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The Sorting Route of Cytochrome \( b_2 \) Branches from the General Mitochondrial Import Pathway at the Preprotein Translocase of the Inner Membrane*

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Cytochrome \( b_2 \) is synthesized in the cytosol with a bipartite presequence. The first part of the presequence targets the protein to mitochondria and mediates translocation into the mitochondrial matrix compartment; the second part contains the sorting signal that is required for delivery of the protein to the intermembrane space. The localization of the structures that recognize the sorting signal is unclear. Here we show that upon import in vivo, the sorting signal of cytochrome \( b_2 \) causes an early divergence from the general matrix import pathway and thereby prevents translocation of a folded C-terminal domain into mitochondria. By co-immunoprecipitations we find that translocation intermediates of cytochrome \( b_2 \) are associated with Tim23, a component of the inner membrane protein import machinery. Cytochrome \( b_2 \) constructs with an alteration in the sorting signal are mistargeted to the matrix of wild-type mitochondria. In mitochondria containing a mutant form of Tim23, however, the translocation of the altered sorting signal across the inner membrane is inhibited, and cytochrome \( b_2 \) is correctly sorted to the intermembrane space. We suggest that the sorting signal of cytochrome \( b_2 \) is recognized within the inner membrane in close vicinity to Tim23.

Nearly all mitochondrial proteins are synthesized by cytosolic ribosomes and posttranslationally imported into the organelle (1–3). Translocation across the outer membrane requires transport through a general import pore that is formed by a complex of Tom proteins. Translocation across the inner membrane involves a common step for all preproteins carrying a presequence and is mediated by a complex of the translocase of the inner membrane, to the peripheral membrane protein Tim44 (8–10), and also directly to the import channel (Tim17-Tim23) (11); therefore, conformational changes of mtHsp70 are directional and can exert a force on the preprotein in transit.

Cytochrome \( b_2 \) of yeast mitochondria has for many years served as a paradigm in elucidating the more complex import pathways of proteins that have a final location in the intermembrane space. In this compartment, mature cytochrome \( b_2 \) (\((\Delta^+)-lactate cytochrome c oxidoreductase\)) is a soluble tetramer with a molecular weight of 12–14. The preprotein contains a bipartite presequence. The first part of the presequence (residues 1–31) mediates translocation across both mitochondrial membranes and is cleaved in the matrix. The second part (residues 32–80) contains the information that is required for sorting of the protein to the intermembrane space. The inner membrane peptidase I, which carries the catalytic site on the intermembrane space side (15), removes the second part of the presequence, yielding the mature protein.

The sorting signal of cytochrome \( b_2 \) resembles the targeting signals of secretory bacterial proteins, suggesting a conservation of targeting mechanisms in mitochondria in line with the endo-symbiotic theory of organelle evolution (16). The sequencing project of the yeast genome, however, has recently demonstrated that a possible conservation of the prokaryotic targeting system does not include a conservation of the Sec machinery of the prokaryotic translocase; homologs of sec genes have not been found in the yeast genome (17). This does not exclude a conservation of mechanistic principles. In a series of studies it has been shown that the sorting signal of cytochrome \( b_2 \) seems to be imported into the matrix in tandem with the first part of the presequence (18–23). These experiments suggest that the sorting signal is subsequently recognized by a separate system besides the import machinery and re-exported to the intermembrane space. Other data have suggested that the sorting signal serves as a stop signal in the import machinery.

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ery and does not proceed into the matrix (24–28). In this concept, the sorting signal leaves the import machinery in the inner membrane laterally, without involvement of a separate reexport system.

In a previous study we used different constructs of cytochrome \( b_2 \) as a molecular ruler to localize the functional sorting signal within the mitochondrion (29). By studying in vitro import into isolated mitochondria, we found that the sorting signal functions already during insertion into the inner membrane. mtHsp70 could exert an unfolding (pulling) activity only on folded domains that were located close to the cytochrome \( b_2 \) presequence. A folded domain located at the C terminus of a cytochrome \( b_2 \) fusion protein was not unfolded and therefore not translocated across the outer membrane, suggesting that the sorting signal directed an early divergence of the preprotein from the mtHsp70-driven matrix import pathway. We now asked whether these in vitro findings were of relevance for protein sorting in vivo. We indeed observed that the sorting signal of cytochrome \( b_2 \) strongly restricts the unfolding activity of the mitochondrial import machinery in intact cells. It prevents import of a folded C-terminal domain and finally leads to retrograde translocation and accumulation of the mature sized protein in the cytosol. To further localize the sub mitochondrial sorting site of sorting of cytochrome \( b_2 \), we characterized a mutant form of the channel protein Tim23 and found that the Tim23-2 mutation suppressed the mis-sorting of a cytochrome \( b_2 \) fusion construct containing an altered sorting signal. Our results indicate a branching site of import pathways in the inner membrane Tim machinery, separating the import pathway of cytochrome \( b_2 \) from the general transport channel of matrix targeted proteins. We suggest that the sorting signal of cytochrome \( b_2 \) is recognized in close vicinity to Tim23.

MATERIALS AND METHODS

**Saccharomyces cerevisiae Strains and Construction of Plasmids**—For expression in yeast, the DNA constructs were cut from pGEM4 plasmids (29, 30) and transferred to the yeast expression plasmid pYE DP 1/8–10 (31). The poEM4 plasmids were cut by HindIII at the 3′-end of the inserts and filled with Klenow fragment, and a BglII linker was inserted. The inserts were subsequently released from the plasmids by cutting with EcoRI and BglII and inserted between the EcoRI and BamHI sites of the vector pYE DP 1/8–10. The plasmids were propagated in the yeast strain 334 (32). This strain has no glucose repression medium containing 3% glycerol to an evisiae—recognized in close vicinity to Tim23.

The presequences of the resulting constructs were sequenced. All DNA inserts were released from the plasmids by MscI–EcoRI and II and inserted between the EcoRI and BamHI sites of the vector pYE DP 1/8–10. The plasmids were propagated in the yeast strain 334 (32). This strain has no glucose repression medium containing 3% glycerol to an evisiae—recognized in close vicinity to Tim23.

**Expression and Localization of Cytochrome \( b_2 \) Constructs in S. cerevisiae**—Yeast cells were grown at 30 °C in selective synthetic complete medium containing 3% glycerol to an \( \Delta \) loci of 0.8–1.2. Galactose was added to a final concentration of 2% to induce the expression of the cytochrome \( b_2 \) fusion proteins. After 4 h of induction, ~20 mg of cells were collected by centrifugation and converted to spheroplasts by enzymolysis treatment as described previously (12). The suspension was divided into 5 aliquots, and the spheroplasts were reisolated by centrifugation (1 min, 16,000 \( \times \) g). Two aliquots were resuspended in 350 μl of cold permeabilization buffer (0.1 μM potassium acetate, 0.2 μM sorbitol, 2 mM MgCl₂, supplemented with 0.02 volumes of 1 mM HEPES-KOH, pH 7.2) to open the plasma membrane (“perm. SP”) (35). The permeabilized spheroplasts were reisolated by centrifugation (10 min, 16,000 \( \times \) g). Pellet and supernatant were separated and the proteins released to the supernatant were precipitated by 10% trichloroacetic acid in the presence of 0.05% sodium deoxycholate. One aliquot of the suspensions of spheroplasts was resuspended in 350 μl of EM buffer (1 mM EDTA, 10 mM MOPS-KOH, pH 7.2) to open the plasma membrane and the outer mitochondrial membrane (“swelling”). The spheroplasts of an additional aliquot were resuspended in EM buffer containing 1% Triton X-100 to lyse all organelles. The latter two samples and one of the samples with permeabilized spheroplasts were treated with protease K (50 μg/ml) to digest the cytochrome \( b_2 \) fusion proteins not protected by membranes. The fifth aliquot of spheroplasts was taken as a control and analyzed directly (“total SP”). Samples were resuspended in 100 μl of sample buffer, and portions of 40 μl were analyzed by SDS-PAGE and immunoblotting with antibodies directed against DHFR. Antibodies directed against the mitochondrial outer membrane protein Tom20 were used to control the fractionation procedure.

To compare the growth rate of different yeast strains (as shown in Fig. 2), the cells were first grown in liquid selective minimal medium at 28 °C containing 2% glucose. The cultures were diluted with Ringer’s solution and spotted on selective minimal medium plates containing 2% glucose or 2% glucose and 2% galactose. After 5 days at 28 °C, cells were scraped from the plates and again diluted with Ringer’s solution and spotted onto plates. Plates were incubated for 5 days at 28 °C.

**Import of Proteins into Isolated Mitochondria**—Yeast cells were grown in YPG medium (1% Bacto-yeast extract, 2% Bacto-peptone, 3% glycerol), and mitochondria were prepared according to published procedures (12). We used the strains PK82 (36), MB3 (WT, Ref. 37), and MB3–46 (tim23-2; Ref. 38). Radiolabeled preproteins were synthesized in rabbit reticulocyte lysate in the presence of [\( ^{35} \)S]Met (ICN Biomedicals Inc.) or in vitro transcription by SP6 RNA polymerase (AmbionCorp., Stratagene) and by coupled transcription/translation with T7 polylerase (Stratagene). Isolated yeast mitochondria (15–25 μg) were incubated with reticulocyte lysate containing the radiolabeled preprotein (5–10% of [\( ^{35} \)S]Met) in import buffer (3% bovine serum albumin (w/v)), 250 mM sucrose, 60 mM KCl, 5 mM MgCl₂, 5 mM sodium malate, 2 mM ATP, 20 mM potassium phosphate, 10 mM MOPS-KOH, pH 7.2) at 37 °C. Reactions were stopped by addition of 1 μl valinomycin and cooling on ice. Samples with a dissipated mitochondrial potential received valinomycin prior to incubation with preprotein. For generation of mitochondria, import reactions were diluted with 9 volumes of EM buffer and left on ice for 30 min. Control mitochondria were diluted with isotonic SEM buffer (EM buffer supplemented with 250 mM sucrose). Proteinase K treatment, resolation of mitochondria, and separation by SDS-PAGE or Tricine-SDS-PAGE have been described previously (39, 40). Autoradiographs were obtained and quantified using a storage PhosphorImaging system (Molecular Dynamics).

**Co-immunoprecipitations**—Specific antibodies were pre-bound to protein A-Sepharose (10 μl wet volume, Pharmacia Biotech Inc.) for 1 h in 480 μl of lysis buffer (1% digitonin (Merck, 1 x recrystallized from ethanol), 10% glycerol (w/v), 50 mM NaCl, 2 mM EDTA, 30 mM HEPES-KOH, pH 7.4). Import reactions were performed for 20 min with 25 μg of mitochondrial protein per lane and 20% of [\( ^{35} \)S]Met reticulocyte lysate. After resolation and washing with SEM buffer, mitochondria were resuspended in lysis buffer supplemented with protease inhibitors (2 μg/ml antipain, 5 μg/ml aprotinin, 0.25 μg/ml chymostatin, 1.25 μg/ml leupeptin, 0.5 μg/ml pepstatin A, 0.25 μg/ml soybean trypsin inhibitor) and shaken end-over-end for 10 min at 8 °C. Unsolubilized material was removed by ultracentrifugation (30 min at 100,000 \( \times \) g). The supernatants were incubated for 1 h at 8 °C by end-over-end shaking with antibodies prebound to protein A-Sepharose. After three washing cycles with lysis buffer, the protein A-Sepharose pellets were heated in sample buffer and applied to SDS-PAGE.

RESULTS

Localization of Different Cytochrome \( b_2 \) Constructs after Import in vivo—Gartner et al. (29) used three building blocks to monitor the sorting and unfolding pathway of cytochrome \( b_2 \) in isolated mitochondria (Fig. 1A) as follows: the bipartite presequence; the ~100-residue non-covalent heme binding domain (HB) of cytochrome \( b_2 \) that forms a tightly folded domain and strictly depends on the function of mtHsp70 for unfolding and translocation across the mitochondrial membrane (26, 41); and the mitochondrial targeting sequence (mTSS) of enzyme dihydrofolate reductase (DHFR) as passenger protein, the unfolding of DHFR requires only a low energy input and thus does not depend on functional mtHsp70 (29, 41). In the in vitro experiments, a heme binding domain located at the C terminus (pd-HDFR-HB) was not imported but got stuck in the mitochondrial import sites. When the intramitochondrial sorting signal was inactivated by deletion

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of a 19-residue segment, the resulting preprotein pb2-DHFR-HB was completely imported (29).

We now expressed the hybrid proteins (Fig. 1A) from a galactose-inducible vector in intact S. cerevisiae cells. To avoid indirect effects of the induction by galactose, a yeast strain with gal11 mutation was employed that cannot utilize galactose as carbon source and lacks a glucose repression of GAL expression (32). After a 4-h induction, cells were isolated and converted to permeabilized spheroplasts (Fig. 1B). We first analyzed two hybrid proteins with a complete presequence and DHFR at the C terminus; the heme binding domain was either directly adjacent to the presequence (pb2-HB-DHFR) or not included (pb2-DHFR). Both proteins were found in the organellar pellet of permeabilized spheroplasts (Fig. 1B, lanes 2 and 8) and protected against protease K (Fig. 1B, lanes 6 and 12) unless the membranes were disrupted with detergent (Fig. 1B, lanes 5 and 11). In a hypotonic buffer (to swell mitochondria and open the intermembrane space), both proteins became accessible to added protease (Fig. 1B, lanes 4 and 10). pb2-HB-DHFR was efficiently processed to the mature sized form (Fig. 1B, lane 1), whereas pb2-DHFR was observed in both the intermediate sized form and the mature sized form (Fig. 1B, lane 7). A slower processing of pb2-DHFR has also been observed in vivo import experiments (29) and may be attributed to a lack of most sequences of mature cytochrome b2. No precursor sized forms of the hybrid proteins were observed. These results indicate an efficient import of the proteins into mitochondria and a correct sorting to the intermembrane space in vivo.

We then studied the localization of the construct pb2-DHFR-HB (Fig. 1B, lanes 13–18). This protein was efficiently processed to the mature sized form; only minute amounts of precursor or intermediate sized forms were observed (Fig. 1B, lane 13). However, the processed protein was mainly found in the cytosolic fraction (Fig. 1B, lane 15) and not protected against proteinase K in permeabilized spheroplasts (Fig. 1B, lane 18). A placement of the heme binding domain at the C terminus of a hybrid protein thus reveals a striking effect on its cellular sorting and prevents a complete import into mitochondria. We will address below (see Fig. 3) the mechanism how a processed protein can be found in the cytosolic fraction.

When the cytochrome b2 sorting signal was inactivated, the resulting hybrid protein pb2-DHFR-HB was found in the organellar fraction (Fig. 1B, lanes 20 and 24). It remained protease-protected also in swollen mitochondria (Fig. 1B, lane 22), demonstrating it was transported across the inner membrane.

These results indicate that pb2-HB-DHFR, pb2-DHFR, and pb2-DHFR-HB were correctly sorted into mitochondria in vivo comparable to the situation in vitro. Mis-sorting of the hybrid protein depends on both the presence of the heme binding domain at the C terminus and an intact sorting signal (pb2-DHFR-HB). To determine the effect on the viability of yeast cells, we expressed the hybrid proteins permanently by grow-
Yeast cells containing the empty vector pYE DP 1/8–10 (−) or the vector with an inserted cytochrome b2 construct (b2-DHFR-HB, b2-DHFR, see Fig. 1A) were grown on selective minimal medium plates containing 2% glucose (Glucose) or 2% glucose and 2% galactose (Galactose) for 5 days at 28 °C. Expression of the hybrid proteins is induced in the presence of galactose.

While pb2-DHFR-HB and pb2-DHFR did not affect cellular growth, cells expressing pb2-DHFR-HB grew poorly. The mis-sorting of pb2-DHFR-HB is thus accompanied by an inhibitory effect on cellular viability.

**Fig. 2. Growth of yeast strains expressing different b2-DHFR constructs.** Yeast cells containing the empty vector pYE DP 1/8–10 (−) or the vector with an inserted cytochrome b2 construct (b2-DHFR-HB, b2-DHFR, see Fig. 1A) were grown on selective minimal medium plates containing 2% glucose (Glucose) or 2% glucose and 2% galactose (Galactose) for 5 days at 28 °C. Expression of the hybrid proteins is induced in the presence of galactose.

**Fig. 3. Import of b2-DHFR hybrid proteins into isolated mitochondria.** A, b2-DHFR-HB is released into the supernatant after processing inside mitochondria. Mitochondria were isolated from a yeast wild-type strain. The hybrid proteins pb2-DHFR-HB and pb2-DHFR (see Fig. 1A) were synthesized in reticulocyte lysate in the presence of [35S]methionine and incubated with isolated mitochondria for 10 min at 12 °C for accumulation in import sites of the mitochondrial membranes (Import). After reisolation, the mitochondria were resuspended in import buffer and incubated for 15 min at 30 °C (Chase). Samples were divided into halves, and one-half was treated with proteinase K (Prot. K). After reisolation of the mitochondria by centrifugation, the mitochondrial pellets (Pel.) and the supernatants (Sup.) were analyzed by SDS-PAGE and autoradiography. i, processing intermediate; m, mature protein. B, time course of the release of b2-DHFR-HB from mitochondria. The experiment was performed as in A, varying the time of chase. The total amount of m-b2-DHFR-HB (pellet + supernatant) present after 60 min of chase was set to 100% (control).
Association of Cytochrome \( b_2 \) Fusion Proteins with the Inner Membrane Translocase Protein Tim23—If the cytochrome \( b_2 \) sorting signal is arrested in the mitochondrial inner membrane, it should be possible to demonstrate interactions of translocation intermediates with distinct components of the inner membrane protein import machinery. By co-immunoprecipitation, we first tested for association of preproteins with Tim23. The following hybrid proteins were used: \( b_2 \)-DHFR with a fully functional cytochrome \( b_2 \) presequence; \( b_2^* \)-DHFR with a partial inactivation of the sorting signal by replacing two positively charged residues (lysine 48 and arginine 49) by uncharged residues (Fig. 4A), the resulting hybrid protein is mistargeted into the matrix space (see below, Fig. 6B) (20, 27); and \( b_2^\Delta \)-DHFR-HB with a complete inactivation of the sorting signal (due to the 19-residue deletion). The hybrid proteins were accumulated in mitochondrial import sites and processed to the intermediate sized form. All three hybrid proteins were found in association with Tim23 (Fig. 4B, lanes 2, 7 and 12), suggesting that cytochrome \( b_2 \) remains in contact with Tim23 irrespective of an alteration (\( b_2^* \)-DHFR) or partial deletion (\( b_2^\Delta \)-DHFR-HB) of the sorting sequence. At least in this stage of translocation, cytochrome \( b_2 \) seems to be imported by the general import channel of matrix targeted proteins. Tim23 is suggested to participate in the constitution of this protein translocation channel (38, 42–48).

Association of Cytochrome \( b_2 \) Fusion Proteins with \( mtHsp70 \)—In parallel, we tested for the interaction of the fusion proteins with \( mtHsp70 \) (Fig. 4B, lanes 4, 9, and 14). Of the three constructs tested, only \( b_2^* \)-DHFR and \( b_2^\Delta \)-DHFR-HB were co-immunoprecipitated in significant amounts. \( b_2 \)-DHFR was only precipitated in minor amounts that were close to the level observed with preimmune serum (Fig. 4B, lane 4 versus lane 1). We conclude that in \( b_2 \)-DHFR the intact sorting signal of cytochrome \( b_2 \) prevents stable binding of the translocation intermediate to \( mtHsp70 \). With \( b_2^* \)-DHFR and \( b_2^\Delta \)-DHFR-HB, \( mtHsp70 \) can gain access to additional segments of the polypeptide chains (Fig. 4B, lanes 9 and 14) that are not accessible when the authentic sorting sequence is present (Fig. 4B, lane 4). \( Tim44 \) serves as a membrane anchor for \( mtHsp70 \) (49–51). No significant association with \( Tim44 \) was observed with either of the three constructs (Fig. 4B, lanes 3, 8, and 13). This result is in agreement with our recent observation that \( Tim44 \) is a component of a separate subcomplex of the import machinery that only transiently interacts with the Tim23-Tim17 core complex (11).

Preprotein Sorting in \( tim23-2 \) Mutant Mitochondria—The yeast mutant \( tim23-2 \) is impaired in preprotein translocation into the mitochondrial matrix \textit{in vivo} and \textit{in vitro} (38, 52). We used \( tim23-2 \) mitochondria to characterize preprotein sorting to the intermembrane space in dependence of the function of the inner membrane Tim machinery. We first tested the stability of the Tim23-Tim17 core complex (44, 46, 47) by co-immunoprecipitations with antibodies against Tim23. The total amounts of Tim23 and Tim17 were comparable between wild-type and mutant mitochondria; however, the stability of the complex with Tim17 was reduced in the \( tim23-2 \) mutant (Fig. 5A). The membrane potential of the mutant mitochondria was intact (not shown). The amounts of \( Tim44 \) and \( mtHsp70 \) were the same in the mitochondria of both strains (Fig. 5A, samples 5 and 6).

We next analyzed the import kinetics of two mitochondrial preproteins, cytochrome \( b_2 \) and the iron/sulfur protein of complex III of the respiratory chain (Rieske Fe/S protein), which are “classical” preproteins in the analysis of mitochondrial sorting pathways. The Fe/S protein is completely imported into the matrix and then exported across the inner membrane to its functional destination (38, 52). We used \( tim23-2 \) mitochondria to characterize preprotein sorting to the intermembrane space in dependence of the function of the inner membrane Tim machinery. We first tested the stability of the Tim23-Tim17 core complex (44, 46, 47) by co-immunoprecipitations with antibodies against Tim23. The total amounts of Tim23 and Tim17 were comparable between wild-type and mutant mitochondria; however, the stability of the complex with Tim17 was reduced in the \( tim23-2 \) mutant (Fig. 5A). The membrane potential of the mutant mitochondria was intact (not shown). The amounts of \( Tim44 \) and \( mtHsp70 \) were the same in the mitochondria of both strains (Fig. 5A, samples 5 and 6).
was synthesized in reticulocyte lysate in the presence of [35S]methionine and imported into wild-type (WT) or tim23-2 mitochondria at 25 °C for the times indicated. In lanes 4 and 8 the membrane potential was dissipated prior to import by including 1 μM valinomycin (Δψ). Import reactions were stopped by addition of valinomycin. All samples were treated with proteinase K (50 μg/ml) to remove non-imported proteins. The mitochondria were reisolated and analyzed by SDS-PAGE and transferred to nitrocellulose. Radiolabeled cytochrome b2*-DHFR and b2*-HB-DHFR were imported into wild-type or tim23-2 mitochondria for 30 min at 25 °C as in A. Import was stopped, and mitochondria were divided into halves. One-half was diluted with cold SEM buffer and left on ice. The other half was subjected to hypotonic swelling and treated with valinomycin. All samples were treated with proteinase K for 30 min. Reisolated mitochondria were washed and proteins were separated by SDS-PAGE and transferred to nitrocellulose. Radiolabeled cytochrome b2*- proteins were analyzed by autoradiography. The amount of endogenous marker proteins (mtHsp70, cytochrome b2) was determined on the same blots by immunodecoration. p, precursor protein; i, processing intermediate; m, mature protein.

shown with the level of mtHsp70 (Fig. 6B, column 1). Import of b2*-DHFR (Fig. 6B, column 3) and b2*-HB-DHFR (Fig. 6B, column 6) behaved like mtHsp70, indicating that they were mistargeted into the matrix.

With tim23-2 mitochondria, however, both constructs were processed further to the mature sized forms (Fig. 6A, lanes 5–7). 30–40% of the imported proteins were processed to the mature forms. The mature forms were protected against proteinase K in intact mitochondria (Fig. 6A, lanes 5–7) but became accessible to the protease after opening of the outer membrane (Fig. 6B, columns 5 and 8). mb2*-DHFR and mb2*-HB-DHFR thus fractionated like mature cytochrome b2, indicating that they were correctly sorted to the intermembrane space in the mutant mitochondria. The processing to the mature forms was abolished by a dissipation of the inner membrane potential (Δψ), demonstrating that it strictly depended on the insertion of the preproteins into the inner membrane.

We conclude that the defect in Tim23 suppresses the sorting defect caused by the amino acid alteration in the pressequence of cytochrome b2.

DISCUSSION

We have characterized the sorting of cytochrome b2 in vivo and in organello and present evidence that its import route...
branches early from the general matrix targeting pathway.

A cytochrome b$_2$ construct with a C-terminal heme binding domain, which is able to form a tightly folded structure (26, 29, 41), cannot be completely imported into mitochondria in vivo. It is processed to the intermediate sized form and, after longer import times, to the mature form. The mature form is then released from the mitochondria and found in the cytosol. Due to the long accumulation in mitochondrial import sites, expression of this preprotein causes a growth defect of intact yeast cells. To translocate the heme binding domain across the mitochondrial membranes, the domain either has to be placed close to the presequence or the sorting signal in the presequence has to be inactivated. In the first case, an interaction of mtHsp70 with the N-terminal portion of the presequence generates a pulling force on the heme binding domain during its entry into/across the outer membrane (29). In the latter case, the preprotein lacking the sorting information is completely imported into the matrix and thus is continuously pulled in by the mtHsp70-driving system. The in vivo experiments show here strongly support the validity of the in vitro import studies published previously (29) which demonstrated that a C-terminal heme-binding domain cannot be imported, indicating that the sorting pathway of cytochrome b$_2$ diverges early from the matrix import pathway (and the mtHsp70-dependent unfolding machinery).

The in vivo import studies bear an important implication on the role of preprotein folding in the cytosol during mitochondrial protein import. Since the heme binding domain located at the C terminus prevents mitochondrial import of a cytochrome b$_2$ construct with a high efficiency (more than 80%), it is most likely that the domain is folded in intact cells as has been observed in the in vitro import system (29). This implies that the 100-residue domain is completely synthesized before translocation into mitochondria, i.e. its import occurs by a post-translational mechanism. Wienhues et al. (55) used the cytosolic enzyme DHFR as passenger protein and a stabilization of its folding by an externally added ligand (aminopterin) to demonstrate a post-translational import mechanism for ~75% of the passenger proteins. With the heme binding domain, we present the first case of an authentic mitochondrial domain that is apparently folded in the cytosol. It has been discussed that mitochondrial protein import occurs mainly co-translationally in vivo (56), and thus preprotein folding should not be relevant. Moreover, cytosolic chaperone proteins could interfere with and prevent folding of protein domains (57, 58). The results of Wienhues et al. (55) and this study, however, provide strong evidence for a post-translational mechanism of mitochondrial protein import.

It has been discussed for many years whether the sorting signal of cytochrome b$_2$ functions during the import reaction by arrest in the inner membrane or whether it requires complete transport into the matrix and becomes functional in a subsequent re-export step (59, 60). In addition to the in vivo results, we show that a mutation affecting a component of the central core of the preprotein translocase in the inner mitochondrial membrane (Tim23) facilitates the recognition of the cytochrome b$_2$ sorting signal. If the cytochrome b$_2$ sorting signal had already left the inner membrane and moved into the matrix to engage a separate export machinery, a further movement of the polypeptide should not be facilitated by structures that had been left behind. If the sorting function were carried out by an independent export system, it is difficult to explain why a mutation of TIM23 should facilitate a subsequent sorting step. The findings reported here thus favor an early recognition of the sorting signal during the entry into the inner membrane. They do not necessarily imply that Tim23 itself recognizes the sorting signal, but Tim23 seems to mark the location where the sorting signal leaves the general matrix import route and moves into a separate branch directed toward the intermembrane space. The mutant Tim23 protein may delay the movement of the modified sorting signal across the inner membrane and thereby reestablish the translocation arrest of cytochrome b$_2$ constructs with a partially inactivated sorting signal. The weakened stability of the Tim23-Tim17 interaction in the tim23-2 mutant mitochondria may facilitate lateral release of the sorting signal from the translocation channel.

An inner membrane localization of the branching site of import pathways is further corroborated by the characterization of translocation intermediates. We find that, after processing to the intermediate sized form, cytochrome b$_2$ is stably inserted in the inner membrane and associates with Tim23 without involvement of mtHsp70 (30, 61; data not shown), in contrast to other proteins that require mtHsp70 to prevent release from the import machinery (62). Tokatlidis et al. (63) recently identified Tim11 as an inner membrane protein that is in close contact to the cytochrome b$_2$ sorting signal during its import and sorting. The authors similarly concluded that the branching of import pathways occurs at the inner membrane. However, the precise function of Tim11 in this process is not yet clear (64). It has been proposed that the biogenesis of cytochrome b$_2$ involves an interaction of the mature part of the protein with the Tim machinery (23, 29, 65). The efficient release of the mature sized cytochrome b$_2$ construct into the cytosol in vivo suggests that such an interaction with the Tim machinery is only transient and of limited stability.

The principle of conservative sorting via the matrix space was originally described for the Rieske Fe/S protein (53). If cytochrome b$_2$ followed a different import pathway, both proteins should reveal differences in the import into mitochondria of the tim23-2 mutant. In fact, the results of our import experiments are in agreement with this prediction. Processing of cytochrome b$_2$ to the intermediate and to the mature protein was not affected in tim23-2 mutant mitochondria. In contrast, the Fe/S protein was only poorly processed to the intermediate form in tim23-2 mitochondria. We conclude that the biogenesis of the Fe/S protein requires transport of the preprotein into the mitochondrial matrix that depends on the intact Tim23-Tim17 complex. The tim23-2 mutation thus reveals a striking difference between the sorting pathways of cytochrome b$_2$ and the Fe/S protein.

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