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Vps41 Phosphorylation and the Rab Ypt7 Control the Targeting of the HOPS Complex to Endosome–Vacuole Fusion Sites

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INTRODUCTION

Membrane fusion depends on multisubunit tethering factors such as the vacuolar HOPS complex. We previously showed that the vacuolar casein kinase Yck3 regulates vacuole biogenesis via phosphorylation of the HOPS subunit Vps41. Here, we link the identified Vps41 phosphorylation site to HOPS function at the endosome–vacuole fusion site. The nonphosphorylated Vps41 mutant (Vps41 S-A) accumulates together with other HOPS subunits on punctate structures proximal to the vacuole that expand in a class E background and that correspond to in vivo fusion sites. Ultrastructural analysis of this mutant confirmed the presence of tubular endosomal structures close to the vacuole. In contrast, Vps41 with a phosphomimetic mutation (Vps41 S-D) is mislocalized and leads to multilobed vacuoles, indicative of a fusion defect. These two phenotypes can be rescued by overproduction of the vacuolar Rab Ypt7, revealing that both Ypt7 and Yck3-mediated phosphorylation modulate the Vps41 localization to the endosome–vacuole junction. Our data suggest that Vps41 phosphorylation fine-tunes the organization of vacuole fusion sites and provide evidence for a fusion “hot spot” on the vacuole limiting membrane.

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the Golgi to the vacuole (Rehling et al., 1999). Importantly, Vps41 becomes phosphorylated at the vacuole by the casein kinase 1 Yck3 (LaGrassa and Ungermann, 2005). In yck3Δ cells, Vps41 accumulates in distinct puncta adjacent to or on the vacuolar membrane in vivo, and yck3Δ vacuoles are less sensitive to Ypt7 inhibitors than wild-type vacuoles in the in vitro vacuole fusion reaction. If Yck3 is overproduced or cells are challenged by osmotic shock, Vps41 phosphorylation is clearly observed in vivo. In addition, we observed a faster recovery of in vivo fusion in yck3Δ cells under highly osmotic conditions (LaGrassa and Ungermann, 2005).

Because we could not exclude an indirect effect of Yck3 on Vps41 due to phosphorylation of other putative substrates, we decided to identify the specific Yck3 phosphorylation sites in Vps41 and analyze the consequences of the corresponding mutations. We now show that Vps41 phosphorylation can be linked to its function at the endosome-vacuole interface.

MATERIALS AND METHODS

Yeast Strains and Molecular Biology

Yeast strains used are listed in Supplemental Table S1. Yeast strains were cultured in YPD medium, except where indicated. Deletions and tagging of genes with green fluorescent protein (GFP) or tandem affinity purification (TAP) tags were performed using homologous recombination of polymerase chain reaction (PCR)-amplified fragments (Pugn-Sancho et al., 1998; Janke et al., 2001). For the expression of Vps41 under the NOP1 promoter, the VPS41 open reading frame was amplified by PCR and inserted into the integrative vector pRS406 containing the NOP1 promoter. The resulting pRS406-NOP1-prVPS41 plasmid was transformed into yck3Δ strains. Point mutations in VPS41 were generated using the QuickChange site-directed mutagenesis kit from Stratagene (La Jolla, CA). The vector coding for the TBC domain of Gyp1, pET22-Gyp1-46 (Wang et al., 2003), was transformed into BL21 Rosetta. Protein expression was induced by addition of 0.5 mM isopropyl-β-D-thiogalactoside (IPTG) to the culture medium overnight at 16°C. Purification was performed using the nickel-nitrilotriacetic acid resin (QIAGEN, Hilden, Germany) and elution with 300 mM imidazole. Buffer exchange to 20 mM piperazine-N,N'-bis[2-ethanesulfonic acid] (PIPES), pH 6.8, 200 mM sorbitol was performed with a PD10 column (GE Healthcare, Munich, Germany).

Microscopy

For GFP microscopy, yeast cells were grown to mid-log phase in YPD or selective medium, collected by centrifugation, washed once with SDC medium containing all amino acids, and immediately analyzed by microscopy. Staining of the cells with N-[3-(trimethylammonium)-propyl]-4-[4-diethylamino-phenylhexatrienyl] pyridinium dibromide (FM4-64) was performed as described previously (LaGrassa and Ungermann, 2005). Briefly, cells were incubated with 30 μM FM4-64 for 15 min and chased for 45 min. Images were acquired with a Leica DM5500 B microscope equipped with a SPOT Pursuit camera using GFP, FM4-64 and differential interference contrast (DIC) filters, and pictures were processed using Adobe Photoshop CS3 (Adobe Systems, Mountain View, CA).

Electron Microscopy (EM) Analysis

Strains grown to exponential phase before being processed for electron microscopy. Permeabilization was performed with SDC medium supplemented with all amino acids, and immediately analyzed by microscopy. Staining of the cells with N-[3-(trimethylammonium)-propyl]-4-[4-diethylamino-phenylhexatrienyl] pyridinium dibromide (FM4-64) was performed as described previously (LaGrassa and Ungermann, 2005). Briefly, cells were incubated with 30 μM FM4-64 for 15 min and chased for 45 min. Images were acquired with a Leica DM5500 B microscope equipped with a SPOT Pursuit camera using GFP, FM4-64 and differential interference contrast (DIC) filters, and pictures were processed using Adobe Photoshop CS3 (Adobe Systems, Mountain View, CA).

RESULTS

Ultrastructural Analysis of yck3Δ Cells

In yck3Δ cells, GFP-Vps41 accumulates in vivo in distinct punctate structures adjacent to the vacuole (LaGrassa and Ungermann, 2005) (Figure 1A). This observation prompted us to analyze yck3Δ cells by electron microscopy. In contrast to wild-type cells, yck3Δ cells contain elongated structures proximal to the vacuole (Figure 1B, A and B), which are in part reminiscent of the class E endosomes observed upon loss of ESCRT subunits (Rieder et al., 1996). The tubular structures may correspond to several flat endosomal cisternae that seem to be stacked onto each other (Figure 1B, C–E). Some structures look like open cups, which may be a result of the cutting procedure (Figure 1B, F–H). We consider it likely that the prominent GFP-Vps41 fluorescence signal corresponds to these stacked structures and those could be late endosomal compartments. This idea is supported by the fact that in yck3Δ cells, we observed colocalization between
GFP-Vps41 and both the endosomal SNARE Pep12 and the cargo protein Cps1 that is sorted to the vacuole via endosomes (Figure 1C).

**Identification of the Yck3 Phosphorylation Site**

One fundamental problem of our EM analysis is the correlation of the altered endosomal morphology to the function of Vps41 because Yck3 has several other targets within the cell, for example, Vam3 (Brett et al., 2008). To unequivocally link the in vivo and in vitro effects observed in the yck3 Δ mutant to Vps41 function, we searched for the phosphorylation sites in the protein. The Vps41 phosphorylation results in a size shift on gels and is observed in vitro if vacuole-containing membranes are incubated in the presence of ATP (Figure 2A). The Vps41 size shift is also detected in vivo but requires the addition of phosphatase inhibitors during cell lysis (LaGrassa et al., 2005; our unpublished observations). Although the deletion of several vacuolar or endosomal proteins involved in fusion did not interfere with Vps41 phosphorylation, any mutation causing Yck3 mis-sorting, such as the truncation of the Yck3 C-terminal domain, abolished Vps41 phosphorylation (Figure 2B and Supplemental Figure S1; Sun et al., 2004). To identify the phosphorylation site, we screened available databases for casein kinase I sites within the Vps41 sequence (NetPhos, http://www.cbs.dtu.dk/services/NetPhos/; ScanSite, http://scansite.mit.edu/) and identified four possible consensus sequences (Figure 2C). The relevant serine and threonine residues were changed into alanines in different combination and the resulting Vps41 mutant forms were expressed in the vps41 Δ background. We then purified membrane fractions and tested for an ATP-dependent mobility shift on SDS-PAGE gels (Figure 2D). Mutations within two regions of Vps41, starting at positions 118 and 364, blocked phosphorylation. Because the deletion of YCK3 results in large vacuoles (LaGrassa and Ungermann, 2005), we tested for vacuole morphology and observed that only the S364, 367, 368, 371, 372A, T376A mutant mimicked the yck3 Δ phenotype and was also located on the vacuolar rim (Figure 2E), whereas the S118, 120, 121A mutant showed fragmented vacuoles indicating a loss-of-function (data not shown). Further analysis of this phosphorylation site by the in vitro phosphorylation assay revealed that the double mutant S367, 368A had reduced mobility shift and the mutations S371,372A impaired Vps41 phosphorylation (Figure 2F), indicating that they are the main sites. We confirmed these results monitoring in vivo Vps41 phosphorylation (data not shown). We therefore decided to conduct further studies with a quadruple mutant of S367, 368, 371, 372A, which we abbreviated Vps41 S-A in the remaining text (or S-D for the phosphomimetic mutant).

**The Vps41 Phosphorylation Status Affects the HOPS Complex Localization**

To address the consequences of Vps41 phosphorylation, we analyzed vacuole morphology in our mutant strains. Whereas the Vps41 S-A or yck3 Δ mutant displayed round vacuoles, the phosphomimetic Vps41 S-D mutant had multilobed vacuoles (Figure 3A). This result is in agreement with our previous studies, which showed that overproduction of Yck3 leads to a decrease in vacuole fusion in vitro, although no fragmentation of vacuoles could be observed in this strain background (LaGrassa and Ungermann, 2005). Consistent with the vacuole morphology phenotype, the GFP-tagged Vps41 S-A mutant localizes to vacuoles and dot-like structures (Figure 3B), resembling wild-type GFP-Vps41 distribution in yck3 Δ cells (LaGrassa and Ungermann, 2005).
In contrast, the S-D mutant was found partially displaced into the cytoplasm, an observation that we confirmed by subcellular fractionation (Figure 3, B and C). Together, these results are consistent with the idea that Vps41 localization is impacted by its phosphorylation status.
To test whether Vps41 phosphorylation status determines the inclusion of this protein in the HOPS complex, we purified TAP-tagged Vps41 variants and the associated proteins by using IgG-Sepharose, and subsequently separated the isolated complexes, which were natively eluted from the IgG beads after TEV protease cleavage, on a gel-filtration column (Figure 4A). As shown previously (Peplowska et al., 2007), the assembled HOPS complex is eluted from the column after a volume of 10–11 ml (fractions 10 and 11), whereas monomeric Vps41 is found in fractions 13 and 14. Our analysis revealed that the HOPS complex is copurified with Vps41 regardless of its phosphorylation status. However, we cannot rule out that the association between Vps41 and the HOPS complex differs quantitatively in the different mutant strains. Compared with previous studies (Peplowska et al., 2007), we find higher amounts of monomeric Vps41 in our preparations. This is most likely due to the use of a NOP1 promoter, which leads to higher expression levels of Vps41.

Because Vps41 is involved in vacuole fusion, but it has also been purified in an intermediate complex together with the CORVET subunit Vps3 (Peplowska et al., 2007), we decided to determine the localization of GFp-tagged HOPS and CORVET subunits in our mutants. In wild-type cells, Vps11 and Vps18 were found in endosomal dots and on the vacuolar rim, whereas Vam6 localized primarily to the vacuolar rim and to some perivacuolar dots (Figure 4B; Nakamura et al., 1997). This accumulation in puncta is enhanced, when the Vps41 S-A mutant was analyzed: All three proteins, Vam6, Vps11, and Vps18, seemed to be enriched in a single dot proximal to or continuous with the vacuolar rim. This distribution is identical to that of the Vps41-GFP S-A mutant (Figure 3B), and it is in agreement with our gel-filtration data indicating that the HOPS complex is assembled in cells expressing the Vps41 S-A variant (Figure 4A). In strong contrast with these observations, GFP-Vam6 was distributed equally along the vacuolar rim in the Vps41 S-D background. Likewise, Vps11 and Vps18 lost their distinct localization and were found on the vacuole and enriched in one or two spots (Figure 4B), which may correspond to endosomes. Statistical analysis of the localization of Vam6, Vps11, and Vps18 in the Vps41 wild type (wt), S-A, and S-D mutant confirmed these conclusions (Figure 4B, bottom). The protein relocalization induced by the Vps41 mutations seems to be exclusively associated to the HOPS subunits as the distribution of neither the late endosomal Rab Vps21, the CORVET subunit Vps3 (Peplowska et al., 2007), the assembled HOPS complex is eluted from the column after a volume of 10–11 ml (fractions 10 and 11), whereas monomeric Vps41 is found in fractions 13 and 14.

Figure 3. Phosphorylation of Vps41 modulates its localization and function. (A) Vacuole morphology in Vps41 mutants. Strains expressing the indicated Vps41 mutants were incubated with FM4-64 and visualized by DIC optics or by fluorescence microscopy. Vps41 S-A carries the S367, 368, 371, 372A point mutations, whereas Vps41 S-D contains the comparable phosphomimetic D mutations. Bar, 10 μm. (B) Localization of Vps41 alanine and aspartate mutants in wild-type and yck3Δ backgrounds. C-terminal GFP-tagged Vps41 was followed by fluorescence microscopy. Bar, 10 μm. (C) Subcellular fractionation of wild-type and Vps41 mutants. Cells expressing C-terminal GFP-tagged Vps41 wild-type or mutant forms were lysed and separated by centrifugation (20,000 × g for 15 min at 4°C) into pellet (P20) and supernatant fractions. The centrifugation of supernatant (100,000 × g for 1 h at 4°C) was performed to isolate pellet (P100) and supernatant (S100) fractions. Proteins within each fraction were analyzed by SDS-PAGE and Western blotting using antibodies against Vps41, Vac8, and the cytosolic protein marker Arc1. T = 50% of total protein used for each separation.

The Vps41 S-A Mutant Accumulates Tubular Membrane Structures Adjacent to the Vacuole

We decided to analyze the ultrastructural changes caused by the Vps41 mutations. By EM, neither wild-type nor the cells expressing the Vps41 S-D mutant showed any significant alterations in their overall cell morphology (Figure 5, A and B). In the Vps41 S-A mutant, in contrast, we observed tubular, stacked membrane structures (Figure 5, C, D, G, and H), which were found proximal to the vacuole (Figure 5, F and I). However, the tubular structures were not as abundant and of the same large size as those detected in yck3Δ cells (Figure 1B). In this strain background, additional putative Yck3 substrates would lack phosphorylation and might contribute to enhanced phenotype of yck3Δ cells (Figure 1B) compared with the cells expressing the Vps41 S-A mutant (Figure 5).
Vps41 Localization Is Linked to the Late Endosome

The morphological similarity between the tubules observed in the yck3Δ and the Vps41 S-A mutant (Figures 1B and 5), and the previously described class E endosomes (Rieder et al., 1996) prompted us to analyze the Vps41 localization in vps27Δ cells. Vps27 belongs to the ESCRT-0 complex involved in the generation of multivesicular bodies (Hurley and Emr, 2006). Interestingly, in wild-type cells Vps41-GFP redistributed partially from the vacuolar rim to the distinctive class E compartment of vps27Δ cells (Figure 6A), whereas GFP-Vam6 did not change its localization (Figure 6B). In the Vps41 S-A mutant, the dot accumulation of Vps41 was enhanced by the VPS27 deletion but did not result in additional, distinct structures (Figure 6A, right). Likewise, GFP-Vam6 was confined to a single dot adjacent to vacuoles in the vps27Δ mutant, with a barely visible signal on the

Figure 4. Effect of Vps41 mutations on HOPS complex assembly and on the localization of various fusion factors. (A) HOPS complex assembly. TAP-tagged Vps41 protein was purified from the indicated yeast strains by using IgG beads, natively eluted by TEV cleavage and the eluted proteins were separated on a Superose 6 column. Proteins in each fraction were TCA precipitated and analyzed by SDS-PAGE and Coomassie staining. Cbp = calmodulin binding peptide. (B) Localization of tethers in Vps41 wild-type and mutant cells. N-terminally GFP-tagged Vam6 and C-terminally GFP-tagged Vps11 and Vps18 were visualized by fluorescence microscopy. Bar, 10 μm. Cells (200) were counted to statistically analyze the distribution of the GFP signals.
vacuolar limiting membrane. Vps41 S-A and Vam6 dots colocalized with the class E compartment labeled with FM4-64 (Figure 6, A and B), indicating that some Vam6 and Vps41 S-A and Vam6 dots colocalized with the class E compartment labeled with FM4-64 (Figure 6, A and B), indicating that some Vam6 and Vps41 S-A and Vam6 dots colocalized with the class E compartment labeled with FM4-64 (Figure 6, A and B), indicating that some Vam6 and Vps41 S-A and Vam6 dots colocalized with the class E compartment labeled with FM4-64 (Figure 6, A and B), indicating that some Vam6 and Vps41 S-A and Vam6 dots colocalized with the class E compartment labeled with FM4-64 (Figure 6, A and B), indicating that some Vam6 and Vps41 S-A and Vam6 dots colocalized with the class E compartment labeled with FM4-64 (Figure 6, A and B), indicating that some Vam6 and Vps41 S-A and Vam6 dots colocalized with the class E compartment labeled with FM4-64 (Figure 6, A and B), indicating that some Vam6 and Vps41 S-A and Vam6 dots colocalized with the class E compartment labeled with FM4-64 (Figure 6, A and B), indicating that some Vam6 and Vps41 S-A and Vam6 dots colocalized with the class E compartment labeled with FM4-64 (Figure 6, A and B), indicating that some Vam6 and Vps41 S-A and Vam6 dots colocalized with the class E compartment labeled with FM4-64 (Figure 6, A and B), indicating that some Vam6 and

Vps41 is also found on late endosomes, a distribution that becomes more apparent in the class E background. This finding is in agreement with previous results from our laboratory, which suggested that the endosomal CORVET tethering complex converts to the HOPS complex in the course of endosome maturation (Peplowska et al., 2007). This conversion is most likely required for efficient HOPS-dependent fusion of matured late endosomes with the vacuole. The cytosolic distribution of Vps41 S-D mutant was not influenced by the VPS27 deletion but an increased vacuole fragmentation was observed (Supplemental Figure S3).

To test whether the puncta where Vps41 and Vam6 concentrate corresponds to an active fusion zone on the vacuole, we challenged vacuoles from the Vps41 S-A strain with high salt to induce fragmentation and monitored fusion upon removal of the salt stress (Bonangelino et al., 2002). When we followed vacuoles over time, we observed that they docked exclusively at zones with strongly enriched Vam6 (Figure 6C). This suggests that vacuoles contain a zone dedicated for fusion, which is enhanced by a block in Vps41 phosphorylation. This idea is also supported by in vitro data where an enrichment of fusion factors at docking zones has been previously reported during the vacuole-vacuole fusion assay (Wang et al., 2003). Our data, however, do not distinguish whether HOPS predefines such a zone, a concept that has to be clarified in future studies.

The Concentration of Vps41 S-A to Endosome–Vacuole Contact Zones Affects the AP-3 Pathway

Cargo proteins destined for the vacuole are transferred either directly from the Golgi to the vacuole by means of the vesicular AP-3 pathway, which is taken by the vacuolar SNARES Vam3 and Nyv1, or reach the vacuole via the endosome. The latter pathway is used among others by the Prc1 (CPY) and Cps1 protein as well as Vam3 and Nyv1 if the AP-3 pathway is blocked. When we analyzed trafficking pathways to the vacuole in our mutant strains, we did not detect major defects in the transport of CPY or autophagic cargo, and we observed efficient sorting of Cps1 into the vacuolar lumen via multivesicular bodies (Supplemental Figure S4; our unpublished observations). We then followed the fate of a synthetic cargo of the AP-3 pathway—a fusion protein of the cytosolic domain of the vacuolar SNARE Nyv1 with the longer transmembrane domain of Snc1. This fusion protein lacks the Golgi-endosome targeting signal and hence is sorted to the plasma membrane if the AP-3 pathway is defective (Reggiori et al., 2000). This effect can be conveniently monitored by fluorescence microscopy. Although the Nyv1-Snc1 fusion protein arrived at the vacuole in cells with wild-type Vps41 or the S-D mutation, some fusion protein was also observed on the plasma membrane in cells expressing Vps41 S-A or lacking Yck3 (Figure 7). This indicates that the AP-3 pathway is impaired under these conditions. Defective protein sorting via the AP-3 pathway in yck3Δ/H9004 cells has also been observed by Anand et al. (2009).

We suggest that the strong accumulation of Vps41 S-A to the distinct fusion “hot spot” on the vacuole—where it can function in the fusion with late endosomes and other vacuoles—restricts its availability for the AP-3 pathway. Alternatively, it is possible that only phosphorylated Vps41 is required in the AP-3 pathway.

Nonphosphorylated Vps41 Confers Fusion Resistance to a GTPase-activating Protein

We previously showed that the in vitro vacuole fusion sensitivity to Ypt7 inhibitors is reduced if Yck3 was lacking from cells (LaGrassa and Ungermann, 2005). If this effect is
linked to Vps41 phosphorylation, the Vps41 S-A mutant should mirror the yck3Δ mutant in the vacuole fusion assay. We generated fusion tester vacuoles carrying this Vps41 mutant form. Vacuole fusion was then monitored using isolated vacuoles from the two tester strains in the established content mixing assay (Haas, 1995). Fusion of yck3Δ and the S-A strains was comparable with wild-type fusion (data not shown). The active GAP domain of Gyp1 has been successfully used as a Rab-specific inhibitor of in vitro vacuole fusion and can block vacuole fusion to the same extent as the Ypt7 GAP Gyp7 (Merz and Wickner, 2004; Brett et al., 2008). If the active GAP-domain of Gyp1 was titrated into

Figure 6. Nonphosphorylated Vps41 and Vam6 are enriched at vacuole fusion sites. (A) Localization of Vps41-GFP in vps27Δ strain. SEY6210 cells expressing C-terminal GFP-tagged wild-type and mutant (S-A) Vps41 were labeled with FM4-64 and analyzed by fluorescence microscopy. Where indicated, VPS27 was deleted. Bar, 10 μm. (B) Localization of GFP-Vam6 in the vps27Δ strain. SEY6210 wild-type and vps27Δ cells expressing N-terminal GFP-tagged Vam6 in the respective Vps41 background were incubated with FM4-64 and analyzed by fluorescence microscopy. Bar, 10 μm. (C) In vivo fusion of vacuoles after relieve from high salt concentration stress. Cells expressing the Vps41 S-A mutant and the N-terminally GFP-tagged Vam6 fusion were incubated with 0.4 M NaCl for 30 min, followed by a wash with YPD medium and grown for the indicated times. Localization of Vam6 and vacuole morphology were monitored by fluorescence microscopy. Bar, 10 μm.
In Vivo Ypt7 Accessibility Depends on the Phosphorylation Status of Vps41

Two additional factors have been implicated in the control of Ypt7. Vam6 has GEF activity (Wurmser et al., 2000), whereas Gyp7 has been identified as a Ypt7-specific GAP, whose activity leads to Ypt7 inactivation and subsequent Gdi1-dependent release from the vacuole (Albert and Gall-witz, 1999). Consequently, we used an overexpression approach to test the effect of Gyp7 on vacuole morphology in the Vps41 mutant backgrounds (Figure 8D). To facilitate the construction of our strain, we generated diploid cells, in which only one copy of Ypt7 is tagged and monitored vacuole morphology by following GFP-Ypt7 and FM4-64 labeling.

For Gyp7 overexpression, we expected an inactivation of Ypt7 and subsequent vacuole fragmentation. This was to some extent the case for cells with wild-type Vps41 and the S-D mutant (Figure 8D). Additionally, we observed Ypt7 redistribution to the cytosol. In contrast, cells expressing Vps41 S-A maintained some Ypt7 associated to the vacuoles and were less responsive to the GAP overproduction (Figure 8D), in complete agreement with the reduced sensitivity in vitro (Figure 8A). Together, only the Vps41 S-A mutant efficiently counteracted the effects of Gyp7 overproduction on the Ypt7 distribution and the vacuole morphology. We assume that this protein variant is more prone to interact with Ypt7 because it binds more efficiently to membranes. Therefore, the Vps41 S-A mutant most likely blocks the access of Gyp7 to Ypt7, which explains the reduced response of this mutant. In combination, our data imply that Vps41 has two binding sites on membranes, which regulate its function: one binding site that is influenced by Yck3-mediated phosphorylation, as well as a Ypt7-dependent binding site.

DISCUSSION

Protein phosphorylation modulates multiple events along the endocytic and exocytic pathways: coat polymerization, membrane tethering, and SNARE assembly (Langer et al., 2007; Preisinger and Barr, 2005). Here, we have analyzed how phosphorylation of Vps41 can control its function in the tethering stage at the endosome/vacuole interface. The phosphorylation site found in Vps41 resembles the casein kinase 1 consensus phosphorylation site: S/T(F)-X_{-1,2}-S/T, where the upstream phosphorylation in residue S364 most probably provides the negative charge required for molecular recognition by the Yck3 kinase (Gross and Anderson, 1998). The identification of the Vps41 phosphorylation sites allowed us to separate Vps41-regulation from Yck3-dependent phosphorylation effects on additional targets within the

Ypt7 Overproduction Can Counteract the Effects of Vps41 Phosphorylation

We then asked whether alteration in the Ypt7 cycle would affect the vacuolar morphology of the different Vps41 mutants. When we tagged Ypt7 N-terminally with GFP and monitored its localization, we detected the protein on vacuoles in wild-type cells as expected (Figure 8B). In the S-A mutant, Ypt7 also accumulated in dots on the vacuolar rim. In contrast, GFP-tagging of Ypt7 in the Vps41 S-D background resulted in a complete vacuole fragmentation. This effect is only evident in combination with the S-D mutation. Our data suggest that the mislocalization of Vps41 S-D together with a Ypt7 protein affected in its functionality by the N-terminal GFP-tag leads to an in vivo fusion defect that is reflected by vacuole fragmentation. If this interpretation was correct, then the untagged Ypt7 should compensate for this defect. This was indeed the case. Overexpression of untagged Ypt7 wild-type rescues the vacuole fragmentation phenotype of the S-D mutant (Figure 8C). Moreover, we observed that more Vps41 S-D localized to the vacuolar rim and prevacuolar dots under these conditions (Figure 8C). We conclude that Vps41 does not solely depend on the Yck3 phosphorylation effects on additional targets within the

Figure 7. The AP-3 pathway is impaired in the Vps41 S-A mutant. Localization of GFP-Nyv1-Snc1TMD in Vps41 wild-type and mutant cells. Cells expressing GFP-tagged Nyv1-Snc1TMD in the indicated Vps41 backgrounds were visualized by fluorescence microscopy. Bar, 10 μm.
cell, in particular other proteins of the endosomal system. For example, the vacuolar SNARE Vam3 has been identified as an additional Yck3 substrate (Brett et al., 2008), but the phosphorylation site remains to be determined. Our data
suggest that nonphosphorylated Vps41, presumably as part of
the HOPS complex, is concentrated in dot-like structures
that correspond to the fusion site between late endosomes
and the vacuole. In fact, Vam6/Vps39 and Vps41 get even
stronger enriched at this site if the ESCRT-0 subunit Vps27
was deleted. Thus, it is likely that the HOPS complex is also
temporarily present on late endosomes to support fusion
with the vacuole. This finding confirms previous studies in
our laboratory, which provided evidence that formation of
the HOPS complex can occur upon subunit exchange of the
homologous endosomal CORVET tethering complex (Peplowska
et al., 2007). The conversion occurs most likely in the
course of endosomal maturation, a feature that was previ-
sously shown for the corresponding Rabs on single endo-
somes in higher eukaryotic cells (Rink et al., 2005). Interest-
ingly, only the Rab5 GTPase Vps21, but not the CORVET
subunits Vps3 or Vps8, is enriched in the class E compart-
ment (our unpublished observations), suggesting once more
that the tether conversion is taking place during endosome
maturation. Our ultrastructural analysis reveals that cells
carrying the nonphosphorylated Vps41 mutant behave very
similar to yck3Δ cells and accumulate tubular endosomal
structures close to the vacuole. The reason for this accumu-
lation is not yet clear, but it is most likely a consequence of
reduced recycling due to impaired mobility of Vps41 under
these conditions.

Our analysis of the Vps41 phosphorylation site also sheds
light on the dynamics of the HOPS complex. All HOPS
subunits analyzed were concentrated together with Vps41 at
the endosome-vacuole fusion site in the nonphosphorylated
Vps41 S-A mutant. In the Vps41 S-D background, in con-
trast, Vps41 was found to a large extent in the cytoplasm,
whereas Vps11, Vps18, and Vam6 were less accumulated in
dots, but still present on the vacuolar rim. This suggests that
Vps41 can operate independently from the remaining HOPS
subunits and could act in the recruitment of the HOPS
subunits to the endosome-vacuole fusion site. Interestingly,
we were able to purify assembled HOPS complex in all Vps41
background strains (Figure 4A), although we cannot
exclude slight changes in the efficiency of HOPS assembly. It
is therefore possible that only the unassembled Vps41 un-
dergoes the phosphorylation-dependent dynamics that are
mimicked by our mutations.

We also observed that the transport of AP-3 cargo is
impaired in cells lacking Vps41 phosphorylation in agree-
ment with Anand et al. (2009). This suggests a positive
feedback regulation: Yck3, sorted to the vacuole via AP-3
Vps41 on AP-3 vesicles might be without consequences as
a different site on vacuoles. A potential phosphorylation of
ding and fusion of AP-3 vesicles, which apparently dock at
this endosomal docking site and make it available for bud-
ment with Anand

mimicked by our mutations.

Vps41 background strains (Figure 4A), although we cannot
we were able to purify assembled HOPS complex in all
Vps41 can operate independently from the remaining HOPS
dots, but still present on the vacuolar rim. This suggests that
Vps41 was found to a large extent in the cytoplasm,
Vps41 S-A mutant. In the Vps41 S-D background, in con-
trast, Vps41 was found to a large extent in the nonphosphorylated
endosome–vacuole interface and thereby liberates Vps41
overproduction. We assume that the efficient binding of the
nonphosphorylated Vps41 to membranes results in a higher
probability to interact with Ypt7, leading to limited accessi-
bility of Ypt7. Moreover, Ypt7 inactivation by Gyp7 might have
only a weak effect, because Vps41 and the HOPS complex do
still efficiently localize independently of Ypt7. The analysis of
the Gyp7 recruitment to membranes is needed to clarify, how
Vps41 S-A can prevent efficient Gyp7 action.

Our data provide evidence for a role of Vps41 and the
HOPS complex at late endosomes. It is possible that the
loading of Ypt7 onto late endosomes and the recruitment of the
HOPS complex are controlled by Vps41, which in turn is
governed by Yck3. It will be important to investigate, how
Vps41 phosphorylation and Ypt7 activation are regulated in
concert and how Yck3 activity is controlled on yeast
vacuoles.

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