Peb1p (Pas7p) Is an Intraperoxisomal Receptor for the NH2-terminal, Type 2, Peroxisomal Targeting Sequence of Thiolase: Peb1p Itself Is Targeted to Peroxisomes by an NH2-terminal Peptide

Jing Wei Zhang and Paul B. Lazarow

Department of Cell Biology and Anatomy, Mount Sinai School of Medicine, New York 10029

Abstract. Peb1 is a peroxisome biogenesis mutant isolated in Saccharomyces cerevisiae that is selectively defective in the import of thiolase into peroxisomes but has a normal ability to package catalase, luciferase and acyl-CoA oxidase (Zhang, J. W., C. Luckey, and P. B. Lazarow. 1993. Mol. Biol. Cell. 4:1351-1359). Thiolase differs from these other peroxisomal proteins in that it is targeted by an NH2-terminal, 16-amino acid peroxisomal targeting sequence type 2 (PTS2). This phenotype suggests that the PEB1 protein might function as a receptor for the PTS2. The PEB1 gene has been cloned by functional complementation. It encodes a 42,320-D, hydrophilic protein with no predicted transmembrane segment. It contains six WD repeats that comprise the entire protein except for the first 55 amino acids. Peb1p was tagged with hemagglutinin epitopes and determined to be exclusively within peroxisomes by digitonin permeabilization, immunofluorescence, protease protection and immuno-electron microscopy (Zhang, J. W., and P. B. Lazarow. 1995. J. Cell Biol. 129:65-80). Peb1p is identical to Pas7p (Marzioch, M., R. Erdmann, M. Veenhuis, and W.-H. Kunau. 1994. EMBO J. 13: 4908-4917). We have now tested whether Peb1p interacts with the PTS2 of thiolase. With the two-hybrid assay, we observed a strong interaction between Peb1p and thiolase that was abolished by deleting the first 16 amino acids of thiolase. An oligopeptide consisting of the first 16 amino acids of thiolase was sufficient for the affinity binding of Peb1p. Binding was reduced by the replacement of leucine with arginine at residue five, a change that is known to reduce thiolase targeting in vivo. Finally, a thiolase-Peb1p complex was isolated by immunoprecipitation. To investigate the topogenesis of Peb1p, its first 56-amino acid residues were fused in front of truncated thiolase lacking the NH2-terminal 16-amino acid PTS2. The fusion protein was expressed in a thiolase knockout strain. Equilibrium density centrifugation and immunofluorescence indicated that the fusion protein was located in peroxisomes. Deletion of residues 6-55 from native Peb1p resulted in a cytosolic location and the loss of function. Thus the NH2-terminal 56-amino acid residues of Peb1p are necessary and sufficient for peroxisomal targeting. Peb1p is found in peroxisomes whether thiolase is expressed or not. These results suggest that Peb1p (Pas7p) is an intraperoxisomal receptor for the type 2 peroxisomal targeting signal.

Analysis of peroxisome biogenesis (peb) mutants suggest that the import of newly synthesized proteins into peroxisomes involves a branched pathway (34, 51). The branches in this pathway are hypothesized to involve receptors for peroxisomal targeting sequences (PTSs) and the common steps in the import pathway presumably include components of the translocation machinery.

As is now well known, there are at least three types of targeting sequences for peroxisomal matrix proteins (proteins inside the organelle). A carboxy-terminal tripeptide, ser-lys-leu, or conservative variants of this sequence, directs diverse proteins to peroxisomes in animals, plants and yeasts (PTS1) (17, 18, 23). An amino-terminal oligopeptide consisting of 11-16 amino acids is necessary and sufficient for the targeting of thiolase to peroxisomes in mammals (32, 44) and Saccharomyces cerevisiae (9, 16). The S. cerevisiae sequence, MSQRRLQSIKDTILVLSA, contains two pairs of amino acids, RL and HL, that are required for the topogenesis and are conserved in the mammalian thiolases. This PTS2 is also found in watermelon.

1. Abbreviations used in this paper: HA, hemagglutinin epitope; pas, peroxisome assembly; peb, peroxisome biogenesis; Peb1p, protein encoded by the PEB1 gene; PTS, peroxisomal targeting sequence.

Address all correspondence to J. W. Zhang, Department of Cell Biology and Anatomy, Box 1007, Mount Sinai School of Medicine, One Gustave Levy Place, New York, NY 10029-6574. Ph.: (212) 241-1749. Fax: (212) 860-1174.
malate dehydrogenase (14), amine oxidase in *Hansenula polymorpha* (11), *Perlp* in *Hansenula polymorpha* (47), and protein(s) in trypansom microbodies (4). Still other peroxosomal proteins contain redundant internal targeting sequences; these include *Candida tropicalis* acyl-CoA oxidase (21, 42) and *S. cerevisiae* catalase A (24).

Mutants in the import of peroxosomal proteins have been isolated from several species (for reviews see 25, 26, 43). Many of them appear to be incapable of importing any matrix proteins into their peroxosomes, regardless of the type of PTS. These data imply that there are common components in the pathway for importing proteins with the various PTSSs. These could include chaperones as well as membrane translocation proteins.

Mutants selectively defective in the import of peroxosomal proteins with a carboxyl-terminal PTS1 have been identified in yeasts and humans (29, 30, 46, 51). Cells carrying these mutations cannot import proteins targeted by a PTS1 into their peroxosomes, but do package normally the peroxosomal proteins bearing other PTSSs. The corresponding genes have been cloned and characterized: *Pas8p* in *Pichia pastoris* (29), *Pas10p* in *S. cerevisiae* (46), and *PXR1* (8) which is identical to PTS1 receptor (13, 48) in humans. *P. pastoris Pas8p* and the human protein bind specifically to a peptide ending with SKL but not to control peptides (8, 13, 29, 48). *S. cerevisiae* *Pas10p* and the human homologue have been shown to interact with proteins ending with SKL, by means of the two hybrid assay (5, 13). Thus, these proteins are thought to be the PTS1 receptor.

*S. cerevisiae* mutant *pebl* (allelic with *pas7*) is defective in importing thiolase into peroxosomes but are competent to import most other peroxosomal proteins including those with PTSSs as well as acyl-CoA oxidase (28, 49, 51). The observed phenotype suggests that the gene product *Peb1p* (*Pas7p*) may be a receptor for the PTS2. We (50) and Marzioch et al. (28) have cloned the *Peb1/pas7* gene by functional complementation. It encodes a 42,320-D, hydrophilic protein with no predicted transmembrane segment. The protein contains six WD repeats, a motif that has been identified in 27 proteins involved in diverse cellular functions (31). The conserved core of the motif begins with Gly-His and after ~27 amino acids, ends with Trp-Asp (WD). Each repeat is thought to fold into three β sheets, separated by turns, and the repeats are believed to associate with one another as dimers or perhaps as multimers. The six WD motifs comprise the large majority of the *Peb1* protein, with the exception of the first 55 amino acids.

We tagged the *Peb1* protein at its carboxy terminus with three copies of the hemagglutinin (HA) epitope and demonstrated that the tagged protein (*Peb1p-HA3*) was functional (50). *Peb1p-HA3* was determined to be associated with peroxisomes by immunofluorescence and equilibrium density centrifugation. When expressed at the wild type level under the control of its own promoter from a single-copy integrating plasmid, all of the *Peb1p-HA3* was found in peroxisomes (within experimental error) as assessed quantitatively by progressive permeabilization of the plasma membrane and intracellular membranes with increasing concentrations of digitonin. We observed that digitonin permeabilization is far gentler, and therefore more reliable for determining intracellular protein distributions, than classical cell homogenization followed by differential and equilibrium density centrifugations. Moreover,

---

**Table 1. Plasmids Used in This Study**

<table>
<thead>
<tr>
<th>Name (Construction)</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>YipPEB1-HA3</td>
<td><em>PEB1</em> tagged with three copies of the HA epitope under the control of its own promoter in an integrating plasmid, pRS306, which has a URA3 marker. (50)</td>
</tr>
<tr>
<td>YcpPEB1-HA3</td>
<td>Triple-tagged <em>PEB1</em> under the control of its own promoter in a centromere plasmid, pRS315, containing a LEU2 marker. This study</td>
</tr>
<tr>
<td>pBXNPEB1-HA3</td>
<td>Triple-tagged <em>PEB1</em> under the control of the GAPDH promoter in a multicopy 2μ plasmid. (50)</td>
</tr>
<tr>
<td>YipPEB1Δ-HA3</td>
<td>Identical to YipPEB1-HA3 except that the nucleotides encoding amino acids 6–55 of <em>Peb1p</em> were deleted by PCR. This study</td>
</tr>
<tr>
<td>Yep352</td>
<td>The part of the <em>PEB1</em> gene encoding amino acids 1–56 of the <em>Peb1p</em> fused in frame with the part of the <em>POT1</em> gene encoding amino acids 17–417 of thiolase, under the control of the <em>Peb1</em> promoter in a multicopy, 2μ plasmid, Yep352. This study</td>
</tr>
<tr>
<td>pGAL4 (DB)-PEB1</td>
<td>The EcoRV-Sacl fragment of the <em>PEB1</em> gene cloned in pPC97 after the <em>GAL4</em> binding domain. (6)</td>
</tr>
<tr>
<td>pGAL4 (TA)-POT1</td>
<td>The transactivation domain (TA) of the <em>GAL4</em> protein in a centromere plasmid. (6)</td>
</tr>
<tr>
<td>pGAL4 (TA)-POT1Δ</td>
<td>Identical to pGAL4 (TA)-POT1 except that the nucleotides encoding the first 16 amino acids of thiolase were deleted. This study</td>
</tr>
<tr>
<td>pGAL4 (TA)-Luciferase</td>
<td>The full length luciferase gene cloned in pPC86 after the <em>GAL4</em> transactivation domain. This study</td>
</tr>
<tr>
<td>pJW30</td>
<td>The 16-bp EcoRI-HindIII fragment of the thiolase gene (<em>POT1</em>) was replaced with the <em>TRP1</em> gene. Used for thiolase disruption to construct strain JW69. This study</td>
</tr>
<tr>
<td>pJW130</td>
<td>The 16-bp EcoRI-HindIII fragment of the thiolase gene was replaced with the <em>URA3</em> gene. Used for thiolase disruption to construct strain JW142. This study</td>
</tr>
<tr>
<td>pRS306</td>
<td>Integrating plasmid. <em>URA3</em>. (41)</td>
</tr>
<tr>
<td>pRS315</td>
<td>Centromere plasmid. <em>LEU2</em>. (41)</td>
</tr>
<tr>
<td>Yep352</td>
<td>2μ <em>URA3</em>. (19)</td>
</tr>
</tbody>
</table>

The Journal of Cell Biology, Volume 132, 1996 326
Table II. Yeast Strain Used in This Study

<table>
<thead>
<tr>
<th>Name</th>
<th>Genotype and/or description</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>JW68-3A</td>
<td>MATa, ura3-1, trpl-1, arg4, ctt1-1 (Wild type)</td>
<td>(49)</td>
</tr>
<tr>
<td>JW69*</td>
<td>MATa, ura3-1, trpl-1, arg4, ctt1-1, pot1::TRP1</td>
<td>This study</td>
</tr>
<tr>
<td>JW75*</td>
<td>MATa, ura3-1, trpl-1, arg4, ctt1-1, pot1::TRP1</td>
<td>(50)</td>
</tr>
<tr>
<td>JW86*</td>
<td>JW 75 transformed with plasmid YipPEB1-HA3</td>
<td>(50)</td>
</tr>
<tr>
<td>JW88*</td>
<td>JW 75 transformed with plasmid pBXNPEB1-HA3</td>
<td>(50)</td>
</tr>
<tr>
<td>2m 1-A4</td>
<td>MATa, peb1-4, leu2-3,112, ura3-1, trpl-1, arg4, ctt1-1</td>
<td>(49)</td>
</tr>
<tr>
<td>JW89</td>
<td>2m1-A4 transformed with plasmid pBXNPEB1-HA3</td>
<td>This study</td>
</tr>
<tr>
<td>JW142*</td>
<td>MATa, ura3-1, trpl-1, arg4, ctt1-1, pebl::pBR3, pot1::URA3</td>
<td>This study</td>
</tr>
<tr>
<td>JW142a</td>
<td>MATa, ura3-1, trpl-1, arg4, leu2, his4, pebl::pBR3, pot1::pBR3, pot1::URA3</td>
<td>This study</td>
</tr>
<tr>
<td>JW161</td>
<td>JW 142a transformed with plasmid YcpPEB1-HA3</td>
<td>This study</td>
</tr>
<tr>
<td>JW162*</td>
<td>JW75 transformed with plasmid YipPEB1-HA3</td>
<td>This study</td>
</tr>
<tr>
<td>JW146*</td>
<td>JW69 transformed with plasmid YepPeb1p::yepl, Thiolase::17,47</td>
<td>This study</td>
</tr>
<tr>
<td>SFY526</td>
<td>MATa, ura3-52, his3-200, ade2-101, lys2-801, trpl-901, leu2-3, 112, can1, gal4-542, gal80-538, URA3::GAL1-LacZ</td>
<td>(1)</td>
</tr>
<tr>
<td>W303a</td>
<td>MATa, ura3-52, his3-200, ade2-101, trpl-901, leu2-3, 112</td>
<td>(36)</td>
</tr>
</tbody>
</table>

* Isogenic with JW68-3A.

It is unknown whether JW142a is CTT1 or ctt1-1.

protease protection studies demonstrated that Peblp-HA3 is inside the peroxisome, in the matrix space, together with thiolase. This was confirmed by immuno-electron microscopy (50).

These observations suggested the hypothesis that Peblp functions as an intra-peroxosomal receptor during the import of thiolase into peroxisomes (50). If this is true, we would expect that Peblp would bind specifically to the NH2-terminal PTS2 of thiolase. We have now tested this prediction by affinity binding experiments, immunoprecipitation and the two-hybrid method. In addition, we have also tested the possibility that the first 55 amino acids of Peblp might be its PTS, in view of the fact this is the only domain of Peblp that is not part of a WD repeat.

Materials and Methods

Media and Culture Conditions

Yeast were precultured twice in rich glucose medium (YPD) to mid log phase and then grown for 18 h in a rich medium containing glycerol and oleic acid (YPGO) as described (51) to induce peroxisomes. Cells were precultured in minimal medium and, at mid-log growth inoculated into liquid YNO medium (50). Cell titers were determined thereafter with a hemocytometer.

Plasmids and Yeast Strains

The plasmids used in these studies are described in Table I. All DNA synthesized by means of the polymerase chain reaction was sequenced for verification. The yeast strains used in this study are listed in Table II. The knockout of the thiolase gene (POT1 [20], which is identical to FOX3 [10]) in strains JW69 and JW142 were verified by immunoblotting with anti-thiolase for the absence of thiolase protein. JW142a was isolated from a tetrad dissection of the diploid (JW142 × W303b) in order to obtain a leu2 marker in the pot1-petb1 double knockout strain.

Immunoprecipitation

Yeast cell extracts were prepared by vortexing with glass beads in breaking buffer (100 mM Tris-HCl, pH 7.0, 1 mM EDTA, 5% glycerol, 0.1% Triton X-100) containing protease inhibitors (45). For immunoprecipitation, 1 μg of monoclonal antibody 12CA5 against the hemagglutinin epitope (HA) was added to 50 μg of cell extract protein and incubated for 1 h at room temperature followed by 1 h at 0°C with gentle rotation. Protein A-Sepharose CL-4B beads (20 μl of a 50% suspension Sigma, P-3391) were added and incubated for 1 h at 4°C. The beads were collected by centrifugation and washed twice with 1 ml washing buffer (100 mM Tris-HCl, pH 7.4, 1 mM EDTA, 5% glycerol, 1% Triton X-100, 200 mM NaCl, 0.5% bovine serum albumin) and twice with breaking buffer. Bound proteins were solubilized with SDS sample buffer. Control samples received 25 μg of HA peptide before immunoprecipitation. According to the manufacturer, protein A is detached by boiling in SDS, and may bind antibodies in subsequent immunoblotting.

Two Hybrid Assay

The two-hybrid assay was based on the method of Fields and Song (12). The tested genes were fused to the DNA-binding domain (DB) of GAL4 or to the trans-activation domain (TA) of GAL4 (Table I) and transformed into the yeast reporter strain SFY526 (1). The transformants were grown in minimal complete glucose medium (39) to mid-log phase and homogenized with glass beads. β-Galactosidase production was measured by immunoblotting.

Affinity Binding Assay

Two oligopeptides were synthesized by the Protein Core Facility (Mount Sinai School of Medicine, New York). The wild type peptide, MSQRLSQKDHVLVSLC, corresponds to the amino-terminal 16 residues of thiolase (16) followed by a cysteine on the COOH-terminus. The mutant peptide, MSQRROSQKDHVLVSLC, is identical except for the Arg at residue five. These oligopeptides were separately coupled to TNB-agarose (Pierce, Rockford, IL) by a disulfide bond according to the manufacturer's instructions. In each case, excess peptide (1 mg) was added to 100 μl of TNB-agarose (50% suspension) bearing 0.25 μmol of TNB. Coupling was >95% efficient in both cases as judged by the release of TNB, which was measured spectrophotometrically at 410 nm. The oligopeptides, coupled to 10 μl of the beads, were incubated with 150 μg of yeast extract protein for 1 h at room temperature in buffer (100 mM sodium phosphate buffer, pH 6.8, 1 mM EDTA) with gentle rotation. The beads were then washed four times with this buffer. The peptides, together with proteins bound to them, were detached from the beads with 10 mM dithiothreitol in the same buffer.

Other Methods

The following methods were from the established protocols: immunofluorescence (49), digitonin permeabilization of cells (51), cell fractionation by differential and density gradient centrifugation (27), yeast genetics (39), yeast transformation (38), DNA manipulation (37), the catalase assay (2), and the fumarase assay (3). Immunoblotting and quantitative analysis of antigens were as described (51); secondary antibodies coupled to horse radish peroxidase for the enhanced chemiluminescence detection step.
Expression of Peblp(1-56)-thiolase(17-417) fusion protein. Yeast cell extracts from wild type JW68-3A (WT), the thiolase knockout strain JW69 (KO), and JW69 transformed with the plasmid encoding Peblp(1-56)-thiolase(17-417) (Fusion, strain JW146) were separated by SDS-PAGE and immunoblotted with anti-thiolase.

Materials
Nycodenz was purchased from Accurate Chemical and Scientific Corporation (Westbury, NY). Digitonin (lot No. 113H0889) was from Sigma (D1407; Sigma Chemical Co., St. Louis, MO). The mouse monoclonal antibody 12CA5, the rabbit anti-thiolase, rabbit anti-phosphoglycerate kinase, and goat anti-catalase A were generous gifts from Drs. Michael Shia (Boston University School of Medicine, Boston, MA), Dr. Wolf Kunau (Bochum, Germany), Dr. Jeremy Thorne (University of California at Berkeley, Berkeley, CA) and Dr. Andreas Hartig (University of Wien, Wien, Austria), respectively. The monoclonal antibody against β-galactosidase was from Promega (Madison, WI). Other reagents were from Promega, Sigma Chemical Co., or New England Biolabs (Beverly, MA). The HA oligopeptide was synthesized by Biosynthesis, Inc. (Lewisville, TX).

Results
The experiments concerning the topogenic information that directs PEB1 to peroxisomes are described first. Thereafter, we report experiments on the interaction of PEB1 with thiolase.

The First 56 Amino Acids of PEB1 Contain a Peroxisomal Targeting Sequence
Suspecting (for reasons described in the Introduction) that the NH2 terminus of PEB1 might contain the peroxisomal targeting signal (PTS), we fused the first 56 amino acids (Peblp(1-56)) in front of a passenger protein that consisted of thiolase without its first 16 amino acids (thiolase(17-417)). Truncated thiolase was chosen because it lacks a PTS (there is no evidence for any other topogenic information in this molecule; 9, 15, 16), is a stable cytosolic protein, and is capable of entering peroxisomes when provided with an amino-terminal topogenic sequence (9, 16). The fusion protein was expressed on an episomal plasmid under the control of the PEB1 promoter in a yeast strain from which the thiolase gene had been knocked out (Tables I and II). The fusion protein (Peblp(1-56)-thiolase(17-417)) had an apparent mass of about 50 kD (Fig. 1, lane 3), consistent with the calculated mass of 49,499 D. As expected, native thiolase was detected only in wild type cells (lane 1). Under these expression conditions, the abundance of the fusion protein in strain JW146 was approximately 1/10 of the abundance of thiolase in wild type cells (assuming that anti-thiolase recognizes the two proteins equally well; compare loads in Fig. 1).

Immunofluorescence analysis with anti-thiolase of cells containing the fusion protein demonstrated a weak punctate staining with a pattern suggestive of peroxisomes (Fig. 2, left). The punctate staining observed with anti-thiolase mostly co-localized with that seen with anti-catalase A (Fig. 2, right), which identifies peroxisomes.

The intracellular location of the (Peblp(1-56)-thiolase(17-417)) fusion protein was also investigated by subcellular fractionation. A postnuclear supernatant fraction was prepared from strain JW146 and separated into an organelle pellet (mainly mitochondria and peroxisomes, ML) and a supernatant (containing cytosol, PS). The fusion protein was mainly (90%) located in the organelle pellet (Fig. 3 A). This organelle fraction was subjected to equilibrium density Nycodenz gradient centrifugation to separate peroxisomes from mitochondria. As shown in Fig. 3 B (top), the peroxisomes (as marked by catalase activity) were well separated from mitochondria (as marked with cytochrome c oxidase). The fusion protein was found at the bottom of the gradient together with catalase (Fig. 3 B, bottom). The fusion protein was enriched, relative to catalase, on the denser side of the peroxisome peak, for reasons as yet unknown. It was also noticed that a band below the fusion was present in the mitochondrial fraction (fractions 4–6); the origin of this band is unknown. In a second experiment, in which the peroxisomes sedimented only half way down the gradient, the fusion protein again accompanied the peroxisomes (data not shown). These cell fractionation data confirm the immunofluorescence double-labeling data that the fusion protein is localized in peroxisomes.
The First 56 Amino Acids of Peb1p Are Required for the Peroxisomal Targeting of Peb1p

We have previously observed that Peb1p, tagged at its carboxy terminus with three copies of the hemagglutinin epitope tag, and expressed at the wild type level under the control of its own promoter (strain JW86), is found entirely within peroxisomes (within experimental error) (50). We now constructed a gene encoding a truncated version of this tagged protein, lacking amino acids 6–55, by means of the polymerase chain reaction. It was similarly expressed under the control of its own promoter, in the pebl knockout strain JW75, on an integrating plasmid (strain JW162). The gene product, named Peb1p(6-55)-HA3, migrated with an apparent mass of 41 kD, consistent with its predicted mass of 40,773 D (Fig. 4, lane 2). The expression level of Peb1p(6-55)-HA3 was comparable to that of the full-length protein in JW86 (Fig. 4, lane 1).

The intracellular location of Peb1p(6-55)-HA3 was analyzed by the progressive permeabilization of spheroplasts with increasing concentrations of digitonin (Fig. 5). As we have shown previously (51), very low concentrations of digitonin are sufficient to release the cytosolic enzyme, phosphoglycerate kinase, from the spheroplasts because of the abundance of sterols in plasma membrane. Much higher concentrations of digitonin are required to permeabilize the peroxisomal membrane (as indicated by the release of catalase activity to the supernatant) and still more digitonin is needed to permeabilize mitochondria (as marked by fumarase activity). The release pattern of Peb1p(6-55)-HA3 was very similar to that of phosphoglycerate kinase (Fig. 5 B), indicating the cytosolic location of...
this truncated protein. This contrasts with full-length Peb1p-HA3 which is inside peroxisomes and emerges with catalase (Fig. 5 A). These data indicate that the NH2-terminal amino acid residues 6-55 are essential for the import of Peb1p into peroxisomes.

Truncated, Cytosolic Peb1p Is Nonfunctional for Importing Thiolase into Peroxisomes

Digitonin permeabilization (Fig. 5 B) together with immunofluorescence analyses (Fig. 6 A) of cells expressing the truncated Peb1p (strain JW162) indicated that thiolase was in the cytosol. This contrasts with the situation in cells expressing the full-length tagged protein, which have been shown to partially package thiolase into peroxisomes (Figs. 5 A and 6 A, strain JW86, discussed in reference 50).

Further evidence for the lack of function of truncated Peb1p came from a test of its capacity to allow cells to grow on oleate as the sole carbon source. Wild type yeast can grow on oleate (YNO plates) by means of the peroxisosomal β-oxidation of this fatty acid. The pebl knockout strain lacks this ability, presumably because thiolase is missing from peroxisomes (Fig. 6 B, strain JW75) (50). Full-length epitope-tagged Peb1p partially restores this
Peb1p-thiolase interaction: two-hybrid assay

Lane 1 2 3 4 5

β-galactosidase
PGK

DNA binding domain — P — P P P
Transactivation domain — T T TΔ Luc

P=Peblp T=thiolase
TΔ=truncated thiolase (Δ1-16)
Luc=luciferase

Figure 7. Peb1p-thiolase interaction detected by the two-hybrid assay. The DNA binding domain (DB) of Gal4p was fused to Peb1p (P) or nothing (−) as indicated. The transactivation (TA) domain of Gal4p was fused to nothing (−), thiolase (T), truncated thiolase lacking the first 16-amino acid residues (TΔ) or luciferase (Luc). These GAL4 fusion proteins were expressed either alone, or in combination as indicated at the bottom of the figure. Protein-protein interaction, causing Gal4p-dependent expression of β-galactosidase, was detected with anti-β-galactosidase antibody. The amount of PGK, also detected by immunoblotting, served as a loading control among the lanes.

Peb1p's Interaction with Thiolase Requires the First 16-amino Acid Residues of Thiolase

The transactivation domain of Gal4p was fused to a truncated version of thiolase lacking the first 16 amino acids. This fusion was co-expressed with the previously tested DNA-binding domain of Gal4p attached to Peb1p: no induction of β-galactosidase occurred (Fig. 7, lane 5). As an additional control, the transactivation domain of GAL4 was fused to the luciferase gene and coexpressed with the GAL4 (DB)-Peb1 fusion gene; no expression of β-galactosidase was detected (lane 5). These results indicate that Peb1p interacts with thiolase, which has a PTS2, but not with luciferase which has a carboxyl-terminal PTS1.

The First 16 Amino Acids of Thiolase are Sufficient for Peb1p Binding

An oligopeptide consisting of the first 16 amino acids of thiolase followed by a cysteine was synthesized and coupled covalently to its COOH-terminus to agarose beads (via an S-S linkage, see Materials and Methods). These beads were used for affinity chromatography with an extract of yeast strain JW88, which contains large amounts of epitope-tagged Peb1p. A substantial amount of Peb1p bound to these beads and (after extensive washing) was detached (together with the peptide) by dithiothreitol (Fig. 8 A, lane 2). The vast bulk of the proteins in the yeast extract did not bind (Fig. 8 A, lanes 1 and 3). Comparison with the starting material (Fig. 8 A, lane 1) by densitometry indicates that about 20% of the Peb1p in the cell extract was recovered in highly purified form by this affinity binding procedure.

As a control, a mutant oligopeptide was synthesized and coupled to agarose beads. The mutant peptide was identical to the wild type peptide except that the fifth amino acid was changed from leucine to arginine. It has been demonstrated that this amino acid substitution (L5R) reduces the import of thiolase into peroxisomes in vivo to 9-12% (16). As seen in Fig. 8 A, lane 3, much less amount of Peb1p bound to the L5R peptide. Densitometry indicated that it amounted to 3% of the applied Peb1p. This result demonstrates that an amino acid among the first 16 that is essential for efficient thiolase import into peroxisomes is also required for efficient Peb1p binding.
Specific binding of Peblp to thiolase targeting sequence. A chemically synthesized peptide, corresponding to the first 16 amino acids of thiolase, followed by cysteine (WT) was coupled by a disulfide linkage to agarose beads as described in Materials and Methods. A mutant peptide, differing only in the replacement of leucine at residue 5 by arginine (L5R), was similarly coupled. Yeast cell extract (150 μg) from strain JW88 expressing epitope-tagged Peblp, was applied to each type of beads. After binding for 60 min, removal of the unbound proteins and repeated washing, the peptides and proteins bound to them were detached from the beads with dithiothreitol. (A) One third of the proteins bound to wild type peptide (WT) or mutant peptide (L5R) were analyzed by immunoblotting with antibody 12CA5. For comparison, 10 μg of the cell extract applied to the beads was analyzed in lane 1. (B) One third of the total proteins bound to the peptides (lanes 1 and 2) or not bound (lanes 3 and 4) were analyzed by SDS-PAGE and Coomassie blue staining.

Discussion

Peblp-PTS2 Binding

These experiments have clearly demonstrated an interaction between Peblp and thiolase. The yeast two-hybrid assay and co-immunoprecipitation showed that Peblp binds to thiolase and that this binding requires the first 16 amino acids of thiolase, which constitute the type 2 targeting sequence (PTS2). Peblp did not bind to luciferase, which is targeted by a PTS1. The PTS2 is sufficient for Peblp binding, as shown by the highly-specific affinity binding of Peblp to an oligopeptide, consisting of the first 16 amino acids of thiolase, coupled to agarose beads. This binding correlated with the topogenic function of the peptide: a single amino acid change (leucine 5 to arginine), which is
known to reduce thiolase import in vivo 8- to 11-fold (16), also reduced Pebp binding about 7-fold. Taken together, these data demonstrate that the PTS2 of thiolase (its first 16 amino acids) is necessary and sufficient to interact with Pebp.

The PTS of Pebp

Pebp has been demonstrated previously to be an intraperoxisomal protein (50). We have now found that Pebp contains a PTS within its first 56 amino acids. This NH2-terminal domain (which is the only part of Pebp not in a WD repeat) is necessary for Pebp to reach peroxisomes, and sufficient to target a passenger protein (truncated thiolase) to peroxisomes. This domain shows no obvious homology to the thiolase PTS2; in particular it lacks the RL and HL dipeptides (or close approximations thereof) that are thought to be required for PTS2 topogenesis. In addition, Pebp probably does not play a role in its own import because a pebp knockout strain can be restored to wild type function by the reintroduction of the PEB1 gene on a plasmid (50). The NH2-terminal topogenic domain of Pebp also does not appear to show any obvious similarity to the internal domains of Candida tropicalis acyl-CoA oxidase (21, 42) or to the internal domain of S. cerevisiae catalase A (24) that target these proteins to peroxisomes. The Pebp PTS appears to be novel.

The Role of Pebp as a PTS2 Receptor

Where in the cell does the interaction between Pebp and the PTS2 occur and how does Pebp function to bring thiolase into the peroxisome? We have considered two models, a co-import model and an intraperoxisomal receptor model. One version of a co-import model was suggested by Marzioch et al. (28) on the basis of their data that Pebp reached peroxisomes by virtue of its association with thiolase, perhaps taking advantage of thiolase’s PTS2 to reach peroxisomes. This version of the co-import model is untenable in view of the fact that Pebp has its own PTS and that Pebp clearly is in peroxisomes in a thiolase knockout strain (Fig. 5).

Co-import?

We might speculate on another hypothetical version of a co-import model. It is theoretically possible that thiolase could bind to Pebp in the cytosol via its PTS2, and then ride piggyback into peroxisomes, directed to the peroxisome by Pebp’s PTS. This would require that the cell make at least as many molecules of Pebp as of thiolase (or at least half as many if all thiolase molecules were to enter peroxisomes as dimers; 15). The steady state abundance of Pebp appears to be far less than that of thiolase. The polypeptide composition of peroxisomes isolated from a pebp knockout strain has been compared with the composition of wild type peroxisomes by silver staining: thiolase was missing, as expected, but no polypeptide with the mass of Pebp was missing (28). This suggests that Pebp, like many other proteins required for peroxisome biogenesis, (e.g., PAF-1; 40), is present at a very low abundance. We may estimate the abundance of Pebp from the data of Fig. 1. The fusion protein (Pebp1.560-thiolase[17-417]) was expressed under the control of the PEB1 promoter on a multi-copy plasmid and its abundance, estimated by immunoblotting with anti-thiolase, was 1/10 that of thiolase itself. Since there are 20–50 copies of the plasmid per cell, the expression level of the fusion protein from a single copy of the gene would be 1/200 to 1/500 of thiolase. Let us assume that anti-thiolase recognizes the fusion protein equally well as thiolase, which is likely because the antibody recognizes truncated thiolase lacking its first 15 amino acids just as well as the full-length thiolase (10). Let us also assume that the steady state expression level of Pebp1.560-thiolase[17-417] is the same as the expression of Pebp. This seems likely because the promoters are the same and the beginning of the proteins (including the translation initiation site) are the same, and peroxisomal proteins turn over synchronously, at least in rat liver (33). In this case, we may infer that Pebp in the wild type cell is 200 to 500 times less abundant than thiolase. This suggests that Pebp is playing a catalytic role, not a carrier role. It is theoretically possible that Pebp might shuttle back out of peroxisomes and re-enter carrying another thiolase molecule, but there is no experimental evidence for protein export from peroxisomes.

An Intra-peroxisomal PTS2 Receptor

The simplest model that is consistent with all of the experimental data is that Pebp functions as an intra-peroxisomal PTS2 receptor. After all, Pebp is found in peroxisomes and it binds the PTS2. In vivo, as suggested previously (50), Pebp might bind newly-synthesized thiolase’s PTS2 as it appears at the inside face of the peroxisome membrane, and then, perhaps together with other proteins, Pebp might “pull” thiolase inside. There is a formal similarity of this proposed mechanism with the role of mitochondrial HSP70 in the import of mitochondrial proteins (22).

If this is correct, we speculate that another PTS2 receptor might function in the cytosol or on the outer surface of the peroxisomal membrane in the initial insertion of the NH2-terminus of thiolase through the peroxisomal membrane. Further research is required to investigate this possibility.

This research was supported by National Institutes of Health grant DK19394. We thank Ms. Xiaoli Cai for her excellent technical assistance. We also thank Dr. Wolf Kunau for anti-thiolase, Dr. Jeremy Thorner for anti-phosphoglycerate kinase, Dr. Michael Shia for antibody 12CA5 and Dr. Andreas Hartig for anti-catalase A.

Received for publication 23 June 1995 and in revised form 2 October 1995.

References


