

Pharmacologic Activation of Integrated Stress Response Kinases Inhibits Pathologic Mitochondrial Fragmentation

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eLife Assessment

This **important** study identifies a new class of small molecules that activate the integrated stress response (ISR) via the kinase HRI. **Convincing** evidence, including the image analysis pipeline, indicates that two of these compounds promote mitochondrial elongation and protect against mitochondrial fragmentation caused by chemical stress conditions or by genetic alterations. These findings open an avenue for new strategies for mitochondrial dysfunction targeting linked to ISR alterations.

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Abstract

Summary

Excessive mitochondrial fragmentation is associated with the pathologic mitochondrial dysfunction implicated in the pathogenesis of etiologically-diverse diseases, including many neurodegenerative disorders. The integrated stress response (ISR) – comprising the four eIF2 α kinases PERK, GCN2, PKR, and HRI – is a prominent stress-responsive signaling pathway that regulates mitochondrial morphology and function in response to diverse types of pathologic insult. This suggests that pharmacologic activation of the ISR represents a potential strategy to mitigate pathologic mitochondrial fragmentation associated with human disease. Here, we show that pharmacologic activation of the ISR kinases HRI or GCN2

promotes adaptive mitochondrial elongation and prevents mitochondrial fragmentation induced by the calcium ionophore ionomycin. Further, we show that pharmacologic activation of the ISR reduces mitochondrial fragmentation and restores basal mitochondrial morphology in patient fibroblasts expressing the pathogenic D414V variant of the pro-fusion mitochondrial GTPase MFN2 associated with neurological dysfunctions including ataxia, optic atrophy, and sensorineural hearing loss. These results identify pharmacologic activation of ISR kinases as a potential strategy to prevent pathologic mitochondrial fragmentation induced by disease-relevant chemical and genetic insults, further motivating the pursuit of highly selective ISR kinase-activating compounds as a therapeutic strategy to mitigate mitochondrial dysfunction implicated in diverse human diseases.

Introduction

The integrated stress response (ISR) comprises four stress-regulated kinases – PERK, PKR, GCN2, and HRI – that selectively phosphorylate eIF2 α in response to diverse pathologic insults.^{1,2} The ISR has recently emerged as a prominent stress-responsive signaling pathway activated by different types of mitochondrial stress.^{3–5} Mitochondrial uncoupling or inhibition of ATP synthase activates the ISR through a mechanism involving the cytosolic accumulation and oligomerization of the mitochondrial protein DELE1, which binds to and activates the ISR kinase HRI.^{6–10} Complex I inhibition can also activate the ISR downstream of the ISR kinase GCN2.¹¹ Further, CRISPRi-depletion of mitochondrial proteostasis factors preferentially activates the ISR over other stress-responsive signaling pathways.¹² These results identify the ISR as an important stress-responsive signaling pathway activated in response to many different mitochondrial insults.

Consistent with its activation by mitochondrial stress, the ISR regulates many aspects of mitochondrial biology. ISR kinases are activated in response to stress through a conserved mechanism involving dimerization and autophosphorylation.^{1,2} Once activated, these kinases phosphorylate eIF2 α , resulting in both a transient attenuation of new protein synthesis and the activation of stress-responsive transcription factors such as ATF4.^{1,2} The ISR promotes adaptive remodeling of mitochondrial pathways through both transcriptional and translational signaling. For example, the activation of ATF4 downstream of phosphorylated eIF2 α transcriptionally regulates the expression of mitochondrial chaperones (e.g., the mitochondrial HSP70 *HSPA9*) and proteases (e.g., the AAA+ protease *LON*), increasing mitochondrial proteostasis capacity during stress.^{13,14} ISR-dependent translational attenuation also enhances mitochondrial proteostasis through the selective degradation of the core import subunit TIM17A, which slows mitochondrial protein import and reduces the load of newly-synthesized proteins entering mitochondria during stress.¹⁵ Apart from proteostasis, transcriptional and translational signaling induced by the activation of ISR kinases also regulates many other mitochondrial functions, including phospholipid synthesis, cristae organization, and electron transport chain activity.^{16–20}

Intriguingly, the morphology of mitochondria is also regulated by ISR signaling. Mitochondrial morphology is dictated by the relative activities of pro-fission and pro-fusion GTPases localized to the outer and inner mitochondrial membranes (OMM and IMM, respectively).^{21,22} These include the pro-fusion GTPases MFN1 and MFN2 and the pro-fission GTPase DRP1, all localized to the OMM. Previous results showed that ER stress promotes adaptive mitochondrial elongation downstream of the PERK arm of the ISR through a mechanism involving the accumulation of the phospholipid phosphatidic acid on the OMM where it inhibits the pro-fission GTPase DRP1.^{19,20,23} This PERK-dependent increase of mitochondrial elongation functions to protect mitochondria during ER stress through multiple mechanisms, including enhanced regulation of respiratory chain activity, suppression of mitochondrial fragmentation, and reductions in the turnover of mitochondria by mitophagy.^{19,20,23} Apart from PERK,

pharmacologic activation of the alternative ISR kinase GCN2 also promotes adaptive mitochondrial elongation.²³ This indicates that mitochondrial elongation may be a protective mechanism that can be pharmacologically accessed by activating multiple different ISR kinases.

Excessive mitochondrial fragmentation is a pathologic hallmark of numerous human diseases, including several neurodegenerative disorders.^{21,24–27} Fragmented mitochondria are often associated with mitochondrial dysfunctions including impaired respiratory chain activity and dysregulation of mitophagy.^{21,24–29} Thus, pathologic increases in mitochondrial fragmentation are linked to many mitochondrial dysfunctions implicated in human disease. Consistent with this observation, interventions that prevent mitochondrial fragmentation have been shown to correct pathologic mitochondrial dysfunction in models of many different diseases.^{30,31} Notably, genetic or pharmacologic inhibition of the pro-fission GTPase DRP1 blocks pathologic mitochondrial fragmentation and subsequent mitochondrial dysfunction in cellular and in vivo models of diverse neurodegenerative diseases, including Charcot-Marie-Tooth Type 2A and Type 2B, spastic paraplegia, optic atrophy, Huntington's disease, Amyotrophic Lateral Sclerosis, and Alzheimer's disease.^{32–43}

The ability of ISR activation to promote mitochondrial elongation suggests that pharmacologic activation of ISR kinases could mitigate the pathologic mitochondrial fragmentation implicated in etiologically diverse human diseases. To test this idea, we probed the potential for pharmacologic activation of different ISR kinases to reduce mitochondrial fragmentation induced by disease-relevant chemical and genetic insults. Previous work identified the small molecule halofuginone as a potent activator of the ISR kinase GCN2 that promotes ISR-dependent, adaptive mitochondrial elongation.^{23,44} However, few other compounds were available that selectively activated other ISR kinases and were suitable for probing mitochondrial adaptation induced by ISR kinase activation.^{23,45} Here, we used a small molecule screening platform to identify two nucleoside mimetic compounds, 0357 and 3610, that preferentially activate the ISR downstream of the ISR kinase HRI. Using these compounds, we demonstrate that pharmacologic HRI activators also promote adaptive, ISR-dependent mitochondrial elongation. We go on to show that pharmacologic activation of the ISR with these compounds prevents DRP1-mediated mitochondrial fragmentation induced by the calcium ionophore ionomycin.^{46,47} Further, we show that compound-dependent activation of the ISR reduces the population of fragmented mitochondria and rescues basal mitochondrial network morphology in patient fibroblasts expressing the D414V variant of the pro-fusion GTPase MFN2 associated with a complex clinical phenotype including ataxia, optic atrophy and sensorineural hearing loss.⁴⁸ These results demonstrate the potential for pharmacologic activation of the ISR to prevent pathologic mitochondrial fragmentation in disease-relevant models. Moreover, our work further motivates the continued development of highly selective activators of ISR kinases as a potential therapeutic strategy to mitigate the pathologic mitochondrial dysfunction implicated in etiologically diverse human diseases.

Results

The nucleoside mimetic compounds 0357 and 3610 preferentially activate the ISR downstream of HRI

The small molecule halofuginone activates the ISR kinase GCN2 and induces ISR-dependent mitochondrial elongation.^{23,44} However, few other compounds are available that selectively activate other ISR kinases through mechanisms that allow for ISR-dependent mitochondrial remodeling.²³ For example, BtdCPU activates the ISR kinase HRI through a mechanism involving mitochondrial uncoupling, precluding its use for probing ISR-dependent protection of mitochondria.²³ To address this limitation and define the potential for pharmacologic activation of other ISR kinases to promote adaptive mitochondrial elongation, we established and implemented a screening platform to identify compounds that activated ISR signaling downstream

of alternative ISR kinases (Fig. 1A). In this screen, we used the ATF4-FLuc translational reporter of the ISR (Fig. S1A). We confirmed that ISR activating stressors including the ER stressor thapsigargin (Tg) and the ATP synthase inhibitor oligomycin A (OA) robustly activated this reporter (Fig. S1B). We then used this reporter to screen the ~3k nucleoside mimetic analog compound library (10 μ M) and monitored ATF4-FLuc activity 8 h after treatment. Our primary screen identified 34 hit compounds that activated the ATF4-FLuc reporter with a robust Z-score >3-fold. We then removed highly reactive compounds and pan-assay interference compounds (PAINS), which reduced the number of hits to 9 (Fig. 1B). These compounds were re-purchased and then tested in dose response for ATF4-FLuc activation (Fig. S1C). This identified compounds 0357 and 3610 as the compounds that most efficaciously activated the ATF4-FLuc reporter, albeit with low potency ($EC_{50} > 10 \mu$ M). We confirmed that co-treatment with the highly selective ISR inhibitor ISRIB^{49,50} blocked ATF4-FLuc activation induced by these compounds, confirming this activation can be attributed to the ISR (Fig. 1C,D). Further, we used qPCR to show that treatment with 0357 or 3610 increased expression of the ISR target genes *ASNS* and *CHAC1* in HEK293 and MEF cells (Fig. S1D,E). Importantly, these compounds did not activate luciferase reporters of other stress-responsive signaling pathway such as the unfolded protein response (UPR; XBP1-RLuc)^{53,54}, the heat shock response (HSR; HSE-FLuc)⁵⁵, or the oxidative stress response (OSR; ARE-FLuc)⁵⁶ (Fig. 1E,F). Further, treatment with these compounds did not induce expression of the UPR target gene *BiP*, the HSR target gene *HSPA1A*, or the OSR target gene *NQO1* in HEK293 cells (Fig. S1F). Finally, treatment with 0357 or 3610 did not significantly reduce viability of HEK293 cells (Fig. S1G). These results indicate compounds 0357 and 3610 preferentially activate the ISR, as compared to other stress responsive signaling pathways.

Next, we sought to identify the specific ISR kinases responsible for ISR activation induced by these two nucleoside mimetics. We monitored the compound-dependent activation of an ATF4-mAPPLE fluorescent reporter stably expressed in HEK293 cells CRISPRi-depleted of each individual ISR kinase (Fig. S1A).^{8,23} We previously used this assay to confirm that halofuginone activates the ISR downstream of GCN2 and BtdCPU activates the ISR downstream of HRI.²³ Treatment with either 0357 or 3610 activates the ATF4-mAPPLE reporter in control cells (Fig. 1G,H). CRISPRi-depletion of *HRI*, but no other ISR kinase, blocked ATF4-FLuc activation induced by these two compounds. This finding indicates that these compounds activate the ISR downstream of HRI. Collectively, these results identify 0357 and 3610 as nucleoside mimetic compounds that preferentially activate the ISR through a mechanism involving the ISR kinase HRI.

Pharmacologic HRI activators promote mitochondrial elongation

Halofuginone-dependent activation of GCN2 promotes adaptive mitochondrial elongation.²³ However, it is currently unclear if pharmacologic activation of other ISR kinases can similarly induce mitochondrial elongation. Here, we tested the ability of our HRI-activating compounds 0357 and 3610 to induce mitochondrial elongation downstream of the ISR. Previously, ISR-dependent mitochondrial elongation was quantified by manually classifying cells as containing fragmented, tubular, or elongated networks.^{19,20} However, since 0357 and 3610 activate ISR signaling to lower levels than that observed for other compounds (e.g., halofuginone), we posited that these compounds may induce more modest mitochondrial elongation that may be difficult to quantify using this manual approach. To address this, we implemented an automated image analysis pipeline using Imaris software to quantify mitochondrial elongation in MEF cells stably expressing mitochondrial-targeted GFP (^{mt}GFP) treated with our compounds (Fig. S2A).⁵⁷ We collected Z-stack confocal images of ^{mt}GFP-expressing MEF cells (MEF^{mtGFP}) and processed images using a deconvolution filter in FIJI to reduce the background and enhance the fluorescent signal. We used the “Surfaces” module on Imaris to generate three-dimensional (3D) segmentation models of mitochondria visible in the deconvolved Z-stacks. Using the surfaces module, we quantified parameters defining mitochondrial shape, including bounding box length, sphericity, and ellipsoid principal axis length (Fig. S2A). Treatment with conditions that induce mitochondrial elongation, such as the ER stressor thapsigargin (Tg) and the GCN2 activator halofuginone (HF),

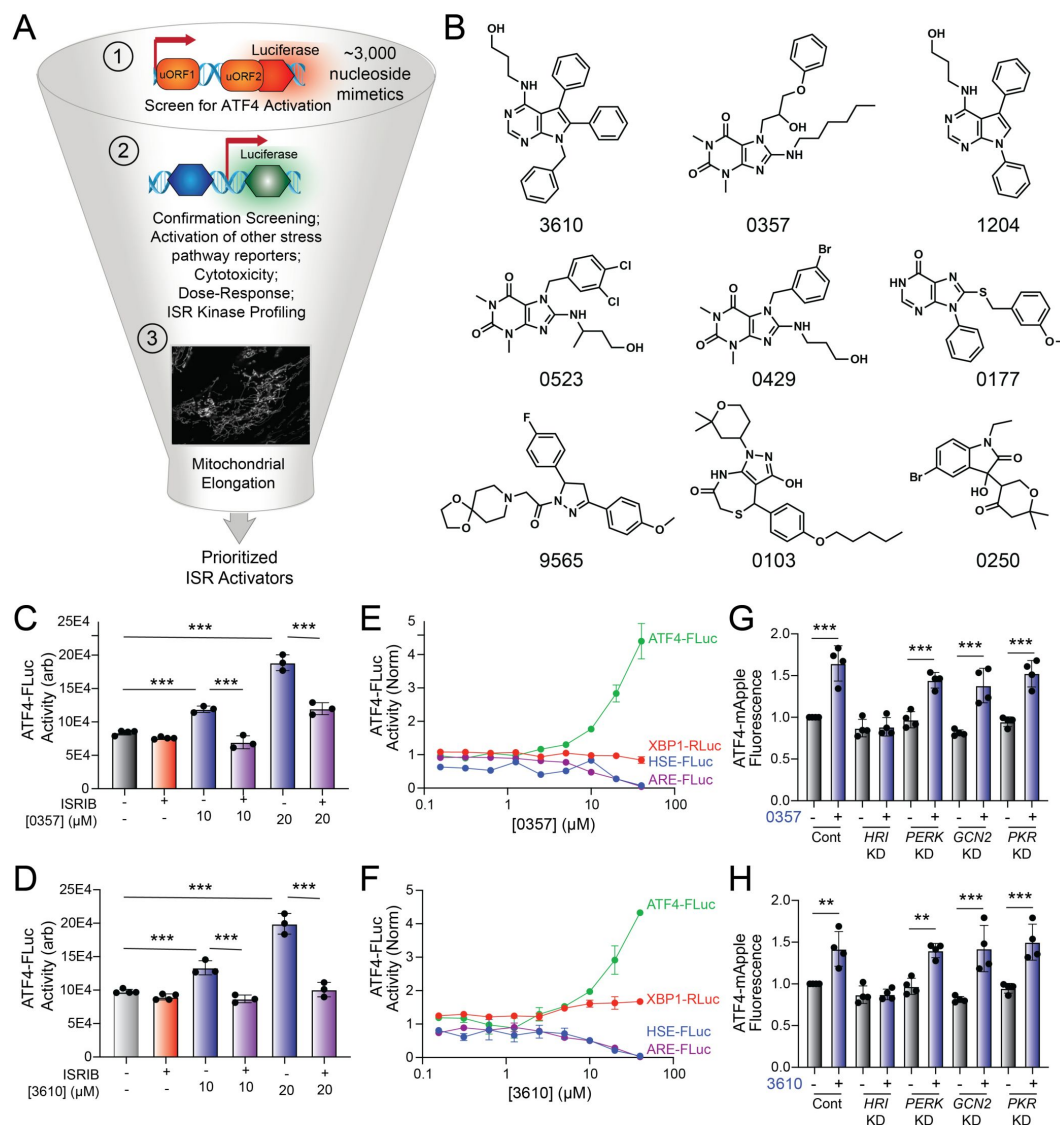


Figure 1.

Identification of nucleoside mimetics that preferentially activate the ISR kinase HRI.

A. Screening pipeline used to identify selective ISR kinase activating compounds that promote protective mitochondrial elongation. **B.** Structures of the top 9 ISR activating compounds identified in our nucleoside mimetic screen. **C,D.** ATF4-FLuc activity in HEK293 cells stably expressing ATF4-FLuc¹⁰ treated for 8 h with the indicated concentration of 0357 (**C**) or 3610 (**D**) in the absence or presence of ISRIB (200 nM). **E,F.** Activation of the ATF4-FLuc ISR translational reporter (green), the XBP1-RLuc UPR reporter (red), the HSE-FLuc HSR reporter (blue) or the ARE-FLuc OSR reporter (purple) stably expressed in HEK293 cells treated with the indicated concentration of 0357 (**E**) or 3610 (**F**) for 16 h. **G,H.** ATF4-mApple fluorescence in HEK293 cells stably expressing ATF4-mApple and CRISPRi depleted of the indicated ISR kinase⁸ treated for 8 h with 0357 (**G**, 20 μM) or 3610 (**H**, 20 μM). ***p*<0.01, ****p*<0.005 for one-way ANOVA.

increased bounding box and ellipsoid principal axis length, while reducing sphericity (**Fig. 2A-D**, **Fig. S2B-D**) – all changes consistent with increases in mitochondrial length. In contrast, treatment with conditions that promote mitochondrial fragmentation, such as the mitochondrial uncouplers BtdCPU and CCCP (both compounds that activate HRI)^{6,23}, reduced bounding box length and ellipsoid principal axis length, while increasing sphericity (**Fig. 2A-D**, **Fig. S2B-D**) – all changes consistent with increased mitochondrial fragmentation.

We next applied this approach to define the impact of our pharmacologic HRI activators on mitochondrial morphology. Treatment with either 0357 or 3610 for 6 h increased both the bounding box and ellipsoid principal axis length, while decreasing mitochondrial sphericity (**Fig. 2A-D**). This result indicates that both these compounds induced mitochondrial elongation. Co-treatment with the selective ISR inhibitor ISRIB blocked these changes in mitochondria shape, indicating that these compounds induce mitochondrial elongation through an ISR-dependent mechanism (**Fig. 2E-H**). ISRIB co-treatment also blocked mitochondrial elongation induced by the ER stressor thapsigargin (Tg) and the GCN2 activator halofuginone (HF), as predicted.^{19,23} These results indicate that, like halofuginone, pharmacologic HRI activators also induce adaptive, ISR-dependent mitochondrial elongation. Further, these results suggest that the pharmacologic activation of different ISR kinases can induce protective elongation of mitochondria in the absence of cellular stress.

Pharmacologic ISR activation suppresses ionomycin-induced mitochondrial fragmentation

The ability for our pharmacologic GCN2 or HRI activators to induce adaptive mitochondrial elongation suggests that enhancing signaling through these kinases may suppress mitochondrial fragmentation induced by pathologic insults such as calcium dysregulation.^{58–61} Treatment with the calcium ionophore, ionomycin, induces rapid, DRP1-dependent mitochondrial fragmentation in cell culture models.^{46,47} We pre-treated MEF^{mtGFP} cells for 6 h with the GCN2 activator halofuginone or our two HRI activating compounds (0357 and 3610) and subsequently challenged these cells with ionomycin. We then monitored mitochondrial morphology over a 15-minute timecourse. As expected, ionomycin rapidly increased the accumulation of fragmented mitochondria in these cells, evidenced by reductions in both bounding box and ellipsoid principal axis length and increases of organelle sphericity (**Fig. S3A-D**). Pre-treatment with the ER stressor thapsigargin, which promotes stress-induced mitochondrial elongation downstream of the PERK ISR kinase, reduced the accumulation of fragmented mitochondria in ionomycin-treated cells (**Fig. 3A-D**), as previously reported.²⁰ Intriguingly, treatment with halofuginone, 0357, or 3610 also reduced the accumulation of fragmented mitochondria in ionomycin-treated cells. Instead, mitochondria in cells pretreated with these ISR kinase activators and challenged with ionomycin demonstrated mitochondrial lengths and sphericity similar to that observed in vehicle-treated MEF^{mtGFP} cells (**Fig. 3A-D**). These results indicate that pharmacologic activation of different ISR kinases can suppress the accumulation of fragmented mitochondria following ionomycin-induced calcium dysregulation.

Pharmacologic activation of ISR kinases restores basal mitochondrial morphology in patient fibroblasts expressing disease-associated MFN2^{D414V}

Over 150 pathogenic variants in the pro-fusion GTPase MFN2 are causatively associated with the autosomal dominant peripheral neuropathy Charcot-Marie-Tooth Type 2A.^{62–64} While these pathogenic variants can impact diverse aspects of mitochondrial biology,⁶³ many, including D414V, lead to increases in mitochondrial fragmentation.^{48,62–64} This can be attributed to reduced activity of MFN2-dependent fusion associated with these variants and a subsequent relative increase of DRP1-dependent mitochondrial fission. We predicted that pharmacologic

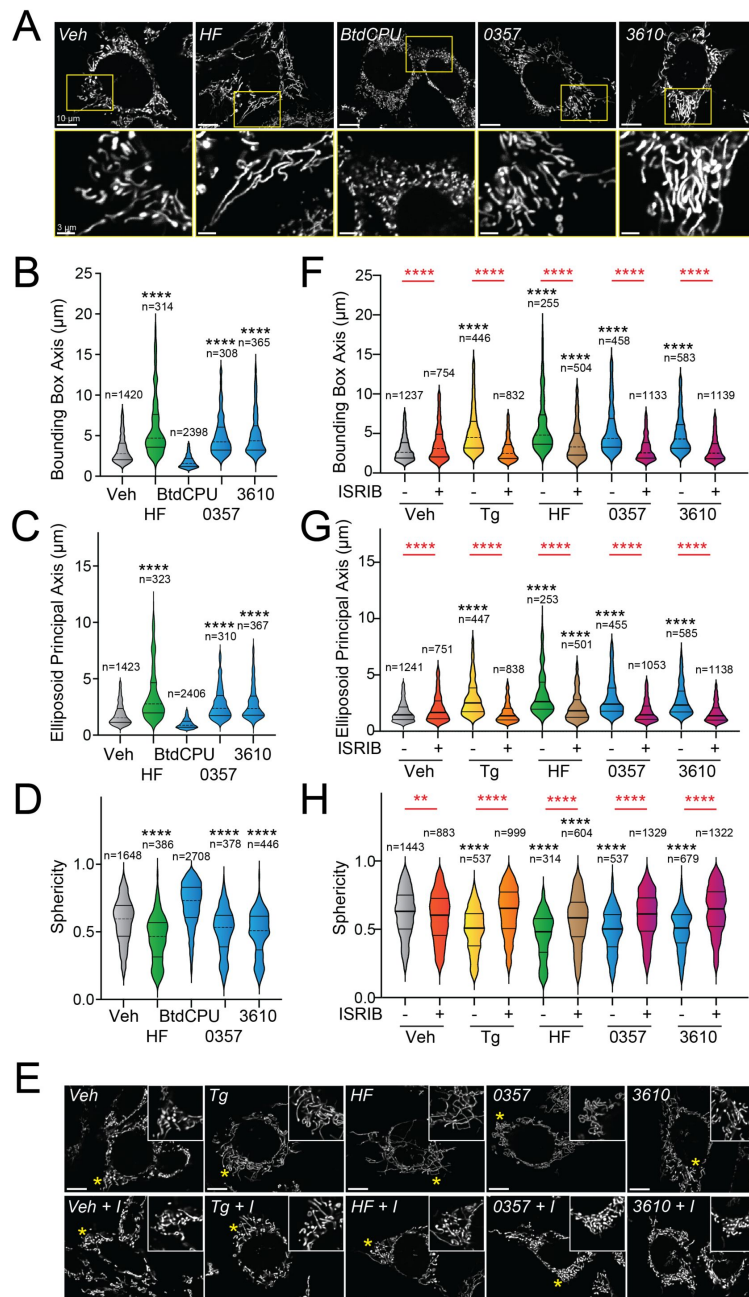


Figure 2.

Pharmacologic HRI activation induces ISR-dependent mitochondrial elongation.

A. Representative images of MEF cells stably expressing mt^{GFP} (MEF mtGFP) treated for 6 h with vehicle (veh), halofuginone (HF, 100 nM), BtdCPU (10 μ M), 0357 (10 μ M) or 3610 (10 μ M). The inset shows a 3-fold magnification of the region indicated by the yellow box. Scale bars, 10 μ m (top) and 3.33 μ m (bottom).

B-D. Quantification of bounding box axis, ellipsoid principal axis, and sphericity from the entire dataset of representative images shown in (A). The number of individual measurements for each condition are shown above.

E. Representative images of MEF mtGFP cells treated for 6 h with vehicle (veh), thapsigargin (Tg; 0.5 μ M) halofuginone (HF, 100 nM), 0357 (10 μ M) or 3610 (10 μ M) in the presence or absence of ISRIB (200 nM). The inset shows 3-fold magnification of the image centered on the asterisks. Scale bars, 10 μ m.

F-H. Quantification of bounding box axis, ellipsoid principal axis, and sphericity from the entire dataset of representative images shown in (E). The number of 3D segmentations used for the individual measurements for each condition are shown above. * $p < 0.05$, **** $p < 0.001$ for Kruskal-Wallis ANOVA. Black asterisks indicate comparison to vehicle treated cells. Red asterisks show comparisons for ISRIB co-treatment.

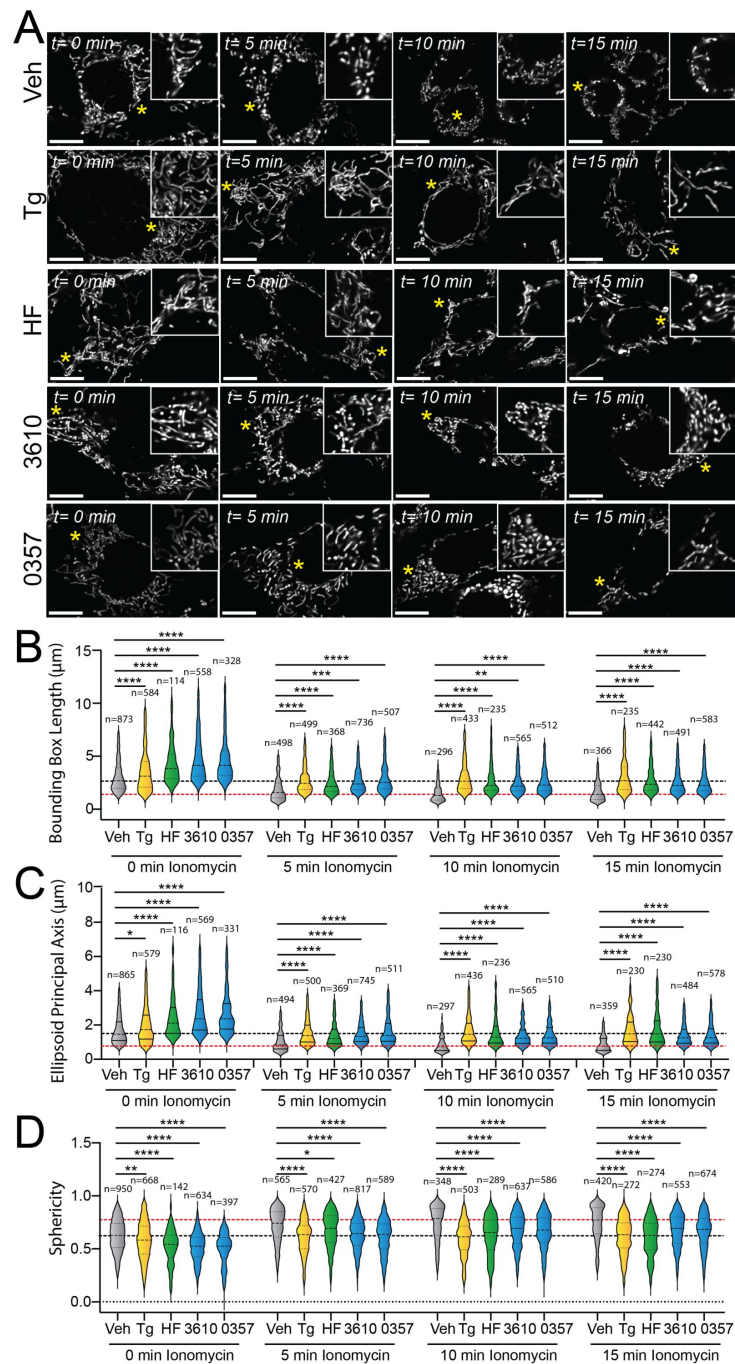


Figure 3.

Pharmacologic activation of ISR kinases prevents ionomycin-dependent accumulation of fragmented mitochondria.

A. Representative images of MEF^{mtGFP} cells pre-treated for 6 h with vehicle (veh), thapsigargin (Tg, 500 nM), halofuginone (HF, 100 nM), 0357 (10 µM) or 3610 (10 µM) and then challenged with ionomycin (1 µM) for the indicated time. The inset shows 3-fold magnification of the image centered on the asterisk. Scale bars, 10 µm. **B-D.** Quantification of bounding box axis length, ellipsoid principal axis length, and sphericity from the entire dataset of representative images shown in (**A**). The black dashed line shows the mean value of vehicle-treated cells prior to ionomycin treatment. The dashed red line shows the mean value of vehicle-treated cells following 15 min treatment with ionomycin. The number of 3D segmentations used for the individual measurements for each condition are shown above. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.005$, **** $p < 0.001$ for Kruskal-Wallis ANOVA. Black asterisks show comparison with vehicle-treated cells.

activation of ISR kinases could rescue mitochondrial network morphology in patient fibroblasts expressing the disease-associated MFN2 variant D414V (MFN2^{D414V}). To test this, we treated wild-type human fibroblasts and patient fibroblasts expressing MFN2^{D414V} with halofuginone or our two HRI activating compounds 0357 and 3610 and monitored mitochondrial network morphology by staining with MitoTracker. As reported previously, MFN2^{D414V}-expressing fibroblasts showed shorter, more fragmented mitochondrial networks, as compared to control fibroblasts, reflected by reductions in both bounding box and ellipsoid principle axis lengths and increased sphericity (Fig. 4A,E, S4A-C).⁴⁸ Treatment with halofuginone, 0357, or 3610 increased mitochondrial length in control fibroblasts (Fig. 4A-D). These changes were inhibited by co-treatment with ISRIB, confirming these effects can be attributed to ISR activation. Intriguingly, all three compounds also increased mitochondrial length and reduced sphericity in MFN2^{D414V}-expressing patient fibroblasts to levels similar to those observed in control fibroblasts, with halofuginone showing the largest effect (Fig. 4E-H). Again, this increase in mitochondrial elongation was reversed by co-treatment with ISRIB. These results show that pharmacologic activation of different ISR kinases can rescue basal mitochondrial morphology in patient fibroblasts expressing the disease-associated MFN2^{D414V} variant that causes dysregulation in various neurological functions including ataxia, optic atrophy, and sensorineural hearing loss.

Discussion

Here, we show that pharmacologic activation of different ISR kinases can prevent mitochondrial fragmentation induced by disease-relevant chemical or genetic insults. We identify two nucleoside mimetic compounds that preferentially activate the ISR downstream of the ISR kinase HRI. We demonstrate that these two HRI activators promote adaptive, ISR-dependent mitochondrial elongation. Further, we show that treatment with these HRI-activating compounds or the GCN2 activator halofuginone prevents the accumulation of fragmented mitochondria induced by Ca²⁺ dysregulation and rescues mitochondrial network morphology in patient fibroblasts expressing the disease-associated, pathogenic D414V variant of MFN2. Collectively, these results demonstrate that pharmacologic activation of different ISR kinases can mitigate pathologic mitochondrial fragmentation induced by diverse disease-associated pathologic insults.

Mitochondrial fragmentation is often induced through a mechanism involving stress-dependent increases in the activity of the pro-fission GTPase DRP1.^{21,28} This has motivated efforts to identify pharmacologic inhibitors of DRP1 to prevent mitochondrial fragmentation and subsequent organelle dysfunction associated with human disease.^{31,38,65} Activation of the ISR kinase PERK during ER stress promotes mitochondrial elongation through a mechanism involving inhibition of DRP1.²⁰ This suggested that pharmacologic activation of other ISR kinases could also potentially inhibit DRP1 and block pathologic mitochondrial dysfunction induced by increased DRP1 activity. Consistent with this idea, we show that pharmacologic activation of the ISR using both GCN2 and HRI activating compounds blocks the accumulation of fragmented mitochondria in ionomycin-treated cells – a condition that promotes mitochondrial fragmentation through increased DRP1-dependent fission.^{46,47} These results support a model whereby pharmacologic activation of different ISR kinases promotes organelle elongation by inhibiting DRP1 and suggests that pharmacologic activation of ISR kinases can be broadly applied to quell mitochondrial fragmentation in the myriad diseases associated with overactive DRP1.

Pathogenic variants in mitochondrial-targeted proteins are causatively associated with the onset and pathogenesis of numerous neurodegenerative disorders, including Charcot-Marie-Tooth (CMT), spinocerebellar ataxia (SCA), and spastic paraplegia.^{21,24,66–69} In many of these diseases, mitochondrial fragmentation is linked to pathologic mitochondrial dysfunctions, such as reduced respiratory chain activity, decreased mtDNA, and increased apoptotic signaling. Intriguingly, pharmacologic or genetic inhibition of mitochondrial fragmentation mitigates cellular and mitochondrial pathologies associated with many of these diseases, highlighting the

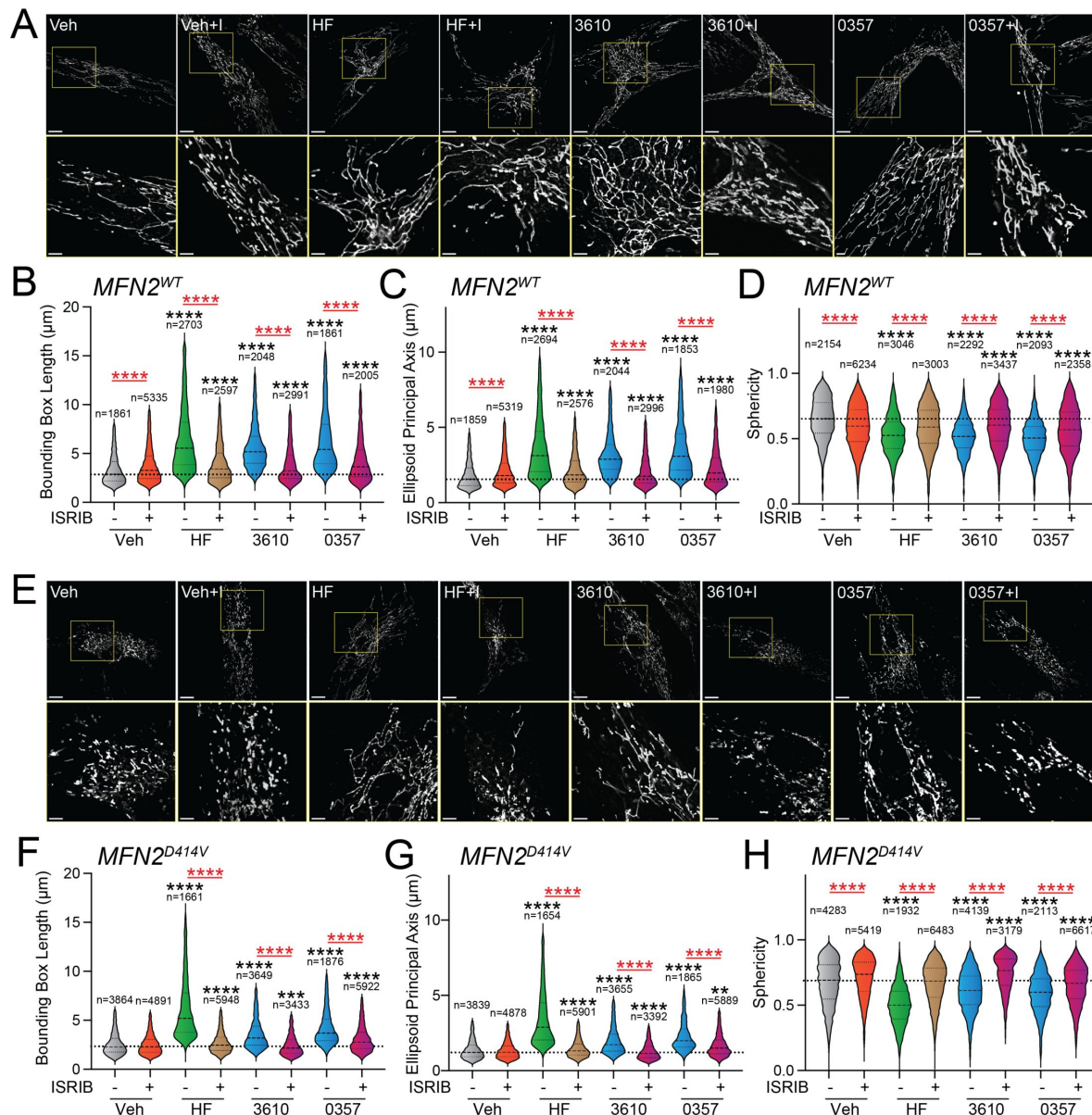


Figure 4.

Pharmacologic activation of ISR kinases rescues basal mitochondrial morphology in patient fibroblasts expressing the disease-associated D414V MFN2 variant.

A. Representative images of control human fibroblasts expressing MFN2^{WT} treated for 6 h with vehicle (veh), halofuginone (HF, 100 nM), 3610 (10 µM), 0357 (10 µM), and/or ISRIB (200 nM). The inset shows 3-fold magnification of the image centered on the asterisks. Scale bars, 15 µm (top) and 5 µm (bottom). **B-D.** Quantification of bounding box axis (**B**), ellipsoid principal axis (**C**), and sphericity (**D**) from the entire dataset of images described in panel **A**. The number of individual measurements for each condition are shown above. **E.** Representative images of patient fibroblasts expressing MFN2^{D414V} treated for 6 h with vehicle (veh), halofuginone (HF, 100 nM), 3610 (10 µM), 0357 (10 µM), and/or ISRIB (200 nM). The inset shows 3-fold magnification of the image centered on the asterisks. Scale bars, 15 µm (top) and 5 µm (bottom). **F-H.** Quantification of bounding box axis (**F**), ellipsoid principal axis (**G**), and sphericity (**H**) from the entire dataset of images described in panel **E**. The number of 3D segmentations used for the individual measurements for each condition are shown above. *p<0.05, ***p<0.005, ****p<0.001 for Kruskal-Wallis ANOVA. Black asterisks show comparison with vehicle-treated cells. Red asterisks show comparisons for ISRIB co-treatment.

critical link between mitochondrial fragmentation and disease pathogenesis.^{33,35,43} Herein, we show that pharmacologic activation of the ISR mitigates mitochondrial fragmentation in patient fibroblasts homozygous for the disease-associated D414V MFN2 variant. This finding highlights the potential for pharmacologic ISR activation to restore basal mitochondrial network morphology in cells expressing pathogenic MFN2 variants, although further study is necessary to determine the impact of ISR activation in cells from heterozygous patients expressing pathogenic MFN2 variants associated with CMT2A, the most common clinical phenotype associated with this disease. Regardless, our results are of substantial interest because over 70% of cases of axonal CMT are associated with pathogenic MFN2 variants, and to date, no disease-modifying therapies are available for any genetic subtype of CMT.^{70,71} Apart from MFN2 variants, our results also highlight the potential for pharmacologic ISR kinase activation to broadly mitigate pathologic mitochondrial fragmentation associated with the expression of disease-related, pathogenic variants of other mitochondrial proteins, which we are continuing to explore.

Apart from morphology, ISR signaling also promotes adaptive remodeling of many other aspects of mitochondrial biology, including proteostasis, electron transport chain activity, phospholipid synthesis, and apoptotic signaling.^{13,20} While we specifically focus on defining the potential for pharmacologic activation of ISR kinases to rescue mitochondrial morphology in disease models, the potential of ISR activation to promote adaptive remodeling of other mitochondrial functions suggests that pharmacologic activators of ISR kinases could more broadly influence cellular and mitochondrial biology in disease states through the adaptive remodeling of these other pathways. For example, we previously showed that halofuginone-dependent GCN2 activation restored cellular ER stress sensitivity and mitochondrial electron transport chain activity in cells deficient in the alternative ISR kinase PERK²³ – a model of neurodegenerative diseases associated with reduced PERK activity such as PSP and AD.^{72,73} Compounds that activate other ISR kinases are similarly predicted to promote the direct remodeling of mitochondrial pathways to influence these and other functions. Thus, as we, and others, continue defining the impact of pharmacologic ISR kinase activation on mitochondrial function, we predict to continue revealing new ways in which activation of ISR kinases directly regulates many other aspects of mitochondrial function disrupted in human disease.

Several different compounds have previously been reported to activate specific ISR kinases.^{23,74–79} However, the potential for many of these compounds to mitigate mitochondrial dysfunction in human disease is limited by factors including lack of selectivity for the ISR or a specific ISR kinase, off-target activities, or low therapeutic windows.²³ For example, the HRI activator BtdCPU activates the ISR through a mechanism involving mitochondrial uncoupling and subsequent mitochondrial fragmentation.²³ Here, we identify two nucleoside mimetic compounds that activate the ISR downstream of HRI and show selectivity for the ISR relative to other stress-responsive signaling pathways, providing new tools to probe mitochondrial remodeling induced by ISR kinase activation. However, the low potency of these compounds limits their translational potential to mitigate mitochondrial dysfunction in disease, necessitating the identification of new, highly-selective ISR kinase activating compounds. As we and others continue identifying next-generation ISR kinase activators with improved translational potential, it will be important to optimize the pharmacokinetics (PK) and pharmacodynamic (PD) profiles of these compounds to selectively enhance adaptive, protective ISR signaling in disease-relevant tissues, independent of maladaptive ISR signaling often associated with chronic, stress-dependent activation of this pathway.^{1,2} As described previously for activators the IRE1 arm of the UPR, such improvements can be achieved by defining optimized compound properties and dosing regimens to control the timing and extent of pathway activity.⁸⁰ Thus, as we and others continue pursuing pharmacologic ISR kinase activation as a strategy to target mitochondrial dysfunction in disease, we anticipate that we will continue to learn more about the central role for this pathway in adapting mitochondria during stress and establish pharmacologic ISR kinase activation as a viable approach to treat mitochondrial dysfunction associated with etiologically-diverse diseases.

Materials and methods

Mammalian Cell Culture

HEK293 cells (purchased from ATCC), HEK293 cells stably expressing XBP1-RLuc^{53,54}, HEK293 cells stably expressing HSE-FLuc, HEK293 cells stably expressing ATF4-mAPPLE (a kind gift from Martin Kampmann's lab)¹⁰ and CRISPRi-depleted of individual ISR kinases (*HRI*, *PKR*, *PERK*, *GCN2*; a kind gift from Martin Kampmann's lab at UCSF)⁸, and MEF^{mtGFP} (a kind gift from Peter Schultz)⁵⁷ were all cultured at 37°C and 5% CO₂ in DMEM (Corning-Cellgro) supplemented with 10% fetal bovine serum (FBS, Gibco), 2 mM L-glutamine (Gibco), 100 U/mL penicillin, and 100 mg/mL streptomycin (Gibco).

Primary fibroblast cells were isolated from partial thickness skin biopsy, as previously described^{48,81}, from a patient who provided written informed consent for research studies using human tissues (University of Calgary Conjoint Research Ethics Board REB17-0850). Cells were cultured in Medium Essential Media (11095080, Gibco), supplemented with 10% Fetal Bovine Serum (12483020, Gibco). Cells were maintained at 37 °C and 5% CO₂. Clinical information regarding this participant was previously reported and included ataxia, optic atrophy, and sensorineural hearing loss.⁴⁸ Exome sequencing in this participant identified a homozygous c.1241A>T variant in *MFN2* (predicted to cause p.(Asp414Val)) and no other pathogenic variants.

Compounds and Reagents

Compound used in this study were purchased from the following sources: thapsigargin (Tg; Cat# 50-464-294 Fisher Scientific), ISRIB (Cat # SML0843, Sigma), CCCP (Cat #C2759, Sigma), BtdCPU (Cat #32-489-210MG, Fisher), halofuginone (Cat #50-576-3001, Sigma), and oligomycin A (S1478, Selleck). The nucleoside mimetic library was purchased from Chem Div. Hit compounds were repurchased from Chem Div.

Measurements of ISR activation in ATF4-reporter cell lines

HEK293 cells stably expressing the ATF4-FLuc, HSE-Fluc, or the ARE-Fluc reporter were seeded at a density of 15,000 cells per well in 384-well white plates with clear bottoms (Greiner). The following day, cells were treated with the indicated compound in triplicate at the indicated concentration for 8h. After treatment, an equal volume of Promega Bright-Glo substrate (Promega) was added to the wells and allowed to incubate at room temperature for 10 minutes. Luminescence was then measured using an Infinite F200 PRO plate reader (Tecan) with an integration time of 1000 ms. This assay was used to both screen the nucleoside mimetic library in triplicate and monitor the activity of hit compounds. HEK293 cells expressing the XBP1-RLuc reporter were tested using an analogous approach to that described above, monitoring RLuc activity using Renilla-Glo reagent (Promega), as previously described.⁵³

HEK293 cells stably expressing the ATF4-mApple reporter and CRISPRi-depleted of specific ISR kinases were seeded at a density of 300,000 cells per well in 6-well TC-treated flat bottom plates (Genesee Scientific). Cells were treated the next day for 16 h with compound at the indicated concentration. Cells were then washed twice with phosphate-buffered saline (PBS) and dissociated using TrypLE Express (ThermoFisher). Cells were then resuspended in PBS and 5% FBS to neutralize the enzymatic reaction. Flow cytometry was performed on a Bio-Rad ZE5 Cell Analyzer monitoring mAPPLE fluorescence (568/592 nm) using the 561 nm green-yellow laser in combination with the 577/15 filter. Analysis was performed using FlowJoTM Software (BD Biosciences).

Quantitative Polymerase Chain Reaction (qPCR)

The relative mRNA expression of target genes was measured using quantitative RT-PCR. Cells were treated as indicated and then washed with phosphate-buffered saline (PBS; Gibco). RNA was extracted using Quick-RNA MiniPrepKit (Zymo Research) according to the manufacturers protocol. RNA (500 ng) was then converted to cDNA using the High-Capacity Reverse Transcription Kit (Applied Biosystems). qPCR reactions were prepared using Power SYBR Green PCR Master Mix (Applied Biosystems), and primers (below) were obtained from Integrated DNA Technologies. Amplification reactions were run in an ABI 7900HT Fast Real Time PCR machine with an initial melting period of 95 °C for 5 min and then 45 cycles of 10 s at 95 °C, 30 s at 60 °C.

qPCR Primers

	Forward	Reverse
<i>M. musculus Chac1</i>	TGACCCTCCTTGAAGACCGTGA	AGTGTTCATAGCCACCAAGCACG
<i>M. musculus RiboP</i>	TGTCATCGCTCAGGGTGTG	AAGCCAAATCCCATGTCTGTC
<i>M. musculus Asns</i>	CCAAGTTCAGTATCCTCTCC	TAATTTGCCACCTTTCTAGC
<i>H. sapiens 36b4</i>	CCACGCTGCTGAACATGC	TCGAACACCTGCTGGATGAC
<i>H. sapiens ASNS</i>	ATCACTGTCGGGATGTACCC	TGATAAAAGGCAGCCAATCC
<i>H. sapiens CHAC1</i>	GTGGTGACGCTCCTTGAAGA	TTCAGGGCCTTGCTTACCTG
<i>H. sapiens HSPA1A</i>	GCTGATGATGGGGTTAACA	GGAGGCGGAGTACA
<i>H. sapiens NQO1</i>	GCCTCCTTCATGGCATAGTT	GGA CTGCACCAGAGCCAT

Fluorescence Microscopy

MEF^{mtGFP} were seeded at a density of 15,000 cells/well in 8-chamber slides (Ibidi) coated with poly-D-lysine (Sigma)⁵⁷. The next day cells were treated with the indicated dose of compound for the indicated time. After treatment, cells were imaged on a Zeiss LSM 880 Confocal Laser Scanning Microscope equipped with a full incubation chamber for regulating temperature and CO₂ during live cell imaging.

Patient fibroblasts were seeded at 70,000 cells per dish in 35 mm dishes with 20mm glass bottoms (D35-20-1.5-N, Cellvis) for live-cell imaging. After 24 hours, the compound treatments were administered at the dosage and for the time points indicated in the figure legends. The mitochondrial network in patient fibroblasts was visualized using 100 nM MitoTracker Green (M7514, Life Technologies)⁸² for 45 minutes, following washing three times with culture media, according to the manufacturer's instructions. The Z-stack images were acquired of patient fibroblasts using an Olympus Spinning Disc Confocal System (Olympus SD OSR) equipped with the Olympus UPlanApo 60XTIRF/1.50 Oil Objective using the CellSense Dimensions software. Acquired Z-stacks were analyzed using AI Machine Learning Segmentation (Imaris), as detailed below.

Quantification of mitochondrial morphology

The z-stack confocal images were processed in FIJI to reduce the background noise and enhance the fluorescent signal. The processed images are then introduced into the developed quantification pipeline in Imaris imaging software. In this approach, mitochondria are segmented in 3D using the "Surfaces" module with a machine-learning algorithm that has been iteratively trained to detect foreground and background pixels in each z-stack, filling blank holes within segments to generate

3D surfaces. The generated surfaces are filtered to include those above a minimum threshold of 250 voxels. While direct length measurements cannot be obtained through the Imaris surface module, indirect measurements of mitochondrial length are inferred from three separate calculations, including (1) object-oriented bounding box axis, (2) ellipsoid axis length, and (3) object sphericity (see **Fig. S2A** [↗](#)). The object-oriented bounding box axis is calculated by measuring the length of the longest or principal bounding-box length of the smallest object-oriented rectangular box that encloses each 3D segmentation. The ellipsoid axis length is calculated by measuring the length of the longest or principal axis of each 3D segmentation. Sphericity is calculated by dividing the longest axis of each 3D segmentation by the length of the perpendicular axis.

Statistical Methods

Data are presented as mean $\pm$ SEM or as violin plots showing the mean and quartiles for the indicated number of measurements. Outliers were removed from datasets describing bounding box length and principal axis length, as appropriate, using the ROUT outlier test in PRISM 10 (GraphPad, San Diego, CA). Normality of datasets from our imaging studies was tested in PRISM 10 (GraphPad, San Diego, CA) using D'Agostino & Pearson, Anderson-Darling, Shapiro-Wilk, and Kolmogorov-Smirnov tests. Statistics were calculated in PRISM 10 (GraphPad, San Diego, CA) and analyzed by one-way ANOVA with Tukey's multiple correction test, Kruskal-Wallis or Mann-Whitney tests for data exhibiting a non-normal distribution, as indicated in the accompanying figure legends. Indications of nonsignificant interactions were generally omitted for clarity.

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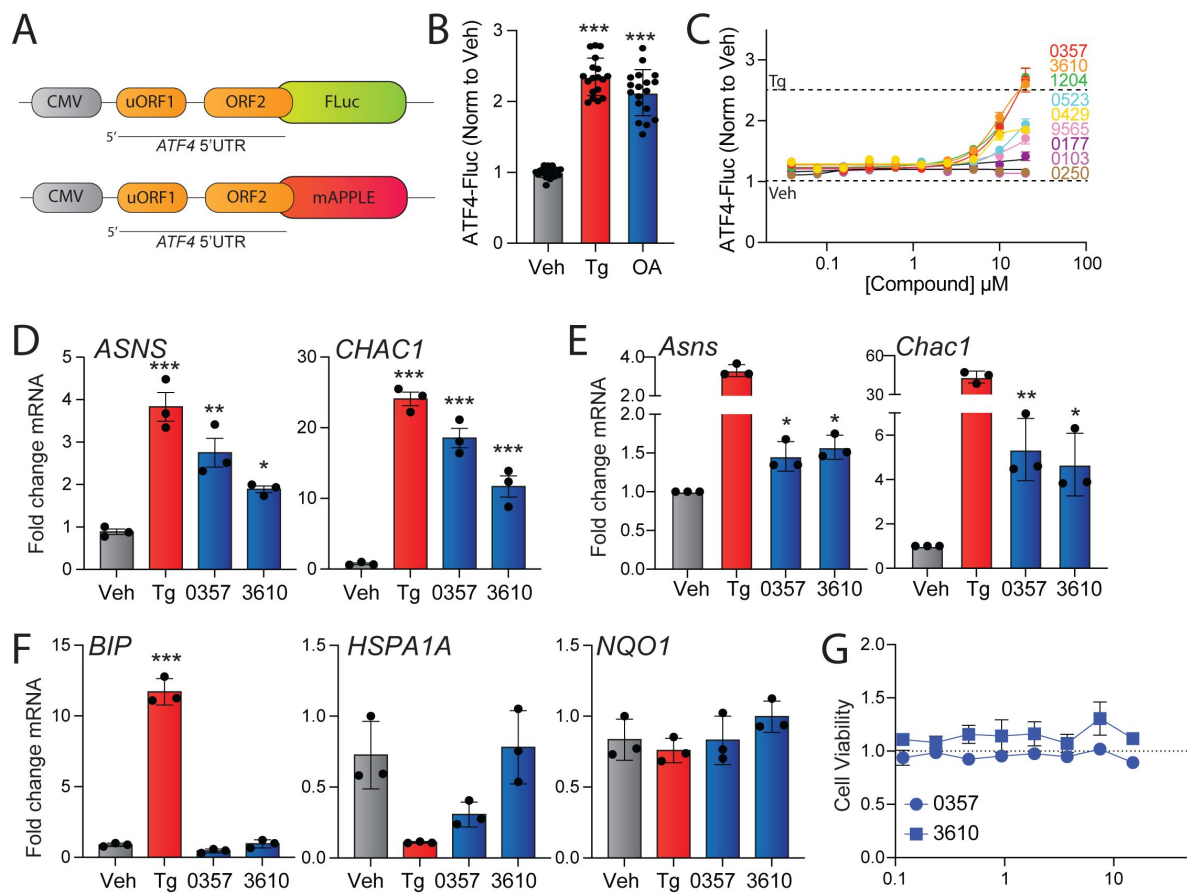


Figure S1

(Supplement to Figure 1). Identification of nucleoside mimetics that preferentially activate the ISR kinase HRI.

A. The ATF4-FLuc and ATF4-mAPPLE reporters containing the 5'UTR of ATF4^{8,10}. **B.** ATF4-Fluc activity, measured by luminescence, in HEK293 cells stably expressing ATF4-FLuc treated for 8 h with vehicle, thapsigargin (Tg, 0.5 μ M), or oligomycin A (OA, 50 ng/mL). **C.** ATF4-Fluc activity, normalized to vehicle, in HEK293 cells stably expressing ATF4-FLuc treated for 8 h with the indicated dose of the indicated compound. The signals observed in veh or thapsigargin (Tg, 0.5 μ M) cells is shown by the dashed lines. Error bars show SEM for n=9 replicates. **D.** Expression, measured by qPCR, of the ISR target genes *ASNS* and *CHAC1* in HEK293 cells treated for 8 h with vehicle, thapsigargin (Tg; 0.5 μ M), 0357 (25 μ M), or 3610 (25 μ M). **E.** Expression, measured by qPCR, of the ISR target genes *Asns* and *Chac1* in MEF cells treated for 8 h with vehicle, thapsigargin (Tg; 0.5 μ M), 0357 (20 μ M), or 3610 (20 μ M). **F.** Expression, measured by qPCR, of the UPR target gene *BIP*, the HSR target gene *HSPA1A*, and the OSR target gene *NQO1* in HEK293 cells treated for 8 h with vehicle, thapsigargin (Tg; 0.5 μ M), 0357 (25 μ M), or 3610 (25 μ M). **G.** Viability, measured by Cell Titer Glo, of HEK293 cells treated for 24 h with the indicated concentration of 0357 or 3610. Error bars show SEM for n=3 replicates. *p<0.05, **p<0.01 ***p<0.005 for one-way ANOVA.

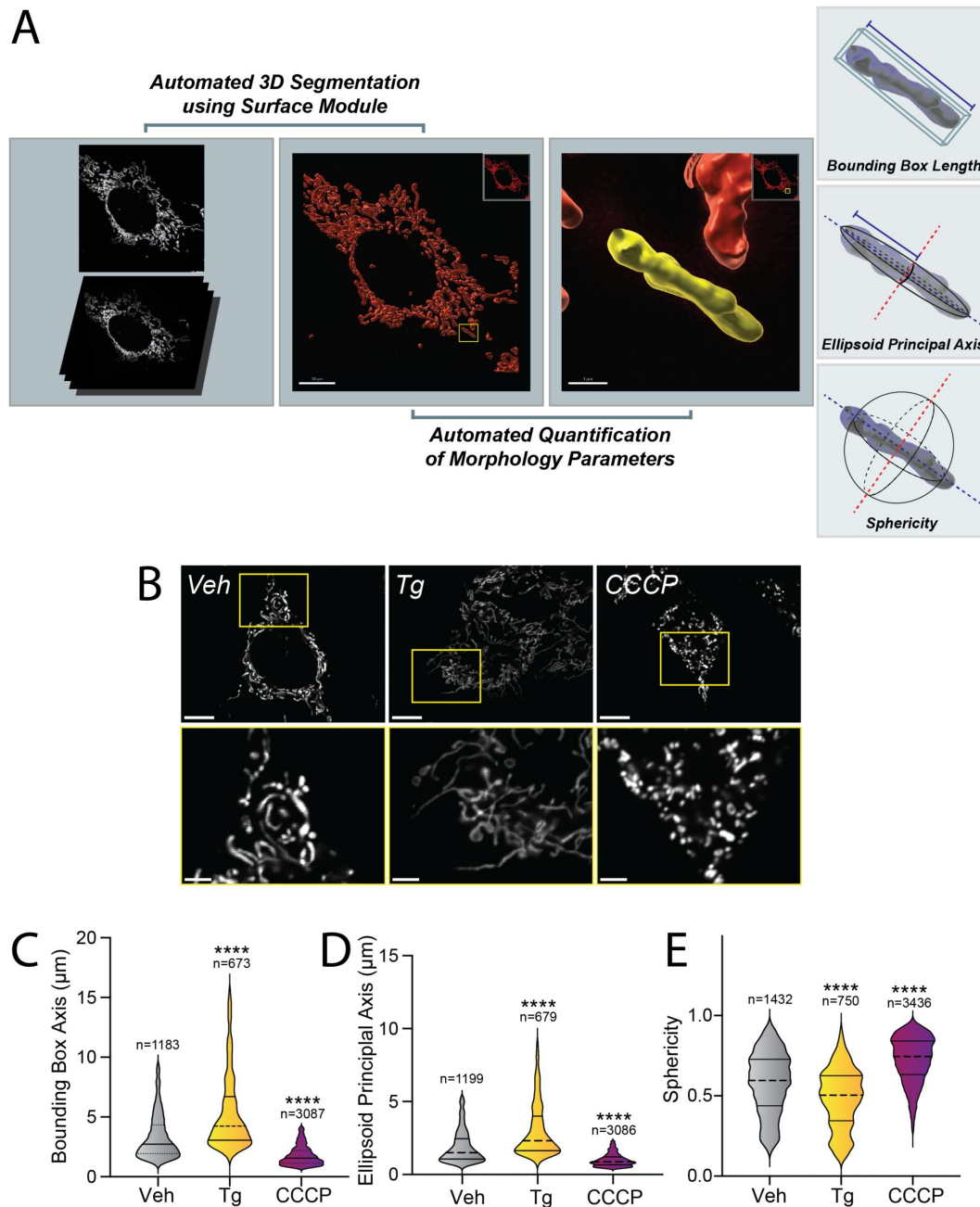


Figure S2

(Supplement Figure 2). Pharmacologic HRI activation induces ISR-dependent mitochondrial elongation.

A. Image processing and analysis workflow to quantify several parameters that define mitochondrial shape. **B.** Representative images of MEF^{mtGFP} cells treated for 6 h with vehicle (veh), thapsigargin (Tg, 500 nM), or CCCP (10 μM). The inset shows a 3-fold magnification of the region indicated by the yellow box. Scale bars, 10 μm (top) and 3.33 μm (bottom) **C-E.** Quantification of bounding box axis, ellipsoid principal axis, and sphericity from the entire dataset of representative images shown in **(B)**. The number of 3D segmentations used for the individual measurements for each condition are shown above. **** $p < 0.001$ for Kruskal-Wallis ANOVA. Black asterisks show comparison with vehicle-treated cells.

Figure S3.

(Supplement to Figure 3). Pharmacologic activation of ISR kinases prevents ionomycin-dependent accumulation of fragmented mitochondria.

A-C. Quantifications of bounding box axis, ellipsoid principal axis, and sphericity of MEF^{mtGFP} cells pre-treated for 6 h with vehicle and then challenged with ionomycin (1 μ M) for the indicated time. Representative images are shown in **Fig. 3A**. The number of 3D segmentations used for the individual measurements for each condition are shown above. **** p <0.001 for Kruskal-Wallis ANOVA. Black asterisks show comparison with vehicle-treated cells at time 0.

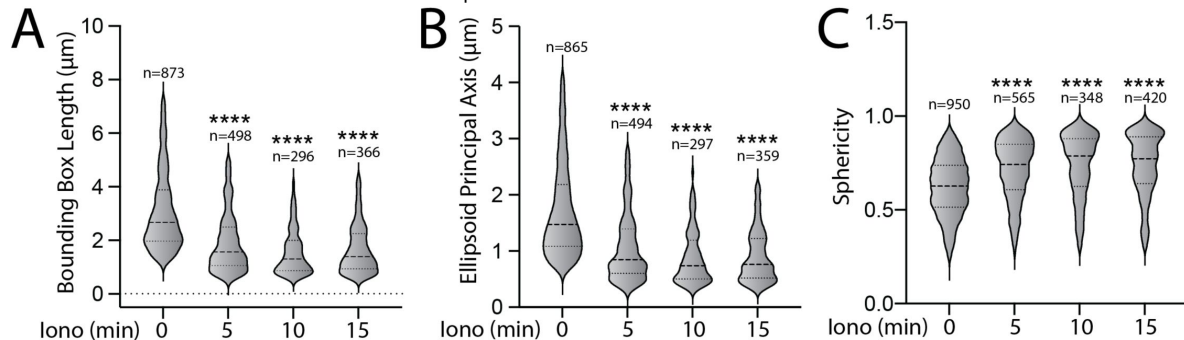
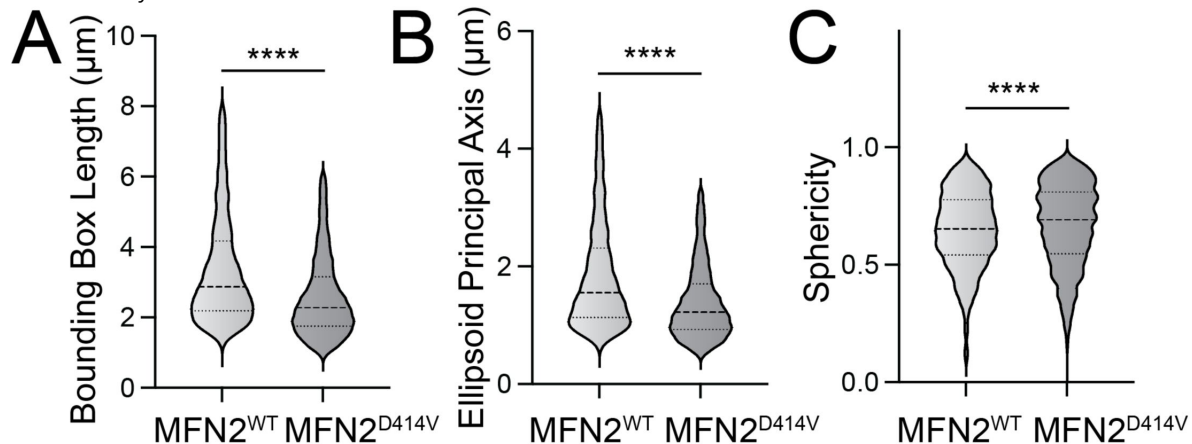


Figure S4

(Supplement to Figure 4). Pharmacologic activation of ISR kinases rescue basal mitochondrial morphology in patient fibroblasts expressing the disease-associated D414V MFN2 variant.

A-C. Bounding box length (**A**), ellipsoid principal axis length (**B**), and sphericity (**C**) in control human fibroblasts expressing MFN2^{WT} or patient fibroblasts expressing MFN2^{D414V}. Representative images are shown in **Fig. 4A,E**. **** p <0.001 for Mann-Whitney t-test.



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Reviewer #1 (Public review):

Summary:

This manuscript (Baron, Oviedo et al., 2024) builds on a previous study from the Wiseman lab (Perea, Baron et al., 2023) and describes the identification of novel nucleoside mimetics that activate the HRI branch of the ISR and drive mitochondrial elongation. The authors develop an image processing and analysis pipeline to quantify the effects of these compounds on mitochondrial networks and show that these HRI activators mitigate ionomycin driven mitochondrial fragmentation. They then show that these compounds rescue mitochondrial morphology defects in patient-derived MFN2 mutant cell lines.

Strengths:

The identification of new ISR modulators opens new avenues for biological discovery surrounding the interplay between mitochondrial form/function and the ISR, a topic that is of broad interest. Conceptually, this work suggests that such compounds might represent new

potential therapeutics for certain mitochondrial disorders. Additionally, the development of a quantitative image analysis pipeline is valuable and has the potential to extract subtle effects of various treatments on mitochondrial morphology.

Weaknesses:

While the ISR modulators described here correct the morphology of mitochondria in MFN2.D414V mutant cells, the impact of these compounds on the function of mitochondria in the mutant cells remains unaddressed. Sharma et al., 2022 provide data for a deficit in mitochondrial OCR in MFN2.D414V cells which, if rescued by these compounds, would strengthen the argument that pharmacological ISR kinase activation is a strategy for targeting the functional consequences of the dysregulation of mitochondrial form.

<https://doi.org/10.7554/eLife.100541.2.sa3>

Reviewer #2 (Public review):

Summary.

Mitochondrial dysfunction is associated with a wide spectrum of genetic and age-related diseases. Healthy mitochondria form a dynamic reticular network and constantly fuse, divide, and move. In contrast, dysfunctional mitochondria have altered dynamic properties resulting in fragmentation of the network and more static mitochondria. It has recently been reported that different types of mitochondrial stress or dysfunction activate kinases that control the integrated stress response, including HRI, PERK and GCN2. Kinase activity results in decreased global translation and increased transcription of stress response genes via ATF4, including genes that encode mitochondrial protein chaperones and proteases (HSP70 and LON). In addition, the ISR kinases regulate other mitochondrial functions including mitochondrial morphology, phospholipid composition, inner membrane organization, and respiratory chain activity. Increased mitochondrial connectivity may be a protective mechanism that could be initiated by pharmacological activation of ISR kinases, as was recently demonstrated for GCN2.

A small molecule screening platform was used to identify nucleoside mimetic compounds that activate HRI. These compounds promote mitochondrial elongation and protect against acute mitochondrial fragmentation induced by a calcium ionophore. Mitochondrial connectivity is also increased in patient cells with a dominant mutation in MFN2 by treatment with the compounds.

Strengths:

- (1) The screen leverages a well-characterized reporter of the ISR: translation of ATF4-FLuc is activated in response to ER stress or mitochondrial stress. Nucleoside mimetic compounds were screened for activation of the reporter, which resulted in the identification of nine hits. The two most efficacious in dose response tests were chosen for further analysis (0357 and 3610). The authors clearly state that the compounds have low potency. These compounds were specific to the ISR and did not activate the unfolded protein response or the heat shock response. Kinases activated in the ISR were systematically depleted by CRISPRi revealing that the compounds activate HRI.
- (2) The status of the mitochondrial network was assessed with an Imaris analysis pipeline and attributes such as length, sphericity, and ellipsoid principal axis length were quantified. The characteristics of the mitochondrial network in cells treated with the compounds were consistent with increased connectivity. Rigorous controls were included. These changes were attenuated with pharmacological inhibition of the ISR.
- (3) Treatment of cells with the calcium ionophore results in rapid mitochondrial

fragmentation. This was diminished by pre-treatment with 0357 or 3610 and control treatment with thapsigargin and halofuginone.

(4) Pathogenic mutations in MFN2 result in the neurodegenerative disease Charcot-Marie-Tooth Syndrome Type 2A (CMT2A). Patient cells that express Mfn2-D414V possess fragmented mitochondrial networks and treatment with 0357 or 3610 increased mitochondrial connectivity in these cells.

Weaknesses:

The weakness is the limited analysis of cellular changes following treatment with the compounds.

(1) Unclear how 0357 or 3610 alter other aspects of cellular physiology. While this would be satisfying to know, it may be that the authors determined that broad, unbiased experiments such as RNAseq or proteomic analysis are not justified due to the limited translational potential of these specific compounds.

(2) There are many changes in Mfn2-D414V patient cells including reduced respiratory capacity, reduced mtDNA copy number, and fewer mitochondrial-ER contact sites. These experiments are relatively narrow in scope and quantifying more than mitochondrial structure would reveal if the compounds improve mitochondrial function, as is predicted by their model.

Comments on revisions:

Many reviewer concerns have been addressed or will be addressed in forthcoming manuscripts.

<https://doi.org/10.7554/eLife.100541.2.sa2>

Reviewer #3 (Public review):

Summary:

Mitochondrial injury activates eIF2 α kinases-PERK, GCN2, HRI and PKR-which collectively regulate the Integrated Stress Response (ISR) to preserve mitochondrial function and integrity. Previous work has demonstrated that stress-induced and pharmacologic stress-independent ISR activation promotes adaptive mitochondrial elongation via the PERK and GCN2 kinases, respectively. Here, the authors demonstrate that pharmacologic ISR inducers of HRI and GCN2 enhance mitochondrial elongation and suppress mitochondrial fragmentation in two disease models, illustrating the therapeutic potential of pharmacologic ISR activators. Specifically, the authors first used an innovative ISR translational reporter to screen for nucleoside mimetic compounds that induce ISR signaling, and identified two compounds, 0357 and 3610, that preferentially activate HRI. Using a mitochondrial-targeted GFP MEF cell line, the authors next determined that these compounds (as well as the GCN2 activator, halofuginone) enhance mitochondrial elongation in an ISR-dependent manner. Moreover, pretreatment of MEFs with these ISR kinase activators suppressed pathological mitochondrial fragmentation caused by a calcium ionophore. Finally, pharmacologic HRI and GCN2 activation was found to preserve mitochondrial morphology in human fibroblasts expressing a pathologic variant in MFN2, a defect that leads to mitochondrial fragmentation and is a cause of Charcot Marie Tooth Type 2A disease.

Strengths:

This well-written manuscript has several notable strengths, including the demonstration of the potential therapeutic benefit of ISR modulation. New chemical entities with which to further interrogate this stress response pathway are also reported. In addition, the authors used an elegant screen to isolate compounds that selectively activate the ISR and identify

which of the four kinases was responsible for activation. Special attention was also paid to a thorough evaluation of the effect of their compounds on other stress response pathways (i.e. the UPR, and heat and oxidative stress responses), thereby minimizing the potential for off-target effects. The implementation of automated image analysis rather than manual scoring to quantify mitochondrial elongation is not only practical but also adds to the scientific rigor, as does the complementary use of both the calcium ionophore and MFN2 models to enhance confidence and the broad therapeutic potential for pharmacology ISR manipulation.

Weaknesses:

The only minor concerns are with regard to effects on cell health and the timing of pharmacological administration.

Comments on revisions:

In this revised manuscript the authors demonstrate that pharmacological activation of the eIF2 α kinases, HRI and GCN2, induce adaptive mitochondrial elongation and suppress mitochondrial fragmentation in two disease models, illustrating the translational potential of pharmacological ISR modulation.

In revising their manuscript the authors adequately addressed the concerns. In response to comments about the potential toxicity of their compounds, 0357 and 3610, the authors furnish evidence that neither compound significantly reduced viability of HEK293 cells (Figure S1G). Understandably, the authors focused the present work on the acute effects of their compounds. Several other attributes are noteworthy: First, that injury attributable to chronic ISR activation in cell culture may ultimately be circumvented by altering the in vivo pharmacodynamic and pharmacodynamic properties of the compounds, thereby preserving the translation potential for these (and related) compounds. Second, the authors also reasonably explain that the rapidity of ionomycin-induced injury, necessitating that the inducers are administered prior to treatment. Their assessment of the effects of the compounds on mitochondrial fragmentation in MFN2 mutant fibroblasts-in combination with the preserved viability of HEK293 cells-is sufficient to demonstrate the practical pharmacological potential for these (or related) agents.

<https://doi.org/10.7554/eLife.100541.2.sa1>

Author response:

The following is the authors' response to the original reviews.

Public Reviews:

Reviewer #1 (Public review):

Summary:

This manuscript (Baron, Oviedo et al., 2024) builds on a previous study from the Wiseman lab (Perea, Baron et al., 2023) and describes the identification of novel nucleoside mimetics that activate the HRI branch of the ISR and drive mitochondrial elongation. The authors develop an image processing and analysis pipeline to quantify the effects of these compounds on mitochondrial networks and show that these HRI activators mitigate ionomycin-driven mitochondrial fragmentation. They then show that these compounds rescue mitochondrial morphology defects in patient-derived MFN2 mutant cell lines.

Strengths:

The identification of new ISR modulators opens new avenues for biological discovery surrounding the interplay between mitochondrial form/function and the ISR, a topic that is of broad interest. It also reinforces the possibility that such compounds might represent new potential therapeutics for certain mitochondrial disorders. The development of a quantitative image analysis pipeline is valuable and has the potential to extract the subtle effects of various treatments on mitochondrial morphology.

We thank the reviewer for the positive feedback on our manuscript. We address all of the reviewer's valuable concerns in the revised submission, as highlighted below.

Weaknesses:

I have three main concerns.

First, support for the selectivity of compounds 0357 and 3610 acting downstream of HRI comes from using knockdown ISR kinase cell lines and measuring the fluorescence of ATF4-mApple (Figure 1G and 1H). However, the selectivity of these compounds acting through HRI is not shown for mitochondrial morphology. Is mitochondrial elongation blocked in HRI knockdown cells treated with the compounds? While the ISRIB treatment does block mitochondrial elongation, ISRIB acts downstream of all ISR kinases and doesn't necessarily define selectivity for the HRI branch of the ISR. Additionally, are the effects of these compounds on ATF4 production and mitochondrial elongation blocked in a non-phosphorylatable eIF2alpha mutant?

We thank the reviewer for highlighting this point. As indicated by the reviewer, we show that compound-dependent increases in mitochondrial elongation are blocked by co-treatment with ISRIB, indicating that this effect can be attributed to ISR activation. We prefer the use of this highly selective pharmacologic approach to block ISR activation, as opposed to the MEF^{A/A} cells, as the use of pharmacologic approaches provide more temporal control over ISR inhibition and can prevent the type of chronic disruption to mitochondria associated with these types of genetic perturbations. However, the reviewer is correct that ISRIB blocks downstream of all ISR kinases, meaning that we cannot explicitly demonstrate that 0357 and 3610 induce mitochondrial elongation downstream of HRI-dependent ISR activation using this tool. Thus, to address this point, we have clarified the discussion of these results to make it clear that our results show that our compounds induce mitochondrial elongation downstream of the ISR, omitting the direct implications of HRI in this phenotype.

This point of selectivity/specificity of the compounds gets at a semantic stumbling block I encountered in the text where it was often stated "stress-independent activation" of ISR kinases. Nucleoside mimetics are likely a very biologically active class of molecules and are likely driving some level of cell stress independent of a classical ISR, UPR, heat-shock response, or oxidative stress response.

A major challenge in defining stress-independent activation of stress-responsive signaling pathways is the fact that the activation of these pathways is often used as a primary marker of cellular stress. While this can be overcome by transcriptome-wide profiling (e.g., RNAseq), the reviewer is correct that our focused profiling of select stress-responsive signaling pathways is insufficient to claim the stress-independent activation of the ISR by our prioritized compounds. To address this, we removed this terminology from the revised submission.

Second, it is difficult for me to interpret the data for the quantification of mitochondrial morphology. In the legend for Figure 2, it is stated that "The number of individual measurements for each condition are shown above." Are the individual measurements

the number of total cells quantified? If not, how many total cells were analyzed? If the individual measurements are distinct mitochondrial structures that could be quantified why are the n's for each parameter (bounding box, ellipsoid principal axis, and sphericity) so different? Does this mean that for some mitochondria certain parameters were not included in the analysis? For me, it seems more intuitive that each mitochondrial unit should have all three parameters associated with it, but if this isn't the case it needs to be more carefully described why.

The number of individual measurements refers to the number of 3D segmentations generated using the “surfaces” module in Imaris. As the reviewer noted, we expect each surface segmentation to represent a single “mitochondrial unit.” We have now further clarified this in the figure legend.

Regarding differences in sample size for each group, we used an outlier test (i.e., ROUT outlier test in PRISM 10) to remove apparent outliers in our data. Often, these outliers result from errors in the automatic quantification that inaccurately merge two mitochondria into one large segmentation. This explains the discrepancy in the number of measurements made for each experimental group. We have made this point more clear in the Materials and Methods section of the revised manuscript.

Third, the impact of these compounds on the physiological function of mitochondria in the MFN2.D414V mutants needs to be measured. Sharma et al., 2021 showed a clear deficit in mitochondrial OCR in MFN2.D414V cells which, if rescued by these compounds, would strengthen the argument that pharmacological ISR kinase activation is a strategy for targeting the functional consequences of the dysregulation of mitochondrial form.

In this manuscript, we demonstrate that pharmacologic activation of the ISR using 0357 and 3610 rescue mitochondrial morphology in patient fibroblasts expressing the disease-associated MFN2^{D414V} mutant. The reviewer is correct that there are other mitochondrial phenotypes linked to the expression of this mutant. We are currently pursuing this question with more potent ISR activating compounds developed in our laboratory identified using the HTS screening platform described in this manuscript. However, this work, which builds on the studies described herein, uses other ISR activating compounds, which we feel would be best described in subsequent manuscripts that can fully define the activity of these new compounds.

Reviewer #2 (Public review):

Summary.

Mitochondrial dysfunction is associated with a wide spectrum of genetic and age-related diseases. Healthy mitochondria form a dynamic reticular network and constantly fuse, divide, and move. In contrast, dysfunctional mitochondria have altered dynamic properties resulting in fragmentation of the network and more static mitochondria. It has recently been reported that different types of mitochondrial stress or dysfunction activate kinases that control the integrated stress response, including HRI, PERK, and GCN2. Kinase activity results in decreased global translation and increased transcription of stress response genes via ATF4, including genes that encode mitochondrial protein chaperones and proteases (HSP70 and LON). In addition, the ISR kinases regulate other mitochondrial functions including mitochondrial morphology, phospholipid composition, inner membrane organization, and respiratory chain activity. Increased mitochondrial connectivity may be a protective mechanism that could be initiated by pharmacological activation of ISR kinases, as was recently demonstrated for GCN2.

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(1) The screen leverages a well-characterized reporter of the ISR: translation of ATF4-FLuc is activated in response to ER stress or mitochondrial stress. Nucleoside mimetic compounds were screened for activation of the reporter, which resulted in the identification of nine hits. The two most efficacious dose-response tests were chosen for further analysis (0357 and 3610). The authors clearly state that the compounds have low potency. These compounds were specific to the ISR and did not activate the unfolded protein response or the heat shock response. Kinases activated in the ISR were systematically depleted by CRISPRi revealing that the compounds activate HRI.

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We appreciate the reviewer's positive response to these aspects of our manuscript. We address the reviewer's valuable comments in the revised submission as highlighted below.

Weaknesses:

The weakness is the limited analysis of cellular changes following treatment with the compounds.

(1) Unclear how 0357 or 3610 alter other aspects of cellular physiology. While this would be satisfying to know, it may be that the authors determined that broad, unbiased experiments such as RNAseq or proteomic analysis are not justified due to the limited translational potential of these specific compounds.

The reviewer is correct. The low potency of 0357 and 3610 limit the translational potential for these compounds. However, building on the work described herein, we recently identified more potent HRI activating compounds with higher translational potential. Using RNAseq profiling, we found that these compounds show transcriptomewide selectivity for the ISR and can promote adaptive remodeling of mitochondrial morphology and function in cellular models of multiple other diseases. These compounds will be further described in subsequent studies that expand on the efforts outlined here demonstrating the potential for pharmacologic HRI activators to promote adaptive mitochondrial remodeling.

(2) There are many changes in Mfn2-D414V patient cells including reduced respiratory capacity, reduced mtDNA copy number, and fewer mitochondrial-ER contact sites. These

experiments are relatively narrow in scope and quantifying more than mitochondrial structure would reveal if the compounds improve mitochondrial function, as is predicted by their model.

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We thank the reviewer for their positive response to our manuscript. We address the reviewer's remaining concerns as outlined below.

The only minor concerns are with regard to effects on cell health and the timing of pharmacological administration.

The two compounds described in this manuscript were found to not induce any overt toxicity over a 24 h period in cell culture models. In the revised manuscript, we show data showing that treatment with increasing doses of either 0357 or 3610 do not significantly reduce cellular viability in HEK293 cells (Fig. S1G).

With regards to treatments, we include all of the relevant information for the timing and dosage of compound treatment in the revised manuscript.

Recommendations for the authors:

Reviewer #1 (Recommendations for Authors)

(1) Figure S1 "B. ATF4-Gluc activity" -> Fluc, The number of replicates is not consistently stated for each experiment. p-values are not given for D and F.

We have changed the legend for Fig. S1B to ATF4-FLuc. We show individual replicates for all experiments for all panels described in this figure, except panels C and G, in the revised Figure S1. We explicitly state the number of replicates in panel C and G in the accompanying figure legend. We have repeated the qPCR described in panels C,F and statistics are included in the revised manuscript.

(2) Figure 2 - no p-values for BtdCPU.

Yes. We found that BtdCPU-dependent increases in mitochondrial fragmentation (described in Fig. 2A-D) were not significant when analyzing *all* the data included in these figures by Brown-Forsythe and Welch ANOVA test. However, the DMSO and BtdCPU conditions were significantly different when directly compared using a Welch's t-test ($p < 0.005$). Since the statistics in this manuscript are being analyzed by ANOVA, we decided not to include a significance marker for BtdCPU, as it was not observed in this more stringent test and is not the main focus of this manuscript.

(3) Figure S4 (Supplement to Figure 5) -> Supplement to Figure 4.

We have corrected this error in the revised manuscript.

(4) Error in references - duplicated 24 and 46, duplicated 10 and 11.

This is now corrected in the revised submission.

Reviewer #2 (Recommendations for the authors):

I would love to see an assessment of mitochondrial function and mtDNA in the D414 cells following treatment.

As indicated above, we are continuing to probe the impact of more potent HRI activating compounds in patient-derived cell models expressing disease-relevant *MFN2* mutants. Initial experiments suggest that this approach can mitigate additional pathologies beyond deficient elongation in these cells, although we are continuing to pursue these results with our improved HRI activating compounds. We are excited by these results, but feel that they are best suited for a follow-up manuscript describing these new HRI activators.

Reviewer #3 (Recommendations for the authors):

The only suggestion to broaden the manuscript's impact might be to perform a basic assessment of the impact of pharmaceutical ISR activation on cell viability. Though mitochondrial elongation is often considered a surrogate for mitochondrial health, whether mitochondrial elongation improves cell viability (or not) would be informative. Similarly, the authors did not address the time-dependent effects of the ISR modulators, choosing to focus on the acute rather more chronic outcomes. Finally, does simultaneous (rather than pre-) treatment with an activator and the ionomycin produce similar effects on mitochondrial morphology, especially since therapeutics are typically administered post-injury?

We now include cell viability experiments showing that the two HRI activators discussed in this manuscript, 0357 and 3610, do not significantly reduce viability in HEK293 cells. This work is included in the revised manuscript (see Fig. S1G).

With respect to acute vs chronic outcomes of ISR activation. As highlighted by the reviewer, we primarily focus this work on defining the impact of acute ISR treatment on mitochondrial morphology. As discussed above, we now show that our prioritized ISR activating compounds 0357 and 3610 do not significantly impact cellular viability over a 24 h timecourse. However, as suggested by the reviewer, additional studies on the potential implications of chronic pharmacologic ISR activation on mitochondrial biology remains to be further explored.

We are continuing to address this in subsequent studies using more potent ISR kinase activating compounds established in our lab. However, we would like to highlight that detrimental phenotypes linked to chronic ISR kinase activation in cell culture does not preclude the translational potential for this approach, as in vivo PK/PD of these compounds can be controlled to prevent complications arising from chronic pathway activity. We previously demonstrated the potential for controlling compound activity through its PK/PD in our establishment of highly selective activators of other stress-responsive signaling pathways such as the IRE1/XBP1s arm of the UPR (e.g., Madhavan et al (2022) *Nat Comm*).

We appreciate the reviewer's comments regarding the timing of compound treatment in them ionomycin experiment. Ionomycin works extremely quick to induce fragmentation (minutes), which would be prior to activation of the ISR induced by these compounds (hours). Thus, co-treatment would lead to fragmentation. It is an interesting question to ask if co-treatment with ISR activators could rescue this fragmentation as the pathway is activated, but we did not explicitly address this question in this manuscript. However, we do show that pharmacologic GCN2 or HRI activators can rescue mitochondrial morphology in patient fibroblasts expressing a *MFN2* mutant, where mitochondria are fragmented, indicating that our approach can restore mitochondrial morphology in this context. We feel that these results, in combination with others described in our manuscript, demonstrate the potential for this approach to mitigate pathologic mitochondrial fragmentation associated with different conditions.

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