The yeast p24 complex is required for the formation of COPI retrograde transport vesicles from the Golgi apparatus

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The p24 family members are transmembrane proteins assembled into heteromeric complexes that continuously cycle between the ER and the Golgi apparatus. These cargo proteins were assumed to play a structural role in COPI budding because of their major presence in mammalian COPI vesicles. However, this putative function has not been proved conclusively so far. Furthermore, deletion of all eight yeast p24 family members does not produce severe transport phenotypes, suggesting that the p24 complex is not essential for COPI function. In this paper we provide direct evidence that the yeast p24 complex plays an active role in retrograde transport from Golgi to ER by facilitating the formation of COPI-coated vesicles. Therefore, our results demonstrate that p24 proteins are important for vesicle formation instead of simply being a passive traveler, supporting the model in which cargo together with a small GTPase of the ARF superfamily and coat subunits act as primer for vesicle formation.

Introduction

COPI vesicle-mediated retrograde transport from the Golgi apparatus to the endoplasmic reticulum (ER) is crucial for eukaryotic cell physiology (Semenza et al., 1990). The molecular mechanisms that drive COPI vesicle generation are not completely understood (Spang, 2002). The current model, known as priming complex model (Springer et al., 1999), proposes that Arf1p, a small GTPase, is attracted to the Golgi membrane, where it is activated by a guanine exchange factor (ArfGEF). Membrane-bound, activated Arf1p then recruits coatamer, a preassembled complex of seven subunits, which forms a priming complex with a GTPase-activating protein (ArfGAP) and a transmembrane protein (cargo or SNARE). Once enough COPI priming complexes are established, they associate laterally to form a larger, polymeric coat on the Golgi membrane. This coat polymerization leads to the deformation of the membrane and, subsequently, to the COPI vesicle generation.

In addition to the coat components, transmembrane proteins might also be important for the budding process by acting as a primer to form priming complexes (Springer et al., 1999). Specific COPI vesicle passengers, such as the members of the p24 family, have been suggested to play a role in COPI vesicle-mediated flow (Stammes et al., 1995; Bremser et al., 1999). The p24 proteins are assembled into heteromeric complexes that continuously cycle between ER and Golgi compartments (Sohn et al., 1996; Rojo et al., 1997; Fullekrug et al., 1999; Belden and Barlowe, 2001b). In yeast, at least four members of the p24 family (Emp24p, Erv25p, Erp1p, and Erp2p) function in the p24 complex (Marzioch et al., 1999). The yeast p24 complex plays a specialized role in selective cargo recruitment into specific ER-derived vesicles (Muñiz et al., 2000, 2001). Nevertheless, this is not likely to be the only function of the p24 complex in the early secretory pathway (Elrod-Erickson and Kaiser, 1996; Bremser et al., 1999; Lavoie et al., 1999; Emery et al., 2003). The p24 proteins have been assumed to play a structural role in COPI vesicle formation because of their ability to bind COPI proteins and their major presence in mammalian COPI vesicles (Stammes et al., 1995; Sohn et al., 1996). Indeed, mammalian p24 cytosolic tails displayed on liposomes can stimulate the formation of COPI vesicles (Bremser et al., 1999). Consistent with these findings and based on further in vitro experiments, it has been proposed that mammalian p24 proteins could inhibit...
The p24 complex is necessary for efficient trafficking from the Golgi to the ER when Glo3p GAP activity is reduced

The data presented in the previous paragraph suggest that the p24 family members play a more active role in the generation of COPI-coated vesicles than previously anticipated. In the wild-type situation, this role may not be essential. However, when the ArfGAP activity provided by Glo3p is missing or compromised, p24 function in COPI vesicle generation could become vital.

To investigate this possibility, we assessed the lack of p24 function in the ret4-1 mutant, a temperature-sensitive mutant allele of GLO3 (Dogic et al., 1999). The T66I mutation in ret4-1, which is localized to the GTPase-activating domain of Glo3p, reduces the GAP activity toward ARF1 in vitro. We found that emp24Δ ret4-1 mutant cells were viable at 24°C, but they grew slower than respective single mutant cells (Fig. 2 A). Furthermore, deleting EMP24 increased the temperature sensitivity of the ret4-1 allele, which is consistent with the observed genetic interaction between emp24Δ and glo3Δ (Fig. 2 A). Next, we investigated whether the emp24Δ deletion aggravates the slight defect of the ret4-1 mutant in retrograde trafficking. Because anterograde and retrograde traffic between the ER and the Golgi are interdependent, a block in retrograde transport usually has an indirect effect on anterograde transport. Thus, we analyzed the post-translational processing of several early secretory pathway cargoes such as the vacuolar hydrolase, carboxypeptidase Y (CPY) (Stevens et al., 1982), and the secreted enzyme invertase (Esmon et al., 1987) in the ret4-1 mutant, as an indirect way to measure defects in retrograde trafficking. Mutations in several COPI genes result in the accumulation of the immature CPY form (p1) at the ER and a general decrease in the glycosylation state of the secreted invertase (Gaynor and Emr, 1997). Likewise, the lack of p24 protein function in a ret4-1 mutant led to an accumulation of the p1 form of CPY (Fig. 2 B) and exacerbated the impairment of the invertase glycosylation and secretion in the single mutants (Fig. 2 C), which is symptomatic of a severe defect in retrograde transport.

To assess more directly the defect of emp24Δ ret4-1 double mutant cells in retrograde trafficking, we determined the secretion of the ER molecular chaperone Kar2p. Most mutants that block retrograde transport secrete elevated levels of ER resident proteins with an HDEL signal, including Kar2p, into the media because the HDEL receptor Erd2p fails to retrieve the ER escaped proteins back from the Golgi (Semenza et al., 1990). Previous studies have shown that overproduction of Erd2p mitigates Kar2p secretion (Semenza et al., 1990; Belden and Barlowe, 2001a). Nevertheless, in some trafficking mutants, such as p24 mutants, the activation of the unfolded protein response (UPR) also contributes to Kar2p secretion by exceeding the capacity of the HDEL-retrieval pathway (Belden and Barlowe, 2001a). Wild-type cells did not secrete Kar2p into the media, but emp24Δ, ret4-1, and emp24Δ ret4-1 cells secreted significant amounts of Kar2p (Fig. 2 D). Interestingly, when ERD2 was overexpressed in emp24Δ and ret4-1 mutants Kar2p is not secreted into the growth media, whereas overexpression of ERD2 in emp24Δ ret4-1 cells did not reduce Kar2p secretion (Fig. 2 D). This defect in Kar2p retention might be due to an exacerbation of the
in *emp24*/*H9004* and *ret4-1* cells, whereas the ER pattern observed in *emp24*/*H9004* and *ret4-1* cells was identical to that in wild-type cells. Together, these data show that *emp24*/*H9004* *ret4-1* double mutant cells exhibit COPI mutant–like phenotypes, supporting the idea of the involvement of the p24 complex in COPI function.

The p24 complex is required for COPI vesicle budding from Golgi membranes

Our genetic and biochemical findings suggest that the p24 complex might participate in retrograde transport from Golgi to ER by promoting the formation of COPI vesicles. We assessed directly this hypothesis by using an in vitro Golgi vesicle budding assay (Spang and Schekman, 1998). Enriched Golgi membranes devoid of ER from wild-type and *emp24*/*H9004* strains were subjected to a vesicle budding assay by incubating them in the presence of GTP. Vesicles containing the COPI cargo Emp47p were produced by wild-type Golgi-enriched membranes (Fig. 3A). In contrast, Golgi membranes from the *emp24* mutant strain failed to form COPI vesicles (Fig. 3A). This result indicates that the p24 complex plays an important role in COPI vesicle generation from Golgi membranes.
Golgi membranes might rescue the emp24/H9004/sec21-1 mutant phenotype. Because ArfGAPs have been shown to potentiate the binding of coatomer to cargo proteins and consequently promote the stabilization of COPI priming complexes (Rein et al., 2002; Lee et al., 2005), we tested whether the temperature sensitivity of emp24/H9004/sec21-1 and erv25/H9004/sec21-1 is suppressed by overexpression of Glo3p and Gcs1p. Indeed, overexpression of GLO3 was able to restore growth of emp24Δ sec21-1 and erv25Δ sec21-1 at the restrictive temperature, whereas overexpression of GCS1 did not rescue the lethal phenotypes (Fig. 4A).

The phenotype enhancement in the emp24Δ sec21-1 mutant might be due to the failure of cargo proteins to create enough priming complexes that would support budding in the absence of p24 proteins. Increasing the stability of coatomer on Golgi membranes might rescue the emp24Δ sec21-1 mutant phenotype. Because ArfGAPs have been shown to potentiate the binding of coatomer to cargo proteins and consequently promote the stabilization of COPI priming complexes (Rein et al., 2002; Lee et al., 2005), we tested whether the temperature sensitivity of emp24Δ sec21-1 and erv25Δ sec21-1 is suppressed by overexpression of Glo3p and Gcs1p. Indeed, overexpression of GLO3 was able to restore growth of emp24Δ sec21-1 and erv25Δ sec21-1 at the restrictive temperature, whereas overexpression of GCS1 did not rescue the lethal phenotypes (Fig. 4A). This result is consistent with the role of Glo3p as a specific component of the COPI vesicle coat through association with the coatomer subunit Sec21p (Lewis et al., 2004), and provides
and IRE1, an ER-localized kinase that activates the UPR, results in slow growth and more severe transport defects (Belden and Barlowe, 2001a). Accordingly, a genetic interaction between emp24Δ and hac1Δ, a transcriptional activator for a set of UPR-regulated genes, was observed during the genetic screen (unpublished data). We wanted to test directly whether UPR activation is responsible for the lack of an obvious retrograde trafficking defect in the emp24Δ H9004 strain. We assessed this possibility by determining whether the Golgi protein Rer1p, which cycles through the ER (Sato et al., 1997), is efficiently recycled back to the ER in an emp24Δ H9004 ire1Δ H9004 strain. We blocked ER exit with the temperature-sensitive sec23-1 (COPII) allele to trap cycling proteins in the ER (Sato et al., 1997). If retrograde transport of Rer1p-GFP depends on both the p24 complex and on UPR, an emp24Δ H9004 ire1Δ H9004 sec23-1 triple mutant strain should not accumulate Rer1p in the ER upon shift to the restrictive temperature (37 °C). As shown in Fig. 5, in sec23-1, emp24Δ sec23-1, and ire1Δ sec23-1 mutant cells at 24 °C, Rer1p-GFP showed punctate staining typical for Golgi in yeast, whereas at 37°C, the ER-characteristic nuclear

further evidence that p24 family proteins are important to stabilize priming complexes on Golgi membranes, which allows efficient polymerization of the COPI coat.

If our hypothesis is correct that p24 proteins are relevant for COPI priming complex formation, they should efficiently recruit COPI coat components such as coatomer and Glo3p. It has already been demonstrated that Emp24p and Erv25p bind coatomer (Belden and Barlowe, 2001b). Next, we tested whether Glo3p is also able to interact specifically with p24 proteins. Peptides corresponding to the C-terminal 10 amino acids of Emp24p or Erv25p were coupled to Sepharose beads and incubated with cytosol. We detected binding of Glo3p to both tail sequences (Fig. 4 B). In contrast, Gcs1p was not recruited to either the Emp24p or the Erv25p tail, supporting the idea that Gcs1p is not part of the COPI coat complex. Furthermore, recombinant Glo3p bound directly to the p24 tails (Fig. 4 C). Our data demonstrate that p24 proteins recruit COPI coat components. Together, our results show that p24 proteins can form COPI priming complexes and that these complexes are required to form retrograde COPI-coated vesicles efficiently from Golgi membranes.

UPR compensates the loss of retrograde transport function in the absence of p24 proteins

We have established in the previous paragraph that p24 complex form priming complexes. However, p24 genes are not essential in yeast. Indeed, deletion of all eight p24 family members does not produce severe transport phenotypes (Springer et al., 2000). Yet, subclasses of secretory proteins accumulate in the ER. How can this apparent discrepancy between the importance of p24 proteins for vesicle generation and the mild phenotypes of their deletion be reconciled? Perhaps a compensatory mechanism exists that helps the cell to cope with the loss of p24 proteins. Indeed, deletion of ERV25 leads to UPR activation (Belden and Barlowe, 2001a). Moreover, the concomitant loss of ERV25 (or EMP24) and IRE1, an ER-localized kinase that activates the UPR, results in slow growth and more severe transport defects (Belden and Barlowe, 2001a). Accordingly, a genetic interaction between emp24Δ and hac1Δ, a transcriptional activator for a set of UPR-regulated genes, was observed during the genetic screen (unpublished data). We wanted to test directly whether UPR activation is responsible for the lack of an obvious retrograde trafficking defect in the emp24Δ strain. We assessed this possibility by determining whether the Golgi protein Rer1p, which cycles through the ER (Sato et al., 1997), is efficiently recycled back to the ER in an emp24Δ ire1Δ strain. We blocked ER exit with the temperature-sensitive sec23-1 (COPII) allele to trap cycling proteins in the ER (Sato et al., 1997). If retrograde transport of Rer1p-GFP depends on both the p24 complex and on UPR, an emp24Δ ire1Δ sec23-1 triple mutant strain should not accumulate Rer1p in the ER upon shift to the restrictive temperature (37 °C). As shown in Fig. 5, in sec23-1, emp24Δ sec23-1, and ire1Δ sec23-1 mutant cells at 24 °C, Rer1p-GFP showed punctate staining typical for Golgi in yeast, whereas at 37°C, the ER-characteristic nuclear
This study further supports the notion that certain transmembrane cargoes, such as the p24 protein family members, might be essential components in the regulation of vesicle formation instead of simply being a passive traveler. p24 proteins could recruit initially the deactivated form of Arf1p, (Gommel et al., 2001) facilitating the formation of a COPI priming complex and subsequently enabling efficient budding. In addition, the ability of p24 proteins to oligomerize and to present multiple coatomer-binding motifs might promote COPI budding by docking coatomer more firmly to the membrane (Bethune et al., 2006). Overexpression of coatomer-binding tails in oligomeric complexes has been shown to overcome the lethality of sec21-3 at the nonpermissive temperature presumably by stabilizing coatomer on the Golgi (Sandmann et al., 2003). Moreover, p24 complex might play a key role in the stabilization of priming complexes by modulating the ArfGAP activity (Goldberg, 2000; Lanoix et al., 2001). Thus, other cargo proteins with lower coatomer affinity, like the single tail exposing Emp47p, could be captured by stabilized priming complexes and then be sorted into COPI vesicles.

This page contains a figure labeled “Figure 5. UPR compensates the loss of retrograde transport function in the absence of p24 proteins. Cells expressing Rer1p-GFP were observed by fluorescence microscopy at 24°C, or after the shift to 37°C for 20 min. Bar, 5 μm.”
Materials and methods

Yeast strains and growth conditions
Strains of Saccharomyces cerevisiae used for this work are listed in Table S1 (available at http://www.jcb.org/cgi/content/full/jcb.200710025/DC1). Standard genetic manipulations were used throughout (Sherman, 1991). Strain RH6148 was made by replacement of EMP24 ORF by natMX (Goldstein and McCusker, 1999) disruption cassette in the Y2292 background. Strain MMY104 was obtained by replacing the entire IRP1 coding sequence of RH1433 with a HphMX disruption cassette [Goldstein and McCusker, 1999]. Strains MMY103 and MMY91 were constructed by crossing MMY104 with RH4443. Strain MMY369 was constructed by crossing RH441 with PC238. Strains MMY409, MMY410, MMY419, and MMY518 were constructed by crossing MMY369 and RH469 with BYG418. Cells were grown in either rich medium YPUD (1% yeast extract, 2% peptone, 2% glucose, and 40 mg/ml each of adenine and uracil) or minimal medium SD (0.67% yeast nitrogen base without amino acids, 2% glucose, 20 μg/ml each of histidine, leucine, and tryptophan, and the required nutrients).

Synthetic lethal screen
Synthetic lethal screen was performed as described by Tong et al. (2001), Synthetic lethal screen and the required nutrients). Cells were grown in either rich medium YPUAD (1% yeast extract, 2% peptone, 2% glucose, and 40 mg/ml each of adenine and uracil) or minimal medium SD (0.67% yeast nitrogen base without amino acids, 2% glucose, and the required nutrients).

Analysis of Kar2 secretion
Assays of ERD2–H9252 fusion construct, pJC31, were performed as described by Cox and Walter (1996). For fluorescence microscopy of GFP-tagged strains, log-phase cells grown in either rich medium YPUAD (1% yeast extract, 2% peptone, 2% glucose, and 40 mg/ml each of adenine and uracil) or minimal medium SD (0.67% yeast nitrogen base without amino acids, 2% glucose, and the required nutrients).

Pulse-chase analysis of CPY and invertase
Radiolabeling and immunoprecipitations were performed as described by Sutterlin et al. (1998). For invertase secretion, cells were induced as described by Küberl et al. (1994) and internal and external invertase was assayed as described by Gaynor and Emr (1997).

Analysis of Kar2 secretion
Extracellular Kar2p secretion was analyzed as described by Belden and Barlowe (2001a).

β-Galactosidase assay
Assays of β-galactosidase activity in extracts of yeast cells containing the UPRE-LacZ fusion construct, pCJ31, were performed as described by Cox and Walter (1996).

In vitro Golgi budding assay
Golgi membranes and COP1 components were purified as described by Sperandio and Schekman (1998). The Golgi budding assay was performed as described by Lewis et al. (2004) with several modifications. For the Golgi budding reactions, membranes were incubated in the presence of 0.1 mM GTP without (coatedlimited conditions) or with an excess of coatomer (250 μg/ml), and Arf1 protein (80 μg/ml) at 30°C for 30 min in a total volume of 180 μl. Samples were loaded on a Ficoll-sucrose gradient consisting of 135 μl of 35, 25, 20, and 15% and 184 μl of 10% Nycodenz in 0.67% yeast nitrogen base without amino acids, 2% glucose, 20 μg/ml each of histidine, leucine, and tryptophan, and the required nutrients).

Pull-down assay
Synthetic peptides corresponding to the C-terminal amino acids of Emp24p (RRFFEVTSLV) and Erv25p (KNFYFFKTTHL) with an N-terminal cysteine residue were generated (JPT Peptide Technologies) and linked to thiopropyl-Sepharose 6B (GE Healthcare) as described by Belden and Barlowe (2001b). Cytochalasin from a pep4 strain (RHF732) was obtained as described by Muñiz et al. (2000). Recombinant Glo3p was purified as described by Rein et al., (2002). In vitro binding reactions were performed as described by Belden and Barlowe (2001b). The immunoblot was quantified by densitometry.

Light microscopy
For fluorescence microscopy of GFP-tagged strains, log-phase cells grown in minimal media were observed directly. Acquisition was performed at 24°C using a Leica DMR microscope equipped with an objective lens (HCX PL APO 63x/1.30 OIL Ph3), a DC 350F camera, and Image Manager 50 v1.20 following the instructions of the manufacturer.

Online supplemental material
Table S1 provides information about the yeast strains used during this study. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200710025/DC1.

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