Mitochondrial Contagion Induced by Parkin Deficiency in *Drosophila* Hearts and its Containment by Suppressing Mitofusin

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ABSTRACT

**Rationale:** Dysfunctional Parkin-mediated mitophagic culling of senescent and/or damaged mitochondria is a major pathological process underlying Parkinson’s Disease and a potential genetic mechanism of cardiomyopathy. Despite epidemiological associations between Parkinson’s Disease and heart failure, the role of Parkin and mitophagic quality control in maintaining normal cardiac homeostasis is poorly understood.

**Objective:** We used germ-line mutants and cardiac-specific RNA interference to interrogate Parkin regulation of cardiomyocyte mitochondria and examine functional crosstalk between mitophagy and mitochondrial dynamics in *Drosophila* heart tubes.

**Methods and Results:** Transcriptional profiling of Parkin knockout mouse hearts revealed compensatory upregulation of multiple related E3 ubiquitin ligases. As *Drosophila* lack most of these redundant genes, we examined heart tubes of *parkin* knockout flies and observed accumulation of enlarged hollow “donut” mitochondria with dilated cardiomyopathy that could be rescued by cardiomyocyte-specific Parkin expression. Identical abnormalities were induced by cardiomyocyte-specific Parkin suppression using two different inhibitory RNAs. Parkin-deficient cardiomyocyte mitochondria exhibited dysmorphology, depolarization, and reactive oxygen species generation without calcium cycling abnormalities, pointing to a primary mitochondrial defect. Suppressing cardiomyocyte mitochondrial fusion in Parkin-deficient fly heart tubes completely prevented the cardiomyopathy and corrected mitochondrial dysfunction without normalizing mitochondrial dysmorphology, demonstrating a central role for mitochondrial fusion in the cardiomyopathy provoked by impaired mitophagy.

**Conclusions:** Parkin deficiency and resulting mitophagic disruption produces cardiomyopathy in part by contamination of the cardiomyocyte mitochondrial pool through fusion between improperly retained dysfunctional/senescent and normal mitochondria. Limiting mitochondrial contagion by inhibiting organelle fusion shows promise for minimizing organ dysfunction produced by defective mitophagic signaling.

**Keywords:** Mitochondrial fusion, mitophagy, cardiomyopathy, Parkin

**Nonstandard Abbreviations and Acronyms:**

- PINK1: PTEN-inducible kinase 1
- Mfn: mitofusin
- FDR: false discovery rate
- GO: Gene ontology
- GFP: green fluorescent protein
- RNAi: RNA interference
- SR: Sarcoplasmic reticulum
- MARF: mitochondrial assembly regulatory factor
- OCT: optical coherence tomography
- ROS: reactive oxygen species
- SOD: superoxide dismutase
- Romo1: ROS modulator 1
- IBR: in-between RING
INTRODUCTION

Dysfunction of the PINK1-Parkin mitochondrial quality control pathway is most widely recognized for its genetic linkage to Parkinson’s disease; accumulating evidence points to an important role of this pathway in normal heart function. Parkin is an E3 ubiquitin ligase recruited to dysfunctional mitochondria through the actions of the kinase PINK1. Mitochondrial levels of PINK1 are chronically suppressed under normal conditions, but mitochondrial senescence or damage that provokes mitochondrial depolarization results in PINK1 accumulation and phosphorylation of mitofusin 2 (Mfn2), the receptor for mitochondrial Parkin recruitment. Parkin-mediated poly-ubiquitination of multiple mitochondrial membrane proteins then selectively targets damaged organelles for mitophagic elimination.

The functional links between PINK1, mitofusins and Parkin were initially revealed by targeting their Drosophila melanogaster gene orthologs and studying skeletal muscle and neuronal mitochondria. Mechanistic foundations for our growing understanding of mitophagic disruption in human Parkinson’s Disease were also established in large part through the use of fruit fly Parkin gene knockout models. Indeed, it is notable that interruption of PINK1 and Parkin in Drosophila melanogaster provokes more severe phenotypes than does the orthologous genetic manipulation in mice, likely because fruit flies lack functionally redundant compensatory pathways present in mammals. Thus, both germ-line ablation and system-wide mutation of the mouse Parkin gene (Park2) fail to evoke more than subtle Parkinson’s Disease phenotypes in mice. Likewise, mice systemically lacking Parkin reportedly have no basal cardiac dysfunction. These findings either impugn the idea that mitochondrial quality control is essential to the mouse brain and heart, or point to induction of as-yet unknown compensatory mechanisms in germ-line parkin null mouse models.

Cardiomyocytes and neurons are both amitotic and therefore unable to repair mitochondrial damage through cell division. Because the brain and heart have a common reliance upon mitochondrial-generated ATP for minute-by-minute functioning, it might be expected that genetic defects in Parkin-mediated mitophagic signaling that impair removal of damaged mitochondria would affect both organs. In support of this notion, and unlike Parkin knockout mice, mice deficient in PINK1 develop progressive cardiomyopathy and evidence of mitochondrial dysfunction as well as features of Parkinson’s disease. Likewise, we recently showed that mice with cardiac myocyte-restricted ablation of Mfn2, which is the obligate mitochondrial Parkin mitophagy receptor, develop cardiomyocyte respiratory impairment and progressive heart failure. These findings may suggest one possible physiological basis for previously described associations between heart failure and Parkinson’s Disease.

Here, we report results of RNA-sequencing studies supporting the notion that compensatory upregulation of alternate E3 ubiquitin ligases can contribute to the absence of severe phenotypes after germ-line park2 ablation. Accordingly, we return to the fruit fly system that has proven utility in mechanistic in vivo studies of Parkin effects in neurons and skeletal muscle, and in which we recently described cardiomyopathy. Because we found that germ-line parkin gene ablation in Drosophila has multiple adverse confounding systemic consequences, we developed cardiomyocyte-specific Parkin suppression flies in which we observed abnormal mitochondrial structure and function, and cardiomyopathy. In this model, we discovered that suppressing mitochondrial fusion (thus preventing fusion-mediated contamination of the normal cardiomyocyte mitochondrial pool by pathologically retained damaged mitochondria) fully rescues mitochondrial dysfunction and cardiomyopathy induced by Parkin deficiency. These findings describe a novel therapeutic strategy for diseases caused by defective mitochondrial quality control: limiting mitochondrial contagion through suppression of organelle fusion.
METHODS

w^{118} (#6326), UAS-mitoGFP (#8442), UAS-GCaMP3 (#32234), Parkin RNAi [#37509 (park KD1) and #38333 (park KD2)], UAS-Parkin (#34748), UAS-SOD1 (#33605), UAS-SOD2 (#24494), and mef-Gal4 (#27390) were obtained from the Bloomington Stock Center. The parkin null mutant, Park^{25} was from L. J. Pallanck (University of Washington, Seattle, WA), UAS-marf RNAi was from M. Guo (University of California, Los Angeles, CA) and UAS-mito-DsRed was from F. Kawasaki (Pennsylvania State University University Park, PN). UAS-ch5-GFP was described previously^{25}. UAS transgenes were expressed in Drosophila cardiomyocytes using the tinC-Gal4 driver from Rolf Bodmer (Sanford-Burnham Medical Research Institute, La Jolla, CA). Studies of Drosophila heart tubes were performed as described^{25, 26}.

RNA-sequencing of Parkin null hearts^{22} was performed as described^{23}.

Expanded Methods are in the Online Supplement.

RESULTS

Compensatory upregulation of multiple E3 ubiquitin ligases in germ-line Parkin null mouse hearts.

To gain insight into why systemic ablation of Parkin has minimal effects on mice^{15, 22} we performed deep mRNA sequencing^{25} of parkin null and wild-type control mouse hearts. Parkin ablation produced a greater than 50% change (False discovery rate [FDR]=0.01; p value <0.005) in steady-state levels of 3,445 of the ~8,000 cardiac mRNAs expressed at levels >1 mRNA copy/cell (3,212 increased; 233 decreased) (Figures 1a, 1b). Gene ontology (GO) analysis revealed dominant effects on metabolic/mitochondrial genes (Figure 1c). Parkin mRNA was absent in knockout hearts, but transcript levels of upstream Parkin activators PINK1 and Mfn2 increased (Figure 1d). Of 15 Parkin-like (i.e. RING1, RING2, and IBR domain) E3 ubiquitinases expressed in hearts, 11 were significantly upregulated in Parkin deficiency (Figure 1e). These results add to accumulating evidence for functional compensation induced by germ-line murine Parkin insufficiency^{24}, suggest how ablation of the parkin gene produces cardiomyocyte mitochondrial enlargement without basal cardiac dysfunction^{16}, and support a re-evaluation of cardiac Parkin biology.

Dilated cardiomyopathy and mitochondrial abnormalities in parkin null flies.

Drosophila melanogaster Parkin null mutants (park -/-) exhibit defective mitochondrial quality control in skeletal muscle^{11}. We recently described heart tube contractile and respiratory impairment in the same line of park-/- flies^{5}. Here, we demonstrated that the cardiomyopathy of Drosophila Parkin deficiency is sustained and we defined the ultrastructural consequences of Parkin ablation on cardiomyocyte mitochondria. One and 4 weeks after eclosure, heart tubes of parkin -/- Drosophila exhibited reduced fractional shortening (Figures 2a, 2b; Online Figure 1a). Ultrastructural examination of parkin -/- heart tubes revealed abnormally enlarged cardiomyocyte mitochondria, many of which had disorganized cristae and/or a characteristic hollow “donut” morphology (Figure 2c). However, germ-line parkin deletion adversely impacted fly size (Online Figure 1b) and markedly reduced longevity (log-rank p<0.001) (Online Figure 1c), as previously reported^{11}. Because the systemic effects and premature lethality of parkin -/- Drosophila confound detailed mechanistic assessments of the cardiac consequences of Parkin deficiency, we developed cardiac-specific Parkin deficient flies.

Cardiac-specific Parkin suppression causes symptomatic heart failure in flies.

We used the tinC4-Gal4 driver to express Parkin inhibitory RNAs and suppress Parkin exclusively in Drosophila cardiomyocytes (UAS-Park RNAi; Figure 3a). As with germ-line parkin ablation, cardiomyocyte-specific Parkin suppression evoked heart tube hypocontractility 1 and 4 weeks
after eclosure (Figure 3b) and increased mitochondrial size imaged with mito-GFP \textsuperscript{25} (Figure 3c). Since longevity was normal in cardiac-specific Parkin deficient flies (log-rank $P=\text{NS}$) (Figure 3d), we determined the impact of cardiomyocyte-autonomous Parkin deficiency on systemic cardiorespiratory function using the negative geotaxis \textit{Drosophila} “stress test” \textsuperscript{26}. Both lines of cardiac-specific Parkin deficient flies displayed accelerated age-related declines in climbing performance (log-rank $P=6.6\times10^{-16}$ for RNAi1 and $1.7\times10^{-13}$ for RNAi2 vs tinc\textsuperscript{Δ4}-Gal4 controls) (Figure 3e).

\textit{Parkin insufficiency causes cardiomyocyte-autonomous cardiomyopathy without altering SR calcium cycling.}

The results of cardiac Parkin suppression indicate that even partial cardiomyocyte Parkin deficiency (see Figure 6g below) can adversely impact cardiac function. We confirmed this finding in germ-line Parkin haploinsufficient flies (\textit{park} +/-), which also developed a cardiomyopathy with mitochondrial abnormalities, despite longer survival than \textit{parkin} -/- flies and normal body size (Online Figures Ila-d). We proved that the cardiomyopathy provoked by germ-line Parkin haploinsufficiency results from cardiomyocyte Parkin deficiency by crossing \textit{park} +/- flies with tinc\textsuperscript{Δ4}-Gal4-driven UAS-Parkin transgenic flies that express Parkin exclusively in cardiomyocytes, which completely normalized cardiac dysfunction (Online Figure Ile).

\textit{Parkin may also modulate endoplasmic reticular calcium release} \textsuperscript{27, 28}. Although sarcoplasmic reticulum (SR) dysfunction is implicated in many cardiomyopathies, cardiomyocyte SR architecture and SR calcium handling were normal in Parkin haploinsufficient \textit{Drosophila} hearts (Online Figure III).

\textit{Parkin insufficiency causes accumulation of dysfunctional cardiomyocyte mitochondria.}

The essential function of Parkin is mediating mitophagic mitochondrial culling \textsuperscript{29, 30}. Consistent with interruption of normal mitophagic quality control caused by \textit{Drosophila} cardiac-specific Parkin deficiency, we observed increases in dysmorphic cardiomyocyte mitochondria and loss of cardiomyocyte mitochondrial nucleoids (see above and Figure 4a). We therefore further interrogated mitochondrial function in Parkin RNAi-expressing hearts and observed a marked increase in the number of depolarized cardiomyocyte mitochondria (Figures 4b, 4c) and greater numbers of mitochondria producing reactive oxygen species (Figure 4d). Evidence for mitochondrial depolarization and ROS production was more common in abnormally large or dysmorphic mitochondria, (Figures 4c, 4d) linking altered structure to dysfunction. Collectively, these data reveal widespread mitochondrial dysfunction in the cardiomyopathy induced by Parkin deficiency.

\textit{Mitochondrial ROS inhibition prevents the cardiomyopathy evoked by cardiac Parkin insufficiency.}

We tested whether the observed increase in mitochondria producing ROS was a cause or consequence of cardiomyopathy in cardiac-specific Parkin deficient flies by crossing them to flies transgenically expressing either soluble (largely cytosolic) superoxide dismutase 1 (SOD1) or mitochondrial localized SOD2 \textsuperscript{31}. Neither SOD1 nor SOD2 alone affected heart tube contraction measured by OCT (Figures 5a, 5b). Strikingly, both SOD1 and SOD2 normalized heart tube contraction and the increase in mitochondrial ROS of cardiomyocyte-specific Parkin-deficient flies (Figures 5a, 5b; Online Figure IV), revealing a role for ROS in cardiac dysfunction that accrues after the dominant Parkin-mediated mitophagic pathway is suppressed.

Because SOD2 is localized to the mitochondrial matrix, its efficacy at preventing the cardiomyopathy implicates mitochondria as the source of toxic ROS under conditions of Parkin insufficiency. Recently, ROS modulator 1 (Romo1) was identified as a major source of ROS originating from the mitochondrial electron transport chain, and Romo1-derived ROS were implicated in cellular senescence \textsuperscript{32}. We considered that Romo1 may be both physically and functionally positioned as the source of ROS produced by abnormal mitochondrial that accumulate after suppression of Parkin. Consistent with this notion, cardiomyocyte-specific RNAi-mediated Romo1 suppression exhibited the same protective effects on heart tube function in cardiomyocyte-specific Parkin-deficient flies as did SOD
expression (Figure 5c). These data further support interruption of normal mitophagic mitochondrial culling and accumulation of toxic damaged organelles as the primary mechanism leading to cardiomyopathy in Parkin-deficient heart tubes.

Suppressing mitochondrial fusion in cardiomyocytes rescues the cardiomyopathy induced by Parkin deficiency without normalizing mitochondrial dysmorphology.

We considered that the increase in ROS-producing and depolarized mitochondria in cardiomyopathic Parkin-deficient cardiomyocytes seems disproportionate because of the unusually low rate of mitochondrial turnover reported for cardiomyocytes in Drosophila and mice. Previous studies suggested a functional interaction between mitochondrial quality control and dynamics pathways. Therefore, we postulated that ongoing mitochondrial fusion might directly contribute to cardiac dysfunction in Parkin-insufficiency by promoting contamination of the normal mitochondrial pool with components of damaged mitochondria that escape mitophagic culling. If this mechanism were correct, then inhibiting mitochondrial fusion would improve both mitochondrial health (by preventing trans-organelle contagion) and heart function (by limiting disproportionate increase in dysfunctional mitochondria) in Parkin deficiency. We tested this hypothesis by suppressing Drosophila cardiomyocyte mitochondrial fusion using cardiac-specific inhibition of MARF (mitochondrial assembly regulatory factor, the Drosophila mitofusin ortholog) on the Parkin RNAi background. Cardiomyocyte-specific Parkin suppression increased heart tube end-systolic and end-diastolic dimensions as expected (Figure 6a, black), and produced mitochondria with decreased mitochondrial DNA (Figure 6b, black), evidence of increased mitochondrial biogenesis (Figure 6c, black), increased mitochondrial ROS (Figure 6d, black), and increased numbers of depolarized organelles (Figure 6e, black). As previously reported, MARF suppression likewise caused a dilated cardiomyopathy (Figure 6a, grey) characterized by mitochondria with fewer genomes, increased ROS, and greater depolarization (Figures 6b, 6d, and 6e, grey), although without evidence for increased biogenesis (Figure 6c, grey). Stunningly, combined cardiac-specific Parkin and MARF suppression normalized heart tube dimension and contractile function (Figure 6a, light grey) and improved each of the indices of mitochondrial health (i.e. limited the proportion of ROS-producing and depolarized organelles and increased mitochondrial DNA) (Figures 6b, 6d, and 6e, light grey). (Note - unlike the Parkin deficient cardiomyopathy, ROS production in the MARF RNAi model is not the major contributory factor; Online Figure V.) The beneficial effects of suppressing mitochondrial fusion seemed unrelated to mitochondrial morphology per se, as the mitochondria of combined Parkin/MARF suppressed cardiomyocytes showed characteristics of both parent lines (i.e. enlarged mitochondria from Parkin deficiency and fragmented mitochondria from MARF suppression; Figure 6f) rather than normalization of organelle morphometry. Furthermore, the benefits of MARF suppression for Parkin insufficient hearts did not reflect normalization of some unexpected evoked increase in MARF, as MARF mRNA levels were normal in Parkin -/- and +/- flies (Figure 6g) and we have previously shown that forced mitofusin expression in Drosophila heart tubes is benign. Instead, genetic epistasis between Drosophila Parkin and MARF/mitofusin uncovers bi-directional contributory roles for mitochondrial dynamics in the cardiomyopathy evoked by interruption of Parkin-mediated mitophagy, and presumably for mitophagy in the cardiomyopathy produced by suppressing mitochondrial fusion.

DISCUSSION

Here we show that cardiomyocyte Parkin is essential to mitochondrial and cardiac hemostasis in Drosophila. This warrants re-evaluation of the notion, derived from absence of a basal cardiac phenotype in parkin null mice, that Parkin is dispensable to normal heart function. By interrogating genetic epistasis between Drosophila Parkin and mitofusin (MARF) we uncover a completely new mechanism for end-organ dysfunction produced by Parkin insufficiency: ongoing mitochondrial fusion contributes to mitochondrial contagion when Parkin signaling (and presumably Parkin-dependent mitophagic elimination of abnormal organelles) is impaired. These findings suggest that general mitochondrial health

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and end-organ function could be preserved in mitophagically impaired tissues through chronic suppression of fusion-induced mitochondrial contamination.

The PINK1-Parkin interaction is central to mitophagic quality control in most tissues, but published studies provide an inconsistent picture of the role of PINK1-Mfn2-Parkin mediated mitophagy in normal hearts. Genetic ablation of mouse PINK1 induces cardiomyopathy and ablation of the critical PINK1-Parkin intermediate, Mfn2, causes a murine cardiomyopathy, but genetic ablation of mouse Parkin had no impact on baseline cardiac function. Rather than accept that upstream activators of Parkin, but not Parkin itself, are essential to normal heart function, we uncovered compensatory upregulation of multiple functionally-related E3 ubiquitin ligases. Functional compensation in Parkin null mice is also observed in neurological tissue and can explain minimal cardiac and neurological phenotypes. As Drosophila have only one Parkin-like protein (Parkin) fruit flies are excellent models of Parkin dysfunction, perhaps explaining why the major mechanistic insights into Parkin-mediated mitophagy and its role in Parkinson’s Disease have derived from work in Drosophila.

Our observation that homozygous and heterozygous germ-line parkin gene ablation and cardiomyocyte-specific Parkin suppression in fruit flies are each detrimental to mitochondrial and cardiac health suggests that a genetic approach in mice that minimizes the opportunity for compensatory regulation of putative alternate mitophagy pathways, such as cardiac-specific Parkin gene ablation, is likely to offer a different view of Parkin’s role in the mammalian heart.

The current studies are an exemplar of functional insights that can accrue from unanticipated genetic interactions revealed through epistasis. We crossed two flies that develop a cardiomyopathy caused by interruption of primary mitochondrial functions (mitochondrial clearance in the cardiac Parkin RNAi and mitochondrial fusion in the cardiac MARF RNAi). The result was flies with normal heart and mitochondrial function, but with mitochondrial structural abnormalities of both parent lines. It may not be intuitively obvious how breeding two cardiomyopathies together can result in a “rescue”, but this result simply reflects functional interconnectivity between mitophagy and fusion. Not only do mitochondrial fusion and mitophagy appear interdependent, but our data suggest that balance between the two processes is essential to overall mitochondrial homeostasis. Thus, a primary disturbance in either the Parkin/mitophagy pathway or the MARF/fusion pathway causes cardiac disease, and restoring balance by concomitant suppression of the other arm is beneficial. Given the unusually slow rate of mitochondrial turnover in hearts compared to other tissues, it will be interesting to use a similar approach to probe the physiological limits of the mitochondrial dynamics/mitophagy equilibrium in other contexts.

A remarkable feature of the Parkin-deficient fly heart is the correlation between abnormal mitochondrial structure (enlarged and/or donut mitochondria) and dysfunction as measured by TMRE staining. Thus, mitochondria exhibit individual organelle abnormalities. This observation is consistent with our paradigm that specific mitochondria that become senescent or are damaged require identification, isolation, and elimination in a manner that preserves members of the normally functioning organelle population. Whereas morphologically and functionally abnormal mitochondria are occasionally observed in normal hearts, Parkin suppression increased the proportion of damaged organelles, presumably because the mitophagic mechanism for their identification and elimination was interrupted. Thus, while it is common to measure mitochondrial respiration, integrity, and toxicity as a population, studies that permit assessments of individual organelles within the overall population can provide insights that might otherwise be overlooked.

Our work offers a new mechanistic paradigm to explain genetic interactions between Drosophila Parkin and mitofusin/MARF. Deng et al described interactions between Parkin and mitochondrial fusion/fission proteins in Drosophila skeletal muscle, attributed to a putative pro-fission (or anti-fusion) activity of Parkin. Although we also found that Parkin-deficient mitochondria are enlarged in Drosophila cardiomyocytes, Parkin overexpression did not induce mitochondrial fragmentation that would be produced by the postulated pro-fission or anti-fusion effect (Online Figure VI). We also did not observe any detrimental effects of Parkin overexpression on normal heart tube function (see Online.
Figure IIe), and inhibiting mitochondrial fusion by suppressing MARF normalized Parkin-deficient heart tube contraction without normalizing mitochondrial morphology. Thus, opposing effects on mitochondrial dynamics cannot explain the genetic epistasis we detected. Instead, our findings are consistent with the schema depicted in Figure 7. When normal mitophagic organelle elimination (Figure 7a) is suppressed by Parkin insufficiency, abnormal “undead” or “zombie” mitochondria accumulate and (as zombies will do) contaminate the normal mitochondrial population by fusing with normal organelles (Figure 7b). Mitochondrial fusion that is ordinarily protective therefore becomes the mechanism for a general contagion of mitochondrial dysfunction. Interrupting mitochondrial fusion prevents contamination of functionally normal mitochondria by virulent zombie mitochondria (Figure 7c), sequestering abnormal mitochondria that can then be removed by alternate, albeit almost certainly less efficient, elimination pathways.

Inhibiting mitochondrial fusion to contain mitochondrial contagion induced by mitophagic dysfunction may have applications in human diseases caused by defective mitochondrial quality control, most notably hereditary Parkinson’s Disease induced by PINK1 and Parkin mutations. We hypothesize that cytotoxicity and end-organ dysfunction can be delayed by interrupting the feed-forward pathway of mitochondrial contamination through suppression of mitochondrial fusion factors. One can envision that the pro-fusion activities of mitofusins 1 or 2 could be suppressed using pharmacological agents that inhibit the critical trans protein-protein interactions mediating mitochondrial tethering and outer membrane fusion. Compared to flies that have only one functional mitofusion protein (outside of male germline cells), mammals that have two mitofusins may offer greater flexibility for manipulating aspects of the mitochondrial fusion-mitophagy interactome. Thus, because mammalian Mfn1 and Mfn2 both promote mitochondrial fusion, it might be advantageous to individually targeted constitutive organelle fusion mediated by Mfn1 while preserving essential elements of mitophagy, cardiomyocyte differentiation, and SR-mitochondrial calcium crosstalk uniquely mediated by Mfn2 5,36, 37. Likewise, the functional redundancy in mammalian mitophagy pathways that initially prompted us to develop the fly as an experimental model for disease caused by cardiac Parkin deficiency will likely enhance the overall efficacy of a therapeutic strategy aimed at reducing the mitochondrial contagion because secondary mammalian mitochondrial quality control mechanisms invoked by Parkin dysfunction will have a greater opportunity to clear damaged organelles.

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DISCLOSURES
None.

REFERENCES


FIGURE LEGENDS

**Figure 1.** Cardiac RNA transcript levels of Parkin pathway factors and Parkin-related E3 ubiquitin ligases in Parkin knockout (KO) mice.  
A and B. Volcano plot (A) and heat maps (B) of cardiac transcriptional changes induced by germ-line Parkin gene ablation in mice.  
C. Gene-ontology analysis of up- (top) and down-regulated mRNAs in Parkin knockout mouse hearts.  
D. mRNA levels of Parkin and upstream Parkin signaling factors Pink1 and Mfn2; Mfn1 is shown for comparison.  
E. Transcript levels of Parkin-related E3 ubiquitin ligases of RING2, RING1, and In Between Ring (IBR) families.  
Gene names are: Arih1, ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein 1; Arih2, ariadne homolog 2; Cul9, cullin 9; Rnf, ring finger protein; Rbck1, RanBP-type and C3HC4-type zinc finger containing 1; Cyhr1, cysteine/histidine-rich 1; Rhx1, ring-box 1; Mib2, mindbomb homolog 2; Polr3k, polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa.  
Values are mean±SEM of RNA sequencing reads per million bases (RPKM) for n=5 wild type (WT) and n=4 germ-line Parkin null (KO) mice.

**Figure 2.** Cardiomyopathy and mitochondrial abnormalities in parkin -/- flies.  
A. Optical coherence tomography (OCT) of heart tube contractions in tincΔ4-Gal4 (Ctrl) and parkin null (-/-) flies 7 days after eclosure.  
B. Bar graphs showing group mean OCT data for end0systolic dimension (ESD) and % fractional shortening.  
C. Transmission electron micrographs showing enlarged mitochondria with disrupted or absent cristae in parkin -/- cardiomyocytes.  
Note characteristic hollow “donut” mitochondrial morphology.  
White scale bars are 1 µm.

**Figure 3.** Cardiomyocyte-specific Parkin suppression induces heart failure and mitochondrial abnormalities in Drosophila.  
A. Parkin targeting by RNAi constructs.  
B. OCT studies showing hypococontractile heart tubes in tincΔ4-Gal4 UAS-Parkin RNAi fly lines.  
Bar graphs show group mean fractional shortening data 7 and 28 days after eclosure (n=15-20/group).  
C. Cardiomyocyte mitochondria visualized by tincΔ4-Gal4-mitoGFP show organelle enlargement and hollow “donut” dysmorphology (arrows).  
Group mean data are to the right (>100 mitochondria analyzed per heart).  
D. Survival analysis of tincΔ4-Gal4 UAS-Parkin RNAi fly lines (n=150/group).  
E. Climbing performance in negative geotaxis test in tincΔ4-Gal4 UAS-Parkin RNAi fly lines (n=150/group).

**Figure 4.** Cardiomyocyte mitochondrial dysfunction induced by Parkin suppression.  
A. Merged confocal analysis of cardiomyocyte mitochondria nucleoids visualized using anti-DNA antibody (green) and cardiomyocyte-specific expression of Mito-DSRed (red).  
Nuclei visualized with DAPI (blue) were digitally masked and mitochondrial DNA content measured using ImageJ.  
Quantitative results are to the right.  
B and C. Depolarization of structurally abnormal mitochondria assessed by rhodamine 123 (Rho) staining.  
Separate tincΔ4-Gal4 driven mito-GFP (green, left) and rhodamine 123 (red, middle) and merged images (right) with representative depolarized (less red staining) mitochondria indicated with arrows.  
C. Representative merged control and Parkin RNAi mito-GFP/rhodamine 123 double stained cardiomyocytes (left) and group quantitative data (right).  
Two of several depolarized mitochondria are indicated by arrows.  
D. Representative merged control and Parkin RNAi mito-GFP/MitoSox double stained cardiomyocytes (left) and group quantitative data (right).  
Three of several ROS-producing mitochondria are indicated by arrows.

**Figure 5.** Mitochondrial ROS production contributes to the cardiomyopathy evoked by Parkin suppression.  
A and B. Results of OCT and MitoSOX studies of cardiomyocyte-specific Parkin RNAi flies without (black) and with (dark grey) concomitant cardiomyocyte-specific expression of SOD1 (A) or SOD2 (B).  
End-systolic dimension (ESD) is on top, % fractional shortening in middle, mitoSOX on bottom.  
C. OCT studies of cardiac Parkin-deficient flies without (black) and with (dark grey) concomitant RNAi-mediated suppression of mitochondrial ROS modulator 1 (ROMO1), a major mitochondrial ROS producing enzyme.  
* = significantly different from Ctrl by ANOVA and Bonferroni test.
**Figure 6.** Interrupting mitochondrial fusion rescues mitochondrial and cardiac dysfunction evoked by Parkin deficiency.  
**A.** Results of OCT studies of Parkin RNAi-expressing fly heart tubes without and with concomitant RNAi-mediated suppression of cardiomyocyte dMfn/MARF (Parkin/MARF RNAi). Normal Ctrl and tincΔ4-Gal4 MARF RNAi results are shown for comparison.  
**B-E.** Mitochondrial function studies of the same groups as (A); **B,** mitoDNA content performed as in Figure 4a; **C,** Tfam mRNA abundance by RT-qPCR; **D,** ROS production performed as in Figure 4d; **E,** mitochondrial depolarization assayed as in Figures 4b, 4c.  
**F.** Mitochondrial morphology assessed by mito-GFP confocal analysis of the same groups. Group histogram data for mitochondrial area are on the left, with representative micrographs on the right. The grey areas depict abnormally small (left) and abnormally large (right) mitochondria defined as the bottom and top decile of the normal control data. The same control data (grey lines) are shown in all three histograms.  
**G.** RT-qPCR of Parkin (top), PINK (middle) and MARF (bottom) mRNA. * = significantly different from Ctrl by ANOVA and Bonferroni test.

**Figure 7.** Schematic diagram depicting interactive mitochondrial dynamics and quality control pathways, as revealed by the current results. Green mitochondria are fully polarized, red mitochondria are fully depolarized, and yellow/orange represent intermediate states.
Novelty and Significance

What Is Known?

- Hearts are mitochondria-rich and require mitochondrial ATP to function.
- Declining cardiac function with age is associated with deterioration of mitochondrial health.
- Damaged cardiac mitochondria must therefore constantly be identified and removed to sustain normal heart function.

What New Information Does This Article Contribute?

- By studying fruit flies we found that the Parkinson’s Disease gene, Parkin, mediates targeting and removal of damaged mitochondria from cardiac myocytes.
- In the absence of Parkin, damaged mitochondria accumulate, fuse with, and contaminate normal mitochondria, spreading organelle damage and causing heart failure.
- Genetically suppressing mitochondrial fusion prevents heart failure in hearts lacking Parkin by interrupting the mitochondrial contagion.

Mitochondrial quality control is critical to normal heart function, but the responsible pathways are unclear. The PINK1-Parkin pathways is the primary mechanism by which dysfunctional mitochondria are identified and selectively eliminated in many tissues and mutations in PINK1 and Parkin cause Parkinson’s Disease in humans. Whereas PINK1 knockout mice develop neurological and cardiac diseases, Parkin knockout mice are inexplicably normal. Here, we uncovered compensatory upregulation of Parkin-like factors in mouse hearts lacking Parkin, explaining this apparent discrepancy. In fruit flies, which do not have multiple compensatory Parkin-like factors, systemic deletion or cardiac-specific suppression of Parkin caused mitochondrial dysmorphology and dysfunction and evoked heart failure. Remarkably, preventing fusion between abnormal and normal mitochondria by suppressing the fusion protein MARF in fly hearts prevented the cardiomyopathy induced by Parkin insufficiency. These results uncover a new mechanism that explains disproportionate cell and end-organ damage when the PINK1-Parkin mitophagy pathway is interrupted: mitochondrial contagion spreads through organelle fusion. Our findings demonstrate the feasibility of moderating organ damage in mitophagically-impaired tissues by targeting mitochondrial fusion.
Figure 1

A.

B. Absolute mRNA expression

C. Normalized mRNA expression

D.

E.
Figure 2
Figure 3

A

B

C

D

E
Figure 5

A  Parkin RNAi with TG SOD1  

B  with TG SOD2  

C  with ROMO1 RNAi  

ESD (μM)  

% shortening  

MitoSOX/MitoTracker  

Legend:

Ctrl  SOD1  Park RNAi  Park RNAi SOD1  

Ctrl  SOD2  Park RNAi  Park RNAi SOD2  

Legend:

Ctrl  ROMO RNAi  Park RNAi  Park RNAi ROMO RNAi  

Legend:

* indicates statistical significance.
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SUPPLEMENTAL MATERIAL

Detailed Methods:

Drosophila Heart Studies. Optical coherence tomography (OCT) was used to image heart tubes of one and four week adult flies on a Michelson Diagnostics (Maidstone, UK) EX 1301 OCT microscope as described previously (1, 2). Image J was used to analyze B-mode images to measure the internal chamber diameter at end-systole (ESD) and end diastole (EDD). % Fractional Shortening (FS) was calculated as (EDD-ESD/EDD).

Phasic calcium transients were measured by expressing UAS-GCaMP3.0 in fly cardiomyocytes and recording changes in the fluorescence intensities using Nikon AZ100 UV fluorescence microscope as described previously (3). One week old adult flies were dissected to expose the heart tube while still attached to the dorsal shell. This preparation was maintained in artificial haemolymph at 18°C during the recording. When measuring caffeine-induced Ca²⁺ release EGTA (8mM/L) was used to stop the heart immediately prior to addition of caffeine (10mM/L) (Sigma).

Confocal and Electron Microscopy. Fly heart tubes were dissected and mounted in haemolymph for live confocal imaging. A Nikon Eclipse Ti confocal system or Carl-Zeiss LSM510-Meta Laser Scanning confocal Microscope were used to image mitochondria in Drosophila cardiomyocytes expressing Tinc Δ4-Gal4 driven UAS-mitoGFP or mito-DSRed. Mitochondrial dimensions were measured using Image J. UAS-GFP-cb5 and Tinc-UAS-DSRed were crossed to Park KO/+ to observe the sarcoplasmic reticulum structure (1).

Rhodamine 123 fluorescence was used to assess mitochondrial membrane potential. Heart tubes were dissected and incubated in Rhodamine 123 (25μM) (Sigma) for 20 min, and then washed for 10 min in phosphate-buffered saline (PBS) prior to confocal imaging.

To assess cardiomyocyte mitochondrial ROS production, dissected heart tubes were incubated in MitoSOX (2.5mM) (Life Technologies) in PBS for 20 minutes at 25°C, washed for 10 min with PBS, and visualized by confocal fluorescent microscopy.

For Drosophila heart tube anti-DNA immunostaining confocal fluorescence studies were performed on freshly isolated drosophila heart tubes. Briefly, fresh dissected heart tubes were fixed with 4%PFA for 5 minutes, and then permeabilized with 1% Triton X-100 for ten minutes. DNA was visualized using mouse monoclonal anti-dsDNA (1:200, Abcam) and Alexa Fluor 546-labeled goat anti-mouse IgG (1:500, Invitrogen).

For EM studies Drosophila heart tubes were fixed in a 2.5% solution of glutaraldehyde (4% PFA, 0.1M cacodylate, and 2.5% glutaraldehyde) (Electron Microscopy Sciences, Hatfield, CA), sequentially stained with osmium tetroxide and uranyl acetate, dehydrated, and embedded in Polybed 812. Tissue was thin sectioned on a Reichert-Jung Ultra-Cut (90nm thick), post stained in uranyl acetate and lead citrate, and viewed on a Jeol electron microscope (JEM-1400) at 5,000 direct magnifications (JEOL, Tokyo, Japan).

Longevity and Climbing Studies. For life span analysis, 150 flies of each genotype were collected within one day of hatching and placed in vials in groups of 25 each. Numbers of dead flies were counted every 2-3 days and surviving flies were flipped into new food vials. Survival curves were compared by Kaplan-Meier analysis and log–rank test.

For assessment of exercise capacity by negative geotaxis, freshly emerged 150 adult flies of each genotype were collected and maintained in 12” X 3.5” clear plastic containers. To examine the climbing ability the flies were displaced to the bottom of the container by quick firm tapping impact and the number of flies that had climbed greater than 10cm within 10 sec was determined daily (2). The climbing curves were compared by Kaplan-Meier analysis and log–rank test.
**Molecular Biology.** For RT-PCR, the total RNA samples were prepared from the whole fly homogenates of parkin -/-, parkin+/+, mef-Gal4>park KD2, mef>UAS park, mef+/+ strains using Trizol. 1 µg of RNA was used to prepare cDNA by random priming and reverse transcription. Primers for real-time qPCR of Parkin are 5’- TAAGCGATGCCACGACAATA and 3’- GCTAAGCGAAGGTTCCTCCT using SYBR green PCR Master Mix (Applied Biosystems).

**Statistical methods.** Microsoft Excel and Sigma Plot were used to analyze numerical data and generate graphs. Student’s t-test (two groups), ANOVA (multiple groups), or log rank test (longitudinal data) were applied as appropriate. Data are presented as mean ± SEM. P<0.05 was considered significant.

**Online Figures:**

**Online Figure I.** Cardiomyopathy in parkin +/- flies. Cardiomyopathy in parkin +/- flies. A. Mean group results of heart tube OCT in TincΔ4-Gal4 (Ctrl) and parkin null (+/-) flies 28 days after eclosure showing end systolic dimension (ESD) and % fractional shortening. B. Photographs of Ctrl and parkin +/- flies 7 days after eclosure; scale is mm. C. Longevity analysis of n=150 flies per group.
Online Figure II. Parkin haploinsufficiency induces cardiomyopathy that is rescued by cardiomyocyte Parkin expression. A. OCT studies of parkin +/- fly heart tubes 28 days after eclosure. B. Longevity analysis of parkin +/- fly lines (n=150 adult flies per line); control (dotted curve) and parkin +/- (50% survival) data from figure 1c are shown for comparison. C. Photographs of Ctrl, parkin +/-, and parkin +/- flies; scale is mm. D. Cardiomyocyte mitochondrial area assessed by confocal of TincΔ4-Gal4 pUAS mito-GFP; parkin +/- heart tubes. E. Heart tube fractional shortening (%FS) assessed by OCT in parkin +/- flies without and with the TincΔ4-Gal4 pUAS-Parkin transgene. Ctrl (+/+)) and TincΔ4-Gal4 pUAS-Parkin (UAS-Parkin) are shown for comparison.
Online Figure III. Sarcoplasmic reticulum (SR) calcium studies in Parkin deficient fly hearts. Top. Confocal analysis of cardiomyocyte SR structure visualized in live heart tubes with TincΔ4-Gal4-cb5-GFP (green) and TincΔ4-Gal4 mitoDSRed (red). High magnification of SR is shown on the right. Bottom. Representative sarcoplasmic calcium transients in spontaneously contracting heart tubes (top) and caffeine-stimulated (arrow) quiescent heart tubes (bottom), measured by TincΔ4-Gal4-GCaMP3 fluorescence. Group mean data of calcium transient amplitude are shown to the right.
Online Figure IV. Comparative effects of SOD1 and SOD2 on two lines of cardiac Parkin RNAi *Drosophila*. **A** and **B**. Results of OCT studies of two lines of cardiomyocyte-specific Parkin RNAi flies without (dark grey) and with (lighter grey) concomitant cardiomyocyte-specific expression of SOD1 (**A**) or SOD2 (**B**). End-systolic dimension (ESD) is on top, % fractional shortening on bottom. Park RNAi1 data are the same as shown in Figure 5, for comparison with Park RNAi2. * = significantly different from Ctrl by ANOVA and Bonferroni test.
Online Figure V. **ROS scavenging has minimal effects on the cardiomyopathy of MARF suppression.** Results of OCT studies of cardiomyocyte-specific MARF suppression, without (black bars) and with (grey bars) concomitant cardiomyocyte-specific expression of SOD1 (left) or SOD2 (right). End-systolic dimension (ESD) is on the top and fractional shortening on the bottom. * = significantly different from TincΔ4-Gal4 control; # = significantly different from MARF RNAi by ANOVA and Bonferroni test.
Online Figure VI. Cardiomyocyte mitochondrial morphology is not changed by overexpression of Parkin. Quantitative assessment of mitochondrial size in control and cardiac Parkin transgenic (TG) fly cardiomyocytes using cardiomyocyte-specific expression of mitochondrial tagged GFP as in Figures 3c and 6f. Representative confocal image of Parkin TG cardiomyocyte mitochondria is on right, showing normal size distribution. Note: OCT of Parkin TG heart tube % shortening is shown in Supplemental Figure S2e.

Online Supplement References

