Pay32p of the Yeast *Yarrowia lipolytica* Is an Intraperoxisomal Component of the Matrix Protein Translocation Machinery

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**Abstract.** *Pay* mutants of the yeast *Yarrowia lipolytica* fail to assemble functional peroxisomes. One mutant strain, *pay32-1*, has abnormally small peroxisomes that are often found in clusters surrounded by membranous material. The functionally complementing gene *PAY32* encodes a protein, Pay32p, of 598 amino acids (66,733 D) that is a member of the tetratricopeptide repeat family. Pay32p is intraperoxisomal. In wild-type peroxisomes, Pay32p is associated primarily with the inner surface of the peroxisomal membrane, but ~30% of Pay32p is localized to the peroxisomal matrix. The majority of Pay32p in the matrix is complexed with two polypeptides of 62 and 64 kD recognized by antibodies to SKL (peroxisomal targeting signal-1). In contrast, in peroxisomes of the *pay32-1* mutant, Pay32p is localized exclusively to the matrix and forms no complex. Biochemical characterization of the mutants *pay32-1* and *pay32-KO* (a *PAY32* gene disruption strain) showed that Pay32p is a component of the peroxisomal translocation machinery. Mutations in the *PAY32* gene prevent the translocation of most peroxisome-bound proteins into the peroxisomal matrix. These proteins, including the 62-kD anti–SKL-reactive polypeptide, are trapped in the peroxisomal membrane at an intermediate stage of translocation in *pay32* mutants. Our results suggest that there are at least two distinct translocation machineries involved in the import of proteins into peroxisomes.

*Peroxisomes* are members of the microbody family of organelles, which also includes the glyoxysomes of plants and the glycosomes of trypanosomes. Peroxisomes are delimited by a single unit membrane and compartmentalize more than 50 enzymes involved in different metabolic functions, most commonly the β-oxidation of fatty acids (Lazarow and de Duve, 1976) and the decomposition of H₂O₂ by catalase (de Duve and Baadhuijn, 1966). Peroxisomes are essential for normal human development and physiology, as shown by the lethality of genetic disorders such as Zellweger syndrome in which peroxisome assembly is disrupted (Lazarow and Moser, 1994). Peroxisomes appear to arise by budding and fission of preexisting peroxisomes (Lazarow and Fujiki, 1985), although some evidence for the de novo formation of peroxisomes has been presented (Waterham et al., 1993).

All peroxisomal proteins are synthesized on free polyribosomes and imported posttranslationally. Two types of peroxisomal targeting signal (PTS)¹ have been identified in peroxisomal matrix proteins. Many matrix proteins are targeted to the peroxisome by tripeptide motifs called PTS1, which are identical to or conserved variants of the prototypical Ser-Lys-Leu PTS1 of firefly luciferase (Gould et al., 1987, 1989, 1990; Aitchison et al., 1991; Swinkels et al., 1992). A second type of peroxisomal targeting signal, PTS2, is found at the amino termini of mammalian and yeast thiolas (Swinkels et al., 1991; Osumi et al., 1991; Glover et al., 1994b; Tsukamoto et al., 1994), yeast amine oxidase (Faber et al., 1995), and watermelon malate dehydrogenase (Gietl et al., 1994). A few peroxisomal matrix proteins are targeted by largely uncharacterized internal PTSs (Small et al., 1988; Purdie et al., 1990; Kragler et al., 1993). There is only limited information on the signals that target proteins to the peroxisomal membrane (McCommon et al., 1994). The only protein components of the peroxisomal targeting machinery so far identified are the PTS1 receptors from yeasts and humans (McCollum et al., 1993; Van der Leij et al., 1993; Dodt et al., 1995; Fransen et al., 1995; Nuttley et al., 1995; van der Klei et al., 1995; Terlecky et al., 1995; Wiemer et al., 1995) and the putative PTS2 receptor of the yeast *Saccharomyces cerevisiae* (Marzioch et al., 1994).

Protein import into peroxisomes has been shown (1) to proceed via two distinct machineries: the cytosol; PNS, postnuclear supernatant; PTS, peroxisomal targeting signal; TPR, tetratricopeptide repeat.

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be energy dependent, requiring ATP hydrolysis but not GTP-hydrolyzing proteins (Imanaka et al., 1987; Rapp et al., 1993; Soto et al., 1993; Wendland and Subramani, 1993); (2) to require cytosolic factors (Wendland and Subramani, 1993), including 70-kD heat shock proteins (Walton et al., 1994); (3) to be dependent on N-ethylmaleimide-sensitive proteins of the peroxisomal membrane (Wendland and Subramani, 1993); and (4) to be saturable and competitive (Walton et al., 1992; Wendland and Subramani, 1993; Miura et al., 1992). Peroxisomes also import oligomeric forms of proteins (Glover et al., 1994a; McNew and Goodman, 1994), which suggests that the peroxisomal translocation machinery can accommodate more than one polypeptide at a time. To date, no component of the peroxisomal translocation machinery itself has been identified. In this paper, we show that the intraperoxisomal protein Pay32p of the yeast *Yarrowia lipolytica* is a component of the peroxisomal translocation machinery for many peroxisomal matrix proteins. We also show that there are at least two distinct pathways for matrix protein translocation across the peroxisomal membrane.

**Materials and Methods**

**Strains and Culture Conditions**

The yeast strains used in this study are listed in Table I. Strains were grown in complete (YEPD, YPBO) or minimal (YND, YNO) media, as required. Media components were as follows: YEPE: 1% yeast extract, 2% peptone, 2% glucose; YPBO: 0.3% yeast extract, 0.5% peptone, 0.5% K2HPO4, 0.5% KH2PO4, 1% Brij 35, 1% (wt/vol) oleic acid; YND: 0.67% yeast nitrogen base without amino acids, 2% glucose; YNO: 0.67% yeast nitrogen base without amino acids, 0.05% (wt/vol) Tween 40, 0.1% (wt/vol) ethanol, 1mM PMSF, 1 µg leupeptin/ml, 1 µg pepstatin/ml, 1 µg aprotinin/ml with or without 0.21 mg NaF/ml. Peroxisomes were purified from the 20KgS fraction of yeast cells (Aitchison et al., 1991), and electron microscopy (Waterham et al., 1992; Nuttley et al., 1994). Mutants were characterized by standard genetic techniques for *Y. lipolytica* (Gaillardin et al., 1973).

**Isolation of the pay32 Mutant Strain**

The *pay32* strain was isolated after chemical mutagenesis of wild type *Y. lipolytica* E122 cells with 1-methyl-3-nitro-1-nitrosoguanidine (Nuttley et al., 1993). The screening protocol included selection for inability to use oleic acid as a carbon source, immunofluorescence microscopy (Nuttley et al., 1993). Leu + colonies were screened on YNO-agar plates for restoration. Plasmid DNA was introduced into cells by electroporation (Nuttley et al., 1993). Leu + transformants that were unable to grow on YNO-agar were further characterized by Southern blotting. pay32::LEU2 integrants were mated to pay32-1 and analyzed for complementation.

**Peroxisome Isolation, Subfractionation, and Extraction**

Fractionation of oleic acid–induced cells into an organellar pellet (20KgP) enriched for peroxisomes and mitochondria, and a supernatant enriched for cytosol (20Kgs) fractions of yeast cells (Aitchison et al., 1991), and electron microscopy (Waterham et al., 1992; Nuttley et al., 1994). Mutants were characterized by standard genetic techniques for *Y. lipolytica* (Gaillardin et al., 1973).

**Table I. Yarrowia lipolytica Strains**

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>E122*</td>
<td>MATA, ura3-302, leu2-270, lys8-11</td>
</tr>
<tr>
<td>22301-3*</td>
<td>MATA, ura3-302, leu2-270, his1</td>
</tr>
<tr>
<td>pay32-1*</td>
<td>MATA, ura3-302, leu2-270, lys8-11, pay32</td>
</tr>
<tr>
<td>PAY32*</td>
<td>MATA, ura3-302, leu2-270, lys8-11, pay32, p32GI (LEU2)</td>
</tr>
<tr>
<td>pay32-KO*</td>
<td>MATA, ura3-302, leu2-270, lys8-11, pay32::LEU2</td>
</tr>
<tr>
<td>pay32-KOB*</td>
<td>MATA, ura3-302, leu2-270, his1, pay32::LEU2</td>
</tr>
<tr>
<td>D32WTB*</td>
<td>MATA/MATb, ura3-302/ura3-302, leu2-270/leu2-270, lys8-11/lys8-11, his1/+, pay32/</td>
</tr>
<tr>
<td>D32KOB*</td>
<td>MATA/MATb, ura3-302/ura3-302, leu2-270/leu2-270, lys8-11/lys8-11, his1/+, pay32/pay32::LEU2</td>
</tr>
</tbody>
</table>

* C. Gaillardin, Thuvaler-Grignon.

*This study.

**Cloning and Characterization of the PAY32 Gene**

The PAY32 gene was isolated from a *Y. lipolytica* genomic DNA library in the autonomously replicating *Escherichia coli* shuttle vector pNiNA445 (Nuttley et al., 1993) by functional complementation of the pay32-1 mutation. Plasmid DNA was introduced into cells by electroporation (Nuttley et al., 1993). Leu + colonies were screened on YNO-agar plates for restoration of the ability to use oleic acid as the carbon source. Complementing plasmids were recovered by transformation into *E. coli*. Standard recombinant DNA methodologies such as enzymatic modification of DNA, DNA fragment purification, and plasmid purification were performed essentially as described in Ausubel et al. (1989).

**DNA Sequencing**

Various restriction endonuclease fragments of the PAY32 gene were cloned into the vectors pGEMSZ(+) and pGEM7Z(+) (Promega, Madison, WI) for dideoxynucleotide sequencing of both strands. The deduced Pay32p amino acid sequence was compared to other known protein sequences using the GENEINFO(R) BLAST Network Service (Blaxter) of the National Center for Biotechnology Information (Bethesda, MD).

**Integrative Disruption of the PAY32 Gene**

A plasmid with a genomic DNA insert containing the PAY32 gene was digested with SpI1, and an ~2.3-kbp SpI1 fragment containing the *Y. lipolytica* LEU2 gene was ligated into this site. In this way, 1.654 bp of the coding region and 74 bp of the 3' untranslated region of the PAY32 gene were replaced with the LEU2 gene. This construct was digested with HindIII to liberate the LEU2 gene flanked by ~1.3 kbp and 1.4 kbp of the 5' and 3' regions of the PAY32 gene, respectively. This linear molecule was used to transform *Y. lipolytica* E122 and 22301-3 strains to leucine prototrophy. Leu + transformants that were unable to grow on YNO-agar were further characterized by Southern blotting. pay32::LEU2 integrants were mated to pay32-1 and analyzed for complementation.
Antibodies

To produce antibodies to Pay32p, a 1,734-bp fragment of the PAY32 gene, which contains both open reading frame and 3' untranslated region and codes for amino acids 47-598 of Pay32p, was excised with SphI, made blunt with T4 DNA polymerase, and inserted into the XmnI site of pMAL-c2 (New England Biolabs, Beverly, MA) in-frame and down-stream of the open reading frame encoding the maltose-binding protein. Antibodies to the fusion protein were raised in guinea pig and rabbit as described previously (Eitzen et al., 1995). Anti-Pay32p antibodies were affinity purified as described by Crane et al. (1994).

Rabbit antibodies to S. cerevisiae peroxisomal acyl-CoA oxidase were a generous gift of Dr. Joel Goodman (University of Texas, Southwestern Medical Center, Dallas, TX). Anti-SKL antibodies were raised in rabbit against the peptide NH$_2$-CRYHLKPLQSKL-CO$_2$H linked to keyhole limpet hemocyanin as described previously (Aitchison et al., 1992). Antibodies to Y. lipolytica peroxisomal thiolase were generated by injection of a thiolase-maltose–binding protein fusion into guinea pig and rabbit.

Immunooaffinity Chromatography

Covalent coupling of affinity-purified rabbit anti-SKL and anti-Pay32p antibodies to protein A–Sepharose (Pharmacia LKB Biotechnology, Piscataway, NJ) and immunooaffinity chromatographic selection of peroxisomal matrix proteins were performed as described by Voos et al. (1994) with the following modifications. The S$_{10}$ containing peroxisomal matrix proteins was diluted with an equivalence of 50 mM Tris–HCl (pH 7.5), 300 mM NaCl, 1% (vol/vol) Triton X-100, 1 mM PMSF, 1 μg leupeptin/ml, 1 μg pepstatin/ml, 1 μg aprozin/ml. The diluted S$_{10}$ (500 μl) was cleared of any nonspecifically binding proteins by incubation for 20 min at 4°C with protein A–Sepharose (50 μl wet volume washed five times in 10 mM Tris–HCl [pH 7.5]). The cleared solution was then subjected to immunooaffinity chromatography. Bound proteins were washed four times in 50 mM Tris–HCl (pH 7.5), 150 mM NaCl, 0.5% (vol/vol) Pay32p Triton X-100, and eluted with 100 mM glycine (pH 2.8). Proteins were precipitated by addition of trichloroacetic acid to 10%, washed in ice-cold 80% (vol/vol) aceton, and then subjected to SDS-PAGE followed by immunoblotting.

For immunoprecipitation of SDS-denatured peroxisomal matrix proteins, the S$_{10}$ was adjusted to 2% SDS, heated at 65°C for 5 min, and processed for immunoprecipitation with anti-SKL and anti-Pay32p antibodies as described (Franzusoff et al., 1991).

Protease Protection

A 20KgP was prepared as described above, except that protease inhibitors were omitted. The 20KgP was gently resuspended in homogenization buffer (1 M sorbitol, 5 mM MES [pH 5.5]). Aliquots containing 240 μg of protein were incubated with 0, 10, 20, or 50 μg of trypsin for 40 min on ice, either in the presence or absence of Triton X-100 at 0.5% (vol/vol) final concentration. The reaction was terminated by addition of trichloroacetic acid to 10% final concentration. The protein precipitates were washed with ice-cold 80% (vol/vol) aceton, and equivalent fractions of each reaction were subjected to SDS-PAGE, followed by immunoblotting with either anti-thiolase, anti-SKL, or anti-Pay32p antibodies.

Immunofluorescence

Immunofluorescence microscopy was performed as described by Aitchison et al. (1992), except that spheroplasts were fixed according to Pringle et al. (1991). Rabbit anti-Pay32p antibodies were affinity purified for immunofluorescence analysis as follows. Whole cell lysates of the pay32-1 mutant grown in YPBO were made in SDS-PAGE sample buffer (2% SDS, 10% [vol/vol] glycerol, 2% [vol/vol] 2-mercaptoethanol, 62.5 mM Tris–HCl, pH 6.8, 0.01% bromophenol blue) as described (Franzusoff et al., 1991). Proteins were separated by SDS-PAGE and transferred to nitrocellulose membranes. Strips of membrane (1 cm × 3 cm) were incubated in 100 mM Tris-HCl, pH 7.0, 6 μM guandine-HCl, 50 mM NaCl for 5 min with gentle agitation at room temperature. After three washes with water (5 min each), the strips were incubated in PBS with 3.7% (vol/vol) formaldehyde for 5 min with gentle agitation at room temperature. The strips were then washed three times with water (5 min each), blocked with PBS containing 1% nonfat dry milk and incubated with anti-Pay32p antisera at dilutions of 1:50, 1:100, and 1:200 in PBS containing 1% nonfat dry milk (~250 μl of diluted antisera was used for each strip) for 30 min with gentle agitation at room temperature. The purified anti-Pay32p antibodies were recovered and used for immunofluorescence microscopy.

Analytical Procedures

Whole cell lysates were prepared as described by Nuttley et al. (1993). Enzymatic activities of catalase (Luck, 1963), isocitrate lyase (Barth and Weber, 1987), malate synthase (Dixon and Kornberg, 1962), 3-hydroxyacyl-CoA dehydrogenase (Osumi and Hashimoto, 1979), and cytochrome c oxidase (Douma et al., 1985) were determined by established methods. SDS-PAGE (Laemmli, 1970) and immunoblotting using a semidry electrophoretic transfer system (model ET-20, Tyler Research Instruments, Edmonton, AB) (Kyhse-Andersen, 1984) were performed as described. Antigen–antibody complexes were detected by enhanced chemiluminescence (Amer sham Life Sciences, Oakville, ON). Densitometry was performed with a LKB Ultrascan XL laser densitometer (LKB Instruments, Bromma, Sweden). Quantification of densitometric signals was done under conditions in which the signal was proportional to the antigen concentration. Protein concentration was determined with a protein assay kit (BioRad Laboratories, Mississauga, ON) using bovine serum albumin as standard. Protein quantification of peroxisomal subfractions was also performed by the method of Schaffer and Weissman (1973).

Results

The pay32-1 Mutant Has Abnormal Peroxisome Morphology

The mutant pay32-1 was initially identified by its inability to grow on media containing oleic acid as the sole carbon source (data not shown). Biochemical characterization showed that pay32-1 had deficiencies in the targeting and import of several peroxisomal matrix proteins (detailed discussion follows), which conforms to the classical pay mutant phenotype.

Electron microscopic analysis of wild-type cells grown in oleic acid–containing (YPBO) medium showed large round peroxisomes well separated from one another and delimited by single membranes (Fig. 1 A). In contrast, peroxisomes from pay32-1 cells were generally smaller than those of wild-type cells and were often found in clusters surrounded by electron-dense membranous material of unknown composition (Fig. 1 B), although loose peroxisomes were also present (Fig. 1 D). The large membranous structures surrounding peroxisomes in pay32-1 cells appear not to be derived from vacuolar, endoplasmic reticular, or Golgi membranes (data not shown).

Immunoelectronmicroscopical analysis showed strong labeling of wild-type peroxisomes with anti-thiolase (Fig. 2 E) and anti-SKL (Fig. 2 F) antibodies. Thiolase and anti-SKL-reactive proteins were also detected in the membranous complexes surrounding peroxisomes of the pay32-1 mutant (arrows in Fig. 2, A and B, respectively). A large immunolabeled peroxisome outside the membranous complex can be seen in Fig. 2 B (P).

Cloning and Analysis of the PAY32 Gene

The PAY32 gene was isolated from a Y. lipolytica genomic DNA library in the autonomously replicating E. coli shuttle vector pNAA445 (Nuttley et al., 1993) by functional
complementation of the mutation in pay32-1 cells. Of the $5 \times 10^3$ transformants screened, one strain, PAY32, was found to have restored growth on oleic acid (data not shown). The strain PAY32 carried the plasmid p32G1, which contains an ~5.4-kbp insert of Y. lipolytica genomic DNA. An ~4.1-kbp region and an overlapping ~3.5-kbp region within this insert were sufficient to functionally complement the pay32-1 mutation (Fig. 3 a). Sequencing within the 3.5-kbp region revealed a 1,794-bp open reading frame encoding a 598-amino acid protein, Pay32p, with a predicted molecular weight of 66,733 (Fig. 3 b).

The sequence of Pay32p shows extensive homology to a family of proteins shown to be essential for peroxisome biogenesis in yeasts and humans: *Pichia pastoris* Pas8p (McCullom et al., 1993), *S. cerevisiae* Pas1p (Van der Klei et al., 1995; van der Klei et al., 1995), and human Pxr1p (Dodt et al., 1995; Fransen et al., 1995; Wiemer et al., 1995). These proteins all share a common structural feature, the tetratricopeptide repeat (TPR) motif, which is a degenerate repeat of 34 amino acids believed to form an interleaving series of $\alpha$-helices (Goebl and Yanagida, 1991). The region of greatest homology among these proteins lies in their TPR domains (data not shown).

It should be noted that the synthesis of Pas8p in pay32-1 cells did not restore growth on oleic acid. Similarly, synthesis of Pay32p in pas8-1 cells did not restore growth on oleic acid. In both cases, the heterologous protein was detectable in immunoblots of whole cell extracts (data not shown). One possible explanation for a negative result of
this type is that Pas8p and Pay32p do not perform the
same function.

Integrative disruption of the PAY32 gene with the Y. lipolytica LEU2 gene was used to create the strains pay32-KO and pay32-KOB in the A and B mating types, respectively. Strains containing a disrupted PAY32 gene were unable to grow on oleic acid (data not shown) and had the same peroxisomal morphology (Figs. 1, C and E, 2, C and D) and peroxisomal protein targeting and import defects (see below) as the original pay32-I mutant. The diploid strain D32WTB, resulting from the mating of the pay32-I strain and the wild-type strain 22301-3, could grow on oleic acid, demonstrating the recessive nature of the pay32-I
mutation. A diploid strain resulting from the mating of
pay32-I and pay32-KOB, D32KOB, was unable to grow
on oleic acid (data not shown), indicating that the authen-
tic PAY32 gene had been cloned.

Expression of the PAY32 gene is inducible by growth on
oleic acid. A small amount of Pay32p is present in wild-
type cells grown in glucose-containing medium. Shifting
cells to oleic acid–containing medium causes an increase in
the level of Pay32p that reaches steady state 3 h after the
shift at a level 10 times that found in glucose-grown cells
(data not shown).
Mutations in the PAY32 Gene Affect the Subcellular Localization but Not the Synthesis of Peroxisomal Proteins

To determine the effects of the pay32-1 and pay32-KO mutations on the level of synthesis of peroxisomal proteins, the wild-type and mutant strains were grown first in glucose-containing (YEPD) medium for 10 h, and then shifted to oleic acid-containing medium (YPBO) for an additional 9 h. Under these conditions, the levels of peroxisomal matrix proteins analyzed (i.e., catalase, isocitrate lyase, malate synthase, 3-hydroxyacyl-CoA dehydrogenase) were assayed. The nucleotide sequence of the PAY32 gene and the deduced amino acid sequence of the wild-type and mutant strains were determined in this study.

Figure 3. Cloning and analysis of the PAY32 gene. (a) Complementing activity of inserts containing the PAY32 gene. The longest line indicates the 4.1-kbp complementing fragment from the original insert in p32G1. The arrow shows the direction and position of the open reading frame of the PAY32 gene. The (+) symbol denotes the ability of an insert to confer growth on oleic acid to pay32-1. The (−) sign denotes the inability of an insert to confer growth on oleic acid to pay32-1. The site of integration of Y. lipolytica LEU2 in the PAY32 gene is shown at the bottom. A, ApaI; E, EcoRI; H, HindII; S, SphI; X, XhoI. (b) Nucleotide sequence of the PAY32 gene and deduced amino acid sequence of Pay32p. The region of TPR motifs is underlined. The nucleotide sequence reported in this paper has been submitted to GenBank with accession number U28155.
crease and reached steady state in the wild-type strain.

The steady-state levels of these proteins in both the pay32-1 and pay32-KO mutants were unchanged vis-à-vis the levels in the wild-type strain (Fig. 4, top panel [catalase (CAT), isocitrate lyase (ICL), malate synthase (MLS), 3-hydroxyacyl-CoA dehydrogenase (HAD)]; Fig. 6, a and b, thiolase; Fig. 8 a, acyl-CoA oxidase; Fig. 8 b, anti-SKL reactive polypeptides). However, the distribution of these proteins between a 20,000 g pellet (20KgP) and a 20,000 g supernatant (20KgS) enriched for cytosol was altered in both mutants as compared to the wild-type strain. A significant fraction of peroxisomal matrix proteins in the wild type strain was associated with the 20KgP, while in the mutant strains these proteins were predominantly localized to the 20KgS (Fig. 4, middle and bottom panels, respectively; Fig. 6, a and b; Fig. 8, a and b).

Peroxisomes were isolated from the wild-type and mutant strains to determine which peroxisome functions were affected by mutations in the PAY32 gene. In the wild-type strain, catalase, isocitrate lyase, and malate synthase activities were found primarily in fractions 1 to 6, with peaks of activity in fraction 4 (Fig. 5 a). Immunoblotting showed that thiolase and anti-SKL-reactive polypeptides were also localized to fractions 1 to 6, with the most intense signals in fraction 4 (Fig. 5, b and c, respectively). Fraction 4 had a density of 1.21 g/cm3. Since all six peroxisomal proteins colocalized to fractions 1 to 6 and as there was essentially no cytochrome c oxidase activity in these fractions, peroxisomes free of mitochondrial contamination were purified in fractions 1 to 6 from the parental strain. Pay32p is also a peroxisomal protein, as it is enriched in the same fractions as are the other peroxisomal proteins (Fig. 5 d).

A similar analysis of the pay32-1 and pay32-KO mutants showed a peak of peroxisomal proteins at a density 1.24 g/cm3 (fraction 2, see Fig. 5). Peroxisome-associated proteins constituted 26.2%, 12.4%, and 3.8% of the 20KgPs of the wild-type, pay32-1 and pay32-KO strains, respectively. The reduced recovery of peroxisome-associated proteins in the pay32 mutant strains may be due to the fact that only single peroxisomes, and not the electron-dense membranous structures surrounding them, are localized to the 20KgP upon subcellular fractionation. However, this is unknown at present.

The fractions most highly enriched for peroxisomes were further analyzed by sucrose-flotation (Heyman et al., 1994). All peroxisomal marker proteins tested floated out of the most dense sucrose and concentrated at the interface between 60 and 35% sucrose at densities of 1.22 g/cm3 and 1.25 g/cm3 for the parental and mutant strains, respectively (data not shown). Therefore, the colocalization of peroxisomal marker proteins in the wild-type strain and in the pay32-1 and pay32-KO mutant strains was not due to the formation of protein aggregates.

A Subset of Peroxisome-associated Proteins Is Translocated Normally into the Matrix of Peroxisomes of pay32 Mutants

Immunoblot analysis of equal quantities of protein from highly purified peroxisomes revealed that thiolase was present in the peroxisomes of the pay32-1 and pay32-KO strains at levels comparable to that found in peroxisomes of the wild-type strain (Fig. 6 c, lanes PER). In peroxisomes from all three strains, thiolase was localized exclusively to the peroxisomal matrix. Subfractionation of peroxisomes showed that thiolase was found only in a 200,000 g supernatant isolated from peroxisomes lysed with Ti8 buffer, which is enriched for peroxisomal matrix proteins (Fig. 6 c, lanes S80k), and protease-protection experiments showed that thiolase in the pay32-KO strain was resistant to protease digestion in the absence of detergent, but was completely digested when the peroxisomal membrane was disrupted with Triton X-100 (Fig. 6 d). Unlike thiolase found in the peroxisomes of the wild-type strain, thiolase in the peroxisomal matrix of the pay32-1 and pay32-KO strains was not proteolytically processed to its mature form (Fig. 6 c). Therefore, thiolase translocation across the peroxisomal membrane does not require proteolytic processing of the thiolase precursor to mature thiolase.

We have measured the specific activities of catalase (Fig. 6, e and f) and malate synthase (Fig. 6, g and h) in
highly purified peroxisomes from wild-type, pay32-1 and pay32-KO cells. No significant differences in specific activities calculated per mg of total peroxisomal protein were found among the three strains (Fig. 6, e and g), suggesting that both catalase and malate synthase, when targeted (bound) to the peroxisome, were translocated normally into the matrix in the pay32-1 and pay32-KO strains. Peroxisome subfractionation experiments also showed that 78–89% of total catalase and malate synthase activities were found in the S18 enriched for peroxisomal matrix proteins (data not shown). It is noteworthy that the specific activities of both catalase and malate synthase, when calculated per mg of peroxisomal matrix protein, were 2–3 times higher in the pay32-1 and the pay32-KO strains as compared to the values for the wild-type strain (Fig. 6, f and h). Therefore, some peroxisome-associated matrix proteins are not efficiently translocated into peroxisomes of the pay32 mutants, and the relative levels of correctly translocated proteins, such as catalase and malate synthase, are selectively enriched in the peroxisomal matrix of the mutant strains.

**Most Matrix Proteins Bound to the Peroxisome Cannot be Translocated Across the Peroxisomal Membrane in the pay32 Mutants**

Subfractionation of peroxisomes from the wild-type strain showed that 76.9 ± 5.0% of total peroxisomal protein was found in the S18 enriched for matrix proteins (Fig. 7 c, solid bar). In contrast, peroxisomal matrix proteins composed 28.8 ± 1.7 and 29.9 ± 2.3% of total peroxisomal protein in the pay32-1 (stippled bar) and pay32-KO (open...
Mutations in the PAY32 gene do not impair the import of thiolase, catalase, and malate synthase into the peroxisomal matrix but do prevent proteolytic processing of the thiolase precursor. (a) Equal fractions (0.2% of the total volume) of the postnuclear supernatant (PNS), 20KgP and 20KgS from the wild-type, pay32-1 and pay32-KO strains were analyzed by immunoblotting with anti-thiolase antibodies. (b) Quantitative analysis of the recovery of thiolase in the 20KgP and 20KgS for the wild-type (solid bar), pay32-1 (stippled bar), and pay32-KO (open bar) strains. Immunoblots as in a were scanned densitometrically. Values reported were standardized to the signals obtained for the PNS of the corresponding strain and are the means ± the standard deviation of three independent experiments. (c) Immunoblot analysis with anti-thiolase antibodies. Peroxisomes from the wild-type (lanes 1), pay32-1 (lanes 2), and pay32-KO (lanes 3) strains were subjected to subfractionation as described in Materials and Methods. Whole peroxisomes (20 μg of protein) were used as starting material for subfractionation. PER, whole peroxisomes (20 μg); S_{THI}, 200,000 g supernatant recovered after peroxisome lysis with Thi8 buffer (step 1); SCO3 and PCO3, 200,000 g supernatant and pellet, respectively, recovered after treatment of the 200,000 g pellet from step 1 (P_{THI}) with 0.1 M Na2CO3 (pH 11). (d) Protease protection analysis. The P_{THI} fraction (240 μg of protein) of the pay32-KO mutant strain was incubated with 0, 10, 20, and 50 μg of trypsin in the absence (−) or presence (+) of 0.5% (vol/vol) Triton X-100 for 40 min on ice. Reactions were terminated by addition of trichloroacetic acid to 10%. Equal fractions of the samples were subjected to immunoblot analysis with anti-thiolase antibodies. (e-h) Specific activities of catalase (e and f) and malate synthase (g and h) in the wild-type (solid bar), pay32-1 (stippled bar), and pay32-KO (open bar) strains. Activities were measured in whole peroxisomes (e and g) and in the S_{THI} enriched for peroxisomal matrix proteins (f and h). Activities were calculated either per mg of total peroxisomal protein (e and g) or per mg of peroxisomal matrix protein (f and h). The values reported are the means ± the standard deviation from three independent experiments.
strain (20.3 ± 2.7% of total peroxisomal protein) were significantly lower than in cells from the mutant strains pay32-1 and pay32-KO (63.1 ± 2.9% and 63.2 ± 4.5%, respectively; Fig. 7c). This shifting of matrix proteins to the peroxisomal membrane in the pay32 mutant strains was confirmed by SDS-PAGE analysis of the various peroxisome subfractions (Fig. 7a). Only a few proteins in whole peroxisomes of the wild-type strain (Fig. 7a, lanes PER, arrows) were missing from the whole peroxisomes of the pay32-1 and pay32-KO mutants, when equal amounts of total peroxisomal proteins were analyzed. Most peroxisomal proteins were found in comparable amounts in peroxisomes of all three strains (Fig. 7a, lanes PER). In the wild-type strain, most peroxisomal proteins were recovered in the matrix fraction (Fig. 7a, S_STi8, lane wt), while in the pay32-1 and pay32-KO strains, most peroxisomal proteins were found tightly associated with the peroxisomal membrane (Fig. 7a, P_PC03, lanes 32-1 and 32-KO, respectively). This tight association of the majority of peroxisomal proteins with the peroxisomal membrane in the mutant strains could also be shown when peroxisomal membrane fractions (P_PC03) were extracted under conditions that solubilize preferentially peripheral membrane proteins (1 M NaCl and 1 M urea). A 62-kD anti-SK1-reactive polypeptide was found among the proteins tightly associated with the peroxisomal membrane in both the pay32-1 and pay32-KO mutants (Fig. 8c, lanes 32-1 and 32-KO, upward pointing arrowheads; Fig. 8e, stippled and open bars, respectively). In peroxisomes isolated from the parental strain, the 62-kD polypeptide was exclusively associated with the peroxisomal matrix (Fig. 8c, S_STi8, lane wt, upward pointing arrowhead; Fig. 8e, solid bar). Treatment of the peroxisomal membrane fraction Pt8 from the pay32-KO strain under conditions that solubilize peripheral membrane proteins (1 M NaCl, 1 M urea, 0.1 M Na2CO3) released some of the 62-kD polypeptide to the soluble (Fig. 8d, lanes S; Fig. 8f, solid bars) fraction, while most of the polypeptide could be solubilized only by treatment with 1% Triton X-100. Protease-protection experiments confirmed that the 62-kD polypeptide was exclusively localized to the matrix of peroxisomes iso-

Figure 7. Mutations in the PAY32 gene prevent translocation of the bulk of peroxisomal matrix proteins across the peroxisomal membrane. (a) Coomassie blue-stained SDS-polyacrylamide gel of whole peroxisomes (PER, 60 μg of protein) and peroxisome subfractions (S_STi8, S_SC03, and P_PC03) of the wild-type (wt), pay32-1 (32-1), and pay32-KO (32-KO) strains. Abbreviations are as in Fig. 6a. Subfractions were isolated from 60 μg of starting purified peroxisomes. (b) The Pt8 of the pay32-KO strain was resuspended in Ti8 buffer, and equal aliquots were treated with one of 1% sodium deoxycholate, 1 M NaCl, 1 M urea, or 1% (wt/vol) Triton X-100. After incubation on ice for 45 min, all samples were separated into supernatant (S) and pellet (P) fractions by centrifugation at 200,000 g for 1 h at 4°C, subjected to SDS-PAGE, and stained with Coomassie blue. Control, sample incubated on ice with Ti8 buffer alone. (c) Peroxisomes isolated from the wild-type (solid bar), pay32-1 (stippled bar), and pay32-KO (open bar) strains were subjected to subfractionation, and the percentage of total peroxisomal protein recovered in each subfraction was determined. The values reported are the means ± the standard deviation from three independent experiments.
Mutations in the PAY32 gene prevent the targeting of acyl-CoA oxidase and a 64-kD anti-SKL reactive polypeptide to peroxisomes and impair the translocation, but not targeting, of a 62-kD anti-SKL reactive polypeptide into peroxisomes. Equal portions (0.2% of the total volume) of the postnuclear supernatant (PNS), the 20KgP and the 20KgS and 10 μg of purified peroxisomes from each of the wild-type and pay32-1 and pay32-KO strains were analyzed by immunoblotting with anti-acyl-CoA oxidase (a) and anti-SKL (b) antibodies. (c) Immunodetection of anti-SKL reactive polypeptides in peroxisomal subfractions. PER lanes contained 20 μg of purified peroxisomes. Peroxisomal subfractions were isolated from 20 μg of starting purified peroxisomes. (c) Recovery of anti-SKL reactive polypeptides in the various peroxisomal subfractions from the wild-type (solid bar), pay32-1 (stippled bar), and pay32-KO (open bar) strains. The percentage of total peroxisomal protein recovered in each subfraction is reported. Values are the means ± the standard deviation of three independent experiments. (d) The PT8 from the pay32-KO strain was treated with various agents and divided into supernatant (S) and pellet (P) fractions as in Fig. 7 b. The control was treated with Ti8 buffer alone. S and P fractions were subjected to SDS-PAGE and immunoblotted with anti-SKL antibodies. (f) Recovery of the 62-kD anti-SKL reactive polypeptide in the S (solid bar) and P (open bar) fractions of d. Localization of anti-SKL reactive polypeptides in peroxisomes of the wild-type (g) and pay32-KO (h) strains by protease protection analysis. Protease protection was carried out as in Fig. 6 b. Arrow, 64-kD anti-SKL reactive polypeptide; upward pointing arrowhead, 62-kD anti-SKL reactive polypeptide; downward pointing arrowhead, 45-kD trypsin-resistant fragment. In contrast, the 62-kD polypeptide was sensitive to protease even in the absence of detergent when peroxisomes were isolated from pay32-KO cells (Fig. 8 h, upward pointing arrowheads), and protease cleavage resulted in a smaller protease-resistant fragment of ~45 kD (Fig. 8 h, downward pointing arrowheads). Therefore, in peroxisomes of the pay32 mutants, a carboxyl-terminal 45-kD fragment reactive with anti-SKL antibodies is protected by the peroxisomal membrane, while an amino-ter-
Mutations in the PAY32 Gene Affect to Varying Matrix Proteins, Including One of the Two Anti-SKL-Reactive Matrix Proteins Across the Peroxisomal Membrane. These Protease.

In the wild-type strain, both acyl-CoA oxidase (data not shown) and the 64-kD peptidase were found in the peroxisomal matrix (Fig. 8c, STi8, lane wt). The 64-kD peptidase is apparently isocitrate lyase (Eitzen, G. A., and R. A. Rachubinski, unpublished results). The specific activity of isocitrate lyase in peroxisomes isolated from the pay32-1 (16.7 ± 3.1 mU/mg prot) and pay32-KO (18.9 ± 3.4 mU/mg prot) mutants did not exceed 4% of the value (492.6 ± 63.8 mU/mg prot) determined for isocitrate lyase in peroxisomes isolated from the wild-type strain. Targeting of the matrix enzyme 3-hydroxyacyl-CoA dehydrogenase was also abolished by mutations in the PAY32 gene (Fig. 4, middle panel). In addition, as mentioned above, a few other peroxisomal matrix proteins also were not associated with peroxisomes isolated from the pay32-1 and pay32-KO mutant strains (Fig. 7a, arrows). In contrast to these proteins, the targeting of catalase, malate synthase (Fig. 4, middle panel), thiolase (Fig. 6, a and b), the 62-kD anti-SKL-reactive polypeptide (Fig. 8b, upward pointing arrowhead), Pay32p (Fig. 9h), as well as most other peroxisomal matrix proteins (Fig. 7a) were only partially reduced.

Pay32p Is an Intraperoxisomal Protein

Antibodies to Pay32p specifically recognized an ~71-kD protein in whole cell extracts prepared from either the wild-type or pay32-1 strains but not the pay32-KO strain (Fig. 9a). The difference between the predicted molecular weight of Pay32p (66,733 D) and its empirical molecular weight (71 kD) has been reported for several other TPR-containing proteins, including p62cdc23 (Sikorski et al., 1993), Pas8p (McCollum et al., 1993) and Pxrlp (Dodd et al., 1995).

Immunoblot analysis revealed that in the wild-type strain, Pay32p was almost exclusively localized to the 20KgP enriched for peroxisomes and mitochondria (Fig. 9b). Densitometric analysis showed that 99.1 ± 0.7% of Pay32p was associated with the 20KgP. This distribution was not affected by the inclusion of NaF to the cocktail of protease inhibitors routinely added to the homogenization buffer (see Materials and Methods). Pay32p also colocalized with peroxisomes isolated from the wild-type strain by sucrose density centrifugation (Fig. 5d). The peroxisomal location of Pay32p was confirmed by double-labeling, indirect immunofluorescence analysis of wild-type cells using anti-Pay32p and anti-thiolase antibodies. The fluorescence patterns generated by these antibodies were superimposable and showed the punctate pattern characteristic of peroxisomes (Fig. 9, i and j).

Despite the fact that a large portion of Pay32p in pay32-1 cells was localized to the cytoplasm (Fig. 9b, 20KgS), the specific amount of Pay32p in highly purified peroxisomes from pay32-1 cells was the same as in peroxisomes purified from cells of the wild-type strain (Fig. 9c, PER, compare lane 32-1 to lane wt). Subfractionation of peroxisomes showed that in cells of the wild-type strain, Pay32p was associated preferentially with the peroxisomal membrane; however, 35% of Pay32p was found in the peroxisomal matrix (Fig. 9c, compare STis, lane wt to PER, lane wt; Fig. 9e, STis, solid bar). In contrast, Pay32p was not associated with the peroxisomal membrane in the pay32-1 mutant but was exclusively localized to the peroxisomal matrix (Fig. 9c, compare STis, lane 32-1 to PER, lane 32-1; Fig. 9e, STis, open bar). Extraction of membranes (PTis) isolated from peroxisomes of the wild-type strain with various solubilizing agents showed that Pay32p fractionated as a peripheral membrane protein that was solubilized to a large extent by either 1 M NaCl or 1 M urea (Fig. 9d, lanes S; Fig. 9e, solid bars) or completely by 0.1 M Na2CO3 (pH 11) (Fig. 9e, solid bar). Protease-protection experiments revealed that in peroxisomes of both the wild-type (Fig. 9g) and pay32-1 (Fig. 9h) strains, Pay32p was resistant to trypsin digestion in the absence of Triton X-100 but was degraded when the peroxisomal membrane was disrupted by the detergent. It is noteworthy that in the presence of detergent, Pay32p in peroxisomes purified from the wild-type strain was more resistant to trypsin treatment than Pay32p in peroxisomes from the pay32-1 strain. A smaller proteolytic fragment of 52 kD was clearly detected after trypsin treatment of peroxisomes of the parental strain only, possibly representing an intermediate of proteolytic digestion (compare Fig. 9g to Fig. 9h). This difference in the protease sensitivity of Pay32p between the wild-type and pay32-1 strains can be explained by a protective action of the components of peroxisomal membrane which can interact with Pay32p in peroxisomes of the parental strain but not in peroxisomes of the mutant strain.

Pay32p Forms a Complex with Anti-SKL-Reactive Poly pep tides In Vivo

Immunofluorinobility chromatography of matrix proteins from peroxisomes of the wild-type strain showed that Pay32p and the 62- and 64-kD anti-SKL-reactive polypeptides could be immunoprecipitated by both anti-Pay32p and anti-SKL antibodies (Fig. 10a). Therefore, Pay32p forms a complex with the anti-SKL-reactive polypeptides. 84.6 ± 9.7% of Pay32p was present in the complex, while 41.3 ± 8.6% of the 62-kD and 21.5 ± 5.4% of the 64-kD anti-SKL-reactive polypeptides were associated with Pay32p (Fig. 10c). The immunoprecipitation of Pay32p and the anti-SKL-reactive polypeptides was specific because (a) under native conditions, anti-SKL antibodies failed to immunoprecipitate Pay32p from the peroxisomal matrix of the
Pay32p is an intraperoxisomal protein associated with both the inner membrane surface and matrix of wild-type peroxisomes. (a) Immunoblot analysis of whole cell extracts (40 μg of protein) probed with anti-Pay32p antibodies. Strains were grown in YPBO for 9 h. (b) Immunoblot analysis of postnuclear supernatant (PNS), 20KgP, and 20 KgS fractions with anti-Pay32p antibodies. Equal portions (0.2% of total volume) of the subfractions were separated by SDS-PAGE. (c) Immunoblot analysis of whole peroxisomes (PER, 60 μg of protein) and peroxisomal subfractions with anti-Pay32p antibodies. Subfractions were prepared from 60 μg starting whole peroxisomes. (d) Quantitative analysis of the distribution of Pay32p in peroxisomal subfractions of the wild-type (solid bar) and the pay32-1 mutant (open bar) strains. Immunoblots as in c were densitometrically scanned. Values reported are standardized to the respective signals obtained for whole peroxisomes (PER) and are the means ± the standard deviation of three experiments. (d) The P18 from the wild-type strain was treated with various agents and divided into supernatant (S) and pellet (P) fractions as in Fig. 7 b. The control was treated with Tris buffer alone. S and P fractions were subjected to SDS-PAGE, transferred to nitrocellulose, and immunoblotted with anti-Pay32p antibodies. (f) Distribution of Pay32p in the S (solid bar) and P (open bar) fractions of d. The values reported are the means ± the standard deviation of three independent experiments. (g and h) Protease protection analysis. The P18 fractions from the wild-type strain (g) and the pay32-1 mutant strain (h) were subjected to digestion with trypsin as in Fig. 6 b. (i and j) Double-labeling, indirect immunofluorescence analysis of wild-type cells using guinea pig anti-thiolase (i) and rabbit anti-Pay32p (j) primary antibodies. Primary antibodies were detected with rhodamine-conjugated donkey anti-guinea pig IgG (i) and fluorescein-conjugated goat anti-rabbit IgG (j) secondary antibodies.
pay32-1 mutant (Fig. 10b), which has no matrix-associated anti-SKL-reactive polypeptides (see Fig. 8c) and (b) Pay32p and the anti-SKL-reactive polypeptides could be immunoprecipitated from wild-type peroxisomal matrix proteins denatured with SDS only by their respective antibodies (data not shown). As expected, Pay32p did not form a complex with either thiolase or acyl-CoA oxidase (Fig. 10a).

Discussion

Here we report the isolation of pay32 mutant strains, their biochemical and morphological characterization, the cloning and sequencing of the PAY32 gene, and the identification and characterization of the PAY32 gene product, Pay32p. While previous studies have revealed the existence of two different peroxisomal targeting pathways that employ different receptors to recognize proteins targeted by PTS1 (McCullum et al., 1993; van der Leij et al., 1993; Motley et al., 1994; Dodt et al., 1995; Wiemer et al., 1995; Fransen et al., 1995; Nuttley et al., 1995; van der Klei et al., 1995; Terlecky et al., 1995) or PTS2 (Marzioch et al., 1994) motifs, this study provides the first evidence that at least two distinct translocation machineries are involved in the import of proteins into peroxisomes.

A Subset of Proteins Is Translocated into the Peroxisomal Matrix Via a Pay32p-independent Pathway(s)

Although the targeting of thiolase, catalase, and malate synthase to the peroxisome is partially reduced by mutations in the PAY32 gene, the peroxisome-bound forms of these proteins are translocated efficiently into the matrix in pay32 mutants. Thiolase, catalase, and malate synthase therefore penetrate peroxisomes via a Pay32p-independent translocation machinery. Y. lipolytica thiolase contains an amino-terminal PTS2 (Berninger et al., 1993) like peroxisomal thiolases from other organisms (Swinkels et al., 1991; Osumi et al., 1991; Glover et al., 1994b; Erdmann, 1994). In contrast, all known peroxisomal catalases and malate synthases are targeted to peroxisomes either by variants of the carboxyl-terminal PTS1 motif or by internal peroxisomal targeting signals (de Hoop and AB, 1992; Roggenkamp, 1992; Kragler et al., 1993; Subramani, 1993). Since peroxisomal targeting signals have been evo-
lutionarily conserved (de Hoop and AB, 1992; Subramani, 1993; Purdue and Lazarow, 1994), the targeting of thiolase and of catalase and/or malate synthase probably occurs via different routes in Y. lipolytica. The existence of a separate targeting route for catalase in Y. lipolytica has been recently demonstrated (Titorenko, V. I., and R. A. Rachubinski, unpublished results). Y. lipolytica could use one Pay32p-independent translocation machinery to translocate proteins targeted by different PTSs via distinct receptors. However, we cannot exclude the possibility that there exists more than one Pay32p-independent translocation machinery. Further analysis of Y. lipolytica pay mutants affected in peroxisomal protein targeting and translocation should reveal which of these two models is representative.

The Pay32p-dependent Translocation Machinery Acts as the Major Pathway for Protein Penetration into the Peroxisomal Matrix

We have shown that two anti-SKL-reactive polypeptides of 62 and 64 kD are localized exclusively to the peroxisomal matrix in the wild-type strain. Only the 62-kD polypeptide was found in peroxisomes of the pay32-1 and pay32-KO mutants, and it was exclusively associated with the peroxisomal membrane. In the mutant strains, the 62-kD polypeptide probably exists as two forms that associate with the peroxisomal membrane. One form (~30–40% of the polypeptide) behaves as a peripheral membrane protein and is apparently associated with the cytoplasmic surface of the peroxisomal membrane, perhaps through interactions with (integral) membrane proteins (see Fig. 8, d and f). The second form (~60–70% of the polypeptide) behaves as an integral membrane protein, with a 45-kD carboxyl-terminal segment apparently embedded in the peroxisomal membrane and a 17-kD segment exposed to the cytoplasm (see Fig. 8, d, f, and h).

Most of the proteins localized to the peroxisomal matrix in the wild-type strain are associated with the peroxisomal membrane in the pay32 mutant strains. Some of these membrane-bound proteins behave like the peripheral form of the 62-kD anti-SKL-reactive polypeptide. They can be solubilized either at high pH or by urea, but treatment with high salt has only a minor effect on their association with the peroxisomal membrane. Other proteins can be released from the peroxisomal membrane only by treatment with detergent and therefore have solubility characteristics of the membrane-embedded form of the 62-kD polypeptide.

From our data, we can conclude that most peroxisomal matrix proteins penetrate peroxisomes via a Pay32p-dependent translocation machinery. Mutations in the PAY32 gene prevent the translocation of peroxisome-associated forms of these proteins into the matrix. Two steps of protein penetration into the peroxisomal matrix are apparently affected in the pay32 mutant strains: (a) embedding of proteins in the peroxisomal membrane and (b) passage of the embedded proteins through the membrane. The fraction of total protein trapped at either of these two stages can vary for different proteins. For example, 30–40% of the 62-kD polypeptide is trapped at the level of the first step, while the remainder of the polypeptide pool is primarily embedded in the peroxisomal membrane, unable to pass through it.

What Role May Pay32p Have in Protein Translocation Across the Peroxisomal Membrane?

Pay32p may function to actively pull PTS1-containing proteins into the peroxisomal matrix, because (a) the intra-peroxisomal pool of Pay32p is dynamically distributed between the inner surface of the peroxisomal membrane and the matrix, (b) the majority of Pay32p in the matrix is present in a complex with SKL-targeted proteins, which dissociate from Pay32p so as to be delivered into the matrix, and (c) mutations preventing the association of Pay32p with the peroxisomal membrane do not prevent the embedding of translocating proteins into the membrane but do impede their being pulled into the matrix, thereby effectively trapping the translocating proteins at the translocon. The saturation of Pay32p-dependent translocans with trapped proteins could prevent many proteins already bound to their peroxisomal receptors on the cytoplasmic surface of the peroxisomal membrane to penetrate the translocon. Indeed, a significant fraction of the proteins normally translocated via a Pay32p-dependent machinery are associated with the cytoplasmic surface of the peroxisomal membrane in pay32 mutants. Proteins that are trapped in the peroxisomal membrane of pay32 mutants and yet are not recognized by anti-SKL antibodies could be targeted by other variants of the PTS1 motif or could exist as intermediate complexes between PTS1-targeted and non-PTS1-targeted proteins formed normally during translocation. The existence of such complexes has been shown previously (Bellion and Goodman, 1987; McNew and Goodman, 1994).

Members of the TPR protein family essential for the import of PTS1-containing proteins have been found in different subcellular compartments: primarily cytoplasmic (S. cerevisiae Pas10p [Van der Leij et al., 1993]; the short form of human Pxr1p [Dodt et al., 1995; Weimer et al., 1995]), associated with the cytoplasmic surface of the peroxisomal membrane (P. pastoris Pas8p [McCollum et al., 1993; Terlecky et al., 1995]; the long form of human Pxr1p [Fransen et al., 1995]), and inside peroxisomes (Y. lipolytica Pay32p). Despite extensive sequence homology, these proteins may still perform distinct functions. Indeed, a model for the action of the short form of human Pxr1p in peroxisomal protein import proposes that this protein acts as a component of a cytoplasmic peroxisomal signal recognition particle, unlike the membrane-anchored Pas8p of P. pastoris or the mitochondrial presquence import receptors MAS20 and MAS70 of S. cerevisiae, even though these proteins are all members of the TPR family (Dodt et al., 1995; Terlecky et al., 1995). We propose that Pay32p of Y. lipolytica acts as an intraperoxisomal component of the matrix protein translocation machinery. An alternative point of view is that PTS1-binding TPR proteins can be organized into a highly integrated system for the import of PTS1-targeted proteins, with the members of TPR protein family being localized to different subcellular compartments. Further analysis is required to distinguish between these possibilities.

How Can Defects in Pay32p Function Impair the Peroxisome Targeting and Translocation of Different Proteins in Distinct Ways?

Mutations in the PAY32 gene have distinct effects on the
targeting and translocation of different peroxisomal matrix proteins: (a) the targeting (binding) of thiolase, catalase, and malate synthase to the peroxisome is partially reduced, while the translocation of the peroxisome-associated forms of these proteins into the matrix appears normal, (b) the targeting of the 62-kD anti-SKL-reactive polypeptide is partially impaired, but the peroxisome-associated form of this polypeptide, as well as most peroxisomal matrix proteins, cannot be translocated across the peroxisomal membrane, and (c) the targeting of acyl-CoA oxidase, 3-hydroxyacyl-CoA dehydrogenase, and the 64-kD anti-SKL-reactive protein, cannot be translocated across the peroxisomal membrane.

How can we explain these data in light of our results? One scenario is that the penetration of proteins into peroxisomes via a Pay32p-dependent translocation pathway could be served by a receptor system consisting of subcomplexes with overlapping substrate specificities but varying affinities for different proteins being imported. The existence of such a receptor system has been demonstrated in mitochondria (Gratzer et al., 1995; Lithgow et al., 1995). Most peroxisomal matrix proteins, including the 62-kD anti-SKL-reactive polypeptide, would show high affinity for this receptor system. These proteins would bind to the components of the peroxisomal membrane much more quickly than would proteins with low affinity for the receptor system. As presented above, mutations in the PAY32 gene could lead to the accumulation of proteins with high affinity on the cytoplasmic surface of the peroxisomal membrane. This accumulation could then interfere with the further binding of proteins with high affinity to the receptor complex serving a Pay32p-dependent translocation machinery, thereby causing a partial defect in their targeting. Under these conditions the targeting (binding) of proteins with low affinity to the receptor system, such as acyl-CoA oxidase, 3-hydroxyacyl-CoA dehydrogenase, and the 64-kD anti-SKL reactive polypeptide, is abolished, thereby causing their mislocalization to the cytoplasm.

While a Pay32p-independent translocation pathway may represent the main route of penetration into the peroxisomal matrix for thiolase, catalase, and malate synthase, these proteins can also use Pay32p-dependent translocons to penetrate the matrix. However, their affinity for the receptor complex serving a Pay32p-dependent translocation machinery may be low. Therefore, in pay32 mutants the targeting (binding) of these proteins (like other proteins with low affinity) to such a receptor complex can be abolished, thereby causing a partial mislocalization of thiolase, catalase, and malate synthase to the cytoplasm.

The results described herein identify Pay32p as an intraperoxisomal component of the translocation machinery for most but not all peroxisomal matrix proteins and provide direct evidence for the existence of multiple pathways of protein translocation across the peroxisomal membrane.

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References


Heyman, J. A., E. Monosov, and S. Subramani. 1994. Role of the PAS1 gene of...
Szilard et al. Protein Translocation into Yeast Peroxisomes