Biogenesis of Porin of the Outer Mitochondrial Membrane Involves an Import Pathway via Receptors and the General Import Pore of the TOM Complex

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Abstract. Porin, also termed the voltage-dependent anion channel, is the most abundant protein of the mitochondrial outer membrane. The process of import and assembly of the protein is known to be dependent on the surface receptor Tom20, but the requirement for other mitochondrial proteins remains controversial. We have used mitochondria from Neurospora crassa and Saccharomyces cerevisiae to analyze the import pathway of porin. Import of porin into isolated mitochondria in which the outer membrane has been opened is inhibited despite similar levels of Tom20 as in intact mitochondria. A matrix-destined precursor and the porin precursor compete for the same translocation sites in both normal mitochondria and mitochondria whose surface receptors have been removed, suggesting that both precursors utilize the general import pore. Using an assay established to monitor the assembly of in vitro–imported porin into preexisting porin complexes we have shown that besides Tom20, the biogenesis of porin depends on the central receptor Tom22, as well as Tom5 and Tom7 of the general import pore complex (translocase of the outer mitochondrial membrane [TOM] core complex). The characterization of two new mutant alleles of the essential pore protein Tom40 demonstrates that the import of porin also requires a functional Tom40. Moreover, the porin precursor can be cross-linked to Tom20, Tom22, and Tom40 on its import pathway. We conclude that import of porin does not proceed through the action of Tom20 alone, but requires an intact outer membrane and involves at least four more subunits of the TOM machinery, including the general import pore.

Key words: mitochondria • protein sorting • porin • Neurospora crassa • Saccharomyces cerevisiae

Introduction

Most mitochondrial precursor proteins are encoded by nuclear genes, synthesized on cytosolic ribosomes and imported into the organelle via the action of complexes comprised of multisubunit translocases in the outer (TOM) and the inner (TIM) mitochondrial membranes (Neupert, 1997; Pfanner et al., 1997; Jensen and Johnson, 1999; Koehler et al., 1999; Bauer et al., 2000). The TOM complex contains surface receptors for the specific recognition of precursor proteins and a general import/insertion pore (GIP) that mediates translocation of precursor proteins into or across the outer membrane. The surface receptors Tom70, Tom22, and Tom20 expose large domains to the cytosol. Precursor proteins are initially recognized by

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Tom20 or Tom70 and are transferred to the central receptor Tom22. The pore-forming component Tom40 and the three small Tom proteins Tom7, Tom6, and Tom5 are integrally embedded in the mitochondrial outer membrane. Together with Tom22, the latter four Tom proteins form the stable ~400-kD core of the outer membrane translocase, termed the TOM complex or GIP complex (Dekker et al., 1998; Hill et al., 1998; Künkele et al., 1998; Ahlting et al., 1999; van Wilpe et al., 1999). Matrix-destined precursors are targeted to mitochondria by a cleavable NH2-terminal presequence, which initially interacts with the receptors of the TOM complex. However, many mitochondrial precursors destined for the inner membrane, the intermembrane space, or the outer membrane are targeted to mitochondria without the aid of a presequence. In several of these proteins such as Tom70 (McBride et al., 1992), Tom22 (Rodriguez-Cousino et al., 1998), BCS1 (Fölsch et al., 1996), and cytochrome c heme lyase (CCHL) (Diekert et al., 1999), a mitochondrial targeting/assembly signal has been identified within the sequence of the mature protein.

Porin, also known as voltage-dependent anion-selective channel (VDAC), is the most abundant protein of the mitochondrial outer membrane and is imported without the aid of a presequence. It is predicted to exist as a β barrel structure similar to its bacterial counterparts (Benz, 1989; Mannella et al., 1996) and forms a pore that allows the passage of small molecules across the membrane. Attempts to characterize possible targeting signals in the porin precursor protein have identified certain residues and regions of the proteins that are involved in its assembly (Hamajima et al., 1988; Smith et al., 1994; Court et al., 1996). However, very little is known about the mechanism whereby the highly structured porin protein is imported and properly assembled in the membrane. Although there is no doubt that the import of mitochondrial porin requires the surface receptor Tom20 (Kleine et al., 1987; Pfäffer and Neupert, 1987; Söllner et al., 1989; Harkness et al., 1994; Schleiff et al., 1997, 1999), the involvement of other mitochondrial factors, including other Tom proteins and the GIP complex, is a subject of debate. On one hand, the import of precursors destined to various mitochondrial compartments could be inhibited by chemical amounts of water-soluble porin at a stage in the import pathway beyond the protease-accessible binding sites. It has been suggested that porin utilizes components of the GIP complex of the outer membrane (Pfäffer et al., 1988; Hönlinger et al., 1996; Dietmeier et al., 1997; van Wilpe et al., 1999). On the other hand, Schleiff et al. (1999) have recently reported that Tom20 alone is sufficient for the insertion and assembly of porin into mitochondria and lipid vesicles. Blocking of the mitochondrial import pore as well as mutations in Tom40 did not inhibit the import of porin. Schleiff et al. (1999) thus proposed a new mechanism of mitochondrial protein import whereby the receptor Tom20 directly catalyzes the insertion and assembly of porin into the outer membrane. The novel mechanism proposed by Schleiff et al. (1999) raises substantial doubts not only about previous studies on the import of porin (Hönlinger et al., 1996; Dietmeier et al., 1997; van Wilpe et al., 1999) but also on the concept of the GIP in general since water-soluble porin was used as the model precursor protein to define the GIP (Pfäffer et al., 1988).

A clarification of the import pathway of porin will thus be of fundamental importance for our understanding of mitochondrial protein import. In the present study, we performed a detailed characterization of porin import in Neurospora crassa and the yeast Saccharomyces cerevisiae to directly determine the role of GIP and individual Tom proteins in import of porin. We have established an assay specific for the assembly of porin imported into isolated yeast mitochondria. Using a collection of mutant mitochondria, competition of precursor proteins for GIP, and cross-linking of porin in transit, we demonstrate that Tom20 alone is not sufficient for porin import. The physiological biogenesis pathway of porin into mitochondria involves several different Tom proteins including the pore Tom40.

### Materials and Methods

**Neurospora Strains and Media**

Growth and handling of *N. crassa* were as described in Davis and De Serres (1970). Strains used in this study were 74-OR23-1 (A), 76-26 (a, his-3, mtrR), and 861 (a, his-3, mtrR, tom22::hygR, tom22* [ectopic copy]). The *tom22* allele contains mutations resulting in several amino acid substitutions in its cytosolic domain (Nargang et al., 1998). The outer mitochondrial membrane of the 861 strain is easily broken during standard mitochondrial isolation procedures.

**Yeast Strains and Media**

The *S. cerevisiae* strains used here are listed in Table I. Cells were grown on YPG (1% [wt/vol] yeast extract, 2% [wt/vol] bactopeptide, 3% [wt/vol] glycerol) or YPD (1% [wt/vol] yeast extract, 2% [wt/vol] bactopeptide, 2% [wt/vol] dextrose) as described (Daum et al., 1982).

### Table I. *S. cerevisiae* Strains Used in This Study

| Strain | Genotype | Reference |
|-------|----------|-----------|
| YPH499 (WT) | MATa ade2-101 his3-Δ200 leu2-Δ1 ura3-52 trp1-Δ63 lys2-801 | Sikorski and Hieter, 1989 |
| MM112-C (tom20A) | MATa ade2-101 his3-Δ200 leu2-Δ1 ura3-52 trp1-Δ63 lys2-801 tomo2::URA3 (Ycp13-TOM22) | Moczko et al., 1994; Hönlinger et al., 1995; Dekker et al., 1998 |
| AH101 (tom7A) | MATa ade2-101 his3-Δ200 leu2-Δ1 ura3-52 trp1-Δ63 lys2-801 tom7::TRP1 | Hönlinger et al., 1996; van Wilpe et al., 1999 |
| O1201 (tom22A) | MATa his3-Δ200 leu2-Δ1 ura3-52 trp1-Δ63 tom22::HIS3 rho0 | Diekert et al., 1997 |
| KD56 (tom5Δ) | MATa ade2-101 his3-Δ200 leu2-Δ1 ura3-52 trp1-Δ63 lys2-801 tom5::HIS3 | Alconada et al., 1995 |
| MM307 (tom6Δ) | MATa ade2-101 his3-Δ200 leu2-Δ1 ura3-52 trp1-Δ63 lys2-801 tom6::URA3 | Blachly-Dyson et al., 1990, 1997 |
| M3 (WT) | MATa lys2 his4 trpl ade2 leu2 ura3 | Blachly-Dyson et al., 1990, 1997 |
| M22-2 (portΔ) | MATa lys2 his4 trpl ade2 leu2 ura3 port1::LEU2 | Blachly-Dyson et al., 1990, 1997 |
| M23-2 (portΔ) | MATa lys2 his4 trpl ade2 leu2 ura3 port2::TRP1 | Blachly-Dyson et al., 1997 |
| KKY3 | MATa his3-Δ200 leu2-3,112 ade2-101 suc2-Δ9 trpl::HIS3 (pRS16-TOM40) | Kassenbrock et al., 1993 |
| KKY3.2 (TK3) (tom40-2) | MATa his3-Δ200 leu2-3,112 ade2-101 suc2-Δ9 trpl::HIS3 (pRS314-tom40-2) | Kassenbrock et al., 1993 |
| KKY3.3 (TK4) (tom40-3) | MATa his3-Δ200 leu2-3,112 ade2-101 suc2-Δ9 trpl::HIS3 (pRS314-tom40-3) | Kassenbrock et al., 1993 |
| KKY3.4 (TK5) (tom40-4) | MATa his3-Δ200 leu2-3,112 ade2-101 suc2-Δ9 trpl::HIS3 (pRS314-tom40-4) | Kassenbrock et al., 1993 |
| KKY3.7 (TK8) (WT) | MATa his3-Δ200 leu2-3,112 ade2-101 suc2-Δ9 trpl::HIS3 (pRS314-TOM40) | This study |
The strains KKY3.2, KKY3.3, and KKY3.4 carry *tom*θ alleles on the plasmid pRS314, whereas the chromosomal copy of *TOM40* has been deleted (Kassenbrock et al., 1993). All mutant alleles were analyzed by DNA sequencing and found to contain several independent mutations. To generate a corresponding wild-type strain (KKY3.7) that similarly expresses *TOM40* from the plasmid, a PCR product of *TOM40* including 334 bp upstream and 345 bp downstream of the *TOM40*-ORF as well as additional restriction sites for XhoI (3' end) and BamHI (5' end) was inserted into XhoI/BamHI cut pRS314 and transferred into KKY3.5 by 5-fluoro-orotic acid–based plasmid shuffling.

**Protein Import into Isolated Mitochondria**

The procedures for standard isolation of *N. crassa* mitochondria (Pfanner and Neupert, 1985) and in vitro import of radiolabeled mitochondrial precursors (Harkness et al., 1994) using trypsin pretreatment in control lanes (Mayer et al., 1993) were as described. In some experiments, chemical amounts of a chimeric precursor were used. The chimeric precursor consists of the NH2-terminal 69 amino acids of the presequence for *N. crassa* ATPase subunit 9 fused to the coding sequence of mouse dihydrofolate reductase (DHFR) (pSu9-DHFR) (Pfanner et al., 1987). The fusion protein with a hexahistidinyl tag at the COOH terminus (pSu9[1–69]-DHFR-his6) was purified by Ni-NTA affinity chromatography from extracts of the *E. coli* strain BL21 carrying the pQE60-pSu9(1–69)-DHFR-his, overexpression vector. Yeast mitochondria were isolated according to published methods (Daum et al., 1982; Rassow, 1999), resuspended in SEM buffer (250 mM sucrose, 1 mM ethylenediaminetetraacetic acid [EDTA], 10 mM morpholinopropanesulfonic acid [MOPS]-KOH, pH 7.2) to a final concentration of 250 μM hexahistidinyl tag at the COOH terminus (pSu9[1–69]-DHFR-his6) was purified by Ni-NTA affinity chromatography from extracts of the *E. coli* strain BL21 carrying the pQE60-pSu9(1–69)-DHFR-his, overexpression vector.

**Assessment of Mitochondrial Outer Membrane Integrity**

Samples of the *N. crassa* mitochondria isolated for import experiments were used to assess outer membrane integrity. The mitochondria (30 μg) were suspended in 100 μL of SEM buffer and incubated with proteinase K (120 μg/ml) at 0°C for 15 min. The reactions were stopped by direct addition of PMSF to a final concentration of 5 mM. Proteins were immediately precipitated with trichloroacetic acid, pelleted by centrifugation, washed with 1 ml of acetone, air dried, suspended in cracking buffer (62.5 mM Tris-HCl, pH 6.8; 2.5% [wt/vol] SDS; 5% [vol/vol] β-mercaptoethanol; 5% [wt/vol] sucrose), and boiled for 5 min. Samples were separated by SDS-PAGE, blotted onto nitrocellulose, and proteins from different mitochondrial compartments were detected using specific antisera. The susceptibility of the intermembrane space protein CCHL to protease K digestion was used as an indicator of outer membrane integrity.

**Blue Native–PAGE**

Blue native (BN)–PAGE was performed as described previously (Schägger and von Jagow, 1991; Schägger et al., 1994; Dekker et al., 1997). In brief, mitochondrial pellets from import reactions (50 μg of protein) were lysed in 45 μl cold digitonin buffer (1% [wt/vol] digitonin, 20 mM Tris-HCl, pH 7.4, 0.1 mM EDTA, 50 mM NaCl, 10% [vol/vol] glycerol, 1 mM PMSF) by carefully resuspending 10 times and incubating for 10 min on ice. After separation on an insoluble material through a clarifying spin (15 min, 16,000 g), 5 μl of sample buffer was added (5% [wt/vol] Coomassie brilliant blue G-250, 100 mM bis-tris, pH 7.0, 500 mM e-aminoacapric acid), and the samples were electrophoresed through a 6–16% polyacrylamide gradient gel at 4°C. The gel was then either stained with Coomassie brilliant blue G-250 and dried, or proteins were transferred onto PVDF membranes by semidy blotting.

**Cross-Linking and Immunoprecipitation**

For cross-linking experiments, radiolabeled precursor was incubated with isolated outer membrane vesicles (OMVs) that were prepared according to Mayer et al. (1993) from *N. crassa* strain 74-OR-1A. After an initial incubation for 2 min on ice, the cross-linking reagent disuccinimidyl glutarate (DSG) (Pierce Chemical Co.) was added for 40 min at 0°C. Excess cross-linker was quenched by the addition of 80 mM glycine (pH 8.0) and incubation for 15 min at 0°C. OMVs were resuspended by centrifugation (20 min, 225,000 g), and aliquots, from before and after addition of the cross-linking reagent, were analyzed. For immunoprecipitation, samples that were incubated with DSG were dissolved in lysis buffer (1% [wt/vol] SDS, 0.5% Triton X-100, 150 mM NaCl, 10 mM Tris-HCl, pH 7.2) and incubated for 5 min at 25°C. The lysed material was diluted 40-fold with lysis buffer lacking SDS and subjected to a clarifying spin (15 min, 20,000 g). The supernatant was incubated with antibodies that were coupled to protein A–Sepharose beads.

**Miscellaneous Methods**

Separation of mitochondrial proteins by SDS-PAGE (Laemmli, 1970) and determination of mitochondrial protein concentration (Bradford, 1976) were performed using previously published procedures. Synthesis and radiolabeling of mitochondrial precursor proteins was performed with rabbit reticulocyte lysate (Amersham Pharmacia Biotech) or the TNT-coupled reticulocyte lysate system (Promega) (Rassow, 1999). Carbonate extraction was performed using a published protocol (Honlinger et al., 1996). Western blotting was performed as previously described (Harlow and Lane, 1999), and, after immunodecoration, proteins were detected by a chemiluminescent system. Bands from autoradiographs were quantified by using a Bio-Rad imaging densitometer (GS-670) and a Molecular Dynam-
sence (A) or presence (B) of 208 rophenylhydrazone were incubated for 15 min at 0
C into two, and one half was incubated for 10 min at 0
C with 3.2
M carbonyl cyanide m-chlorophenylhydrazone were incubated for 15 min at 0°C in the absence (A) or presence (B) of 20 µg/ml trypsin. After inactivation of the trypsin by soybean trypsin inhibitor, each sample was split into two, and one half was incubated for 10 min at 0°C with 3.2
M pSu9(1–69)-DHFR. Radiolabeled porin precursor was then added and further incubated at 15°C (A) or 25°C (B) for the indicated periods. At the end of the import reactions proteinase K (100 µg/ml) was added, proteins were analyzed by SDS-PAGE, and imported porin was quantified.

A

Figure 2. Insertion of porin is inhibited by blocking the translocation pore with import intermediates. N. crassa mitochondria (30 µg protein per import reaction) in import buffer containing 2 mM NADH, 2 mM ATP, and 37 µM carbonyl cyanide m-chlorophenylhydrazone were incubated for 15 min at 0°C in the absence (A) or presence (B) of 20 µg/ml trypsin. After inactivation of the trypsin by soybean trypsin inhibitor, each sample was split into two, and one half was incubated for 10 min at 0°C with 3.2
M pSu9(1–69)-DHFR. Radiolabeled porin precursor was then added and further incubated at 15°C (A) or 25°C (B) for the indicated periods. At the end of the import reactions proteinase K (100 µg/ml) was added, proteins were analyzed by SDS-PAGE, and imported porin was quantified.

B

Results

Reduction of Porin Import into Mitochondria with a Fragile Outer Membrane

The mitochondrial outer membrane of certain mutant strains of N. crassa is easily broken during standard mitochondrial isolation procedures (Nargang et al., 1998; Grad et al., 1999). In such mitochondria, we found that most precursor proteins were imported with the same efficiency as in mitochondria with intact outer membranes. An exception was the precursor of porin, which was imported at reduced levels. This is shown in Fig. 1 A where mitochondria, isolated by standard procedures from a control strain (WT) and a tom22 mutant strain susceptible to opening of the outer membrane during isolation under standard conditions (tom22861) (Nargang et al., 1998), were used to assess the import of the precursors of the β subunit of the mitochondrial ATPase (F1β) and porin. The import of F1β was virtually indistinguishable in the two strains, whereas porin import was significantly reduced in the mutant. Quantification of the levels of import in tom22861 relative to the control strain in three separate experiments gave averages of 91% for F1β and 34% for porin.

To examine mitochondria for outer membrane damage in the preparations used for the import experiments, we determined the levels of proteins from different mitochondrial compartments after the addition of proteinase K. The level of the soluble intermembrane space protein, CCHL, served as a measure for the degree of damage to the outer membrane. Broken outer membranes allow access of externally added proteinase K to the intermembrane space, thereby reducing the amount of CCHL. As shown in the upper panel of Fig. 1 C, the level of CCHL in control mitochondria was virtually unaffected by added proteinase K (13% reduction), whereas in mutant mitochondria the proteinase had a much greater effect (53% reduction). These data demonstrate that little or no damage has occurred to the outer membrane of the control mitochondria, whereas the integrity of the outer membrane in the mutant mitochondria isolated under standard conditions was considerably reduced. The level of a matrix protein, mtHsp70, was unaffected by treatment of mitochondria with proteinase K in both strains, indicating that the inner membrane was intact (Fig. 1 C, second panel). The large hydrophilic domain of the Tom20 receptor protein is exposed to the cytosol and its digestion to characteristic proteolytic fragments (Tom20') serves as a control for the effectiveness of the proteinase digestion in both strains (Fig. 1 C, third panel). Levels of the outer membrane proteins Tom20 and porin (Fig. 1 C, lower panel) were similar in the control mitochondria and the damaged mutant mitochondria, confirming that no significant amount of the outer membrane was lost during isolation of mitochondria from the mutant strain. Therefore, the increased accessibility of the intermembrane space protein CCHL to proteinase K is due only to breaks in the membrane that made the compartment more accessible. Exposure of isolated mitochondria to proteinase K had no effect on endogenous porin levels in either strain, showing that once integrated into the outer membrane the protein was fully protected, even in the mitochondria of tom22861. Direct examination of the import blots for porin levels (Fig. 1 B) verified this observation. Thus, the observed decrease in import of radiolabeled porin cannot be attributed to enhanced degradation of imported porin molecules in mitochondria containing opened outer membranes by the proteinase K treatment that follows the import reaction. We conclude that other mitochondrial factors in addition to Tom20 are required for high efficiency import of porin.

A Matrix-destined Precursor Protein and the Porin Precursor Compete for the Same Translocation Sites

To investigate the role of TOM complex components in porin insertion, we added excess amounts of a matrix-destined precursor protein to saturate import sites and then evaluated the effect on the import of porin into mitochon-
and the signals were detected by chemiluminescence. (Ass. Porin) Complexes of assembled porin. (C) Wild-type mitochondria (50 μg protein) were treated with sodium carbonate, and the membrane pellet was subjected to BN-PAGE and immunodecoration with antibodies against porin (lane 2). Nontreated mitochondria are shown as control (lane 1).

dria in vitro. Chemical amounts of a fusion protein consisting of the presequence of F0-ATPase subunit 9 and pSu9-DHFR were added to N. crassa mitochondria under conditions where completion of import to the matrix was prevented by dissipation of the inner membrane potential with the protonophore carbonyl cyanide m-chlorophenyl hydrazone. Subsequent import of radiochemical amounts of porin precursor was reduced about fourfold relative to import with no competitor present (Fig. 2 A). This indicates that the pSu9-DHFR and porin compete for similar sites required for insertion. To determine if the inhibitory effect was due solely to competition for binding sites on the receptors of the outer membrane (Tom20/Tom22), or if it also involved the actual import pore, the experiment was repeated using mitochondria pretreated with trypsin to remove the surface receptors. Under these conditions, receptor-dependent precursors enter mitochondria at a lower rate due to “bypass import,” which occurs via direct interaction with the GIP (Pfaller et al., 1989). As expected for trypsinized mitochondria, the import of porin was reduced relative to untreated mitochondria even without the addition of excess amounts of competing pSu9-DHFR precursor (Fig. 2 B).

However, the saturation of the pore with excess precursor substantially decreased the level of porin import even via the bypass route. Since the binding of the competing precursor was also reduced in the bypass route, lower levels of competition were expected. As the matrix-destined pSu9-DHFR precursor was found to be in the vicinity of the Tom40 pore component under similar “bypass” conditions (Rapaport et al., 1997), the data suggested that the import of porin is also dependent on components of the TOM complex that make up the translocation pore. Therefore, we decided to perform a detailed analysis for the requirement of individual Tom proteins in import of porin.

**Imported Porin Selectively Assembles into Preexisting Porin Complexes**

To establish a specific assay for the import of porin, we characterized the properties of yeast mitochondrial porin (also termed porin1). Mitochondria from yeast wild-type and a porin-deficient strain (por1Δ) (Blachly-Dyson et al., 1990) were separated by SDS-PAGE and stained with Coomassie brilliant blue G-250. The mutant mitochondria selectively lacked a protein band at 30 kD, the expected size of porin (Fig. 3 A, lane 2); the identity as porin was confirmed by immunodecoration (not shown). A quantification revealed that porin is 1 of the 10 most abundant proteins of mitochondria.

To assess the native state of porin, isolated yeast mitochondria were lysed with the mild nonionic detergent digitonin and subjected to BN-PAGE. Porin, detected by immunodecoration, migrated mainly in two complexes, an ~200-kD complex and an ~440-kD complex (Fig. 3 B, lane 1). Additionally, a complex of ~400 kD was present with lower abundance (Fig. 3 B, lane 1). In the por1Δ mitochondria, all three complexes were missing, indicating that they represent genuine porin-containing complexes (Fig. 3 B, lane 2). Besides porin1, yeast mitochondria contain a homologous protein, termed porin2, that is expressed at low level and does not reveal a detectable pore activity (Lee et al., 1998). The porin complexes of por2Δ mitochondria were indistinguishable from those of wild-type mitochondria (Fig. 3 B, lane 3), confirming that they are porin1 specific. The finding of several yeast porin complexes may be related to the observation in mammalian mitochondria that the integral membrane protein porin forms complexes with peripherally associated proteins from the cytosol/intermembrane space (Beutner et al., 1996). To investigate the relative stability of the porin complexes, the mitochondria were extracted with sodium carbonate, at pH 11.5, before BN-PAGE. Under these conditions, only the complex of 200 kD was stable (Fig. 3 C, lane 2 vs. lane 1), indicating that this complex represents the stable membrane-integrated core of the porin complexes.

We used the characteristic behavior of mature endogenous porin on BN-PAGE to establish a specific assay for the correct import and assembly of in vitro-synthesized porin precursors. Porin was synthesized in rabbit reticulocyte lysate in the presence of [35S]methionine/cysteine and
imported into isolated wild-type mitochondria. The mitochondria were reisolated, lysed in digitonin-containing buffer, and subjected to BN-PAGE and digital autoradiography. The radiolabeled porin was found in three high molecular weight complexes with a mobility indistinguishable from that of endogenous porin (Fig. 4 A, lanes 1–3). When por1Δ mitochondria were employed, however, none of the three high molecular weight complexes was observed (Fig. 4 A, lanes 4–6, and B), indicating that preexisting porin was required for the assembly of the radiolabeled porin. por2Δ mitochondria behaved like wild-type mitochondria (Fig. 4 A, lanes 7–9 vs. 1–3, and B). With all three types of mitochondria, a low molecular weight form of porin was found, likely representing the monomeric form of the porin precursor that was associated with mitochondria yet not assembled (Fig. 4 A). Additionally, radiolabeled porin was found at an ~100-kD position (Fig. 4 A, asterisk). The formation of this species required the presence of preexisting porin (Fig. 4 A, lanes 4–6), raising the possibility that it represents an assembly intermediate of porin. Since the 100-kD band does not represent a major form of mature porin (Fig. 3 B) and is observed to variable...
extent (depending on the yeast strain used), we only used the mature 200–440-kD complexes to determine the efficiency of assembly of radiolabeled porin. We conclude that BN-PAGE of digitonin-lysed mitochondria represents a specific assay to determine correct import and assembly of porin in yeast.

**Assembly of Porin Requires Tom20, Tom22, Tom5, and to a Lower Degree Tom7**

Mitochondria were isolated from yeast strains with single deletions of TOM22, TOM20, TOM7, TOM6, or TOM5. The steady-state levels of most mitochondrial marker proteins, including the respective other components of the TOM complex and the TIM machinery (shown here with Tim44), were found to be similar to those of wild-type mitochondria (Fig. 5 A) (Alconada et al., 1995; Höninger et al., 1996; Dietmeier et al., 1997; Dekker et al., 1998; van Wilpe et al., 1999). This was explained in the following way: mutations impairing the function of the TOM complex result in slower mitochondrial protein import that consequently becomes rate-limiting for mitochondrial and cellular growth. The strain lacking Tom20, however, is an exception since tom20Δ mitochondria are known to have a strongly reduced level of Tom22 (Lithgow et al., 1994). Therefore, we used a tom20Δ strain that additionally ex-

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**Figure 5. Import of porin requires components of the GIP.** (A) Levels of Tom proteins in mitochondria isolated from yeast strains lacking individual TOM genes (Table I). Isolated mitochondria (25 μg protein per lane) were subjected to SDS-PAGE and immuno-decoration with antibodies directed against the indicated proteins. Tim44, translocase of inner membrane subunit of 44 kD. (B) Import and assembly of radiolabeled porin. The experiment was performed as described in the legend to Fig. 4 A, except tom mutant mitochondria were used, and import was performed for the indicated periods. (Non-ass. Porin) Porin precursor in the low molecular weight range that is associated with mitochondria but not assembled. (C) Quantification of assembled porin. Hatched bars, high molecular weight complexes of assembled porin (440 and 400 kD); white bars, total assembled porin (440, 400, and 200 kD complexes together). The total amount of assembled radiolabeled porin in wild-type mitochondria after 15 min was set to 100% (control).
Mitochondria lacking one of the small Tom proteins re-
of porin inserted in vitro (Fig. 5, B and C, lanes 6 and 12). chondria were almost completely deficient in the assembly conclusion of Schleiff et al. (1999). However, The Journal of Cell Biology, Volume 152, 2001 296 assembly of porin was strongly reduced in used are selectively defective in only one Tom protein. (Fig. 5 A, lower left panel). Thus, the mutant mitochondria, followed by BN-PAGE. As-
pressed TOM22 from a high copy number plasmid (Table components modulating the dynamics of the TOM machinery; they function at least in part in an antagonistic manner to support assembly (Tom6) and dissociation (Tom7) of the GIP complex (Alconada et al., 1995; Hönlinger et al., 1996; Dekker et al., 1998). Although we did not observe a major porin assembly defect with tomtom7a mitochondria (Fig. 5, B and C, lanes 4 and 10), tomtom22A mitochondria revealed a moderate reduction of assembly for the two high molecular weight forms (440 and 400 kD) of porin (Fig. 5 B, lanes 5 and 11, and C, first row, lanes 5 and 11). The tomtom40-3 mutant mitochondria also displayed a differential effect on the amount of low molecular weight (monomeric) porin precursor that is associated with mitochondria but not assembled. Although the level of monomeric porin was unaltered in tomtom7Δ (and tomtom6Δ) mitochondria, a clear reduction was found with tomtom22Δ, tomtom20Δ, and tomtom5Δ mitochondria (Fig. 5 B). The most severe block was again observed in tomtom22Δ mitochondria (Fig. 5 B, lanes 6 and 12). Therefore, Tom20, Tom22, and Tom5 are involved in the stable association of the porin precursor with mitochondria.

We conclude that the import of porin into mitochondria not only requires Tom20 but also components of the GIP complex, in particular Tom22 and Tom5. Of the two components modulating the dynamics of the TOM machinery, the dissociating component Tom7 stimulates porin assembly. However, an actual requirement for the import pore itself that is formed by Tom40 (Hill et al., 1998; Künkele et al., 1999) cannot be proven with these experiments.

Two New Mutant Alleles of Tom40 Cause a Defect in Porin Import

Tom40 is an essential yeast protein; therefore, deletion mutants are not viable (Baker et al., 1990). A conditional mutant allele of Tom40 has been characterized, termed tomtom40-3 (isp42-3 in the old nomenclature) (Kassenbrock et al., 1993; Pfanner et al., 1996; Schleiff et al., 1999). We used the BN-PAGE assay to analyze assembly of porin in tomtom40-3 mitochondria. For comparison, radiolabeled porin was incubated with isolated mitochondria of the corresponding wild-type strain. After lysis in digitonin and BN-PAGE, assembled porin was mainly found in the 200-kD complex and to a smaller degree in the 440-kD complex (Fig. 6 A, lanes 1–3). Immunodecoration of preexisting porin revealed an indistinguishable behavior on BN-PAGE, confirming the specificity of the assay (not shown). (A higher molecular weight species [~500 kD] was a mitochondrial complex not related to porin that became nonspecifically radiolabeled.) The two major assembly complexes (200 and 440 kD) of porin are thus observed in different strain backgrounds (with variations in the relative amounts). When radiolabeled porin was incubated with tomtom40-3 mitochondria, we did not observe any significant defect in import and assembly of porin (Fig. 6 A, lanes 4–6, and B), demonstrating that tomtom40-3 mitochondria indeed are not deficient in porin biogenesis. This is in agreement with results reported by Schleiff et al. (1999).

Two possibilities are conceivable to explain this result. Tom40 is not involved in import of porin at all, or the competence of Tom40 with regard to porin assembly is not compromised in cells harboring the allele tomtom40-3. The...
PCR mutagenesis of TOM40 (Kassenbrock et al., 1993) had yielded several further uncharacterized mutant alleles that confer temperature-sensitive growth. Like tom40-3 and the corresponding wild-type strain, all these strains harbor a chromosomal deletion of TOM40 and express Tom40 from a plasmid. We performed an initial screen of the mutant strains in order to select strains where mitochondrial marker proteins, including Tom proteins, are present in normal amounts to minimize indirect effects of the mutations. We then selected two mutant strains, termed tom40-2 and tom40-4. The TOM40 ORFs of the two new alleles were sequenced, demonstrating their independence (Fig. 7 A). Each allele led to several amino acid alterations; additionally, a premature stop in tom40-4 led to a Tom40 lacking 17 amino acid residues at the COOH terminus (Fig. 7 A).

Mitochondria were isolated from the tom40-2 and tom40-4 strains as well as the corresponding wild-type. We first assessed the steady-state levels of several mitochondrial marker proteins by immunodecoration (Fig. 7 B). All Tom proteins analyzed along with other marker proteins for the outer membrane, inner membrane, and matrix were present in wild-type levels. Notably the levels of Tom40 and preexisting porin were not changed (Fig. 7 B). Moreover, the complexes of preexisting porin of wild-type and both mutant mitochondria were indistinguishable on BN-PAGE (not shown), excluding that defects in assembly of in vitro–imported porin would be caused by a lack of preexisting porin complexes. As expected, Tom40 from tom40-4 mitochondria showed a higher electrophoretic mobility consistent with the COOH-terminal truncation. Most importantly for the question addressed in this study, the levels of Tom20 were unchanged by the Tom40 mutations (Fig. 7 B). We further analyzed if the 400-kD GIP complex (TOM core complex) was properly assembled in the mutant mitochondria. The mitochondria were lysed with digitonin, separated by BN-PAGE and decorated with anti-Tom5. No difference in the mobility of the GIP complex was detectable in the mutant mitochondria (Fig. 7 C). We tested if the mutant mitochondria were impaired in the translocation of preproteins through the GIP by using a matrix-targeted fusion protein between an NH2-terminal portion of the precursor of cytochrome b2 and DHFR (b2-DHFR). The import of the preprotein into both mutant mitochondria was significantly inhibited compared with the corresponding wild-type mitochondria (Fig. 7 D).

We then incubated radiolabeled porin with isolated wild-type, tom40-2, and tom40-4 mitochondria and analyzed them by BN-PAGE. The assembly of porin was inhibited in the mutant mitochondria (Fig. 8 A, lanes 4–9). A quantification

Figure 7. Two new mutant alleles of TOM40. (A) Predicted amino acid sequences (single letter code) of wild-type Tom40 and the two mutant alleles tom40-2 and tom40-4. Alterations to the wild-type sequence are indicated in bold. (B) Steady state levels of mitochondrial proteins. Isolated mitochondria (25 μg protein per lane) from wild-type or tom40 mutant yeast strains were separated by SDS-PAGE using the Tris-tricine buffer system (Schägger and von Jagow, 1987), followed by immunodecoration with antibodies directed against the indicated yeast proteins. Tom40', truncated form of Tom40. AAC, ADP/ATP carrier; Ssc1, matrix Hsp70; Mge1, matrix co-chaperone of the GrpE-type. (C) Presence of the 400-kD GIP complex in the tom40 mutant mitochondria. Isolated mitochondria (50 μg protein per lane) were lysed in digitonin-containing buffer and subjected to BN-PAGE, followed by immunodecoration with antibodies directed against Tom5. (D) Import of a matrix-targeted preprotein is inhibited in the tom40 mutant mitochondria. The fusion protein b2-DHFR (1 μg protein per lane) was imported into isolated mitochondria (50 μg protein per lane) for the indicated time points. The processed form of the protein was detected by immunodecoration.
showed a 60–70% reduction of porin assembly compared with the wild-type mitochondria (Fig. 8 B). Since the levels of all marker proteins analyzed along with the GIP complex are not disturbed in the mutant mitochondria, we conclude that a functional Tom40 is required for the biogenesis of porin.

Cross-Linking of the Porin Precursor to Tom20, Tom22, and Tom40

To obtain independent evidence for the involvement of components of the GIP complex in porin import, we performed cross-linking of porin precursor molecules during the import process. Radiolabeled porin precursor was accumulated as an import intermediate in *Neurospora* OMVs by incubation at 0°C. Addition of the homobifunctional cross-linking reagent, DSG, led to cross-linking of porin to each of Tom20, Tom22, and Tom40 (Fig. 9). Cross-linked Tom40 products tend to appear as multiple bands on SDS-PAGE, probably caused by the existence of different conformations of Tom40 molecules in the membrane (Rapaport et al., 1997, 1998; Kanamori et al., 1999). The abundance of the adduct with Tom20 is at least partly due to the fact that the experiments are performed at 0°C, which insures that cross-linking occurs before the porin precursor becomes fully inserted. These conditions also favor association of porin with the receptor rather than with pore components. Nonetheless, the data clearly show that both Tom22 and Tom40 are in the vicinity of the porin precursor during import. No cross-linking of endogenous porin, the most abundant outer membrane protein, to Tom40 was observed (not shown), demonstrating the specificity of the cross-linking approach and excluding that the observed cross-linking of porin precursor to Tom40 could be explained as random interactions between assembled porin with Tom40. Although the levels of cross-linking of the porin precursor to the GIP complex components are low, they are comparable to those observed previously for the matrix-destined precursor pSu9-DHFR imported under similar conditions (Rapaport et al., 1997) and suggest that the initial stages of import for the two pre-
cursors occur via a similar pathway. As observed with matrix-targeted preproteins (Neupert, 1997; Pfanner et al., 1997), Tom20 may thus interact first with the porin precursor, followed by Tom22 and Tom40.

Discussion

Porin is not only the most abundant protein of the mitochondrial outer membrane, it is 1 of the 10 most abundant proteins found in mitochondria. It has been reported that porin is imported via a pathway that is radically different from that of other mitochondrial proteins since the proposed pathway utilizes only the receptor Tom20 for both recognition and membrane insertion of the precursor protein (Schleiff et al., 1999). It is possible that porin utilizes an unorthodox mechanism because it is a β-barrel protein, whereas most mitochondrial proteins, known to be imported via receptors and the GIP, contain α-helical portions. Although another putative β-barrel protein, Tom40, was found to be imported via the GIP (Rapaport and Neupert, 1999), its biogenesis pathway may represent a special situation since Tom40 forms the major component of the GIP itself. Therefore, we performed an analysis of the import pathway of porin in Neurospora and yeast mitochondria and provide evidence that the physiological import pathway into mitochondria is not mediated by Tom20 alone but requires several components of the GIP complex.

Initially, we observed that Neurospora mitochondria with fragile outer membranes were deficient in porin import. Similarly, Smith et al. (1994) reported that the import of porin was reduced in wild-type yeast mitochondria containing ruptured outer membranes. In the previous study with yeast mitochondria, a loss of Tom20 was not excluded. In this report, we analyzed the level of Tom20 in the Neurospora mitochondria and found that it was unchanged. Although these experiments cannot discriminate whether factors of the outer membrane or intermembrane space are impaired, the result with Neurospora mitochondria indicated that Tom20 alone was not sufficient for porin import and thereby prompted a characterization of the import pathway of porin.

Several observations show that the translocation pore of the TOM complex is involved in the import of the porin precursor. As reported previously, an excess of water-soluble porin competes with the translocation of various precursors at the level of the GIP (Pfaller et al., 1988). We have now demonstrated that the reciprocal is also true. When an excess of a matrix-destined precursor was incubated with mitochondria before addition of porin precursor, the import of porin was decreased. The competing effect is not limited to the receptor binding stage but is also observed in trypsin-treated mitochondria which are devoid of surface receptors. Thus, it appears that trypsin-resistant components of the TOM complex, such as Tom40, are involved in porin import. Furthermore, peptides resembling either matrix targeting signals, or signal–anchor sequences, are also able to inhibit insertion of porin into the outer membrane at a GIP-like step (Millar and Shore, 1996).

We have established a specific assay to directly monitor the assembly of in vitro-imported porin into preexisting porin complexes and thus exclude possible pitfalls that might arise when the import of porin is analyzed only by protease protection or resistance to alkaline pH (Schleiff et al., 1999). Using this assay, we have analyzed two new mutant alleles of yeast tom40 (tom40-2 and tom40-4) and indeed found that functional Tom40 is required for efficient import of porin. In the tom40 mutant mitochondria, the other Tom proteins, including Tom20, are present in normal amounts, demonstrating a specific effect of the Tom40 alterations on the import of porin. We also tested the tom40-3 strain used before by Schleiff et al. (1999) and confirmed that there is no inhibition of porin import in this strain in contrast to mitochondria from strains harboring alleles tom40-2 and tom40-4. Porin precursor accumulated at an intermediate stage of import could be cross-linked to Tom40. Therefore, the precursor must be in the immediate neighborhood of the import channel during its translocation. A similar pattern of cross-linking adducts was seen during low temperature import of pSu9-DHFR (Rapaport et al., 1997); this argues strongly in favor of precursors entering the GIP.

An involvement of the GIP complex in the import of porin is substantiated by analyzing the role of Tom22, the central receptor and organizer of the GIP complex. Mutant mitochondria lacking Tom22 are severely impaired in porin import, and the porin precursor can be cross-linked to Tom22 in wild-type OMVs. Moreover, lacking Tom5 are inhibited in porin import, as are mutant mitochondria lacking Tom20. We conclude that the import of porin requires the coordinated action of several Tom proteins: the receptors Tom20 and Tom22, and the small subunit Tom5 that aids in transfer of preproteins to the Tom40 channel. It is not excluded that under certain conditions, e.g., addition of urea or guanidinium chloride (Xu and Colombini, 1996), a fraction of porin may insert into artificial membranes (Schleiff et al., 1999). Our study demonstrates, however, that in a more physiological situation, i.e., with mitochondrial membranes, porin follows a complex import pathway involving two receptors and the GIP complex of the outer membrane.

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