Overexpression of Catalase Targeted to Mitochondria Attenuates Murine Cardiac Aging

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Background—Age is a major risk factor for cardiovascular diseases. Although mitochondrial reactive oxygen species have been proposed as one of the causes of aging, their role in cardiac aging remains unclear. We have previously shown that overexpression of catalase targeted to mitochondria (mCAT) prolongs murine median lifespan by 17% to 21%.

Methods and Results—We used echocardiography to study cardiac function in aging cohorts of wild-type and mCAT mice. Changes found in wild-type mice recapitulate human aging: age-dependent increases in left ventricular mass index and left atrial dimension, worsening of the myocardial performance index, and a decline in diastolic function. Cardiac aging in mice is accompanied by accumulation of mitochondrial protein oxidation, increased mitochondrial DNA mutations and deletions and mitochondrial biogenesis, increased ventricular fibrosis, enlarged myocardial fiber size, decreased cardiac SERCA2 protein, and activation of the calcineurin–nuclear factor of activated T-cell pathway. All of these age-related changes were significantly attenuated in mCAT mice. Analysis of survival of 130 mice demonstrated that echocardiographic cardiac aging risk scores were significant predictors of mortality. The estimated attributable risk to mortality for these 2 parameters was 55%.

Conclusions—This study shows that cardiac aging in the mouse closely recapitulates human aging and demonstrates the critical role of mitochondrial reactive oxygen species in cardiac aging and the impact of cardiac aging on survival. These findings also support the potential application of mitochondrial antioxidants in reactive oxygen species–related cardiovascular diseases. (Circulation. 2009;119:2789-2797.)

Key Words: aging ■ diastole ■ mitochondria ■ oxidant stress ■ survival

Cardiovascular diseases are highly prevalent in the geriatric population. Age is a major risk factor for cardiovascular disease, at least in part because it prolongs exposure to hypertension, diabetes mellitus, hypercholesterolemia, and other cardiovascular risks. However, intrinsic cardiac aging, the slowly progressive structural changes and functional declines with age, also makes the heart more susceptible to stress and contributes to increased cardiovascular mortality and morbidity in the elderly.

Clinical Perspective on p 2797

Epidemiological data from the Framingham Heart Study and the Baltimore Longitudinal Study on Aging showed that in healthy populations there is an age-dependent increase in the prevalence of echocardiographic left ventricular (LV) hypertrophy, a decline in diastolic function, relatively preserved systolic function (ejection fraction) at rest, but a decline in exercise capacity (maximal ejection fraction) and an increased prevalence of atrial fibrillation.1 LV hypertrophy is well known to increase the risk of coronary heart disease, stroke, and sudden death. Diastolic heart failure, heart failure with diastolic dysfunction but preserved systolic function, plays a major role in congestive heart failure and exercise intolerance in the elderly population. Given demographic projections, heart failure is likely to become the major cause of hospital admissions and mortality in North America.2

According to the mitochondrial variant of the free radical theory of aging, reactive oxygen species (ROS) produced mainly in the mitochondria attack mitochondrial constituents, causing mitochondrial DNA (mtDNA) damage and mitochondrial dysfunction, leading to further production of ROS, increases in oxidative damage to lipids and proteins, and declines in cellular and organ function that contribute to death.3 We have recently shown that although both point mutations and deletions in mtDNA...
accumulate with aging, mtDNA deletions are likely to drive the aging process. As a vital organ rich in mitochondria and high in oxygen use, the heart is especially prone to oxidative damage. Together with the fact that cardiovascular diseases are the leading cause of death in humans, we hypothesized that in the absence of other cardiovascular risks, cardiac aging is a predictor of mortality.

In this report, we have made use of a transgenic mouse model in which catalase is overexpressed and targeted to mitochondria (mCAT) to clearly define cardiac aging phenotypes in a murine model of aging and investigate their plausible molecular mechanisms, to investigate the impact of reductions in mitochondrial ROS on cardiac aging, and to investigate the impact of cardiac aging on all-cause mortality.

Methods

See the online-only Data Supplement for additional details.

Animal Longevity Cohort and Echocardiography

C57Bl6 mice in the longevity cohort were maintained as described. This study included a cross-sectional sample of 170 mice from this cohort, with 20 to 30 mice in each group. Mice were not subjected to any invasive experimentation other than echocardiography. Echocardiography was performed with an Acuson CV-70 (Siemens Medical Systems, Malvern, Pa) using standard imaging planes: M-mode, conventional, and tissue Doppler imaging. All protocols were approved by the University of Washington Institutional Animal Care and Use Committee.

Biochemical and Molecular Analysis

Gene expression, mtDNA copy number, and mutation frequency assays were performed with quantitative polymerase chain reaction. Mitochondrial protein carbonyl and calcineurin activity assays were determined with commercial kits. Measurement of cardiac angiotsins was performed with a tandem quadruple mass spectrometry coupled to high-performance liquid chromatography. For study of calcium transients, cardiomyocytes were isolated by an enzymatic method, loaded with Fluo-4, and electrically stimulated at 1 Hz. Calcium transient fluorescence was collected with an IonOptix system (IonOptix, Milton, Mass).

Statistics and Survival Analysis

Continuous variables with normal distribution are presented as mean ± SEM. Those significantly skewed are presented as box plots (median, 25%, 75%) with an x within the box to indicate the mean. Standard t tests, ANOVA, and linear regression were applied as appropriate to detect the statistical differences between genotypes or age groups. Probability values were shown uncorrected for multiple testing. To be more conservative, a Bonferroni correction (n = 2) can be applied to t test comparisons between young wild-type (WT) and old WT and between old WT and old mCAT groups, after which P < 0.025 would be considered significant. To investigate the effect of cardiac aging on survival, we chose variables representing structure (LV mass index [LVMI]) and function (myocardial performance index [MPI]) a priori to create a cardiac aging risk score. Univariate Cox regression was used to verify a strong association between these variables and mortality. We then included both age-adjusted functional decline (MPI) and structural changes (LVMI) in a multivariate analysis to generate the semiparametric maximum likelihood estimate of the best-fitting linear combination of MPI and LVMI score in predicting subsequent mortality (β2 MPI + β3 LVMI in model 1 in the Table). We define this linear combination as the cardiac aging risk score; Kaplan–Meier curves stratified on the risk score tertiles are used to illustrate the differences in risk as the score increases. Log-rank test probability values serve

### Table. Cox Regression Models Predicting Mortality

<table>
<thead>
<tr>
<th>Predictors</th>
<th>Hazard Ratio</th>
<th>P</th>
<th>95% CI</th>
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<tbody>
<tr>
<td>Univariate Cox model</td>
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<td></td>
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<tr>
<td>Age, mo</td>
<td>1.18</td>
<td>&lt;0.001</td>
<td>1.11–1.26</td>
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<td>Men vs women</td>
<td>1.20</td>
<td>0.46</td>
<td>0.74–1.94</td>
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<tr>
<td>MPI,† (0.1 unit)</td>
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<td>&lt;0.001</td>
<td>1.16–1.58</td>
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<td>LVMI,† mg/g</td>
<td>1.44</td>
<td>0.002</td>
<td>1.15–1.80</td>
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<tr>
<td>Multivariate Cox model 1</td>
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<tr>
<td>Age, mo</td>
<td>1.15</td>
<td>&lt;0.001</td>
<td>1.07–1.23</td>
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<tr>
<td>MPI,† (0.1 unit)</td>
<td>1.26</td>
<td>0.005</td>
<td>1.07–1.48</td>
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<tr>
<td>LVMI,† mg/g</td>
<td>1.12</td>
<td>0.41</td>
<td>0.86–1.45</td>
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<tr>
<td>Age, mo</td>
<td>1.16</td>
<td>&lt;0.001</td>
<td>1.09–1.24</td>
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<tr>
<td>Cardiac aging score T2‡</td>
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<td>0.067</td>
<td>0.96–3.39</td>
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<tr>
<td>Cardiac aging score T3‡</td>
<td>2.88</td>
<td>0.003</td>
<td>1.43–5.82</td>
</tr>
</tbody>
</table>

*The hazard ratio rises by a factor of 1.35 for every 0.1-unit difference in MPI.
†Hazard ratios associated with LVMI are calculated as for MPI.
‡Cardiac aging risk score = β2 MPI + β3 LVMI, calculated from the multivariate Cox model 1, and presented as the middle (T2) or high (T3) vs lower (T1) tertile.

as descriptive statistics for the strength of the differences in survival between tertiles. To approximate the attributable risk fraction of cardiac aging on mortality, we calculated the difference between the incidence of the all-cause mortality rate of mice with risk scores in the highest tertile and the incidence in those with scores in the middle and lowest tertiles.

Results

MCAT Attenuates the Cardiac Aging Phenotype

There were no differences in body weight or food consumption between mCAT and WT mice. There were no significant differences with age or genotype in blood pressure, heart rate, pulse pressure, fasting plasma glucose, or total cholesterol in the mouse longevity cohort (Table I of the online-only Data Supplement). This is consistent with a low incidence of conventional cardiovascular risks in these C57Bl6 mice.

Echocardiography was performed in 90 mCAT and 80 WT littermate mice across a wide range of ages in a mouse longevity cohort. Despite the absence of cardiovascular risk factors, we found significant age-dependent linear trends for all parameters (P < 0.001 for all except fractional shortening, P = 0.005). LVMI (Figure 1A) was 76% higher in the oldest group compared with the young adult group. Left atrial dimension was significantly increased by 35% with age (Figure 1B). Systolic function measured by fractional shortening showed a 12% decline from young adult to the oldest group (Figure 1C). Tissue Doppler imaging revealed an age-dependent decline in Ea/Aa, from 1.69 ± 0.3 in young adult to 0.95 ± 0.4 in the oldest (Figure 1D). The prevalence of diastolic dysfunction, defined as Ea/Aa < 1,9 was dramatically increased to 55% in the oldest age group (Figure 1E). The MPI was significantly increased (worsened) with age (Figure 1F), consistent with the age-related declines in systolic and diastolic function. These abnormalities closely mimic the age-related echo-
cardiographic changes previously reported in healthy human populations.1

The age-related changes in all of the above echocardiographic findings were significantly delayed and attenuated in age-matched mCAT littermates. In the oldest group, mCAT significantly reduced the age-related increase in LVMI by 39%, the percent of mice with diastolic dysfunction by 69%, the MPI by 67%, and the age-related decrease in Ea/Aa by 59% (Figure 1). The genotype difference in the linear rate of change with age (the genotype-by-slope interaction) was highly significant for all outcomes (P<0.001 for all except fractional shortening, P=0.03).

To confirm the protective effects of mCAT on cardiac aging, we performed a cross-sectional study of 42 additional old WT and mCAT C57BL6 mice (age, 27 to 29 months) in which cardiac tissue harvest was also performed within 24 hours after echocardiography. The protective effects of mCAT on echocardiographic parameters were fully reproduced in this independent data set (online-only Data Supplement Table II).

Histological analysis of tissue showed that compared with young WT (4 months of age), old WT mice had significantly larger myocardial fiber width (Figure 2A and 2B) and a higher cross-sectional area with fibrosis (Figure 2C and 2D). Both cardiomyocyte hypertrophy and ventricular fibrosis were significantly attenuated in age-matched old mCAT mice. There was no genotype difference in young adults. Moreover, myocardial fiber width by image analysis was highly correlated with LVMI determined by echocardiography (R²=0.73, P<0.01; online-only Data Supplement Figure I).

MCAT Protects Against Mitochondrial Oxidative Damage and DNA Mutations in the Aged Heart

As an extension to our earlier findings that mCAT protected cardiac mitochondrial aconitase enzymes from oxidative damage,7 we further found that protein carbonyls, an indicator of oxidative damage, increased significantly in cardiac mitochondria with age and was significantly reduced in old mCAT mice (Figure 3C). Aging is associated with increased mtDNA mutations and deletions,4,10 as well as extensive morphological damage in mitochondria shown by electron micrographs (online-only Data Supplement Figure II). Using the newly developed random mutation capture assay, we found that cardiac mtDNA point mutation and deletion frequencies both significantly increased by 3-fold with aging.11 The mCAT genotype significantly reduced DNA point mutation and deletion frequencies to levels more comparable to those of young animals (Figure 3A and 3B). We found that mtDNA copy number increased in the aged heart (Figure 3D) and was accompanied by upregulation of transcription factors involved in mitochondrial biogenesis (Figure 3E), consistent with reports that oxidative stress induces mitochondrial biogenesis.12 Most of these changes were significantly reduced in old mCAT mice, including an attenuated increase in mtDNA copy number and reduced

Figure 1. Echocardiography of mice from different age groups in the longevity cohort. Age-related changes in (A) LVMI (mg/g body weight); (B) left atrial (LA) dimension (mm); (C) fractional shortening (FS%; (D) Ea/Aa measured by tissue Doppler imaging of the mitral annulus; (E) proportion of mice with diastolic dysfunction defined as Ea/Aa < 1; and (F) MPI. There was a significant linear increase across ages for all outcomes (P<0.001 for all except for FS, P=0.005, fit linearly to a continuous age function), mCAT mice had a significantly lower rate of progression with age in all of the above measurements vs WT (P<0.001 for all except for FS, P=0.03, for an interaction between age-slope and genotype). Ninety mCAT and 80 littermate WT mice were examined, with ∼20 mice in each age and genotype group.

Figure 2. Cross-sectional study of cardiac pathology. A, Old WT (OWT) mice had larger myocardial fiber width than old mCAT (OmCAT) mice (trichrome stain, ×400; scale bar=10 μm). B, Quantitative analysis showed a significant increase in myocardial fiber width in aged heart, which was significantly attenuated in OmCAT mice. C, OWT mice had more fibrosis (blue; trichrome, ×20) than OmCAT mice, as shown by quantitative image analysis of the percent fibrotic area in aged hearts, which was significantly attenuated in OmCAT mice (D). YWT indicates young WT; YmCAT, young mCAT.
induction of peroxisome proliferator-activated receptor gamma coactivator-1 alpha (PGC-1α) and transcription factor A, mitochondrial (TFAM) but not nuclear respiratory factors 1 and 2 (NRF-1 and NRF-2) mRNA (Figure 3D and 3E).

Plausible Mechanisms of Cardiac Hypertrophy in the Aged Heart and the Effect of mCAT

To investigate the potential mechanisms of aging-associated cardiac hypertrophy, we measured the activation of calcineurin–nuclear factor of activated T-cell (NFAT) and phospho-ERK1/2 pathways, which are known to mediate pathological and compensated hypertrophy, respectively.13 Both the phosphorylation of ERK1/2 and the total ERK1/2 protein levels did not change significantly with age (data not shown). However, we found that the calcineurin-NFAT pathway was activated in cardiac aging. Activity of calcineurin, a phosphatase that activates NFAT by dephosphorylation, was found to increase significantly with age (Figure 4A). Downstream of calcineurin, NFAT3 activity was increased in aged heart as shown by stronger DNA binding activity (Figure 4B) and increased transcription of NFAT target genes, including modulatory calcineurin interacting protein-1 and atrial and brain natriuretic peptides (Figure 4C). Furthermore, we found that GATA4, a cofactor of NFAT3,14 was activated in aged heart, as shown by increased phosphorylation of GATA4 at serine 105 (Figure 4D). The age-dependent activation of calcineurin-NFAT and GATA4 was significantly reduced in old mCAT hearts (Figure 4A through 4D).

Plausible Mechanisms of Diastolic Dysfunction in the Aged Heart and Effect of mCAT

Several factors have been reported to cause diastolic dysfunction, including impaired myocardial relaxation resulting from...
decreased calcium reuptake and increased myocardial stiffness. Increased fibrosis in aged heart and amelioration of fibrosis in mCAT mice were described above.

Sarco(endo)plasmic reticulum Ca ATP-ase (SERCA2) and the sodium-calcium exchanger (NCX) are key proteins in calcium reuptake that assist in myocardial relaxation during the diastolic phase. They were examined by Western blots in aged heart. Quantitative analysis revealed that SERCA2 protein decreased by 52% in aged WT heart compared with young WT heart (P < 0.01). SERCA2 was much better preserved in old mCAT heart compared with old WT littermates (Figure 5A). NCX protein increased by 103% in the aged WT heart compared with the young WT heart (Figure 5B). The increase was significantly less in old mCAT hearts compared with old WT hearts. Interestingly, we found an inverse correlation between the level of NCX and SERCA2 proteins (Figure 5C). This novel observation suggests that NCX may be upregulated in the aged heart to compensate for the decline in SERCA2. Levels of total and phosphorylated phospholamban, which inhibits SERCA2 activity in its dephosphorylated form, did not change significantly with age (Figure 5E).

To further investigate plausible mechanisms of diastolic dysfunction in the aged heart, we analyzed the relationships of myocardial fiber width, ventricular fibrosis, and SERCA2 protein with diastolic dysfunction. Univariate analysis showed that cardiomyocyte hypertrophy and ventricular fibrosis were significantly associated with the presence of diastolic dysfunction (Figure 6A and 6B). These findings were consistent with the fact that both ventricular hypertrophy and fibrosis would increase myocardial stiffness. The level of SERCA2 protein was dramatically decreased in mice with age-related diastolic dysfunction (Figure 6C). Multivariate regression modeling showed that SERCA2 was the strongest predictor of Ea/Aa, an indicator of diastolic function (P < 0.01; online-only Data Supplement Table III).

To further investigate the role of SERCA2 in aging, we examined [Ca^{2+}]i transients in ventricular myocytes isolated from mouse hearts, loaded with the Ca^{2+} indicator dye Fluo-4, and paced at 1 Hz. Compared with young cardiomyocytes, old WT cardiomyocytes had significantly lower [Ca^{2+}]i transient amplitude and slower rates of decay, whereas old mCAT cardiomyocytes had significantly preserved calcium transient amplitude and decay rates (Figure 6D and 6E). Stimulation with caffeine, which opens ryanodine receptors and unloads the sarcoplasmic reticulum calcium, showed that old WT cardiomyocytes had significantly lower sarcoplasmic reticulum calcium loads. This is consistent with the lower [Ca^{2+}]i transient amplitude observed in old WT cardiomyocytes. Inhibition of SERCA2 with cyclopiazonic acid (5 μmol/L) completely abolished the beneficial effects of mCAT on calcium transient amplitude and rate of decay (Figure 6D and 6F), suggesting that the protective effect of mCAT in aged cardiomyocytes is mediated by better preservation of SERCA2 activity. Overall, the decline of ventricular SERCA2 thus appeared to be the most important factor associated with age-dependent cardiac diastolic dysfunction, presumably by causing impaired myocardial relaxation.

Increased Cardiac Angiotensin II in Aging

Angiotensin II (Ang II) is known to induce cardiomyocyte hypertrophy and apoptosis, increase cardiac fibrosis, and impair cardiomyocyte relaxation, compatible with all of the above aging-related changes. We therefore measured the cardiac Ang II octapeptide in young and old LV tissue using mass spectrometry. Cardiac Ang II concentrations...
increased significantly with age (Figure 5D). mCAT did not appear to reduce the age-related increase in cardiac Ang II, suggesting that the mechanism of mCAT protection is downstream of Ang II.

Cardiac Aging Phenotype as Predictors of Follow-Up Mortality

To investigate whether the cardiac aging phenotype determined by echocardiography is a predictor of follow-up mortality, we performed survival analysis of 130 old WT and mCAT mice that underwent echocardiography at midlife (age, 16 to 24 months) in the longevity cohort. Univariate Cox regression analyses verify that age, MPI, and LVMI were significant predictors of mortality (the Table). A multivariate Cox model was used to estimate the best linear combination of these variables ($\beta_2$ MPI + $\beta_3$ LVMI) to create a cardiac aging risk score for each mouse based on these variables. Cox regression adjusted for age at the time of echocardiography (Cox model 2) verifies that this risk score provides a biologically meaningful measure of the risk of death; mice in the highest tertile (T3) had a significantly increased hazard of all-cause mortality, with a hazard ratio of 2.88 (95% confidence interval, 1.43, 5.82; $P=0.003$), compared with mice in the lowest tertile of cardiac aging score (T1) (the Table and Figure 7A). As evidence for our hypothesis, we found a marked difference in the distribution of cardiac aging risk scores between mCAT and WT mice: At midlife, the proportions of mCAT mice in T1, T2, and T3 were 91%, 48%, and 24% versus 9%, 52%, and 76% for WT ($\chi^2=39.4, P<10^{-5}$). Kaplan–Meier analysis based on tertiles of cardiac aging risk scores calculated separately for WT and mCAT mice also stratified each of these genotypes into high- and low-mortality-risk groups (Figure 7B and 7C, respectively).

To study the relative contribution of cardiac aging to mortality, we estimated the incidence of all-cause mortality in mice that reached their natural end of life. The
incidence of mortality in the highest tertile of cardiac aging score (T3) versus those in the lower 2 tertiles of cardiac aging score was 16.2% and 7.3%, respectively. The attributable risk fraction indicated that 55% of mortality risk was attributable to the cardiac aging risk score. This is the first such analysis of cardiac functional parameters with aging that has been reported. Thus, cardiac aging is a significant predictor of mortality in mice despite the absence of hypertension, diabetes, or hypercholesterolemia, and the cardiac aging phenotype appears to contribute to approximately half of the mortality risk in the mouse longevity cohort.

Discussion

Our results demonstrate that overexpression of mCAT protects mice from cardiac aging, providing direct evidence for the role of mitochondrial ROS in the aging of this vital organ. Several lines of evidence support this conclusion. In WT mice from the longevity cohort, we found age-dependent LV hypertrophy and a decline in cardiac performance (especially diastolic function), concomitant with the accumulation of oxidized mitochondrial proteins, mtDNA mutations, increased ventricular fibrosis, cardiomyocyte hypertrophy, a decline in SERCA2 protein, and activation of the calcineurin-NFAT pathway in the aged heart. These age-related alterations took place in the absence of significant cardiovascular risks such as diabetes, hypertension, or hypercholesterolemia, suggesting that these findings are primary changes of cardiac aging rather than secondary to other diseases. mCAT littermates were partially protected from all of the above age-related cardiac alterations, suggesting that these aging changes are related in substantial part to chronic ROS exposure and emphasizing the role of mitochondrial ROS in cardiac aging. Interestingly, we did not observe any additional benefit in protection against cardiac aging in mice with higher versus lower mCAT cardiac expression (online-only Data Supplement Table II), which is consistent with our previous observation that lifespan is not associated with the level of mCAT expression. 

We have suggested that the location of the catalase, ie, targeting to mitochondria, is more important than the magnitude of catalase expression. Here, we show that mtDNA point mutations and deletions in the heart increased significantly with age but that the antioxidant function of mCAT protects cardiac mtDNA from these age-related mutations. These age-associated mtDNA point mutations had a spectrum similar to that observed in oxidative DNA damage. Furthermore, because oxidative stress has been shown to induce mitochondrial biogenesis, we also found that mtDNA copies increased in aged heart, with upregulation of transcription factors involved in mitochondrial biogenesis. These phenomena were reduced in old mCAT mice, suggesting that mitochondrial biogenesis in the aging heart is mediated by oxidative damage to mitochondria.

To investigate the signaling in age-associated cardiac hypertrophy, we examined 2 major pathways of cardiac hypertrophy, MEK1/2-ERK1/2 and calcineurin pathways, which are central regulators of compensated and pathological hypertrophy, respectively. Although we did not find increased expression or phosphorylation of ERK1/2 in aging, we found that the calcineurin-NFAT pathway was significantly activated in the aged heart. Calcineurin activity was increased by ~4-fold in the aged heart (Figure 4A). This phoshatase activates the transcription factor NFAT. Activated NFAT translocates into nucleus, where it interacts with the transcription factor (GATA4) to initiate transcription of hypertrophic fetal genes such as atrial and brain natriuretic peptides. Electrophoretic mobility shift assay showed that NFAT DNA binding activity is increased in aged heart (Figure 4B), consistent with increased mRNA levels of atrial and brain natriuretic peptides and modulatory calcineurin interacting protein-1 (Figure 4C). Furthermore, we found an age-dependent increase in GATA4 phosphorylation at Ser105 (Figure 4D), which has been reported to enhance its activity of DNA binding and transcription activation. The activation of the calcineurin-NFAT pathway in age-associated cardiac hypertrophy was partially protected by mCAT, suggesting an interaction between ROS and hypertrophic signaling mediators. Although myocardial ROS has been implicated in the generation of cardiac hypertrophy and dysfunction, as shown by the antihypertrophic effect of several antioxidants, the in vivo evidence for direct links between hypertrophic mediators and ROS has been scant. ROS might cause oxidative and nitrative modification of signaling proteins and may thereby modulate signal transduction and transcriptional and translational regulation. However, further studies are needed to elucidate the exact mechanism of these interactions.

Upstream of the above signaling pathways, Ang II induces cardiomyocyte hypertrophy and apoptosis, increases cardiac fibrosis, and impairs cardiomyocyte relaxation, all consistent with our observed age-related changes. Inserra et al proposed that Ang II is a crucial mediator of cardiovascular aging. They recently showed that long-term inhibition of Ang II reduces cardiac pathology and prolongs rat survival. Consistent with this, we found that cardiac Ang II concentrations increased significantly with age. Cardiac Ang II levels in old mCAT mice were similar to those in old WT mice despite mCAT protection against cardiac aging, suggesting that mCAT acts downstream of Ang II. Ang II is known to promote superoxide generation through NADPH oxidase, to uncouple endothelial nitric oxide synthase, and to stimulate mitochondrial H2O2 production in vascular endothelial cells in vitro. Although blocking Ang II signaling provides survival benefit in patients with heart disease, the efficacy of such drugs for retarding intrinsic cardiac aging remains unknown.

Diastolic dysfunction is well documented in human cardiac aging. Impaired myocardial relaxation caused by functional decline in calcium handling proteins and increased myocardial stiffness related to cardiac hypertrophy and fibrosis are common causes of diastolic dysfunction. Among these, the decline in SERCA2 protein is the strongest predictor of diastolic dysfunction in aged mice (online-only Data Supplement Table III). We and others have found that old WT cardiomyocytes have a lower amplitude and prolonged decay rate of calcium transients, and we have shown that old mCAT cardiomyocytes have calcium transient profiles...
more comparable to young cardiomyocytes (Figure 6E). Significantly lower sarcoplasmic reticulum calcium loads in old WT cardiomyocytes (shown by caffeine stimulation; Figure 6D) are best explained by a chronic reduction in SERCA2 protein levels in old hearts because dephosphorylated phospholamban did not change significantly with age (Figure 5E) and the beneficial effect of mCAT was completely abolished when SERCA2 was inhibited by cyclopyrazonic acid (Figure 6E). Our data also show that NCX is upregulated in aged heart when SERCA2 is decreased. Such declines in SERCA2 and increases in NCX expression have previously been reported in cardiac aging in response to Ang II and in heart failure.35–37 Ren et al28 reported that overexpression of catalase in cardiomyocytes attenuated aging-induced cardiomyocyte relaxation dysfunction by increasing NCX rather than preserving SERCA2. In contrast, mCAT preserves SERCA2 in old mice, and upregulation of NCX is less apparent.

Although mice are the best-studied experimental model of mammalian aging, little evidence has directly linked the senescence of vital organs with survival. Echocardiographic data of our mouse longevity cohort suggested that both cardiac hypertrophy (increased LVMi) and functional decline (increased MPI) are significant predictors of mortality. We generated the cardiac aging risk score for each mouse in the cohort, estimated by the linear regression model of LVMi and MPI (Cox model 1, the Table), and showed that the cardiac aging risk score is an independent predictor of mortality. Estimation by an epidemiological approach suggested that approximately half of the natural deaths in the cohort were attributable to cardiac aging. Study of the end-of-life pathology of this longevity cohort has indicated that cardiac pathology was a contributing cause of death in about half of the C57BL6 mice,29 consistent with the estimated attributable risk fraction for cardiac aging by echocardiography, suggesting that cardioprotection likely contributes to the lifespan extension previously observed in mCAT mice.30 Such demonstration of improved organ function during aging may be even more relevant to human health than observations of extended longevity,30 and this report shows that the murine model of cardiac aging is well suited for this approach.

Conclusions

Our data emphasize the roles of mitochondrial ROS in cardiac aging, which is an independent predictor of mortality in mouse longevity cohort. This study also suggests potential clinical applications of mitochondria-targeted antioxidant drugs in cardiovascular diseases, despite the disappointing results from nontargeted antioxidants.

Source of Funding

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Disclosures

None.

References

24. Lim CC, Apstein CS, Colucci WS, Liao R. Impaired cell shortening and relengthening with increased pacing frequency is intrinsic to the
Old age is a major risk factor for cardiovascular disease because it prolongs exposure to hypertension, diabetes, hypercholesterolemia, and other cardiovascular risks. However, intrinsic cardiac aging, the slowly progressive structural changes and functional declines with age, also makes the heart more susceptible to stress and contributes to increased risk of cardiovascular mortality and morbidity in the elderly. Using echocardiography, we showed that cardiac aging in mice recapitulates human cardiac aging as documented by prior epidemiological studies: age-dependent increases in left ventricular mass index and diastolic dysfunction and worsening myocardial performance index. Cardiac aging in the mouse is accompanied by increases in mitochondrial protein oxidation, DNA deletions, mitochondrial biogenesis, and ventricular fibrosis, as well as decreased cardiac SERCA2 and activation of the calcineurin–nuclear factor of activated T-cell pathway. Although mitochondrial reactive oxygen species have been proposed as a cause of aging, their role in cardiac aging is unclear. We have previously shown that overexpression of catalase targeted to mitochondria (mCAT) prolongs the murine median lifespan by 17% to 21%. In this study, we demonstrated that all of the age-related changes were significantly attenuated in mCAT mice. Survival analysis showed that echocardiographic parameters are a significant predictor of mortality in mice, even in the absence of hypertension, diabetes, or hypercholesterolemia. This study emphasizes the critical role of mitochondrial reactive oxygen species in cardiac aging and the impact of cardiac aging on survival. These findings also suggest that mitochondria-targeted antioxidants may have a role in treating or preventing reactive oxygen species–related cardiovascular diseases, despite the disappointing results of clinical trials using nontargeted antioxidants.
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SUPPLEMENTAL MATERIAL (Dai, et al)

Expanded Methods

Animal Longevity Cohort

Mice (C57Bl6) were housed as previously described \(^1\), fed regular chow diet (irradiated Picolab Rodent Diet 20 #5053, PMI Nutrition International, Brentwood, MO) and reverse osmosis water. They were kept in a barrier specific-pathogen-free facility maintained at 70-74°F, 45-55% humidity, with 28 air changes/hour and 12/12-h light/dark cycle. Mice were selected for echocardiography using consecutive identification numbers assigned at birth.

All animals in the longevity cohort were not subjected to any invasive experimentation other than echocardiography. All animal experiments were approved by the University of Washington Institutional Animal Care and Use Committee.

Echocardiography

A reduced dose of ketamine/xylazine (65mg/kg and 4.4 mg/kg, respectively), providing adequate sedation but minimal cardiac suppression, was used to minimize the effect of anesthesia or stress on cardiac function. The mice were placed in a lateral decubitus position on a heat-pad to maintain the body
temperature at 37°C. Transthoracic echocardiography was performed with
Acuson CV-70 (Siemens) equipped with a 13 MHz-transducer. Images were
collected and stored as a digital cine loop for measurements and calculations.
Standard imaging planes, M-mode, conventional and Tissue Doppler, and
functional calculations were performed according to American Society of
Echocardiography guidelines. The parasternal long-axis view was used for the
measurement of the left atrium (LA) dimension, the left ventricle (LV) wall
thickness and chamber dimension. These parameters were applied to
estimate the fractional shortening and LV mass. The apical long-axis view was
used to obtain the pulsed-waved Doppler of mitral inflow, aortic ejection,
isovolemic contraction and relaxation time as well as Tissue Doppler Imaging
of the mitral annulus (Ea/Aa). MPI (Tei index) was calculated as the ratio of the
sum of isovolemic contraction and relaxation time to LV ejection time \(^2\). For
both pulsed-wave and tissue Doppler recording, a sample size of 0.2 mm was
used. A sweep speed of 40 mm/s was used for M-mode and Doppler studies.

Quantitative Pathology

One day after echocardiography, the second series of 42 old mice (24 MCAT,
18 WT) aged 24-29 months were euthanized for cross-sectional study of heart
pathology. Trichrome and H&E staining was performed. Myocardial fiber width was quantified as the average fiber width of 40-50 longitudinal sections of myocytes from 4-5 high power field images per heart section (400x).

Ventricular fibrosis was quantified from Trichrome stained sections, in which the percentage of blue-green area was measured relative to the total cross-sectional area of the ventricles.

**The random mutation capture assay** of mt DNA point mutations was performed as previously described \(^3,4\) with slight modifications. Briefly, a crude mitochondrial fraction was isolated, followed by mtDNA purification and extensive mtDNA digestion with TaqI endonuclease. Real-time PCR was performed with two primer sets. The first primer set, mTaq634, flanks a TaqI restriction site. Termed PCR A, this sequence is amplified only if there is a mutation within the TaqI restriction site. The second primer set, termed control primers, amplifies an adjacent region not containing a TaqI restriction site, is performed to quantitate the total amount of mtDNA template in the sample (called PCR B). In addition, a standard curve using control primers is generated in parallel to control for PCR efficiency and to set an independent standard for the quantification of WT and mutant mtDNA molecules. Using a
comparative PCR-strategy, WT and mutant molecules are quantified, and the amount of mutant molecules is divided by the amount of WT molecules in order to calculate the mutation frequency. This strategy requires a 100% digestion of mtDNA molecules with WT TaqI restriction sites, although rare WT molecules may persist. To correct for the presence of these rare WT mtDNA molecules, the product of PCR A was further digested using TaqI endonuclease, and the fraction of mutant, or undigested PCR-product, (250 bp, called C) vs WT or digested (150 bp, called D) was quantified using Agilent Bioanalyzer DNA-1000 microelectrophoresis (Agilent Technologies, Germany). The mtDNA mutation frequency was estimated as relative quantity of C/(C+D) x A/B/4. The sequences for mTaq634 forward and reverse primers are

ACTCAAAAGGACTTGGCGGTA & AGCCCATTTCTTCCCATTTC,

respectively and for control forward and reverse primers are

TCGGCGTAAACGTGTCAACT & CCGCCAA GTCCTTTGAGTTT,

respectively. Detection of deletions was performed with the same method using a different set of primers flanking multiple Taq I restriction sites located several kb apart. PCR amplification does not take place unless all restriction sites are lost by a segmental deletion, which renders the DNA molecule
resistant to Taq I cleavage. The primers for deletion assay are
AGGCCACCACACTCCTATTG and AATGCTAGGCCTTTGATTGG.

**Measurement of mitochondrial protein carbonyl**

LV tissues were homogenized in mitochondrial isolation buffer (sucrose
250mM, 1mM EGTA, 10mM HEPES, 10mM Tris-Hcl, pH7.4) using glass-grind
homogenizer, then the lysates were centrifuged at 800g for 10 minutes. The
supernatants were further centrifuged at 4000 g for 30 min at 4ºC. The crude
mitochondrial pellets were then resuspended in small volume of isolation
buffer and sonicated on ice. The mitochondrial extracts were treated with 1%
streptomycin sulfate to precipitate mitochondrial nucleic acids. The enriched
mitochondrial proteins (use 1µg) were assayed using protein carbonyl ELISA
based on derivatization of the carbonyl group with dinitrophenylhydrazine
(DNPH), followed by anti-DNPH antibody (OxiSelect protein carbonyl ELISA,
Cell Biolabs, San Diego, CA).

**Quantitative PCR**

The quantitation of relative gene expressions was performed using
Taqman Gene Expression Assays with Applied Biosystem 7900 real time PCR
machine. The genes include: PGC1-α (Mm00731216), TFAM (Mm00447485),
NRF-1 (Mm00447996), NRF-2 (Mm00487471), ANP (Mm01255747), BNP
(Mm 00435304) and MCIP-1 (Mm00517094). All expression assays were normalized to 18S RNA.

Mitochondrial DNA copy number was quantified using quantitative PCR of total DNA extracts from cardiac tissues. Mitochondrial DNA copies were estimated by the ratio of the amount of mitochondrial gene NADH dehydrogenase 1 (ND1) and a single-copy nuclear gene cytochrome P4501A1 (cyp1A1). Primers used were: ND1 (For: GAACGCAAAATCTTAGGGTACATACA, Rev: GCCGTATGGACCAACAATGTT, probe: 6FAM-CTACGAAAAGGCCC) and cyp1A1 (For:GACACAGTGATTGGCAGAGATC, Rev:AACGGATCTATGGTCTGACCTGT, probe: 6FAM-CTCAGCTGCCCTATCTGGAGG CCTTC)

Calcineurin assay and NFAT Electrophoretic Mobility Shift Assay (EMSA)

Measurement of calcineurin activity (phosphatase PP-2B) was performed using colorimetric calcineurin activity assay kit (Calbiochem), according to manufacturer’s protocol. For NFAT EMSA, consensus NFATc oligonucleotides (sc-2577, Santa Cruz) were labeled with \[^{32}P\]dATP using T4 Polynucleotide kinase (New England Biolab). Nuclear fraction of cardiac tissues was extracted
using nuclear extraction kit (Millipore), then quantified with Bradford assay. Fifteen µg of nuclear extracts were incubated at room temperature for 1 hour with 1.23 µg of poly (dl/dC), 20 mM Tris, pH 7.5, 100 mM NaCl, 1.6 mM DTT, 10% glycerol, 1mM EDTA, 5 – 10 x 10⁵ cpm of [³²P]dATP-NFATc oligonucleotide. It was then separated in non-denaturing polyacrylamide gels (6%) at 150 V for 2-3 hrs in Tris-borate-EDTA buffer, pH 8.0. After electrophoresis, the gels were dried, and radioactive protein-DNA bands were detected by autoradiography.

**Western Blot**

LV tissues were homogenized in iced-cold lysis buffer containing protease and phosphatase inhibitors, then analyzed by standard western blots. Total protein (10-25 µg) were separated on 4–20% polyacrylamide gradient gels and transferred to nitrocellulose membranes, then blocked with 5% milk in Tris-buffer solution with 1% Tween-20. Membranes were incubated with primary antibodies for 2 hours at room temperature or overnight at 4°C. The primary antibodies include: rabbit polyclonal anti-SERCA2 (Novus Biologicals), anti-NCX and GATA4 (Santa Cruz), p-GATA4 S105 (Abcam), anti phospho-ERK1/2 and anti-ERK1/2 (Chemicon), anti-phopho-phospholamban and anti-phospholamban (Millipore) as well as anti-GAPDH (Cell Signaling). The
secondary antibody was donkey anti-rabbit antibody (Thermo-Scientific). The
antigen-antibody complexes were detected by the enhanced chemi-
luminescence method (Thermo-scientific). The relative band density was
quantified by using Image Quant ver.2.0 and reported as a ratio to GAPDH as
an internal control. All samples were normalized to the same cardiac protein
sample.

**Calcium transients study**

Ventricular cardiomyocytes were dissociated using standard enzymatic
methods, then maintained in Dubelcco's MEM and loaded with
acetoxyethyl-ester form of Fluo-4 (50uM), a calcium indicator dye, at room
temperature for 30 min. Field stimulation was performed using IonOptix
Myopacer (IonOptix Corp, Milton, MA, USA) stimulator at a frequency of 1 Hz.
Olympus IX-70 inverted microscope coupled with IonOptix photometry system
was used to collect calcium transients fluorescence signals from
cardiomyocytes. The \([\text{Ca}^{2+}]_i\) was estimated using the equation: 
\[ C = \frac{K_d \times R}{(K_d/C_0+1-R)^6} \]
where \(R\) denotes \(F/F_0\), \(K_d\) is the dissociation constant of Fluo-4
(600nM), and \(C_0\) is the resting \([\text{Ca}^{2+}]_i\) (=150nmol/L). The Ca-transient
amplitude was reported as \(F/F_0\), where \(F_0\) is the diastolic fluo-4 fluorescense.
The exponential fit of the Ca-transient decay was applied to estimate the
decay rate constant $\lambda (s^{-1})$. The amplitude of the Ca-transient evoked by the application of 20 mM caffeine was used as an indicator of SR Ca$^{2+}$ content. To ensure steady-state SR Ca$^{2+}$ load, cells were subjected to a minimum of 10 preconditioning pulses (1 Hz) before caffeine was applied. Cyclopyrazonic acid (5 µM) was applied to investigate the contribution of SERCA2 to the Ca-transients.

**Measurement of cardiac angiotensins by mass spectrometry (MS)**

LV tissues were homogenized and centrifuged at 3000g for 10 min at 4°C, then 3x volume of absolute ethanol was added to the supernatant on ice for 30 min, followed by centrifugation at 14,000rpm for 15 min at 4°C. The final supernatant containing peptides was dried and resuspended in 20 µL of buffer A (5% acetonitrile, 0.1% formic acid). The analysis was carried out on a tandem quadrupole MS/MS system (TSQ Ultra, Thermo Fisher) coupled to a HPLC (Surveyor, Thermo Fisher) with a flow splitter system. Samples were loaded on a 75µm x 250mm column packed in house with 4µm RP-C12 beads (Jupiter, Phenomenex). The following pairs of precursor>fragments were selected for the MS method: 523.8> 263.1, 400.2, 513.3, 676.3, 775.4, and 931.5 and were correspondent to the formation of y2, y3, y4, y5, y6 and y7-ions from the doubly charged species of the peptide DRVYIHPF (Ang II).
The pair 523.8>263.1 gave the strongest signal and was used for quantitation, whereas other transitions were used for confirmation. Samples were eluted in a 60min gradient from 5 to 80% of buffer B (80%acetonitrile, 0.1% formic acid). The flow rates were approximately 5μL/min and 250nL/min for loading and gradient elution, respectively. External calibration method with synthetic angiotensin II peptide was used for quantification.
Supp Table 1. Biochemical and physiological data for young and old WT and MCAT mice

<table>
<thead>
<tr>
<th></th>
<th>Young (5-8 months)</th>
<th>Old (24-28 months)</th>
<th>ANOVA</th>
<th>p*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>WT</td>
<td>MCAT</td>
<td>WT</td>
<td>MCAT</td>
</tr>
<tr>
<td>Body weight (g)</td>
<td>28±6</td>
<td>29±6</td>
<td>30±4</td>
<td>31±4</td>
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<tr>
<td>Systolic BP (mmHg)</td>
<td>102±18</td>
<td>107±19</td>
<td>96±15</td>
<td>102±10</td>
</tr>
<tr>
<td>Diastolic BP (mmHg)</td>
<td>81±18</td>
<td>85±20</td>
<td>74±12</td>
<td>75±13</td>
</tr>
<tr>
<td>Mean arterial pressure (mmHg)</td>
<td>88±18</td>
<td>91±20</td>
<td>81±13</td>
<td>83±12</td>
</tr>
<tr>
<td>Pulse pressure (mmHg)</td>
<td>21±5</td>
<td>20±3</td>
<td>21±5</td>
<td>23±6</td>
</tr>
<tr>
<td>Heart rate (bpm)</td>
<td>624±105</td>
<td>646±121</td>
<td>601±116</td>
<td>569±118</td>
</tr>
<tr>
<td>Glucose (mg/dL)</td>
<td>107±16</td>
<td>110±11</td>
<td>95±8</td>
<td>93±7</td>
</tr>
<tr>
<td>T-cholesterol (mg/dL)</td>
<td>97±28</td>
<td>89±21</td>
<td>89±30</td>
<td>77±11</td>
</tr>
</tbody>
</table>

* p-values of Two-way ANOVA models including age, genotype and age*genotype interaction
Supp Table 2. Cross-sectional echocardiography in the second series of old WT and MCAT mice, and absence of differences in MCAT mice with higher vs. lower transgene expression.

<table>
<thead>
<tr>
<th></th>
<th>Old WT</th>
<th>Old MCAT</th>
<th>p</th>
<th>Low MCAT</th>
<th>High MCAT</th>
</tr>
</thead>
<tbody>
<tr>
<td>n</td>
<td>17</td>
<td>25</td>
<td></td>
<td>13</td>
<td>12</td>
</tr>
<tr>
<td>Age (months)</td>
<td>28.3 ± 0.65</td>
<td>27.6±0.7</td>
<td>0.32</td>
<td>28 ± 0.76</td>
<td>27.4 ± 0.7</td>
</tr>
<tr>
<td>Male (%)</td>
<td>52.9</td>
<td>52</td>
<td>0.41</td>
<td>53.9</td>
<td>50</td>
</tr>
<tr>
<td>MCAT/GAPDH mRNA (arbitrary unit)</td>
<td></td>
<td></td>
<td>0.5 ± 0.03</td>
<td>1.16 ± 0.15</td>
<td></td>
</tr>
<tr>
<td>Echocardiography:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LVMI (mg/g)</td>
<td>4.4 ± 0.4</td>
<td>2.8±0.2</td>
<td>0.0001</td>
<td>3 ± 0.2</td>
<td>2.7 ± 0.3</td>
</tr>
<tr>
<td>LA dimension (mm)</td>
<td>2.0 ± 0.1</td>
<td>1.7±0.1</td>
<td>0.04</td>
<td>1.8 ± 0.1</td>
<td>1.7 ± 0.1</td>
</tr>
<tr>
<td>FS (%)</td>
<td>46.9± 1.1</td>
<td>47.8±1.1</td>
<td>0.55</td>
<td>47±1.7</td>
<td>48.4±1.2</td>
</tr>
<tr>
<td>Ea/Aa</td>
<td>0.87±0.1</td>
<td>1.34±0.1</td>
<td>0.001</td>
<td>1.35±0.1</td>
<td>1.25±0.1</td>
</tr>
<tr>
<td>Diastolic dysfunction (%)</td>
<td>64.8</td>
<td>20</td>
<td>0.003</td>
<td>23.1</td>
<td>16.7</td>
</tr>
<tr>
<td>MPI</td>
<td>0.85±0.05</td>
<td>0.54±0.03</td>
<td>0.001</td>
<td>0.55±0.06</td>
<td>0.57±0.03</td>
</tr>
</tbody>
</table>
Supp Table 3. Multivariate regression model predicting Ea/Aa (diastolic function)

<table>
<thead>
<tr>
<th></th>
<th>β</th>
<th>p</th>
<th>95% C.I.</th>
</tr>
</thead>
<tbody>
<tr>
<td>SERCA2 protein</td>
<td>0.58</td>
<td>0.01</td>
<td>0.16</td>
</tr>
<tr>
<td>Fibrosis (%)</td>
<td>0.03</td>
<td>0.19</td>
<td>-0.01</td>
</tr>
<tr>
<td>Myocyte width</td>
<td>-0.02</td>
<td>0.25</td>
<td>-0.07</td>
</tr>
</tbody>
</table>
Supp Fig 1. Linear regression demonstrated that myocardial fiber width was strongly correlated with LV mass index by echocardiography.
Supp Fig 2. Transmission electron micrographs of cardiac mitochondria from young Wt (4 months old), very old Wt and Mcat (36 months old), n=3 each group. Relative number of damage mitochondria was quantified blindly from 8-10 images from different fields (15000x magnification). Damage mitochondrion was defined as loss of electron density in more than 20% of the area of a mitochondrion.
Supp References: