Nutrient regulation of oligopeptide transport in 
*Saccharomyces cerevisiae*

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Small peptides (2–5 amino acid residues) are transported into *Saccharomyces cerevisiae* via two transport systems: PTR (Peptide Transport) for di-/tripeptides and OPT (OligoPeptide Transport) for oligopeptides of 4–5 amino acids in length. Although regulation of the PTR system has been studied in some detail, neither the regulation of the OPT family nor the environmental conditions under which family members are normally expressed have been well studied in *S. cerevisiae*. Using a *lacZ* reporter gene construct fused to 1 kb DNA from upstream of the genes *OPT1* and *OPT2*, which encode the two *S. cerevisiae* oligopeptide transporters, the relative expression levels of these genes were measured in a variety of environmental conditions. Uptake assays were also conducted to measure functional protein levels at the plasma membrane. It was found that *OPT1* was up-regulated in sulfur-free medium, and that Ptr3p and Ssy1p, proteins involved in regulating the di-/tripeptide transporter encoding gene *PTR2* via amino acid sensing, were required for *OPT1* expression in a sulfur-free environment. In contrast, as measured by response to toxic tetrapeptide and by real-time PCR, *OPT1* was not regulated through Cup9p, which is a repressor for *PTR2* expression, although Cup9p did repress *OPT2* expression. In addition, all of the 20 naturally occurring amino acids, except the sulfur-containing amino acids methionine and cysteine, up-regulated *OPT1*, with the greatest change in expression observed when cells were grown in sulfur-free medium. These data demonstrate that regulation of the OPT system has both similarities and differences to regulation of the PTR system, allowing the yeast cell to adapt its utilization of small peptides to various environmental conditions.

INTRODUCTION

During studies of peptide transport in *Candida albicans*, it was noted that the yeast was able to transport peptides consisting of two to five amino acid residues. The cloning of a peptide transporter gene, *CaPTR2*, accounted for the phenotype of di-/tripeptide transport (Basrai et al., 1995), but clearly a second transporter responsible for tetra-/penta-peptide uptake was present in this organism. It was this conclusion that led Lubkowitz et al. (1997) to clone *CaOPT1*, the tetra-/pentapeptide transporter from *C. albicans*. It was shown that CaOpt1p was not a member of either the ABC or the PTR membrane transport families: CaOpt1p contained neither the nucleotide-binding domain of the ABC family nor the conserved PTR family motifs. Two *Saccharomyces cerevisiae* ORFs, YJL212C and YPR194C, later named *OPT1* and *OPT2*, respectively, were subsequently cloned and identified by function as encoding oligopeptide transporters (Hauser et al., 2000). The phenotype of strains expressing either *S. cerevisiae OPT* gene was similar to that of a *S. cerevisiae* strain expressing *CaOPT1*, in that they were able to transport tetra-/pentapeptides (Hauser et al., 2000; Lubkowitz et al., 1997). *OPT1* was also cloned in another study and given the name *HGT1*, since it was also identified as a GSH transporter (Bourbouloux et al., 2000). Little information was obtained regarding the regulation of these *OPT* genes, except that their expression was very low under normal growth conditions, requiring expression under a constitutive promoter to reveal their function as oligopeptide transporters (Hauser et al., 2000; Lubkowitz et al., 1998). Some information regarding expression of *OPT1* and *OPT2* may be extracted from the *S. cerevisiae* microarray expression database, as mentioned below. There is an additional putative *S. cerevisiae OPT* gene that was identified by homology (Yen et al., 2001). This ORF, named YGL114w, has been examined rigorously now by sequence comparison and the protein it encodes does not appear to be a true member of the OPT family, despite having slight sequence similarity to *S. cerevisiae* Opt1p and Opt2p (Wiles et al., 2006).
The number of identified genes encoding oligopeptide transporters has increased recently. Plants such as Arabidopsis thaliana (Osawa et al., 2006) and Oryza sativa (rice) (Cagnac et al., 2004) have been shown to contain multiple OPT homologues, and some information has been generated regarding expression of OPT genes in plants. Koh et al. (2002) found that AOPT3 expression is required for embryonic growth of A. thaliana, which has nine OPT genes. The same group also found that the other AOPT genes are expressed in different plant tissues during different developmental stages (Osawa et al., 2006). The genome of the pathogenic yeast C. albicans contains seven OPT genes as determined by sequence homology. Lorenz et al. (2004) observed up to 30-fold induction of three of these OPTs upon phagocytosis by macrophages, but no induction of the other four family members in the same species. Thus, having a multiplicity of OPT genes in a single species provides the opportunity for differential expression of the individual genes under various environmental or developmental conditions.

Although there appear to be only two members of the OPT family in S. cerevisiae, a few microarray studies have shown differential regulation of ScOPT1 and ScOPT2 under stress or nutrient limitation conditions. In response to nitrogen depletion, OPT1 was induced (Gasch et al., 2000); another group observed that OPT1 was up-regulated when cells were grown in a limited source of sulfur but not when cells were grown in a limited source of nitrogen (Boer et al., 2003). These two results seem to conflict with each other with respect to the regulation of OPT1 by nitrogen starvation, although the media, strains and growth conditions were different in these two studies.

While these microarray data have been gathered for only a few environmental conditions that regulate OPT expression in S. cerevisiae, the regulation of PTR2, the gene encoding the di-/tripeptide transporter in S. cerevisiae, has been well characterized. Earlier studies indicated that dipeptide transport was increased when cells were grown on the sole, poor nitrogen source allantoin (Island et al., 1987). When cells are grown on a poor nitrogen source, PTR2 expression is induced by the nitrogen catabolite repression pathway (Magasanik & Kaiser, 2002). Levels of Ptr2p at the membrane drop dramatically within 30 min of addition of a rich nitrogen source, such as ammonium sulfate (S. Minkin and J. M. Becker, unpublished). In addition, expression of both PTR2 and Ptr2p is increased when cells are exposed to micromolar levels of amino acids, with tryptophan and leucine being the best inducers; PTR2 mRNA levels peak at 40 min when induced with leucine (Perry et al., 1994) and dipeptide transport peaks at 4 h when induced with tryptophan (Island et al., 1987). This amino acid induction of PTR2 is regulated through the amino acid receptor Ssy1p (Didion et al., 1998).

Ssy1p is an integral membrane protein that interacts with Ptr3p and Ssy5p to form the SPS complex (Forsberg et al., 2001). Ssy1p is also required for the induction of genes encoding amino acid transporters, AGP1, BAP1, BAP2, GAP1, GNP1, TAT1 and TAT2 in S. cerevisiae (Kodama et al., 2002). Upon receptor activation by amino acids, the signal is transduced by the SPS complex that processes the transcription factors Stp1p and Stp2p, which then migrate to the nucleus (Andreason et al., 2006). In addition, dipeptides initiate the degradation of the repressor Cup9p, which results in transcription of PTR2 (Hauser et al., 2001) by an SPS-independent pathway (Byrd et al., 1998; Turner et al., 2000). Our lab has recently completed a comprehensive study of S. cerevisiae genes involved in dipeptide utilization that has revealed a total of 42 genes involved in the expression of PTR2 (Cai et al., 2006).

Because expression of genes encoding the amino acid and di-/tripeptide transporters in S. cerevisiae is affected by nitrogen supply, we tested the effect of nitrogen constraints on OPT expression. We also tested the effect of sulfur and carbon constraints on expression because of findings by both Gasch et al. (2000) and Boer et al. (2003). Additionally, the roles of Ptr3p and Ssy1p in OPT1 expression were investigated, since these proteins are known to play a role in the gene expression of amino acid and di-/tripeptide transporters. We were also interested in whether each individual OPT or YGL114wp protein had an effect on the expression of OPT1 or OPT2, and if the genes were autoregulated. Our results demonstrated that the absence of sulfur, but not nitrogen or carbon, and the addition of all naturally occurring amino acids, except the sulfur-containing amino acids methionine and cysteine, led to SPS-dependent induction of OPT1 and increased transport of a pentapeptide.

**METHODS**

**Media.** Strains were maintained on synthetic complete (SC) medium made using the original recipe for yeast nitrogen base with 2 % glucose without amino acids (Wickerham, 1946, 1951). Modifications were made to Wickerham’s formulation to create media with specific nutrient reductions as shown in Supplementary Table S1, available with the online journal. Reduced carbon medium contained 25 % of the amount of glucose found in SC. Reduced nitrogen medium contained 10 % of the amount of ammonium sulfate found in SC, with the sulfate added back via sodium sulfate. Reduced sulfur medium contained no ammonium sulfate and 10 % of the amount of magnesium sulfate found in SC; with the magnesium added back via the corresponding chloride salts. Furthermore, reduced nitrogen and sulfur medium had no ammonium sulfate and 10 % of the magnesium sulfate found in SC; 10 % of the ammonium and 90 % of the magnesium were added via their chloride salts. Modifications were also made to SC to create media with no carbon, no nitrogen, no sulfur, and with neither nitrogen nor sulfur. In media with either no nitrogen or no sulfur, the corresponding chloride salts were added to maintain the correct concentration of other nutrients. Allantoin SC medium was made from 1-7 g yeast nitrogen base 1-1 (Difco) without (NH4)2SO4 or amino acids, 20 % glucose, and 1 % allantoin as nitrogen source. As needed, 20 μg uracil ml−1 or 30 μg leucine ml−1 were supplemented.

**Strain construction.** Single gene knock-outs of OPT1, OPT2, YGL114W, PTR3 and SSY1, and double knock-outs of PTR3 and SSY1, and PTR3 and OPT1, were created in the S. cerevisiae FY2
strain background (MATa ura3-52) (Winston et al., 1995) using the drug resistance cassettes KanMX4, providing resistance to G418, HphMX3, providing resistance to hygromycin B, and NatMX3, providing resistance to clonNAT (nourseothricin) (Goldstein & McCusker, 1999; Guldener et al., 1996). YEPD (1%, w/v, yeast extract; 2%, w/v, peptone; 2% glucose) was used in the construction of knock-out strains, with final concentrations of 200 μg G418 ml⁻¹, 300 μg hygromycinB ml⁻¹ or 100 μg clonNAT ml⁻¹ (Werner BioAgents) added when appropriate. FY2 was used for genomic DNA was ethanol precipitated and resuspended in 100 μl 100 mM NaCl, 10 mM Tris/HCl pH 8.0, 1 mM EDTA pH 8.0, and 7% DMSO was included in the PCR for amplifying the NatMX3 cassette due to its high G/C content. The components were combined on ice and immediately placed at 95 °C for 5 min to begin the reaction. The reaction conditions were as follows: 40 cycles of 1 min at 95 °C, 1 min at 52 °C for KanMX4 (Guldener et al., 1996), 55 °C for HphMX3 or 52 °C for NatMX3, and 3 min at 72 °C. An additional 7 min at 72 °C were added for extension, followed by a hold at 4 °C. The PCR products were visualized on a 1% agarose/TAE gel with subsequent staining by ethidium bromide, and purified using a SOPE column (Open Biosystems).

The amplified knock-out cassettes were transformed into the required strain following a well-established protocol (Gietz & Woods, 2002). In brief, cells to be transformed were harvested in exponential phase and made competent with lithium acetate. They were allowed to recover for 2 h in YEPD at 30 °C, with shaking at 200 r.p.m., before being plated on YEPD containing the appropriate drug. Drug-resistant (presumed knock-out) colonies were picked and streaked for isolation after 4 days of incubation.

Gene knock-outs were confirmed by PCR and Southern blotting using yeast genomic DNA. For purifying the DNA, 5 ml cultures were grown overnight at 30 °C, with shaking at 200 r.p.m., in YEPD. The cells were harvested in a tabletop centrifuge at top speed for 5 min, and resuspended in 500 μl sterile water. The cells were again pelleted at top speed, this time in a microfuge, and resuspended in 300 μl breaking buffer (2%, w/v, Triton X-100, 1%, w/v, SDS, 100 mM NaCl, 10 mM Tris/HCl pH 8.0, 1 mM EDTA pH 8.0), and 450 mg glass beads and 300 μl phenol/chloroform/isoamy alcohol (24: 24: 1, by vol.) were added to the tube. The tube was vortexed at top speed for 3 min, then 100 μl TE buffer was added, and the tube vortexed briefly. The sample was again microfuged at top speed for 5 min, and the aqueous layer was transferred to a new tube. The genomic DNA was ethanol precipitated and resuspended in 100 μl sterile water.

For PCR confirmation of the strains, primers were designed to anneal to sequences flanking the knocked-out region in the genomic DNA (Table 1). The PCR mixtures and conditions were as described above except that 8 ng genomic DNA was used as the template and the annealing step was carried out at 54 °C.

Southern blotting was carried out using 20 μg genomic DNA digested overnight in a volume of 200 μl with 10 μl restriction enzyme, one of two enzymes chosen for each gene, one cutting only flanking the ORF, the other cutting internally. BamHI flanked OPT1, OPT2 and YGL114W, while KpnI cut OPT1, FspI cut OPT2 and BglII cut YGL114W. PTRA was flanked by FspI and cut by SacI, and SY1 was flanked by XhoI and cut by HindIII. Enzymes were used as recommended by New England BioLabs. Also included was genomic DNA from the parent strain FY2. After digestion, DNA was ethanol precipitated, resolved on a 0.7%-agarose/TAE gel and blotted.

Probes were constructed by PCR amplification of the ORF from genomic DNA using probe primers specific for each gene (Table 1). The PCR mixtures and conditions were as described for PCR analysis of the knock-outs except that the annealing temperature was 55 °C. Purified PCR product was labelled using a random-prime labelling technique as follows: 50 ng DNA was incubated for 1 h at 37 °C with 3 μg random 9-mer or 5 μg random 6-mer, 1 x label buffer (900 μM HEPES, 100 μg MgCl₂), 50 mM dNTP (no ATP), 10 mM DTT, 3 μl [³²P]dATP (50 μCi = 1-85 MBq) and 1 μl Klenow enzyme (Fisher Scientific) in 20 μl total volume. A spin-column purification was performed to purify the radioactive probe, using either Bio-Spin chromatography columns (Bio-Rad) or ProbeQuant micro columns (Amersham/GE Healthcare). Hybridization was carried out at 65 °C overnight. The blot was then placed against a Molecular Dynamics phosphor screen (Amersham/GE Healthcare) overnight, and the screen analysed on a STORM 840 densitometer with ImageQuant (Amersham/GE Healthcare).

**Plasmid constructions containing a reporter gene.** The promoters of OPT1, OPT2 and YGL114W were cloned into pYLZ6 (Hermann et al., 1992) upstream of the gene encoding β-galactosidase. The region 1 kb upstream of each ORF, including the start codon, was amplified by PCR. Primers (Table 1) were designed for homologous recombination into the plasmid, which had been linearized at the HindIII site. PCR conditions to amplify the promoters were as follows: 2 units Pfu DNA polymerase (Stratagene), 1 pmol primer, 200 μM dNTPs, 1 x buffer (supplied with enzyme), 2-5 mM MgCl₂ and 8 ng genomic DNA. The components were combined on ice and immediately placed at 95 °C for 5 min to begin the reaction. Forty cycles of PCR were carried out as follows: 45 s at 95 °C, 45 s at 53 °C, and 5 min at 72 °C. An additional 7 min at 72 °C was added for extension, followed by a hold at 4 °C. The reaction products were visualized and purified as described for strain construction. Each product and the linearized plasmid were used to co-transform FY2 following the protocol by Gietz & Woods (2002). Plasmid transformants and cells transformed to make use of homologous recombination were picked after 2–3 days of growth on SC medium. Plasmids were recovered with a Zymoprep kit (Zymo Research) and sequenced. These new plasmids were named pYLZ6-OPT1, pYLZ6-OPT2 and pYLZ6-YGL114W after the genes whose promoters they contained.

*Escherichia coli* was used for amplification of plasmids. Transformations were carried out using DH5α heat-shock competent cells (Invitrogen). The manufacturer’s protocol was followed, with 10 ng plasmid DNA. For plasmid preps, Wizard Plus SV miniprep DNA purification spin columns (Promega) were used. E. coli containing plasmid was maintained on LB (1%, w/v, tryptone, 0-5%, w/v, yeast extract, 1%, w/v, sodium chloride) with 100 μg ampicillin ml⁻¹.

**Growth curve assays.** To determine growth curves or gene expression levels in these media, cells were first grown overnight in SC, harvested at top speed in a tabletop centrifuge, and washed twice with cold water. The various media were then inoculated at 5 x 10⁵ cells ml⁻¹, and the OD₅₅₀ of each culture was measured every 2 h for 12 h and compared to a standard curve constructed for each knock-out strain.

**β-galactosidase assays.** Assays for β-galactosidase activity were conducted using a protocol modified from that of Hoffman et al. (2002). Cells containing the empty vector pYLZ6 or the vector containing 1 kb DNA from upstream of the gene of interest (pYLZ6-OPT1, pYLZ6-OPT2 or pYLZ6-YGL114W) were scraped from a fresh plate and grown overnight in 25 ml SC. They were harvested in a tabletop centrifuge at high speed at 4 °C, and washed three times with cold water. Cells were inoculated into fresh media at 5 x 10⁶ cells ml⁻¹ and grown for 2–12 h. If amino acids were added, this was carried out simultaneously to the addition of the cells, at
Table 1. Primers used in the construction of plasmids and strains or real-time RT-PCR

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence (5' to 3')</th>
<th>Comment</th>
</tr>
</thead>
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<tr>
<td>KO_029_F</td>
<td>GGTACGAAATACACAACGTAGCGGTTATCATGCACTCTCACAGCTGAAACCTGTTCCGTACGC</td>
<td>YFR029W (PTR3) knock-out</td>
</tr>
<tr>
<td>KO_029_R</td>
<td>GTGAAATATTGGCCTTACATTTTGAGTTCGTCCGGGATGGCCATAGGCGCCTAGAGATGGATCTG</td>
<td>YFR029W (PTR3) knock-out</td>
</tr>
<tr>
<td>KO_114_F</td>
<td>CCGTTAAGATTCATAACCTGCTAATCTGGACACATTTGAAACCTGTTCCGTACGC</td>
<td>YGL114W knock-out</td>
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<tr>
<td>KO_114_R</td>
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<td>YGL114W knock-out</td>
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<td>KO_160_F</td>
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<td>YDR160W (SSY1) knock-out</td>
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<tr>
<td>KO_160_R</td>
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<td>KO_194_F</td>
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<td>YPR194C (OPT2) knock-out</td>
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<tr>
<td>KO_194_R</td>
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<tr>
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<tr>
<td>KO_212_R</td>
<td>CACCACTTTATCTAACCACATTATTTTGATTAGAAGAAGTCAACAGCTGAAACCTGTTCCGTACGC</td>
<td>YPR194C (OPT2) knock-out</td>
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<tr>
<td>212prom_pYLZ_F</td>
<td>GCCAGTTAACATCAAGCTTAGGATTCCTAATTACCTAACAGCTGAAACCTGTTCCGTACGC</td>
<td>Creation of pYlZ6-OPT1</td>
</tr>
<tr>
<td>212prom_pYLZ_R</td>
<td>CACCACTTTATCTAACCACATTATTTTGATTAGAAGAAGTCAACAGCTGAAACCTGTTCCGTACGC</td>
<td>Creation of pYlZ6-OPT1</td>
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<td>194prom_pYLZ_F</td>
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<td>ACT1 (F)</td>
<td>CACCATGTGCCAGTGATT</td>
<td>Real-time PCR for amplification of ACT1 amplicon</td>
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<tr>
<td>ACT1 (R)</td>
<td>CAACTCCAGGAGACGACTT</td>
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<td>OPT1 (F)</td>
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<td>PTR2 (R)</td>
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<td>Real-time PCR for amplification of PTR2 amplicon</td>
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concentrations required to fulfil auxotrophic requirements (see Supplementary Table S2 available with the online journal). When needed, GSH was added at 250 μM. Aliquots were harvested as described above for the growth assay. Using a black 96-well plate, 100 μl cells at 1 × 10⁸ cells ml⁻¹ were added to each well. A fluorescent di-β-D-galactopyranoside (FDG; Molecular Probes/Invitrogen) stock solution was made with 100 μM FGF in 25 mM Pipes (pH 7.2). The stock solution was combined 1:1 with a 5 % Triton X-100, 250 mM Pipes (pH 7.2) solution; 20 μl of this final solution was added to each well. The 96-well plate was incubated at 37 °C in the dark for 4 h. It was then read with a Wallac Victor² fluorescence multi-well plate reader (PerkinElmer) with excitation at 485 nm and emission at 530 nm. Background levels were determined using FY2 transformed with the empty vector pYLYZ6 grown in SC.

**Leu-enkephalin uptake assays.** Cells containing the empty plasmid pYLYZ6 were grown in SC or no sulfur medium, with or without amino acids or GSH, as described for β-galactosidase assays. Cultures were harvested at 4 °C by centrifugation at top speed in a tabletop centrifuge, washed twice with cold 2 % glucose, and resuspended at 2 × 10⁸ cells ml⁻¹. These cells were then combined with an equal part of 2 × uptake medium (2 % glucose, 400 μM citric acid/potassium phosphate buffer pH 5-5, 250 μM [³H]Leu-enkephalin at 1 μCi ml⁻¹ (37 kBq ml⁻¹)) and incubated for 10 min at 30 °C, after which the cells were filtered using a vacuum manifold fitted with 0-45 μm nitrocellulose filters (Millipore). The filters were then washed with 4 ml ice cold water, and were dissolved with CytoScint (MP Biomedicals) and counted with a scintillation counter. Preliminary experiments showed that uptake was linear at least 10 min.

**Toxic halo assays.** The sensitivity of various strains to the toxic dipeptide Ala-Eth (AE) or toxic tetrapeptide Lys-Leu-Ala-Eth (KLAE) was measured as previously described (Island et al., 1987). Eth (ethionine) is a toxic analogue of methionine, and its intracellular accumulation results in cell death. Yeast cells capable of transporting the toxic peptide die as a result of uptake of the peptide and subsequent intracellular release of ethionine. Cells with defective dipeptide or tetrapeptide transport will survive as indicated by a reduced halo or no halo in the halo assay system. Strains with the genetic background FY2, which is considered to be wild-type with respect to this assay, and FY2 strains carrying deletions in OPT1, OPT2 and CUP9, were grown overnight at 30 °C in allantoin SC + Ura medium. Cells were harvested and washed three times with sterile, distilled water, counted by haemocytometer, and adjusted to 5 × 10⁶ cells ml⁻¹. One millilitre cell suspension was added to 0-8 % noble agar (3 ml) and plated onto solid (2 % agar) allantoin or sulfur. Under the conditions used for these experiments, 10 % of the sulfur or nitrogen and 25 % of the carbon were sufficient for full growth during the 12 h incubation period.

**Real-time RT-PCR.** Approximately 3 × 10⁶ cells of the tested deletion strains opt1, opt2 and cup9, and wild-type (FY2), were grown overnight in allantoin SC + Ura + Leu medium. The overnight cultures were harvested, transferred into the same fresh medium, and grown for 3 h. Yeast total RNA was isolated using a RiboPure-yeast kit (Ambion). The amount of total RNA was quantified by measuring absorbance at 260 nm. To check that the genomic DNA had been eliminated, the obtained total RNA was used as the template to PCR amplify the target genes, and no PCR product was obtained. cDNA was synthesized using M-MLV reverse transcriptase (Invitrogen; 400 U) in a reaction mixture containing 1 μg oligo(dT), 1 mM deoxynucleoside triphosphates, 14 U anti-RNase and 1 μg total RNA at 42 °C for 45 min, and the reaction was stopped after 5 min by incubation at 72 °C.

Real-time PCR analysis was performed using the Opticon DNA engine (MJ Research) with the QuantiTect SYBR Green PCR kit (Qiagen). The primers used for detecting the expression of OPT1, OPT2, PTR2 and ACT1 are shown in Table 1. The resulting PCR products were about 100 bp. The reaction contained 12-5 μl x quantitive PCR reaction mix, 15 pmol primers, run with 1 cycle of 50 °C for 2 min, 95 °C for 15 min, followed by 40 cycles of 95 °C for 15 s, 54 °C for 30 s and 72 °C for 15 s. The Ct value, the cycle when the sample fluorescence exceeded the threshold above background fluorescence, was determined using the DNA engine software program. The copy number of OPT1, OPT2, PTR2 and ACT1 genes in the tested strains was calculated based on a standard curve. The ratio was calculated by the fold-change of the target genes (OPT1, OPT2 or PTR2) in the cup9 strain compared to that of the wild-type, divided by the fold-change of ACT1 in the cup9 strain compared to that of the wild-type. The ratio of the fold-change in the wild-type was standardized to 1-0.

**RESULTS**

**Determination of growth curves in media with reduced nutrients or without nutrients**

The growth of wild-type (FY2) cells was observed in several media variations in order to determine at what point growth slowed due to nutrient restriction. SC medium (Wickerham yeast nitrogen base with 2 % glucose, without amino acids) was varied by reducing or eliminating the source of carbon, nitrogen or sulfur. Wild-type cells, inoculated at 5 × 10⁷ cells ml⁻¹ from a primary culture grown in SC, were grown in these media for 12 h to determine exponential-phase growth. When grown in SC medium, exponential growth of wild-type cells continued throughout the 12 h incubation (Fig. 1). Growth of cells in media without a nitrogen source, or without nitrogen and sulfur, slowed after a few hours compared to the growth of cells in SC. In the sulfur-free medium, growth was the same as that of wild-type for the first 8 h and then growth slowed considerably, while cells grown with no carbon did not divide at all. There were no apparent differences among the growth curves of wild-type cells grown in SC and cells grown in media with reduced carbon, nitrogen or sulfur. Under the conditions used for these experiments, 10 % of the sulfur or nitrogen and 25 % of the carbon were sufficient for full growth during the 12 h incubation period.

Growth curves of each of the mutant strains carrying deletions of the OPT genes, singly or in combination, were also examined to determine if the deletions affected growth under these nutrient constraints (data not shown). All deletion strains except for the ygl114wA strain grew at the same rate as wild-type in the various media. When the ygl114wA strain was grown in SC, its growth was compromised and was comparable to wild-type grown without nitrogen. Not only did the ygl114wA strain have limited growth in liquid media, but also its colony and culture colour on SC agar plates was white in comparison to wild-type S. cerevisiae, which was cream coloured. There was no visible microscopic difference between ygl114wA and wild-type under growth conditions used in this study (data not
shown). Under these conditions, experiments showed that OPT1 and OPT2 deletion did not affect growth, and that starvation for sulfur appeared to manifest itself at 8 h whereas nitrogen starvation manifested itself at an earlier time, and the cells did not tolerate growth without a carbon source. However, the concentration used in this study for reduced carbon, nitrogen and sulfur did not affect growth noticeably. These conditions formed the basis for further studies of OPT1 and OPT2 expression.

OPTp–lacZ expression under limited nutrient conditions

To create reporter systems for measuring transcription of the oligopeptide transporter genes in response to various environmental conditions, the lacZ coding region was placed under the control of the promoters of OPT1, OPT2 or YGL114W. We chose to use the low-copy-number plasmid pYLZ6 that was constructed specifically for the study of promoters by measurement of β-galactosidase activity in S. cerevisiae (Hermann et al., 1992). The segment of DNA 1 kb upstream of the ORFs of OPT1, OPT2 and YGL114W, including the start codon, was amplified and cloned into pYLZ6, immediately upstream of the lacZ gene. Cells of the wild-type strain FY2, harbouring pYLZ6-OPT1, pYLZ6-OPT2 or pYLZ6-YGL114W, were grown for 12 h in each of the previously tested media. Cells were harvested every 2 h after inoculation of SC-grown cells into fresh media and tested for β-galactosidase activity. Cells containing pYLZ6-OPT1 grown without sulfur showed increased β-galactosidase activity by 6 h, indicating that OPT1 was up-regulated in response to lack of this nutrient (Fig. 2). OPT2 and YGL114W were not up-regulated by sulfur starvation (data not shown). In addition, no changes in OPT1, OPT2 or YGL114W gene expression were observed when cells were incubated without carbon or grown without nitrogen, or when grown in any of the reduced nutrient media.

OPT1p–lacZ expression in the presence of amino acids

In S. cerevisiae, the gene encoding the di-/tripeptide transporter, PTR2, is up-regulated in a SPS-dependent fashion by the addition of leucine to the growth medium. We tested whether leucine also induced OPT1 and whether this was influenced by the sulfur content of the medium. Because the cell growth slowed after 8 h when cells were grown with no sulfur, cells of the strain FY2 bearing pYLZ6-OPT1 were grown for 8 h in either SC or no sulfur media containing leucine or no added amino acids. Cells grown overnight in SC were placed into fresh medium with or without sulfur and with or without leucine and assessed for β-galactosidase activity every 2 h for 8 h (Fig. 3). Leucine addition resulted in increased expression of OPT1 in the presence or absence of sulfur at the 4, 6 and 8 h time points; the highest induction of leucine was at the 6 h time point. Because of these results and because an appreciable increase of OPT1 expression was seen at 6 h growth without sulfur (threefold

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**Fig. 1.** Growth curves in reduced nutrient media and media lacking nutrients. Wild-type cells (FY2) were grown for 12 h in SC, reduced nitrogen, no nitrogen, reduced sulfur, no sulfur, reduced nitrogen and reduced sulfur, no nitrogen or sulfur, reduced carbon, or no carbon media. Cell density was measured every 2 h. The growth curves were conducted in quadruplicate, with nearly identical growth patterns obtained. ▼, SC; ■, reduced nitrogen or reduced sulfur or reduced carbon or reduced nitrogen and sulfur; △, no sulfur; ○, no nitrogen; +, no nitrogen and no sulfur; ▽, no carbon.

**Fig. 2.** Sulfur-free medium induces OPT1 expression. Wild-type cells (FY2) harbouring pYLZ6-OPT1, pYLZ6-OPT2 or pYLZ6-YGL114W were grown in SC medium. Additionally, cells containing pYLZ6-OPT1 were grown in medium lacking sulfur. Aliquots were taken every 2 h for 12 h, and assayed for β-galactosidase activity, in quadruplicate. Error bars represent the SEM. β-Galactosidase activity was reported as relative fluorescence. ●, OPT1–lacZ no sulfur; ■, YGL114W–lacZ SC; □, OPT2–lacZ SC; ○, OPT1–lacZ SC.

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increase, Fig. 2), the 6 h time point was chosen for all further experiments.

The induction of OPT1p–lacZ was then assayed after growth in SC and no sulfur media with each of the 20 naturally occurring amino acids individually present (Fig. 4). Leucine and tryptophan induced OPT1 about threefold when cells were grown in SC in comparison to the no amino acid addition control. In contrast, when cells were grown in sulfur-free medium, most amino acids, except cysteine and methionine, greatly induced OPT1 expression. The acidic amino acids – aspartic acid and glutamic acid – were the best inducers of OPT1, followed by tyrosine, when added to medium lacking sulfur. The sulfur-containing amino acids, cysteine and methionine, did not induce OPT1 under these conditions; methionine even down-regulated OPT1 about twofold in both SC and no sulfur media.

**OPT1p–lacZ expression in deletion strains**

Because both Ptr3p and Ssy1p are known to induce gene expression of amino acid and di-/tripeptide transporters by sensing amino acids, including leucine, we tested whether these proteins were also involved in the regulation of the gene encoding the oligopeptide transporter Opt1p. Additionally, we tested whether Opt1p autoregulated its gene expression and whether expression of OPT2 affected the expression of OPT1. Cells of the six knock-out strains, opt1Δ, opt2Δ, ptr3Δ, ssy1Δ, ptr3Δ ssy1Δ and ptr3Δ opt1Δ, and the wild-type strain FY2, were transformed with pYLZ6-OPT1 and grown for 6 h in the presence or the absence of: leucine; methionine or cysteine (which did not induce OPT1 expression); aspartic acid, glutamic acid or tyrosine (the best inducers of OPT1 when cells were grown without sulfur); or GSH (γ-Glu-Cys-Gly). GSH was tested because Opt1p is the sole transporter of GSH into *S. cerevisiae* (Bourbouloux et al., 2000). These strains were then assayed for β-galactosidase activity (Fig. 5).

When knock-out strains were grown in either SC or no sulfur medium supplemented with leucine, OPT1p–lacZ expression in the strains with the single gene knock-outs opt1Δ and opt2Δ was generally slightly higher in the absence of sulfur, with or without leucine addition, compared to the response of the wild-type (Fig. 5A). In contrast, OPT1p–lacZ expression in strains containing deletions of ptr3 and ssy1, genes encoding proteins in the SPS sensor complex, was not up-regulated in the presence of leucine. In fact, OPT1p–lacZ was not induced in any strain containing a knock-out of either ptr3 or ssy1, regardless of whether cells were grown in either SC or no sulfur media, with or without any addition of leucine.

When the sulfur-containing amino acids, methionine and cysteine, were added to SC or no sulfur medium, OPT1p–lacZ was not up-regulated in any of the deletion mutants or in wild-type cells (Fig. 5B). Similarly, the effect of no sulfur medium was not seen when the medium was supplemented...
with GSH with one exception. The only strain to retain the up-regulation of OPT1 in this instance was opt1Δ (Fig. 5B).

The effect of PTR3, SSY1, OPT1 and OPT2 on the expression of OPT1p–lacZ was also examined in the presence of the inducing amino acids aspartic acid, glutamic acid and tyrosine (Fig. 5C). Similar to results observed upon the addition of leucine (Fig. 5A), the absence of PTR3 and SSY1 eliminated the induction of OPT1 in the presence of the acidic amino acids and tyrosine when cells were grown in sulfur-free medium. Unlike induction by leucine, the absence of OPT1 and OPT2 affected OPT1p–lacZ expression when cells grown without sulfur were supplemented with aspartic acid, glutamic acid or tyrosine (Fig. 5C). Without OPT1 or OPT2, OPT1p–lacZ expression was reduced by 25% upon addition of aspartic acid, as was OPT1p–lacZ expression when opt1Δ cells were supplemented with glutamic acid. OPT1 was only slightly induced in opt2Δ cells when glutamic acid was added. When either OPT was knocked-out, OPT1p–lacZ expression was reduced by more than 60% when sulfur-free medium was supplemented with tyrosine.

The effect of the ORF YGL114W was also investigated as to its potential role in OPT1 expression. Because ygl114wΔ cells grew poorly even in SC (data not shown), the yield of cells from 2 l primary culture was only enough to investigate the effect of YGL114W on OPT1p–lacZ expression in SC and medium lacking sulfur, each with or without leucine or cysteine. Under all six conditions, these cells showed OPT1 expression that was barely above background levels. Thus, the result of the influence of YGL114W on expression of OPT1 could not be calculated with this strain.

**Leu-enkephalin uptake under different nutrient conditions**

To complement the OPT1 gene expression data, the initial rate of uptake of Leu-enkephalin, a known pentapeptide substrate of Opt1p (Hauser et al., 2000), was measured to assess the functionality of Opt1p. Cells grown under the same conditions used in the lacZ study were assayed for their ability to accumulate [3H]Leu-enkephalin over 10 min (Fig. 6). FY2 cells harbouring the empty vector pYLZ6 were grown in either SC or no sulfur medium, with or without amino acids and GSH (Fig. 6A). Consistent with the lacZ assay results, growth in the presence of either cysteine or GSH did not increase Leu-enkephalin uptake, and the addition of methionine reduced transport of Leu-enkephalin to half of that observed in FY2 cells grown in SC. Growth in sulfur-free medium with the addition of aspartic acid, glutamic acid, or tyrosine increased the ability of the cells to transport the pentapeptide (Fig. 6B). Leucine increased the transport capability of FY2 when grown without sulfur, but did not increase transport when cells had been grown in SC supplemented with leucine, even though β-galactosidase activity suggested leucine increased OPT1 expression in this medium.

When opt2Δ cells were tested for their ability to accumulate [3H]Leu-enkephalin (Fig. 6B), results were consistent with those of the lacZ assay; compared to FY2, Leu-enkephalin uptake was reduced when aspartic acid was supplemented and similar to unsupplemented SC when tyrosine was added. The effect of the absence of PTR3, SSY1 and OPT1 on Leu-enkephalin uptake was tested after cells were grown without sulfur and supplemented with leucine (Fig. 6C). As expected, leucine did not lead to increased uptake in ptr3Δ or ssy1Δ cells. The opt1Δ strain showed background to be half that of the wild-type strain grown in SC.

**Regulation of peptide transport by the addition of leucine and by CUP9**

To test the effect of Cup9p and the addition of leucine on peptide utilization, the sensitivity of wild-type and cup9 strains to AE and KLAE was examined with or without the addition of leucine (Fig. 7). Deletion of CUP9 increased the sensitivity to AE and KLAE in the presence or absence of leucine (compare A to B, C to D, E to F, and G to H). We also found that the sensitivity of wild-type to AE and KLAE was regulated by leucine (compare A to E, and C to G) but that leucine did not markedly affect AE and KLAE sensitivity in the cup9 deletion strain (compare B to F, and D to H). The opt1 deletion strain showed the same sensitivity to AE and KLAE as the wild-type, and the opt2 deletion strain showed the same sensitivity to AE as the wild-type but no sensitivity to KLAE (data not shown), demonstrating that KLAE is transported by Opt2p and not by Opt1p.

To further determine whether Cup9p regulated the expression of OPT1 and OPT2, the expression level of these genes was measured by real-time RT-PCR in the wild-type and cup9 deletion strain (Fig. 8). ACT1 was used as the internal control for gene expression, and PTR2 was measured as well due to its known regulation by Cup9p. The expression of PTR2 in the cup9 strain was more than 500-fold higher than the wild-type, while the expression of OPT2 was 12-fold higher in the cup9 strain. There was no
difference in OPT1 expression level in the wild-type strain in comparison to that of the cup9 strain.

**DISCUSSION**

This paper represents an advancement in the understanding of the regulation of OPT1 in *S. cerevisiae*. Previously, limited information was known about the transcriptional regulation of the OPT genes in *S. cerevisiae*, although some evidence was available regarding native conditions for transcription for members of the OPT family in other species (Hauser et al., 2001). Here we show that absence of sulfur in the medium up-regulates expression of OPT1–lacz, determined by β-galactosidase assays, and Opt1p, determined by uptake assays. Boer et al. (2003) found similar up-regulation
of OPT1 transcription in microarray studies of chemostat cultures grown with limited sulfur. Unlike these authors, we observed no change in OPT1 expression in the absence of carbon for up to 10 h in batch culture, whereas they observed the down-regulation of OPT1 under conditions limiting carbon. Gasch et al. (2000) detected a great increase in OPT1 expression by microarray analysis when cells were depleted of nitrogen in batch culture, yet our study, as well as that of Boer et al. (2003), did not observe this. All three studies used different strain backgrounds considered to be wild-type, which may explain the variations in results obtained. PTR2, the gene encoding the di-/tripeptide transporter in S. cerevisiae, is also regulated by limited nutrient conditions. The expression of this transporter gene is up-regulated when cells are grown on a poor nitrogen source (Perry et al., 1994).

The substrates of Ptr2p are similar to those of Opt1p in that both permeases transport small peptides, but perhaps the physiological roles of these peptide transporters are more different than initially thought. Ptr2p, which transports dipeptides and tripeptides, is likely present to scavenge amino acids as a nitrogen source, whereas the studies presented herein indicate that a function of Opt1p, which transports GSH and tetra-/pentapeptides, may be to obtain sulfur for the cell. Opt1p does not transport all tetrapeptides, however, as indicated by the observation that KLAE was equally toxic to the opt1 deletion strain and the wild-type, whereas KLAE was not toxic to the opt2-deletion strain (data not shown). These results suggest that KLAE is not a substrate of Opt1p but is transported by Opt2p. The role of Opt1p as the yeast GSH transporter (Bourbouloux et al., 2000) may be primary with peptide transport perhaps serving a secondary function as an amino acid and sulfur scavenger from sulfur-containing peptides. This conclusion is based on the observation explored herein that sulfur regulates OPT1 expression in S. cerevisiae. However, it can be inferred from the regulation of OPT1 by amino acids that there is a role for Opt1p in yeast amino acid metabolism as well.

Our data indicate that OPT1 is differentially regulated by various amino acids when starved for sulfur. Of the 20 naturally occurring amino acids, the acidic amino acids – aspartic acid and glutamic acid – up-regulate OPT1 to the greatest degree, followed by tyrosine. Only the sulfur-containing amino acids do not up-regulate OPT1 expression in sulfur-free medium. Additionally, GSH does not up-regulate OPT1. We were not able to analyse the effect of leucine on the regulation of Opt1p function in the KLAE halo assay since the opt2 deletion strain showed no sensitivity to KLAE, indicating that KLAE is not a substrate of Opt1p (data not shown). It is likely that when these sulfur-containing compounds are transported into the cell, they supply it with enough sulfur to negate the effect of the sulfur-free medium. When opt1Δ cells are grown in medium lacking sulfur that has been supplemented with GSH, OPT1p–lacz expression is up-regulated to the same extent as if it were grown in sulfur-free medium without any additions (Fig. 5B). Since Opt1p, which also functions as the GSH transporter, is absent, the cell is not able to take up the sulfur supplied GSH. Thus OPT1p–lacz is up-regulated since it is essentially still in a sulfur-free environment. Unlike cysteine and GSH, however, methionine down-regulated OPT1p–lacz and Opt1p when cells were grown in sulfur-free media. Perhaps in a natural environment the presence of certain amino acids indicates to the cell that particular peptides are available for scavenging. Another explanation for the regulatory phenomena observed is that no sulfur in the environment is a signal to the cell that there is a lack of, or at least very few, amino acids available. The presence of extracellular methionine is a signal that there is enough sulfur, and therefore sufficient amino acids being taken into the cell, which results in OPT1 down-regulation.

Of all the 20 amino acids tested, leucine and tryptophan up-regulated OPT1p–lacz to the highest level when cells were grown in SC medium. Similarly, the addition of leucine to the medium caused a significant increase in sensitivity to KLAE in the wild-type and opt1-deletion strains, from which it can be inferred that there is a role for leucine in the regulation of OPT2 expression. This is similar to PTR2 and BAP2 induction – leucine and tryptophan are the best inducers (Didion et al., 1998). Yet the fold induction of these genes due to these amino acids is dramatically different. PTR2p–lacz is up-regulated 100-fold upon the addition of tryptophan or leucine (V. Narita and J. M. Becker, 2000).

![Image](http://mic.sgmjournals.org)

**Fig. 8.** The expression of OPT1, OPT2 and PTR2 in the wild-type and cup9 strains grown in allantoin SC medium + Ura + Leu. The expression level was measured by real-time RT-PCR analysis and shown as a ratio calculated by the fold-change of the target gene (OPT1, OPT2 or PTR2) in the cup9 strain compared to that of the wild-type, divided by the fold-change of ACT1 in the cup9 strain compared to that of the wild-type. The ratio of the fold-change in the wild-type was standardized to 1:0. Black bars, OPT1/ACT1; hatched bars, OPT1/ACT1; white bars, PTR2/ACT1.
unpublished data), whereas OPT1 is up-regulated about 10-fold. Leucine and tryptophan induce OPT1 when cells are grown without sulfur, but only moderately when compared to the other amino acids.

The amino acid sensor Ssy1p and its associated protein Ptr3p are responsible for the regulation of genes encoding amino acid transporters and the regulation of PTR2. The SPS system has the greatest response to leucine and tryptophan (Didion et al., 1998) but is able to sense all other amino acids except proline and arginine in assays measuring AGP1p–lacz expression (Iraqui et al., 1999). Here we show that both SSY1 and PTR3 are also required for induction of OPT1. A microarray study investigating the effects of the SPS sensor system responding to leucine (Forsberg et al., 2001) found less than a twofold change in OPT1 expression, but the medium in which the cells were grown contained sulfur, so increased expression would not be expected. Our data show that the presence of both Ssy1p and Ptr3p is required for expression of OPT1p–lacz when cells are grown in a sulfur-free environment – even in the absence of inducing amino acids. This suggests the possibility that the SPS system has the additional role of a sulfur sensor.

When cells are grown in sulfur-free medium, OPT2 is required for the induction of OPT1p–lacz by glutamic acid, and OPT1 and OPT2 are required for the induction of OPT1p–lacz by tryptophan (Fig. 5C). If one of the OPT genes is not present at the plasma membrane, perhaps the yeast cell is able to recognize the need for a greater number of oligopeptide transporters and up-regulate either OPT1 gene to compensate for this deficiency. This may suggest that intracellular peptides, although rapidly degraded upon entry (Hauser et al., 2000), may be involved in signalling to regulate the expression of the OPT family. Indeed, the expression of the gene encoding the di-/tripeptide transporter, PTR2, is regulated by dipeptides binding to Ptr3p/Ubr1p, which then degrades the PTR2 repressor Cup9p (Turner et al., 2000).

The sensitivity of the cup9 deletion strain to KLAЕ did not change upon addition of leucine, suggesting that the regulation of OPT2 by Cup9p is independent of leucine induction. A similar observation was made for the Cup9p regulation of PTR2 (Byrd et al., 1998). In addition, the sensitivity to AE and KLAЕ was increased in the cup9 deletion strain, which suggests that Cup9p regulates PTR2 and OPT2 expression (Fig. 7). In the direct analysis of gene expression by RT-PCR, the expression of OPT1 was not affected by cup9 deletion, whereas the expression of OPT2 increased 12-fold and PTR2 increased over 500-fold (Fig. 8). The observation that the halo assay does not directly reflect the large differences in gene expression indicates that regulatory interactions are superimposed upon gene expression that control the ability of the cell to accumulate the toxic peptides (Cai et al., 2006). Nevertheless, these studies show that Cup9p contributes to regulation of OPT2 expression, but not OPT1 expression. More studies will be needed to understand the regulator network of OPT1 and OPT2 expression in the detail now known for PTR2 expression (Cai et al., 2006).

No difference was seen in either OPT2 or YGL114W expression when cells were grown either without various nutrients or with reduced amounts of the nutrients, as compared to growth in SC (data not shown). These genes are, therefore, regulated by different conditions than those tested in this study. Perhaps there is a different physiological state in which Opt2p is the preferred oligopeptide transporter, and its favoured substrate is something other than a peptide. It may be that Opt2p transports a variety of biological molecules, some of which include peptides such as KLAЕ. For instance, Opt1p transports both Leu-enkephalin and GSH, but has a higher affinity for the latter, which is not a true peptide, yet Opt1p does not transport KLAЕ. Also the PTR family is able to transport β-lactams (Meredith & Boyd, 2000) even though its primary role is di-/tripeptide transport.

The role of the protein Ygl114wp is currently unknown. We could not detect OPT1p–lacz expression in the ygl114w strain, but conditions required to grow the strain were different than those required to grow cultures of all other deletion mutants and wild-type. Therefore, we were unable to draw any conclusions from the experiment. Yen et al. (2001) have postulated that YGL114W encodes a transporter that is a member of the OPT family. When we overexpressed YGL114W in a strain with the knock-outs opt1Δ, opt2Δ and leu2Δ, we observed no growth of cells when grown in the presence of either Leu-enkephalin, a substrate for Opt1p, or KLL, a substrate for Opt2p (A. M. Wiles and J. M. Becker, unpublished). Nevertheless, cells lacking YGL114W double only every 12 h when grown in SC medium, and culture colour is different than that of wild-type.

We have presented direct evidence that OPT1 and Opt1p expression is dependent on the sulfur content of the medium. Additionally, we show for the first time that expression is induced by all but the sulfur-containing amino acids, and that expression is dependent upon the presence of PTR3 and SSY1. This extends the roles of Ptr3p and Ssy1p to regulation of all known peptide and amino acid permeases in yeast. The differential regulation of the PTR and OPT systems allows yeast to adapt its utilization of small peptides to obtain optimal growth in a variety of environmental conditions.

REFERENCES


