ESCRT-I components of the endocytic machinery are required for Rim101-dependent ambient pH regulation in the yeast *Yarrowia lipolytica*

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Ambient pH signalling involves a cascade of conserved Rim or Pal products in ascomycetous yeasts or filamentous fungi, respectively. Insertional mutagenesis in the yeast *Yarrowia lipolytica* identified two components of the endosome-associated ESCRT-I complex involved in multivesicular body (MVB) vesicle formation, YIVps28p and YIVps23p. They were shown to be required at alkaline pH, like Rim factors, for transcriptional activation of alkaline-induced genes and repression of acid-induced genes. The constitutively active *YIRIM101-1119* allele, which suppresses the pH-signalling defects of *Ylr* mutations, also suppresses *Ylv* defects in pH response, but not in endocytosis. The contribution of the ESCRT-III component Snf7p could not be assessed due to the essential nature of this component in *Y. lipolytica*. Unlike Rim factors, YIVps4p, a component of the MVB pathway acting downstream from ESCRT complexes, seems not to be required for the alkaline response. In *Y. lipolytica*, all *vps* mutations including those affecting *YIVPS4*, affected growth at acidic pH, a feature not exhibited by *Ylr* mutations. These results suggest that Rim and Vps pathways cooperate in ambient pH signalling and that this relation is conserved across the full range of hemiascomycetous yeasts.

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INTRODUCTION

Yarrowia lipolytica is a non-pathogenic saprophytic yeast that colonizes various food products and natural environments (Barth & Gaillardin, 1997). A recent genomic survey confirmed that it is very distantly related to *Saccharomyces cerevisiae* and *Candida albicans* (Dujon *et al.*, 2004). Like *C. albicans* and many other fungi, it secretes proteases whose expression is tightly controlled by a combination of environmental stimuli, including nutrient availability and ambient pH (Ogrydziak *et al.*, 1977, 1993). *Y. lipolytica* secretes either an acidic protease encoded by the *AXP1* gene at acidic pH, or an alkaline protease encoded by the *XPR2* gene at neutral/alkaline pH. Previous work showed that pH-dependent expression of the *XPR2* gene was achieved through activation of a conserved signalling pathway regulating the expression of many pH-dependent genes (Gonzalez-Lopez *et al.*, 2002; Lambert *et al.*, 1997; Tréton *et al.*, 2000). This pathway, called Pal in filamentous fungi and Rim in yeasts, was initially described as a pH-response pathway in *Aspergillus nidulans* (Caddick *et al.*, 1986), and was later identified in *Y. lipolytica* (Lambert *et al.*, 1997), and several other ascomycetes including *C. albicans* (Ramon *et al.*,

1999), *S. cerevisiae* (Lamb *et al.*, 2001) and other fungi (Peñalva & Arst, 2002, 2004). The current model states that at alkaline pH, a cascade of six *PAL* or five *RIM* genes activates the zinc finger transcriptional factor PacC/Rim101p through a complex C-terminal proteolytic processing event involving the PalB/Rim13p protease. The PacC/Rim101p truncated form is able to activate alkaline-pH-responsive genes and to repress acid-induced genes (for a review see Peñalva & Arst, 2002, 2004). Direct interaction of Rim13p/PalB and Rim101p/PacC could not, however, be observed, and the only direct interactions detected in two-hybrid screens of Pal/Rim components were between Rim20p/PalA and Rim101p/PacC (Vincent *et al.*, 2003; Xu & Mitchell, 2001).

In *Y. lipolytica*, screening of an insertional library for altered expression of either acidic or alkaline protease genes, or both, revealed besides components of the Rim pathway, other potential regulators of protease expression, in particular YIVps28p (Gonzalez-Lopez *et al.*, 2002). Mutations in *YIVPS28* conferred an *Xpr2*[−] phenotype like *Ylr* mutations. But, in contrast to *Ylr* mutations, they clearly interfered with the capacity of the strains to execute the yeast–hyphae transition (Gonzalez-Lopez *et al.*, 2002).

In *S. cerevisiae*, Vps28p is a class E component of the endosomal-sorting complex ESCRT-I (Katzmann *et al.*, 2001). This complex participates in the recognition of

Abbreviation: MVB, multivesicular body.

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both ubiquitinated endocytic and biosynthetic cargos that are targeted to the multivesicular body (MVB) vesicles to be ultimately delivered to the lumen of the vacuole when the MVB fuses with this organelle (Futter *et al.*, 1996). In contrast, transmembrane proteins that remain in the limiting membrane of the MVB are either delivered to the limiting membrane of the vacuole, or recycled to the plasma membrane or the Golgi (Lemmon & Traub, 2000). The MVB-sorting pathway thus affects both endocytosis and exocytosis of membrane-anchored proteins. It is conserved from yeast to higher eukaryotes, and is required for a growing list of cellular functions that includes downregulation of receptors and transporters, regulation of the immune response and even the budding of certain viruses like human immunodeficiency virus (for a review see Katzmann *et al.*, 2002).

Therefore, the question was whether *Ylups28* mutations affected expression of protease genes through an indirect effect on protein expression, or through a specific interference with the Rim signalling pathway. This last hypothesis was particularly attractive since interactions had been detected during a whole-genome screen of two-hybrid interactants in *S. cerevisiae*, between Rim20p and two other Vps components, Snf7p and Vps4p, and Rim13p and Snf7p (Ito *et al.*, 2001). Snf7p is a component of the ESCRT-III complex (Babst *et al.*, 2002a), which acts downstream from ESCRT-I and ESCRT-II complexes in the MVB pathway, whereas the Vps4p/End13p AAA ATPase acts at the end of the endocytic cycle to dissociate the ESCRT-III complex from the endosomal membrane (Babst *et al.*, 1998). Subsequent observations in *A. nidulans*, *S. cerevisiae* and *C. albicans* confirmed that Snf7p indeed interacted physically with Rim20p/PalA (Bowers *et al.*, 2004; Ito *et al.*, 2001; Vincent *et al.*, 2003; Xu *et al.*, 2004). Analysis of mutations affecting the interaction domain of Rim20p showed that both Rim20p–Rim101p and Rim20p–Snf7p interactions were required for Rim101p processing (Xu *et al.*, 2004). The interaction between Rim20p and Vps4p was also observed in another two-hybrid analysis (Bowers *et al.*, 2004), but its *in vivo* significance was later questioned since Vps4p does not appear to be required for Rim101p processing in *S. cerevisiae* (Kullas *et al.*, 2004). Indeed, both Snf7p and Vps4p were shown to interact with Bro1p/Vps31p (Gavin *et al.*, 2002), a Rim20p/PalA paralogue, which is another soluble class E factor required for MVB sorting but not for pH sensing (Odorizzi *et al.*, 2003). The interaction between Rim13p and Snf7p has not been confirmed by other studies. Finally, a systematic phenotypic analysis of a nearly complete collection of gene-deletion mutants of *S. cerevisiae* indicated that several *vps* mutant strains exhibited impaired growth at alkaline pH or in the presence of high concentrations of monovalent cations (Giaever *et al.*, 2002), two phenotypes that are characteristic of *rim* mutants in this organism (Lamb *et al.*, 2001).

More recently, and while our work was in progress, definite evidence for a functional link between the Rim and Vps pathways was obtained in the yeasts *S. cerevisiae* and *C.*

albicans. In *C. albicans*, a mutant strain inactivated for the *CaSNF7* gene displayed all the phenotypes expected for a *Carim* mutant strain (pH and ion sensitivity during growth, and the absence of alkaline-induced filamentation and Rim101p processing) and was suppressed by a constitutively active form of CaRim101p (Kullas *et al.*, 2004). Other *vps* mutants affecting different ESCRT-I, -II and -III components were shown, in a separate study, to exhibit morphological defects characteristic of *rim* mutants (Xu *et al.*, 2004). In *S. cerevisiae*, mutations in several ESCRT-I, -II and -III components affected processing of the transcriptional activator Rim101p, as would do, for example, a *rim20* mutation (Xu *et al.*, 2004). Interestingly in this last study, not all ESCRT-encoding genes were required for the processing of Rim101p, and none of the non-ESCRT *vps* genes were. The theory that not the whole endocytic pathway was involved in pH signalling was further confirmed by the observation that Vps4p defects had no drastic effect on Rim101p processing either in *S. cerevisiae* or in *C. albicans* (Kullas *et al.*, 2004; Xu *et al.*, 2004).

This paper reports on the characterization of *vps* mutant strains in *Y. lipolytica*. It confirms the conservation of a functional link between the components of the endocytic pathway and pH signalling, and the absence of an involvement of Vps4p, over the full range of ascomycetous yeasts. We further show that *SNF7* is an essential gene in *Y. lipolytica*. This last observation may explain why ESCRT components were not easily, or not at all, identified in exhaustive screens for genes affecting pH signalling in *Y. lipolytica* and *A. nidulans*.

METHODS

Strains, sequence data and gene designation. The bacterial strains used for transformation and amplification of recombinant DNA were *Escherichia coli* DH5 α and SURE (Stratagene). Yeast strains are described in Table 1. Previously reported *Y. lipolytica* mutations in *pal1* (*pal1-26*) and *pal4* (*pal4-24*) (Lambert *et al.*, 1997) were shown to be specifically complemented by *YIRIM13* and *YIRIM20*, respectively (data not shown), and have been designated *rim13-26* and *rim20-24* mutations, respectively.

Unless otherwise stated, all sequence data were obtained from the complete genome sequence of *Y. lipolytica* (<http://cbi.labri.fr/Genolevures/>; Dujon *et al.*, 2004). Systematic gene nomenclature referring to this project is given in the text where appropriate.

Culture media and phenotypic tests. Complete YPD medium, minimal YNB-glucose medium, derepressing (Y) medium and protease-inducing medium (YPDm) have been described previously (Blanchin-Roland *et al.*, 1994; Lambert *et al.*, 1997). Solid and liquid media were buffered at pH 4.0 (with 0.2 M sodium citrate buffer), pH 7.0 (with 0.2 M sodium phosphate buffer) or pH 8.0 (with 25 mM Tris/HCl) and supplemented with 0.1 g uracil l⁻¹. The pH of liquid media was stable within 0.3 pH units during growth. The Lac⁺ phenotype was screened on Y medium buffered at pH 7.0, as previously described (Gonzalez-Lopez *et al.*, 2002).

Growth at various pHs was assayed by spotting serial threefold dilutions of exponential-phase cultures in YPD liquid medium, on plates buffered either with 0.2 M citrate-phosphate buffer at pH 3.5, or with 0.2 M MOPS for assays at pH 7.0–8.5. Crossing of compatible

Table 1. Strains

Strain	Relevant genotype	Source
AM3	<i>MAT A, ura3-302, leu2-270, lys11-23, XPR2, LEU2, XPR2':lacZ</i>	Lambert <i>et al.</i> (1997)
AM4	<i>MAT B, ura3-302, leu2-270, his-1, XPR2, LEU2, XPR2':lacZ</i>	Lambert <i>et al.</i> (1997)
E122	<i>MAT A, ura3-302, leu2-270, lys11-23</i>	E. Fabre*
SY12	<i>MAT A, ura3-302, leu2-270, lys11-23, XPR2, LEU2, AXPI':gusC, XPR2':lacZ</i>	Gonzalez-Lopez <i>et al.</i> (2002)
AM319ΔC	<i>MAT A, ura3-302, leu2-270, lys11-23, XPR2, LEU2, XPR2':lacZ, RIM101-1119</i>	Lambert <i>et al.</i> (1997)
LAM26-03	<i>MAT A, ura3-302, leu2-270, XPR2, LEU2, XPR2':lacZ, pal1-26/rim13-26</i>	Lambert <i>et al.</i> (1997)
SBR116	<i>MAT A, ura3-302, leu2-270, XPR2, LEU2, XPR2':lacZ, pal1-26/rim13-26, RIM101-1119</i>	This study
CGL-U15u	<i>MAT A, ura3-302, leu2-270, lys11-23, XPR2, LEU2, AXPI':gusC, XPR2':lacZ, vps23-U15</i>	This study
SBR117	<i>MAT A, ura3-302, leu2-270, lys11-23, XPR2, LEU2, AXPI':gusC, XPR2':lacZ, vps23-U15, RIM101-1119</i>	This study
CGL-Y2u	<i>MAT A, ura3-302, leu2-270, lys11-23, XPR2, LEU2, AXPI':gusC, XPR2':lacZ, vps28-Y2</i>	This study
SBR118	<i>MAT A, ura3-302, leu2-270, lys11-23, XPR2, LEU2, AXPI':gusC, XPR2':lacZ, vps28-Y2, RIM101-1119</i>	This study
SBR114u	<i>MAT A, ura3-302, leu2-270, lys11-23, XPR2, LEU2, AXPI':gusC, XPR2':lacZ, vps4Δ14</i>	This study
SBR119	<i>MAT A, ura3-302, leu2-270, lys11-23, XPR2, LEU2, AXPI':gusC, XPR2':lacZ, vps4Δ14, RIM101-1119</i>	This study
SY1364	<i>MAT A, ura3-302, leu2-270, lys11-23, XPR2, LEU2, AXPI':gusC, XPR2':lacZ, vps4^{K172A}, URA3, vps4Δ14</i>	This study

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Y. lipolytica auxotrophs, diploid sporulation and spore isolation was done as described previously (Gonzalez-Lopez *et al.*, 2002). Dilutions of spore suspensions were plated on complete medium and colonies were tested on appropriate media.

DNA and RNA techniques. Standard recombinant DNA techniques were performed essentially as previously described (Gonzalez-Lopez *et al.*, 2002). Sequences were obtained from the DNA sequencing department of Eurogentec. They were assembled and annotated using the GCG package. All transformation events were checked by colony PCR using PuRe Taq Ready-To-Go PCR beads (Amersham) and confirmed by Southern blotting.

Gene expression was determined by real-time quantitative RT-PCR using a LightCycler (Roche Molecular Biochemicals). Cells were grown at 28 °C in Y medium buffered either at pH 4 or 8, and harvested at the exponential phase (OD₆₀₀ about 0.6). Total RNA was extracted with the RNeasy mini-kit from Qiagen and then treated by DNase I (Qiagen). The cDNA was synthesized from 1 µg total RNA according to the manufacturer's protocol of the SuperScript II RNase H⁻ reverse transcriptase kit (Invitrogen). Primer sets for the genes were as follows: *ACT20-ACT21r* for *ACT1*, *XPR210-XPR211r* for *XPR2*, *PHR112-PHR113r* for *PHR1*, *RIM104-RIM105r* for *RIM101* and *PHR203-PHR204r* for *PHR2* (Table 2). The PCR parameters were 95 °C for 8 min, followed by 45 cycles at 95 °C for 10 s, 55 °C for 7 s, and 72 °C for 10 s. A negative control with sterile water was performed for each

primer set. The threshold cycle (Cp) was determined as the cycle above which the fluorescence signal produced by the SYBRGreen I dye, reached a baseline level. The expression levels of the genes were determined relative to the expression of the *ACT1* gene, which was uniform, as confirmed by Northern experiments (data not shown). For each gene, experiments were carried out at least four times, using two cDNA samples from two (or in a few cases three) independent cultures. Statistical analysis was performed using Student's *t*-test. A *P* value lower than 0.05 was considered as significant.

Deletion of *YIVPS4* and *YISNF7*. To create null versions of *YIVPS4* and *YISNF7*, a disruption cassette was constructed according to Fickers *et al.* (2003). First, the promoter and the terminator regions of each gene were amplified separately using the SY12 genomic DNA as template. The promoter and terminator regions of *YIVPS4* were amplified with the primers V4BP1/VPS4P2 and VPS4T1/V4XT2, as ~0.99 and ~0.89 kb fragments, respectively (Table 2). For *YISNF7*, the promoter and terminator regions were amplified with the primers V32XP1/VPS32P2 and VPS32T1/V32BT2, as ~1.00 and ~1.15 kb fragments, respectively. Primers VPS4P2 and VPS4T1, and primers VPS32P2 and VPS32T1 all contain the meganuclease I-SceI recognition sequence. For each gene, the resulting promoter-I-SceI and I-SceI-terminator fragments were then annealed and further amplified by using primers V4BP1/V4XT2 or V32XP1/V32BT2. The resulting promoter-I-SceI-terminator cassettes were then digested by *Bam*HI/*Xba*I and cloned into pBluescript KS+, digested by the same

Table 2. Primers

Primer	Sequence 5' to 3'
V4BP1	AGAGCGGATCCGTTGTTACCGGTAGCTAGTGCCTCTG
VPS4P2	ATTACCCTGTTATCCCTATGTGTGGGTGGTTGGGTTAATACC
VPS4T1	TAGGGATAACAGGGTAATCATCGGAGCAGCAATAACTAACGTTTG
V4XT2	TCCCCTCTAGAAACCACTCTTCTGCGTGAGGGTATGCC
VPS4ka5	CCGGTACCGGAGCGTCGTACCTGGCCAAG
VPS4ka3r	CCAGGTACGACGCTCCGGTACCGGGGGGT
V32XP1	CGGTAATCTAGATATGAGATGGTCCGAAAGCAACCGAAG
VPS32P2	ATTACCCTGTTATCCCTATGTTGTATGATTATGGTGATGTTTGTGGTG
VPS32T1	TAGGGATAACAGGGTAATGGGAACTGGAACCAAGGATACCGAG
V32BT2	GATGATGGATCCTTACATGGCTAGTACTCCCTGCACTC
ACT20	TCCAGGCCGTCTCTCCC
ACT21r	GGCCAGCCATATCGAGTCGCA
XPR210	AACTTCGCTGACACACAGAACG
XPR211r	AGAGAGCTGCGGATCGGC
PHR112	CCCTCTGGCTGACCCCAAG
PHR113r	TCAGGTAGATGCCAGCATCGT
RIM104	GGCTCCGCTGAGAAGCTCTAC
RIM105r	ATCCTGAGGTCGCTTGAACG
PHR203	ACAACCTGTCTTCGCAGATGGC
PHR204r	GGTTCCGACCTTGGGGGTG

enzymes, to generate plasmids pINA1344 (promoter-terminator of *VPS4*) and pINA1346 (promoter-terminator of *SNF7*). The loxR-URA3-loxP module was rescued from JMP113 (Fickers *et al.*, 2003), by *I-SceI* digestion, and cloned into pINA1344 and pINA1346 at the *I-SceI* site, generating plasmids pINA1345 and pINA1347, respectively. The disruption cassettes, PUTV4 and PUTV32, were generated by PCR amplification using the primers V4BP1/V4XT2 with pINA1345 plasmid DNA as the template, and V32XP1/V32BT2 with pINA1347 plasmid as template, respectively. The PUTV4 cassette was integrated by double crossover at the *YIVPS4* locus into the SY12 strain to generate strain SBR114 (*Ylvps4Δ14* allele). The PUTV32 cassette was used in the same way to delete *SNF7* in the haploid strain SY12 or one copy of *SNF7* in the diploid strain AM3/AM4. To carry out the deletion of *SNF7* by pop-in/pop-out, the disruption vector pINA1356 was obtained by ligating the *Bam*HI-*Xba*I insert of pINA1346 described above, carrying the promoter-*I-SceI*-terminator cassette, into the integrative *URA3* plasmid pINA300' digested with *Bam*HI/*Nhe*I.

Production of ATP-binding site mutant *YIVps4p*-(K172A). Site-directed mutagenesis of the ATP-binding site of *Vps4p* was performed by the overlapping PCR technique to create a mutated *Vps4p* with a Lys172Ala substitution. Two PCR products were amplified with SY12 genomic DNA as a template, using primers V4BP1-VPS4ka3r and VPS4ka5-V4XT2. These PCR products, containing the mutation in their overlapping regions, were mixed and amplified with the flanking primers to generate a full-length PCR product containing the internal mutation. This PCR product was digested by *Bgl*II/*Xba*I and then inserted into pINA300' digested by *Bam*HI/*Nhe*I, to generate plasmid pINA1357, which was confirmed by sequencing. The *Nhe*I-digested pINA1357 was targeted to the promoter of *VPS4* in strain SBR114u to give strain SY1364.

Cloning of the *YISNF7* gene. The *Y. lipolytica* wild-type *SNF7* gene was amplified from SY12 genomic DNA by the Expand High Fidelity PCR system from Roche with primers V32XP1/V32BT2. The

PCR product carrying *SNF7* was digested with *Xba*I, and then inserted into the replicative *LEU2* plasmid pINA240 digested by *Nru*I/*Nhe*I to give pINA1355, which was checked by DNA sequencing.

Introduction of the *YIRIM101-1119* truncated allele into *Ylvps* mutant strains. *YIURA3* was excised from strains CGL-U15 (*Ylvps23-U15* allele), CGL-Y2 (*Ylvps2-Y2* allele) and SBR114 (*Ylvps4-14* allele), by using plasmid pUB4-CRE as previously described (Fickers *et al.*, 2003) to give strains CGL-U15u, CGL-Y2u and SBR114u, respectively. The *Dra*III-digested pINA1119 (Lambert *et al.*, 1997) was targeted to the terminator of *YIRIM101* in these resulting *Ura*⁻ strains, and in LAM26-03 strain (*rim13-26* allele). Secondary *Ura*⁻ clones were selected on 5-fluoroorotic acid medium, and recombination events leaving the *YIRIM101-1119* truncation were selected (strains SBR116–SBR119, see Table 1).

Staining with FM4-64. FM4-64 localization experiments were done using a modification of the protocol described by Vida & Emr (1995). Yeast cells were grown in YPD to an OD₆₀₀ of about 0.6. Cells (5 ml culture volume) were harvested, incubated in 150 µl YPD containing 40 µM FM4-64 (Molecular Probes) for 30 min at 0 °C, washed three times on ice, and further incubated in 200 µl YPD for 20 min at 18 °C. An aliquot of cells was centrifuged, resuspended in water and visualized by differential interference contrast (DIC) and fluorescence microscopy using an Olympus U-RFL-T microscope with a CoolSNAP camera.

RESULTS

Isolation of the *Ylvps23-U15* mutant

To identify potential regulators affecting the expression of either acidic (Axp1p) or alkaline (Xpr2p) proteases, or both, in *Y. lipolytica*, mutant strains had previously been isolated from the SY12 strain mutagenized by a library of genomic

fragments transposed by the mTnY11-transposon (Gonzalez-Lopez *et al.*, 2002). Characterization of mutations affecting the expression of *XPR2* alone, or both *XPR2* and *AXP1*, identified five *YRIM* and five non-*RIM* genes. Fourteen additional mutations resulted from integrations at other loci and were characterized only by *in silico* analysis of the sequences flanking the transposon (Gonzalez-Lopez *et al.*, 2002). PCR analysis, carried out as previously described (Gonzalez-Lopez *et al.*, 2002), showed that homologous integration of the transposed genomic DNA fragments had occurred in three of these mutant strains. Only one of these showed a genetic linkage between the protease phenotype and the *URA3*-labelled transposon, as checked by mating against the SY12 isogenic derivative AM4 (data not shown). The complete sequence of the disrupted ORF was assembled from overlapping flanking regions and by primer walking (accession no. AJ509167); it was identical to that of YALI0F19272g later found in the complete genome assembly (Dujon *et al.*, 2004).

This mutant strain was affected in a gene orthologous to *S. cerevisiae* *VPS23*, which encodes a component of the ESCRT-I complex required for sorting membrane proteins into the MVB pathway (Katzmann *et al.*, 2001), as was *YIVPS28* previously identified in the same screening (Gonzalez-Lopez *et al.*, 2002). *YIVPS23* encodes a predicted protein of 378 aa (accession no. AJ509167) displaying 36 % identity with *Homo sapiens* TSG101 (accession no. AAC52083), 34 % with *Drosophila melanogaster* TSG101 (accession no. AF315343), 28 % with *S. cerevisiae* *Vps23p*/Stp22p (Li *et al.*, 1999) and with *C. albicans* CA2343/orf19.2343 (<http://genolist.pasteur.fr/CandidaDB/>). Comparison of the *Y. lipolytica* amino acid sequence with its homologues showed a conservation of the domain structure predicted for ScVps23p and TSG101 (Katzmann *et al.*, 2001): a N-terminal domain homologous to ubiquitin-conjugating enzymes, but unlikely to catalyse ubiquitination because of the substitution for the C residue that binds ubiquitin, a Pro-rich region, a coiled-coil region (positions 218–251 and 265–299) and a conserved C-terminal portion. The YlmTn1 insertion truncates *YIVps23p* at aa 150 (*Ylvps23-U15*).

Role of *YIVPS23* and *YIVPS28* in alkaline- or acidic-pH responses

To establish whether *YIVPS* genes are involved in ambient pH signalling, we assessed the effects of *Ylvps* mutations on the transcription of different pH-regulated genes by real-time quantitative PCR on total RNA extracted from cultures grown in Y medium at pH 4.0 and 8.0, using actin transcript as a reference. We chose the alleles *Ylvps23-U15* (the only mutation available affecting this gene) and *Ylvps28-Y2*, which truncates *Vps28p* at aa 87. As ambient alkaline-pH-responding genes, we chose, as previously, *XPR2* and *YIPHR1* (accession no. YALI0D04851g) (Gonzalez-Lopez *et al.*, 2002) plus *YRIM101*. Since expression of the acidic-protease gene *AXP1* was shown to be independent of the Rim pathway, we chose as acidic pH-responding gene *YIPHR2* (accession no. YALI0D06039g), a homologue of

CaPHR2 known to be expressed at acidic pH only in *C. albicans* (Muhlschlegel & Fonzi, 1997). As a control of the effect of *rim* mutations on the expression of these genes, we chose one *Yrim* mutant, carrying the *Yrim13-26* mutation (see Methods) that displays a typical Rim phenotype (Gonzalez-Lopez *et al.*, 2002).

At pH 8.0, both *Ylvps23-U15* and *Ylvps28-Y2* mutations significantly decreased *YRIM101* expression (more than 2 times compared to wild-type, *P* values ≤ 0.01), reduced *YIPHR1* expression more than 20 times and nearly abolished *XPR2* transcription (Fig. 1a). These observations were fully confirmed by measuring the expression of the *XPR2':lacZ* fusion integrated at the *XPR2* locus of these strains and by Northern blotting (data not shown). At pH 4.0, no or very little transcription of these alkaline reporter genes could be detected (Fig. 1b). Thus, like *YRIM13* and other *YRIM* genes (Gonzalez-Lopez *et al.*, 2002; Lambert *et al.*, 1997), *YIVPS23* and *YIVPS28* are absolutely required for transcriptional activation of alkaline-induced genes at pH 8.0. In both *Ylvps* mutant strains, as in the *Yrim13-26* mutation strain, at alkaline pH, expression of the acid-induced gene *YIPHR2* derepressed more than 20 times over the wild-type level at the same pH, reaching its level at acidic pH in the reference strain (Fig. 1a, b).

Yrim mutants induce a characteristic growth defect at alkaline pH and have no effect on growth at acidic pH (Gonzalez-Lopez *et al.*, 2002; Fig. 2a). The growth of the *Ylvps* mutant strains was slightly affected at acidic pH and drastically affected at alkaline pH, even more than that of the *Yrim13-26* mutant (Fig. 2a). All these results strongly suggest that *YIVPS23* and *YIVPS28* genes are, like *YRIM* genes, required for sensing ambient pH and adjusting cellular responses to it.

A C-terminal truncated allele of *YRIM101* suppresses *Ylvps23* and *Ylvps28* mutations at both pHs

In order to test whether pH effects observed in the *Ylvps* mutants were mediated through the Rim pathway, we checked whether a dominant, constitutively active, truncated form of YIRim101p was able to suppress *Ylvps* mutations for their defects in alkaline and acidic responses. To address this question, we replaced the wild-type *YRIM101* allele by the most truncated allele, *YRIM101-1119* (Lambert *et al.*, 1997), in the *Ylvps23-U15* and *Ylvps28-Y2* mutants and in the *Yrim13-26* mutant (see Methods). The *VPS⁺* AM319ΔC strain (Lambert *et al.*, 1997), where *YRIM101-1119* replaces the wild-type *YRIM101* allele, was used as a control. As shown on Fig. 1, expression of the *YRIM101-1119* allele efficiently suppressed the defective alkaline-induced gene expression observed in the *Yrim13-26* and *Ylvps* mutants, and resulted in expression levels not significantly different from those observed in the RimSL control strain (χ^2 0.99). At both alkaline and acidic pH, the two alkaline-induced genes, *XPR2* and *PHR1*, were induced more than 10 times over the levels measured in the

Fig. 1. Expression patterns of alkaline-induced genes (*XPR2*, hatched bars, *PHR1*, white bars and *RIM101*, black bars) and acid-induced genes (*PHR2*, grey bars) in *Y. lipolytica* strains at pH 8.0 (a) and pH 4.0 (b). The strains were SY12 (WT), LAM26-03 (*rim13*), CGL-U15u (*vps23*), CGL-Y2u (*vps28*), AM319ΔC (RimSL), SBR116 (*rim13*+RimSL), SBR117 (*vps23*+RimSL), SBR118 (*vps28*+RimSL), SBR114u (*vps4*) and SBR119 (*vps4*+RimSL). RimSL stands for the YIRIM101-1119 constitutively active, truncated allele. The levels of mRNA were measured by quantitative RT-PCR and expressed as a percentage of the constitutive expression level of the actin gene. Results are the mean $\pm$ SD of four quantifications.

unsuppressed mutants at the same pH. At both pHs, *RIM101* itself was induced 2–5 times over the mutant levels at the same pH ($P \leq 0.01$). The acid-induced gene *PHR2* was repressed more than 10 times at alkaline pH, and about 3 times ($P \leq 4 \times 10^{-4}$) at acidic pH, relative to its level in the *vps* mutants (Fig. 1a, b). Taken together, these results indicate

that *Ylps* mutations, like *Yrim* mutations, can be bypassed by expressing a constitutively active form of YIRim101p.

Expression of the YIRIM101-1119 allele rescues the alkaline-sensitive growth phenotype of the *Yrim13-26* mutant and generates a mild acid-sensitive phenotype (Fig. 2a, RimSL

Fig. 2. Effects of the different mutations on *Y. lipolytica* sensitivity to ambient pH. Droplets of serial dilutions of late-exponential-culture cells in YPD medium were deposited on solid YPD medium buffered at pH 3.5 with 0.2 M citrate buffer, and at pH 7.0, 8 and 8.5 with 0.2 M MOPS buffer, and incubated at 28 °C for 40 h. The strains were (a) LAM26-03 (*rim13*); CGL-U15u (*vps23*), CGL-Y2u (*vps28*), SY12 (WT), AM319ΔC (RimSL), SBR116 (*rim13*+RimSL), SBR117 (*vps23*+RimSL) and SBR118 (*vps28*+RimSL). (b) SY12 (WT); SBR114u (Δ*vps4*), SBR119 (Δ*vps4*+RimSL) and SY1364 (*vps4KA*).

or *rim13*+RimSL). Both effects were observed when this activated form was expressed in *Ylvs28-Y2* and *Ylvs23-U15*, the acid-sensitive phenotype being exacerbated in these strains compared to *Ylrim13-26* (Fig. 2a).

All these results confirmed that (i) like *Ylrim* mutations, *Ylvs23* and *Ylvs28* mutations are suppressed by a constitutively active form of YIRim101p, suggesting that their effects at alkaline pH are mediated through YIRim101p, (ii) unlike *Ylrim* mutant strains, *Ylvs* mutant strains display a strong alkaline-sensitive growth phenotype and an acid-sensitive phenotype that is exacerbated when the alkaline response is turned on at acidic pH, suggesting that their response to ambient pH is affected both in Rim-dependent and in Rim-independent ways.

YISNF7* is an essential gene in *Y. lipolytica

In *S. cerevisiae*, Vps23p and Vps28p are both components of the ESCRT-I complex (Katzmann *et al.*, 2001). We wondered whether Snf7p, which is known to interact with Rim20p in *S. cerevisiae*, *A. nidulans* and *C. albicans* (see Introduction), was also involved in pH regulation. The YALI0C16027g sequence encodes a predicted protein of 215 aa that matches putative orthologous gene products in other species, with the following identity scores: 49 % with *S. cerevisiae* Snf7p, 50 % with *C. albicans* Snf7p (CA4903 <http://genolist.pasteur.fr/CandidaDB/>), 43 % with *Schizosaccharomyces pombe* Spac1142.07c (CAB77014.1), 47 % with *Neurospora crassa* hypothetical protein (CAD70846.1) and 41 % with *H. sapiens* CHMP4b (CAC14088.1). Like its homologues, YISnf7p presents several putative coiled-coil regions (positions 14–48, 53–85 and 149–173).

As *SNF7* is non-essential in *S. cerevisiae* and *C. albicans*, we first tried to delete the *YISNF7* coding sequence in the haploid strain SY12 (see Methods). We got only two disruptants from several transformation assays, most transformants resulting from ectopic integrations. The two clones were not affected in endocytosis and displayed no pH-response defect (data not shown). In order to rule out that a functionally redundant protein may compensate for the loss of YISnf7p, we searched for possible YISnf7p homologues within the *Y. lipolytica* genome. Only two distant paralogues YIVps20p (28 % identity) and Mos10p/Vps60p (33 % identity) were identified, as would be the case in *S. cerevisiae* for a search of ScSnf7p paralogues. We wondered if the presence of suppressing mutation(s) in the *YIRIM101* gene may account for the lack of phenotypes for *Ylsnf7Δ* strains. The sequence of the *YIRIM101* locus was checked entirely in these strains, but no mutation could be detected. We thus assumed that *YISNF7* might be essential. Therefore, two strategies were developed to disrupt this gene. (i) One *YISNF7* allele of the diploid strain AM3/AM4 was disrupted as before, with selection for Ura⁺ isolates. Deletion of one *YISNF7* allele was confirmed by PCR and Southern blotting for several transformants. Two independent diploids were sporulated and their progeny was studied by random spore analysis. Among a total of 153 fast-growing

auxotrophic segregants, none were Ura⁺ (i.e. disrupted for *YISNF7*), whereas the other auxotrophic markers segregated normally. Twelve very slow-growing colonies were later observed on the plates; they were all Ura⁺, and upon a PCR test were shown to be disomic, carrying both a normal and a deleted copy of *YISNF7* (data not shown). We concluded, therefore, that the *YISNF7* gene was essential for spore germination and/or vegetative growth. (ii) The plasmid pINA1356, carrying an internal deletion of the whole *YISNF7* coding sequence, was integrated by a single crossing-over event into the promoter of the *YISNF7* gene in the haploid strain E122, with selection for Ura⁺. This created a wild-type copy and a deleted copy integrated in tandem in the genome and flanking the *URA3* marker. The resulting strain was then transformed with the Leu⁺ replicative plasmid pINA1355 carrying the wild-type *YISNF7* gene, with selection for unstable Leu⁺ clones. Secondary Ura[−] clones were selected on 5-fluoroorotic acid medium and screened for the occurrence of recombination events leaving the *Ylsnf7-1356* deletion. Six Ura[−] Leu⁺ transformants, carrying the expected deletion of the genomic *YISNF7* allele and a free pINA1355 plasmid (as shown by *E. coli* transformation), were tested for the stability of the Leu⁺ marker. No loss of the replicative plasmid was observed among more than 600 clones tested, after 30 generations on non-selective medium, thus confirming that the *YISNF7* gene was essential for the viability of the cells during vegetative growth.

***YIVPS4* does not appear to be required for the Rim101-dependent pH response**

We wondered whether Vps4p (Babst *et al.*, 1998), which acts downstream from the three ESCRT complexes and has been reported to interact with Rim20p (Bowers *et al.*, 2004), was also involved in pH regulation in *Y. lipolytica*. A putative homologue (accession no. YALI0B16368g) of this gene was identified in the *Y. lipolytica* genome. The predicted 428 aa YIVps4p protein matches putative homologues in other species with the following identity scores: 77 % with *C. albicans* Vps4p (CA1340; <http://genolist.pasteur.fr/CandidaDB/>), 73 % with *S. cerevisiae* Vps4p, 67 % with *A. nidulans* hypothetical protein AN3061.2 (EAA63632.1), 63 % with *Schizosaccharomyces pombe* Spac2G11.06 (CAA91171.1), 61 % with *H. sapiens* Vps4-2 (AAG33022.1) and 60 % with *Mus musculus* Skd1p (AAD47570.1). Like its homologues, YIVps4p displays the three-domain structure postulated for ScVps4p (Babst *et al.*, 1998): the N-terminal domain with a putative coiled-coil motif (position 51–80), one central AAA domain containing the AAA-protein family signature (position 263–281), two consensus ATP-binding sites consisting of a Walker A box motif (position 172–179) and a version of the Walker B motif called the DEAD box (position 229–242) and the highly charged C-terminal domain.

To assess the effects of *YIVPS4* on pH response, the phenotype of the SBR114 strain, carrying the null mutation *YIΔvps4-14*, was established (see Methods). The effects of the *YIVPS4* deletion on the expression of alkaline- and

acid-induced genes were assessed by real-time quantitative PCR, at pH 4.0 and 8.0 (Fig. 1). At alkaline pH, in *Ylvs4Δ-14*, the transcript levels of *XPR2*, *YIPHR1*, *YIRIM101* and *YIPHR2* varied by a factor of less than two compared to the wild-type strain, less than observed in the *rim13*, *vps23* and *vps28* mutants (see above). At acidic pH, *XPR2* and *YIPHR1* showed significantly more expression than in these mutants ($P < 0.01$), whereas the level of expression of the acid-induced gene *YIPHR2* was barely affected (less than twofold, $P \times 10^{-5}$). These results indicate that the *Ylvs4Δ* mutation affects the pH response much less severely than the *Yrim13*, *Ylvs23* and *Ylvs28* mutations at alkaline pH, and affects the pH response in an opposite way with respect to alkaline-induced genes at acidic pH. These complex effects might partly relate to the slow growth of this mutant. Indeed, the deletion of *YIVPS4* conferred a pronounced growth defect on cells grown on YPD medium at all pH values tested (Fig. 2b).

Next, we checked whether expression of the constitutively active, truncated form *YIRIM101-1119* was able to suppress the defects of the *Ylvs4Δ-14* mutant, as it did for the *rim13*, *vps23* and *vps28* mutants. To address this question, we replaced the wild-type *YIRIM101* allele by the most truncated allele, *YIRIM101-1119* (Lambert *et al.*, 1997), in the *Ylvs4Δ-14* mutant strain (see Methods). As shown in Fig. 2(b), expression of the *YIRIM101-1119* allele did not rescue the growth defects of *Ylvs4Δ-14*, at all pH values tested. At both alkaline and acidic pHs, the *YIRIM101-1119* allele failed to restore the expression of the two alkaline-induced genes, *XPR2* and *PHR1*, in the *Ylvs4Δ-14* mutant (Fig. 1a, b).

Vps4p exhibits an ATPase activity, which is required in *S. cerevisiae* for the dissociation of ESCRT complexes at the end of the MVB cycle (Babst *et al.*, 1998), and has been proposed as an interactant of Rim20p (see Introduction). In order to check whether the growth defect of *Ylvs4Δ-14* was due to the loss of the ATPase activity or to the loss of the protein itself, we constructed the SY1364 strain (see Methods; Table 1) where a K172A mutation specifically destroys the ATP-binding site of Vps4p. Correct expression of the mutated allele, which is expected to display a dominant negative phenotype on endocytosis (Babst *et al.*, 1997), was checked by its ability to block endocytosis in a *YIVps4⁺* background, as checked by FM4-64 staining (data not shown). As shown in Fig. 2(b), the growth of the *Ylvs4^{K172A}* mutant was as severely affected as the growth of *Ylvs4Δ-14* at all pH values tested. Taken together, these results suggest that effects of the *Ylvs4Δ-14* mutation mostly result from an endocytic Rim-independent defect on cell physiology.

Ylvs* mutants exhibit endocytic defects not suppressed by the C-terminal truncated allele of *RIM101

In order to confirm that the *vps* mutations indeed affected the MVB pathway in *Y. lipolytica*, the endocytic defects of *Ylvs4Δ-14*, *Ylvs23-U15* and *Ylvs28-Y2* mutant strains

were visualized with the fluorescent dye FM4-64, a lipophilic dye that binds to the plasma membrane, is internalized and then delivered to the vacuolar membrane (Vida & Emr, 1995). Cells were labelled with FM4-64 at 0 °C, then warmed to 18 °C and assessed for the distribution of FM4-64. By 20 min, FM4-64 could be seen on the vacuole limiting membrane in the wild-type cells. In contrast, in all the mutant strain cells, the bulk of FM4-64 remained in small compartments adjacent to the vacuole (Fig. 3). These structures are highly reminiscent of class E compartments, which accumulate proteins destined to the vacuole in class E *vps* mutants in *S. cerevisiae* (Rieder *et al.*, 1996; Vida & Emr, 1995). When the constitutively active *YIRIM101-1119* allele was expressed in *Ylvs4Δ-14*, *Ylvs23-U15* and *Ylvs28-Y2* cells, the bulk of FM4-64 remained in small compartments adjacent to the vacuole (Fig. 3), as in the parental mutant strains. These results show that mutations in *YIVPS4*, *YIVPS23*, *YIVPS28* indeed lead to a membrane-trafficking defect that, as expected, is independent of the status of the Rim pathway.

DISCUSSION

At the late endosome, the MVB pathway sorts endosomal proteins destined for the lumen of the vacuole (resident hydrolases for proper localization and endocytosed activated cell-surface proteins for downregulation) away from proteins destined for the limiting membrane of the vacuole or to be recycled back to the plasma membrane or Golgi complex. The MVB pathway involves several class E Vps factors, some of them organized in three distinct endosome-associated protein complexes called ESCRT complexes (Babst *et al.*, 2002a, b; Bowers *et al.*, 2004; Katzmann *et al.*, 2001). Previous reports pointed toward possible interactions between components of the MVB pathway and of the Rim pathway devoted to pH sensing in ascomycetes. The interactions of Snf7p with Rim20p homologues are conserved across evolution from *S. cerevisiae* Rim20p to *A. nidulans* PalA and to human AIP1/Alix homologues (Bowers *et al.*, 2004; Ito *et al.*, 2001; Vincent *et al.*, 2003).

Here we report on the characterization of *Ylvs* mutations affecting the ESCRT-I complex of the MVB pathway in *Y. lipolytica*. We show that *Ylvs23* and *Ylvs28* mutations not only affect the endocytic pathway, as expected from the function of the proteins encoded by their homologues in *S. cerevisiae* and *C. albicans* (Rieder *et al.*, 1996; Vida & Emr, 1995; Kullas *et al.*, 2004; Cornet *et al.*, to be published), but also that the mutant strains have a bona fide Rim phenotype, as described in these two other yeasts (Kullas *et al.*, 2004; Xu *et al.*, 2004; unpublished data). The proteins are required for growth at alkaline pH (Fig. 2), activation of alkaline-induced genes and repression of an acid-induced gene, like *YIPHR2* (Fig. 1). All the defects in the alkaline response are suppressed at least partially by the constitutively active *RIM101-1119* allele expressing a truncated form of the downstream transcriptional activator Rim101p. The suppressive effect of the truncated form of Rim101p suggests

Fig. 3. FM4-64 staining in the *Y. lipolytica* mutants. The strains were SY12 (WT), SBR114u ($\Delta vps4$); CGL-U15u (*vps23*), CGL-Y2u (*vps28*), SBR119 ($\Delta vps4$ +RimSL), SBR117 (*vps23*+RimSL) and SBR118 (*vps28*+RimSL). They were incubated with 40 μ M FM4-64, as described in Methods, and visualized by fluorescence microscopy. The left side of each panel shows FM4-64 fluorescence, while the right side shows DIC images.

that these MVB components act upstream from Rim101p. In agreement with findings reported in *S. cerevisiae* and *C. albicans*, we showed that *Ylups4* does not appear to be required for activation of the Rim pathway in *Y. lipolytica*. This suggests that part of the MVB pathway only is required for ambient pH signalling in all ascomycetous yeasts. An attractive hypothesis would be that early steps of endocytosis including formation, but not dissociation, of the ESCRT complexes mediate signalling by the postulated membrane receptors Rim21p/PalH and/or Rim9p/PalI (Peñalva & Arst, 2004), and lead to recruitment by Snf7p of the cytoplasmic Rim machinery (Kullas *et al.*, 2004; Xu *et al.*, 2004).

During this work, we observed that *YIPHR2* behaved as expected for a bona fide acid-induced gene. *YIPHR2* was derepressed at alkaline pH in *YIRim13*, *Ylups23* or *Ylups28* mutant strains to identical levels, close to those observed at pH 4.0 in the wild-type strain (Fig. 1). It was repressed in these three backgrounds to similar levels at pH 4.0 upon expression of the artificially truncated form of YIRim101p. This repression was incomplete in all cases, suggesting that our construct YIRim101-1119p does not perfectly mimic the physiologically active form of YIRim101p, as previously reported (Gonzalez-Lopez *et al.*, 2002; Lambert *et al.*, 1997). These results show that, like *C. albicans*, *Y. lipolytica* expresses two isoforms of the surface proteins Phr1p/Phr2p with inverted pH-regulation patterns, both YIRim101p-dependent (Muhlschlegel & Fonzi, 1997). A search in the promoters of *YIPHR1* and *YIPHR2* for GCCARG, the putative consensus binding site for YIRim101p (Blanchin-Roland

et al., 1994; Lambert *et al.*, 1997), identified one such site in *YIPHR1* (position -139 from ATG) and three in *YIPHR2* (positions -302, -296 and -224 from ATG). Further work is needed to confirm the role of the putative YIRim101p-binding sites identified so far in the promoters of these acid- and alkaline-induced genes.

Besides effects on endocytosis and alkaline-pH sensing, our results evidenced other effects associated with mutations in *VPS* genes in *Y. lipolytica*. *Ylups* mutants appear more sensitive to acidic and alkaline pH than *Ylrin* mutants (Fig. 2), and the induction of an alkaline response, by a constitutively active form of the Rim101p regulator, is more deleterious at acidic pH for *Ylups23* and *Ylups28* than for *Ylrin* mutants (Fig. 2). This exacerbated defect could be explained by the fact that the growth of *Ylups* mutant strain was already affected at acidic pH, whereas the growth of *Ylrin* mutants was not. These defects suggest that ambient pH might influence MVB pathway activity *in vivo*, as has been suggested by Xu *et al.* (2004).

A puzzling observation is that only two ESCRT-I component encoding genes were identified in our initial mutagenesis. This may seem surprising in view of the different *VPS* genes reported in *S. cerevisiae*, from the screening of a haploid deletion-strain library, as being required for growth at mild alkaline pH (Serrano *et al.*, 2004), or functioning in the Rim101p pathway (Barwell *et al.*, 2005). This last exhaustive screening revealed the genes already shown to be involved in Rim101p processing (Xu *et al.*, 2004), as

encoding components of either the ESCRT-I (Vps23, Vps28, Vps37), the ESCRT-II (Vps22, Vps25, Vps36) or the ESCRT-III sub-complex (Vps20, Vps32). Although our screen was not exhaustive, it identified most (i.e. five out of six) of the *RIM* genes, but only two out of the eight *VPS* genes, so far identified in *S. cerevisiae* as affecting Rim101p processing. It is even more surprising to observe that no *vps* mutant at all was identified in *A. nidulans*, in exhaustive screens for defects in pH signalling (Peñalva & Arst, 2004). Recent reports suggest that fungi do have homologues of the *VPS* genes (Read & Kalkman, 2003). The fact that *YISNF7* was found to be essential, the *Ylvps4Δ* mutant strain grows very poorly, and *Ylvps23* and *Ylvps28* mutations mildly affect growth at all pH conditions tested (Fig. 2), even at pH 7.0, may offer a general clue to this apparent paradox. A likely hypothesis is that most, if not all, *VPS* genes are essential, or are required to avoid major growth defects in *A. nidulans* and to a lesser extent in *Y. lipolytica*. In *S. cerevisiae*, although *vps* mutant strains were reported to be viable, a careful analysis shows that many, including *vps23* and *snf7*, may present severe growth defects on several types of media, including complete medium, after 20 or more generations (Giaever *et al.*, 2002; see also <http://www.yeastgenome.org/>). In *C. albicans*, the growth of the *snf7Δ/snf7Δ* mutant is significantly reduced on complete medium and drastically impaired at alkaline pH (Kullas *et al.*, 2004). Since pH signalling is not an essential function in fungi under most circumstances, it might be that endocytosis is required for cellular growth.

In *Y. lipolytica*, transition from unicellular yeast-type growth to filamentous hyphal growth is not pH dependent, contrary to what is observed in *C. albicans* (Fonzi, 2002). We notice that all *Ylvps* mutants tested show a strong defect in hyphal formation not suppressed by expression of the truncated, active form of YlRim101p, contrary to *Ylrim* mutants, which display near normal morphogenesis at all pH conditions tested (Gonzalez-Lopez *et al.*, 2002; data not shown). In contrast to this, all *C. albicans rim* or *vps* mutant strains present defects in hyphal formation and these defects are either totally, in *Carim* mutants, or at least partially, in *Cavps* mutants, bypassed by the expression of the constitutive form of CaRim101p (Kullas *et al.*, 2004; Xu *et al.*, 2004). Taken together, these results suggest that *VPS* genes might be required directly for hyphal growth in *Y. lipolytica* and probably also in other fungi, but that this function has been taken over by the Rim pathway in *C. albicans*. This may further explain why *VPS* genes were not identified during hunts for mutant strains defective in pH response in *A. nidulans*. Further work is thus needed to assess the involvement of *VPS* genes in pH sensing and control of cellular morphology in diverse fungal species.

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