIns4P to PtdIns4,5P2 before secretory vesicles reach the PM. It is assumed that Pik1-generated PtdIns4P serves as a specific docking epitope on the Golgi membrane for recruitment of other proteins that are involved in vesicle formation and trafficking. Although certain yeast proteins have PH domains (Levine and Munro, 2002) and PH-like domains (Li et al., 2002) that mediate their Pik1-dependent and PtdIns4P-specific localization to the Golgi, these polypeptides are not individually required for secretion. Recently, an automated global screen for mutations synthetically lethal with a pik1Δ allele implicated Gyp2, the cognate GAP for a Golgi-specific Rab family member (Ypt31), as a potential candidate (Sciorra et al., 2005). Gyp2 contains a conserved GRAM domain (Doerks et al., 2000), which is a structural motif that resembles that of PH domains (Begley et al., 2003). Whether GRAM domains bind PIPs is, however, somewhat controversial (Begley et al., 2003). Moreover, mutations in the GRAM domain that make Gyp2 nonfunctional in vivo did not alter the subcellular distribution of GFP-Gyp2 nor is a gyp2Δ mutant inviable. Hence, the identity of the PtdIns4P-binding protein(s) required for secretion remains elusive.

In this regard, one study showed that PI4KIIIβ (but not its kinase activity) is necessary to recruit Rab11 (the mammalian Ypt31 orthologue) to the Golgi, and that this interaction is important for subsequent membrane traffic from the Golgi to the PM (de Graaf et al., 2004). However, in addition to the tagged PI4KIIIβ derivatives followed, catalytically active endogenous PI4KIIIβ was present in the same cells. In yeast, it is claimed that Lsb6 contributes to endosome motility independent of its own ability to generate PtdIns4P (Chang et al., 2005), but Sst4 at the PM could supply PIPs for endocytosis and control of actin dynamics.

In any event, it seems well established that one vital function of Pik1 is executed at the Golgi. However, as shown here, it is not sufficient for cell viability to restrain Pik1 to the cytosol or even to Golgi membranes. When expressed alone, Pik1-CAAX, which is stable, fully catalytically active, present abundantly at the Golgi, and able to generate copious amounts of PtdIns4P at the Golgi—as judged by decoration with a PtdIns4P-specific reporter, GFP-2X-PH-domainDab2 (Levine and Munro, 2002; unpublished data)—was unable to support viability of pik1Δ cells. Thus, the essential functions of Pik1 are not confined to the Golgi and to the secretory process. Indeed, when Pik1-CAAX was coexpressed with Pik1(Δ10-192) (which is only feebly active, unable to complement a pik1Δ mutation, and largely confined to the nucleus), the simultaneous presence of these two proteins was able to rescue the viability of pik1Δ cells. When Pik1-CAAX was coexpressed with catalytically inactive Pik1(Δ10-192), the cells were dead, confirming that PtdIns4P supplied by Pik1 in the nucleus is essential for cell function.

There is considerable evidence that PtdIns4,5P2 is present in the S. cerevisiae nucleus and is cleaved by the PLC61 orthologue, Plc1 (Flick and Thorner, 1993), to generate IP3 and other more highly phosphorylated IP3s derived from it, which have apparent roles in regulating mRNA export (York et al., 1999), modulating transcription (Odom et al., 2000) perhaps via chromatin-remodeling complexes (Shen et al., 2003; Steger et al., 2003), and influencing telomere length (York et al., 2005). Our results pinpoint Pik1 as the PI4K that is responsible for supplying the nuclear pool of PtdIns4P and, because Mss4 also traffics to the nucleus, at least some of this lipid is presumably converted to PtdIns4,5P2 to supply the substrate for Plc1. Like Pik1 and Mss4, Plc1 also undergoes active nucleocytoplasmic shuttling (Huynh, 1998). Thus, the cell brings the necessary machinery into the nucleus to ensure that these products are generated in situ. Given that IP3s are small enough to freely traverse the nuclear pore complex by passive diffusion, it is perhaps not surprising that generation of IP3s in the cytosol by contrived means is sufficient to support their nuclear functions (Miller et al., 2004). However, we find that when Plc1 is confined to the nucleus by point mutations that ablate its Xpo1-dependent nuclear export sequence, the rate and extent of IP3 production and generation of its more highly phosphorylated derivatives is elevated (unpublished data). Thus, most likely, soluble IP3s normally are generated locally within the nucleus via Plc1-dependent cleavage of the PtdIns4,5P2 supplied by Pik1 and Mss4 action.

However, plc1Δ mutants are viable (under nonstressful conditions; Flick and Thorner, 1993), whereas pik1Δ mutations are lethal under all conditions (Flanagan et al., 1993). Therefore, the PtdIns4P (and/or PtdIns4,5P2) derived from Pik1 action in the nucleus is not solely used as the substrate for Plc1, but must have some other essential function(s). Current evidence suggests that this essential role might be transcription. Mammalian tumor suppressor protein, ING2, is a member of a family of at least six, highly related chromatin-associated proteins and contains a plant homeodomain (PHD) motif that reportedly binds PtdIns4,5P2 and PtdIns5P (Gozani et al.,

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2003). Four close relatives of ING2 exist in the *S. cerevisiae* genome, all contain PHD motifs, and all are components of nuclear chromatin remodeling machines involved in gene regulation. Whether yeast PHD proteins bind PIPs is not known.

Also, tethering of transcription factors to integral membrane proteins on the inner face of the yeast nuclear envelope seems to have a critical role in regulating the expression of certain essential genes during the unfolded protein response and presumably during adaptation to other cellular stresses (Brickner and Walter, 2004). Perhaps Pik1-generated PIPs affect organization, stability, or function of the nuclear envelope proteins required for this transcriptional control. However, like other secretory blocks, shift of *pik1α* mutants to restrictive temperature induces robust UPR-*lacZ* reporter expression (unpublished data); hence, sustained Pik1-dependent PIP production is not needed, at least for the unfolded protein response. Potential involvement of Pik1-derived products in transcriptional regulation may be coupled to a perhaps related phenomenon. Certain proteins that reside in the nucleus rapidly relocalize to the cytosol when the secretory pathway is compromised (Nanduri et al., 1999). The so-called cell integrity MAPK signaling pathway initiated by Pkc1 is reportedly necessary for this response (Li et al., 2000; Nanduri and Tartakoff, 2001). When a secretion-defective mutant (sec6-4) was shifted to restrictive temperature for only 10 min, all nuclearly associated Pik1 was lost (Walch-Solimena and Novick, 1999).

Hence, Pik1 may be a protein that rapidly relocalizes to the cytosol upon secretory stress. Nucleocytoplasmatic shuttling of Pik1 may, therefore, be under regulation and Pik1 itself (or some component involved in its nucleocytoplasmic transport) may be a target of Pkc1 or of the MAPK (Mpk1/Slt2) it activates.

### Materials and methods

#### Construction of plasmids

Plasmids (Table I) were constructed using standard recombinant DNA methods. *Escherichia coli* strain DH5α and NM522 were used to manipulate and propagate plasmids. PCR was performed using *Pfu* DNA polymerase (Stratagene); all constructs were verified by dideoxy chain terminaton sequencing. To produce kinase-dead Pik1, DNA fragments encoding a D918A mutation were generated by PCR using appropriate primers and incorporated by homologous recombination-mediated double strand break repair in vivo via cotransformation with acceptor vectors linearized with *PstI* and *BglII* (pTS12 and pTS16), *BglII* and *BspEII* (pTS13) or *Nhel* and *Saci* (pTS15) in strain BJ2407. Plasmid DNA recovered from the resulting Leu+ or Trp+ transformants was rescued and amplified in *E. coli*. A YEp24-based plasmid encoding PEP24 (p)y2802; gift of E.W. Jones, Carnegie Mellon University, Pittsburgh, PA) was used to allow sporulation of the protease-deficient diploid strain BJ2407. GEX2TK-KAP95-His6 (gift of M. Rexach, Stanford University, Stanford, CA) was used to prepare GST-Kap95His6 in *E. coli*.

#### Yeast strains, growth conditions, and tetrad dissections

Yeast strains used in this study are listed in Table II. Standard rich (YP) and synthetic complete media (Sherman et al., 1986) were supplemented with either 2% glucose, 2% raffinose, or 2% galactose and with appropriate nutrients to maintain selection for plasmids. Yeast was cultivated at 30°C, unless otherwise stated. Standard methods for DNA-mediated transformation, sporulation, tetrad dissection, and other genetic manipulations of yeast cells were used (Guthrie and Fink, 1991). To generate a novel pik1 null allele, a KANMX4 cassette, flanked by short stretches (45 bp) of homology to sequences immediately upstream and downstream of the Pik1 coding region in the yeast genome, was amplified in a standard PCR reaction using pFA6a-KANMX4 as the template. The resulting DNA fragments were introduced by DNA-mediated transformation into strain BJ2407, and the cells were plated on YPD medium containing 200 μg/liter G418 sulfate (Meditech Inc.). Candidate antibiotic-resistant integrants were streaked on the same medium containing G418 and authentic transplacement of the Pik1 locus by the pik1::KANMX4 allele on one homologue was verified by analytical PCR using appropriate primers. Strains YTS129 and YTS131 were generated in a similar manner, using strain BY4743 and BY2407 (Hendricks et al., 1999). Table I. Plasmids used in this study

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<td>PIK1</td>
<td>mycPIK1</td>
<td>Hendricks et al., 1999</td>
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<td>PIK1</td>
<td>mycPIK1</td>
<td>Hendricks et al., 1999</td>
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<td>GAL1</td>
<td>mycPIK1(D918A)</td>
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<td>mycPIK1(Δ302-785)</td>
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<td>TEV</td>
<td>GFP(S65T)·KanMX6</td>
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<td>PEPl</td>
<td>E.W. Jones</td>
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<td>tac</td>
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<td>SEC7·DsRed</td>
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</tbody>
</table>

<sup>α</sup>All pTS plasmids are based either on pRS314 (TRP1) or pRS315 (LEU2) (Sikorski & Hieter, 1989).
appropriate primers to replace the PSE1 or MTR10 chromosomal loci, respectively, with a KANMX4 cassette. A one-step PCR-based technique for targeted modification of chromosomal loci (Longtine et al., 1998) was used to generate FRQ1-GFP. In brief, oligonucleotide primers with 5'-ends corresponding, respectively, to the last 40 bp of the FRQ1 ORF (forward) or to the first 40 bp downstream of the respective stop codons (reverse), and with 3'-ends to allow in-frame amplification of the GFP (S65T)/KanMX6 cassette, were used for PCR with PfA6a-GFP/KanMX6-KanMX6 as the template. The resulting DNA products were purified, introduced by transformation into strain BY4743, and G418-resistant transformants were selected. Genomic DNA was prepared from candidate clones to verify its integration by homologous recombination at the FRQ1 locus and sequenced to confirm the integrity of the construct. For integration of YIp lac204/T/C-SEC7/DsRed.14, the plasmid was cut with Bsu36I before transformation.

Fluorescence microscopy and indirect immunofluorescence
To view GFP and/or DsRed fusion proteins, cells were grown to mid-exponential phase and examined directly under a fluorescence microscope equipped with appropriate band-pass filters for detection of each protein. To counterstain for DNA, cells were incubated in growth medium with 2 μg/ml Hoechst 33258 (Invitrogen) for 15 min before viewing. Unless otherwise noted, expression of GFP fusion proteins under control of the GAL1 promoter was induced by adding galactose (2% final concentration) to the culture and, after 45 min, glucose was added (2% final concentration) to repress further expression and the cells were grown for 1 h. To localize GFP-Pik1 in strains SWY1312 and SWY1313, cells first were grown at 26°C, shifted to 37°C for 1 h, and then galactose was added to induce GAL1 promoter-driven expression. After 3 h, the cells were viewed by fluorescence microscopy. To localize GFP-Pik1 in strains YTS0012 and W303-1a (kap600 and KAP60p, respectively), cells were grown at 30°C, shifted to 37°C for 1 h, and then galactose was added to induce GAL1 promoter-driven expression. After 3 h, the cells were viewed by fluorescence microscopy.

Table II. Strains used in this study

<table>
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<tr>
<th>Strain</th>
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<tr>
<td>B2168</td>
<td>MAa leu2 trpl phen2-40 pep4-3 gal2</td>
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<td>CFY13</td>
<td>hsc83::EU2 pep4::URA3 (derived from B2168)</td>
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<td>BYB67</td>
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treated as just described, but incubated at 37°C for as long as 5 h after galactose induction.

BY676 cells carrying plasmids for the GAL1 promoter-driven expression of either mycPik1, mycPik1(D10-192) or mycPik1-CCAAX were grown to A₆₀₀nm = 0.5, induced by addition of galactose (2% final concentration) for 90 min, fixed, and prepared for indirect immunofluorescence. Cells were incubated with a solution (1 mg/ml) of affinity-purified anti-Myc mAb 9E10 that was diluted 1:150 in PBS, pH 7.3, containing 1 mg/ml BSA (PBSA) for 2 h at RT, washed three times with PBSA, and then incubated for 1 h with FITC-conjugated secondary antibody (Jackson ImmunoResearch Laboratories) that was diluted 1:700 in PBSA. To counter-stain for DNA, DAPI was added (1 μg/ml final concentration) for 90 min, fixed, and prepared for indirect immunofluorescence.

Preparation of yeast cell extracts and immunoprecipitation
Yeast cell lysis, preparation of extracts, and immunoprecipitations were performed as described previously (Hendricks et al., 1999; Hutter et al., 2003).

Online supplemental material
Supplemental materials and methods section describe the following protocols: negative stain and immunogold EM; preparation of Kap95-His6 and in vitro binding studies; in vitro kinase assay; and in vitro binding studies; invertase secretion measurement; and protocols: negative stain and immunogold EM; preparation of Kap95-His6 and in vitro binding studies; invertase secretion measurement; and measurements of PI4,5P2 (a phosphatidylinositol-specific phospholipase C) activity. Fig. S2 shows purified import substrate to mammalian nuclear import pathway for the transcription factor TFIIS. Emr2p is a karyopherin involved in the nuclear transport of messenger RNA binding proteins. For yeast, EM, and B. Glick, K.B. Hendricks, E.W. Jones, S. Patel, M. Rexach, B.Q. Wang, K. Weis, and S. Wente for strains, plasmids, or advice.

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