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Conserved motifs reveal details of ancestry and structure in the small TIM chaperones of the mitochondrial intermembrane space.

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Abbreviations: TOM, translocase of the outer mitochondrial membrane; TIM, translocase of the inner mitochondrial membrane; SAM, sorting and assembly machinery in the outer mitochondrial membrane; AAC, ATP/ADP carrier; HMM, hidden Markov model; DAPI, 4',6-diamidino-2-phenylindole.

ABSTRACT

The mitochondrial inner and outer membranes are composed of a variety of integral membrane proteins, assembled into the membranes post-translationally. The small TIMs are a group of ~10 kDa proteins that function as chaperones to ferry imported proteins across the mitochondrial intermembrane space to the outer and inner membranes. In yeast there are five small TIM proteins: Tim8, Tim9, Tim10, Tim12 and Tim13, with equivalent proteins reported in humans. Using hidden Markov models we find that many eukaryotes have proteins equivalent to the Tim8 and Tim13 and the Tim9 and Tim10 subunits. Some eukaryotes provide “snapshots” of evolution, with a single protein showing the features of both Tim8 and Tim13, suggesting that a single progenitor gene has given rise to each of the small TIMs through duplication and modification. We show that no “Tim12” family of proteins exist, but rather that variant forms of the cognate small TIMs have been recently duplicated and modified to provide new functions: the yeast Tim12 is a modified form of Tim10, while in humans and some protists variant forms of Tim9, Tim8 and Tim13 are found instead. Sequence motif analysis reveals acidic residues conserved in the Tim10 substrate-binding tentacles, whereas more hydrophobic residues are found in the equivalent substrate-binding region of Tim13. The substrate-binding region of Tim10 and Tim13 represents an independent domain, the acidic domain from Tim10 can be attached to Tim13 converting the Tim8/Tim13 complex so that the Tim9/Tim10 complex becomes dispensable. The conserved features in the Tim10 and Tim13 subunits provide distinct binding surfaces to accommodate the broad range of substrate proteins delivered to the mitochondrial inner and outer membranes.

INTRODUCTION

Mitochondria are found ubiquitously in eukaryotes where they house 10-20% of the cellular proteome (Sickmann et al. 2003; Gabaldon and Huynen 2004; Ohlmeier et al. 2004; Prokisch et al. 2004; Reichert and Neupert 2004), with up to a thousand proteins of varying biochemical properties having to be imported into the organelle and sorted to one of the four sub-mitochondrial compartments. A series of molecular machines in the outer and inner mitochondrial membranes are responsible for the import and assembly of mitochondrial proteins (Pfanner and Geissler 2001; Herrmann and Neupert 2003; Koehler 2004a; Pfanner et al. 2004; Dolezal et al. 2006). These machines: the TOM complex, SAM complex, TIM23 complex, TIM22 complex and OXA1 complex, are composed of forty or more subunit parts that function as distinct modules. Some of the modules found in the yeast protein import machinery are conserved in animals and plants, while others seem to be more restricted in their distribution suggesting they have arisen more recently (Dolezal et al. 2006). Comparative analysis of the protein import machinery from various eukaryotic groups provides a powerful means to address how the component parts combine to form functional machines, and how the machines handle the broad range of substrate proteins imported into mitochondria.

The several hundred membrane proteins imported into mitochondria enter an aqueous channel in the TOM complex, enabling their translocation across the outer membrane (Brix, Dietmeier, and Pfanner 1997; Dietmeier et al. 1997; Schatz 1997; Pfanner et al. 2004). Those proteins destined for assembly into the outer membrane are then transferred to the SAM complex. Most of the proteins destined for the inner membrane, including the abundant metabolite carrier proteins, are transferred instead to the TIM22 complex. It remains unclear how a given substrate protein is recognized for specific delivery to either the SAM or TIM22 complex, but it is known that both transfer reactions require the assistance of the small TIM chaperones (Rehling et al. 2003; Koehler 2004a; Koehler 2004b; de Marcos-Lousa, Sideris, and Tokatlidis 2006). The small TIMs are a group of ~10 kDa proteins originally characterised by a unique arrangement of cysteines: two sequence motifs of CX_3C separated by 11-16 residues (Koehler 2004b). This superfamily of proteins, referred to as zf-Tim10DDP (PF02953), is collected together as a single group by the Conserved Domain Database (Marchler-Bauer et al. 2005) because of the common features centred around the conserved CX_3C sequences. The cysteines contribute to two pairs of disulfide bonds that maintain the structural integrity of the proteins (Allen et al. 2003; Webb et al. 2006).

In yeast there are five members of the zf-Tim10DDP family: according to their approximate molecular weight in kDa these proteins are called Tim8, Tim9, Tim10, Tim12 and Tim13. Three of these, Tim9, Tim10 and Tim12 are essential for cell viability while the genes encoding the other two, Tim8 and Tim13, can be deleted without obvious effects on cell growth (Koehler et al. 1999). Tim9 and Tim10 combine to form a $\alpha_3\beta_3$ hexamer, and the function of this Tim9/Tim10 complex has been studied in detail (Koehler et al. 1998b; Adam et al. 1999; Luciano et al. 2001; Curran et al. 2002a; Curran et al. 2002b; Truscott et al. 2002; Lu et al. 2004; Lu and Woodburn 2005; Webb et al. 2006). The essential Tim12 sits as a peripheral subunit on the inner membrane TIM22 translocase, where it appears to help unload substrates delivered by the Tim9/Tim10 complex (Koehler et al. 1998a; Sirrenberg et al. 1998; Bauer et al. 1999; Endres, Neupert, and Brunner 1999; Muhlenbein et al. 2004). Tim8 and Tim13 form a second $\alpha_3\beta_3$ hexameric complex which appears to perform analogously to the Tim9/Tim10 complex in delivering substrate proteins to the outer and inner membranes (Koehler et al. 1999; Curran et al. 2002b; Davis et al. 2000). This redundancy of function and the non-essential nature of the genes encoding Tim8 and Tim13 leaves open the question of why these two small TIMs are needed in yeast.

Due to the sequence conservation in the small TIMs, BLAST searches with the yeast sequences revealed corresponding human proteins. The Tim9/Tim10 complex from humans is involved in inner membrane protein insertion (Bauer et al. 1999; Muhlenbein et al. 2004) and its crystal structure was recently solved (Webb et al. 2006). It consists of a ring-shaped hexamer formed from alternating Tim9 and Tim10 subunits. The Tim8/Tim13 complex is also found in humans and a mutation in one of the genes encoding Tim8 leads to Mohr-Tranebjaerg syndrome (Koehler et al. 1999; Bauer and Neupert 2001; Roesch et al. 2002).

We have taken a comparative genomics approach using hidden Markov models (HMMs) to comprehensively screen for small TIM sequences and to discriminate conserved features within the small TIM family. We have assessed the role of the small TIM proteins in delivery of substrates to the mitochondrial membranes, addressing three questions. Firstly, does a signature motif exist that defines each of the five small TIM sub-families? Secondly, how do these defining motifs relate to the three dimensional structure of the small TIM proteins and their capability for recognition and binding of substrates? Thirdly, can these motifs be used to

determine whether or not all organisms encode and rely on Tim12 and both the Tim9/Tim10 and Tim8/Tim13 complexes?

The comprehensive sequence analysis made possible with the hidden Markov models shows some eukaryotes have a reduced number of small TIMs, with only two or three genes present. While some apicomplexan parasites like the malaria-causing *Plasmodium* have clear and distinct Tim9, Tim10, Tim8 and Tim13 subunits, the genome of a related apicomplexan, *Theileria parva*, encodes a Tim9 and a Tim10 and then has a third gene that encodes a hybrid Tim8-Tim13 protein while other apicomplexans, in the genus *Cryptosporidium*, have only the hybrid Tim8-Tim13 protein. This work suggests that the small TIM chaperones were present in the last common ancestor to the eukaryote lineage, and that distinct features in the four types of small TIMs are critical: they have been maintained, or independently evolved, to be present in diverse eukaryotes. Distinct features identified in substrate-binding domains of the Tim10 and Tim13 subunits provides for the broadest range of substrate proteins to be collected and ferried across the mitochondrial intermembrane space.

MATERIALS AND METHODS

Hidden Markov models

The initial set of small TIM sequences gathered from BLAST searches were aligned using ClustalX (Jeanmougin et al. 1998) and the alignment was used to generate a Neighbor-Joining phylogenetic tree that clustered the sequences into four main groups, with each of the cognate small TIMs from yeast sitting in one of the four groups. The sets representing Tim8, Tim9, Tim10, and Tim13 contained 16, 15, 13, and 9 sequences respectively. The grouped sequences were then used to construct HMMs which in turn were used to search the UniProt database for related proteins.

The HMMs were built with the program HMMER 2.3.2 (Durbin 1998). The best multiple alignment for each family of sequences was obtained with ClustalW (Thompson, Higgins, and Gibson 1994) and t-coffee (Notredame, Holm, and Higgins 1998). The two alignment programs produced different best alignments, and we built two sets of HMMs (corresponding to ClustalW and t-coffee alignments) for each family of sequences (Tim8, Tim9, Tim10 and Tim13). The resulting HMMs were used to scan UniProt database release 7.2 (Swiss-Prot release 49.2 and TrEMBL release 32.2) (Bairoch et al. 2005) and also to scan protein data sets from the *Trichomonas vaginalis* and *Encephalizoon cuniculi* genomes individually, as previously described (Dolezal et al. 2006). The results of all HMM searches were manually examined. The sequences used to construct the HMM were detected from within the UniProt search with scores better than $E = 10^{-40}$. Novel sequences retrieved with scores $E < 10^{-5}$ were proteins of 50-100 residues that carry the twin CX_3C motif and were considered members of the small TIM family. Sequences which scored poorer than $E = 10^{-4}$ were larger than 100 residues, did not carry the twin CX_3C motif, and were therefore discarded. Many of these were proteins of known function and have predicted (helix-rich) coiled-coil domain structures.

Motif analysis to distinguish four small TIM families

Proteins deemed to belong to one of the four small TIM families were used to define sequence motifs. Note, the hybrid Tim8-Tim13 sequences were not included for motif analysis. The program MEME version 3.5.2 (Bailey and Elkan 1994) was used and in the first step we searched each given protein family for the single strongest motif present in the sequences, the rationale being that if all sequences were correctly assigned to a small TIM family they should have at least one common motif. Consequently, any sequence which did

not have this motif was removed from further analysis. This resulted in the removal of one sequence from the initial Tim8, Tim9 and Tim10 sets. The resulting Tim8, Tim9, Tim10, and Tim13 sets containing 33, 40, 33 and 25 sequences, respectively, were used in further motif analysis. In the second step, we checked for possible motifs that occur as repetitions (MEME 'anr' distribution option). No such motifs were found in any of the four protein families. Finally, the three most prominent motifs in each family were searched for. The motifs were constrained to be between 5 and 128 residues, with the E-value not to exceed 1e-10. Motifs that were present in all sequences of a sub-family are represented in the logos in Figure 1 and have the following characteristics: Tim9 Motif (E-value = 10^{-1115}), Tim10 Motifs 1 and 2 (E-values = 10^{-543} and = 10^{-448}), Tim8 Motifs 1 and 2 (E-values = 10^{-400} and = 10^{-211}), Tim13 Motifs 1 and 2 (E-value = 10^{-396} = 10^{-335}). No other characteristic motifs were found. From past experience we know that the output of a MEME motif search (including the exact beginning or end of a motif) may be affected by input parameters (V. Likić, unpublished). To test for reliability in the predicted motifs, we ran five repeats of motif elucidation with different input parameters. For each family of sequences the resulting motifs were confirmed.

In order to map the critical residues within the motifs onto the crystal structure of Tim9/10, the information content (Shannon uncertainty) (Schneider and Stephens 1990) was calculated for each column in seperate multiple alignments of Tim9 and Tim10 using the Biopython tools (http://biopython.org) and assuming a uniform background symbol distribution. These values were mapped to the coordinates of the Tim9/Tim10 heterohexamer crystal structure (pdb accession 2BSK) (Webb et al. 2006) using the occupancy field of the pdb format and analysed using VMD (version 1.8.4) (Humphrey, Dalke, and Schulten 1996).

RNAi knockdowns of Tim8-13 and TIM translocase core in Trypanosoma brucei

RNAi-mediated ablation of the *T. brucei* Tim8-13 and TIM translocase core was performed using stem loop constructs containing the puromycine resistance gene as described (Bochud-Allemann and Schneider 2002). The constructs correspond to the sequence of the entire open-reading frame of *T. brucei* Tim8-13 and TIM translocase genes. Transfection of *T. brucei* (strain 29-13), selection with antibiotics, cloning and induction with tetracycline were done as described (McCulloch et al. 2004).

Binding assays with the yeast Tim8/Tim13 complex

PVDF membranes of 13mer peptides with a ten amino acid overlap were synthesised by automated spot synthesis (JPT Peptide Technologies, Berlin, Germany). Binding of Tim13 was performed as described (Vergnolle et al. 2005) with the following modifications: Tim13 antibodies were used to detect bound proteins, and signals were quantified using ImageQuant software (Molecular Dynamics). Transmembrane segments were predicted for Tim22 using DAS (Cserzo et al. 1997) and multiple sequence alignments as previously described (Chan et al. 2006) and for Aac2 by alignment with the bovine AAC crystal structure (Pebay-Peyroula et al. 2003).

RESULTS

There are four, distinct small TIM families: Tim8, Tim9, Tim10 and Tim13

Tim9, Tim10, Tim8, Tim13 and Tim12 were first identified in yeast (Jarosch et al. 1996; Koehler et al. 1998b; Sirrenberg et al. 1998) and a thorough characterization of the homologs of these proteins in humans has been done (Bauer et al. 1999; Jin et al. 1999). Starting with the functionally characterised small TIMs from yeast and humans, BLAST searches were used to gather an initial set of 53 small TIM sequences. From a phylogenetic analysis, these cluster into four groups with each of the groups containing at least one of the cognate small TIMs from yeast (data not shown). The Tim12 and Tim10 sequences from yeast sit in a single group.

The grouped sequences were then used to construct four hidden Markov models, one describing each of the small TIM sub-families. The HMMs were used to extract related sequences from UniProt 7.5 sequence data. Those sequences that had been used to construct the HMM were recognised in UniProt with scores of $E \leq 10^{-40}$. This then constitutes a "perfect match" in this search. All of the novel sequences retrieved with scores above $E = 10^{-5}$ are proteins of 50-100 residues, carry the twin CX_3C motif and were therefore collected as members of the small TIM family. The 141 small TIM sequences discovered here come from a broad range of eukaryotes, but none were found in prokaryotes. A number of complete genome sequence data sets are present in UniProt, and the small TIM proteins discovered in these organisms are listed in Table 1.

Each of the four small TIM families was then analysed for motifs, in order to determine those features that distinguish each of the four families. The motifs are represented in Figure 1. In all Tim9 sequences, a single motif exists with fifteen residues situated between the two CX_3C sequences. Numerous key residues in the motif are highly conserved as judged by the height of the character in the sequence logo (Figure 1). In the other TIM families there are two motifs, which are broken by the insertion of a variable number of residues: in Tim10, there are 15-21 residues between the twin CX_3C sequences, in Tim8 there are 14-18 residues while the Tim13 sequences have 11-14 residues inserted between the twin CX_3C sequences. The region between the twin CX_3C sequences is known to form a structured loop (Webb et al. 2006), which could accommodate the variable number of residues. The conserved, diagnostic motifs found here include and extend well beyond the twin CX_3C sequences, with the key residues conserved within each motif distinguishing the four families. For example, there are

several conserved acidic residues in the N-terminal region of all the Tim10 sequences that are not found in the other small TIMs.

Tim12-type proteins are the result of recent gene duplication events

While only four characteristic families of small TIMs can be recognised, in many organisms for which complete sequence data is available, five distinct small TIM proteins were found: one corresponding to each of the cognate families and a fifth isoform that fits less well to the criteria shown in any of the conserved motifs. The best studied of these is the yeast Tim12, a peripheral component of the TIM22 complex (Koehler et al. 1998a; Sirrenberg et al. 1998). Tim12 appears to serve as a docking point for the substrate-Tim9/Tim10 complex. Yeast Tim12 matches the Tim10 motif, though poorly compared to *bona fide* Tim10 homologues. A peripheral small TIM component of the TIM22 complex has also been described in humans (Muhlenbein et al. 2004), but this small TIM (Q9Y5J6) best matches the sequence criteria of the Tim9 HMM ($E = 10^{-46}$) rather than the Tim10 HMM ($E = 6.10^{-5}$). Thus it seems that the TIM22 complex subunit can be of either type of small TIM. Furthermore, of the four species of *Plasmodium* for which complete genome data are available, two have a variant TIM that matches the Tim8 HMM while two species have a variant that matches the Tim13 HMM ($E \sim 10^{-5}$ to10^{-8} in all cases). This would suggest that the acquisition of a fifth, "Tim12" type, subunit might have occurred relatively recently and have come about independently in various lineages of eukaryotes. In keeping with this proposal plants, filamentous fungi and several, diverse groups of protists have no apparent variant form of small TIM available to fulfil this function. Presumably in these organisms the import pathway has evolved such that substrate-loaded small TIM complexes can dock to the TIM22 complex directly, without the assistance of a pre-bound Tim12 subunit.

Mapping the conserved residues onto the structural framework of the Tim9/Tim10 complex

The structure of the Tim9/10 complex from humans was recently solved by X-ray crystallography (Webb et al. 2006). This provides a framework to analyse the conserved features of each of the small TIMs. Many of the highly conserved residues pinpointed in the motif analysis are involved in forming contacts between the Tim9 and Tim10 subunits. Two independent types of Tim9-Tim10 interface alternate in the hexamer. In one, F29 and F36 of Tim9 pack against side chains of Y58, K32 and the C54-C29 disulphide of Tim10 (Figure 2A), and a conserved ion pair is formed between E45 of Tim9 and K57 of Tim10. In the other interface, the most highly conserved contacts are the inter-subunit ion pairs D52

(Tim9)…R62 (Tim10), and E47 (Tim10)…K55 (Tim9) (Figure 2B). These molecular interfaces are thus strong but potentially labile, benefiting a chaperone function. In short, conserved residues on either face of Tim9 and Tim10 subunits are critical to hexamer assembly.

As a result of these inter-subunit contacts, the flat or 'upper' face of the hexamer has a highly conserved surface (Figure 2C). The conserved patches are discontinuous due to non-conserved sequences in the loop between the twin CX_3C motifs in each subunit. These 'cys-loops' divide the conserved surface into two patches: the first comprising Tim10 residues K32, G46, E47, C33-C50, R53 and Tim9 residues F36 and K55. A second, smaller, patch forms from Tim9 residues E45 and C32-C48. Most of the conserved residues are involved in contacts that determine the conformation of the cys-loops, and hence the surface complementarity of Tim9 and Tim10 subunits. The cysteine residues in the twin CX_3C motifs are invariant, and form disulphides that constrain the ends of each helix between the cys-loops, possibly also promote the propeller topology of the assembly. Conservation of the upper surface makes it an attractive proposition for docking to other components of the import machinery, though the underlying reason for conservation of these residues is in maintaining the structural integrity of the hexameric assembly prior to substrate binding. The equivalent of E45 in the yeast Tim9, for example, has been implicated in formation of a stable hexamer (Leuenberger et al. 2003).

Substrate-binding regions in the Tim9/Tim10 and the Tim8/Tim13 complexes

When Tim10 is purified in isolation from Tim9, it exists in a small soluble form that might be either a monomer or dimer (Vial et al. 2002; Webb et al. 2006). The purified Tim10 subunit binds the inner membrane substrate AAC in a manner similar to the Tim9/Tim10 complex, whereas Tim9 alone does not bind at all (Vergnolle et al. 2005). To test whether either Tim8 or Tim13, or both, subunits are responsible for binding substrate proteins, a cellulose filter carrying 103 peptides representing the ADP/ATP carrier protein (AAC), a substrate of the small TIM chaperones, was incubated with purified Tim8 or Tim13. A discrete set of spots, highlighting the peptides bound by Tim13, can be seen on the filter (Figure 3A, upper panel). The peptides bound by Tim13 correspond to the hydrophobic transmembrane domains of AAC. These same regions of AAC are bound by Tim10 and the native Tim9/Tim10 complex (Curran et al. 2002a; Vasiljev et al. 2004; Vergnolle et al. 2005).

Binding of Tim8 to the same filter was barely detectable (Figure 3A, lower panel), suggesting Tim13 functions as the substrate sensor in the Tim8/Tim13 complex. Likewise, using a cellulose filter carrying peptides from the inner membrane protein Tim22, the Tim13 subunit binds to discrete peptides on the membrane while Tim8 bound only weakly to one peptide spot (Figure 3B). As is the case for its binding to AAC, Tim13 binds peptides corresponding to the predicted transmembrane regions of the Tim22 substrate. Tim10 and Tim13 therefore act as substrate-binding subunits for their respective complexes, by binding to hydrophobic transmembrane segments of their substrate proteins. While the capacity for binding unstructured peptides segments as revealed by peptide-filter assays can be modified *in vivo*, through partial folding of the substrate or by competition between the Tim9/Tim10 and Tim8/Tim13 complexes, these results make clear that the Tim10 and Tim13 subunits are capable substrate-binding subunits.

Motif analysis described a highly conserved N-terminal region in both Tim13 and Tim10 (Figure 1). The N-terminal residues of Tim10 featuring in this motif are required for substrate binding (Vergnolle et al. 2005) and form three “tentacles” extending down from the inner ring of helices in the Tim9/Tim10 hexamer (Webb et al. 2006). Mapping the conserved residues from the Tim10 motif onto the structure (Figure 4A) suggests the acidic region does not make contact with neighbouring Tim9 subunits. Given that this N-terminal domain of Tim10 is apparently structurally independent of the rest of the complex (Vial et al. 2002; Lu et al. 2004; Webb et al. 2006), it should be possible to graft the substrate-binding domain in place of the equivalent substrate-binding region of the Tim13 subunit, and convert Tim8/Tim13 to a complex that binds the substrates of Tim9/Tim10. To test this proposition, the N-terminal residues of Tim13 were replaced with those of Tim10 to create the fusion protein $Tim13^{10}$ (Figure 4B). Conserved acidics (D31 in Tim10 and E48 in Tim13) sit nine residues N-terminal to the first cysteine in each protein, and this position was used as “splicing” site. A single-copy plasmid driving expression of $Tim13^{10}$ was transformed into *tim10*^{ts} yeast cells. The *tim10*^{ts} mutants carry a destabilising mutation in the *tim10* gene and at 37^{o}C the expression of Tim10 and Tim9 is inhibited (Koehler et al. 1998b). The cells die at 37^{o}C because there is at least one essential substrate of the Tim9/Tim10 complex that can not be carried by the Tim8/Tim13 complex. The *tim10*^{ts} cells are rescued by expression of $Tim13^{10}$ (Figure 4B) demonstrating that $Tim13^{10}$ can account for the essential function of Tim10.

Organisms lacking a Tim8/Tim13 complex?

Some organisms appear to lack genes that would encode Tim8 and Tim13 family members. *Dictyostelium discoideum* is a case in point where very clear Tim9 and Tim10 subunits are found while no other small TIM sequences are present in the completely sequenced genome (Table 1). Further species of eukaryotes for which complete genome data is available also lack Tim8 and Tim13 proteins. However *Theileria parva, Leishmania major, Trypanosoma cruzi* and *Trypanosoma brucei* show intriguing sequences that might represent ancestral-type composite Tim8-13 proteins.

The kinetoplastida represents some of the earliest diverging forms of eukaryotes and include the human pathogens *L. major*, *T. cruzi* and *T. brucei*. Each of these organisms has three small TIMs. In *T. brucei* the first TIM matches both the Tim9 model and Tim10 model (E = 10^{-6}, E = 2.10^{-7}, respectively) and the second protein specifically matches the Tim10 HMM (E = 2.10^{-5}). The third sequence has limited conservation to any of the four TIM families, but conserved residues within the N-terminal half of the protein most closely match the signatures of Tim13, and conserved residues within the C-terminal half most closely match the signatures of Tim8.

Little is known about the protein import apparatus in the kinetoplastid mitochondrion. However, a few of the most conserved components of the protein import machinery have been annotated within the completely sequenced genomes (El-Sayed et al. 2005) including the inner membrane translocase *Tb*11.01.4870, a member of the Tim17/Tim22/Tim23 family of proteins (PF02466) that would serve as the core of the inner membrane (TIM) protein translocase. Despite having only one Tim22/Tim23 translocase and only three small TIMs, the overall pathway for import of carrier proteins must be conserved between humans and *Leishmania* as a mammalian carrier protein is imported into mitochondria of transfected *L. major* promastigotes, such that the carrier is functional and represented 4.7% of the total mitochondrial protein (Alvarez-Fortes et al. 1998).

Depletion of this protein by RNAi in cultured procyclic form parasites gives a mitochondrial defect, with the normally reticular mitochondrion becoming a globular mass as judged from immunofluorescent staining of the mitochondrial matrix protein Hsp60 (Figure 5B). The defect, seen in 60-75% of cells after 72 hours of treatment (Figure 5C), might reflect the

paucity of protein insertion into the mitochondrial membranes, and is distinct from the morphology after RNAi treatment of other essential proteins (Esseiva et al. 2004; Smid et al. 2006). Over the same timecourse, RNAi treatment to deplete the Tim8-13 of *T. brucei* yields the same growth phenotype and mitochondrial defect, (Figure 5B, 5C) demonstrating that this small TIM protein functions as a crucial component in the mitochondria of these kinetoplastids.

Complete genome sequence data is also available for three groups of apicomplexan parasites, seven species in all from *Plasmodium*, *Cryptosporidium* and *Theileria*. *Cryptosporidium parvum* and *Cryptosporidium hominis* have only relic mitochondria, the mitosome, with a greatly reduced set of proteins targeted to this organelle (Riordan et al. 2003; Putignani et al. 2004; Slapeta and Keithly 2004; Henriquez et al. 2005); the genomes of these organisms encode only one small TIM, which has the characteristics of both Tim8 and Tim13 (Table 1). In *Theileria parva*, three proteins are encoded: the first matches the Tim9 HMM ($E = 10^{-41}$) and the second matches the Tim10 HMM ($E = 9.\ 10^{-9}$). The third small TIM from *T. parva* matches both the HMM for Tim13 ($E = 6.\ 10^{-7}$) and the HMM for Tim8 ($E = 10^{-41}$). In the genome sequence of the four diverse species of *Plasmodium*, four cognate small TIMs were detected. Each is remarkably similar to the Tim9, Tim10, Tim8 and Tim13 proteins found in humans and yeast (Table 1).

DISCUSSION

Protein import into mitochondria is a ubiquitous process in eukaryotes (Dolezal et al. 2006). From work done in yeast and in humans, the small TIMs function to collect substrate proteins from the TOM complex and deliver them to either the TIM22 complex in the inner membrane or the SAM complex in the outer membrane. The TOM, TIM22 and SAM complexes appear to be present in all eukaryotic lineages (Dolezal et al. 2006), suggesting the mechanism for the import of membrane proteins follows is conserved.

Distinguishing roles for the Tim8/Tim13 and Tim9/Tim10 complexes

Recent functional analyses rule out the prospect that the two small TIM complexes selectively deliver substrates to either the outer membrane or to the inner membrane (Leuenberger et al. 1999; Davis et al. 2000; Curran et al. 2002b; Truscott et al. 2002; Hoppins and Nargang 2004). Both Tim8/Tim13 and Tim9/Tim10 complexes are required for the efficient delivery of outer membrane substrates (Hoppins and Nargang 2004; Wiedemann et al. 2004) and both complexes assist in the delivery of some inner membrane proteins. Recently, Davis et al. (2006) used cross-linking assays to comprehensively map the binding sites for Tim8/Tim13 and Tim9/Tim10 on the substrate protein Tim23. Specific sites were identified on Tim23 to which structurally-defined chaperone complexes bound: rather than general binding to hydrophobic regions of Tim23, specific cross-links indicated that Tim8/Tim13 bind to a few specific sites around the hydrophobic regions and that the Tim9/Tim10 complex binds selectively to other, specific sites around these hydrophobic regions on each molecule of substrate (Davis et al. 2006). Substrates like Tim23 and Tim22 are essential proteins, and in the absence of the (essential) Tim9/Tim10 complex the Tim8/Tim13 complex alone is insufficient to deliver some essential substrates to the inner membrane.

The identity of the residues conserved in the tentacles of Tim10 and the equivalent region of Tim13 differ, with numerous alanine residues more diagnostic of the Tim13 substrate-binding segment. This provides distinct characteristics for the binding of substrates: we note that Tim13 binds best to the last transmembrane segment of the Tim22 substrate (Figure 4B) while Tim10 binds best to the second transmembrane segment (Vasiljev et al. 2004). For the AAC peptides, Tim13 binds best to those corresponding to transmembrane segments 2, 3 and 5 while the Tim9/10 complex preferentially binds the peptides from transmembrane segments

3 and 4 (Lu et al. 2004). Furthermore, *in organello*, Tim8/Tim13 and Tim9/Tim10 are positioned at precise locations along the imported substrate Tim23, demonstrating each complex has preferred binding sites (Davis et al. 2006). The N-terminal tentacle of both Tim10 and Tim13 predict highly for propensity to form a coiled coil (Vergnolle et al. 2005; data not shown). This structural feature may also contribute to substrate binding; in coils, the chaperone's α-helical tentacles might shield hydrophobic helical segments of substrate.

In yeast, the *TIM8* and *TIM13* genes are not essential for cell viability and *Dictyostelium discoideum* lacks Tim8 and Tim13 proteins. The Tim9 and Tim10 in *D. discoideum* are typical, with very high matches to the respective HMM ($E = 10^{-35}$ and 10^{-44}). This suggests that a single small TIM complex is sufficient to mediate targeting of all membrane protein substrates in this organism. Too little is known about mitochondrial protein targeting in *D. discoideum* yet, but its various substrate proteins might be less diverse in their sequence characteristics – which might in turn explain how a single small TIM complex could deliver all protein substrates to the outer and inner membranes. We suggest that the advantage to most organisms in having distinct Tim8/Tim13 and Tim9/Tim10 complexes comes in the increased range of substrates that can be bound; with the somewhat different substrate-binding tentacles in the Tim13 and Tim10 subunits providing a broader capability for the substrates that can be recognized and delivered to the TIM22 and SAM complexes for assembly.

The primitive condition: acquisition and diversification of the small TIMs

Our HMM analysis detects no proteins widely found in bacteria that might represent an ancestor chaperone from which the small TIMs have been derived, and we suggest that this family of chaperones was derived by the host cell in order to facilitate membrane protein transfer across the intermembrane space to the inner membrane; a pathway not pre-existing in the bacterial endosymbiont. The distinct "primitive" conditions, found in this study, each contribute something to a new understanding of how the small TIM proteins came about.

Firstly, some eukaryotes have no small TIMs, demonstrating that small TIMs are not essential for mitochondrial biogenesis *per se*. During the first phases of mitochondrial evolution, targeting of membrane proteins could have proceeded in the absence of small TIMs. *Encephalitozoon cuniculi* is a microsporidian, and these organisms diverged early

from the animal and fungal lineage. Microsporidians have massively reduced genomes, and in particular have highly simplified mitochondria (referred to as “mitosomes”) with no electron transport chain, no ATP synthase and no mitochondrial metabolite carriers in their inner membranes (Katinka et al. 2001). The remnant mitochondrion in microsporidians probably houses relatively few proteins apart from the simplified mitochondrial protein import apparatus and FeS cluster biosynthetic machinery, and therefore has relatively few proteins assembled into the mitosomal membranes. The widespread distribution of small TIM proteins in other eukaryotes suggests an early origin for the family and that microsporidians have therefore lost their TIMs as part of their genome reduction. Microsporidians retain a Tom40 that must be assembled into the outer membrane and a vestigial SAM complex (Katinka et al. 2001; Dolezal et al. 2006), and a Tim22/Tim23 that must be assembled in the inner membrane (Katinka et al. 2001), thereby demonstrating that even in the absence of small TIMs mitochondrial membrane protein assembly can be achieved. A similar situation is seen in *Trichomonas vaginalis*, which might also have a reduced membrane protein complexity and shows an absence of small TIMs. These eukaryotes provide proof-of-principle for a situation in the earliest eukaryotes, when relatively few membrane proteins were coded on nuclear genes and in need of import.

The composite small TIM found in species of *Cryptosporidium*, *Theileria*, *Leishmania* and *Trypanosoma*, with the combined sequence characteristics of Tim8 and Tim13, supports our suggestion that a single gene might be enough to encode a functional chaperone. In particular, species of *Cryptosporidium* appear to have only this small TIM. Again, this represents proof-of-principle that in simple eukaryotes a single gene encoding a suitable hybrid protein, such as Tim8-13, could form a functional chaperone.

We suggest that early eukaryotes carried a single small TIM, and that duplication of this gene gave rise to both the Tim10 and Tim13 type chaperones in the mitochondrial intermembrane space. Further gene duplications, and co-dependent mutations created the Tim9- and Tim8-type subunits, providing in each the necessary inter-subunit contacts to give rise to heteromeric complexes. Much more recently, gene duplication events have given rise to the “Tim12” subunit found attached to the TIM22 complex in the mitochondrial inner membrane. The development of Tim9/Tim10 and Tim8/Tim13 complexes may have occurred very early, so that all eukaryotes inherited a full set of the four cognate small TIMs. Alternatively, some of the duplication events may have occurred in parallel, in distinct lineages, with correlated

mutations giving similar outcomes in the Tim9 and Tim8 families. With such small, simply structured proteins, this alternative represents a reasonable proposition.

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FIGURE LEGENDS

Figure 1. Motif representation of the four cognate small TIM families. Sequence Logos (Crooks et al. 2004) describing the conserved sequence motifs in each of the small TIMs are shown. These centre around the conserved twin CX_3C residues. In the case of Tim10, Tim8 and Tim13 the motif is broken in two due to a variable number of residues in the interhelical loop region. The highly conserved N-terminal region in the Tim10 sequences corresponds to the region of the protein that binds substrate (Vergnolle et al. 2005).

Figure 2. Conserved residues sit at the inter-subunit contacts of the Tim9/Tim10 hexamer. (A) This view shows the interface between the "front" face of Tim9 (cyan cylinders) and the "back" face of Tim10 (blue/white/red surface). The most conserved residues in contact across this interface are aromatics (Tim9-F29, Tim-F26 and Tim10-Y58), which pack against one of the two strictly conserved disulphide bonds in Tim10 (C54-C29) (B) Flipped 180^o, the view of the interface where the "back" face of Tim9 (transparent grey cylinders) contacts the "front" face of Tim10 (blue/white/red surface). In addition to the ionic interactions between Tim10-D52/Tim9-R62 and Tim10-E47/Tim9-K55, the conserved L43 of Tim10 packs against the acyl chain region of Tim9-K55 which "threads" through the loop of Tim10. The sidechains of the most conserved residues (>3.46 bits, 80^{th} percentile) in Tim9 are shown as orange spheres (C) The conserved core residues of the Tim9/Tim10 complex are also partially exposed on the top surface of the hexamer. Residues from Tim9 (grey labels) and Tim10 (orange labels) with side-chains contributing to the conserved patches are identified.

Figure 3. Substrate recognition by Tim13 and Tim8. (A) Thirteen-mer peptide assemblies (see Methods) representing AAC (the Aac2 protein from *S. cerevisiae*) were screened with purified Tim13 (upper panel) or Tim8 (lower panel) proteins. Bound protein was blotted to PVDF membranes and probed with antibodies that detect Tim13 or Tim8. Immunolocalisation of the respective small TIMs shows the pattern of peptides to which they bind, and the immunoblots are shown along with a graphical representation of relative amount of binding to each peptide spot. The positions of predicted transmembrane domains and loops, according to peptide number, are indicated below the graphs. (B) Thirteen-mer peptide assemblies (see Methods) representing Tim22 from *S. cerevisiae* were analysed as described above.

Figure 4. Conserved residues in the Tim10 tentacles. (A) The conserved residues in the first twenty residues of the N-terminal segments are mapped onto each of the three Tim10 subunits. The conserved acidic residues are labelled. Shaded purple are further conserved residues M18, L15, A11 and A10. (B) Wild-type or *tim10*^{ts} yeast cells were transformed with a parent plasmid or with the plasmid encoding the Tim13^{10} fusion protein. Equal cell numbers were serially-diluted on plates that were then incubated at either the permissive (25^{o}C) or non-permissive (37^{o}C) growth temperature.

Figure 5. Depletion of TIM function leads to mitochondrial morphology defects and cell death in *T. brucei*. (A) Growth curves in the absence (-Tet) and presence (+Tet) of tetracycline of representative clonal *T. brucei* RNAi cell lines. Cell growth stops 50 hours after the addition of the tetracycline inducer. (B) Analysis of mitochondrial morphology in uninduced (0h) and induced (72h) TIM translocase core *Tb*11.01.4870 and Tim8-13 RNAi cell lines using immunofluorescence. Upper panel, Nomarski image. Lower panel, immunofluorescence staining with Hsp60 antiserum (red) and DAPI stain for DNA (blue). Bar = 20 μm. (C) Time course of appearance and extent of mitochondrial fragmentation observed in induced TIM translocase core *Tb*11.01.4870 and Tim8-13 RNAi cell lines (n > 200 cells for each time point).

TABLE LEGEND

Table 1. Patterns of distribution of the small TIMs in eukaryotes. Hidden Markov models were built to describe Tim9, Tim10, Tim8 and Tim13 and used to search genome sequence data. The organisms listed each have completely sequenced genomes. The column “other” includes the Tim12 protein from yeast and humans, both of which have been shown to be located on the surface of the TIM22 translocase ([8] - weak similarity to Tim8, [9] - strong similarity to Tim9, [10] - weak similarity to Tim10, [13] - weak similarity to Tim13).

REFERENCES

Adam, A., M. Endres, C. Sirrenberg, F. Lottspeich, W. Neupert, and M. Brunner. 1999. Tim9, a new component of the TIM22.54 translocase in mitochondria. Embo J **18**:313-319.

Allen, S., H. Lu, D. Thornton, and K. Tokatlidis. 2003. Juxtaposition of the two distal CX3C motifs via intrachain disulfide bonding is essential for the folding of Tim10. J Biol Chem **278**:38505-38513.

Alvarez-Fortes, E., L. M. Ruiz-Perez, F. Bouillaud, E. Rial, and L. Rivas. 1998. Expression and regulation of mitochondrial uncoupling protein 1 from brown adipose tissue in Leishmania major promastigotes. Mol Biochem Parasitol **93**:191-202.

Bailey, T. L., and C. Elkan. 1994. Fitting a mixture model by expectation maximization to discover motifs in biopolymers. Proc Int Conf Intell Syst Mol Biol **2**:28-36.

Bairoch, A., R. Apweiler, C. H. Wu, W. C. Barker, B. Boeckmann, S. Ferro, E. Gasteiger, H. Huang, R. Lopez, M. Magrane, M. J. Martin, D. A. Natale, C. O'Donovan, N. Redaschi, and L. S. Yeh. 2005. The Universal Protein Resource (UniProt). Nucleic Acids Res **33**:D154-159.

Bauer, M. F., and W. Neupert. 2001. Import of proteins into mitochondria: a novel pathomechanism for progressive neurodegeneration. J Inherit Metab Dis **24**:166-180.

Bauer, M. F., U. Rothbauer, N. Muhlenbein, R. J. Smith, K. Gerbitz, W. Neupert, M. Brunner, and S. Hofmann. 1999. The mitochondrial TIM22 preprotein translocase is highly conserved throughout the eukaryotic kingdom. FEBS Lett **464**:41-47.

Bochud-Allemann, N., and A. Schneider. 2002. Mitochondrial substrate level phosphorylation is essential for growth of procyclic Trypanosoma brucei. J Biol Chem **277**:32849-32854.

Brix, J., K. Dietmeier, and N. Pfanner. 1997. Differential recognition of preproteins by the purified cytosolic domains of the mitochondrial import receptors Tom20, Tom22, and Tom70. J Biol Chem **272**:20730-20735.

Chan, N. C., V. A. Likic, R. F. Waller, T. D. Mulhern, and T. Lithgow. 2006. The C-terminal TPR domain of Tom70 defines a family of mitochondrial protein import receptors found only in animals and fungi. J Mol Biol **358**:1010-1022.

Crooks, G. E., G. Hon, J. M. Chandonia, and S. E. Brenner. 2004. WebLogo: a sequence logo generator. Genome Res.

Cserzo, M., E. Wallin, I. Simon, G. von Heijne, and A. Elofsson. 1997. Prediction of transmembrane alpha-helices in prokaryotic membrane proteins: the dense alignment surface method. Protein Eng **10**:673-676.

Curran, S. P., D. Leuenberger, W. Oppliger, and C. M. Koehler. 2002a. The Tim9p-Tim10p complex binds to the transmembrane domains of the ADP/ATP carrier. Embo J.

Curran, S. P., D. Leuenberger, E. Schmidt, and C. M. Koehler. 2002b. The role of the Tim8p-Tim13p complex in a conserved import pathway for mitochondrial polytopic inner membrane proteins. J Cell Biol.

Davis, A. J., N. B. Sepuri, J. Holder, A. E. Johnson, and R. E. Jensen. 2000. Two intermembrane space TIM complexes interact with different domains of Tim23p during its import into mitochondria. J Cell Biol **150**:1271-1282.

Davis, A.J., N.N. Alder, R.E. Jensen, and A.E. Johnson. 2006. The Tim9p/10p and Tim8p/13p Complexes Bind to Specific Sites on Tim23p during Mitochondrial Protein Import. Mol Biol Cell [Epub ahead of print] PMID: 17122363

de Marcos-Lousa, C., D. P. Sideris, and K. Tokatlidis. 2006. Translocation of mitochondrial inner-membrane proteins: conformation matters. Trends Biochem Sci **31**:259-267.

Dietmeier, K., A. Honlinger, U. Bomer, P. J. Dekker, C. Eckerskorn, F. Lottspeich, M. Kubrich, and N. Pfanner. 1997. Tom5 functionally links mitochondrial preprotein receptors to the general import pore. Nature **388**:195-200.

Dolezal, P., V. Likic, J. Tachezy, and T. Lithgow. 2006. Evolution of the molecular machines for protein import into mitochondria. Science **313**:314-318.

Durbin, R., S.R. Eddy, A. Krogh, G. Mitchison. 1998. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. Cambridge University Press.

El-Sayed, N. M., P. J. Myler, G. Blandin, M. Berriman, J. Crabtree, G. Aggarwal, E. Caler, H. Renauld, E. A. Worthey, C. Hertz-Fowler, E. Ghedin, C. Peacock, D. C. Bartholomeu, B. J. Haas, A. N. Tran, J. R. Wortman, U. C. Alsmark, S. Angiuoli, A. Anupama, J. Badger, F. Bringaud, E. Cadag, J. M. Carlton, G. C. Cerqueira, T. Creasy, A. L. Delcher, A. Djikeng, T. M. Embley, C. Hauser, A. C. Ivens, S. K. Kummerfeld, J. B. Pereira-Leal, D. Nilsson, J. Peterson, S. L. Salzberg, J. Shallom, J. C. Silva, J. Sundaram, S. Westenberger, O. White, S. E. Melville, J. E. Donelson, B. Andersson, K. D. Stuart, and N. Hall. 2005. Comparative genomics of trypanosomatid parasitic protozoa. Science **309**:404-409.

Endres, M., W. Neupert, and M. Brunner. 1999. Transport of the ADP/ATP carrier of mitochondria from the TOM complex to the TIM22.54 complex. Embo J **18**:3214-3221.

Esseiva, A. C., A. L. Chanez, N. Bochud-Allemann, J. C. Martinou, A. Hemphill, and A. Schneider. 2004. Temporal dissection of Bax-induced events leading to fission of the single mitochondrion in Trypanosoma brucei. EMBO Rep **5**:268-273.

Gabaldon, T., and M. A. Huynen. 2004. Shaping the mitochondrial proteome. Biochim Biophys Acta **1659**:212-220.

Henriquez, F. L., T. A. Richards, F. Roberts, R. McLeod, and C. W. Roberts. 2005. The unusual mitochondrial compartment of Cryptosporidium parvum. Trends Parasitol **21**:68-74.

Herrmann, J. M., and W. Neupert. 2003. Protein insertion into the inner membrane of mitochondria. IUBMB Life **55**:219-225.

Hoppins, S. C., and F. E. Nargang. 2004. The Tim8-Tim13 complex of Neurospora crassa functions in the assembly of proteins into both mitochondrial membranes. J Biol Chem **279**:12396-12405.

Humphrey, W., A. Dalke, and K. Schulten. 1996. VMD: visual molecular dynamics. J Mol Graph **14**:33-38, 27-38.

Jarosch, E., G. Tuller, G. Daum, M. Waldherr, A. Voskova, and R. J. Schweyen. 1996. Mrs5p, an essential protein of the mitochondrial intermembrane space, affects protein import into yeast mitochondria. J Biol Chem **271**:17219-17225.

Jeanmougin, F., J. D. Thompson, M. Gouy, D. G. Higgins, and T. J. Gibson. 1998. Multiple sequence alignment with Clustal X. Trends Biochem Sci **23**:403-405.

Jin, H., E. Kendall, T. C. Freeman, R. G. Roberts, and D. L. Vetrie. 1999. The human family of Deafness/Dystonia peptide (DDP) related mitochondrial import proteins. Genomics **61**:259-267.

Katinka, M. D., S. Duprat, E. Cornillot, G. Metenier, F. Thomarat, G. Prensier, V. Barbe, E. Peyretaillade, P. Brottier, P. Wincker, F. Delbac, H. El Alaoui, P. Peyret, W. Saurin, M. Gouy, J. Weissenbach, and C. P. Vivares. 2001. Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi. Nature **414**:450-453.

Koehler, C. M. 2004a. New developments in mitochondrial assembly. Annu Rev Cell Dev Biol **20**:309-335.

Koehler, C. M. 2004b. The small Tim proteins and the twin Cx3C motif. Trends Biochem Sci **29**:1-4.

Koehler, C. M., E. Jarosch, K. Tokatlidis, K. Schmid, R. J. Schweyen, and G. Schatz. 1998a. Import of mitochondrial carriers mediated by essential proteins of the intermembrane space. Science **279**:369-373.

Koehler, C. M., D. Leuenberger, S. Merchant, A. Renold, T. Junne, and G. Schatz. 1999. Human deafness dystonia syndrome is a mitochondrial disease. Proc Natl Acad Sci U S A **96**:2141-2146.

Koehler, C. M., S. Merchant, W. Oppliger, K. Schmid, E. Jarosch, L. Dolfini, T. Junne, G. Schatz, and K. Tokatlidis. 1998b. Tim9p, an essential partner subunit of Tim10p for the import of mitochondrial carrier proteins. Embo J **17**:6477-6486.

Leuenberger, D., N. A. Bally, G. Schatz, and C. M. Koehler. 1999. Different import pathways through the mitochondrial intermembrane space for inner membrane proteins. Embo J **18**:4816-4822.

Leuenberger, D., S. P. Curran, D. Wong, and C. M. Koehler. 2003. The role of Tim9p in the assembly of the TIM22 import complexes. Traffic **4**:144-152.

Lu, H., A. P. Golovanov, F. Alcock, J. G. Grossmann, S. Allen, L. Y. Lian, and K. Tokatlidis. 2004. The structural basis of the TIM10 chaperone assembly. J Biol Chem **279**:18959-18966.

Lu, H., and J. Woodburn. 2005. Zinc binding stabilizes mitochondrial Tim10 in a reduced and import-competent state kinetically. J Mol Biol **353**:897-910.

Luciano, P., S. Vial, M. A. Vergnolle, S. D. Dyall, D. R. Robinson, and K. Tokatlidis. 2001. Functional reconstitution of the import of the yeast ADP/ATP carrier mediated by the TIM10 complex. Embo J **20**:4099-4106.

Marchler-Bauer, A., J. B. Anderson, P. F. Cherukuri, C. DeWeese-Scott, L. Y. Geer, M. Gwadz, S. He, D. I. Hurwitz, J. D. Jackson, Z. Ke, C. J. Lanczycki, C. A. Liebert, C. Liu, F. Lu, G. H. Marchler, M. Mullokandov, B. A. Shoemaker, V. Simonyan, J. S. Song, P. A. Thiessen, R. A. Yamashita, J. J. Yin, D. Zhang, and S. H. Bryant. 2005. CDD: a Conserved Domain Database for protein classification. Nucleic Acids Res **33**:D192-196.

McCulloch, R., E. Vassella, P. Burton, M. Boshart, and J. D. Barry. 2004. Transformation of monomorphic and pleomorphic Trypanosoma brucei. Methods Mol Biol **262**:53-86.

Muhlenbein, N., S. Hofmann, U. Rothbauer, and M. F. Bauer. 2004. Organization and function of the small Tim complexes acting along the import pathway of metabolite carriers into mammalian mitochondria. J Biol Chem **279**:13540-13546.

Notredame, C., L. Holm, and D. G. Higgins. 1998. COFFEE: an objective function for multiple sequence alignments. Bioinformatics **14**:407-422.

Ohlmeier, S., A. J. Kastaniotis, J. K. Hiltunen, and U. Bergmann. 2004. The yeast mitochondrial proteome, a study of fermentative and respiratory growth. J Biol Chem **279**:3956-3979.

Pebay-Peyroula, E., C. Dahout-Gonzalez, R. Kahn, V. Trezeguet, G. J. Lauquin, and G. Brandolin. 2003. Structure of mitochondrial ADP/ATP carrier in complex with carboxyatractyloside. Nature **426**:39-44.

Pfanner, N., and A. Geissler. 2001. Versatility of the mitochondrial protein import machinery. Nat Rev Mol Cell Biol **2**:339-349.

Pfanner, N., N. Wiedemann, C. Meisinger, and T. Lithgow. 2004. Assembling the mitochondrial outer membrane. Nat Struct Mol Biol **11**:1044-1048.

Prokisch, H., C. Scharfe, D. G. Camp, 2nd, W. Xiao, L. David, C. Andreoli, M. E. Monroe, R. J. Moore, M. A. Gritsenko, C. Kozany, K. K. Hixson, H. M. Mottaz, H. Zischka, M. Ueffing, Z. S. Herman, R. W. Davis, T. Meitinger, P. J. Oefner, R. D. Smith, and L. M. Steinmetz. 2004. Integrative analysis of the mitochondrial proteome in yeast. PLoS Biol **2**:e160.

Putignani, L., A. Tait, H. V. Smith, D. Horner, J. Tovar, L. Tetley, and J. M. Wastling. 2004. Characterization of a mitochondrion-like organelle in Cryptosporidium parvum. Parasitology **129**:1-18.

Rehling, P., K. Model, K. Brandner, P. Kovermann, A. Sickmann, H. E. Meyer, W. Kuhlbrandt, R. Wagner, K. N. Truscott, and N. Pfanner. 2003. Protein insertion into the mitochondrial inner membrane by a twin-pore translocase. Science **299**:1747-1751.

Reichert, A. S., and W. Neupert. 2004. Mitochondriomics or what makes us breathe. Trends Genet **20**:555-562.

Riordan, C. E., J. G. Ault, S. G. Langreth, and J. S. Keithly. 2003. Cryptosporidium parvum Cpn60 targets a relict organelle. Curr Genet **44**:138-147.

Roesch, K., S. P. Curran, L. Tranebjaerg, and C. M. Koehler. 2002. Human deafness dystonia syndrome is caused by a defect in assembly of the DDP1/TIMM8a-TIMM13 complex. Hum Mol Genet **11**:477-486.

Schatz, G. 1997. Just follow the acid chain. Nature **388**:121-122.

Schneider, T. D., and R. M. Stephens. 1990. Sequence logos: a new way to display consensus sequences. Nucleic Acids Res **18**:6097-6100.

Sickmann, A., J. Reinders, Y. Wagner, C. Joppich, R. Zahedi, H. E. Meyer, B. Schonfisch, I. Perschil, A. Chacinska, B. Guiard, P. Rehling, N. Pfanner, and C. Meisinger. 2003. The proteome of Saccharomyces cerevisiae mitochondria. Proc Natl Acad Sci U S A **100**:13207-13212.

Sirrenberg, C., M. Endres, H. Folsch, R. A. Stuart, W. Neupert, and M. Brunner. 1998. Carrier protein import into mitochondria mediated by the intermembrane proteins Tim10/Mrs11 and Tim12/Mrs5. Nature **391**:912-915.

Slapeta, J., and J. S. Keithly. 2004. Cryptosporidium parvum mitochondrial-type HSP70 targets homologous and heterologous mitochondria. Eukaryot Cell **3**:483-494.

Smid, O., E. Horakova, V. Vilimova, I. Hrdy, R. Cammack, A. Horvath, J. Lukes, and J. Tachezy. 2006. Knock-downs of iron-sulfur cluster assembly proteins ISCS and ISCU down-regulate the active mitochondrion of procyclic trypanosoma brucei. J Biol Chem.

Thompson, J. D., D. G. Higgins, and T. J. Gibson. 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Res **22**:4673-4680.

Truscott, K. N., N. Wiedemann, P. Rehling, H. Muller, C. Meisinger, N. Pfanner, and B. Guiard. 2002. Mitochondrial import of the ADP/ATP carrier: the essential TIM complex of the intermembrane space is required for precursor release from the TOM complex. Mol Cell Biol **22**:7780-7789.

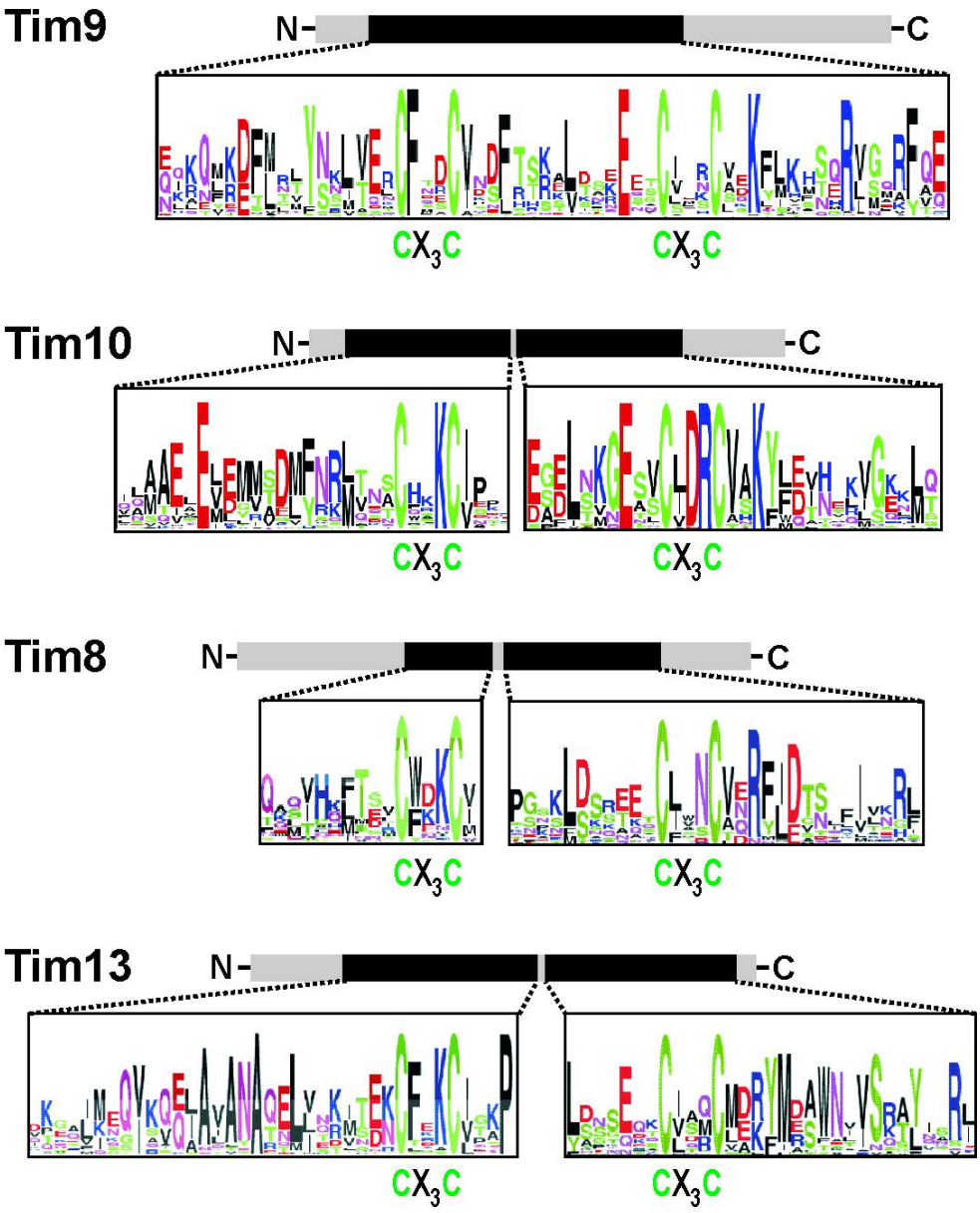
Vasiljev, A., U. Ahting, F. E. Nargang, N. E. Go, S. J. Habib, C. Kozany, V. Panneels, I. Sinning, H. Prokisch, W. Neupert, S. Nussberger, and D. Rapaport. 2004. Reconstituted TOM core complex and Tim9/Tim10 complex of mitochondria are sufficient for translocation of the ADP/ATP carrier across membranes. Mol Biol Cell **15**:1445-1458.

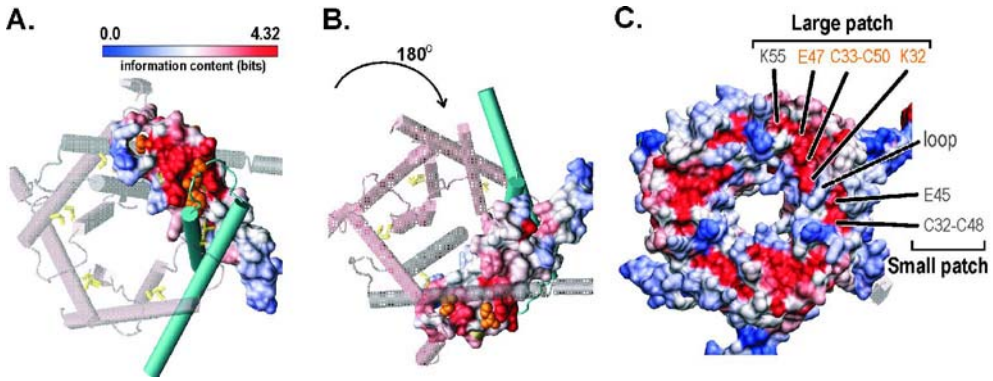
Vergnolle, M. A., C. Baud, A. P. Golovanov, F. Alcock, P. Luciano, L. Y. Lian, and K. Tokatlidis. 2005. Distinct domains of small Tims involved in subunit interaction and substrate recognition. J Mol Biol **351**:839-849.

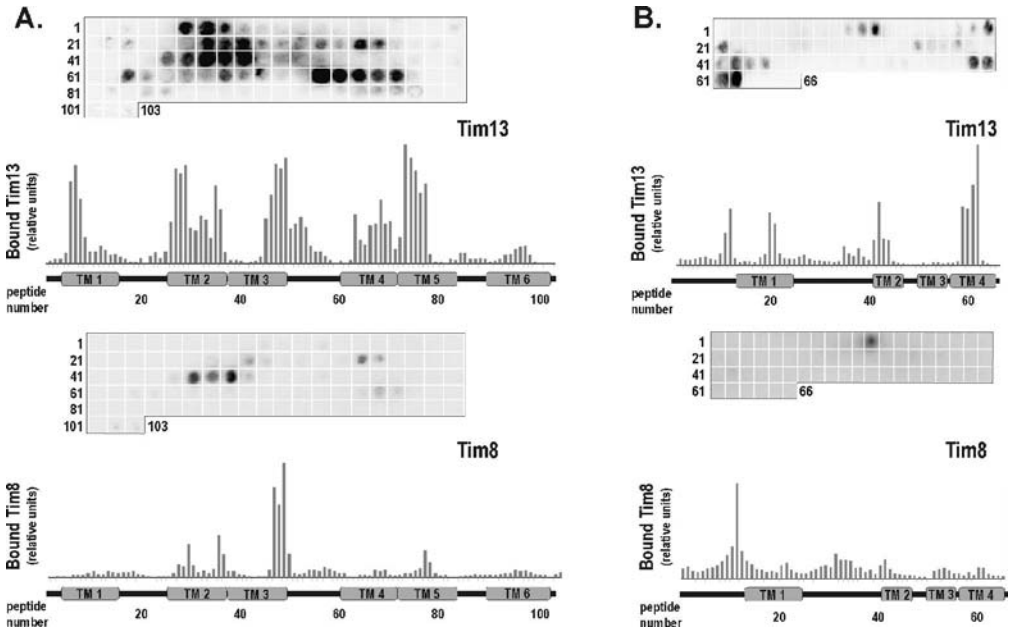
Vial, S., H. Lu, S. Allen, P. Savory, D. Thornton, J. Sheehan, and K. Tokatlidis. 2002. Assembly of Tim9 and Tim10 into a functional chaperone. J Biol Chem **277**:36100-36108.

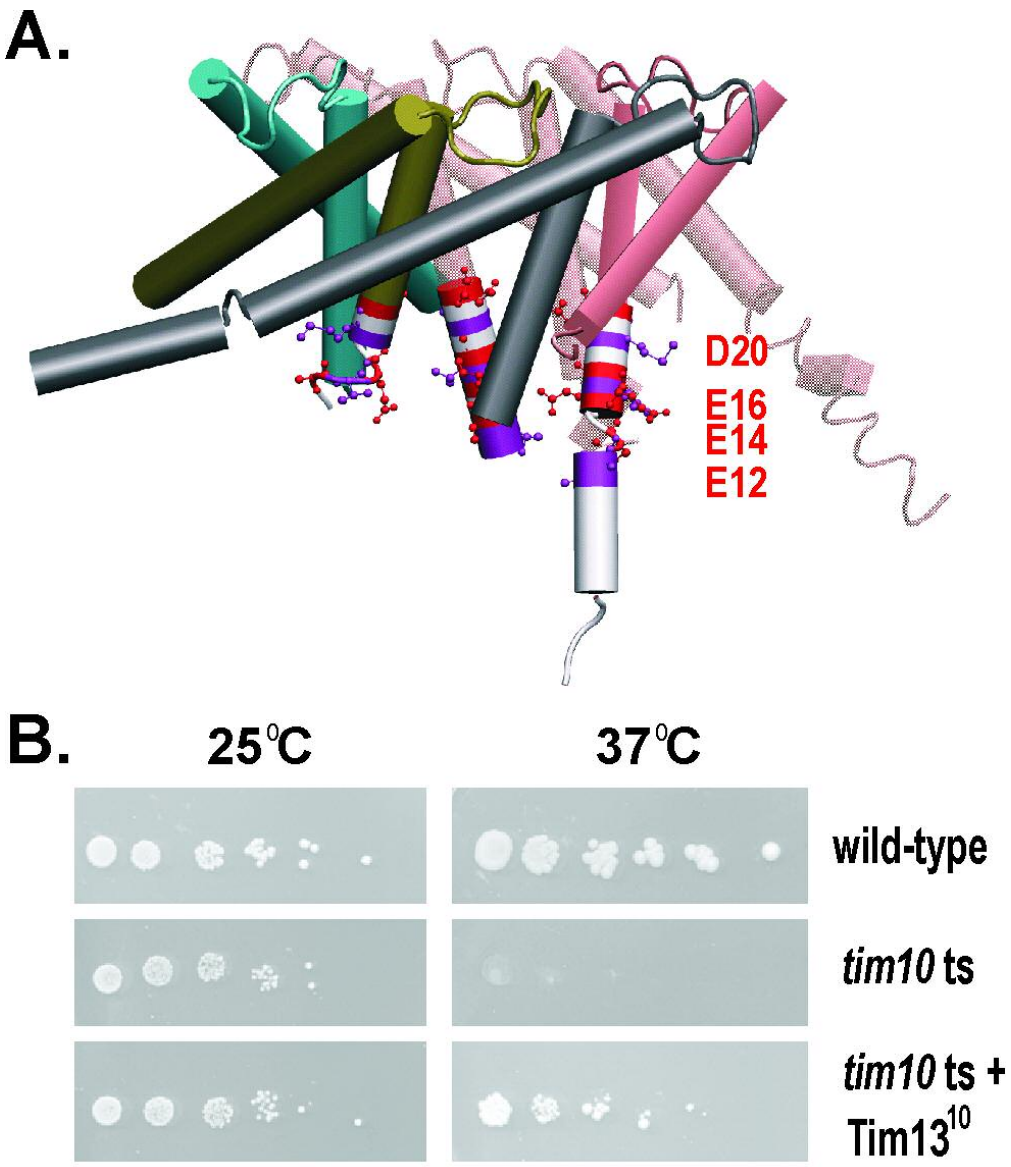
Webb, C. T., M. A. Gorman, M. Lazarou, M. T. Ryan, and J. M. Gulbis. 2006. Crystal structure of the mitochondrial chaperone TIM9.10 reveals a six-bladed alpha-propeller. Mol Cell **21**:123-133.

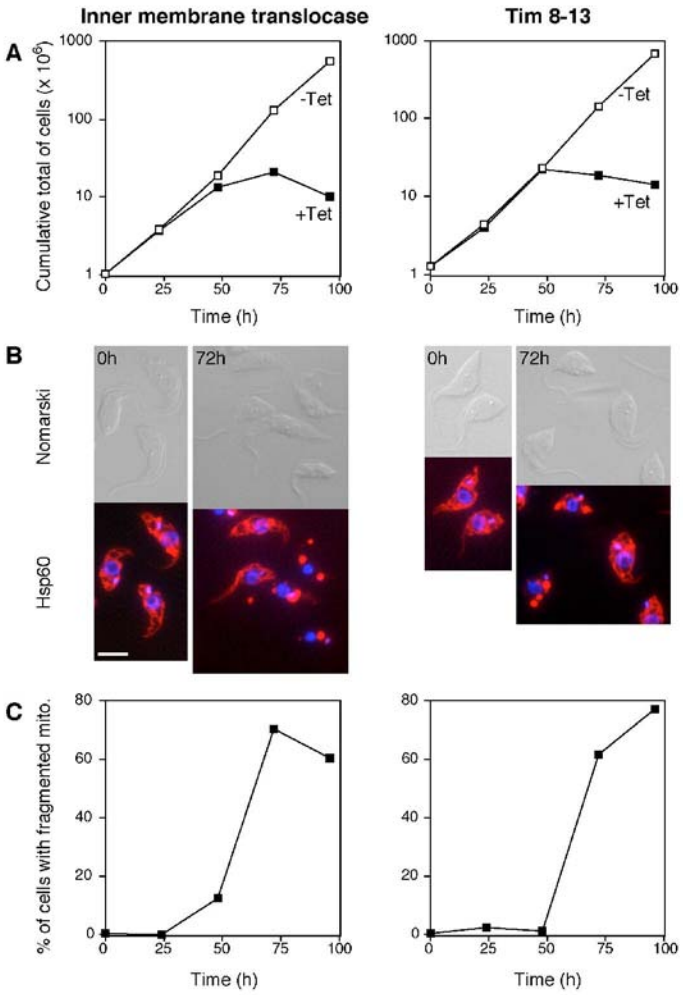
Wiedemann, N., K. N. Truscott, S. Pfannschmidt, B. Guiard, C. Meisinger, and N. Pfanner. 2004. Biogenesis of the protein import channel Tom40 of the mitochondrial outer membrane: intermembrane space components are involved in an early stage of the assembly pathway. J Biol Chem.











	Tim9	Tim10	Tim8	Tim13	other
Fungi					
Saccharomyces cerevisiae	O74700	P87108	P57744	P53299	P32830[10]
Neurospora crassa	Q8J1Z1	Q9C0N3	Q9Y8C0	Q7SBR3	none
Eremothecium gossypii	Q757S0	Q759W7	Q75DU7	Q75F72	AAS51609[10]
Encephalitozoon cuniculi	none	none	none	none	none
Animals					
Homo sapiens	Q9Y5J7	P62072	O60220 Q9Y5J9	AAF15101 AAF15102	Q9Y5J6[9]
Mus musculus	Q9WV98	P62073	Q9WVA2 P62077	P62075 BAB22536	Q9WV96[9]
Danio rerio	Q9W762	Q6DI06	Q6DEM5	Q6DGJ3	Q568N4
Caenorhabditis elegans	Q17754	Q9Y0V6	Q9N408	O45319	Q9Y0V2[9]
Drosophila melanogaster	Q9VYD7	Q9W2D6	Q9Y1A3	Q9VTN3	Q9Y0V3[9]
Plants					
Arabidopsis thaliana	Q9XGX9	Q9ZW33	Q9XGY4	Q9XH48	none
Oryza sativa	Q9XGX7	Q7XI32	Q6Z1H2	Q7XUM9	none
Protists					
Dictyostelium discoideum	EAL71103	EAL64919	none	none	none
Plasmodium falciparum	Q8ID24	Q8I5W2	Q8ILN5	Q8I500	Q8I472[13]
Plasmodium bergheii	Q4YMY2	Q4YCZ6	Q4Z7J2	Q4Z4Q5	Q4Z7B6[13]
Plasmodium chabaudi	Q4XVQ0	Q4XF82	CAH85260	Q4XDV1	Q4Y1F0[8]
Plasmodium yoelli	Q7RCS2	Q7RBI2	Q7R8G4	Q7RH88	Q7RFP3[8]
Theileria parva	EAN34037	EAN34123	EAN30577		none
Cryptosporidium parvum	none	none	EAK90166		none
Cryptosporidium hominis	none	none	EAL36478		none
Leishmania major	CAJ03937	CAJ05328	CAJ04425		none
Trypanosoma brucei	AAX69615	AAX80231	EAN79502		none
Trypanosoma cruzi	EAN98593	EAN94952	EAN92571		none
Trichomonas vaginalis	none	none	none	none	none

Hidden Markov models were built to describe Tim9, Tim10, Tim8 and Tim13 and used to sift the data in UniProt. The listed organisms have complete genome sequences represented in UniProt.

[8] - weak similarity to Tim8
[9] - strong similarity to Tim9, functional studies reveal the protein to be located on the inner membrane and part of the TIM22 complex in humans (ref)
[10] - weak similarity to Tim10, functional studies show the protein to be located on the inner membrane and part of the TIM22 complex in yeast (ref)
[13] - weak similarity to Tim13