Loss of Mitofusin 2 Promotes Endoplasmic Reticulum Stress*

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*Running Title: Mfn2 and ER stress

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Background: The role of Mfn2 in ER stress has not been examined previously.

Results: ER stress upregulates Mfn2. Ablation of Mfn2 delays translational recovery, alters late UPR signaling and increases cell death during ER stress.

Conclusion: Mfn2 influences whether the UPR is adaptive or apoptotic.

Significance: Mfn2 is an ER stress-inducible factor that contributes to ER homeostasis.

SUMMARY

The outer mitochondrial membrane GTPase mitofusin 2 (Mfn2) is known to regulate endoplasmic reticulum shape in addition to its mitochondrial fusion effects. However, its role in ER stress is unknown. We report here that induction of ER stress with either thapsigargin (TG) or tunicamycin (TM) in mouse embryonic fibroblasts leads to up-regulation of Mfn2 mRNA and protein levels with no change in the expression of the mitochondrial shaping factors Mfn1, Opal, Drp1 and Fis1. Genetic deletion of Mfn2 but not Mfn1 in mouse embryonic fibroblasts (MEFs) or cardiac myocytes in mice led to an increase in the expression of the ER chaperone proteins. Genetic ablation of Mfn2 in MEFs amplified ER stress and exacerbated ER stress-induced apoptosis. Deletion of Mfn2 delayed translational recovery through prolonged eIF2α phosphorylation associated with decreased GADD34 and p58IPK induction and elevated CHOP induction at late time points. These changes in the unfolded protein response were coupled to increased cell death reflected by augmented caspase 3/7 activity, lactate dehydrogenase release from cells and an increase in propidium iodide-positive nuclei in response to TG or TM treatment. In contrast, genetic deletion of Mfn1 did not affect ER stress-mediated increase in ER chaperone synthesis or eIF2α phosphorylation. Additionally, ER stress-induced CHOP, GADD34 and p58IPK induction and cell death were not affected by loss of Mfn1. We conclude that Mfn2 but not Mfn1 is an ER stress-inducible protein that is required for the proper temporal sequence of the ER stress response.

The endoplasmic reticulum (ER) is a highly dynamic organelle consisting of interconnected tubules involved in the synthesis, folding and transport of secretory and membrane proteins (1). It also serves as a site for calcium storage (2). Perturbing the protein synthetic machinery or ER Ca²⁺ homeostasis will induce a condition that is referred to as ER stress (3,4). ER stress activates complex cytoplasmic and nuclear signaling pathways collectively called the unfolded protein response (UPR) (5). Initially, the UPR seeks to reestablish ER homeostasis via translational attenuation to decrease ER load, transcriptional activation of chaperone genes to increase the folding capacity of the ER, and activation of the ER associated degradation machinery to clear misfolded proteins (6-8). If ER stress is unresolved, apoptosis is triggered (9,10). ER stress
is linked to the pathophysiology of numerous diseases including diabetes, atherosclerosis and Alzheimer’s disease (11-13). Experimentally, ER stress can be induced by tunicamycin, that inhibits N-glycosylation of nascent ER proteins by preventing UDP-GlcNAc-dolichol phosphate GlcNAc-phosphate transferase activity (14), or thapsigargin (TG) that inhibits ER Ca\(^{2+}\) ATPase leading to the depletion of ER calcium stores (15).

Three ER transmembrane proteins are instrumental in coordinating the UPR signal. These proteins are inositol-requiring transmembrane kinase and endoribonuclease 1α (IRE1α), activation transcription factor 6 (ATF6) and protein kinase-like ER kinase (PERK). In response to ER stress, IRE1α catalyzes Xbp1 mRNA splicing leading to the generation of an active transcription factor which translocates to the nucleus and activates the transcription of genes involved in protein folding and degradation to restore ER homeostasis (16). ATF6 is transported to the Golgi complex where it is cleaved by proteases to yield a transcription factor, that activates the expression of genes involved in protein folding (17,18). In addition to this transcriptional regulation, PERK phosphorylates eukaryotic initiation factor 2α (eIF2α) leading to the rapid attenuation of protein translation (7,19-21). This translational attenuation is transient because the production of proteins required for increased ER capacity is required during the later phase of the stress response. Thus, during the late phase, the stress-induced phosphatase GADD34 and the PERK inhibitor P58 IPK mediate the dephosphorylation of eIF2α to restore protein translation (22,23). Ultimately, if the ER stress is not mitigated, eIF2α phosphorylation promotes apoptosis through the induction of C/EBP homologous protein (CHOP).

The mitofusins, Mfn1 and Mfn2 are transmembrane GTPAses located on the outer mitochondrial membrane (OMM) that participate in the fusion of this organelle (24). Complete ablation of either mitofusin protein leads to embryonic lethality in mice, whereas mutations in human MFN2 are associated with Charcot-Marie-Tooth type IIa, a peripheral neuropathy (25,26). It has been reported that mitofusins are required for neuronal function and for maintenance mitochondrial DNA (mtDNA) in skeletal muscle of mice (27,28). Recently, the targeted ablation of either Mfn1 or Mfn2 in cardiac myocytes was shown to result in the diminution or enlargement of mitochondrial size, respectively, with little or no deterioration of cardiac function (29,30). Loss of either Mfn1 or Mfn2 delays oxidative stress-induced loss of mitochondrial membrane potential and mitochondrial permeability transition pore (MPT) activation. In contrast, the simultaneous ablation of both mitofusins in cardiac myocytes leads to severe cardiac dysfunction and gross deformities in mitochondrial structure (31).

Although Mfn1 and Mfn2 are highly homologous, studies have shown that they are not functionally redundant. In this regard, Mfn2 has been shown to exert extra-mitochondrial functions (32). Mfn2 differs from Mfn1 in that it is also present in the ER where it regulates ER shape, tethers ER and mitochondria, and regulates mitochondrial uptake of Ca\(^{2+}\) released by the ER (33). This study also demonstrated that the mutations in MFN2 associated with Charcot-Marie-Tooth type IIa syndrome selectively affect ER tubulation and tethering to the mitochondria. Ablation of the Mfn2 gene has also been shown to uncouple mitochondria from the ER increasing the distance between these organelles in cultured cells and interfering with interorganelle Ca\(^{2+}\) transport (33). In contrast, the sarcoplasmic reticulum-mitochondria distance is not affected when Mfn2 was ablated in adult cardiac myocytes where these structures appear to be locked into a tight crystalline-like array (29).

In this work, we provide evidence for the first time that Mn2 but not Mfn1 is upregulated upon the induction of ER stress. Moreover, ablation of Mfn2 but not Mfn1 in cultured mouse embryonic fibroblasts (MEFs) or adult cardiac myocytes in vivo led to an up-regulation of ER chaperone proteins both at baseline and in response to treatment with TG or TM in MEFs. Loss of Mfn2 was found to sensitize cells to ER stress-induced cell death by increasing caspase activity and augmenting CHOP induction. These findings suggest that Mfn2 but not Mfn1 is an ER stress regulatory protein that is necessary for the homeostasis of the ER.

**EXPERIMENTAL PROCEDURES**

**Isolation and culture of primary mouse embryonic fibroblasts** – Primary MEFs were isolated in accordance with the University of
Boston Animal Care and Use Committee. Using a protocol modified from Kamijo et al. (34), pregnant female mice with either loxP flanked Mfn1 or loxP flanked Mfn2 genes were sacrificed on day E14.5 of gestation by CO2 asphyxiation and mouse embryos explanted. Following removal of the head, heart and liver, embryos were rinsed with phosphate-buffered saline, minced, and digested with trypsin (0.25% solution containing 0.5 mM EDTA) for 15 minutes at 37°C, using 3 ml per embryo. Trypsin was inactivated by addition of DMEM containing 10% fetal bovine serum and penicillin/streptomycin. Cells from embryos were plated into 150 mm diameter culture dishes and incubated at 37°C in a 5% CO2 humidified chamber. Plating after disaggregation of embryo cells was considered passage 1. Cells were then subcultured in 35mm dishes, 6- or 12-well plates for experimentation.

**Adenoviral transfection** – MEFs were transfected with 50 multiplicity of infection of replication-deficient adenoviruses carrying the cre recombinase gene (AdCre), Null gene (AdNull), or green fluorescent protein (AdGFP) for 48 or 72 hours. Viruses were purchased from Vector Biolabs. Adenoviruses were delivered to the cells for four hours, and then the medium was changed to fresh DMEM. The cells were transfected with adenovirus 24 or 48 hours before treatment with Thapsigargin or Tunicamycin at the indicated concentrations to induce ER stress. Functional expression was confirmed by appropriate immunoblot analysis or real-time PCR. Transfection efficiency using these conditions was about 80%. Sample size is equal to at least five per group per treatment.

**ER stress induction** – MEFs treated as mentioned above were subjected to ER stress by treatment with 0.1 μmol/L of TG (for 0.5 or 18 hours) or 0.5 μg/ml of TM (for 1 or 18 hours). In case of TG, after 0.5 hour of TG treatment, medium was changed to fresh DMEM and cells allowed to recover. Tunicamycin (TM) inhibits N-glycosylation of nascent ER proteins (14), while thapsigargin (TG) depletes ER calcium stores by inhibiting ER Ca\(^{2+}\) ATPase (15).

Cardiac myocyte-specific ablation of Mfn1 and Mfn2 in mice – Mice with cardiac myocyte specific deletion of Mfn1 (Mfn1 CKO) and Mfn2 (Mfn2 CKO) were generated as previously described (29,30), and mice were handled according to the regulations of the Institutional Animal Care And Use Committee (IACUC) of Boston University School of Medicine.

**Protein extraction** – Total cellular proteins were isolated from MEFs treated as mentioned above. Monolayer cultures of MEFs were washed with PBS, harvested in ice-cold lysis buffer (containing 20 mMol/L Tris-HCl, 150 mMol/L NaCl, 1 mMol/L Na2EDTA, 1 mMol/L EGTA, 1% (v/v) Triton, 2.5 mMol/L sodium pyrophosphate, 1 mMol/L glycero phosphatase, 1 mMol/L Na3VO4, 1 μg/mL leupeptin, 0.1% (v/v) protease inhibitor cocktail, and 1 mMol/L PMSF) using a cell scraper. Extracts were sonicated and the resulting lysates centrifuged at 15000 x g for 5 minutes at 4°C to remove cell debris. Total protein was estimated using bicinchoninic acid assay. Lysates were immediately frozen in liquid nitrogen and stored at - 80°C until used. Total cellular protein was also isolated from hearts of WT, Mfn2 CKO and Mfn1 CKO mice as previously described (30).

**Western blotting** – Twenty five micrograms of protein was applied to each lane of a 10% Tris-glycine SDS-PAGE gel and electroblotted onto PVDF membranes. Reagent-grade nonfat milk (Bio-Rad) 5% (w/v) in Tris buffered saline was used for blocking. Blots were incubated with anti-Mfn2 (1:2000, Sigma), anti-Mfn1 (1:1000, NeuroMab) anti-Grp94 (1:4000, Santa Cruz), anti-Grp78 (1:1000, Santa Cruz), anti-CHOP (1:1000; Santa Cruz), anti-GADD34 (1:1000, Santa Cruz), anti-p-Elf2α (1:1000, Cell Signaling), anti-eIF2α (1:2000, Cell Signaling), anti-p-58IPK (1:2000, Cell Signaling) or α-tubulin (1:2000, cell signaling), as primary antibodies overnight at 4°C. Blots were then incubated for one hour with 0.1μg/mL of secondary antibody (goat anti-rabbit IgG-HRP conjugated, goat anti-mouse IgG-HRP conjugated, goat anti-rat IgG-HRP conjugated) and detected with an enhanced chemiluminescent detection system (Pierce). Densitometry was performed using non-saturated chemiluminescent membranes exposed using Fuji LAS-4000 bio-imaging analyzer and quantified using ImageJ software. Multiple exposures from every experiment were used to confirm that the signal was within the linear range. Levels of proteins of interest were normalized to α-tubulin, and then expressed as a percentage of control (set at 100%).

**PCR** – Total RNA was extracted with Trizol reagent (Invitrogen). Total RNA (1 μg) was
subjected to reverse transcriptase reaction to synthesize the cDNA using SuperScript™ III First-Stand Synthesis System (Invitrogen). Quantification of cDNAs was by real-time PCR (RT-PCR) using SYBR® Green (Applied Biosystems). These quantities were expressed relatively to that of the Gapdh gene. All primer sequences for genes shown in Figure are available upon request. All primers were purchased from Integrated DNA Technologies.

Assessment of ER and mitochondrial morphology – ER and mitochondrial morphology was evaluated in Mfn2loxP MEFs cultured on 3mm glass bottom dishes (MatTak). MEFs were transfected with AdCre to ablate Mfn2 or treated with 0.1µM TG for 18 hours to induce ER stress. MEFs were then transfected with either a vector encoding the ER targeting sequence of calreticulin fused to the 5’ end of DsRed2 (Clontech) to evaluate ER morphology or stained with 50nM mitotracker green (Molecular Probes) to evaluate mitochondrial morphology. Using confocal microscopy, DsRed2 was excited with the 543nm laser set at 40% power while Mitotracker green was excited with the 488nm laser set at 7% power and visualized with a 63x oil immersion lens (Plan-Apochromat; NA 1.5). All experimental groups were repeated three times.

Cell death assays – Cell death was assessed for MEFs by measuring LDH release spectrophotometrically using a commercially available kit (Sigma) following ER stress induction. The results were expressed as LDH release relative to total LDH in the cells and normalized to untreated control. Similarly treated MEFs were also stained with the fluorescent DNA-binding dyes DAPI (10 μg/ml) and propidium iodide (PI; 10 μg/ml) for 1 hour similar to previous work (35,36). The stained nuclei were then visualized using a LUCPlanApo 10X/0.4 objective on an Olympus Inverted fluorescence microscope and Xcite 120 Fluor light source (level of 12%). Filters used included 350/50 nm excitation and 470/40 nm emission filters for DAPI and 560/40 nm excitation and 630/60 nm emission filters for PI. Exposure duration was set at 100 ms for DAPI and 500 ms for PI. Four fields per treatment were counted, treatments were done in duplicates and data were expressed as percent PI-positive nuclei/total nuclei. Sample size is equal to six per group per treatment. Apoptosis was also assessed by measuring caspase-3/7 activity in whole cell lysates using Caspase Glo kit (Promega) according to the manufacturer’s instructions. Briefly, equal volumes of whole cell lysate (30 μg) and caspase reagent were mixed and incubated in the dark for 1 hour at room temperature. Bioluminescence was measured using an Infinite® M1000 microplate reader (TECAN) and expressed in percent luminescence (normalized to control). Sample size is equal five per group per treatment.

Statistical Analysis – Results are shown as mean ± S.E. The statistical analysis (Graph Pad 4.0) was conducted using student’s t test or by one-way ANOVA followed by Dunnett’s Test, as appropriate. Differences were considered statistically significant if \( P<0.05 \).

RESULTS

Mfn2 is up-regulated by ER stress– To establish a link between ER stress and the expression of proteins involved in mitochondrial dynamics, mouse embryonic fibroblasts (MEFs) were treated with TG (0.1µmol/L), that depletes ER Ca2+, or TM (0.5 µg/µL), that inhibits ER N-glycosylation, for 18 hours to induce ER stress. Treatment with TG induced Mfn2 transcript levels 1.9 fold (\( P<0.05 \)) and TM induced Mfn2 transcript levels by 1.8 fold (\( P<0.05 \)), as determined by quantitative RT-PCR (Fig. 1A). Neither TG- nor TM-induced ER stress altered the transcript levels of other outer mitochondrial membrane fusion protein Mfn1. Furthermore, these agents did not influence the transcript levels of other proteins involved in mitochondrial fission and fusion including Opa1, Drp1 or Fis1. Treatment of MEFs with TG or TM also led to the upregulation of Mfn2 but not Mfn1 protein levels by a factor of 2 (Fig. 1B). The induction of Mfn2 paralleled the increase in the levels of the ER chaperone proteins Grp78 and Grp94. Taken together, the above results suggest that among mitochondrial fission and fusion proteins, Mfn2 is selectively upregulated by ER stressors.

Ablation of Mfn2 augments ER chaperone expression– The accumulation of unfolded proteins in the ER lumen induces the selective induction of chaperone proteins (21). To determine if Mfn2 affects this arm of the UPR response, an adenoviral vector expressing cre recombinase (AdCre) was used to ablate Mfn2 by transducing...
MEFs isolated from Mfn2\textsuperscript{floxflox} mice. The transfection efficiency for the AdCre was estimated to be greater than 80% based upon transfection with an adenoviral vector that expresses the GFP reporter gene (Fig. 2A). Forty eight hours after transfecting primary MEFs with AdCre, total cellular proteins were harvested and protein levels were evaluated via western immunoblot analysis. Immunoblots for Mfn1 and Mfn2 showed significant reductions in Mfn2 but no change in Mfn1 levels compared with MEFs treated with a control adenovirus lacking the Cre transgene (AdNull) (Fig. 2B).

To determine the effects of Mfn2 ablation on the unfolded protein response (UPR), control and Mfn2 deficient MEFs were evaluated for ER chaperone protein expression under baseline conditions and in response to treatment with TG or TM. Ablation of Mfn2, augmented baseline Grp78 expression and, to a lesser extent, Grp94 expression (Fig. 2C). As expected, treatment with TG or TM led to increased expression of Grp78 and Grp94, and the induction of these proteins was generally higher in Mfn2-ablated MEFs compared with control. Additionally, real time PCR showed significantly up-regulated mRNA levels of ATF4 and Grp94 for AdCre-treated MEFs compared with control MEFs at baseline (Fig. 2D). In contrast, ablation of Mfn2 did not affect levels of calreticulin, either at baseline or under ER stress conditions (data not shown). Mfn2 ablation did not affect mRNA levels of the mitochondrial fusion factors Mfn1 and Opa1, nor the expression of the mitochondrial fission factors Drp1 and Fis1 (Fig. 2D).

In contrast to Mfn2 ablation, the selective ablation of Mfn1, achieved by treating Mfn1\textsuperscript{floxflox} MEFs with AdCre (Fig. 3A), did not affect either baseline or ER stress-induced chaperone expression (Fig. 3B). Quantitative transcript analysis also did not reveal significant changes in the mRNA levels of factors involved with the regulation of mitochondrial fusion and fission (data not shown). Overall, the above results suggest a role for Mfn2 but not Mfn1 in ER stress signaling.

Loss of Mfn2 alters ER and mitochondrial morphology—The effects of Mfn2 ablation and ER stress on mitochondria and ER shape were analyzed by confocal microscopy in Mfn2\textsuperscript{floxflox} MEFs. In control MEFs, the ER appeared as interconnected networks. The induction of ER stress with TG or ablation of Mfn2 had similar effects on ER morphology, resulting in the formation of dilated and aggregated structures as shown by DsRed fluorescence (Fig. 4 upper panel). Similarly, both ER stress and ablation of Mfn2 resulted in similar alterations to the mitochondrial network. While mitochondrial structure was mostly tubular-like in control MEFs, mitochondria from MEFs subjected to ER stress or deficient in Mfn2 expression showed a fragmented phenotype, as shown by mitotracker Green fluorescence (Fig. 4 lower panel).

Ablation of Mfn2 in cardiac myocytes in vivo augments ER chaperone expression—Mice with targeted deletion of either Mfn1 or Mfn2 in cardiac myocytes are viable and survive through adulthood (29,30). Since Mfn2 ablation augments the expression of ER stress makers in MEFs, we sought to confirm these findings in vivo in mice with cardiac myocyte-specific deletion of Mfn2 (Mfn2 CKO mice). Although ablation of Mfn2 in the heart did not significantly change the expression of other mitochondrial fusion (Mfn1 and Opa1) or fission (Drp1 and Fis1) factor mRNA levels, the transcript levels for ER stress response markers, ATF4 and Grp94 were significantly elevated in heart (Fig. 5A). Western blotting also revealed augmented expression of the UPR-inducible proteins Grp94 and Grp78, and a smaller but reproducible increase in calreticulin in hearts of Mfn2 CKO compared to wild type (WT) mice (Fig. 5B). In contrast, cardiac myocyte-specific ablation of Mfn1 (Mfn1 CKO) did not affect the expression levels of Grp94, Grp78, or calreticulin (Fig. 5C).

Loss of Mfn2 affects UPR signaling—ER stress is associated with the temporal regulation of UPR proteins. Therefore, time course studies analyzing the expression of Mfn2 and known ER stress proteins were performed in MEFs treated with TG. Mfn2 up-regulation occurred in the late phase of ER stress (8 hours) and was accompanied by increases in CHOP, Grp94, Grp78, GADD34 and p58IPK expression (Fig. 6A,B). The upregulation of Mfn2 was preceded by the transient upregulation of eIF2\textalpha phosphorylation.

Phosphorylation and dephosphorylation of eukaryotic initiation factor 2 (eIF2\textalpha) is a critical early step in the regulation of protein synthesis during ER stress (20-23). Therefore, we
determined whether loss of Mfn2 affects the phosphorylation status of eIF2α during the early and late stages of the UPR. In the absence of ER stress, loss of Mfn2 did not affect baseline phosphorylation of eIF2α (data not shown). In control MEFs, brief treatment with TG (0.5 hours) or TM (1 hour) was associated with a profound increase in eIF2α phosphorylation (Fig. 6C,D). This early increase in eIF2α phosphorylation was not altered by the ablation of Mfn2. In contrast, levels of phosphorylated eIF2α remained elevated at late time points (18 hours) after treatment with TG or TM in Mfn2-ablated MEFs compared with control MEFs. An analysis of multiple time course experiments revealed that Mfn2 ablation led to 5.4±1.2 fold and 4.7±1.5 fold elevations in eIF2α phosphorylation in TG- and TM-treated cells, respectively, at the 18 hour time point (P<0.01).

Thus, Mfn2 ablation does not affect the early TG- or TM-mediated increases in eIF2α phosphorylation, but delayed the dephosphorylation of eIF2α that occurs at later time points. Consistent with this observation, Mfn2 ablation led to 40.5±3.6% and 23.8±4.7% reductions in the level of GADD34 and P58IPK, that promote eIF2α dephosphorylation at the late time points (Fig. 6C). Quantitative analyses revealed that Mfn2 ablation led to 40.5±3.6% and 23.8±4.7% reductions in the level of GADD34 (P<0.05), and 44.8±4.2% and 22.6±6.4% reductions in the level of P58IPK (P<0.05) in the TG- and TM-treated cells, respectively, at the 18 hour time point. In contrast, loss of Mfn1 did not alter either UPR mediated PERK-eIF2α phosphorylation or GADD34 and P58IPK induction during late ER stress (Fig. 6E). Taken together, these data suggest that Mfn2 is induced during late UPR signaling and that this induction is essential for the dephosphorylation of eIF2α and the induction of GADD34 and P58IPK.

**DISCUSSION**

The present study examined the role of the mitochondrial fusion protein Mfn1 and Mfn2 in the ER stress response. The data show that: 1) Pharmacologic induction of ER stress will up-regulate Mfn2 but not Mfn1 levels in MEFs. 2) Deletion of Mfn2, but not Mfn1, in the heart or in MEFs up-regulates the expression of ER stress proteins. 3) Loss of Mfn2 prolongs eIF2α phosphorylation and diminishes the induction of GADD34 and P58IPK in MEFs, indicative of an impairment in a recovery from translational repression. 4) Ablation of Mfn2 augments ER stress-induced CHOP induction and caspase activation. 5) Mfn2 deficiency sensitizes MEFs to ER stress-induced death. 6) Unlike Mfn2 ablation, Mfn1 ablation did not affect the expression of ER stress proteins involved in translational recovery, nor ER stress-mediated CHOP induction and cell death. Thus, our study provides the first demonstration that Mfn2 is an ER stress inducible protein that is required for the adaptation of the ER to stress.

We initially observed that inducers of ER stress led to the elevated expression of Mfn2. Mfn2 was induced by altering ER Ca2+ signaling with TG, inhibiting protein N-glycosylation with TM or by inhibiting the ER-Golgi trafficking of newly synthesized proteins through treatment with Brefeldin A (data not shown). Despite the differences in action of these pharmacological agents, the time course and extent of Mfn2
upregulation was similar, suggesting that Mfn2 induction is a general feature of the ER stress response. This effect was highly specific for Mfn2, and the induction of ER stress had no effect on the expression of other mitochondrial shaping proteins including Mfn1, Opa1, Drp1 and Fis1. The specificity of Mfn2 induction by ER stress is particularly striking in light of the observation that ER stress is associated with marked changes in the morphology of the mitochondrial network (see Fig. 4). Finally, starvation (38), cold (39) and oxidative stress (40) have all been reported to upregulate Mfn2 expression. Because these stresses are also associated with the development of ER stress (41,42), it is possible that the ER-mediated induction of Mfn2 is central to the regulation of this factor.

Like many other stress-induced signaling pathways, the UPR can exert both protective and detrimental effects on the cell (43). The strength and duration of the ER stress are critical determinants of whether the UPR exerts either a pro-survival or a pro-death signal. It is widely accepted that the initial UPR responses are oriented toward protection and the resolution of the ER stress. In contrast, UPR pathways activated late in ER stress can enhance apoptosis that is necessary for removal of irreversibly damaged cells (44,45). In this regard, early and late UPR signals function in concert to temporally modulate translational activity. Early in ER stress, eIF2 is inactivated by phosphorylation to suppress protein synthesis (46,47). Later stages of the UPR require the synthesis of new stress-induced proteins, and eIF2α is dephosphorylated through the actions of GADD34 and P58IPK (22,46,47). Several groups have reported that excessive phosphorylation of eIF2α leads to ATF4-mediated CHOP induction, resulting in apoptosis (10,48). Here, it is shown that loss of Mfn2 does not affect the proximal effectors of the UPR, such as the rapid phosphorylation of eIF2α. Instead, Mfn2 is upregulated during the later stages of the ER stress response, and at these time points it appears to be required for the release from translational repression (Fig. 9). Consistent with this hypothesis, ablation of Mfn2 in MEFs led to prolonged eIF2α phosphorylation and reductions in GADD34 and P58IPK expression that serve to dephosphorylate and reactivate eIF2α. Mfn2 ablation also led to a propagation of the pro-apoptotic UPR program, as indicated by CHOP induction and caspase activation, and led to greater cell death in response to ER stress. CHOP is regulated by the ATF transcription factor, and ATF expression is enhanced by the phosphorylation of eIF2α at Ser51 (19). In agreement with these observations, we report that ATF expression is elevated in MEFs lacking Mfn2. Thus, it appears that the increased cell death caused by Mfn2 ablation is due to the activation of eIF2α-ATF-CHOP signaling, that may result from an impairment in the recovery from translational repression.

It is widely appreciated that both Mfn1 and Mfn2 control mitochondrial morphology by mediating the fusion of these organelles (49). It is also appreciated that mitochondria are juxtaposed with the ER. This close association is believed to be important in controlling lipid metabolism and Ca2+ transmission from the ER to the mitochondria (49). Recently, it has been shown that Mfn2 is present in the ER and that it tethers the ER and mitochondria (33). In the absence of Mfn2, ER structure is altered and the distance between the ER and mitochondria is increased, diminishing mitochondrial Ca2+ uptake. Notably, Mfn1 was found to have no detectable role in controlling ER shape or ER-mitochondrial communication. Here, we show that Mfn2, but not Mfn1, is regulated by ER stress and that it has an essential role in the UPR program. Furthermore, ER stress and Mfn2 ablation promote similar morphological changes to both the mitochondrial and ER networks. While these observations suggest that a dynamic interplay between mitochondrial and the ER may be required for an appropriate UPR, further studies are required to discern whether or not the ER-mitochondria bridging function of Mfn2 mediates these actions on the UPR. In this regard, it has been reported that re-expression of Mfn2 forms with a mutation in the GTPase domain that causes Charcot-Marie-Tooth syndrome, or ablation of the p21-Ras binding domain, are sufficient to rescue the mitochondrial shape phenotype in Mfn2-/- MEFs, but had no effect on the altered ER morphology (33).

We also observed that cardiac myocyte-specific ablation of Mfn2, but not Mfn1, led to ER stress marker (e.g. Grp78, Grp94) expression in the heart. We have previously reported that Mfn2 ablation in cardiac myocytes leads to modest
hypertrophy and only a small diminution in function when mice were stimulated with isoproterenol (29). In contrast to MEFs, ablation of Mfn2 in adult cardiac myocytes protected against cell death in response to a variety of stresses. In addition to having a pro-apoptotic role, ER stress can have a protective role in cardiac myocytes as well as other cell types through chaperone protein induction (50-52). In myocytes, ischemia will activate Grp78 expression via an ATF6-dependent mechanism, eliciting a preconditioning effect (53). It has also been reported that ER stress will activate autophagy in myocytes and promote cell survival (54). Thus, ER stress can fortify a cell against insults, but can also lead to cell death depending upon the strength and the duration of the ER stress. Based upon these considerations, it is reasonable to speculate that the induction of chaperone proteins in the hearts of Mfn2 CKO mice contributes to their enhanced resistance to pro-apoptotic stresses.

In light of the above considerations, it should also be noted that studies report different effects of Mfn2-deficiency in different cell types (32,55,56). Discordant results with cardiac myocytes have also been reported. For example, Mfn2 ablation in cultured neonatal cardiac myocytes leads to cell death (57), whereas Mfn2 expression is reported to promote cell death in both neonatal cardiac myocytes and a cardiac myocyte cell line (40). In our own studies, we found that Mfn2-deficiency in cardiac myocytes protects the heart from ischemia-reperfusion injury, protects adult cardiac myocytes from oxidative stress-induced loss of mitochondrial membrane potential, and diminishes the sensitivity of mitochondria to undergo mitochondrial permeability transition (MPT) (29). In contrast, we also found that siRNA knockdown of Mfn2 in cultured neonatal cardiac myocytes sensitized these cells to oxidative stress-induced loss of mitochondrial membrane potential and cell death (29). It is conceivable that these different effects of Mfn2 are due to differences in the quantity and organization of mitochondrial and, perhaps, ER networks within a particular cell type. For example, adult myocytes contain highly abundant mitochondria that are packed into a high ordered array that may favor the propagation of mitochondrial depolarizing events throughout the cell (58-61), thereby making these cells highly sensitive to cell death that is mediated by mechanisms that involve mitochondria. In contrast, neonatal myocytes are fibroblast-like and contain a much smaller number of mitochondria that are loosely organized within the cell. Thus, we speculate that the likelihood of a coordinated MPT is reduced in neonatal myocytes and MEFs. In these cell types, other effects of Mfn2 ablation, such as the status of the pro- or anti-apoptotic arms of the UPR, may predominate in the control of cell fate. Collectively, these data suggest that the actions of Mfn2 are likely to be highly dependent upon cellular context that can be influenced by the state of cellular differentiation, mitochondrial density and, perhaps, the status of the ER.

In summary, we have identified Mfn2 as a new regulator of the ER stress response. We show that it is selectively upregulated in response to ER stress, whereas other mitochondrial shaping proteins are not. Furthermore, we show that Mfn2 is essential for an appropriate elaboration of the UPR and ER homeostasis.

REFERENCES

**FOOTNOTES**

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FIGURE LEGENDS

FIGURE 1. ER stress upregulates Mfn2 expression in fibroblasts. MEFs were subjected to ER stress with 0.1µM thapsigargin (TG) or 0.5µg/µL tunicamycin (TM) for 18 hours. A. Real time PCR was performed to determine the mRNA levels of mitochondrial fusion proteins (mitofusin 1 (Mfn1), mitofusin 2 (Mfn2) and optic atrophy 1 long variant (Opa1)), and mitochondrial fission proteins (dynamin-related protein (Drp1) and mitochondrial fission protein 1 (Fis1)). B. Endogenous expression of mitochondrial fusion proteins (Mfn1 and Mfn2) and of ER chaperones (Grp78 and Grp94) determined by western blotting and densitometric quantification of immunoblots for Mfn1 and Mfn2. Results are expressed as means ± SEM, n=5/group, *P<0.05 vs. Control.

FIGURE 2. Ablation of Mfn2 in fibroblasts promotes ER chaperone protein expression. LoxP flanked Mfn2 MEFs were transfected with an adenoviral vector expressing Cre (AdCre) to delete Mfn2, or control virus (AdNull) for 48 hours. A. Fluorescent microscopy was used to determine transfection efficiency in AdCre transfected cells. Transfection efficiency was found to be greater than 75%. B. Whole cell lysates were extracted from similarly treated MEFs and immunoblotted for Cre recombinase, Mfn1 and Mfn2. A representative immunoblot is shown. Blots were quantified by densitometry and levels of Mfn1 and Mfn2 are expressed relative to α-tubulin. C. MEFs from Control and Mfn2 -deficient MEFs were subjected to ER stress with 0.1µM TG or 0.5µg/µL TM for 18 hours and immunoblotted for the ER chaperone proteins Grp94 and Grp78. D. Quantitative RT-PCR was performed to determine the mRNA levels of Mfn1, Mfn2, Opa1, Drp1, Fis1, ATF4 and Grp94. Results are expressed as means ± SEM, n=5/group *P<0.05 vs. TG or TM.

FIGURE 3. Loss of Mfn1 does not affect ER chaperone protein expression. LoxP flanked Mfn1 MEFs were transfected with AdCre to delete Mfn1 or control virus (AdNull) for 72 hours. A. Whole cell lysates were immunoblotted for Cre recombinase, Mfn1 and Mfn2, and α-tubulin was used as a loading control. B. Similarly treated MEFs were subjected to ER stress with 0.1µM TG or 0.5µg/µL TM for 18 hours were immunoblotted for the ER chaperone proteins Grp94 and Grp78. Results are expressed as means ± SEM, n=5/group *P<0.05 vs. TG or TM.

FIGURE 4. Loss of Mfn2 alters ER and mitochondrial morphology. LoxP flanked Mfn2 MEFs transfected with an adenoviral vector expressing Cre (AdCre) to delete Mfn2, or control virus (AdNull) for 48 hours were treated with TG to induced ER stress. Upper panel: Control and Mfn2-deficient MEFs were transfected with a vector encoding the ER targeting sequence of calreticulin fused to DsRed2 and ER visualized using confocal microscopy. Lower panel: Control and Mfn2-deficient MEFs were loaded with 100nM Mitotracker green and mitochondria visualized using confocal microscopy.

FIGURE 5. Cardiac myocyte-specific deletion of Mfn 2 but not Mfn1 upregulates ER chaperone expression in vivo. A. Quantitative RT-PCR was performed on transcript-encoded cDNA isolated from
wild-type (WT) and from Mfn2 CKO hearts to determine the mRNA levels of mitochondrial fusion proteins (Mfn1, Mfn2 and Opa1), mitochondrial fission proteins (Drp1 and Fis1), activating transcription factor 4 (ATF4) and glucose regulated protein 94 (Grp94). B. Whole cell lysates isolated from hearts of wild-type mice or with specific cardiac myocytes deletion of Mfn2 (Mfn2 CKO) were immunblotted to detect endogenous levels of the ER chaperone proteins Grp94, Grp78, and calreticulin. Even though Mfn2 deletion in the heart did not significantly alter Mfn1 levels, it activated ER stress as reflected by immunoblots showing augmented Grp94, Grp78, and calreticulin levels. Immunoblots were quantified by densitometry and GRP94, GRP78 and calreticulin levels are expressed relative to the α-tubulin loading control. C. Western blot analysis was performed to detect endogenous levels of Grp94, Grp78, and calreticulin in the heart of specific cardiac myocytes deletion of Mfn1 (Mfn1 CKO) relative to that in WT. Mfn1 deletion in the heart did not activate ER stress. Results are expressed as means ± SEM, n=4-6/group, *P<0.05 vs. WT.

FIGURE 6. Loss of Mfn2 affects UPR signaling in a time-dependent manner. A. Time courses of Mfn2 and of ER stress protein inductor in MEFs treated with 0.1 µM TG for the indicated time points. B. Densitometric quantification of time course of Mfn2 and ER stress proteins. C. Control and Mfn2 deficient MEFs were treated with 0.1 µM TG (0.5 or 18 hours). Cell extracts were prepared from these cells and immunobblotted for phosphorylated elf2α, total elf2α, GADD34 and p58IPK. D. Cell extracts from control and Mfn2-deficient MEFs treated with 0.5 µg/µLTM for (1 or 18 hours) were immunobblotted for phosphorylated elf2α, total elf2α, GADD34 and p58IPK. E. Total cell extracts from Control and Mfn1 deficient MEFs treated with 0.1µM TG or 0.5µg/µLTM for 18 hours were immunobblotted for phosphorylated elf2α, total elf2α, GADD34 and p58IPK. Results are expressed as means ± S.E. n=4/group. *P< 0.05 vs. TG or TM. CHOP induction is statistically significant at all time points. Phosphorylated elf2α (P-elf2α) levels differ from control at 30 minute, 4 hour, 8 hour and 18 hour time points (P<0.05).

FIGURE 7. Loss of Mfn2 activates the maladaptive UPR. Total cell lysates from control, and Mfn2-deficient MEFs were subjected to ER stress with 0.1µM TG or 0.5µg/µL TM for 18 hours were immunobblotted for CHOP (A) or assayed for Caspase 3/7 activity (B). C. Cell lysates from control and Mfn1-deficient MEFs subjected to ER stress with 0.1 µM TG or 0.5 µg/µL TM for 18 hours were immunobblotted for CHOP and α-tubulin. Blots were subjected to densitometry and CHOP levels were quantified relative to α-tubulin expression. *P<0.05 vs. TG or TM; n=4-6/group.

FIGURE 8. Loss of Mfn2 sensitizes MEFs to ER stress-induced cell death. A. Control and Mfn2 deficient MEFs treated with 0.1 µM TG and 0.5 µg/µLTM for 18 hours and stained with DAPI and propidium iodide (PI) to evaluate cell death. B. The media from the same cultures were assayed for LDH release. C. Control and Mfn1-deficient MEFs were treated with 0.1 µM TG and 0.5 µg/µL TM for 18 hours and stained with DAPI and PI. Results expressed as means ± SEM, n=4-6/group, *P<0.05 vs. TG or TM.

FIGURE 9. Schematic model of the involvement of mitofusin 2 in UPR signaling. Cross arrows indicate inhibition while other arrows designate positive signaling. Under ER stress conditions, early UPR involves elf2α phosphorylation leading to translational attenuation, while late UPR response involves GADD34 and P58IPK mediated elf2α dephosphorylation and CHOP induction. Ablation of Mfn2 inhibits GADD34 and P58IPK expression, enhances CHOP induction and promotes cell death.
Figure 1

A

Fold Change in Transcript (Relative to Control)

Mfn1  Mfn2  Opa1  Drp1  Fis1

Control  TG  TM

B

Protein Levels (% of Control)

Mfn1  Mfn2

Control  TG  TM

*
Figure 2

A

Bright field  GFP Fluorescence

B

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<tr>
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<td>α-tubulin</td>
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Protein Levels (% of AdNull)

Mfn1  Mfn2

Protein Levels (% of AdNull)

0  20  40  60  80  100  120  140

*
Figure 2

C. Western blot analysis showing the expression of Grp78, Grp94, and α-Tubulin in AdCre and AdNull groups. The blots are shown for TG and TM conditions.

D. Relative transcript level of Grp78, Grp94, Mfn1, Mfn2, Opa1, Drp1, Fis1, and ATF4 in AdNull and AdCre groups. The bars represent % of AdNull control.
Figure 3

A

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B

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Protein Levels (% of AdNull)

- **Mfn1**: AdNull 80 ± 10, AdCre 100 ± 10 (p < 0.05)
- **Mfn2**: AdNull 90 ± 10, AdCre 95 ± 10

% of Control

- **Grp78**: AdNull 100 ± 10, AdCre 150 ± 10
- **Grp94**: AdNull 100 ± 10, AdCre 200 ± 10

- **TG**
  - AdNull: 80 ± 10, AdCre: 120 ± 10
  - TG: 100 ± 10, TM: 150 ± 10
Figure 5

A

mRNA Levels (% of WT)

WT
Mfn2 CKO

Mfn1 Mfn2 Opa1 Drp1 Fis1 ATF4 Grp94

B

Grp78
Grp94
Calreticulin
α-tubulin

RT-qPCR

WT
Mfn2 CKO

Mfn1 Mfn2 ATF4

C

Protein Levels (% of WT)

WT
Mfn1 CKO

Grp78
Grp94
Calreticulin
α-tubulin
Figure 6

(A) TG time course (hours)

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</table>

(B) Fold Increase

- Mfn2
- P-eIF2α
- CHOP
- GADD34
- P58IPK

* Significant difference
### Figure 6

#### C

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<td>TG</td>
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</tr>
<tr>
<td>AdCre</td>
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</table>

#### GADD34

- Early: 
  - TG: -
  - AdCre: -

- Late: 
  - TG: +
  - AdCre: +

#### P58\textsuperscript{IPK}

- Early: 
  - TG: -
  - AdCre: -

- Late: 
  - TG: +
  - AdCre: +

#### P-eIF2\textalpha{}

- Early: 
  - TG: -
  - AdCre: -

- Late: 
  - TG: +
  - AdCre: +

#### elf2\textalpha{}

- Early: 
  - TG: -
  - AdCre: -

- Late: 
  - TG: +
  - AdCre: +

#### D

<table>
<thead>
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<tr>
<td>AdCre</td>
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</table>

#### GADD34

- Early: 
  - TG: -
  - AdCre: -

- Late: 
  - TG: +
  - AdCre: +

#### P58\textsuperscript{IPK}

- Early: 
  - TG: -
  - AdCre: -

- Late: 
  - TG: +
  - AdCre: +

#### P-eIF2\textalpha{}

- Early: 
  - TG: -
  - AdCre: -

- Late: 
  - TG: +
  - AdCre: +

#### elf2\textalpha{}

- Early: 
  - TG: -
  - AdCre: -

- Late: 
  - TG: +
  - AdCre: +
Figure 6

<table>
<thead>
<tr>
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<tr>
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Figure 7

**A**

**Mfn2\(^{loxP}\) MEFs**

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<tbody>
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</tr>
<tr>
<td>TM</td>
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</table>

**CHOP levels (% of Control)**

![CHOP levels graph](image)

**B**

**Mfn2\(^{loxP}\) MEFs**

<table>
<thead>
<tr>
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<th>AdCre</th>
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<tbody>
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<td>TG</td>
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<td>+</td>
</tr>
<tr>
<td>TM</td>
<td>-</td>
<td>+</td>
</tr>
</tbody>
</table>

**Caspase 3/7 Activity (% of AdNull)**

![Caspase activity graph](image)

**Western Blot**

- CHOP
- α-tubulin
Figure 9

ER stress $\rightarrow$ eIF2\(\alpha\) $\leftrightarrow$ eIF2\(\alpha\)\,-P $\rightarrow$ GADD34 $\leftarrow$ Mfn2

P58\(^{IPK}\)

CHOP $\rightarrow$ Cell death

Early $\rightarrow$ Late