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Heart Failure with Preserved Ejection Fraction: Molecular Pathways of the Aging Myocardium

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Abstract

Age-related diastolic dysfunction is a major factor in the epidemic of heart failure. In patients hospitalized with heart failure, diastolic heart failure is now as common as systolic heart failure. We now have many successful treatments for HFrEF, while specific treatment options for HFpEF patients remain elusive. The lack of treatments for HFpEF reflects our very incomplete understanding of this constellation of diseases. There are many pathophysiological factors in HFpEF, but aging appears to play an important role. Here we propose that aging of the myocardium is itself a specific pathophysiological process. New insights into the aging heart, including hormonal controls and specific molecular pathways such as microRNAs, are pointing to myocardial aging as a potentially reversible process. While the overall process of aging remains mysterious, understanding the molecular pathways of myocardial aging has never been more important. Unraveling these pathways could lead to new therapies for the enormous and growing problem of HFpEF.

Keywords

Aging; diastolic dysfunction; diastolic heart failure; cardiac hypertrophy

I. THE SIGNIFICANCE OF HFpEF AND AGING

For thousands of years, if people were lucky enough to survive childhood illnesses and reach adulthood, they had a good chance of living into their 50's and 60's.¹ However, routine survival into the 80's and 90's is a truly new event in human life. As the world's population ages, the prevalence of age-related diseases is growing dramatically. In the United States, for example, one in every eight Americans is now above age 65, and by 2030 the proportion of Americans over 65 will reach 19%.² Heart failure affects ~1% of individuals over 50 and

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increases progressively with age.³ Thus, with the ongoing steep rise in the world population of elderly individuals⁴, age-related heart failure is certain to become an increasingly prevalent health condition and a leading cause of mortality in the elderly.^{5,6} Although heart failure traditionally is associated with reduced contractile function of the myocardium, dilation of the left ventricle, and reduced ejection fraction, there is a growing epidemic of heart failure accompanied by preserved ejection fraction (HFpEF).⁷ This form of heart failure usually has a normal sized left ventricle, often but not always with hypertrophy and is characterized by a global impairment of depressed cardiovascular function.⁸ Approximately 50% of patients hospitalized for heart failure have HFpEF, and the mortality risk for these patients is equivalent to those with heart failure accompanied by reduced ejection fraction (~50% die within 3 years^{9–11}).

Recent studies have defined aging as one factor in the HFpEF epidemic.^{12, 13} Echocardiographic studies often reveal normal or near normal ejection fraction in elderly patients with heart failure, with abnormal diastolic relaxation and left ventricular filling.^{14–16} As observed by Borlaug et al, LV stiffness increases progressively with age despite reduction in arterial load.¹⁶ Abnormal diastolic filling is associated with female gender, obesity, age >65 years, hypertension, renal disease and diabetes, suggesting that distinct risk factors and pathological mechanisms underlie these conditions.^{6, 12}

An overview of HFpEF with particular emphasis on the clinical aspects will be provided in the accompanying review by Kass and colleagues.¹⁷ Here we specifically review molecular insights into age-related contributors to changes in myocardial function, an area of paramount importance, which may also affect globally cardiovascular reserve. Understanding the molecular events in myocardial aging will be essential to developing treatments for the types of heart failure we will see in this century.

II. DISSECTING THE COMPONENTS OF MYOCARDIAL REMODELING IN AGE-RELATED HFpEF

Aging is an evolutionarily conserved yet poorly understood process that leads to deterioration of many physiological functions over the lifespan of an organism.¹⁸ Studies have suggested that aging may contribute independently to deterioration of diastolic function.¹⁹ Normal cardiac aging is characterized by structural and functional changes. Increased cardiomyocyte size, increased apoptosis with decreased myocyte number, increased collagen deposition and also functional changes at the cellular level may all contribute to abnormal diastolic function with normal aging²⁰. The consequences of these changes are an increase in left ventricular diastolic stiffness with aging.^{19, 21} In both the Baltimore Longitudinal Study on Aging and the Framingham Heart Study, left ventricular hypertrophy increased with age, while systolic function was maintained.²² However, while cardiomyocyte hypertrophy occurs in aging human hearts, co-morbid diseases such as hypertension also are much more common in the elderly, complicating our understanding of the effects of aging.²³ Left ventricular diastolic filling rate deteriorates with progressive age²⁴ and this decline is observed as early as age 20 years in humans.²⁵ By 80 years of age, the reduction in early diastolic filling is as profound as 50%.²⁵ Adult mammalian heart replenishes its cardiomyocyte pool both during physiological aging and in response to

injury^{26–28}; cardiomyocyte refreshment, which occurs at a low rate (~1%/year) in youth, appears to slow even further with advancing age.²⁶ Aging does not appear to affect the low rate of cardiomyocyte apoptosis in normal human hearts.²⁹ In the myocardial extracellular matrix, aging leads to increased deposition of extracellular matrix components, principally collagen, with increased fibril diameter and collagen cross-linking, an increase in the ratio of type I to type III collagen, decreased elastin content, and an increase in fibronectin.^{13, 30–37} These changes may contribute to exercise intolerance with advancing age, though skeletal muscle function declines with age, as well.^{15, 20}

Models of cardiac aging

Cardiac aging in rodents recapitulates many changes observed in humans, with age-dependent increases in left ventricular mass index as well as impaired left ventricular filling.^{22, 38} Studies have documented an age-dependent increase in cardiomyocyte size in wild-type mice,^{39–41} and age-dependent cardiomyocyte hypertrophy also occurs in rats.⁴² Studies of rodents suggest multiple potential mechanisms of cardiomyopathy in aging. For example, cardiac angiotensin II levels are higher in senescent animals.⁴³ Adrenergic and cholinergic signaling may also play a role, as mice with disruption of the type 5 adenylyl cyclase are protected from age-related cardiac hypertrophy and fibrosis,⁴⁰ and mice with reduced function of the choline transporter exhibit age-dependent decreases in fractional shortening and increases in ventricular size and fibrosis.⁴⁴ Mitochondrial dysfunction likely also contributes, as the aging myocardium exhibits increased mitochondrial protein oxidation and increased mitochondrial DNA mutations.²² In addition to cardiomyocyte hypertrophy, aging mice develop progressive myocardial fibrosis, associated with molecular signatures of immune cell and inflammatory dysregulation.⁴⁵ Furthermore, cardiomyocyte stability and intercellular mechanical and functional coupling may be perturbed in aged animals due to disruption of junctional adhesion proteins.⁴⁶

III. AGE RELATED DETERMINANTS OF DIASTOLIC DYSFUNCTION

The development of heart failure symptoms in patients with diastolic dysfunction has profound implications, as it carries a 60% 5-year mortality prognosis.⁵ What tips patients into the symptomatic phase is unknown, as patients are known to have impaired diastolic filling before symptoms emerge.^{5, 13, 14} Aging may play a fundamental role in modifying both the passive stiffness of the myocardium as well as the active diastolic relaxation properties of the myocytes.

Myocardial Interstitial Fibrosis

Interstitial fibrosis is a hallmark of cardiac aging and a major contributor to myocardial stiffness.^{47, 48} The myocardial extracellular matrix (ECM) is not just a passive scaffold for tissue architecture but also a dynamic participant in cellular signaling.^{20, 49} Studies have shown more than doubling of extracellular matrix content in the myocardium of senescent rats.^{41, 47, 48} The collagenous weave is not only thicker but increased cross-linking among the collagen filaments confers greater rigidity to the myocardium.²⁰ Fibroblasts are the principal cells secreting extracellular matrix components, including collagen, fibronectin, and laminin. In aging as well as under a wide range of hypertrophic stimuli, fibroblasts

undergo activation and phenotypic transformation to myofibroblasts, which are characterized by expression of the contractile protein alpha-SMA.^{49–51} Myofibroblasts control ECM composition by regulating the secretion and activity of proteolytic enzymes, including members of the family of matrix metalloproteinases (MMPs) and their inhibitors plasminogen activator inhibitor 1 (PAI-1) and tissue inhibitors of matrix metalloproteinases (TIMPs).⁵¹ Fibroblasts are under the active control of multiple signaling hormones and cytokines,^{49, 51} and the pro-fibrotic neurohormonal cascades relevant to cardiac aging are discussed below.

TGF- β Signaling Pathway

TGF β is one of the most extensively studied fibroblast-activating growth factors. It mediates myofibroblast transformation as well as transcriptional suppression of the MMPs, thus tipping the proteolytic balance towards net matrix accumulation.^{48, 52–55} Brooks et al studied heterozygous TGF β (+/-) deficient mice which at 24 months of age exhibited decreased myocardial fibrosis with a total of 4% interstitial collagen as opposed to 10% observed in wild type mice.⁵⁵ The loss of one TGF β allele also contributed to improved myocardial compliance and performance. Blocking TGF β activity through administration of a neutralizing antibody attenuates diastolic dysfunction in a pressure overload model of cardiac hypertrophy.^{54, 55} TGF β expression is also upregulated by angiotensin II signaling through the AT1 receptor.^{56, 57} Angiotensin II increases TGF β 1 mRNA and protein expression levels in both cardiomyocytes and fibroblasts.^{56–62} Administration of ACE inhibitors or AT1 receptor blockers ameliorates cardiac hypertrophy and decreases TGF β 1 levels, implicating TGF β as a mediator of ATII effects.^{61, 62} Furthermore, Schultz et al have demonstrated that TGF- β 1 -/- mice (bred on immunocompromised Rag1 -/- background to protect from lethality of complete TGF β 1 loss) are protected from the hypertrophic effects of Angiotensin II stimulation.⁶³ Angiotensin II also activates cardiac fibroblast function through signaling via endothelin-1 (ET-1), IL-6 and periostin.^{48, 56, 64}

Downstream TGF β signaling pathways have been extensively studied. TGF β binds to the constitutively active type II receptor (T β RII) at the surface of the target cell and subsequently recruits and phosphorylates a type I receptor (T β RI), also known as ALK5.⁵⁹ Downstream, Smad2 and Smad3 are activated through phosphorylation by ALK5, and form a complex with Smad4 that translocates to the nucleus and affects gene expression.^{48, 59} Non-Smad signaling pathways mediated by TGF β include Erk, JNK, p38 MAPK.^{59, 60} Although these downstream signaling pathways have not been explored extensively in the context of cardiac aging, their role in pro-fibrotic signaling has been shown in a number of animal models.^{48, 52}

Oxidative Balance

Another important contributor to activation of pro-fibrotic signaling pathways in the aging myocardium is the presence of a positive oxidative balance.^{41, 65} Increased levels of reactive oxygen species (ROS) in the senescent myocardium can cause direct TGF β activation resulting in upregulation of its downstream effector connective tissue growth factor (CTGF).^{59, 65} Indeed, NADPH oxidase 4 dependent generation of hydrogen peroxide is required for TGF- β 1-induced conversion of cardiac fibroblasts to myofibroblasts.⁶⁵

Furthermore, scavenging of reactive oxygen species through mitochondrially-targeted catalase expression ameliorates the age-related myocardial fibrosis.⁴¹ Other TGF β activators include thrombospondin-1 as well as enzymes such as MMP-2, MMP-9 and plasmin which through their proteolytic activity also regulate the kinetics of TGF β release from the ECM.^{59, 66, 67}

Matrix Metalloproteinases

Many of the matrix metalloproteinases family of enzymes as well as their inhibitors have been explored in the context of cardiac aging. Epidemiological studies have shown correlations between increasing age and regulation of these enzymes.^{68, 69} Aging may produce a shift in the balance between matrix metalloproteinases and tissue inhibitors of matrix metalloproteinases that ultimately translates in increased matrix accumulation. In a study of healthy subjects with no prior diagnoses of cardiovascular disease, Bonnema et al showed that age correlates with an increase in MMP-2, MMP-7, TIMP-1, -2 and -4 levels, as well as with a decrease in MMP-9 plasma levels.⁶⁸ Analysis of Framingham subjects has also shown an age dependent increase in TIMP-1 plasma levels that was related to major cardiovascular risk factors and to indices of LV hypertrophy.⁷⁰ Direct genetic evidence from animal models for the specific role of these enzymes in aging-related ventricular remodeling are lacking. Chiao et al conducted a genetic study in which MMP-9 null mice of all age groups showed no variation in ventricular filling, unlike wild-type senescent mice where impaired diastolic filling occurs with aging.⁷¹ This functional preservation in MMP-9 deficient mice correlates with attenuation of the fibrotic remodeling observed with age.

Titin and Myocyte Stiffness

Titin has been identified as a major molecular determinant of myocyte stiffness.⁷²⁻⁷⁹ As the largest molecular component of the myocyte structure spanning from Z disk to the M band of the sarcomere, it has been shown to modulate cardiomyocyte passive stiffness through its I-band region, which has spring-like properties that regulate early diastolic recoil and late diastolic resistance to stretch.^{78, 79} Titin modulates its stiffness through post-translational modifications, including phosphorylation by protein kinases A, C-alpha and G, which decrease its compliance.⁷⁸⁻⁸⁴

In HFpEF patients, titin is largely hypophosphorylated.⁸⁰ A proposed mechanism by the Paulus group postulates that the increased oxidative stress in diastolic dysfunction depletes the nitric oxide (NO) reserve, thus lowering PKG activity.^{73, 74} Furthermore, the abundant ROS generate disulfide bridges that shorten titin's N2B segment, increasing its stiffness.⁸³ Relative hypophosphorylation of the stiff N2B titin isoform ultimately increases resting tension of cardiomyocytes that contributes to the high diastolic LV stiffness observed in failing human hearts and restoring phosphorylation of the titin N2B segment in elderly hypertensive dogs lowered diastolic LV stiffness.⁷⁶ In addition, multiple transgenic mouse models have been created showing that the absence of either the N2B or PEVK segment, or shortening the tandem immunoglobulin segment, is sufficient to increase myocardial stiffness and cause impaired diastolic filling.^{77, 79, 83} Thus, titin is emerging as an important mediator of diastolic dysfunction, but the effects of aging on titin are incompletely described.

Calcium Signaling and Active Diastolic Relaxation

In addition to the above discussed changes in passive myocardial stiffness, impairment in active diastolic relaxation has been well documented in diastolic dysfunction.^{85–88} Cardiac relaxation occurs when Ca^{2+} reuptake into the sarcoplasmic reticulum occurs through sarcoplasmic/endoplasmic reticulum Ca^{2+} ATPase (SERCA) or extruded extracellularly through the sarcolemmal $\text{Na}^+/\text{Ca}^{2+}$ exchanger (NCX). Regulation of SERCA channel activity occurs through interaction with the regulatory protein phospholamban (PLN). In its unphosphorylated state, PLN interacts with SERCA2a and decreases its affinity for Ca^{2+} . Phosphorylation of PLN by PKA and Ca^{2+} /calmodulin-dependent protein kinase (CaMK) disrupts this inhibitory interaction and augments the SERCA pump activity.⁸⁹

Myocardial preparations from experimental models of impaired diastolic function have revealed a decreased rate of intracellular Ca^{2+} decay resulting in prolonged action potential and impaired diastolic filling.^{87, 88} Studies have been equivocal correlating expression levels of calcium handling proteins and aging-related HFpEF. Brian et al and others have shown that human SERCA2a levels correlate inversely with age, while Babušíková et al and others have shown no changes in SERCA2a protein or mRNA expression levels in senescent murine myocardium compared to young control animals.^{90–95} When SERCA levels are reported together with PLN levels, the evidence has suggested decreased SERCA2a/PLN ratio with age.^{92, 95, 96} Restoring the SERCA/PLN balance through gene transfer of the SERCA2a protein in senescent rat myocardium improves age-related diastolic dysfunction.^{97, 98}

Conflicting results have been reported regarding protein and mRNA expression levels of RyR, L-type Ca^{2+} channels, and NCX.^{98–102} However, more recent evidence suggests the role of post-translational modification of the Ca^{2+} -handling proteins in modifying their activity level. Specifically, in multiple separate studies it has been shown that the increased oxidative stress observed in senescent myocardium leads to oxidative damage of the SERCA pump, thus decreasing its Ca^{2+} sequestering activity and prolonging diastolic relaxation.^{91–93} Phosphorylation is another mechanism of post-translational signaling control in Ca^{2+} homeostasis.⁹¹ The aged myocardium has lower responsiveness to beta-adrenergic stimulation, and this has been shown to translate into reduced PKA and CaMK mediated phosphorylation of PLN and RyR, thus decreasing Ca^{2+} handling rate.¹⁰²

Aging-Related Diastolic Dysfunction and Mitochondria

Both animal and human studies have shown that with aging, mitochondrial DNA accumulates mutations with reported increases as much as 16-fold, and the components of the mitochondrial apparatus function at a decreased level.^{103–105} Vermulst et al showed that mitochondrial DNA deletions play much greater role than point mutations in premature cardiac aging.^{104, 105} In a genetic murine model, mice with homozygous mutation of mitochondrial polymerase γ ($\text{Polg}^{\text{m/m}}$) exhibit accelerated aging including cardiac senescence features such as cardiac hypertrophy and dysfunction.¹⁰³ The loss of mitochondrial polymerase proofreading capacity leads to deficiently functioning components of the cellular energetics machinery that contribute directly to increased oxidative stress. The specific role of mitochondria in myocyte oxidative stress is supported

by the finding that overexpression of catalase targeted to mitochondria (mCAT) but not targeted to peroxisomes (pCAT) protects against cardiac hypertrophy, fibrosis, and failure.^{106, 107} Dai et al show that mCAT mice exhibit significantly attenuated cardiac aging as demonstrated by increased left ventricular myocardial index, myocardial performance index and E/A ratio on echocardiography.^{41, 107} On a histopathological level, mice with overexpressed mitochondrial catalase exhibit decreased myocardial hypertrophy and interstitial fibrosis, as well as about 20% lifespan extension.

Dysfunctional mitochondria are eliminated by mitophagy, a specialized form of macroautophagy^{108, 109} This process is particularly important in cells like cardiomyocytes where autophagy is the major determinant in protein and organelle turnover.¹¹⁰ Macroautophagy efficiency progressively declines in cardiomyocytes during aging.^{111, 112} As a result, dysfunctional mitochondria that are more prone to release ROS accumulate within aging cardiomyocytes contributing to increase oxidative stress.¹¹³

The renin-angiotensin aldosterone system is a driver of mitochondrial dysfunction.^{114, 115} Dai et al have shown elevated myocardial levels of angiotensin II in aging hearts.¹¹⁴ Angiotensin II signals through binding to the angiotensin receptor-1 (ATR1), a Gαq coupled receptor, which has been shown to stimulate the NOX4 isoform of NADPH oxidase on the mitochondrial membrane.^{114, 115} Reactive oxygen species generated by NADPH oxidase sets off a ROS-mediated-ROS generation propagating a vicious cycle of oxidative stress damaging mitochondrial components further exacerbating the above cycle.^{116, 117} Thus, activation of angiotensin II signaling may promote myocardial aging.

IV. MOLECULAR PATHWAYS IN AGE-RELATED DIASTOLIC DYSFUNCTION

The NO-cGMP-PKG signaling axis/Inflammation

Aging is associated with a systemic proinflammatory state, so called ‘inflamm-aging’, that may lead to a functional decline in multiple organs even in absence of a specific disease¹¹⁸ and can activate signaling cascades leading to myocardial structural and functional remodeling.^{119–126} Indeed, multiple cross-sectional studies show that increasing age is associated with elevated circulating levels of inflammatory markers, including TNFα, IL-6, IL-18, MCP-1, soluble ST2, and pentraxin 3 (Figure 1).^{119, 121, 124} An emerging theory for the pathogenesis of HFpEF proposes that a systemic proinflammatory state produced by comorbidities, including aging, causes coronary microvascular endothelial inflammation. This inflammation ultimately results in increased interstitial fibrosis and cardiomyocytes stiffness that contributes to high diastolic left ventricular stiffness and heart failure development.¹¹⁹ Moreover, the presence of circulating pro-inflammatory cytokines is predictive of the development of heart failure symptoms.¹²⁴

Inflamed coronary microvascular endothelial cells, as evidenced by the upregulated expression of endothelial adhesion molecules including vascular cell adhesion molecule (VCAM-1) and E-selectin in myocardial samples from HFpEF patients,^{119, 127, 128} produce reactive oxygen species.^{129–135} Increases in reactive oxygen species can cause reduction in bioavailability of nitric oxide (NO) for adjacent cardiomyocytes. Reduced NO causes decreases in cGMP levels, which in turn decreases protein kinase G (PKG) activity in

cardiomyocytes. The inflamed endothelium enables binding and translocation of inflammatory cells, further propagating an inflammatory state within myocardium.¹¹⁹ Low PKG activity translates into cardiomyocyte hypertrophy and hypophosphorylation of titin, thereby increasing stiffness. Stiff cardiomyocytes and increased collagen deposition by myofibroblasts cause diastolic LV impairment.¹¹⁹

Neurohormonal pro-fibrotic signaling through angiotensin II and endothelin is also facilitated by the presence of endothelial inflammation.^{47, 119, 131} Counterbalancing the effect of the oxidative stress on cGMP levels with long-term use of sildenafil has shown benefit for diastolic LV function.¹³¹ However, in the largest trial studying PDE5 inhibitors, the RELAX study (Evaluating the Effectiveness of Sildenafil at Improving Health Outcomes and Exercise Ability in People With Diastolic Heart Failure), sildenafil showed no effect on exercise tolerance in the enrolled subjects with HFpEF.¹³⁶

V. METABOLISM AND CARDIAC AGING

Reducing calorie intake in many species leads to increased longevity and slows the aging effects in key organ systems.^{137, 138} In fact, Doppler studies in humans practicing caloric restriction reveal no changes in systolic function but improved diastolic function.¹³⁹ In rats, caloric restriction improves calcium handling and diastolic function.¹⁴⁰ It was long thought that lower calorie intake leads to diminished metabolism-associated “wear and tear” by decreasing generation of harmful metabolic byproducts, such as reactive oxygen species. However, further studies have shown the activation of “longevity pathways” that control genes protective against apoptosis and maladaptive remodeling.^{141, 142}

For example, the sirtuins (silent information regulators, SIRT6) as well as the IGF-1/Akt pathways have been identified as key nutrient sensors involved in cardiac and organismal longevity. Conserved from lower organisms, such as yeast, flies and worms, up to humans, the 7 members of the sirtuins class are diversely positioned in the nucleus and cytosol responding to the cellular energy balance through their NAD⁺ cofactor.^{142–149} The characterization of the role of the first member of this class, Sirt1, in cardiac aging has yielded equivocal results. Alcendor et al have shown that low (2.5-fold) to moderate (7.5-fold) cardiac-specific overexpression of Sirt1 in a transgenic mouse model attenuated age-dependent cardiac remodeling and dysfunction, as well as served a cardioprotective role in the presence of oxidative stress (such as paraquat administration) through FOXO-dependent signaling.¹⁴⁵ In contrast, high expression levels (12.5-fold) of Sirt1 increased baseline myocyte oxidative stress, apoptosis and cellular hypertrophy that reflected in a functional deterioration of the heart.¹⁴⁵ In addition, Sirt1 haploinsufficiency ameliorates the extent of cardiac hypertrophy in the presence of a pressure overload stimulus.¹⁴⁹ Sundaresan et al demonstrated that the pro-hypertrophic properties of Sirt1 are mediated through crosstalk with the Akt pathway, which participates in cell survival, protein synthesis and metabolism. Sirt1 deacetylates Akt, thus freeing it to bind and activate PIP3.^{150, 151} Sirt1 also deacetylates PDK1 allowing Akt phosphorylation by this phosphokinase, thus augmenting Akt activity by as much as ~1000-fold. Sirt1, therefore, plays a dual function in cardiac aging.^{150–152}

Another member of the sirtuin family, Sirt3, is a NAD⁺ dependent histone deacetylase primarily localized to the mitochondrial membrane that has been shown to regulate pathways in energy metabolism, apoptosis and reactive oxygen species synthesis.^{153–157} Sirt3 knockout mice do not exhibit grossly different phenotype but microscopic examination reveals premature aging including mitochondrial swelling, cellular hypertrophy and fibrosis as early as 13 months of age.^{153–155} Sirt3 ^{-/-} mice also demonstrate greater susceptibility to stress such as transverse aortic banding, to which they respond with an exaggerated hypertrophy and fibrosis.^{153–155} On the contrary, Sirt3 overexpression is cardioprotective in the setting of hypertrophy induced by stimulation with angiotensin II or isoproterenol.¹⁵⁴ Hafner et al proposed a mechanism of Sirt3 to involve prevention of mitochondrial dysfunction by way of decreasing the activity of the mitochondrial permeability transition pore (mPTP) through deacetylation of its regulatory component cyclophilin D.¹⁵⁴ Furthermore, Sirt3 activates FOXO3a-mediated expression of the anti-oxidant enzymes superoxide dismutase and catalase.¹⁵⁸

Recent studies have shed light on the crosstalk between Sirt6 and the IGF-1/Akt pathway and its cardiac effects.^{150, 157} Sirt6 ^{-/-} mice exhibit the most progerian phenotype of all sirtuin knockout animal models.¹⁵⁰ These transgenic mice are severely hypoglycemic and die within 1 month of age. Sundaresan et al showed that myocardial samples from humans with heart failure as well as from mouse models of cardiac hypertrophy induced by transverse aortic constriction, angiotensin II or isoproterenol showed markedly reduced Sirt6 levels.¹⁵⁷ Both single and double Sirt6 knock-out mice develop significant cardiac hypertrophy and dysfunction.¹⁵⁷ The myocardium of these animals exhibits fibrosis, myocyte hypertrophy, apoptotic and fetal gene expression. Sirt6 overexpression, on the other hand, protects remodeling and dysfunction in the presence of hypertrophic stimuli.¹⁵⁷ Sirt6 is, thus, a major regulator on the crossroads of two nutrient-sensing pathways.

Sirt7 is another sirtuin family member and similar to Sirt6, its downregulation through double gene knock-out in a mouse model leads to myocardial hypertrophy and decreased lifespan.¹⁵⁹ However, much less extensive evidence exists for Sirt 7 and the rest of the sirtuin enzymes on their roles on cardiac aging. The Sirt proteins through their complex interactions with multiple signaling pathways involved in nutrient responses and mitochondrial function are emerging as important therapeutic targets in the context of cardiac aging.

VI. NOVEL DISCOVERIES IN CARDIAC AGING

SMP30

Senescence marker protein 30 (SMP30), a 34-kDa protein, ubiquitously expressed in human organs and preserved across species, has recently been identified as another player in cardioprotection in the setting of aging-associated myocardial changes.^{160, 161} Misaka et al demonstrated that SMP30 is a marker of cardiac senescence as levels of this protein decrease in the murine myocardium with aging by as much as 40%.^{162, 163} SMP30 has been shown to play a role in multi-organ senescence, including brain, lungs and kidneys.¹⁶² Misaka's laboratory created an Ang II-induced model of cardiac hypertrophy and showed that SMP30 knock-out mice exhibit greater myocardial remodeling when exposed to

angiotensin II.^{162, 163} They also demonstrated that SMP30 deficiency leads to increased myocardial oxidative stress concomitant with increased NADPH oxidase activity. SMP30, therefore, may tip the redox balance in the aging heart.

GDF11

The quest for a humoral factor that can rejuvenate aging phenotypes has been long-standing. Recently, growth differentiation factor 11 (GDF11), a member of the activin/TGF- β superfamily, has been identified as a factor that carries the potential to reverse aging-related cardiac remodeling.¹⁶⁴ Heterochronic parabiosis, an experimental procedure whereby two animals of different ages are joined together, identified GDF11 as a candidate hormone that controls the aging myocardial phenotype. Further elucidation of how GDF11 fits in the multiple signaling cascades identified to play a role in cardiac aging is pending.

miRNA Signaling

MicroRNAs (miRNAs) are endogenous small noncoding RNAs, 20–23-nucleotides in length, which have emerged as important post-translational regulators of numerous cardiovascular processes, from myocardial infarction to cardiac aging.^{165–167} They are characterized by target promiscuity, as a single miRNA is known to target the expression of up to 100 of genes by hybridization with complementary sequences on mRNAs and thus triggering their degradation or translational inhibition.¹⁶⁵ Expressional survey of the 17–92 miRNA cluster in the aging heart has implicated miRNA 18 and miRNA 19 as potential regulators of aging cardiomyopathy through their targeting of pro-fibrotic pathways involving TGF-beta and TSP-1 signaling.¹⁶⁸ Another study conducted in vitro has also shown that miRNA-22 is upregulated with age in mouse fibroblast isolates.¹⁶⁹ The authors identified mimecan (osteoglycan, described together with TGF-beta1 and beta2) as its target under inverse regulation relationship.¹⁶⁹

More recently, exciting studies have revealed that miR-34a has been implicated in cardiac aging.^{170–173} Predominantly expressed by cardiomyocytes, miR-34a is upregulated in aging mouse hearts as well as in human heart biopsies (~2-fold).¹⁷⁰ The role of miR-34a in cardiac aging has been linked to regulation of apoptosis. Using microRNA target prediction tools, Boon et al identified Ppp1r10 (PNUTS) as a downstream target which is downregulated by miR-34a (luciferase assays have shown direct targeting of mi-34a to the 3'UTR of PNUTS).¹⁷⁰ PNUTS has known antiapoptotic effects - it reduces telomere attrition in vitro and DNA damage through the DNA damage response pathways involving CHK2 activation in the presence of TRF2.^{170–173} miRNAs are opening new potential therapeutic frontiers in cardiac aging but additional studies delineating their biology in aging are needed.

Telomere attrition

Telomere shortening may contribute to functional decline in different tissues, including myocardial tissue.¹⁷⁴ Telomere shortening has been recently identified as a biomarker of lifetime stress, as early as in childhood¹⁷⁵ and this stress-related telomere shortening could be responsible for accelerated biological aging.¹⁷⁶ Telomere dysfunction-induced cellular phenotypes characterized by proliferative arrest, apoptosis, and senescence may be less relevant considering that genesis of cardiomyocytes occurs at a low rate by the division of

pre-existing cardiomyocytes during normal aging.¹⁷⁷ Interestingly, however, telomeres may regulate functional changes in cardiomyocytes. p53 activation induced by telomere dysfunction may directly affect function of mitochondria and metabolism in cardiomyocytes by repressing peroxisome proliferator-activated receptor gamma coactivator (PGC)-1 α and PGC-1 β thus contributing to the development of an aging dysfunctional phenotype.¹⁷⁸

VII. FUTURE DIRECTIONS AND THERAPEUTIC IMPLICATIONS

In the twenty-first century we are seeing our rapidly aging population afflicted with a cardiovascular syndrome that we are ill prepared to face therapeutically, as we simply don't understand the disease. It is common practice to use HFpEF as a term covering a syndrome that is likely a set of diseases of diverse pathophysiologies. Careful dissection of the various pathophysiological factors at play in this clinical syndrome is important in order to design effective therapeutics (Figure 2).

Systemic inflammation could be a common pathway toward diastolic dysfunction. However, recent discoveries of new molecular pathways in aging suggest that we are at the very beginning of understanding the specific role that aging plays in the myocardium. As these new pathways are explored, it raises the exciting possibility that some effects of myocardial aging are potentially reversible.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Nonstandard Abbreviations and Acronyms

MMPs	matrix metalloproteinases
TIMPs	tissue inhibitors of matrix metalloproteinases
CTGF	connective tissue growth factor

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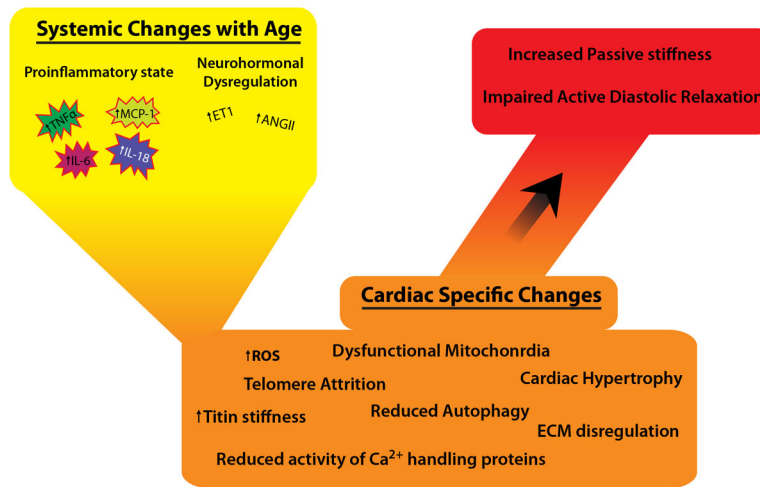


Figure 1. Aging itself leads to molecular changes that contribute to diastolic impairment
Age is associated with systemic changes and myocardial molecular dysfunction that translate into structural changes believed to contribute to HFpEF.

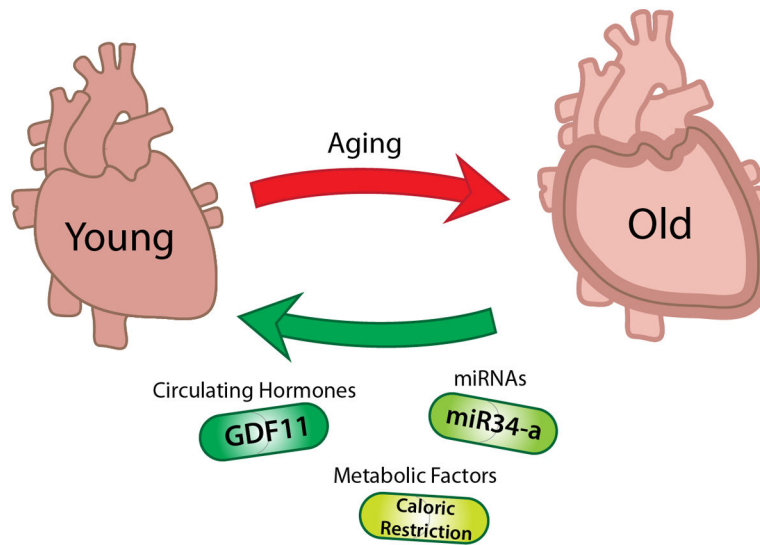


Figure 2. New molecular pathways in aging biology could lead to new treatments of age-related diastolic heart failure

Existing therapies for systolic heart failure have been unsuccessful at treating HFpEF. Novel therapeutic pathways including microRNAs, metabolic factors and age-dependent circulating hormones offer the new opportunities for developing successful treatments.