Overproduction of translation elongation factor 1-α (eEF1A) suppresses the peroxisome biogenesis defect in a Hansenula polymorpha pex3 mutant via translational read-through

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Abstract
In eukaryotes, elongation factor 1-α (eEF1A) is required during the elongation phase of translation. We observed that a portion of the cellular eEF1A colocalizes with purified peroxisomes from the methylotrophic yeast Hansenula polymorpha. We have isolated two genes (TEF1 and TEF2) that encode eEF1A, and which are constitutively expressed. We observed that overproduction of eEF1A suppressed the peroxisome deficient phenotype of an H. polymorpha pex3-1 mutant, which was not observed in a strain deleted for PEX3. The pex3-1 allele contains a UGG to UGA mutation, thereby truncating Pex3p after amino acid 242, suggesting that the suppression effect might be the result of translational read-through. Consistent with this hypothesis, overexpression of the pex3-1 gene itself (including its now untranslated part) partly restored peroxisome biogenesis in a PEX3 null mutant. Subsequent co-overexpression of TEF2 in this strain fully restored its peroxisome biogenesis defect and resulted in the formation of major amounts of full-length Pex3p, presumably via translational read-through.

Introduction
The eukaryotic translation elongation factor 1-α (eEF1A) is essential for the delivery of aminoacyl-tRNA (aa-tRNA) molecules to the ribosome during the elongation phase of translation (Riis et al., 1990; Merrick, 1992). Similar to EF-Tu, its bacterial and mitochondrial counterpart, eEF1A binds aa-tRNA and GTP to form a ternary complex (eEF1A/GTP/aa-tRNA), which delivers the charged aa-tRNA to the A site of the ribosome at the expense of GTP hydrolysis. In addition to its role in translation elongation, eEF1A also appears to control the accuracy of translation. Mutations are known to occur in Saccharomyces cerevisiae eEF1A which increase the level of mistranslation and result in frameshifting as well as read-through at stop codons. Furthermore, it was demonstrated that changes in the level of S. cerevisiae eEF1A parallel changes in the misreading of nonsense codons (for review see Valente & Kinzy, 2003). Similar effects have been observed in the yeast Podospora anserina (Silar & Picard, 1994; Silar et al., 2000).

In addition to a role in translation, eEF1A has also been demonstrated to function in multiple other cellular processes (see Lamberti et al., 2004) including, among others, apoptosis, ubiquitin-mediated protein degradation, calmodulin binding and actin binding, and bundling. Initially, these additional roles for eEF1A were observed exclusively in higher eukaryotes. However, recently it has been demonstrated that eEF1A is also an actin-binding and bundling protein that affects the actin cytoskeleton in S. cerevisiae (Munshi et al., 2001). Strikingly, it has been observed that, like eEF1A, actin also has a role in the translational fidelity in baker’s yeast (Kandl et al., 2002).

Here we show that in the methylotrophic yeast Hansenula polymorpha a portion of the cellular eEF1A cofractionates with peroxisomes. Peroxisomes are essential, inducible
Materials and methods

Strains and media

The H. polymorpha strains used in this study are listed in Table 1 and were grown in batch cultures on (1) mineral medium (MM; van Dijken et al., 1976) using glucose (0.5% w/v), ethanol (0.5% v/v), glycerol (0.5% v/v), methanol (0.5% v/v) or glycerol + methanol (0.1% + 0.5% v/v, respectively) as carbon sources, and ammoniumsulphate (0.25% w/w) or D-alanine (0.25% w/w) as nitrogen sources; or on (2) rich medium (YPD) containing 1% (w/v) peptone and 1% (w/v) glucose. Transformants were selected on YND plates containing 0.67% (w/v) yeast nitrogen base without amino acids (Difco), 1% (w/v) peptone and 1% (w/v) glucose. Transformants were selected on YND plates containing 0.67% (w/v) yeast nitrogen base without amino acids (Difco), 1% (w/v) peptone and 1% (w/v) glucose. Transformants were selected on YND plates containing 0.67% (w/v) yeast nitrogen base without amino acids (Difco), 1% (w/v) peptone and 1% (w/v) glucose. Transformants were selected on YND plates containing 0.67% (w/v) yeast nitrogen base without amino acids (Difco), 1% (w/v) peptone and 1% (w/v) glucose. Transformants were selected on YND plates containing 0.67% (w/v) yeast nitrogen base without amino acids (Difco), 1% (w/v) peptone and 1% (w/v) glucose. Transformants were selected on YND plates containing 0.67% (w/v) yeast nitrogen base without amino acids (Difco), 1% (w/v) peptone and 1% (w/v) glucose.

Escherichia coli DH5α and C600 (Sambrook et al., 1989) were used for plasmid constructions and were cultured on (1) LB medium supplemented with the appropriate antibiotics or on (2) M9 medium with the appropriate vitamins, amino acids and nucleotides (Sambrook et al., 1989).

Table 1. Hansenula polymorpha strains used in this study

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>NCYC495</td>
<td>leu1.1 ura3</td>
<td>Gleeson &amp; Sudbery (1988)</td>
</tr>
<tr>
<td>CBS4732</td>
<td>Prototrophic</td>
<td>CBS culture collection</td>
</tr>
<tr>
<td>tef1</td>
<td>NCYC495 tef1::CaLEU2 ura3</td>
<td>This study</td>
</tr>
<tr>
<td>tef2</td>
<td>NCYC495 tef2::HpURA3 leu1.1</td>
<td>This study</td>
</tr>
<tr>
<td>TEF2-lacZ</td>
<td>NCYC495::PTEF1TEF1-lacZ CaLEU2 ura3</td>
<td>This study</td>
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<tr>
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<td>NCYC495::PTEF2TEF2-lacZ CaLEU2 ura3</td>
<td>This study</td>
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<td>Baerends et al. (1996)</td>
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<td>pex3-1 containing plasmid overexpressing the TEF2 gene</td>
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<td>Baerends et al. (2000)</td>
</tr>
<tr>
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<td>This study</td>
</tr>
<tr>
<td>KEF9-6</td>
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</tr>
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<td>KEF2-1:p&lt;sub&gt;AOX&lt;/sub&gt;-TEF2</td>
<td>KEF2-1 with integrated pHIPZ4-TEF2 plasmid</td>
<td>This study</td>
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<tr>
<td>KEF9-6:p&lt;sub&gt;AOX&lt;/sub&gt;-TEF2</td>
<td>KEF9-6 with integrated pHIPZ4-TEF2 plasmid</td>
<td>This study</td>
</tr>
<tr>
<td>pex3 [pRBG61]</td>
<td>pex3 with plasmid containing p&lt;sub&gt;AOX&lt;/sub&gt;-MYC-PEX3</td>
<td>Haan et al. (2002)</td>
</tr>
</tbody>
</table>

Ca, C. albicans; Hp, H. polymorpha; mc, multicopy.
sequences determined from the purified protein. PCR amplification with the primers Hp52-1 (5'-AAA GGT ACC GTN CCN TTY GTN CCN AT-3') – based on amino acids Thr-Val-Pro-Phe-Val-Pro-Ile of peptide p52-33 – and Hp52-3 (5'-TCT TCT AGA GGV ARY CTV ARN GGY TTR TC-3') – based on amino acids Asp-Lys-Pro-Leu-Arg-Leu-Pro of peptide p52-31 – resulted in the amplification of a specific 200-bp fragment from wild-type *H. polymorpha* genomic DNA, which was cloned in pUC19. Sequencing of the PCR fragment revealed high sequence similarity to genes encoding eEF1A. In addition, Southern blot hybridization demonstrated the presence of two genes encoding p52 in the *H. polymorpha* genome. Subsequently, the cloned fragment was used as a probe to isolate the *H. polymorpha* TEF1 gene by colony hybridization using a *H. polymorpha* genomic library in plasmid pHRP2 (Faber *et al*., 1992). Four positive clones were obtained, of which plasmid pKEF3 contained the entire TEF1 gene. The TEF2 gene was apparently not present in this gene library, but was shown to be located on a 4.5-kb HindIII genomic *H. polymorpha* fragment by Southern blot hybridization (data not shown). Subsequently, a small gene library was constructed in pUC19 using HindIII-digested *H. polymorpha* genomic DNA (fragment sizes 4–5 kb). A clone containing TEF2 was identified by colony hybridization and designated as pKEF5.

For the determination of the nucleotide sequence of TEF1, subclones were generated in Bluescript II SK+ (Stratagene Inc., San Diego, CA) that were sequenced using the T7 polymerase system (Pharmacia). For TEF2 a series of nested deletions was generated by the limited exonuclease III digestion method (Sambrook *et al*., 1989), and these deletions were sequenced on an ABI 313A automatic sequencer (Applied Biosystems Inc.) using the Taq Dye Deoxy Terminator Cycle Sequencing Kit. In addition, several selected oligonucleotides were synthesized to complete or confirm certain portions of the TEF1 and TEF2 DNA sequences. *BLAST* algorithms (Altschul *et al*., 1997) were used to screen databases at the National Center for Biotechnology Information (Bethesda, MD). The nucleotide sequences of *H. polymorpha* TEF1 and TEF2 were deposited at GenBank and were assigned the accession numbers AY179868 (TEF1) and AY179869 (TEF2).

**Construction of TEF1 and TEF2 null mutants**

To disrupt TEF1, we constructed plasmid pKEF403, a pUC19 derivative that contains the *Candida albicans* LEU2 gene (Genbank accession number AF000121) flanked by the promoter region of TEF1 (up to the HpaI site at nt 936 of AY179868) and the 3′ end of the TEF1 coding sequence (downstream from the EcoRV site at nt 1135 of AY179868). This will result in a deletion of the region of TEF1 encoding amino acids 9 to 74. For the TEF2 disruption, the HpaI–NcoI (blunted by Klenow treatment) fragment of pKEF5 (nt 794–1388 of AY179869, the region of TEF2 encoding amino acids 9–207) was replaced by a 2.3-kb BamHI (blunted by Klenow treatment) fragment containing the *H. polymorpha* URA3 gene (Merckelbach *et al*., 1993), resulting in plasmid pKEF504. Subsequently, a 3.6-kb PvuII–PstI fragment of pKEF403 (TEF1) or a 2.9-kb PvuII fragment of pKEF504 (TEF2) was used to transform *H. polymorpha* NCYC495 (leu1.1 ura3) (see Fig. 1). Leucine (TEF1) or uracil (TEF2) prototrophic transformants were screened by Southern blot analysis for proper disruption (data not shown). Crossing of the tef1 (ura3) and tef2 (leu1.1) strains and random spore analysis of the resulting diploids were performed according to Titorenko *et al*. (1993).

**Construction of TEF gene fusions with the E. coli lacZ gene**

To enable quantitative measurement of the expression levels of *H. polymorpha* TEF1 and TEF2 we constructed plasmids containing the TEF1 and TEF2 coding regions in-frame fused to the lacZ gene of *E. coli* (AE3). The fusion TEF1 and TEF2 were constructed by linking the TEF1 and TEF2 coding sequences to the lacZ gene through a unique HindIII site (Fig. 1). To obtain a 2.8-kb HindIII genomic fragment containing the TEF1 coding region (up to the HpaI site at nt 936 of AY179869, the region of TEF1 encoding amino acids 208–471) a 4.5-kb HindIII genomic fragment was used as a probe to isolate a 4.8-kb HindIII genomic fragment from the *H. polymorpha* genome. Subsequently, the cloned fragment was used to construct pKEF504 containing the lacZ gene 4–5 kb. A clone containing TEF2 was identified by colony hybridization using a *H. polymorpha* genomic library in plasmid pHRP2 (Faber *et al*., 1992). Four positive clones were obtained, of which plasmid pKEF3 contained the entire TEF1 gene. The TEF2 gene was apparently not present in this gene library, but was shown to be located on a 4.5-kb HindIII genomic *H. polymorpha* fragment by Southern blot hybridization (data not shown). Subsequently, a small gene library was constructed in pUC19 using HindIII-digested *H. polymorpha* genomic DNA (fragment sizes 4–5 kb). A clone containing TEF2 was identified by colony hybridization and designated as pKEF5.

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**Construction of TEF gene fusions with the E. coli lacZ gene**

To enable quantitative measurement of the expression levels of *H. polymorpha* TEF1 and TEF2 we constructed plasmids...
pKEF411 and pKEF506 harbouring in frame fusion genes between the TEF1 and TEF2 genes and the E. coli lacZ gene lacking a start codon (from plasmid pMLB1034; Silhavy et al., 1984), respectively. In pKEF411 and pKEF506, lacZ was placed downstream from a 2-kb EcoRV–HpaI fragment (TEF1) or a 1.4-kb HindIII–HpaI (TEF2) fragment comprising the promoter region and the first eight codons of the indicated TEF gene. In addition, both plasmids contain the C. albicans LEU2 gene. To enable integration at the homologous locus in the H. polymorpha genome, plasmids pKEF411 and pKEF506 were linearized with NcoI and EcoRI in the TEF1 and TEF2 promoter regions, respectively, and transformed into H. polymorpha (leu1.1 ura3) (Fig. 1). Leucine prototrophic transformants were analysed by Southern blot analysis for proper single-copy integration (data not shown).

**Overexpression of TEF2 in H. polymorpha**

To enable overproduction of eEF1A in H. polymorpha, the entire TEF2 coding region was placed under the control of the strong inducible H. polymorpha AOX promoter. First a HindIII site was introduced upstream of the TEF2 gene by PCR using primer TEF2-H (5′-TGA AAG CTT CAA AAT GGG TAA AG-3′). After subcloning in pBlue-script (Stratagene) – a plasmid designated pB-TEF2-rec – a 2.2-kb HindIII–SmaI fragment containing the entire TEF2 coding region was inserted between the HindIII and SmaI sites of pHIPX4 (Gietl et al., 1994). The resulting plasmid, designated pHIPX4-TEF2, was transformed into various H. polymorpha pex-null mutant strains.

**Generation of polyclonal antibodies against eEF1A**

The region comprising amino acids 9 to 459 of H. polymorpha eEF1A was produced in E. coli as part of a fusion protein with maltose-binding protein (MBP) using the Protein Fusion and Purification System (New England Biolabs, Beverly, MA). To this end, a 3-kb Hpal–HindIII fragment of pKEF5 was cloned between the Asp700I and HindIII sites of the pMAL-c2 vector resulting in plasmid pKEF500. Production and purification of the fusion protein was performed according to the instructions of the supplier of the system. Purified MBP-eEF1A fusion protein was used to immunize a rabbit.

**Isolation of the mutant PEX3 gene from H. polymorpha pex3-1**

The mutant PEX3 locus was amplified from the genome of the peroxisome deficient H. polymorpha strain pex3-1 by PCR using primers PER9-1A (5′-AGA GGA TCC CGG GTT CGT TCT CTG TGA TAC-3′) and PER9-1B (5′-GTC GTC GAC GAT ATC TAA TCA GTA TAC ATG C-3′). The resulting 1.45-kb PCR fragment was digested with BamHI and Sall and inserted in BamHI+Sall-digested pBluescript, resulting in plasmid pH-pex3-1. Subsequently, two independently isolated clones were sequenced.

**Overexpression of mutant versions of PEX3 in a H. polymorpha pEX3 null mutant**

To overexpress MYC-tagged versions of the pex3-1 gene in a H. polymorpha mutant lacking PEX3, we constructed plasmids pX4-MYC-pex3-1ORF and pX4-MYC-pex3-1total. For pX4-MYC-pex3-1ORF, we digested plasmid pRBDG60 – a derivative of pRBDG61 (Haan et al., 2002) containing the wild-type MYC-PEX3 gene in the vector pHIPX4 – with HindIII and SmaI, and inserted a 0.75-kb HindIII–EcoRV fragment of pH-pex3-1. This fragment exclusively contains the 242 aa ORF of the pex3-1 gene. For pX4-MYC-pex3-1total, we inserted the entire mutant pex3-1 allele from pH-pex3-1 as a 1.35-kb HindIII–Sall fragment between the HindIII and Sall sites of pRBDG60. Both plasmids were subsequently integrated in the P_AOX locus of the genome of the H. polymorpha PEX3 null mutant. Proper integration of the plasmids was confirmed by Southern blotting (data not shown). Strains with multiple copies of the expression cassettes in their genomes (designated KEF2-1 and KEF9-6, respectively) were selected for further study.

To enable co-overexpression of MYC-tagged versions of the pex3-1 gene and the TEF2 gene we used plasmid pHIPZ4-TEF2. This plasmid was constructed by inserting a 2.2-kb HindIII–XbaI fragment from pH-TEF2-rec, containing the entire TEF2 gene, between the HindIII and XbaI sites of vector pHIPZ4 (Salomons et al., 2000), which contains the H. polymorpha AOX promoter and a zeocin resistance gene. Subsequently, pHIPZ4-TEF2 was linearized with Asp718I and integrated into the genomes of H. polymorpha KEF2-1 and KEF9-6.

**Biochemical techniques**

Hansenula polymorpha protoplasts were generated and lysed according to Van der Klei et al. (1998). Postnuclear supernatants were loaded on to discontinuous sucrose gradients as described by Douma et al. (1985). Fractions of gradients were analysed for sucrose concentrations and alcohol oxidase (AO; Verduyn et al., 1984) and cytochrome c oxidase (COX; Douma et al., 1985) activities. Protein concentrations were determined using the Bio-Rad Protein Assay system using bovine serum albumin as a standard. β-galactosidase activity measurements were performed according to Miller (1972) using crude extracts of H. polymorpha cells prepared with glass beads as described by Waterham et al. (1994). For
Western blots, cell extracts of *H. polymorpha* cells were prepared using the TCA method (Baerends et al., 2000). Sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) and Western blotting were performed by established procedures. Western blots were decorated with polyclonal antibodies against various *H. polymorpha* proteins.

**Electron microscopy**

Cells were fixed and prepared for electron microscopy and immunocytochemistry as described previously (Waterham et al., 1994). Immunolabeling was performed on ultrathin sections of Unicryl-embedded cells using specific antibodies against selected *H. polymorpha* proteins.

**Results**

**Isolation of the *H. polymorpha* TEF1 and TEF2 genes encoding eEF1A**

*Hansenula polymorpha* cells, subjected to methylotrophic growth conditions, contain many peroxisomes that harbour enzymes involved in the metabolism of methanol: alcohol oxidase (AO) dihydroxyacetone synthase (DHAS) and catalase (CAT) (Veenhuis et al., 1978; for a recent review see van der Klei et al., 2006). AO and DHAS constitute the majority of the proteins present in peroxisomes (Fig. 2). We observed that in addition to these proteins fractions enriched in peroxisomes, obtained by sucrose density centrifugation of homogenized protoplasts, also contain a relatively dominant protein band of c. 52 kDa (designated p52). Microsequencing of this protein band identified two peptides with high similarity to eukaryotic eEF1A.

To confirm (partial) colocalization of eEF1A with peroxisomes, we determined eEF1A levels in fractions of sucrose density gradients prepared from a postnuclear supernatant (PNS) of methanol/ammoniumsulphate-grown wild-type cells, we determined eEF1A levels in fractions of sucrose density gradients prepared from a postnuclear supernatant of *H. polymorpha*. To enable this, polyclonal antibodies were raised against selected proteins.

In many yeast species eEF1A is encoded by at least two genes (Schirmaier & Philippsen, 1984; Sundstrom et al., 1987, 1990). In order to isolate the gene(s) encoding eEF1A, we designed degenerate primers based on the peptide sequences and obtained a specific *H. polymorpha* DNA fragment by PCR. Sequence analysis demonstrated that the isolated fragment indeed contained part of a *H. polymorpha* gene encoding eEF1A. Southern blot hybridization with genomic DNA of *H. polymorpha* using the cloned PCR fragment as a probe (Fig. 4) revealed that the *H. polymorpha* genome contains two genes encoding eEF1A (TEF1 and TEF2), which were isolated and sequenced.

Analysis of the sequences revealed that TEF1 and TEF2 differ only six nucleotides in the region encoding eEF1A (1380 bp). In contrast, the promoter and terminator regions of the genes are rather dissimilar. As was observed for *S. cerevisiae* and *C. albicans* (Schirmaier & Philippsen, 1984; Sundstrom et al., 1990), in *H. polymorpha* the two genes encode an identical protein. *Hansenula polymorpha* eEF1A is highly similar to its orthologues from other eukaryotes (81–93% identity) but also shows similarity to prokaryotic EF-Tu proteins (c. 30% identity).

**Deletion of *H. polymorpha* TEF1 and TEF2**

In order to analyse the effect of deletion of TEF1 and/or TEF2 in *H. polymorpha*, we constructed strains tef1 and tef2 (see Fig. 1). In eukaryotes, eEF1A is an essential protein (Cottrelle et al., 1985). To investigate this also for *H. polymorpha*, we crossed the tef1 and tef2 strains and subjected prototrophic diploids to random spore analysis. Phenotypic analysis of the progeny from these diploids resulted in a TEF1/TEF2: tef1/tef2: tef1/tef2
segregation of 1 : 1 : 1 : 0 (n = 504), confirming the inviability of a tef1/tef2 double deletion mutant.

We also analysed the effect of the deletion of either TEF1 or TEF2 on growth of H. polymorpha on medium with different carbon and nitrogen sources. Growth of tef1 cells was significantly retarded on media containing methanol/ammonium sulphate or methanol/D-alanine (Table 2). As growth on these substrates involves peroxisomal enzymes, a possible explanation could be that peroxisome formation was affected in tef1 cells. To study this we performed an ultrastructural analysis of tef1 cells grown on methanol/ammonium sulphate media, which indicated that the cells contained normal peroxisomes similar to WT controls (data not shown). Furthermore, immunocytochemistry using specific antibodies against AO and CAT showed no significant mislocalization of these peroxisomal matrix proteins in tef1 cells (data not shown).

**Hansenula polymorpha TEF1 and TEF2 are constitutively expressed genes**

The data presented above suggest that *H. polymorpha* TEF1 and TEF2 may not be expressed to the same extent and/or that their expression levels/profiles may depend on the carbon/nitrogen sources used for growth. To understand more about the expression levels/profiles of TEF1 and TEF2, we placed a TEF-lacZ fusion gene containing the first eight codons of TEF1/TEF2 fused in frame to the *E. coli* lacZ gene under the control of the genomic TEF1 and TEF2 promoters, respectively (see Fig. 1), and determined ß-galactosidase activities in crude extracts of cells grown under various conditions. We also determined eEF1A protein levels in *H. polymorpha* wild-type, tef1 and tef2 cells by Western blotting using samples taken at different time-intervals during growth on YPD medium. The results of these experiments demonstrate (1) that both TEF1 and TEF2 promoters are active on all media tested, with the lowest expression levels on medium with methanol/D-alanine as carbon/nitrogen source (Table 3); (2) that eEF1A is constitutively present during growth of *H. polymorpha* on YPD...
Table 2. Growth characteristics of Hansenula polymorpha strains on different carbon and nitrogen sources

<table>
<thead>
<tr>
<th>Carbon/nitrogen source</th>
<th>Doubling time t_d (h)</th>
<th>Yield (OD_{663 nm})</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Wild-type</td>
<td>tef1</td>
</tr>
<tr>
<td>Glucose/NH_4^+</td>
<td>1.6</td>
<td>1.5</td>
</tr>
<tr>
<td>Ethanol/NH_4^+</td>
<td>1.8</td>
<td>1.8</td>
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<td>2.0</td>
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<tr>
<td>Methanol/D-alanine</td>
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<td>4.7</td>
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</table>

The indicated Hansenula polymorpha strains were grown at 43°C in mineral medium supplemented with various carbon and nitrogen sources. The data represent the average of three independent experiments. The optimal doubling time (t_d) was calculated from growth curves. The yield represents the final OD_{663 nm} of the cultures.

Table 3. Expression of the Hansenula polymorpha TEF1 and TEF2 genes

<table>
<thead>
<tr>
<th>Strain</th>
<th>Glucose/ NH_4^+</th>
<th>Glucose/D-alanine</th>
<th>Methanol/ NH_4^+</th>
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<tbody>
<tr>
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<td>3120</td>
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<td>2630</td>
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<tr>
<td>TEF2-lacZ</td>
<td>2620</td>
<td>1770</td>
<td>1870</td>
<td>1350</td>
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<tr>
<td>Ratio TEF1/TEF2</td>
<td>1.57</td>
<td>1.76</td>
<td>1.61</td>
<td>1.95</td>
</tr>
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</table>

Cells of the indicated Hansenula polymorpha strains were cultivated to the mid-exponential growth phase on mineral medium with the indicated carbon and nitrogen sources and β-galactosidase activities were measured in crude cell extracts. No significant β-galactosidase activity (< 50 U mg⁻¹) was observed in wild-type Hansenula polymorpha cell extracts. The ratio between the expression levels of TEF1 and TEF2 on the various media is also indicated.

medium (Fig. 5a); and (3) that the expression of the TEF1 gene is c. 1.5- to 2-fold higher than that of TEF2 (Table 3). As a result, extracts of tef1 cells grown on methanol/D-alanine have the lowest eEF1A levels (Fig. 5b).

Overproduction of eEF1A suppresses the peroxisome biogenesis defect in a Hansenula polymorpha pex3-1 mutant

Our data indicate that depletion of eEF1A has no effect on peroxisome formation in a wild-type background. We next examined the possibility that overproduction of eEF1A might suppress the peroxisome biogenesis defect of Hansenula polymorpha pex mutants defective in peroxisome formation (for an overview of the PEX genes present in fungi see Kiel et al., 2006). Overproduction was confirmed by Western blotting using specific antibodies against eEF1A (data not shown). Ultrastructural analysis demonstrated that exclusively in the pex3-1 mutant (Baerends et al., 1996) partial suppression of the peroxisome biogenesis defect had occurred. Unlike wild-type Hansenula polymorpha cells, which contain many peroxisomes (Fig. 6a), peroxisomal structures are not detectable in pex3-1 cells (Fig. 6b; see also Baerends et al., 1996). Overproduction of eEF1A in pex3-1 cells resulted in the formation of a single peroxisome in a number of cells (Fig. 6c). Immunocytochemistry demonstrated that this single organelle contained significant amounts of peroxisomal matrix proteins (Fig. 6d, shown for AO).

To understand whether the partial suppression of the peroxisome biogenesis defect in the pex3-1 mutant was allele-specific, we also investigated whether overproduction of eEF1A could restore peroxisome biogenesis in a pex3 null mutant. Ultrastructural analysis of cells of this mutant overexpressing TEF2 did not show any visible
peroxisome formation, clearly implying that the pex3-1 allele was essential for the suppression effect (data not shown).

**Co-overexpression of the pex3-1 allele and TEF2 fully restores peroxisome biogenesis in a pex3 strain**

In order to obtain more information as to why eEF1A overproduction partly suppressed the peroxisome biogenesis defect in the pex3-1 mutant, we decided to investigate this mutant in more detail. Sequencing of the mutant allele resulted in the identification of a G1925A mutation in the PEX3 sequence (see Genbank U37763) that changed codon 243 from UGG (Trp) to UGA (Ter). Thus, the pex3-1 allele could still produce a C-terminally truncated protein with a calculated Mr of 28 kDa. However, Western blot analysis failed to detect any protein of this size in crude extracts of pex3-1 cells (Fig. 7a), suggesting that either the truncated protein or the mRNA encoding it may be unstable in the cell.

In eukaryotes, eEF1A plays a crucial role in translation elongation. However, additional roles for this protein (e.g. regulating translational fidelity or bundling of actin filaments) have also been proposed. We reasoned that upon eEF1A overproduction, the nonsense codon in pex3-1 mRNA might be occasionally misread, resulting in the production of a minor amount of functional Pex3p. To test this possibility, we constructed *H. polymorpha* pex3 strains that overexpressed two different versions of the mutant pex3-1 allele. In the first strain (KEF2-1), only the protein-coding portion of the pex3-1 allele (up to nt 1997 in
H. polymorpha pex3 tagged at their 5' and 3' ends. As a control, H. polymorpha pex3 [pRBG61] was used which contains a 5' MYC-tagged wild-

type PEX3 gene under the control of its endogenous promoter (Haan et al., 2002).

Ultrastructural analyses of methanol-induced cells of the strains KEF2-1 and KEF9-6 revealed dramatic differences in their peroxisomal profiles. As shown before (Haan et al., 2002), expression of MYC-PEX3 by its endogenous promoter fully complemented the peroxisome biogenesis defect of the pex3 strain and many large peroxisomes were formed in control cells (data not shown). In KEF2-1 cells, the production of the truncated MYC-tagged protein resulted in the formation of small membranous structures (Fig. 8a), which contained the peroxisomal membrane protein Pex14p (inset in Fig. 8b), but harboured only little matrix protein (Fig. 8b, shown for AO). KEF9-6 cells showed a heterogeneous population in that some cells contained a few, very large peroxisomes which harboured most peroxisomal matrix proteins (Fig. 8c and d; shown for AO). In other cells only a single peroxisome was present and AO was located in both the peroxisome and a cytosolic crystalloid (Fig. 8e). Despite this partial restoration of the peroxisome biogenesis defect, KEF9-6 cells were unable to grow on methanol as sole carbon and energy source.

Biochemical analyses revealed that cells of KEF2-1 and KEF9-6 produced an c. 35-kDa protein that was recognized by the α-MYC antibodies (Fig. 7b). In both cases the amount of truncated protein produced by these overexpression strains approximately equalled that produced by the strain expressing wild-type MYC-PEX3 by the much weaker endogenous promoter. Assuming that translational read-through of the pex3-1 allele had caused the major ultrastructural differences observed between the two strains, some wild-type MYC-Pex3p should have been formed in KEF9-6 cells. Although such a protein band is not visible in Fig. 7b, a very long exposure of a similar Western blot demonstrated the presence of a minute amount of a protein of the expected size in extracts of KEF9-6 cells, which was absent in extracts of pex3 and KEF2-1 cells (Fig. 7c).

To definitively prove that eEF1A overproduction could result in translational read-through of the pex3-1 allele, we also overexpressed TEF2 in strains KEF2-1 and KEF9-6. Analysis of the growth characteristics of the resulting strains, KEF2-1::AOX-TEF2 and KEF9-6::AOX-TEF2, demonstrated that eEF1A overproduction rescued the inability of strain KEF9-6 to utilize methanol as the sole source of carbon and energy, a hallmark of the presence of functional peroxisomes. In contrast, strain KEF2-1::AOX-TEF2 remained unable to grow on methanol. Biochemical analyses of these strains revealed that KEF9-6::AOX-TEF2 cells produced almost wild-type levels of full-length MYC-Pex3p in addition to the truncated MYC-Pex3-1 protein (Fig. 7d). In contrast, overproduction of eEF1A in strain KEF2-1 failed to result in any synthesis of full-length MYC-Pex3p.

![Fig. 7. Detection of mutant forms of Pex3p.](image-url)
Discussion

We have identified and cloned two genes encoding eEF1A in *H. polymorpha*. In this yeast, both genes are constitutively expressed. As expected, deletion of both genes was lethal. Deletion of the *TEF1* gene resulted in reduced growth on media containing methanol and D-alanine. Our data demonstrate that under these cultivation conditions, the
expression of both TEF genes is relatively low. We presume that upon deletion of TEF1, the gene with the highest expression, the remaining level of eEF1A in the cells is not sufficient to fully support a normal growth rate.

Furthermore, we found that eEF1A overproduction suppressed the peroxisome deficient pex3-1 mutant that contains a UGG to UGA mutation in PEX3, resulting in premature translation termination. A similar suppression was also observed upon overexpression of the pex3-1 allele in pex3 cells, while additional co-overproduction of eEF1A in this strain restored the ability of the cells to utilize methanol as the sole carbon and energy source. Our data indicate that the partial suppression of the peroxisome biogenesis defect in the pex3-1 mutant upon eEF1A overproduction was presumably not caused by a direct interaction between eEF1A and the truncated pex3-1 gene product. Rather, we presume that the increased eEF1A levels caused enhanced translational read-through of the stop codon in the pex3-1 mRNA, resulting in the formation of a minute amount of full-length Pex3p, which nevertheless remained below the limit of our detection. This assumption was confirmed by the observation that significant amounts of full-length MYC-Pex3p were present in a strain co-overproducing eEF1A and MYC-Pex3p(Trp243Ter). Such a suppression phenomenon is consistent with observations made in other yeast species regarding a role for eEF1A in translational fidelity (Song et al., 1989; Silar & Picard, 1994; Silar et al., 2000). Previously, we have observed a direct relation between the level of Pex3p and the number of peroxisomes in H. polymorpha (Baerends et al., 1996). In line with this is the observation that eEF1A overproduction in pex3-1 cells only allows the formation of a single peroxisome per cell. Recently, eEF1A was also isolated as a suppressor of the Yarrowia lipolytica pex1-1 (pay41) mutant, which is affected in peroxisome biogenesis and unable to grow on oleate as the sole carbon and energy source (V.I. Titorenko, unpublished data). It is tempting to assume that also in this case read-through of a stop codon has resulted in the formation of sufficient amounts of wild-type Pex1p to allow growth on media containing oleate.

The current analysis was initiated by the finding that a portion of eEF1A copurifies with peroxisomes (Figs 2 and 3). A number of recent proteomics studies on highly purified peroxisomes confirm that eEF1A associates with these organelles (see Schäfer et al., 2001; Marelli et al., 2004; our unpublished data). Several explanations could possibly clarify this phenomenon. eEF1A is a rather basic protein (pI = 9.1), which might bind rather nonspecifically to negatively charged membranes. Alternatively, eEF1A may perform a specific function at peroxisomes e.g. in localized translation (Condeelis, 1995; Gonsalvez et al., 2005). Currently, our data do not allow us to discriminate between these possibilities.

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References
Hansenula polymorpha eEF1A and peroxisomes


