Cardiovascular homeostasis dependence on MICU2, a regulatory subunit of the mitochondrial calcium uniporter


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Contributed by Christine E. Seidman, September 8, 2017 (sent for review June 26, 2017; reviewed by Kenneth E. Bernstein and Elizabeth Murphy)

Comparative analyses of transcriptional profiles from humans and mice with cardiovascular pathologies revealed consistently elevated expression of MICU2, a regulatory subunit of the mitochondrial calcium uniporter complex. To determine if MICU2 expression was cardioprotective, we produced and characterized *Micu2*−/− mice. Mutant mice had left atrial enlargement and *Micu2*−/− cardiomyocytes had delayed sarcomere relaxation and cytosolic calcium reuptake kinetics, indicating diastolic dysfunction. RNA sequencing (RNA-seq) of *Micu2*−/− ventricular tissues revealed markedly reduced transcripts encoding the apelin receptor (*Micu2*−/− vs. wild type, *P* = 7.8 × 10−6), which suppresses angiotensin II receptor signaling via allosteric transinhibition. We found that *Micu2*−/− and wild-type mice had comparable basal blood pressures and elevated responses to angiotensin II infusion, but that *Micu2*−/− mice exhibited systolic dysfunction and 30% lethality from abdominal aortic rupture. Aneurysms and rupture did not occur with norepinephrine-induced hypertension. Aortic tissue from *Micu2*−/− mice had increased expression of extracellular matrix remodeling genes, while single-cell RNA-seq analyses showed increased expression of genes related to reactive oxygen species, inflammation, and proliferation in fibroblast and smooth muscle cells. We concluded that *Micu2*−/− mice recapitulate features of diastolic heart disease and define previously unappreciated roles for *Micu2* in regulating angiotensin II-mediated hypertensive responses that are critical in protecting the abdominal aorta from injury.

**Significance**

Hypertension increases the risk for development of abdominal aortic aneurysms, a silent pathology that is prone to rupture and cause sudden cardiac death. Male gender, smoking, and hypertension appear to increase risk for development of abdominal aortic aneurysms by provoking oxidative stress responses in cardiovascular tissues. Here we uncovered unexpected linkages between the calcium-sensing regulatory subunit of the mitochondrial calcium uniporter complex. We test the hypothesis that *Micu2* is a critical responder to cardiovascular stress. From studies of *Micu2*−/− mice, we report unexpected phenotypes that link mitochondrial calcium sensing and cardiovascular stress responses.


The authors declare no conflict of interest.

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This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1711303114/-/DCSupplemental.
Results

We performed a bioinformatic screen to identify stress-responsive molecules in cardiomyopathy by intersecting differentially expressed genes from nine left ventricle (LV) transcriptome datasets: seven from human heart tissue from patients with HCM (SI Appendix, Table S1), and two from mouse models of HCM (Myh6 p.R403Q) (1) and DCM (Pth p.R9C) (27). Approximately 300 genes were differentially expressed in both mouse cardiomyopathy datasets. Intersecting this list with the seven human transcriptomes identified only 6 genes that were consistently expressed in the same direction among all nine transcriptome profiles that could plausibly function in the stress response. Three of these genes participate in pathways involving cell growth and metabolism, including IGFBP6 (insulin growth factor binding protein 6), PRKAB2 (the beta-2 non-catalytic subunit of AMP-activated protein kinase), and RHEB (a small GTPase superfamily member that functions in insulin/TOR/S6K signaling). Another gene, DAPK3 (expression of the death-associated protein kinase 3), participates in apoptosis pathways. Two mitochondrial proteins were also identified: UCP2 (mitochondrial uncoupling protein), that encodes an inner-membrane transporter, and MICU2 (mitochondrial calcium uptake 2), a regulatory subunit of the mitochondrial calcium uniporter complex that localizes to the mitochondrial intermembrane space, where it senses calcium levels to gate the activity of the mitochondrial calcium uniporter pore (28-31).

Recent studies link the mitochondrial calcium uniporter complex pore to both skeletal muscle and cardiac phenotypes. MCU is the uniporter’s pore-forming subunit that, in combination with essential MCU regulator (EMRE), forms a functional channel in vivo (32, 33). Under basal conditions, MCU-EMRE is kept in the closed position by the calcium-sensing MICU1–MICU2 heterodimer that resides in the mitochondrial intermembrane space. In response to a threshold spike in calcium, the MICU1–MICU2 complex disinhibits the pore to allow calcium entry into mitochondria. Mice lacking Muc are impaired skeletal muscle metabolism and peak performance (34, 35). Similarly, in the heart, MUCU participates in matching cardiac metabolism to contractile stress (36, 37) and also impacts heart rate (38). Although a global Muc knockout mouse and cardiac-specific Muc deficiency did not cause overt heart deficits at baseline or with isoproterenol infusion or transverse aortic constriction, rapid physiologic fight-or-flight responses were impaired (34-38). Moreover, mice expressing a dominant-negative Muc had altered cardiac oxygen utilization, cytoplasmic Ca\(^{2+}\) homeostasis, and pathologic responses to ischemia-reperfusion injury (39).

These data prompted us to prioritize MICU2 for further study. We hypothesized that if increased MICU2 expression was cardioprotective, deletion of MICU2 would promote cardiovascular dysfunction. To test this model, we generated a Micu2\(^{-/+}\) mouse using a gene-trap vector (Fig. 1A and SI Appendix, Fig. S1A). Micu2\(^{-/+}\) and Micu2\(^{-/-}\) mice bred and produced offspring in Mendelian ratios, had comparable sizes and activity levels to wild-type littermates, and routinely lived for >18 mo. Micu2\(^{-/-}\) mice had ∼50% normal levels of Micu2 transcripts in hepatic, renal, and cardiac tissue. Transcript levels were further reduced in Micu2\(^{-/-}\) mice (SI Appendix, Fig. S1B). We did not detect Micu2 protein in LV, aorta, or liver tissues from Micu2\(^{-/-}\) mice by immunoblotting (Fig. 1 B and C and SI Appendix, Fig. S2). Consistent with prior results of RNAi targeting Micu2 in mouse liver (28), both Micu1 and Muc protein levels were significantly reduced in live tissue from Micu2\(^{-/-}\) mice (SI Appendix, Fig. S2C). We also confirmed prior studies that demonstrate that Micu2\(^{-/-}\) mitochondria take up a high-concentration pulse of calcium more slowly than wild-type mitochondria (likely due to the reduction in Muc levels) (28) but more rapidly take up lower-concentration pulses of calcium (SI Appendix, Fig. S3). These data are consistent with Micu2 setting the calcium threshold for the uniporter (30). Given these findings, we concluded that Micu2\(^{-/-}\) mice had reduced levels of Micu2 protein and activity.

Cardiac structure and function of Micu2\(^{-/-}\) mice were studied by histology, electron microscopy, and longitudinal echocardiography. Myocardial cellularity, cardiomyocyte size, and myocardial fibrosis in Micu2\(^{-/-}\) and wild-type littermate mice were indistinguishable and sarcomere structure was normal (Fig. 1D). By contrast, electron microscopy revealed that in Micu2\(^{-/-}\) mice (Fig. 1E), mitochondria were 20% smaller (P = 0.003) and 5% more eccentric (P = 0.002) than mitochondria from wild-type mice. Crista structure appeared normal.

Longitudinal echocardiography revealed that Micu2\(^{-/-}\) mice had normal LV dimensions and fractional shortening (Table 1) but developed isolated left atrial (LA) enlargement at 16 to
18 mo of age (20% increased diameter, *P* = 0.01). LA enlargement can reflect the cumulative effect of increased diastolic LV pressure due to diastolic dysfunction (40, 41).

To better understand this diastolic dysfunction in mutant mice, we profiled sarcomere contractility and cytosolic calcium transients in single cardiomyocytes from three pairs of wild-type mice and *Micu2−/−* littermates (ages 6 to 8 wk). Although the extent and rate of contraction were comparable in *Micu2−/−* and wild-type cardiomyocytes, relaxation rates were slower (*P* = 0.02) in *Micu2−/−* cardiomcytes ([SI Appendix, Table S2](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/TableS2)). The magnitude of calcium flux in *Micu2−/−* and wild-type cardiomyocytes was similar; however, the time constant for calcium reuptake was increased (*P* = 0.03) in *Micu2−/−* cardiomyocytes (Fig. 2 and [SI Appendix, Table S3](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/TableS3)). From these profiles, we deduced that slower reuptake of cytosolic calcium by *Micu2−/−* cardiomyocytes could retard relaxation and contribute to diastolic dysfunction.

Next, we analyzed the LV transcriptome in 18-wk-old *Micu2−/−* and wild-type mice by RNA sequencing (RNA-seq). Among the differentially expressed genes, the sarcomeric reticulum Ca²⁺-ATPase (SERCA2a) encoded by *Atp2a2* ([Dataset S1](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/DatasetS1); *P* < 2 × 10⁻²⁰⁶) was significantly increased, likely as a compensatory response for increased cytosolic calcium in *Micu2−/−* cardiomyocytes. Database for Annotation, Visualization, and Integrated Discovery (DAVID) gene set enrichment analyses of 700 differentially expressed genes identified several gene ontologies with significant dysregulation ([Fig. 3 and Datasets S1 and S2](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/DatasetsS1S2)), including sarcomere genes (*P* = 6 × 10⁻⁶⁸), bZIP transcription factors (*P* = 1.1 × 10⁻⁴⁵), stress response genes (*P* = 0.01), and ribosomal proteins (*P* = 0.002).

We partitioned differentially expressed genes into those primarily expressed in cardiomyocytes (*n* = 64) and nonmyocytes (*n* = 89) based on greater than fivefold difference in normalized transcript levels ([42]). Differentially expressed genes found in both compartments were excluded. Notably, cell-specific pathway analysis identified enrichment in sarcomere genes (*P* = 2.5 × 10⁻⁵⁰) and oxidative phosphorylation (*P* = 3.9 × 10⁻³⁵) in cardiomyocytes and bZIP transcription factors in nonmyocytes (*P* = 2.9 × 10⁻⁶⁰). Among 1,100 genes that encode mitochondrial proteins ([43, 44]), only 46 genes were differentially expressed ([odds ratio 1.1, *P* = NS (not significant)]). Two of the most significant changes in transcripts from *Micu2−/−* LV ([Dataset S1](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/DatasetS1)) were a 1.6-fold decrease in the contractile protein gene *Myh7* (*P* < 1e⁻⁵⁰) and a 2.9-fold decrease in the apelin receptor (*Apln*: *P* = 1e⁻⁰⁴). The findings were independently confirmed by qPCR ([Fig. 3B](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/3B)). Notably, two dysregulated bZIP proteins, ATF3 (activating transcription factor 3) and C/EBP-B (CCAAT/enhancer-binding protein beta), regulate apelin expression in response to stress ([45]).

Given these transcriptional data, we hypothesized that *Micu2−/−* mice would be particularly sensitive to angiotensin II, since the apelin receptor suppresses angiotensin II type 1 receptor signaling via allosteric transinhbitition ([46, 47]). As angiotensin II stimulates cardiac hyper trophy ([48]), we also expected that this provocation could increase diastolic dysfunction in *Micu2−/−* mice. Homozygous *Micu2−/−* mice, heterozygous *Micu2+/−* mice, and wild-type littermates were infused with 1.2 mg kg⁻¹·d⁻¹ of angiotensin II to increase systolic blood pressure over baseline by 25 mmHg (*P* < 0.001; [SI Appendix, Fig. S4](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/SIAppendix)). After 2 wk of treatment, all mice showed increased expression in sarcomere wall thickness, suggesting a comparable degree of hypertrophic remodeling (Table 2). However, *Micu2−/−* and *Micu2+/−* but not wild-type mice had significantly increased fractional shortening in comparison with baseline (*P* = 0.04 and *P* = 0.002, respectively).

Unexpectedly, 3 of 14 *Micu2−/−* but no wild-type mice died during angiotensin II infusion (*P* = 0.03; [Fig. 4A](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/4A)). Autopsies revealed that all three had ruptured abdominal aortic aneurysms, we extended these studies to assess whether loss of *Micu2* impacted blood pressure and stress-induced vascular responses. Infusion of low (1.2 mg kg⁻¹·d⁻¹) or high (2.4 mg kg⁻¹·d⁻¹) doses of angiotensin II showed dose-dependent but equivalent increases in blood pressure in both *Micu2−/−* and wild-type mice ([SI Appendix, Fig. S4](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/SIAppendix)).

Abdominal ultrasonography of untreated *Micu2−/−* mice (*n* > 8) showed slightly larger (5%) aortic artery diameters than wild-type mice (*P* = 0.003). Neither low nor high doses of angiotensin II infusion altered abdominal aortic diameters in wild-type mice, but *Micu2−/−* mice had dose-dependent increases in aortic diameters (*P* = 0.0006; [Fig. 4B](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/4B)). Excluding mice with aortic rupture, a conservative estimate of the angiotensin II-induced aortic dilatation was at least 4.5-fold increased in *Micu2−/−* compared with wild-type mice.

Serial analyses of high-dose angiotensin II infusions revealed 10% increased abdominal aortic dimensions at day 2 in both *Micu2−/−* and wild-type mice. At day 4 and thereafter, aortic dimensions of wild-type mice remained unchanged while *Micu2−/−* mouse aortas continued to enlarge (*P* = 0.005; [Fig. 4C](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/4C) and [SI Appendix, Table S4](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/SIAppendix)).

To consider if this vascular pathology was blood pressure-mediated or angiotensin II-specific, we treated mice with norepinephrine (5.6 mg kg⁻¹·d⁻¹). Using norepinephrine to increase blood pressures to equivalent levels induced by low-dose angiotensin II ([SI Appendix, Fig. S4](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/SIAppendix)) did not induce aortic aneurysms in *Micu2−/−* or wild-type mice ([Fig. 4B](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/4B)).

Table 1. Echocardiographic assessment of cardiac structure and function in aged *Micu2−/−* mice

<table>
<thead>
<tr>
<th></th>
<th>WT (SD)</th>
<th><em>Micu2−/−</em> (SD)</th>
<th><em>P</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>Left atrial diameter, mm</td>
<td>1.46 (0.06)</td>
<td>1.76 (0.08)</td>
<td>0.01</td>
</tr>
<tr>
<td>Interventricular septum, mm</td>
<td>0.92 (0.02)</td>
<td>0.87 (0.03)</td>
<td>0.11</td>
</tr>
<tr>
<td>Posterior wall, mm</td>
<td>0.82 (0.04)</td>
<td>0.85 (0.02)</td>
<td>0.43</td>
</tr>
<tr>
<td>LV diameter, mm</td>
<td>3.32 (0.18)</td>
<td>3.48 (0.17)</td>
<td>0.53</td>
</tr>
<tr>
<td>Fractional shortening, %</td>
<td>49 (4.0)</td>
<td>48 (2.0)</td>
<td>0.97</td>
</tr>
</tbody>
</table>

Statistics are means (SD). *P* values were calculated from a two-sided t test with five or six animals, age 15 to 18 mo, in each group.

![Fig. 2. Functional analysis of isolated *Micu2−/−* cardiomyocytes. Representative tracings of (A) single-myocyte sarcomere length (plotted as % of resting length) and (B) calcium flux (plotted as normalized Fura-2 intensity) in *Micu2−/−* mice and wild-type littermates. *Micu2−/−* cardiomyocytes had slower repolarization kinetics, as evidenced by both decreased sarcomere relaxation velocity (A, Inset) and increased time constant (tau, the exponential decay of the ventricular pressure during isovolumic relaxation) for calcium reuptake (B, Inset) compared with wild-type cardiomyocytes (*Micu2+/−*, *n* = 22 cells; wild type, *n* = 31 cells; t test). Error bars denote standard deviation.](https://www.pnas.org/lookup/suppl/doi:10.1073/pnas.202010192/-/DCSupplemental/2)
Aneurysms arise from abnormalities of the intima, media, or adventitial layers of vascular beds that include fibroblast, smooth muscle, and endothelial cells. As histopathology of aortic aneurysms from $\text{Micu2}^{-/-}$ mice did not implicate a vascular layer or cell lineage (Fig. 4A, Inset), we attempted to deconvolute transcriptional changes by single-cell RNA-seq (49). From angiotensin II-treated $\text{Micu2}^{-/-}$ and wild-type aortas, we isolated 60 smooth muscle and fibroblast cells ($\text{SI Appendix}$, Fig. S6A) and 10 endothelial cells (likely due to smaller cell diameters that escaped microfluidic capture chips). The relative distribution of captured cell types was the same in $\text{Micu2}^{-/-}$ and wild-type aortas ($P = NS$).

Among aortic cells from wild-type mice, the distribution of $\text{Micu2}$ expression did not differ by cell type ($P = NS$). $\text{Micu2}$ was robustly expressed in 50% of endothelial, 23% of smooth muscle, and 18% of fibroblast cells, indicating that $\text{Micu2}$ deficiency could affect each cell lineage.

Two patterns of altered gene expression were observed: differences in the absolute expression levels (quantitated by a Wilcoxon test on median differences; $\text{SI Appendix}$, Fig. S6B) and differences in the number of cells expressing an appreciable level of genes (quantitated with a Fisher test; $\text{SI Appendix}$, Fig. S6C). Too few endothelial cells were captured to identify genes exceeding the significance threshold (Bonferroni adjustment for significance was set at $P < 10^{-4}$ to reflect 5,000 expressed genes), but differential expression was identified in six smooth muscle cell genes and five fibroblast genes.

Among the six genes differentially expressed in $\text{Micu2}^{-/-}$ smooth muscle cells, we observed increased expression of genes associated with inflammation and reactive oxygen species (ROS) ($\text{SI Appendix}$, Figs. S6 B and C). Significantly more $\text{Micu2}^{-/-}$ (96%) than wild-type (29%) smooth muscle cells expressed extracellular glutathione peroxidase ($\text{Gpx3}$), the inflammatory cytokines $\text{Tnf}$ and $\text{Ccl11}$, and the transcription factor $\text{If2}$, which is associated with inflammation (50). Although the majority of $\text{Micu2}^{-/-}$ and wild-type smooth muscle cells expressed metallothionein (Mt1) that contributes to cardiovascular protection in high-ROS states (51), the median expression was ninefold higher in $\text{Micu2}^{-/-}$ smooth muscle cells ($P = 7.5 \times 10^{-9}$).

The five differentially expressed genes in $\text{Micu2}^{-/-}$ fibroblasts are involved in proliferation, inflammation, and ROS ($\text{SI Appendix}$, Figs. S6 B and C). More $\text{Micu2}^{-/-}$ fibroblasts (80%) than wild-type fibroblasts (10%) expressed the proproliferative transcription factor $\text{Myc}$ ($P = 1.5 \times 10^{-5}$) (52). Most $\text{Micu2}^{-/-}$ (88%) but few wild-type (10%) fibroblasts expressed $\text{Epm1}$, which induces EGFR autophosphorylation and activates cell adhesion and migration ($9.6 \times 10^{-5}$) (53–55). $\text{Micu2}^{-/-}$ fibroblasts also showed significant differential gene expression of inflammatory and ROS genes, including decreased expression of $\text{Pmo3}$ and $\text{Sod3}$, which reduce ROS free radicals (56, 57), and increased expression of the inflammatory mediator $\text{Il6}$ (58).

**Table 2. Cardiac structure and function in $\text{Micu2}^{-/-}$ mice after 2 wk of angiotensin II treatment**

<table>
<thead>
<tr>
<th></th>
<th>WT (SD)</th>
<th>$\text{Micu2}^{-/-}$ (SD)</th>
<th>$P$</th>
</tr>
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<tbody>
<tr>
<td>Systolic blood pressure, mmHg</td>
<td>141 (9.8)</td>
<td>142 (9.8)</td>
<td>0.94</td>
</tr>
<tr>
<td>Intraventricular septum, mm</td>
<td>0.89 (0.02)</td>
<td>0.82 (0.06)</td>
<td>0.28</td>
</tr>
<tr>
<td>Posterior wall, mm</td>
<td>0.82 (0.04)</td>
<td>0.82 (0.02)</td>
<td>0.99</td>
</tr>
<tr>
<td>LV diameter, mm</td>
<td>3.25 (0.11)</td>
<td>3.58 (0.15)</td>
<td>0.09</td>
</tr>
<tr>
<td>Fractional shortening, %</td>
<td>36 (1.2)</td>
<td>28 (1.9)</td>
<td>0.006</td>
</tr>
<tr>
<td>Systolic strain, %</td>
<td>$-19.3$ (2.1)</td>
<td>$-13.8$ (2.5)</td>
<td>0.007</td>
</tr>
</tbody>
</table>

Statistics are mean (SD). $P$ values were calculated from a two-sided $t$ test with four to eight male mice, age 6 to 8 wk, in each group following 2 wk of angiotensin II infusion (1.2 mg kg$^{-1}$ d$^{-1}$).
cardiovascular homeostasis in health and disease. Loss of Micu2 produced cardiac diastolic dysfunction with LA enlargement, abnormalities that are likely secondary to delayed calcium reuptake and decreased relaxation rates by cardiomyocytes. Micu2 depletion did not significantly alter gene expression of Mcu or Micu1, but protein levels of both were reduced. Hence, the cellular consequences of Micu2 loss are attributable to the combination of two effects: (i) a decrease in the threshold for mitochondrial calcium uptake due to loss of the gatekeeping activity of Micu2; and (ii) overall loss of mitochondrial calcium uptake by the uniporter due to destabilization of Mcu and the entire complex. Moreover, changes in protein levels of Mcu and Micu1 after genetic ablation of Micu2 indicate that homeostatic interactions among components of the mitochondrial calcium uniporter complex may be important for stability. The resultant altered calcium dynamics was associated with pathologic transcriptional signatures in cardiomyocytes and nonmyocytes. Gene expression in Micu2−/− hearts was characterized by sarcomere dysregulation, stress response pathways, and altered expression of sarcomere genes and the bZIP family of transcription factors, molecules that contribute to cardiomyopathy pathogenesis and that regulate apelin signaling (2, 3, 59, 60).

In the setting of cardiovascular disease, Micu2 expression was particularly important. Hypertensive Micu2−/− mice had both diastolic and systolic dysfunction, as evidenced by decreased fractional shortening and altered systolic strain measurements. Despite these functional abnormalities, LV dimensions in Micu2−/− mice remained normal. As such, hypertensive Micu2−/− mice may provide a first step toward the development of an animal model for heart failure with preserved ejection fraction, a prevalent and poorly understood human disease (61).

The molecular mechanisms for diastolic dysfunction are incompletely understood. At the cellular level, cardiomyocyte relaxation requires tightly bound actin–myosin filaments to detach, a process mediated in part by calcium removal. Reduced or delayed calcium reuptake into the sarcoplasmic reticulum (SR) or mitochondria or removal from cardiomyocytes can delay relaxation (62). In addition, abnormal mitochondrial calcium homeostasis can influence NADPH levels and the redox state of cardiomyocytes to perturb relaxation. Consistent with these observations, malfunction of multiple calcium-handling proteins propel heart failure, including SERCA2a and its modulator phospholamban (PLB), the SR Ca2+ release channel and its modulator FKBP12.6 protein 12.6 (FKBP12.6), and the sodium–calcium exchanger (63–66).

We suggest that Micu2 contributes to restoration of diastolic calcium levels by sensing cytosolic levels and dynamically gating calcium uptake of the mitochondrial calcium uniporter, similar to activities of PLB or FKBP12.6 proteins. Consistent with this model, we note that hepatocyte mitochondria from Micu2−/− mice, which lack multiple calcium-buffering mechanisms, uptake high concentrations of calcium significantly more slowly than wild-type mitochondria (28), likely due to destabilization of the entire channel complex. While cardiomyocytes have multiple pathways to remove high concentrations of calcium that occur with each contraction, fine-tuning by mitochondrial calcium uptake may also be important in cardiac calcium dynamics and could account for the decreased cytosolic calcium reuptake that we observed in Micu2−/− cardiomyocytes.

Several recent studies have probed how changes in components of the mitochondrial calcium uniporter complex regulate and integrate mitochondrial and cellular calcium homeostasis (29, 67). Micu2-null mice on an isogenic C57/B6 background are viable and have minimal basal abnormalities, whereas Micu1-null mice on an isogenic C57/B6 background exhibit perinatal mortality due to mitochondrial calcium overload (68, 69). A challenge in interpreting the consequences of genetic loss of one of these subunits is that they can cross-stabilize each other in a tissue-specific manner. The consensus in the field is that Micu1 functions as an essential gatekeeper that regulates calcium influx into the mitochondria (70). The inhibitory activity of

**Discussion**

Our data establish a critical role for Micu2, and presumably the mitochondrial calcium uniporter channel complex, in maintaining

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**Fig. 4.** Micu2−/− mice are susceptible to angiotensin II (Ang2)-induced aortic aneurysms. (A) In response to angiotensin II (1.2 mg/kg, *P* = 0.03) infusion, Micu2−/− mice had abdominal aortic aneurysms and 30% of mice had lethal ruptures. (A, Inset) Representative abdominal aorta histological sections after 2 wk of angiotensin II infusion demonstrated grossly similar histologic patterns. Electron microscopy of Micu2−/− mouse aorta and liver showed no mitochondrial abnormalities (SI Appendix, Fig. S5). (B) Abdominal aortic (AbAo) diameter measured at baseline and 2 wk after angiotensin II infusion identified slightly enlarged diameters in Micu2−/− mice (*n* > 10) at baseline that was exaggerated with increasing angiotensin II dose (2.4 mg/kg). Aorta diameter did not change in response to norepinephrine. (C) Serial measurements of Micu2−/− and wild-type mice showed differential aortic enlargement by day 4 of angiotensin II infusion (2.4 mg/kg) (*n* = 5 mice, *t* test at each time point). Bars indicate standard deviation.
Transcriptional dissection of aortic aneurysm. (Values are shown. mice (3) compared with wild-type mice (n = 3) identified gene sets with increased (shaded bars) and decreased (clear bars) expression. GF, growth factor. Bonferroni-corrected P values are shown. (B) RNA-seq pathway enrichment analysis of mouse aorta tissue after angiotensin II infusion (1.2 mg/kg for 2 wk) identified three notable changes in gene sets. (C) Fold change of selected genes with known roles in aneurysm formation after angiotensin II (1.2 mg/kg) versus basal state with significant differential expression by RNA-seq.

Micu2 is dependent on its physical association with Micu1. At low calcium concentrations, heterodimers between Micu1 and Micu2 negatively regulate calcium import by Mcu, while at high calcium concentrations, the Micu1–Mico2 inhibition is relieved and calcium uptake occurs (31). Oxidative stress imposes further modification of a cysteine residue in Mico2 that results in conformational changes of the pore-forming unit and persistent mitochondrial uptake of calcium (71). Responses to changes in the mitochondrial calcium uniporter complex further impact calcium homeostasis. For example, marked depletion (80%) of Mico2 expression in cardiomyocytes reduces the activity and expression of the mitochondrial sodium–calcium exchanger, so as to maintain normal cytosolic calcium (36). By contrast, cytosolic calcium is increased in cardiomyocytes that chronically express a dominant-negative Mico2 construct (39) or, as described here, lack the pore’s inhibitory subunit Micu2, without changes in the expression of the mitochondrial sodium–calcium exchanger but with increased SERCA2a activity (39) or expression (Dataset S1). Collectively, these data point to the multiple integrated mitochondrial and cytosolic strategies to maintain calcium homeostasis in cardiomyocytes and other cells.

Our studies uncovered unexpected and critical roles for physiological regulation of the mitochondrial calcium uniporter complex to maintain calcium homeostasis in vascular tissues. In the setting of angiotensin II-induced hypertension, Micu2−/− mice were prone to lethal abdominal aortic aneurysms. Transcriptional profiles of the Micu2−/− aorta implicated molecules and pathways known to promote aneurysm formation, including the proinflammatory state, increased extracellular matrix remodeling, and cellular proliferation (72–76). Matrix metalloproteinase 3 (Mmp3), which degrades collagen, fibronectin, laminin, and elastin, had significantly increased expression (77). Mmp3 gene polymorphisms are associated with aneurysm formation in human patients (78, 79), and deletion of Mmp3 in mice reduces aneurysm formation (74). The expression of Col3a1 and Col2a1, molecules that cause vascular disease in Ehlers–Danlos syndrome (80–82), were increased in angiotensin II-treated Micu2−/− mice, a finding suggestive of active collagen degradation from increased Mmp3 expression. Angiotensin II increased the expression of other genes implicated in human aneurysms, most notably Fbn1 (tibrillin-1, mutated in Marfan syndrome) and Tgfβ2 (transforming growth factor beta-2, mutated in Loehs–Dietz syndrome) (83–85).

Two calgranulins, S100a8 and S100a4, that were decreased in untreated Micu2−/− mice and increased after angiotensin II infusion were well-calcium to directly link altered calcium flux to aneurysm. Calgranulins are a family of small acidic calcium signaling proteins that promote inflammation and vascular disease by activating the receptor for advanced glycation end products (RAGE) (86), and are linked to vascular dysfunction and atherosclerosis (87, 88). S100a4 is strongly up-regulated in human thoracic aortic aneurysms (89) and intracranial aneurysms (90). Mechanistically, silencing S100a4 decreases vascular smooth proliferation and matrix metalloproteinase expression (89).

Notably, Micu2−/− mice did not develop aneurysms in the setting of norepinephrine-induced hypertension, a finding that implicates angiotensin II-specific signaling. Angiotensin II has been shown to activate noncanonical TGFβ signaling (ERK1/2) via protein kinase C (83–85, 91–93). Recent studies of Fbn1−/− mice (modeling Marfan syndrome) treated with calcium channel blockers had accelerated thoracic aortic aneurysm expansion and rupture through a protein kinase C-mediated pathway, further implicating cross-talk between calcium signaling, TGFβ, and aneurysms (94). Clinical evidence also supports the link between calcium and aneurysm formation. A retrospective study of human patients identified the use of calcium channel blockers as an independent risk factor for abdominal aortic aneurysms (95). These data and our findings motivate further investigations into mitochondrial calcium homeostasis and aneurysm formation.

Angiotensin II and loss of the Micu2 paralog and binding partner Micu1 can trigger oxidative stress and vascular dysfunction (96, 97). These data, combined with our transcriptional analyses, implicate oxidative stress in the pathogenesis of aneurysm in angiotensin II-treated Micu2−/− mice. While atherogenic mice are thought to develop abdominal aortic aneurysms via reactive oxygen species (98, 99), the Micu2−/− mice described here implicate abnormal mitochondrial calcium handling. It is notable that these two pathways, oxidative stress and mitochondrial calcium transport by the uniporter, have recently been mechanistically linked at a molecular level (71, 100). Further elucidation of the mitochondrial molecules and pathways that impact stress-induced calcium signaling are expected to further insights into disease pathogenesis and perhaps uncover novel therapeutic strategies to treat abdominal aortic aneurysms.

Materials and Methods

The Micu2 mice were derived from the gene-trap allele (Micu2; OST409343) that was generated by the Texas A&M Institute for Genomic Medicine. The
Vitr 37 viral plasmid was used to insert a splice acceptor, β geo (I-galactosidase/neomycin) cassette, synthetic polyA signal transfection blocker, and PGK promoter/BTK exonic donor cassette, all flanked by two viral long-terminal repeat segments in-between exons 4 and 5 of the Micu2 locus. Mice were derived and backcrossed onto the C57/B6 background for >10 generations. All animal experiments and procedures were reviewed and approved by the Institutional Animal Care and Use Committee at Harvard Medical School.

Immunobots. Immunobots were performed using antibodies from Sigma (Micu1, Micu, actin), Abcam (HPRE6, ATP5a), and BD Biosciences (TIIIM23). Antibodies against Micu2 and HIE were produced in collaboration with Bethyl.

Mouse Liver Mitochondrial Isolation and Calcium Uptake Analysis. Mitochondria were isolated from mouse liver using differential centrifugation as previously described (28) and resuspended in 220 mM mannitol, 75 mM sucrose, 10 mM Heps (pH 7.4), 1 mM EDTA, and 0.2% BSA and kept on ice. Calcium uptake assays were performed by adding 120 μg mitochondria to 150 μL buffer containing 125 mM KCl, 2 mM K2HPO4, 1 mM MgCl2, 20 mM Heps at pH 7.2, 5 mM glutamate and malate, and 1 μM Oregon Green- Bapta6F. Fluorescence was monitored using a PerkinElmer Envision plate reader in response to various pulses of CaCl2. The relative rate of calcium uptake is reported using a linear fit of fluorescence from 30 to 40 s (n = 3).

Mouse Echocardiography and Abdominal Ultrasoundography. Mice were anesthetized with an isoflurane vaporizer (VetEquip), and each limb was placed on an ECG leads on a Vevo Mouse Handling Table (VisualSonics), maintaining the body temperature at 37 °C during the study. Transthoracic echocardiography and transabdominal ultrasoundography were performed using the Vevo 2100 High-Resolution In Vivo Micro-Imaging System and MS550D transducer (VisualSonics), with heart rate at 500 to 550 beats per min. The images were acquired as 2D (left parasternal long and short axes), M-mode (left parasternal short axis), speckle tracking, and transabdominal 2D measurements. Measurements were averaged from images acquired during three consecutive heart beats. All echocardiogram and sonogram measurements were performed with an experienced operator blinded to mouse genotype. Differences between groups of mice were determined using the unpaired Student’s t test.

Single-Cardiomyocyte Functional Profiling. Ventricular cardiomyocytes from three pairs of adult wild-type and Micu2−/− littermates at 6 to 8 wk of age, on 3 separate days, were isolated via a Langendorff-perfused heart preparation using enzymatic digestion as previously described (101). After isolation, the cells were suspended in Tyrode’s buffer with gradually increasing Ca2+ concentrations (0.06, 0.6, and 1.2 mM, pH 7.4 at room temperature) and loaded with 2 μM Fura-2 AM calcium indicator (Molecular Probes) as previously described (102). Myocytes were washed three times for 10 to 15 min with 1.2 mM Ca2+ Tyrode’s solution containing 250 μM probenecid to retain the indicator in the cytosol. The experiments were then performed at room temperature in 1.2 mM Ca2+ Tyrode’s solution containing 140 mM NaCl, 4.5 mM KCl, 0.5 mM MgCl2, 5 mM glucose, and 10 mM Hepes, pH adjusted to 7.4 with NaOH.

Cardiomyocytes were electrically paced at 60 beats per min via platinum wires. Sarcomere shortening/relengthening and Fura-2 fluorescence ratios (which reflect the intracellular calcium transients) were simultaneously recorded and determined from discrete striation positions on the myocyte wires. Sarcomere shortening/relengthening and Fura-2 fluorescence ratios (which reflect the intracellular calcium transients) were simultaneously recorded and determined from discrete striation positions on the myocyte using a dual-excitation fluorescence imaging/contractility recording system (IonWizard SarcLen detection and PMT acquisition fluorescence system; IonOptix). Sarcomere length and Ca2+ transients were analyzed using IonOptix transient analysis software. Myocytes included in the study were rod-shaped with a clear striation pattern, quiescent in the absence of electrical stimulation, and with a resting sarcomere length of more than 1.6 μm. At least seven myocytes were profiled from each animal. Statistical analysis was performed with a two-sample, one-tailed Student’s t test.

Electron Microscopy. LV tissue from three pairs of wild-type and Micu2−/− littermates at 18 wk of age were evaluated in a blinded fashion with seven repeat observers. Some fields per mouse imaged at 1,900× resolution on a Tecnai G2 Spirit BioTWIN transmission electron microscope (FEI). The average mitochondrial size and eccentricity were automatically quantified with CellProfiler (Broad Institute).

Pharmacologic Manipulation with Angiotensin II. Hypertension was induced in mice by chronic infusion with angiotensin II (Sigma-Aldrich) dissolved in saline at 1.4 mg·kg−1·d−1 or 2.8 mg·kg−1·d−1 or norepinephrine dissolved in saline at 5.6 mg·kg−1·d−1, via an osmotic minipump for 2 wk (103).

Blood Pressure Measurement. Systolic blood pressure was measured in trained conscious mice, maintained at normal body temperature, using a BP-2000 Analysis System (Visitech Systems) as previously described (104). Mice were “trained” to the procedure twice daily for 3 consecutive days, and data were recorded over the following 2 d. Statistical analyses are from 10 readings for each mouse.

Transcriptome-Wide Analyses. Human tissue samples from HCM patients were obtained from study participants undergoing either myectomy heart surgery, cardiac transplant surgery, or valve replacement surgery with informed consent, using IRB-approved protocols at Brigham and Women’s Hospital. RNA from human tissues and mouse LV was prepared and RNA-seq libraries were constructed and analyzed as previously described (105). Uniform amplification of the cDNA library was achieved with amplification cycling before the reaction reached saturation, as determined by quantitative PCR. Aorta RNA-seq libraries were constructed with the Nextera library preparation method (106). To reduce biological variation in mouse specimens, RNA was pooled from three biological replicates for LV samples and angiotensin II-treated aorta samples. For the basal aorta RNA-seq samples, libraries from three biological replicates for each genotype (Micu2−/− and wild type) were constructed and the libraries were sequenced individually.

Libraries were sequenced on an Illumina HiSeq 2000 sequencer with 50-bp paired-end reads. Following sequencing, alignment of reads to the mm10 genome was performed with Bowtie and TopHat (107). Gene expression profiles were constructed by tallying reads on gene loci, using a Bayesian P value to assess the significance of gene expression differences between pooled samples (108). Cuffdiff 2 was used for assessing the significance of gene expression differences in aorta RNA-seq library replicates (109). Genes were considered differentially expressed if there was >40% increase or decrease in fold change with P < 10−3. The DCM mouse model and HCM mouse model transcriptome datasets were previously described (110, 111).

Gene ontology pathway enrichment analysis was performed with DAVID (112).

Single-Cell RNA-Seq. Mouse aortas were dissected and digested into single cells using collagenase. Cells were captured, and RNA was extracted and amplified into cDNA libraries using the Fluidigm C1 system as previously described (113). Libraries were sequenced on an Illumina HiSeq 2000 sequencer with 50-bp paired-end reads. Reads were aligned using TopHat. The expression of known markers for vascular lineages was used to classify each cell as a smooth muscle cell (Acta2, Tagln, Myh11), fibroblast (Vim), or endothelial cell (Pecam1, Tek, Cad5). Cells lacking any of these markers were classified as “undetermined.” Wilcox and Fisher test P values were calculated in the R statistical computing environment, version 2.15.0 (www.r-project.org).

ACKNOWLEDGMENTS. We thank Dr. Richard Mitchell for helpful discussions. A.G.B. was supported by NIH Graduate Fellowship T32GM007753. K.J.K. was supported by a graduate research fellowship from the National Science Foundation. Y.S. received support from the Helen Hay Whitney Foundation. This work was supported by a gift from W. Dan and Pat Wright (to V.K.M.) and grants from Fondation Leducq (to J.G.S. and C.E.S.) and the Howard Hughes Medical Institute (to V.K.M. and C.E.S.).


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