High confidence ATFS-1 target genes for quantifying activation of the mitochondrial unfolded protein response

Sonja K Soo1,2 and Jeremy M Van Raamsdonk1,2,3,4§

1Department of Neurology and Neurosurgery, McGill University, Montreal, Quebec, Canada
2Metabolic Disorders and Complications Program, and Brain Repair and Integrative Neuroscience Program, Research Institute of the McGill University Health Centre, Montreal, Quebec, Canada
3Division of Experimental Medicine, Department of Medicine, McGill University, Montreal, Quebec, Canada
4Department of Genetics, Harvard Medical School, Boston, MA, USA
§To whom correspondence should be addressed: jeremy.vanraamsdonk@mcgill.ca

Abstract

The mitochondrial unfolded protein response (mitoUPR) is an evolutionarily conserved pathway that restores homeostasis to the mitochondria after various disturbances. This pathway has roles in both resistance to exogenous stressors and longevity. The mitoUPR is mediated by the transcription factor ATFS-1/ATF-5, which modulates the expression of genes involved in protein folding, metabolism and stress resistance. MitoUPR activation in C. elegans is most commonly evaluated through transcriptional reporter strains for the mitochondrial chaperones HSP-6 and HSP-60. In order to obtain a more comprehensive view of transcriptional changes resulting from activation of the mitoUPR, we compared gene expression changes from three different mitoUPR-activating interventions: mutation of nuo-6, RNA interference (RNAi) knockdown of spg-7, and constitutive activation of ATFS-1. We specifically focused on gene expression changes that are dependent on ATFS-1. From this comparison, we identified 61 high confidence target genes that can be used to monitor mitoUPR activation. Notably, neither hsp-6 nor hsp-60 were significantly upregulated under all three mitoUPR activating conditions. We ranked the 61 genes according to the magnitude of upregulation and identify multiple genes that may serve as robust readouts of mitoUPR activation.
Figure 1. Levels of gene expression under conditions of mitoUPR activation: To compare the efficacy of using different target genes to monitor activation of the mitoUPR, we examined the expression of each gene under conditions of ATFS-1 activation. To activate ATFS-1, we used a nuo-6 mutation (blue bars) or the constitutively active atfs-1(et15) and atfs-1(et17) mutations (green bars). ATFS-1 activation was prevented using an atfs-1 deletion mutation gk3094 in wild-type and nuo-6 worms (red bars and purple bars, respectively). Expression is shown as a percentage of wild type worms (white bars). A. There is a significant increase in hsp-6 mRNA under conditions of ATFS-1 activation that is prevented by disruption of atfs-1. B. The levels of hsp-60 are not increased in nuo-6 mutants or either constitutively active atfs-1 mutants. C-F. The mitoUPR target genes C01G1.7, F22B3.7, cyp-14A4 and clec-17 exhibit a marked increased in expression under conditions of ATFS-1 activation with a magnitude much greater than hsp-6. G-J. The mitoUPR target genes hrg-9, K09E9.1, cdr-2 and F15B9.10 show a large increase in expression relative to their standard deviation under conditions of ATFS-1 activation. K-N. The expression of mitoUPR target genes cdr-2, F15B9.10, C07G1.7 and hrg-9 show increased expression in nuo-6 worms by quantitative RT-PCR. O. Heat map comparing the expression of identified mitoUPR target genes between wild-type and long-lived mitochondrial mutant isp-1 worms. All but 4 of the 61 genes are significantly upregulated in isp-1 mutants. Expression levels in panels A-J were determined from our previously published RNA sequencing data (Wu et al., 2018). Expression represents counts per million from six biological replicates that has been normalized to wild-type. Heat map was generated using our previously published RNA sequencing data (Senchuk et al., 2018). Error bars indicates SEM. **p<0.01, ***p<0.001. Statistical significance was assessed using a one-way ANOVA with Dunnett’s multiple comparison test, except in panels K-N where a student’s t-test was used.

Description

The mitochondrial unfolded protein response (mitoUPR) is a stress response pathway that promotes cell survival and restores mitochondrial function when mitochondrial health is compromised (Haynes et al. 2013; Jovaisaite et al. 2014; Shipilka and Haynes 2018). While a mitoUPR was first reported in mammalian cells (Zhou et al. 2002), the initial work on the mitoUPR in C. elegans was performed by Yoneda et al. who found that treatment with ethidium bromide, which affects the replication and expression of mitochondrial DNA, increased the expression of the mitochondrial chaperone gene hsp-6 (Yoneda et al. 2004). Based on this observation, they generated hsp-6p::gfp and hsp-60p::gfp reporter strains to further study the mitoUPR. They found that either RNA interference (RNAi) targeting spg-7, the worm homolog of paraplegin, or RNAi targeting other genes encoding mitochondrial proteins resulted in activation of the hsp-6p::gfp and hsp-60p::gfp reporter strains (Yoneda et al. 2004).

The hsp-6p::gfp and hsp-60p::gfp reporter strains were used to identify other components of the mitoUPR including the transcriptional regulator UBL-5, the transcription factor DVE-1, the protease ClpP, the protease import channel HAF-1, and the transcription factor ATFS-1 (Benedetti et al. 2006; Haynes et al. 2007; Haynes et al. 2010; Nargund et al. 2012). Under normal conditions, the mitoUPR transcription factor, ATFS-1, is imported into the mitochondria through the HAF-1 import channel and degraded by the protease ClpP. However, when mitochondria are impaired, ATFS-1 import into the mitochondria is blocked. Instead, the nuclear localization signal (NLS) of ATFS-1 drives ATFS-1 into the nucleus. In the nucleus, ATFS-1 acts with DVE-1 and UBL-5 to upregulate genes that restore mitochondrial homeostasis, including genes involved in mitochondrial protein folding and metabolism. In addition to responding to disruptions in mitochondrial function and integrity, the mitoUPR also plays important roles in resistance to stress (Pellegrino et al. 2014; Campos et al. 2021; Soo et al. 2021) and longevity (Durieux et al. 2011; Houtkooper et al. 2013; Bennett et al. 2014; Wu et al. 2018).

Previous studies from our laboratory and others have used RNA sequencing (RNA-seq) or microarrays to examine gene expression under conditions that induce ATFS-1 activation. Nargund et al. identified 366 genes that are upregulated by spg-7 RNAi in an ATFS-1-dependent manner (Nargund et al. 2012). We previously identified 1704 genes that are upregulated in nuo-6 mutants in an ATFS-1-dependent manner (Senchuk et al. 2018; Wu et al. 2018) and 529 genes that are upregulated in both atfs-1(et15) and atfs-1(et17) constitutively active atfs-1 mutants (Rauthan et al. 2013; Wu et al. 2018).

In order to establish a list of mitoUPR target genes that are consistently upregulated across all three ATFS-1-activating conditions, we examined the overlap between these datasets. We identified a total of 61 genes that are upregulated in nuo-6 worms in an ATFS-1-dependent manner, upregulated by spg-7 RNAi in an ATFS-1-dependent manner, and upregulated in both atfs-1(et15) and atfs-1(et17) constitutively active mutants (Extended data, Column A,B). Surprisingly, neither hsp-6 nor hsp-60 were among the 61 genes on this list. In fact, hsp-60 was not identified in any of the three datasets. It is uncertain why spg-7 RNAi increases fluorescence in the hsp-60p::GFP reporter strain (Yoneda et al. 2004) but hsp-60 was not identified as one of the genes upregulated by spg-7 RNAi (Nargund et al. 2012). One possibility may be that hsp-60 expression is primarily upregulated during development in response to spg-7 RNAi and other mitochondrial insults. Then the half-life of the HSP-60:GFP protein might allow the increase in HSP-60:GFP to still be observed at adulthood even after the hsp-60 mRNA has returned to baseline.
In order to rank the different mitoUPR target genes, each gene was scored by adding together their expression levels in *nuo-6, atfs-1(et15)* and *atfs-1(et17)* mutants and subtracting their expression level in *nuo-6;atfs-1* mutants. By this metric, 42 of the 61 mitoUPR target genes exhibited a higher score than *hsp-6* (Extended data, Column J). The top genes of *C07G1.7, F22B3.7, cyp-14A4,* and *clec-17* had scores ranging from 17084-21882, compared to a score of 350 for *hsp-6*. The expression of these genes compared to *hsp-6* and *hsp-60* is shown in Fig 1A-F.

In order to control for variability, we divided this score by the average standard deviation from WT, *atfs-1(gk3094), nuo-6, nuo-6;atfs-1(gk3094), atfs-1(et15) and atfs-1(et17).* By this metric, 27 of the 61 mitoUPR target genes showed a higher score than *hsp-6* (Extended data, Column K). The top genes of *C07G1.7, hrg-9, K09E9.1, cdr-2* and *F15B9.10* had variability-corrected scores of 26-38 compared to 15 for *hsp-6*. The expression of these genes is shown in Fig 1G-J.

To determine if these mitoUPR target genes are being activated directly by binding of ATFS-1, we examined the data from a previous chromatin immunoprecipitation sequencing (ChIP-seq) experiment that identified genes bound by ATFS-1 after treatment with spg-7 RNAi (Nargund et al. 2015). We found that 22 of the 61 mitoUPR target genes exhibited binding of ATFS-1 after spg-7 RNAi (Extended data, Column L). This suggests that the expression of these genes is directly modulated by ATFS-1, while the expression of the other mitoUPR target genes may be regulated indirectly, or perhaps bound by ATFS-1 under different conditions than were utilized in the ChIP-seq study.

Our results suggest that the genes identified here may be better for monitoring the activation of the mitoUPR by quantitative RT-PCR or RNA-seq than *hsp-6* and *hsp-60*. To that end, we have designed and validated primers for quantitative RT-PCR to measure the levels of two of the highest-ranked direct targets, *cdr-2* and *F15B9.10*, and two of the highest ranked indirect targets, *C07G1.7* and *hrg-9*. We confirmed that all four sets of primers can efficiently measure activation of the mitoUPR in *nuo-6* worms compared to wild-type worms (Fig 1K-N).

Finally, to validate this list of 61 genes for monitoring the activation of the mitoUPR, we examined the long-lived mitochondrial mutant *isp-1*, which we have previously shown to have increased activation of a *hsp-6p::gfp* reporter strain and significantly overlapping gene expression changes with constitutively active *atfs-1* mutants (Wu et al. 2018). 57 of the 61 genes were found to be significantly upregulated in *isp-1* mutants (Extended data, Fig 1O).

Overall, this work has identified a gene expression signature that can be used to monitor the activation of the mitoUPR by quantitative RT-PCR or RNA-seq, microarray or qPCR studies. These genes can be used to complement the use of *hsp-6p::gfp* and *hsp-60p::gfp* reporter strains, and may provide a more robust measure of mitoUPR activation in studies measuring mRNA.

**Methods**

**Request a detailed protocol**

**Strains.** Worms were grown on NGM plates seeded with OP50 bacteria at 20°C. We previously performed RNA sequencing on wild-type(N2), *atfs-1(gk3094), nuo-6(qm200), nuo-6(qm200);atfs-1(gk3094), atfs-1(et15), atfs-1(et17) and isp-1(qm150)* worms (Senchuk et al. 2018; Wu et al. 2018). This RNA sequencing data was re-analyzed to generate Figure 1, panels A-J and Figure 1, panel O. The quantitative RT-PCR results in Figure 1, panels K-N were generated for this publication using wild-type and *nuo-6(qm200)* worms

**Quantitative RT-PCR.** Worms from an overnight limited lay were allowed to grow to the prefertile young adult stage. Worms were washed three times with M9 buffer and frozen in Trizol. RNA was isolated by phenol-chloroform extraction using Trizol reagent as previously described (Machiela et al. 2016). RNA was converted to cDNA using a High Capacity cDNA Reverse Transcription Kit (Life Technologies) according to the manufacturer’s protocol. qPCR was performed in a Viaa 7 RT-PCR machine from Applied Biosystems real-time thermal cycler using PowerUp SYBR Green Master Mix kit (Applied Biosystems). RNA was collected from three biological replicates and normalized to the levels of *act-3*. Primer sequences:

- *cdr-2* (L: CGAGCCTCATTTGAAAGAA, R: GCATCTGCCGCCGTGAACCTT)
- *F15B9.10* (L: CCGGACAGTTTCAAAGAATGC, R: CACTGAGGATCCAATGTCCA)
- *hrg-9* (L: TGGAATATTGAGTGGCGTTG, R: CCTCCTCTACTTGGTGCATGT)
- *C07G1.7* (L: CGAGCCTCATTTGAAAGAA, R: GCATCTGCCGCCGTGAACCTT)

**Analysis of gene expression data.** Lists of differentially expressed genes were obtained from (Nargund et al. 2012; Wu et al. 2018). The raw data from these experiments is available on NCBI GEO (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38196, https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE110984). We used BioVenn (https://www.biovenn.nl/index.php) to generate lists of overlapping gene expression between gene sets. Genes upregulated in *nuo-6* worms in an ATFS-1-dependent manner are genes that are upregulated in *nuo-6* mutants but not *nuo-6;atfs-1* mutants. To rank
mitoUPR target genes, expression of each gene was normalized to wild-type. The score for each gene was determined by summing the normalized expression in nuo-6, atfs-1(et15) and atfs-1(et17) mutants and subtracting three times the expression in nuo-6/atfs-1 mutants. To generate a variability-corrected score, this score was divided by the average standard deviation for each of the strains. Binding of ATFS-1 was determined from a previous chromatin immunoprecipitation (ChIP) study (Nargund et al. 2015). Data from this study is available on NCBI GEO: [https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE63803](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE63803).

### Reagents

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
<th>Source</th>
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<tbody>
<tr>
<td>N2</td>
<td>wild-type</td>
<td>Wild isolate from Bristol</td>
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<tr>
<td>MQ1333</td>
<td>nuo-6(qm200)</td>
<td>Yang, Hekimi. 2010.</td>
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<tr>
<td>VC3201</td>
<td>atfs-1(gk3094)</td>
<td><em>C. elegans</em> Reverse Genetics Core Facility at the University of British Columbia</td>
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<td>MQ887</td>
<td>isp-1(qm150)</td>
<td>Feng et al. 2001.</td>
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<tr>
<td>JVR477</td>
<td>nuo-6(qm200); atfs-1(gk3094)</td>
<td>Wu et al. 2018.</td>
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**Extended Data**


**References**


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