High aggregation sensitivity of mammalian mitochondrial elongation factor Tu (Tufm) as a sensor for organellar stress

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Running title: *Protein aggregation in heat-stressed mitochondria*

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Keywords: Mitochondria, heat-stress, proteomic analysis, protein aggregation, protein translation, mitochondrial elongation factor Tu, Tufm, preprotein import

Abstract

As proteins in mammalian cells exhibit optimal stability at natural temperatures, small temperature variations may cause unfolding and subsequent non-specific aggregation. As this process leads to a loss of function of the affected polypeptides as well as to further cytotoxic stress, aggregate formation has been recognized as a major pathogenic factor in human diseases. In this study we determined the impact of physiological heat stress on mammalian mitochondria on a proteomic level. The overall solubility of endogenous mitochondrial proteins was only marginally affected by a treatment at elevated temperatures. However, we identified a small subset of polypeptides that exhibited an exceptionally high sensitivity to heat stress. The mitochondrial translation elongation factor Tu (Tufm), a protein essential for organellar protein biosynthesis, was highly aggregation-prone and lost its solubility already under mild heat stress conditions. In parallel, mitochondrial translation as well as the import of cytosolic proteins was defective in heat stressed mitochondria. We propose that a shutdown of endogenous protein synthesis concomitant with a reduced preprotein import has a protective function by attenuating the proteotoxic stress caused by an accumulation of nascent polypeptides with a high tendency to misfold.

Introduction

Mitochondria are organelles that fulfill many essential cellular tasks in addition to their traditionally established functions in energy metabolism. These functions are dependent on the enzymatic activities provided by many different mitochondrial polypeptides, of which the majority is encoded in the nucleus while only a few polypeptides are generated by the endogenous mitochondrial protein bio-synthesis machinery. The mitochondrial fitness is therefore dependent on a coordinated expression of both nuclear and mitochondrial genes. The mechanisms underlying this coordination process, in particular during adaptation to various stress conditions, are still only inadequately known and are an active field of cell biological research (1).

To maintain mitochondrial functions under normal and stress conditions, a mitochondria-specific protein quality control (PQC) system, consisting of chaperones and proteolytic enzymes, protects the structural integrity of endogenous polypeptides or removes terminally misfolded proteins (2). Apart from a loss of important enzymatic activities, an accumulation of misfolded proteins can also lead to aggregation reactions that result in further structural and functional damage of the cells. As shown in other organelles or in the cytosol, the activity of the PQC system is mainly aimed at the prevention of an accumulation of cellular protein

aggregates (3). The proteotoxic effects of aggregates are best exemplified in the occurrence of so-called protein-folding diseases, in particular neurodegenerative diseases that are caused by or at least correlated with the accumulation of specific protein aggregates (4). The chronic expression of aggregation–prone proteins such as pathological poly-glutamine proteins in these diseases declines the protein homeostasis of the cell, which results in further misfolding and aggregation of metastable proteins. Further the overall capacity of protein homeostasis is declined in aging cells, which results in an increased risk of accumulation of toxic protein aggregates (5,6). Research efforts over the past decade have established that mito-chondrial dysfunction plays a major role in the etiology of many neurodegenerative diseases (7) as well as in aging processes (8).

Besides mutations and translation errors, there are also environmental stress conditions, which cause protein misfolding and consequently lead to aggregation processes (9). Elevated temperatures or heat stress at non-lethal levels represent a prominent cause of polypeptide denaturation and functional inactivation. As already small increases in temperature can lead to protein unfolding and aggregation, elevated growth temperatures represent a substantial challenge to cellular survival (10). However small increase of the optimal physiological temperature could also be positively for organisms under specific circumstances as fever in vertebrates has evolved as a survival benefit by regulating the immune system and protecting the organism against infection (11).

Elevated temperatures activate a cellular heat shock response by inducing the synthesis of heat shock proteins that help to maintain protein homeostasis and ensure the survival of the cell (12). The heat shock response is based on a specific transcriptional response regulated by heat shock transcription factors (HSF) that induce the synthesis of a specific set of molecular chaperones during stress (13). If this protein quality control system is overwhelmed, cells have additional protective mechanisms to deal with aggregated proteins, like sequestration to specific compartments, disaggregation and refolding to a native protein structure, clearance by autophagy as well as asymmetric distribution of aggregates during cell division (9,14).

Although substantial information on the stress-related reactivity of the cytosolic compartment has been obtained, so far there is only little known about the aggregation behavior of endogenous mitochondrial proteins under stress conditions and the effect on the overall mitochondrial function. Previous studies in *S. cerevisiae* have shown that key mitochondrial metabolic enzymes are aggregating and become inactivated under elevated temperatures. The aggregation propensity was modulated by mitochondrial chaperones and the Pim1 protease in the matrix compartment (15). Interestingly, mitochondrial proteins were over-represented in a screen of aging-related protein aggregation in *C. elegans*, connecting mitochondrial protein aggregation with age-related diseases (16).

In this work, we studied the impact of mitochondrial protein aggregation reactions at different stress conditions under *in vivo* like conditions in mitochondria isolated from mammalian cells. We identified aggregation–prone mitochondrial proteins by performing a quantitative proteomic analysis determining the changes in protein solubility after heat stress. In particular, we treated isolated intact mitochondria with high temperature to induce protein aggregation and characterize the changes in protein abundance using 2-dimensional differential gel electrophoresis (2D-DIGE). The quantification of the protein spot pattern revealed the identification of temperature sensitive proteins, whose aggregation behavior was characterized in more detail. Finally, we tested the impact of heat stress on the mitochondrial protein biogenesis reactions by assessing mitochondrial translation as well as the efficiency of polypeptide import.

Results

General effects of heat stress on cells and isolated mitochondria.

In order to test the effects of heat stress on mitochondria in intact HeLa cells we analyzed the morphology of mitochondria by fluorescence microscopy. Cells were incubated for 2 h at 45°C compared to cells growing at the physiological temperature of 37°C. The mitochondrial morphology was analyzed using fluorescently labeled antibodies detecting the mitochondrial matrix proteins Hsp60 (60 kDa heat shock protein) and Tufm (mitochondrial elongation factor Tu) as well as the mitochondrial inner membrane proteins Sdha (flavoprotein subunit of the succinate dehydrogenase) and F1ß (ATP synthase subunit beta). The fluorescence microscopic analysis showed that the shape of the mitochondria changed from the typical filamentous network structure, which spread into the periphery of the cell to a more condensed structure around the nucleus after heat shock (Fig. 1A).

To determine the effects of heat stress on the functional integrity of mitochondria, we measured typical metabolic properties of mitochondria, like the inner membrane potential ($\Delta\psi$), the accumulation of reactive oxygen species (ROS), and the mitochondrial ATP levels. The membrane potential of HeLa cells was analyzed by staining with the potential-dependent mitochondrial dye tetramethylrhodamine (TMRE) and subsequent flow cytometry. As control for a depleted mitochondrial membrane potential cells were treated with 0.1 µM valinomycin before TMRE staining. We observed that the mitochondrial membrane potential was decreased by about 30% after heat stress at 45°C for 2.5 h (Fig. 1B, left). The production of ROS was assayed by a staining with the mitochondria-specific superoxide-reactive dye MitoSOX™. As control we used a treatment with menadione (100 µM f. c.), a vitamin K_3 metabolite that generates superoxide radicals (17). The analysis by flow cytometry showed a decreased production of reactive oxygen species of about 30-40% after incubation at 45°C for 2.5 h compared to unstressed cells (Fig. 1B, right). We also investigated the temperature dependence of the membrane potential in isolated mitochondria. To monitor the change in membrane potential mitochondria were stained with TMRE and the fluorescence was measured in a microplate reader. Mitochondrial membrane potential was already significantly diminished after 20 min incubation at elevated temperatures. As shown in Fig. 1C membrane potential started to decrease after an incubation at 37°C indicating that isolated mitochondria were more sensitive to increased temperatures as mitochondria in whole cells. At 42°C, representing physiological heat stress, the membrane potential decreased for about 70% and was almost completely abolished after a severe heat treatment at 45°C. We were also interested if there is a change in the ATP levels in isolated mitochondria after incubation at elevated temperatures. Our results showed that there was already a decrease of about 25% in the mitochondrial ATP content after 20 min incubation at 25°C, which was increased after heat shock, resulting in a decrease of more than 80% compared to pre-heat shock levels (Fig. 1D).

To investigate the physical integrity of the heat stressed mitochondria, we treated them with proteinase K (PK) after a 20 min incubation at 42°C and 25°C (control). PK digests exposed proteins, which are not protected by intact mitochondrial membranes. Western blot analysis showed that there was no digestion of any soluble matrix proteins like Trap1 (heat shock protein 75 kDa), Mpp (mitochondrial-processing peptidase) and Tufm in both heat stressed and unstressed mitochondria, which suggests that the mitochondrial inner membrane was still intact after heat treatment (Fig. 1E). The translocase of the mitochondrial inner membrane Tim23 was slightly digested by PK in the heat stressed sample indicating that the mitochondrial outer membrane was partially damaged by the incubation at elevated temperatures. In order to proof that the used conditions were sufficient for protein digestion, we used 0.5% (v/v) Triton X-100 for complete lysis of the mitochondria. All proteins were digested in lysed mitochondria using a PK

concentration of 1.25 µg/ml and 20 min incubation, except for Mpp, which was just partially digested.

As one of the main functions of mitochondria is the ATP production by electron transfer through the membrane bound complexes I-V (18), we investigated if there is a structural change in the complexes of the respiratory chain after heat stress. For this purpose the heat shock was performed as described before in isolated mitochondria. Afterwards a separation of the respiratory chain complexes was done under native conditions via Blue-native polyacrylamide gel electrophoresis (BN-PAGE) and analyzed by Western blot using antibodies against subunits of the five different complexes. The experiment showed no significant change in the composition of complexes, despite small changes in complex II and IV (Fig. 1F). We also investigated the enzymatic activities of malate dehydrogenase (MDH) and alpha-ketoglutarate dehydrogenase complex (KGDHC) enzymes as representatives of the tricarboxylic acid cycle (TCA) under heat stress conditions. Activities were tested after 20 min incubation of isolated mitochondria at 42°C compared to 25°C. The MDH activity showed no change after heat shock whereas the KGDHC activity was reduced to 65% of the activity compared with the treatment at 25°C (Fig. 1G), which could indicate a thermo-dependent inactivation of KGDHC.

These results showed that even if the mitochondria and the respiratory chain complexes of the inner membrane are still intact there is a clear temperature-dependent decrease of metabolic functions like an impairment of enzymatic activity and energy production as well as a drop in membrane potential in heat-stressed mitochondria.

Analysis of the mitochondrial proteome under heat stress.

As we have established that heat stress caused functional defects in mitochondria, we determined the effects of heat stress on the structural integrity of the mitochondrial proteome by identifying polypeptides that are prone to aggregate at elevated temperatures. As described above, we treated isolated mitochondria for 20 min at a physiological heat stress temperature of 42°C and 25°C as control. Afterwards mitochondria were lysed by detergent treatment and centrifuged at 125,000 x*g* in order to separate aggregated proteins, which go to the pellet fraction, from soluble proteins, which remain in the supernatant (15,19). To detect quantitative changes in the mitochondrial proteome, we used two-dimensional differential gel electrophoresis (DIGE), which allows the simultaneous separation of three different fluorescently labeled samples on one gel to exclude inter-gel variations. The gels were scanned with dye specific wavelengths and gel matching was performed to detect and quantify the protein spots in the respective samples. Spot detection as well as determination of spot intensities were performed using the Delta2D software (DECODON). For the quantitative analysis, data of two independent experiments, each consisting of triplicates for stressed and unstressed samples were used. On average, a total of 300-400 spots per gel have been detected. The protein spots were manually excised from spots of the Coomassie-stained master gels containing proteins of isolated HeLa mitochondria. Excised spots were digested by trypsin and analyzed by mass spectrometry. In order to obtain a consistent and comparable protein spot pattern, we analyzed the polypeptides present in the supernatant fractions of the different samples. A reduced or absent spot intensity in the supernatant of heat-treated mitochondria in comparison to the control sample would indicate potential aggregation-prone polypeptides that lost their solubility. The short time of incubation at elevated temperature essentially excluded the chance that the reduction of protein amount was caused by degradation processes.

An overlay of the 2D gels obtained after heat-shock treatment allowed a direct comparison of mitochondrial polypeptide solubility. Proteins present in the soluble proteome of the heat-stressed sample were displayed in green, those of the control sample were stained in red resulting in a yellow color overlay picture for protein spots that did not show a change in abundance after the heat shock (Fig. 2A). Therefore red spots would

represent proteins present in reduced amounts in the heat stress samples indicating a potential temperature-dependent aggregation. Overall, the abundance of soluble proteins did not change significantly after the heat shock treatment, indicating a high general temperature stability of the mitochondrial proteome, However, there were 10 protein spots, which were consistently absent in the soluble mitochondrial proteome after heat stress in all six experiments of which 4 proteins could be identified by mass spectrometry. Two of the proteins, Pdia3 (protein disulfide-isomerase A3) as well as Hyou1 (hypoxia up-regulated protein 1), were proteins, which were assigned by the database to be localized in the lumen of the endoplasmatic reticulum. The contamination of ER proteins in the samples could be explained by to the isolation procedure of mitochondria using standard differential centrifugation method that would not be able to completely remove all ER proteins from the mitochondria fraction. However two of the identified proteins were mitochondrial proteins. The mitochondrial Lon protease homolog (LonP1) showed a partial aggregation after heat shock. The most prominent protein spot, which was completely disappearing after heat treatment was the mitochondrial elongation factor Tu (Tufm). This result was consistent for all six gels (Fig. 2A, detail sections).

We also compared the results for the 17 identified mitochondrial proteins (Table 1; Fig. S1) and quantified the abundance in the soluble proteome after heat shock compared to the control. The spot intensities for each gel were normalized by the total sum of spot intensity at 25°C for each gel (Fig. 2B). There was no significant decrease of abundance in the soluble proteome after heat shock for the majority of proteins, whereas a significant decrease in abundance was observed for the protease LonP1 (about 40%) and Tufm (about 70%) after heat shock. The protein amounts of Sdha (flavoprotein subunit of the succinate dehydrogenase), Hsp60 (60 kDa heat shock protein), and HspA9 (70 kDa heat shock protein) showed only a small decrease of about 5-15%, whereas the other proteins exhibited no significant decrease in the soluble fraction after heat stress compared to the control.

Overall these results of the proteomic analysis showed that the mitochondrial proteome is relatively resistant against heat stress as the vast majority of mitochondrial proteins are not prone to aggregate. Strikingly one of the mitochondrial proteins, the translation-related protein Tufm, exhibited a very thermolabile behavior by aggregating completely under heat stress.

Aggregation behavior of Tufm during stress.

Having determined that Tufm is the most prominent protein disappearing from the soluble fraction under heat stress conditions, we wanted to confirm if this behavior was due to protein aggregation and which relevance a potential aggregation has on the functionality of affected mitochondria. In order to get more information about a temperature-dependent aggregation of Tufm in comparison to other mitochondrial proteins, we incubated isolated mitochondria at control temperature (25°C) as well as under mild and strong heat shock conditions (37°C, 42°C, and 45°C). Although a temperature of 37°C can be considered as physiological in HeLa cells, our results (Fig. 1C) have indicated that isolated mitochondria showed already some temperature-sensitivity under this condition.

Isolated HeLa mitochondria were lysed after heat treatment and aggregated proteins (pellet) were separated from the soluble proteins (supernatant) by high-speed centrifugation and analyzed by SDS-PAGE and Western blot. In addition to Tufm, the aggregation behavior of the elongation factor Tsfm, which is associated with Tufm during translation inducing GDP to GTP exchange (20), as well as the mitochondrial ribosomal protein Mrpl38 was investigated. A significant amount of Tufm and Tsfm as well as Mrpl38 was recovered in the pellet already at 37°C and their aggregation tendency increased further with higher temperatures (Fig. 3A). Notably, at 42°C Tufm and Mrpl38 were not detected any more in the supernatant fraction, indicating a complete aggregation. The mitochondrial matrix

proteins Aco2 and Hsp60 also started to aggregate at 37°C, but not as strong as Tufm. Whereas Aco2 was completely aggregated after incubation at 45°C, part of Hsp60 stayed soluble. The translocase of the inner mitochondrial membrane Tim23 served as a control, which showed no temperature-dependent aggregation.

To investigate if other stress conditions such as the formation of reactive oxygen species also induced an aggregation of mitochondrial proteins, mitochondria were treated with menadione. Isolated mitochondria were incubated with different menadione concentrations and aggregated and soluble proteins were separated and analyzed as described above. Under oxidative stress conditions we observed no aggregation for the mitochondrial matrix proteins Aco2 and Sod2 as well as for the outer membrane control protein Vdac (Fig. 3B). Whereas just a small subset of Hsp60 aggregated after treatment with high menadione concentrations, significant amount of the elongation factor Tufm aggregated in a concentration-dependent manner, starting at 0.5 mM menadione. However, compared to the temperature behavior of Tufm, there was still a substantial amount of soluble protein detected in the supernatant, indicating that Tufm may be more sensitive to heat than to oxidative stress.

Molecular chaperones are the most prominent cellular enzymes involved in aggregation prevention and refolding of heat-denatured proteins (21). As most molecular chaperones require ATP for their activity, we wanted to determine if there is an ATP-dependence of Tufm aggregation. Isolated HeLa mitochondria were heat stressed at 42°C in the presence and absence of ATP. Aggregates and soluble proteins were isolated and analyzed as described before. It was shown that although there was an ATP-effect after heat shock visible for the shock protein Hsp60, which was more stable in the presence of ATP, there was no change of the Tufm as well as Tsfm, Mrpl38 and Aco2 aggregation (Fig. 3C), indicating that at least under the chosen conditions there is no aggregation-protective effect for the analyzed proteins mediated by mitochondrial chaperones.

Tufm is a GTPase, which hydrolyzes GTP as energy source for conformational changes in the process of transferring the aminoacyl-tRNA to the A-site of the ribosome (20). As the presence or absence of guanine nucleotides might influence protein stability of Tufm, we also determined the influence of GTP on its temperature-dependent aggregation. Isolated mitochondria were heat stressed in absence and presence of GTP and aggregates were isolated and analyzed as described above. As shown in Fig. 3D there was no GTP dependence of the aggregation of Tufm at 42°C as well as for Tsfm. The ribosomal protein Mrpl38 was already present in the pellet fraction at 25°C in the same amount as after heat shock and there was no visible change in the presence of GTP.

Time-dependence of aggregation under heat stress.

The kinetics of the mitochondrial protein aggregation was studied by incubation of isolated mitochondria for several time points from 0 to 60 minutes at heat stress and control conditions. Aggregated proteins were analyzed by SDS-PAGE and Western blot. The percentage of aggregation was calculated by the amount of aggregated protein compared to the total protein amount (Fig. 4). The mitochondrial elongation factors Tufm and Tsfm both exhibited remarkable fast aggregation kinetics. These proteins started to aggregate already after 2 min incubation at 42°C and practically reached a maximal level already after 5 min. The protein amounts in the pellet did not increase significantly over time any more, indicating a very thermolabile behavior. The ribosomal protein Mrpl38 also showed a fast aggregation kinetics with around 50% aggregation after 5 min, which increased over time up to 70%. However 10% of Mrpl38 was already detected in the pellet fraction without any heat stress indicating a temperature independent tendency to sediment under the used centrifugation conditions, most likely due to its association with ribosomes. It should be noted that Tufm, Tsfm, and Mrpl38 showed also some aggregation at control conditions (25°C) after longer incubation times indicating an intrinsic low stability. In

contrast to the former proteins, Aco2 and Hsp60 showed slower aggregation kinetics after heat shock. Whereas just 15-20% of these proteins were found aggregated after 5 min, the amount of aggregated protein increased over time up to 90% (Aco2) and 60% (Hsp60) after 60 min heat shock. Tim23 served as a control for a heat-stable protein that only showed a minor aggregation propensity (less than 20%) even after 1 h of heat shock. These observations indicate that in particular the translation factors Tufm and Tsfm are extremely thermo-sensitive and aggregate very quickly under heat shock conditions.

Properties of Tufm aggregates.

In order to analyze the nature of the Tufm aggregates we analyzed their sedimentation behavior by differential centrifugation. Isolated mitochondria were subjected to a heat treatment as described before and after lysis of the mitochondria aggregated proteins were fractionated at different centrifugal forces to get information about size and density of the formed aggregates. Whereas Tufm and Tsfm were soluble at control conditions and just small amounts were detected in the pellet fraction after 125,000 x*g*, after heat shock aggregates were already detected after a low spin step (5 min at 1600 x*g*) suggesting that they represent rather big aggregates (Fig. 5A, left panel). After 20 min centrifugation at 20,000 x*g* the Tufm aggregates were completely sedimented, which caused us to keep this as standard condition for isolating aggregates in the following experiments. As it could be assumed that elongation factors might also sediment due to a possible attachment to the ribosome in the process of translation, we compared the sedimentation behavior of Tufm with the ribosomal protein Mrpl38. In contrast to Tufm, at control conditions (25 °C) Mrpl38 was mainly detected in the pellet fraction after 40 min centrifugation at 125,000 x*g*. This indicated that the presence of Mrpl38 in the pellet is due to the sedimentation of whole ribosomal subunits after high-speed sedimentation. However, after heat stress also Mrpl38 partially aggregated, as indicated by sedimentation already at lower centrifugation speeds. Still a significant amount of Mrpl38 could be found in the putative ribosome pellet, while none of the elongation factor components were present in this fraction, at least under heat stress conditions. Hence, the sedimentation behavior of Tufm and Tsfm represented a genuine aggregation phenomenon independent of the behavior of ribosomal proteins. This result was confirmed by analyzing the heat-stress aggregates by sucrose gradients, which also showed an independent aggregation behavior of Tufm and Mrpl38 (Fig. S2) as well as there was no influence of high salt concentrations on the heat-induced Tufm aggregation detected indicating no ionic binding between the protein and the ribosome present (Fig. S3).

Although the less thermo-sensitive proteins Aco2 and Hsp60 were still partial soluble after heat stress, the stress-induced aggregates were also found already in the low speed pellets (5 min centrifugation at 20,000 x*g*). The control protein Tim23 was not aggregating after heat stress (Fig. 5A, right panel). That the pelleted material of Tufm represented genuine aggregates was confirmed by their resistance against the proteolytic digestion of the proteinase K. Heat-treated mitochondria were lysed with the non-denaturing detergent Triton X-100 and then incubated with different proteinase K concentrations. Whereas Tufm under control conditions (25 °C) was completely digested already at very low protease concentrations, after heat shock the aggregated protein was completely resistant against proteinase K digestion (Fig. 5B). In comparison, the mitochondrial matrix protein Trap1 was only partially digested by proteinase K both under control and stress condition, indicating an intrinsic protease resistance. An investigation of the mitochondrial protein levels over 6 h under heat stress incubation (42°C) and control (30°C) conditions showed that there was no change in the total protein amounts (Fig. 5C). This verified that the decrease in the soluble amounts of the proteins Tufm and Tsfm was indeed caused by a heat–induced aggregation and not due to proteolytic degradation.

As the elongation factor Tufm exhibited a strong aggregation propensity after heat stress, we wanted to investigate if the solubility of the protein could be recovered

over time after the heat stress has ceased. For this purpose heat-stressed mitochondria were subjected to a recovery incubation at 30°C for 15, 60 and 120 min. During recovery mitochondria were supplied with an ATP regenerating system and mitochondrial substrate molecules to keep them fully energized. Aggregates and soluble proteins were separated as described before by centrifugation and analyzed by SDS-PAGE and Western blot. In the tested time range no solubilization of Tufm aggregates nor any of the other aggregated polypeptides was observed (Fig. 5D), indicating that mammalian mitochondria did not exhibit a strong disaggregation activity.

Mitochondrial protein biosynthesis under heat stress.

As the elongation factor Tufm promotes the binding of aminoacyl-tRNA to the A-site of the ribosome during protein translation (22), we wanted to investigate the correlation between the thermal aggregation of Tufm and its effect on mitochondrial translation reactions. We investigated the impact of heat stress on the translation efficiency in isolated mitochondria by checking radiolabeled translation products after different times of pre-incubation of isolated mitochondria at 42°C. Newly synthesized proteins encoded in the mitochondrial genome were detected by an incubation with ^{35}S-labeled amino acids methionine/cysteine for 45 min (Fig. 6A right panel). The labeled protein bands could be assigned to subunits of mitochondrial respiratory chain complexes NADH dehydrogenase, Cytochrome *c* oxidase, Cytochrome *bc*1 complex and ATP-Synthase (23) (Fig. 6A left panel). Control samples were treated with cycloheximide or chloramphenicol to inhibit translation reactions. After two minutes of heat stress the amount of newly translated proteins is comparable to the control conditions whereas with increasing incubation times at 42°C the amount of translation products decreased significantly (Fig. 6A, see also quantification 6B). As shown for control and heat stressed samples both cycloheximide and chloramphenicol blocked the mitochondrial translation completely (Fig. 6A). A quantification of the overall translation efficiency (sum of total radioactivity per lane) revealed that there is a clear correlation between the time of heat stress and the decline of mitochondrial translation efficiency (Fig. 6B). While after 2 min of heat stress the level of freshly translated proteins was still comparable to the control conditions, translation efficiency decreased to less than 20% after 20 min. It was also shown that the *in organello* translation after 20 min heat stress could not be recovered after two hours at 25°C (Fig. S4).

As mitochondrial function depends both on endogenous translation as well as cytosolic translation of nuclear-encoded mitochondrial proteins and their subsequent import, we tested if there is also an impact of heat stress on the import efficiency in addition to the observed impairment of mitochondrial translation. We performed *in vitro* import experiments using an [^{35}S]-labeled artificial mitochondrial preprotein Su9(70)-DHFR into fully energized isolated mitochondria at 25 °C after the mitochondria were subjected to a pre-incubation at heat stress temperatures for 20 min. A proteinase K treatment was used to remove non-imported preproteins and, as negative control, an import reaction where the membrane potential ($\Delta\psi$) was depleted before import was started. We observed that the import reaction was strongly influenced by heat stress (Fig. 6C). Whereas after the pre-incubation at 37°C the amount of imported protein was still comparable to the control condition, import efficiency decreased substantially after a heat shock at 42°C and was completely depleted after a severe heat shock at 45°C. This showed that after heat shock not only the new translation of mitochondrially encoded proteins broke down, but also no cytosolically translated proteins were imported into the mitochondria. As both processes are affected, this resulted in a complete shutdown of mitochondrial protein biogenesis under heat shock conditions.

We also determined if the newly imported proteins are prone to aggregate under heat stress. We performed an *in vitro* import of [^{35}S]-labeled genuine mitochondrial preproteins Trap1 (heat shock protein 75 kDa) and Mdh2 (malate dehydrogenase) into isolated energized

mitochondria under normal temperature (30°C) as described above. Directly after import, mitochondria were exposed to various temperatures to induce aggregation. After lysis of mitochondria, aggregates were separated from soluble proteins by centrifugation and analyzed by SDS-PAGE and Western Blot. The newly imported preproteins Trap1 and Mdh2 were analyzed by autoradiography (Fig. 6D, upper panel) while already present endogenous Trap1 and Mdh2 were detected by immuno-decoration (Fig. 6D, lower panel). As the amount of the radioactive labeled imported proteins was too low to be detected by antibodies, both protein species could be distinguished. The freshly imported proteins were both aggregating in a temperature-dependent manner. After incubation at 37°C the imported Trap1 and Mdh2 partially accumulated in the pellet fraction although soluble polypeptides could still be detected in the supernatant. The amounts of aggregated preprotein increased strongly at 42°C and 45°C. The same behavior could also be detected for endogenous Trap1, which was also aggregating with rising temperatures (Fig. 6D, bottom panel). In contrast the endogenous Mdh2 showed no aggregation and stayed soluble even at incubation at 45°C. These observations indicated that newly imported proteins are highly sensitive to thermal aggregation independently of the thermodynamic stability of the native folding state under steady-state conditions.

Discussion

Heat stress typically exerts a dramatic effect on the organization of eukaryotic cells characterized by the damage of the cytoskeleton, fragmentation of organelles, swelling of the nucleus, formation of stress granules and arrest of the cell cycle (10). These deleterious effects are largely based on the denaturation and misfolding of the involved polypeptides, eventually leading to the formation of protein aggregates. Protein aggregation itself can present additional pathological challenges to the functional integrity of cells (5). As mitochondria represent semi-autonomous organelles within their eukaryotic host, their reactivity to diverse stress conditions has to be analyzed separately from the generally cellular reactivity. Therefore, we focused in our study on the heat-sensitivity of mammalian mitochondria and their polypeptides on a proteomic level. Heat stress had an obvious general effect on mitochondria as the overall mitochondrial shape in intact HeLa cells changed from the typical form of a tubular network, which is evenly distributed within the cell (24) to a more condensed structure concentrated near the nucleus. This observation confirms a previous electron-microscopic study in mammalian cells, which showed an increasing number of mitochondria at the nucleus in contrast to the cell periphery after heat stress, most likely due to a heat-dependent damage of the cytoskeleton (25).

The heat stress-induced structural changes of mitochondria were accompanied by a significant decrease of the inner membrane potential as well as a drop in mitochondrial ATP concentration. This decrease in energetic efficiency occurred despite mitochondrial membranes remained largely intact, demonstrating that mitochondria were not completely destroyed during the stress treatment. Heat stress of intact cells also caused a significant decrease of the amount of reactive oxygen species inside mitochondria, which could add to the pathological insult of heat shock conditions. Furthermore, our analysis revealed that the overall composition and structure of the mitochondrial respiratory chain complexes was not affected by heat stress, indicating a direct negative effect of heat stress on enzymatic function. This was confirmed by a decrease of enzymatic activity of a key metabolic mitochondrial enzyme KGDHC, an observation that was previously made also in fungal mitochondria (26). Interestingly a decreased KGDHC activity was also observed in brain mitochondria of patients of Alzheimer disease (27), which could indicate an influence of aggregation of KGDHC in the onset of the disease.

The primary goal of this work was to characterize the impact of heat stress on the mitochondrial proteome in order to identify proteins, which are prone to misfolding and aggregation. We performed

a quantitative analysis of the 2D-PAGE spot pattern of total protein extracts obtained from isolated mitochondria that were subjected to a short heat shock treatment representing physiological heat stress conditions. These native protein samples were subjected to a high-speed centrifugation step to distinguish soluble from aggregated polypeptides. Our analysis indicated a remarkable stress resistance of the mitochondrial protein as most polypeptides stayed soluble after a treatment with elevated temperatures. The observation that the mitochondrial proteome exhibits an overall resistance against stress conditions was already revealed by a previous proteomic analysis of heat-aggregating proteins in yeast mitochondria (15). The observations in both studies that just a small subset of mitochondrial proteins aggregate under heat stress supports the idea that the heat sensitivity of a cell does not depend on a general denaturation of proteins and a loss of the overall proteome function (28) but rather on the deactivation of few or single essential proteins with key physiological functions (29,30). Interestingly, the two mitochondrial matrix proteins identified as aggregation-prone candidates represented key elements of the mitochondrial protein homeostasis machinery: the mitochondrial translation factor Tu (Tufm) and the AAA+ protease Lon homolog (LonP1). While Tufm polypeptides were highly sensitive to an exposure to elevated temperature, LonP1 showed an intermediate behavior with most of the protein in a soluble state. In this context, the homolog of the protease LonP1, called Pim1, had been established as a major factor preventing a negative impact of heat-dependent aggregation by removing misfolded polypeptides (15,31). As proteases from the Lon family exhibit both chaperone and protease activities (32), an association of at least a part of the Lon proteins with the misfolded polypeptides in the aggregate pellet could be expected. However, our observations would indicate that the case of Tufm aggregation represents a different biochemical phenomenon. In *S. cerevisiae,* the homolog of elongation factor Tu (Tuf1) was not identified as a prominently aggregating polypeptide (15). In fungal mitochondria rather key enzymes of the major metabolic pathways aggregated under heat stress, causing large-scale metabolic inactivation. A more detailed analysis of the aggregation behavior of Tufm revealed that it is a very thermo-labile protein that started to aggregate already under mild heat shock conditions and after a short exposure to elevated temperatures. Although not identified from our 2D-gel spot pattern, we observed that the mitochondrial elongation factor Ts (Tsfm), a close partner protein and guanine nucleotide exchange factor for Tufm (20), showed the same heat-dependent aggregation behavior. The elongation factors, as they were originally described in bacteria, were labeled according to their thermostability as unstable (u) and stable (s) (33,34), however more detailed later studies did not support this strong difference (35).

We also characterized the behavior of selected other mitochondrial proteins to compare their aggregation tendency. The Krebs cycle enzyme aconitase, Aco2, previously identified as a meta-stabile polypeptide (15,36), also exhibited significant aggregation, but to an extent that was much smaller than the mitochondrial elongation factors. The same behavior was observed for the matrix chaperone Hsp60. In both cases, the majority of the respective polypeptides remained soluble. Interestingly, the mitochondrial ribosomal protein Mrpl38, which was used as a control protein, showed an intermediate behavior – an expected temperature-independent sedimentation due to its association with ribosomal particles as well as some temperature-dependent aggregation. The different sedimentation behavior of Mrpl38 and Tufm clearly demonstrates that the temperature-induced aggregation is a genuine property of Tufm and not due to a co-sedimentation with the ribosome. Further it was verified that the decrease of soluble proteins was not due to proteolytic degradation during heat stress. As the formation of reactive oxygen species also represents an important stress factor for mitochondria (37), we observed that the solubility of Tufm was also severely compromised under oxidative stress conditions however less pronounced compared to heat shock. The aggregation

of Tufm as well as Tsfm was neither dependent on mitochondrial ATP nor GTP concentrations. This suggests that mammalian mitochondria lack a significant chaperone activity that would be able to prevent a temperature-dependent aggregation. Interestingly, we also did not observe a recovery of protein solubility when mitochondria were put back to normal temperature conditions, indicating that a chaperone-dependent dis-aggregation capacity is absent in mammalian mitochondria. Disaggregation has been demonstrated in fungal mitochondria under *in vivo* conditions (38,39), correlating with the presence of a specific member of the Hsp100 chaperone family, Hsp78, which is lacking in metazoan organisms. This disaggregation activity was also shown to have a major impact on the recovery of mitochondrial protein biosynthesis after heat stress. Although a principal disaggregation activity has been shown with mammalian chaperones in *in vitro* reactions (40,41), direct evidence for aggregate solubilization is still lacking for mammalian cellular systems. Under this assumption, it is conceivable that mammalian cells lack - but also may not need - a general capability to recover aggregated polypeptides, both in the cytosol as well as in mitochondria.

The exceptionally high thermo-lability of the translation factors Tufm and Tsfm and their complete deactivation by a stress-induced aggregation reaction suggested a major impact on the efficiency of the endogenous mitochondrial translation activity at elevated temperatures. Whereas only limited observations are available for mito-chondrial EF–Ts (42), proteins from the elongation factor Tu (EF-Tu) family are highly conserved proteins found in bacteria, plant chloroplasts, mitochondria and eukaryotic cytoplasm. Tufm, in cooperation with the nucleotid exchange factor Tsfm, facilitates the binding of aminoacyl-tRNA (aa-tRNA) to the acceptor site of the mitochondrial ribosome, thereby controlling translation progress in the elongation phase (43). In our system, translation of mitochondrially encoded proteins showed a strong impairment with increasing exposure to heat stress. The time course of decreased translation efficiency essentially followed the kinetics of Tufm and Tsfm aggregation, indicating that the decreased solubility of the elongation factors correlates with the decreased translation rate at elevated temperatures. This observation suggests that the thermo-labile elongation factors may serve as a stress-triggered switch to quickly shut-off mitochondrial synthesis of new polypeptides in order to prevent an accumulation of misfolded protein species.

Interestingly, previous experiments indicated an involvement of the bacterial and plant homologs of the EF-Tu in heat stress reactions although the postulated cellular mechanism underlying this effect was different. For example, heat stress induced synthesis of EF-Tu in maize chloroplasts, suggests an important role in development of thermotolerance (44). Similarly, other abiotic stresses like salinity, water restriction, and hypothermia in different plant species result in upregulation of gene expression of both plastids EF-Tu as well as cytosolic EF-1α (33). Based mainly on experiments using the recombinant proteins in *in vitro* assays, a chaperone-like activity has been postulated for EF-Tu homologs derived from mammalian mitochondria (45), bacteria (46,47) as well as from plant chloroplasts. Although there seemed to be a correlation between a putative prevention of thermal protein aggregation by EF-Tu with improved heat tolerance in plants (48,49), so far it is not entirely clear, how relevant this activity is in the *in vivo* situation.

In general, newly synthesized proteins exhibit an increased sensitivity to heat stress due to their incomplete folding state in contrast to long-lived proteins, which frequently results also in their ubiquitin-dependent degradation (50). Stalling the biosynthesis of proteins during stress conditions would therefore be beneficial for the cell in terms of limiting the amount of potential aggregation prone proteins. Indeed, a general heat stress-induced inhibition of protein synthesis, except for heat shock proteins, was already described for cytosolically synthesized proteins in HeLa cells. The inhibitory effect is also exerted on the translational level and is caused by a phosphorylation of the

translation initiation factor eIF2α (51,52). In addition, a heat-induced formation of stress granules in the cytosol has been described as a cellular mechanism for the prevention of an overloading of the protein quality control system by newly synthesized polypeptides (53). The formation of stress granules, which consist of non-translated mRNA, RNA-binding proteins, translation initiation factors and 40S ribosomal subunits, is initiated by the block of translation initiation due to phosphorylation of eIF2α under heat stress (54). An eIF2α-mediated translational shutdown has been also described as a major factor of the ER stress response (55). A recovery from stress conditions then includes a partial disassembly of stress granules as well as restoration of translation (53,56). However, in isolated mitochondria we were not able to detect a recovery of the solubility of aggregated translation factors Tufm and Tsfm as well as a recovery of the mitochondrial translation. As our study used *in organello* conditions, where potential compensatory mechanisms of the cell by heat shock-induced changes of protein expression were not possible, we cannot exclude that an increased biosynthesis of mitochondrial chaperones in intact cells might recover translational efficiency after heat stress conditions have ceased.

An important aspect of mitochondrial protein biogenesis is the fact that only a minority of the resident proteins is provided via mitochondrial translation. The vast majority of mitochondrial proteins is encoded in the nucleus and imported after their synthesis in the cytosol (57). Hence, an unilateral shut-down of mitochondrial translation would only exacerbate the problem of an accumulation of misfolded polypeptides inside mitochondria. Interestingly, we observed under *in vivo* like conditions that the import efficiency of cytosolic proteins was strongly decreased at elevated temperatures. This correlated with the observation that similar to nascent proteins at the ribosome, also newly imported polypeptides in mitochondria are highly sensitive to heat stress and prone to aggregation. Although a mitochondrial unfolded protein response (mtUPR) has been described as a potential protective mechanism against the accumulation of misfolded mitochondrial polypeptides (58), no specific effect of this stress-regulatory process on mitochondrial protein biosynthesis has been described so far. Thus, a translation shutdown by Tufm aggregation in combination with a decrease in import efficiency would effectively prevent an accumulation of misfolded polypeptides in mitochondria under heat stress – representing a protective mechanism to prevent further proteotoxic insults on organellar function. Hence, our observations support the notion that organellar EF-Tu proteins represent important components of the stress-protective cellular processes responsible for protein homeostasis.

Experimental Procedures

Cells and culture conditions

HeLa cells were cultured in Roswell Park Memorial Institute medium (RPMI medium), supplemented with 10% (v/v) fetal calf serum (FCS), 2 mM L-glutamine, 100 units/ml penicillin, 100 µg/ml streptomycin. Cells were grown in tissue culture dishes at 37°C in 5% CO_2 and routinely passaged by trypsinization at ratios 1:3 to 1:6 every 48 to 72 h.

Immunocytochemistry

For fluorescence microscopy 3×10^4 cells per well were grown over night on coverslips. For heat shock, culture medium was changed with 45°C preheated medium and cells were incubated in an incubator at 45°C for 2 h. After heat treatment cells were incubated for 5 min at 37°C in fixing solution (4% (w/v) paraformaldehyde, 10% (w/v) sucrose in 1x phosphate-buffered saline (PBS), pH 7.2) and permeabilized with 0.5% triton X-100 in PBS for 10 min at RT. Cover slips were washed three times in PBS after each step. After 1 h incubation in blocking solution (0.2% (w/v) bovine serum albumin (BSA) in PBS) samples were incubated over night with different primary antibodies (1:250 dilution in blocking solution). Flourophore coupled secondary antibodies Alexa Fluor 488 and 594 (Invitrogen) were used to generate fluorescence signals. Microscopic pictures were obtained using $EVOS_{Fl}$ Cell Imaging System (Peqlab) with a 40x objective lens.

Flow cytometry

Membrane potential was assayed by an incubation of cultures cells for 10 min at 37°C with 0.5 µM tetrymethylrhodamine ethyl ester (TMRE). As control, a sample was treated with valinomycin (f.c. 0.1 µM) for 30 min at 37°C. The generation of ROS was determined using the mitochondrial superoxide indicator MitoSOX™ (Thermo Fisher Scientific). Cells were incubated with the indicator dye for 10 min at 37°C. As positive control, cells were treated with 100 µM menadione for 15 min at 37°C. Cells were harvested by trypsinization and washed twice in PBS containing 0.2% (w/v) BSA. Fluorescence of 20,000 cells for each sample was analyzed using the flow cytometer CyFlow space CY-S3001 (Partec).

Mitochondrial aggregation assay

Mitochondria were isolated from cultures cells essentially as described (59). For each sample 30 µg of fresh mitochondria were resuspended in 100 µl resuspension buffer (500 mM sucrose, 160 mM KAc, 40 mM HEPES/KOH pH 7.6, 10 mM MgAc, 5 mM glutamate, 5 mM malate, 1 mM DTT). For analysis of the nucleotide dependence the resuspension buffer was supplemented either with 5 mM adenosine triphosphate (ATP), creatine phosphate (20 mM) and creatine kinase (4 µg/ml) or with 2.5 mM guanosine triphosphate (GTP). Mitochondria were either pre-incubated for 20 min at indicated temperatures (25°C-45°C) or in presence of different concentrations of menadione (0-2 mM) at 25°C. After incubation mitochondria were reisolated by centrifugation (12,000 x*g*, 10 min, 4°C) and pellets were lysed in lysis buffer (0.5% (v/v) Triton X-100, 200 mM KCl, 30 mM Tris/HCl pH 7.4, 5 mM EDTA, 0.5 mM PMSF, 1x protease inhibitors) by vigorous shaking for 10 min at 4°C. Soluble proteins were separated from aggregated proteins by centrifugation at 20,000 x*g* for 20 min at 4°C. The supernatants were precipitated with TCA and pellets were re-extracted in 100 µl lysis buffer by shaking as described above. After a second centrifugation step at 20,000 x*g* for 20 min at 4°C supernatants were discarded and the pellet was resuspended in 1x Laemmli SDS-PAGE buffer (2% (w/v) sodium dodecyl sulfate (SDS), 10% (v/v) glycerol, 60 mM Tris/HCl pH 6.8, 5% (w/v) β-mercaptoethanol, 0.02% (w/v) bromophenol blue). Samples were analyzed by SDS-PAGE and Western blot.

To distinguish between aggregate sizes, different centrifugation steps were applied. After the first low spin step at 1,600 x*g* for 5 min the supernatant was collected and centrifuged at 20,000 x*g* for 5 min, following a 20 min centrifugation at the same spin. After the last spin at 125,000 x*g* for 40 min the supernatant was precipitated with TCA. All pellets were resuspended in 1x laemmli buffer and analyzed as described above.

For recovery from aggregation, 30 µg of mitochondria were resuspended in 100 µl buffer containing ATP (250 mM sucrose, 80 mM potassium acetate, 20 mM HEPES/KOH pH 7.6, 5 mM magnesium acetate, 5 mM glutamate, 5 mM malate, 5 mM KP_i pH 7.4, 2 mM ATP, 1 mM DTT) to keep them fully energized. After heat stress for 20 min at 42°C samples were incubated for up to 2 h at 30°C. Samples were lysed, centrifuged and analyzed as described above.

Proteinase K treatment of mitochondria

For determination of the integrity of mitochondria, mitochondria were treated after heat stress with 1.25 µg/ml proteinase K for 20 min. Treatments were stopped by 15 min incubation with 1.5 mM PMSF and following precipitation by TCA. As control for successful digestion by proteinase K samples in parallel were lysed with lysisbuffer (0.5% (v/v) Triton X-100, 200 mM KCl, 30 mM Tris/HCl pH 7.4, 5 mM EDTA, 0.5 mM PMSF, 1x protease inhibitors) and incubated with proteinase K. In order to test the protease resistence of aggregates, lysed mitochondria were incubated with 0.25 µg/ml or 0.5 µg/ml proteinase K for 5, 10 and 20 min. After 15 min incubation with PMSF samples were precipitated with TCA.

Membrane potential measurement

30 µg mitochondria were resuspended in potential buffer (600 mM sorbitol, 20 mM KPi, pH 7.2, 10 mM $MgCl_2$, 10 mM glutamate, 5 mM malate, 0.1% (w/v) BSA) and incubated with 1 µM TMRE for 10 min at 30°C. Negative control samples were treated with valinomycin for 10 min at 30°C prior TMRE incubation. All samples

were washed with potential buffer and TMRE fluorescence (excitation: 540 nm, emission: 585 nm) was measured in a microplate reader (Infinite M200 PRO, Tecan).

Determination of ATP content in isolated mitochondria after heat shock

The mitochondrial ATP content was measured by a luciferase based ATP assay (ATP Determination kit, Invitrogen). Isolated energized mitochondria were either analyzed directly or after 20 min incubation at 25°C or 42°C. The ATP assay was performed according to the manufacture`s instructions and luminescence was measured in a microplate reader.

Enzymatic assays

Activities of malate dehydrogenase (MDH) and alpha-ketoglutarate dehydrogenase complex (KGDHC) were measured in isolated mitochondria (100 µg/sample for MDH and 200 µg/sample for KGDHC activity assay) after incubation for 20 min at 25°C (control) or 42°C (heat shock) in resuspension buffer (500 mM sucrose, 160 mM KAc, 40 mM HEPES/KOH pH 7.6, 10 mM MgAc, 5 mM glutamate, 5 mM malate, 1 mM DTT). After reisolation of the mitochondria at 12,000 x*g* for 10 min at 4°C, the mitochondrial pellets were lysed in 50 µl homogenization buffer (0.5% Triton X-100, 50 mM Tris/HCl pH 7.4) and shaken at maximum speed for 10 min at room temperature. The respective reaction mixtures (MDH activity assay: 50 mM Tris/HCl pH 7.4, 0.5 mM oxalacetic acid and 75 µM NADH; KGDHC activity assay: 50 mM Tris/HCl pH 7.4, 50 mM KCl, 5 mM alpha-Ketoglutarate, 2 mM $MgCl_2$, 0.3 mM thiamine pyrophosphate, 0.3 mM coenzyme A and 2 mM NAD^+) were pre-warmed at 37°C, the lysed mitochondria were added and enzyme activities were measured at 340 nm every 15 sec for 10 min in a photometer (BioPhotometer plus, Eppendorf) by either decrease of NADH absorption (MDH) or increase of NADH absorption (KGDHC).

Blue Native SDS-PAGE

40 µg of isolated mitochondria were resuspended in resuspension buffer (500 mM sucrose, 160 mM KAc, 40 mM HEPES/KOH pH 7.6, 10 mM MgAc, 5 mM glutamate, 5 mM malate, 1 mM DTT), incubated for 20 min at 25°C (unstressed) or 42°C (heat stress) and afterwards solubilized in digitonin lysis buffer (0.4% (w/v) digitonin, 50 mM NaCl, 20 mM Tris/HCl, pH 7.4, 2 mM EDTA pH 8.0, 1 mM PMSF, 10% (v/v) glycerol) by pipetting (20x) and shaking for 10 min at 4°C at maximum speed. 10x loading dye (5% (w/v) Coomassie blue G–250, 500 mM ε-amino n-caproic acid, 100 mM Bis-Tris-HCl pH 7.0) was added and samples were applied to a 5-16% polyacrylamide gradient gel. The samples were analyzed by Western blot using antibodies against subunits of the respiratory chain complexes as indicated.

2-D gel electrophoresis

Isolated mitochondria (150 µg total protein) were dissolved in resuspension buffer (500 mM sucrose, 160 mM KAc, 40 mM HEPES/KOH pH 7.6, 10 mM MgAc, 5 mM glutamate, 5 mM malate, 1 mM DTT) and incubated for 20 min at 25°C (control) or 42°C (heat stress). After centrifugation at 12,000 x*g* for 10 min at 4°C mitochondria were lysed in lysis buffer (0.5% Triton X-100, 200 mM KCl, 30 mM Tris/HCl pH 7.4, 5 mM EDTA, 0.5 mM PMSF, 1x protease inhibitors) by vigorous shaking for 10 min at 4°C. The aggregated proteins were separated ultracentrifugation at 125,000 x*g* for 40 min. Supernatants were precipitated with TCA and re-suspended in IEF lysis buffer (7 M urea, 2 M thiourea, 4% (w/v) CHAPS, 10 mM DTT, 1x protease inhibitors, 40 mM Tris/HCL pH 8.8) and lysed by 10 min of shaking at maximum speed at 4°C. Control, heat stressed and standard samples were labeled with CyDye DIGE Fluor minimal dyes (GE Healthcare). The pooled samples were diluted in rehydration buffer (7 M urea, 2 M thiourea, 2% (w/v) CHAPS, 20 mM DTT, 0.8% (v/v) Pharmalyte™ 3–11 NL, small amount of bromophenol blue) and applied to a 18 cm non-linear, pH 3–11 Immobiline™ Dry Strip (GE Healthcare) in an IPGphor isoelectric focusing system (GE Healthcare). In parallel, one sample containing 400 µg total mitochondria was precipitated with TCA, resuspended in rehydration buffer and applied to a strip as described above. Protein spots were detected by Coomassie blue G–250 staining and

manually excised for analysis by mass spectrometry.

Immobiline strips were rehydrated in-gel rehydration for 12 h at 30 V. Afterwards protein focusing was conducted stepwise for respectively 1 h at 200 V, 500 V and 1000 V followed by a slow increase (2 h and 30 min) to 8000 V for 3 h and finally decrease to 500 V for 2 h and 30 min. Focused strips were incubated in equilibration buffer (6 M urea, 1.5 mM Tris/HCl pH 8.8, 50% (v/v) glycerol, 1% (w/v) SDS) containing 1% (w/v) dithiothreitol (DTT) for equilibration followed by an incubation in equilibration buffer containing 2.5% (w/v) iodacetamide for reduction. Both incubations were performed for 15 min in the dark. Proteins were separated by SDS-PAGE on a 11% polyacrylamide gel for 1 h at 0.5 W per gel followed by 1.5 W per gel over night at 20°C in an Ettan™ DALT*six* system (GE Healthcare). Proteins were detected by fluorescence scanning using the Fluoro Image Analyzer FLA-5100 (Fujifilm) and obtained protein spots were analyzed by the Delta2D software (DECODON). For each gel spot intensities were normalized by the total sum of spot intensity at 42°C divided by the total sum of spot intensity at 25°C and the average of six different gels as well as the standard error of the mean (SEM) was calculated. The significance was calculated using GraphPad Prism 6 software via 1-way ANOVA of all samples to a control of 100% (Dunnett`s multiple comparisions test). A p–value ≤ 0.001 was considered significant and indicated by asterisks.

Peptide preparation and MALDI–TOF analysis

Manually exised protein spots were washed and destained stepwise with water, 50% acetonitrile (ACN) and 100% ACN. Gel pieces were dried in a vacuum concentrator (ScanVac, Labogene) for 30 min at 40°C and 1000 x*g* and afterwards stepwise reduced with 20 mM dithiothreitol (DTT) in 50 mM ammonium bicarbonate for 30 min at 55°C and alkylated with 40 mM iodacetamide (IAA) in 50 mM ammonium bicarbonate for 30 min at room temperature in the dark. After washing, the gel pieces were dehydrated with 100% ACN and dried in a vacuum concentrator. Proteins were digested with sequencing grade trypsin (400 pg/gel piece in 50 mM ammonium bicarbonate) at 37°C over night. The peptide extract was collected and the remaining peptides were extracted with 50% ACN. The peptides were dried in a vacuum concentrator and stored at –20°C. Peptides were dissolved in 8 µl 0.1% trifluoroacetic acid (TFA). 1 µl was dried on an AnchorChip 384 target plate (Bruker Daltonik GmbH, Bremen, Germany). Matrix solvent (85% acetonitrile, 0.1% TFA, 1 mM $NH_4H_2PO_4$) was saturated with α-Cyano-4-hydroxycinnamic acid at room temperature. The solution was diluted 1:30 with matrix solvent and 1 µl of the diluted matrix solution was added to the dried peptides.

MALDI MS and MS/MS measurements were run with an automated method on a Bruker Autoflex III spectrometer in positive reflectron mode. 4000 MS1 spectra were recorded (700–3150 m/z), processed by FlexAnalysis 3.3 software and sent to ProteinScape 3.0 for evaluation. Suitable peptide ions were subjected to MS/MS analyses (LIFT-process without collision gas) with acquisition of 10000 spectra per precursor. Peptide identification was done with an in house Mascot server version 2.4 (Matrix Science Ltd, London, UK) searching human sequences in the SwissProt database. Oxidation of methionine and carbamidomethyl on cysteine were set as variable modification. Identifications that were only based on MS1 data (peptide mass fingerprint) were inspected manually for number of identified peptide peaks, completeness of assignment, and mass errors.

Preprotein import into mitochondria

In vitro import was performed as described (59), using the radiolabeled substrate proteins Su9(70)-DHFR, Trap1 and Mdh2, which were synthesized by *in vitro* transcription and translation in rabbit reticulocyte lysate. For each import reaction 50 µg of fresh isolated energized mitochondria were used that were either heat-shocked before the import reaction to assess tha import efficiency or after the import reaction to test if fresh imported proteins were prone to aggregate. The heat shock was performed in resuspension buffer (see above) for 20 min at respective temperatures. Control

samples without membrane potential ($\Delta\psi$) mitochondria were pretreated with antimycin, valinomycin and oligomycin. The import reaction was performed for 40 min at 30°C and stopped by adding 0.5 µM valinomycin. Where indicated, samples were treated with 50 µg/ml proteinase K for 30 min at 4°C to digest non-imported proteins. Samples were analyzed by SDS-PAGE and autoradiography.

***In organello* translation**

50 µg of fresh isolated mitochondria were resuspended in resuspension buffer (see above) and incubated 2-20 min at 42°C and 25°C. After reisolation of the mitochondria (12,000 x*g*, 10 min, 4°C) pellets were resuspended in translation buffer (645 mM sorbitol, 160 mM KCl, 21.5 mM Tris/HCl pH 7.4, 21.5 mM ADP, 13.5 mM $MgSO_4$, 3.2 mg/ml BSA, 14 µM amino acid mix w/o methionine, 0.53 mM GTP, 180 mM creatine phosphate, 4 µg/ml creatine kinase, 1.2 mg/ml α-keto-glutarate). Where indicated cycloheximide (f. c. 100 µg/µl) or chloramphenicol (f. c. 100 µg/µl) were added. After pre–incubation of the samples for 3 min at 30°C and shaking at 300 rpm, newly synthesized mitochondrial proteins were labeled by adding [^{35}S]-methionine/ cysteine (f. c. 22 µCi/µl). The samples were incubated for 45 min at 30°C and labeling was stopped by adding MOPS/Met buffer (1 M MOPS, pH 7.2, 200 mM methionine, f. c. 50 mM) and incubating for 30 min at 30°C. Mitochondria were washed once with washing buffer (0.6 M sorbitol, 1 mM EDTA, 5 mM methionine) and samples were analyzed by SDS-PAGE on a 15% polyacrylamide gel containing 1.1 M urea and autoradiography.

Acknowledgements

We are grateful to M. Fuhrmann and B. Gehrig for expert technical assistance. We thank W. Jaworek, K. Pollecker and Dr. G. Cenini for discussion and critical comments on the manuscript. Work in the authors laboratory was supported by the Deutsche Forschungsgemeinschaft (grant VO 657/5-2 to W.V.).

Conflict of interest

The authors declare that they have no conflicts of interest with the contents of this article.

References

1. Quiros, P. M., Mottis, A., and Auwerx, J. (2016) Mitonuclear communication in homeostasis and stress. *Nat. Rev. Mol. Cell Biol.* 17, 213-226
2. Voos, W. (2013) Chaperone-protease networks in mitochondrial protein homeostasis. *Biochim. Biophys. Acta* 1833, 388-399
3. Balchin, D., Hayer-Hartl, M., and Hartl, F. U. (2016) In vivo aspects of protein folding and quality control. *Science* 353, aac4354
4. Chiti, F., and Dobson, C. M. (2017) Protein Misfolding, Amyloid Formation, and Human Disease: A Summary of Progress Over the Last Decade. *Annu. Rev. Biochem.* 86, 27-68
5. Hipp, M. S., Park, S. H., and Hartl, F. U. (2014) Proteostasis impairment in protein-misfolding and -aggregation diseases. *Trends Cell Biol.* 24, 506-514
6. Labbadia, J., and Morimoto, R. I. (2015) The biology of proteostasis in aging and disease. *Annu. Rev. Biochem.* 84, 435-464
7. Lin, M. T., and Beal, M. F. (2006) Mitochondrial dysfunction and oxidative stress in neurodegenerative diseases. *Nature* 443, 787-795
8. Osiewacz, H. D. (2010) Role of mitochondria in aging and age-related disease. *Exp. Gerontol.* 45, 465
9. Tyedmers, J., Mogk, A., and Bukau, B. (2010) Cellular strategies for controlling protein aggregation. *Nat. Rev. Mol. Cell Biol.* 11, 777-788
10. Richter, K., Haslbeck, M., and Buchner, J. (2010) The heat shock response: life on the verge of death. *Mol. Cell* 40, 253-266

11. Evans, S. S., Repasky, E. A., and Fisher, D. T. (2015) Fever and the thermal regulation of immunity: the immune system feels the heat. *Nat. Rev. Immunol.* 15, 335-349
12. Lindquist, S. (1986) The heat-shock response. *Annu. Rev. Biochem.* 55, 1151-1191
13. Morimoto, R. I. (1998) Regulation of the heat shock transcriptional response: cross talk between a family of heat shock factors, molecular chaperones, and negative regulators. *Genes Dev.* 12, 3788-3796
14. Bruderek, M., Jaworek, W., Wilkening, A., Rüb, C., Cenini, G., Förtsch, A., Sylvester, M., and Voos, W. (2017) IMiQ: a novel protein quality control compartment protecting mitochondrial functional integrity. *Mol. Biol. Cell* in press, doi: 10.1091/mbc.E1017-1001-0027
15. Bender, T., Lewrenz, I., Franken, S., Baitzel, C., and Voos, W. (2011) Mitochondrial enzymes are protected from stress-induced aggregation by mitochondrial chaperones and the Pim1/LON protease. *Mol. Biol. Cell* 22, 541-554
16. David, D. C., Ollikainen, N., Trinidad, J. C., Cary, M. P., Burlingame, A. L., and Kenyon, C. (2010) Widespread protein aggregation as an inherent part of aging in C. elegans. *PLoS Biol.* 8, e1000450
17. Chaput, M., Brygier, J., Lion, Y., and Sels, A. (1983) Potentiation of oxygen toxicity by menadione in Saccharomyces cerevisiae. *Biochimie* 65, 501-512
18. Friedman, J. R., and Nunnari, J. (2014) Mitochondrial form and function. *Nature* 505, 335-343
19. Mogk, A., Tomoyasu, T., Goloubinoff, P., Rüdiger, S., Roder, D., Langen, H., and Bukau, B. (1999) Identification of thermolabile Escherichia coli proteins: prevention and reversion of aggregation by DnaK and ClpB. *EMBO J.* 18, 6934-6949
20. Cai, Y. C., Bullard, J. M., Thompson, N. L., and Spremulli, L. L. (2000) Interaction of mitochondrial elongation factor Tu with aminoacyl-tRNA and elongation factor Ts. *J. Biol. Chem.* 275, 20308-20314
21. Bukau, B., Weissman, J., and Horwich, A. (2006) Molecular chaperones and protein quality control. *Cell* 125, 443-451
22. Ott, M., Amunts, A., and Brown, A. (2016) Organization and Regulation of Mitochondrial Protein Synthesis. *Annu. Rev. Biochem.* 85, 77-101
23. Chomyn, A. (1996) In vivo labeling and analysis of human mitochondrial translation products. *Methods Enzymol.* 264, 197-211
24. Lackner, L. L. (2014) Shaping the dynamic mitochondrial network. *BMC Biol.* 12, 35
25. Welch, W. J., and Suhan, J. P. (1985) Morphological study of the mammalian stress response: characterization of changes in cytoplasmic organelles, cytoskeleton, and nucleoli, and appearance of intranuclear actin filaments in rat fibroblasts after heat-shock treatment. *J. Cell Biol.* 101, 1198-1211
26. Bender, T., Leidhold, C., Ruppert, T., Franken, S., and Voos, W. (2010) The role of protein quality control in mitochondrial protein homeostasis under oxidative stress. *Proteomics* 10, 1426-1443
27. Huang, H. M., Zhang, H., Xu, H., and Gibson, G. E. (2003) Inhibition of the alpha-ketoglutarate dehydrogenase complex alters mitochondrial function and cellular calcium regulation. *Biochim. Biophys. Acta* 1637, 119-126
28. Ghosh, K., and Dill, K. (2010) Cellular proteomes have broad distributions of protein stability. *Biophys. J.* 99, 3996-4002
29. Chang, R. L., Andrews, K., Kim, D., Li, Z., Godzik, A., and Palsson, B. O. (2013) Structural systems biology evaluation of metabolic thermotolerance in Escherichia coli. *Science* 340, 1220-1223
30. Leuenberger, P., Ganscha, S., Kahraman, A., Cappelletti, V., Boersema, P. J., von Mering, C., Claassen, M., and Picotti, P. (2017) Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. *Science* 355, eaai7825
31. Bezawork-Geleta, A., Brodie, E. J., Dougan, D. A., and Truscott, K. N. (2015) LON is the master protease that protects against protein aggregation in human mitochondria through direct degradation of misfolded proteins. *Sci. Rep.* 5, 17397

32. Rep, M., van Dijl, J. M., Suda, K., Schatz, G., Grivell, L. A., and Suzuki, C. K. (1996) Promotion of mitochondrial membrane complex assembly by a proteolytically inactive yeast Lon. *Science* 274, 103-106
33. Fu, J., Momcilovic, I., and Vara Prasad, P. V. (2012) Roles of Protein Synthesis Elongation Factor EF-Tu in Heat Tolerance in Plants. *J. Botany* 2012, 8
34. Lucas-Lenard, J. (1971) Protein biosynthesis. *Annu. Rev. Biochem.* 40, 409-448
35. Arai, K., Kawakita, M., and Kaziro, Y. (1974) Studies on the polypeptide elongation factors from E. coli. V. Properties of various complexes containing EF-Tu and EF-Ts. *J. Biochem.* 76, 293-306
36. Bota, D. A., and Davies, K. J. (2002) Lon protease preferentially degrades oxidized mitochondrial aconitase by an ATP-stimulated mechanism. *Nat. Cell Biol.* 4, 674-680
37. Ott, M., Gogvadze, V., Orrenius, S., and Zhivotovsky, B. (2007) Mitochondria, oxidative stress and cell death. *Apoptosis* 12, 913-922
38. Röttgers, K., Zufall, N., Guiard, B., and Voos, W. (2002) The ClpB homolog Hsp78 is required for the efficient degradation of proteins in the mitochondrial matrix. *J. Biol. Chem.* 277, 45829-45837
39. Germaniuk, A., Liberek, K., and Marszalek, J. (2002) A bichaperone (Hsp70-Hsp78) system restores mitochondrial DNA synthesis following thermal inactivation of Mip1p polymerase. *J. Biol. Chem.* 277, 27801-27808
40. Nillegoda, N. B., and Bukau, B. (2015) Metazoan Hsp70-based protein disaggregases: emergence and mechanisms. *Front. Mol. Biosci.* 2, 57
41. Rampelt, H., Kirstein-Miles, J., Nillegoda, N. B., Chi, K., Scholz, S. R., Morimoto, R. I., and Bukau, B. (2012) Metazoan Hsp70 machines use Hsp110 to power protein disaggregation. *EMBO J.* 31, 4221-4235
42. Xin, H., Woriax, V., Burkhart, W., and Spremulli, L. L. (1995) Cloning and expression of mitochondrial translational elongation factor Ts from bovine and human liver. *J. Biol. Chem.* 270, 17243-17249
43. Mai, N., Chrzanowska-Lightowlers, Z. M., and Lightowlers, R. N. (2017) The process of mammalian mitochondrial protein synthesis. *Cell Tissue Res.* 367, 5-20
44. Bhadula, S. K., Elthon, T. E., Habben, J. E., Helentjaris, T. G., Jiao, S., and Ristic, Z. (2001) Heat-stress induced synthesis of chloroplast protein synthesis elongation factor (EF-Tu) in a heat-tolerant maize line. *Planta* 212, 359-366
45. Suzuki, H., Ueda, T., Taguchi, H., and Takeuchi, N. (2007) Chaperone properties of mammalian mitochondrial translation elongation factor Tu. *J. Biol. Chem.* 282, 4076-4084
46. Caldas, T. D., El Yaagoubi, A., and Richarme, G. (1998) Chaperone properties of bacterial elongation factor EF-Tu. *J. Biol. Chem.* 273, 11478-11482
47. Kudlicki, W., Coffman, A., Kramer, G., and Hardesty, B. (1997) Renaturation of rhodanese by translational elongation factor (EF) Tu. Protein refolding by EF-Tu flexing. *J. Biol. Chem.* 272, 32206-32210
48. Rao, D., Momcilovic, I., Kobayashi, S., Callegari, E., and Ristic, Z. (2004) Chaperone activity of recombinant maize chloroplast protein synthesis elongation factor, EF-Tu. *Eur. J. Biochem.* 271, 3684-3692
49. Ristic, Z., Bukovnik, U., Momcilovic, I., Fu, J., and Vara Prasad, P. V. (2008) Heat-induced accumulation of chloroplast protein synthesis elongation factor, EF-Tu, in winter wheat. *J. Plant Physiol.* 165, 192-202
50. Medicherla, B., and Goldberg, A. L. (2008) Heat shock and oxygen radicals stimulate ubiquitin-dependent degradation mainly of newly synthesized proteins. *J. Cell Biol.* 182, 663-673
51. Duncan, R., and Hershey, J. W. (1984) Heat shock-induced translational alterations in HeLa cells. Initiation factor modifications and the inhibition of translation. *J. Biol. Chem.* 259, 11882-11889
52. Wek, R. C., Jiang, H. Y., and Anthony, T. G. (2006) Coping with stress: eIF2 kinases and translational control. *Biochem. Soc. Trans.* 34, 7-11
53. Buchan, J. R., and Parker, R. (2009) Eukaryotic stress granules: the ins and outs of translation. *Mol. Cell* 36, 932-941

54. Kedersha, N. L., Gupta, M., Li, W., Miller, I., and Anderson, P. (1999) RNA-binding proteins TIA-1 and TIAR link the phosphorylation of eIF-2 alpha to the assembly of mammalian stress granules. *J. Cell Biol.* 147, 1431-1442
55. Ron, D. (2002) Translational control in the endoplasmic reticulum stress response. *J. Clin. Invest.* 110, 1383-1388
56. Cherkasov, V., Hofmann, S., Druffel-Augustin, S., Mogk, A., Tyedmers, J., Stoecklin, G., and Bukau, B. (2013) Coordination of translational control and protein homeostasis during severe heat stress. *Curr. Biol.* 23, 2452-2462
57. Chacinska, A., Koehler, C. M., Milenkovic, D., Lithgow, T., and Pfanner, N. (2009) Importing mitochondrial proteins: machineries and mechanisms. *Cell* 138, 628-644
58. Jovaisaite, V., and Auwerx, J. (2015) The mitochondrial unfolded protein response-synchronizing genomes. *Curr. Opin. Cell Biol.* 33, 74-81
59. Becker, D., Richter, J., Tocilescu, M. A., Przedborski, S., and Voos, W. (2012) Pink1 kinase and its membrane potential ($\Delta\psi$)-dependent cleavage product both localize to outer mitochondrial membrane by unique targeting mode. *J. Biol. Chem.* 287, 22969-22987

Table 1. Quantitative changes in the solubility of mitochondrial proteins under heat stress.

Nr.	Protein	Description	UniProt entry	Size [kDa)	pI	Rel. amount [%]
1	Aldh2	Aldehyde dehydrogenase	P05091	54.34	5.76	103 ± 4
2	Atp5B	ATP synthase subunit beta	P06576	51.69	4.74	115 ± 2
3	C1qbp	Complement component 1 Q subcomponent–binding protein	Q07021	23.74	4.06	108 ± 3
4	Cps1	Carbamoyl–phosphate synthetase 1	A0A024R454	160.35	6.32	113 ± 4
5	Sdha	Succinate dehydrogenase [ubiquinone] flavoprotein subunit	P31040	67.99	6.69	79 ± 9
6	Ech1	Delta(3,5)–Delta(2,4)–dienoyl–CoA isomerase	Q13011	32.15	6.36	139 ± 20
7	Echs1	Enoyl–CoA hydratase	P30084	28.29	5.91	125 ± 5
8	Glud1	Glutamate dehydrogenase 1	P00367	55.93	7.21	125 ± 5
9	Hsp60	60 kDa heat shock protein	P10809	57.88	4.96	83 ± 4
10	HspA9	Stress–70 protein	P38646	68.66	5.23	93 ± 4
11	LonP1	Lon protease homolog	P36776	99.23	5.7	54 ± 3
12	Pdhb	Pyruvate dehydrogenase E1 component subunit beta	P11177	35.85	5.23	108 ± 6
13	Prdx3	Thioredoxin–dependent peroxide reductase	P30048	21.5	6.14	104 ± 6
14	Oxct1	Succinyl–CoA:3-ketoacid coenzyme A transferase 1	P55809	52.01	6.33	116 ± 5
15	StomL2	Stomatin–like protein 2	Q9UJZ1	35.63	5.13	121 ± 6
16	Tufm	Elongation factor Tu	P49411	44.97	6.75	28 ± 3
17	Vdac1	Voltage–dependent anion–selective channel protein 1	P21796	30.8	9.2	114 ± 7

Relative amounts of proteins remaining in the supernatant after heat shock were calculated as described in Fig. 2B. Identities of protein spots were analyzed by mass spectrometry in this study and by comparison with previous mass spectrometry results. Protein descriptions were assigned according to database (www.uniprot.org). Molecular weight and pI were calculated using SerialCloner 2-6 by subtracting the transit peptide, which is cleaved after import, from the polypeptide chain, except for Vdac1 as this mitochondrial outer membrane protein exhibits no transit peptide.

Figure legends

Figure 1. General effects of heat stress on HeLa cells and isolated mitochondria.
A) Analysis of the mitochondrial morphology of HeLa cells after heat stress by fluorescence microscopy. HeLa wild-type were treated for 2 h at indicated temperatures and analyzed immunofluorescence using antibodies against the mitochondrial proteins Hsp60, Tufm, Sdha, and F1ß. Scale bar: 10 µm. B) Flow cytometry analysis of HeLa cells after heat stress. Left: Analysis of mitochondrial membrane potential by TMRE staining. Black: negative control (valinomycin treatment), white: control at 37°C, grey: heat stress at 45°C for 2.5 h. Right: Detection of reactive oxygen species using the mitochondria-specific superoxide-reactive dye MitoSOX^{TM}. Black: positive control (menadione-treatment), white: control at 37°C, grey: heat stress at 45°C for 2.5 h. Results shown are representatives for two independent experiments. C) Membrane potential of isolated mitochondria after 20 min incubation at different temperatures. The potential was measured by TMRE fluorescence in a microplate reader. Shown are the means of the relative values of the respective sample compared to the control sample at 25°C (n=3) and the standard error of the mean (SEM). D) ATP content in isolated mitochondria after heat shock. The ATP concentration was determined as described in experimental procedures either directly ("before") or after 20 min incubation at 25°C or 42°C ("after") E) Integrity of mitochondria after heat stress. Incubation of isolated HeLa wild–type mitochondria at 25°C and 42°C for 20 min and following 20 min treatment with proteinase K (PK) at the indicated concentrations. Mitochondria were lysed prior the treatment with buffer containing 0.5% Triton X-100 as control for a sufficient PK treatment. F) Analysis of the mitochondrial protein complexes in isolated mitochondria after heat stress (20 min, 42°C) compared to unstressed conditions (20 min, 25°C). Mitochondria were analyzed by BN–PAGE or SDS–PAGE and Western blot. Antibodies against subunits of the complex I (NDUFA9), complex II (SDHA), complex III (UQCRC2), complex IV (COX4) and complex V (F1ß) were used. G) Enzymatic activity assays of mitochondrial enzymes after heat shock. Activities of malate dehydrogenase (MDH) and alpha-ketoglutarate dehydrogenase complex (KGDHC) were measured as described after incubation of isolated mitochondria for 20 min at 25°C and 42°C. Values shown are means +/- SEM of the ratio of the activity after heat stress compared to control conditions.

Figure 2. Proteomic analysis of the mitochondrial proteome under heat stress.
A) 2D-DIGE spot pattern of heat treated mitochondria. Gel shows an overlay of total soluble protein samples from control (25°C; *red*) and heat-treated (20 min at 42°C; *green*) mitochondria. The gel shown is a representative example of three experiments. Protein spots of the mitochondrial elongation factor Tu (Tufm) are shown enlarged for all six gels analyzed (insets). M_r: relative molecular mass. B) Quantification of selected protein spots. Shown are relative differences of spot intensities between control and heat-stressed mitochondria. Average spot intensities in control samples were set to 100%. Spot detection and quantification were done using the Delta2D software (DECODON). Error bars indicate the standard error of the mean (SEM). The significance was calculated via one-way ANOVA using the Dunnett`s multiple comparisons test. A *p*–value ≤ 0.001 was considered significant and is indicated by asterisks.

Figure 3. Aggregation behavior of mitochondrial elongation factor Tu during stress.
A) Aggregation under heat stress. Isolated mitochondria were incubated for 20 min at indicated temperatures and aggregates were separated by centrifugation at 20,000 x*g*. Total lysates (T), supernatants (Sup) and pellets (Pel) were analyzed by SDS-PAGE and Western blot. B) Aggregation under oxidative stress. Isolated mitochondria were treated with menadione as indicated for 20 min and analyzed as described above. C) ATP dependence of Tufm aggregation. Isolated mitochondria were heat stressed for 20 min at 42°C in presence and absence of ATP (f.c. 5 mM) and analyzed as described above. Asterisk in lane 4 indicate that less sample was loaded due to loss of sample material during the procedure. D) GTP dependence of Tufm aggregation. Isolated mitochondria were heat stressed in presence and absence of GTP (f.c. 2.5 mM) and analyzed as describe above.

Figure 4. Time dependence of aggregation under heat stress.
Time dependence of aggregation of mitochondrial proteins after heat stress. After incubation of isolated mitochondria at 42°C for indicated times aggregates were analyzed by SDS-PAGE and Western blot. Percentage of aggregation was calculated by the ratio of aggregated protein (pellet) compared to the total protein (supernatant + pellet). Shown are mean values of three experiments; error bars indicate the standard error of the mean (SEM).

Figure 5. Nature of Tufm aggregates after heat stress.
A) Analysis of aggregate size after heat stress. Isolated mitochondria were incubated for 20 min under stress (42°C) and control (25°C) conditions. Protein aggregates were fractionated by differential centrifugation (supernatants of each centrifugation step were transferred to the next centrifugation step). B) Protease resistance of Tufm aggregates. Isolated mitochondria were incubated for 20 min at indicated temperature. Mitochondria were lysed with 0.5% Triton X-100 and digested with indicated concentrations of proteinase K. C) Degradation of mitochondrial proteins during heat stress. Intact energized mitochondria were incubated for up to 6 h at 30°C (control) and 42°C (heat stress). Protein was precipitated with TCA and analyzed by SDS–PAGE and Western blot using the indicated antibodies. D) Recovery of aggregation after heat shock. Isolated mitochondria were heat stressed at 42°C for 20 min and afterwards incubated for up to 2 h at 30°C. During the recovery incubation, mitochondria were energized and supplied with ATP. Supernatants (Sup) and pellets (Pel) were separated by centrifugation and analyzed by SDS PAGE and Western blot.

Figure 6. Translational control under heat stress.
A) *In organello* translation of mitochondria-encoded proteins. Isolated mitochondria were heat stressed at 42°C for up to 20 min (control sample 25°C) and newly translated mitochondrial proteins were labeled with [^{35}S]-Met/Cys. Samples were treated with cycloheximide and chloramphenicol to impede cytosolic or mitochondria translation. Left panel: Bands representing mitochondria-encoded subunits are indicated (ND, NADH dehydrogenase; CO, cytochrome *c* oxidase; A, ATP-synthase; Cyt b, cytochrome *bc1* complex). B) Quantitative analysis of *in organello* translation of mitochondria-encoded proteins after heat shock. Shown are mean relative values and SEM of total incorporated radioactivity (n=3; control values at 25°C were set to 100%). C) Mitochondrial protein import after heat stress. *In vitro* import of [^{35}S]Met/Cys-labeled preprotein SU9(70)DHFR in energized isolated mitochondria after pre-incubation at indicated temperatures for 20 min. The import was performed under standard conditions. Where indicated, the membrane potential (ΔΨ) was depleted before import. Non-imported preproteins were digested by incubation with proteinase K (PK) [f.c. 50 µg/ml] after the import reaction. Imported proteins were analyzed by SDS-PAGE and detected by digital autoradiography. p: precursor, m: mature protein. D) Comparison of heat-induced aggregation of newly imported and endogenous proteins. After *in vitro* import of [^{35}S]Met/Cys-labeled preproteins Trap1 and Mdh2 as described above, mitochondria were subsequently heat-shocked for 20 min at indicated temperatures. Aggregates were separated by centrifugation and supernatants (Sup), pellets (Pel) as well as total amounts were analyzed by SDS–PAGE and Western blot (ΔΨ, inner membrane potential; PK, proteinase K treatment). The newly imported proteins were detected by autoradiography (top panel) whereas endogenous steady-state amounts of Trap1 and Mdh2 were detected by immunodecoration with specific antibodies (bottom). Asterisks indicate lanes where less sample was loaded. p: precursor protein, m: mature protein.

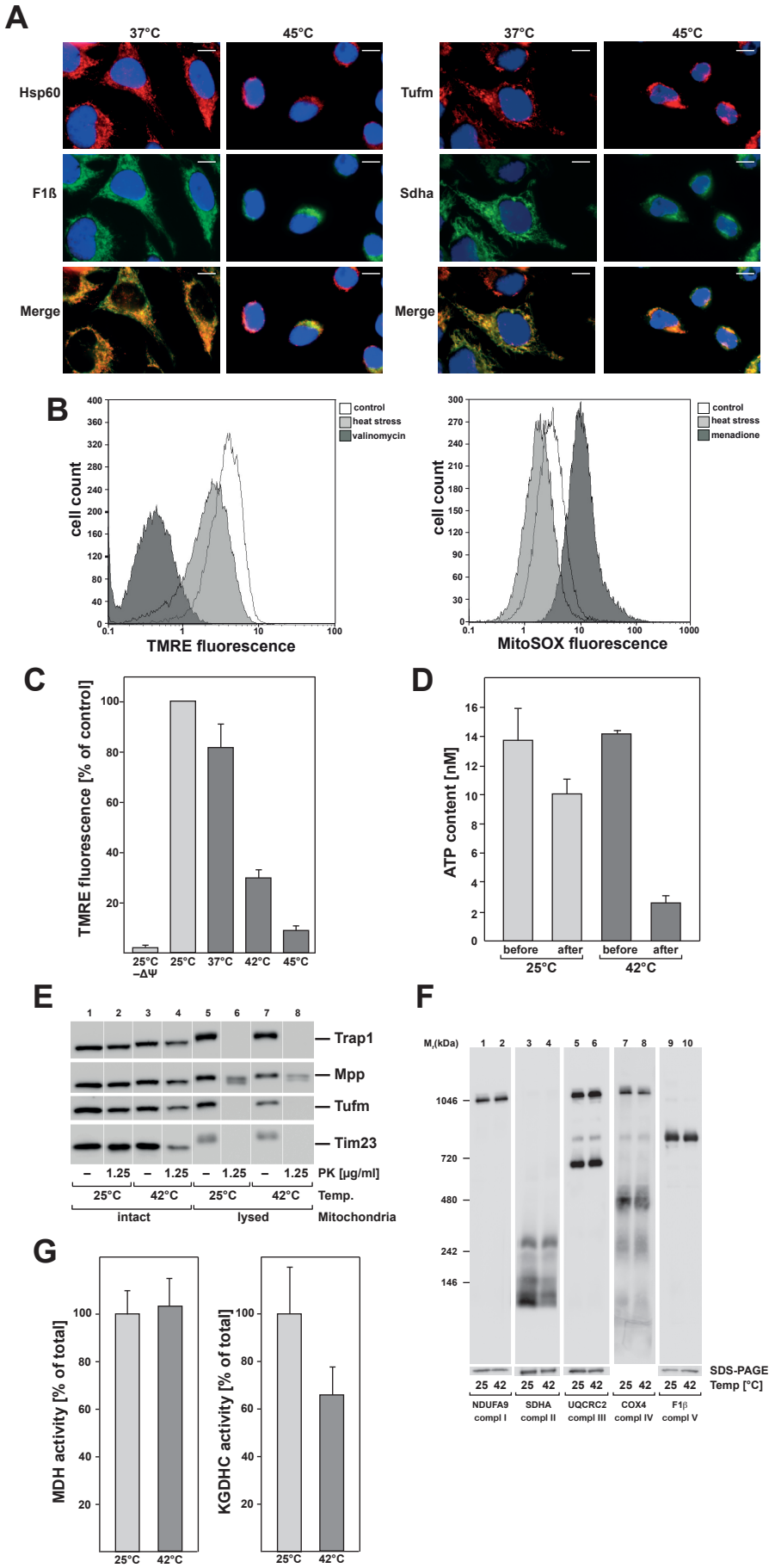
A
37°C
45°C
Hsp60
F1ß
Merge
Tufm
Sdha
B
control
heat stress
valinomycin
menadione
cell count
TMRE fluorescence
MitoSOX fluorescence
C
TMRE fluorescence [% of control]
25°C −ΔΨ
25°C
37°C
42°C
45°C
D
ATP content [nM]
before
after
E
Trap1
Mpp
Tufm
Tim23
PK [µg/ml]
Temp.
Mitochondria
intact
lysed
F
M_r(kDa)
1046
720
480
242
146
SDS-PAGE
Temp [°C]
NDUFA9 compl I
SDHA compl II
UQCRC2 compl III
COX4 compl IV
F1β compl V
G
MDH activity [% of total]
KGDHC activity [% of total]

Figure 1

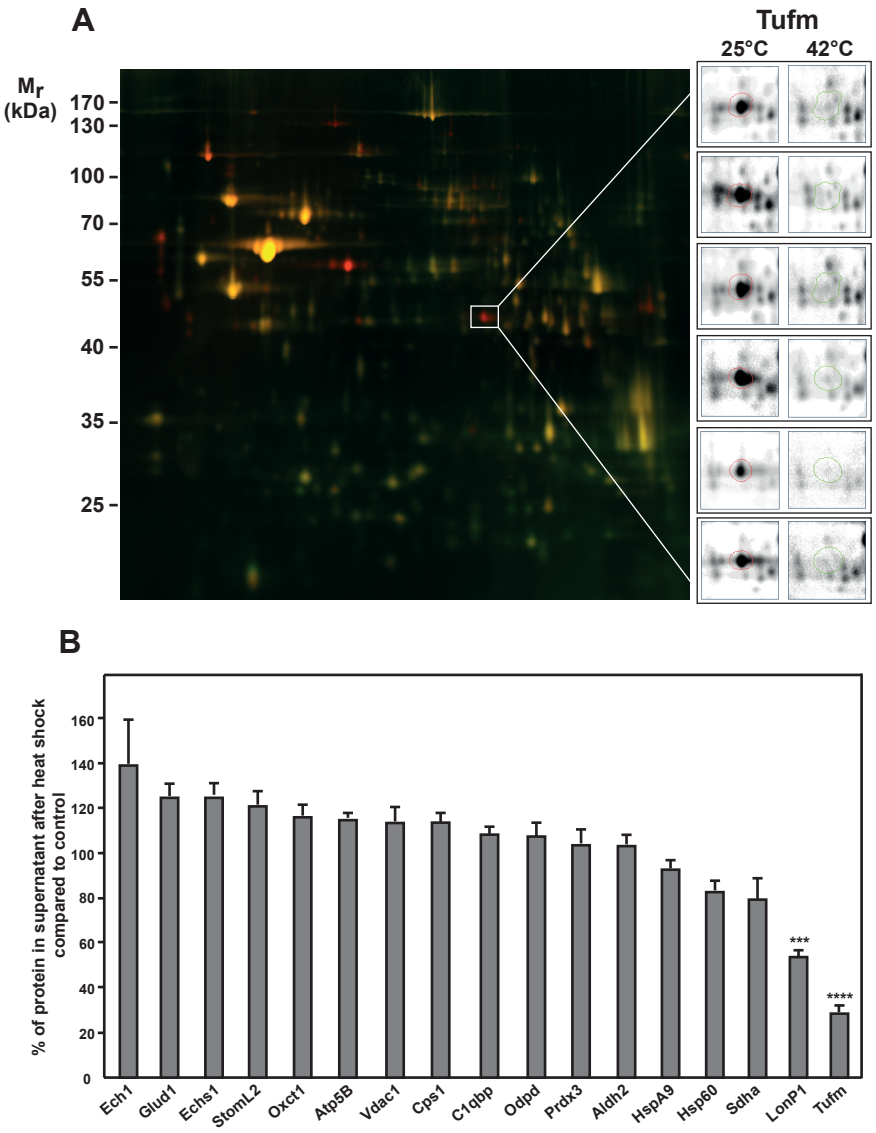
A
Tufm
25°C
42°C
Mr
(kDa)
170
130
100
70
55
40
35
25
B
% of protein in supernatant after heat shock compared to control
160
140
120
100
80
60
40
20
0
***
****
Ech1
Glud1
Echs1
StomL2
Oxct1
Atp5B
Vdac1
Cps1
C1qbp
Odpd
Prdx3
Aldh2
HspA9
Hsp60
Sdha
LonP1
Tufm

Figure 2

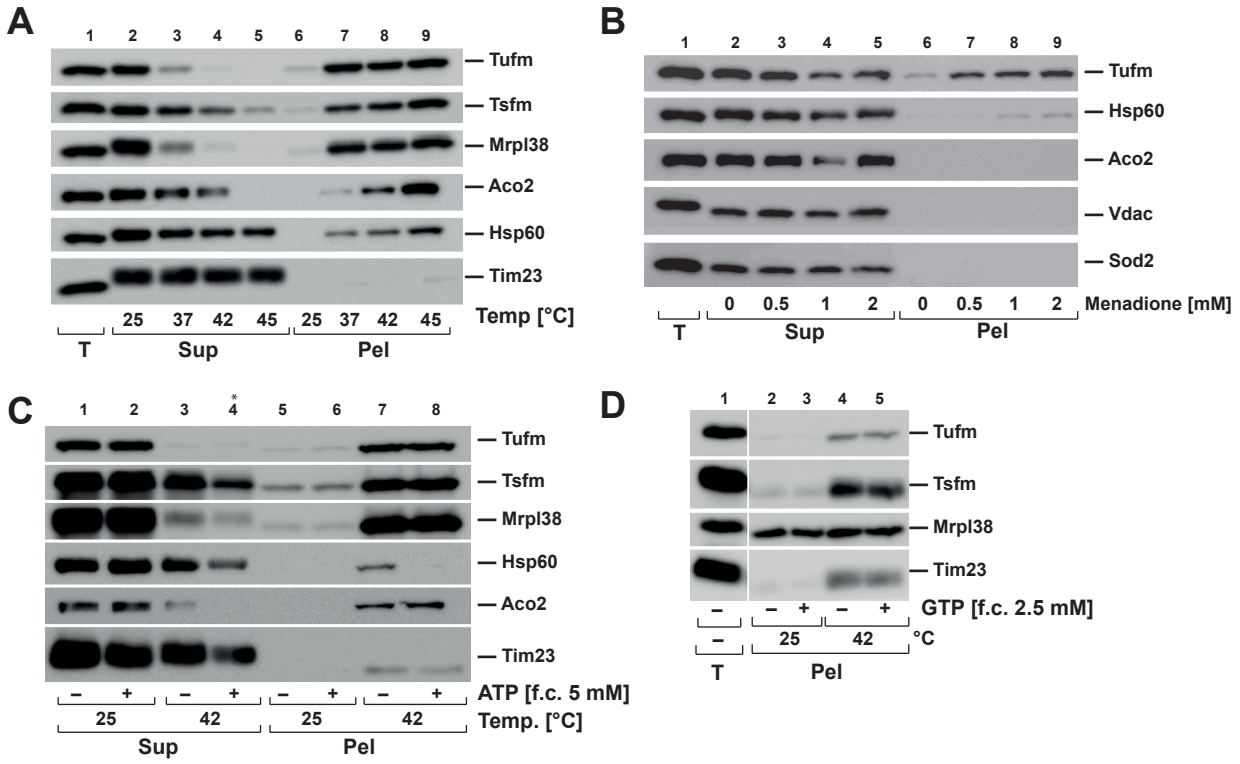
A
1 2 3 4 5 6 7 8 9
Tufm
Tsfm
Mrpl38
Aco2
Hsp60
Tim23
25 37 42 45 25 37 42 45
Temp [°C]
T
Sup
Pel
B
1 2 3 4 5 6 7 8 9
Tufm
Hsp60
Aco2
Vdac
Sod2
0 0.5 1 2 0 0.5 1 2
Menadione [mM]
T
Sup
Pel
C
1 2 3 4* 5 6 7 8
Tufm
Tsfm
Mrpl38
Hsp60
Aco2
Tim23
– + – + – + – +
ATP [f.c. 5 mM]
25 42 25 42
Temp. [°C]
Sup
Pel
D
1 2 3 4 5
Tufm
Tsfm
Mrpl38
Tim23
– – + – +
GTP [f.c. 2.5 mM]
– 25 42
°C
T
Pel

Figure 3

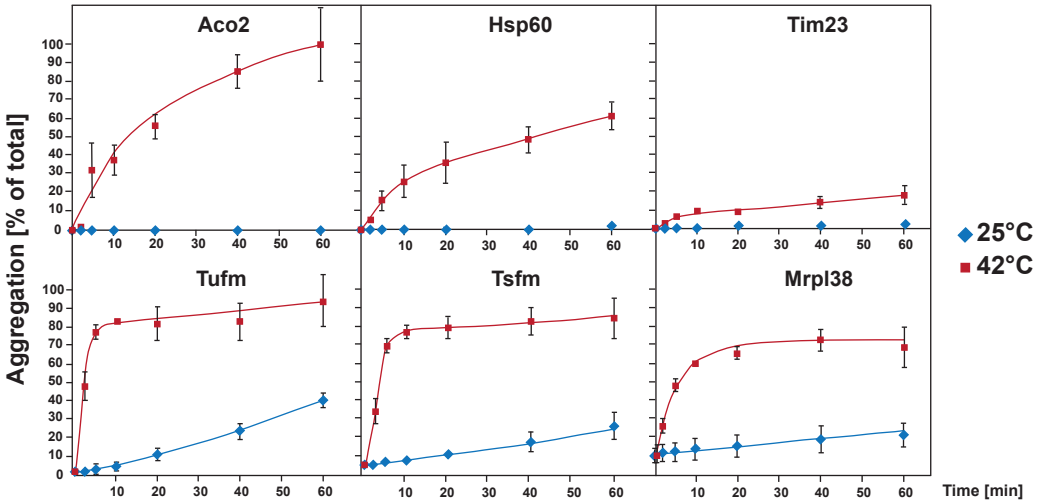
Aco2
Hsp60
Tim23
Tufm
Tsfm
Mrpl38
Aggregation [% of total]
Time [min]
25°C
42°C

Figure 4

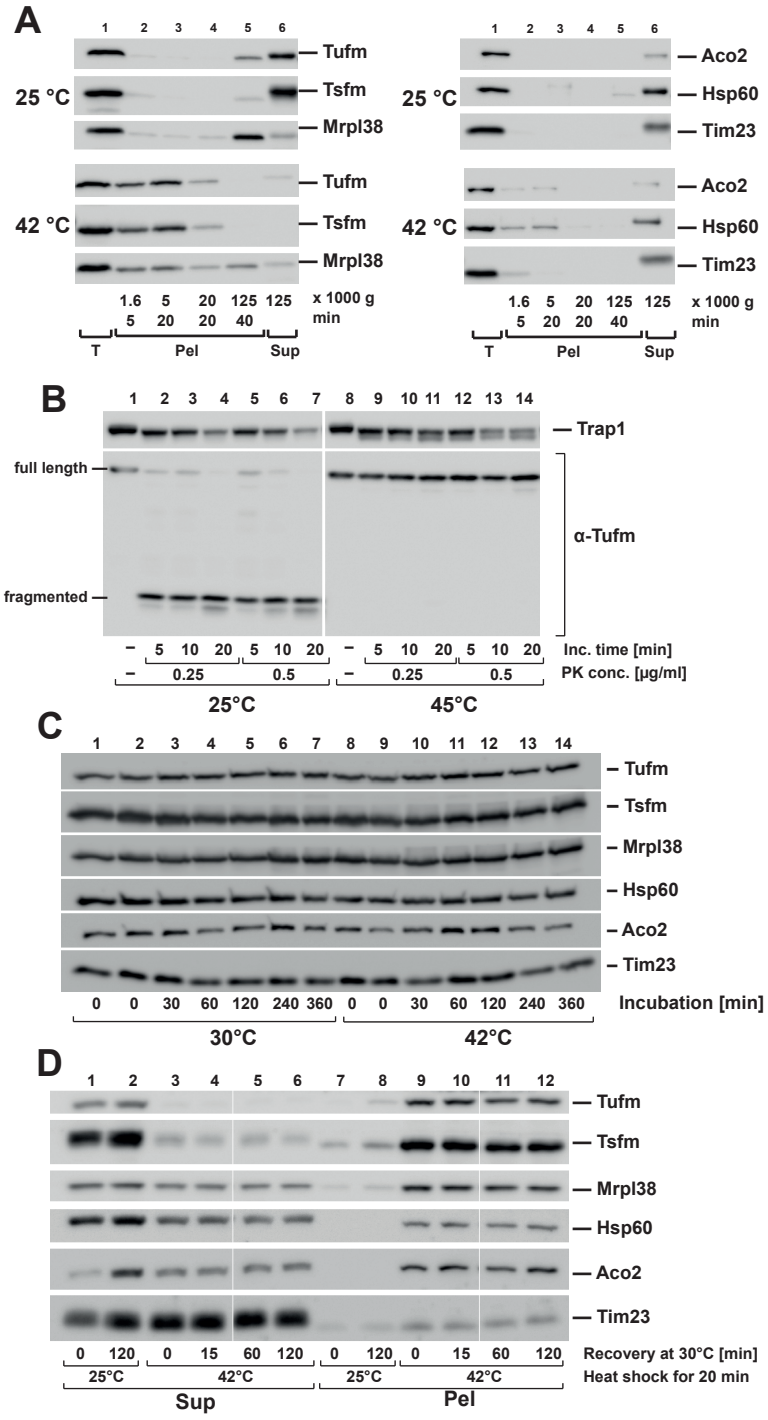
A
1 2 3 4 5 6
Tufm
Tsfm
Mrpl38
25 °C
42 °C
Aco2
Hsp60
Tim23
1.6 5 20 125 125
5 20 20 40
x 1000 g
min
T
Pel
Sup
B
1 2 3 4 5 6 7 8 9 10 11 12 13 14
Trap1
full length
fragmented
α-Tufm
– 5 10 20 5 10 20
Inc. time [min]
– 0.25 0.5
PK conc. [µg/ml]
25°C
45°C
C
Tufm
Tsfm
Mrpl38
Hsp60
Aco2
Tim23
0 0 30 60 120 240 360
Incubation [min]
30°C
42°C
D
1 2 3 4 5 6 7 8 9 10 11 12
0 120 0 15 60 120
Recovery at 30°C [min]
25°C
42°C
Heat shock for 20 min
Sup
Pel

Figure 5

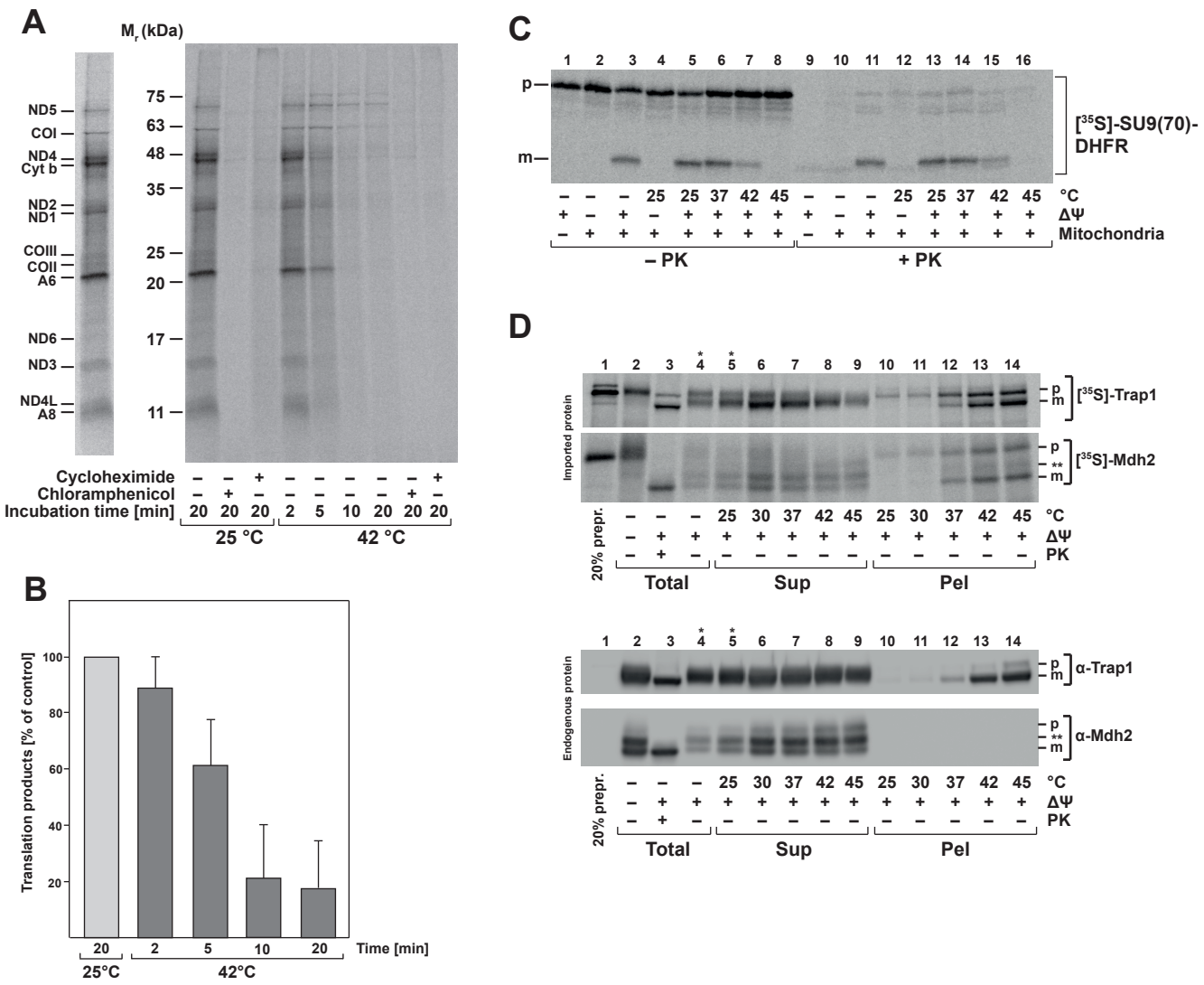
A
M_r (kDa)
ND5
COI
ND4
Cyt b
ND2
ND1
COIII
COII
A6
ND6
ND3
ND4L
A8
75
63
48
35
25
20
17
11
Cycloheximide
Chloramphenicol
Incubation time [min]
25 °C
42 °C
B
Translation products [% of control]
Time [min]
25°C
42°C
C
p
m
[35S]-SU9(70)-DHFR
°C
ΔΨ
Mitochondria
– PK
+ PK
D
Imported protein
[35S]-Trap1
[35S]-Mdh2
20% prepr.
PK
Total
Sup
Pel
Endogenous protein
α-Trap1
α-Mdh2

Figure 6