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## Targeting Age-Related Pathways in Heart Failure

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### Abstract

During aging, deterioration in cardiac structure and function leads to increased susceptibility to heart failure. The need for interventions to combat this age-related cardiac decline is becoming increasingly urgent as the elderly population continues to grow. Our understanding of cardiac aging, and aging in general, is limited. However, recent studies of age-related decline and its prevention through interventions like exercise have revealed novel pathological and cardioprotective pathways. In this review, we summarize recent findings concerning the molecular mechanisms of age-related heart failure and highlight exercise as a valuable experimental platform for the discovery of much-needed novel therapeutic targets in this chronic disease.

A major risk factor for heart failure (HF) and overall cardiovascular disease is age. Approximately 1% of individuals aged over 50 years are affected by HF, and this number doubles with each decade of life,<sup>1</sup> making HF the major cause of mortality in the elderly.<sup>2</sup> This is a matter of increasing concern in the United States, where the population aged 65 and over increased from 40 million in 2007 to 51 million in 2017 and is projected to reach 95 million in 2060.<sup>2</sup> Given this dramatic growth in the aged population, age-related HF represents one of the greatest challenges confronting global health care today.

Undoubtedly, an important part of the explanation for increased HF with increasing age lies in greater time for exposure to injurious stimuli, such as hypertension, metabolic stress, or ischemic injury. The heart's limited endogenous capacity for repair or regeneration implies that heart function

at any specific time reflects the cumulative burden of prior insults. Thus, it makes sense that older patients would have a greater impairment of cardiac reserves and elevated HF risk.

However, even in the absence of overt injury, structural and functional changes occur in the heart as it ages, which seem to contribute to the increased susceptibility to HF in older adults.<sup>3,4</sup> Normal aging is generally accompanied by a thickening and stiffening of the left ventricular walls, particularly the interventricular septum, an increase in left atrial dilation, and an overall increase in cardiac fibrosis.<sup>5</sup> Although resting cardiac function is not markedly impaired in the aged heart, both subclinical diastolic and systolic dysfunction are present.<sup>6,7</sup> However, the most notable functional change observed in the aged heart is the progressive decline in cardiac reserve, which not only contributes to the age-related decline in exercise capacity<sup>8-10</sup> but interestingly is also a major pathophysiological feature of HF with preserved ejection fraction, the most common form of HF in older adults.<sup>11,12</sup>

Although aging has long been considered an unmodifiable consequence of passage of time (chronological aging),<sup>13</sup> the observation that the rate of age-related deterioration (biological aging) differs substantially across species, individuals, and organs,<sup>14</sup> has led to a more nuanced understanding of biological aging as mutable and potentially amenable to manipulation. Thus, we and others have proposed that understanding the underlying biology of cardiac aging could potentially lead to the discovery of novel therapeutic targets for age-related cardiovascular diseases. Indeed, accumulating evidence suggests that it may be possible to target age-related pathways to counteract and even reverse some of the structural and functional changes that drive age-related HF.<sup>15,16</sup> Epidemiological data support the idea that age-related cardiac decline can also be modulated by lifestyle factors, such as diet and exercise, and experimental studies in animals suggest that behavioral, pharmacological, and genetic interventions can slow or accelerate age-related changes and the development of HF.<sup>15-17</sup> These studies suggest protective physiological pathways can counteract the effects of aging and prolong cardiac health.

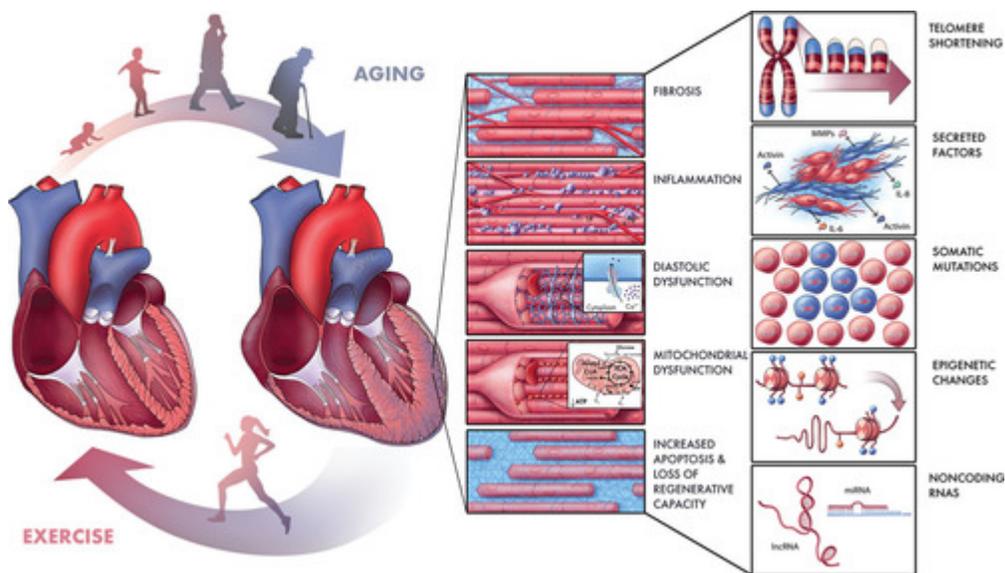
One of the most striking behavioral modulators of cardiac aging is physical activity, which seems to prevent or mitigate cardiovascular disease in older adults and the elderly.<sup>18-21</sup> There is growing evidence that exercise is associated with lower HF risk and attenuation of age-associated intermediate phenotypes such as cellular senescence, telomere length, and cell survival signaling.<sup>22-25</sup> Although much of the human data suggesting that exercise can attenuate cardiac aging is cross-sectional and observational in nature, multiple prospective studies suggest exercise is capable of mitigating or even partially reversing at least some of the cardiac aging phenotypes associated with HF.<sup>26-29</sup> Thus, investigation into the physiological effects of exercise has the potential to complement therapeutic insights derived from investigation of the mechanisms of cardiac decline. Deciphering the mechanisms underlying the beneficial effects of exercise on cardiac aging could be helpful in the development of therapeutic interventions to curtail or even reverse age-related functional decline in the heart.

This review summarizes the pathophysiological changes in the aging heart, recent advances in our understanding of the underlying molecular mechanisms, and the potential therapeutic implications. The cardioprotective effects of exercise will also be discussed, with emphasis on the potential value

of exercise as an experimental paradigm for discovering cardioprotective pathways that can be exploited for prevention and treatment of aged-related HF.

## Pathophysiological Processes Driving Cardiac Aging

Both systemic and cardiac-specific changes in cellular physiology likely contribute to age-related alterations in heart structure and function (Figure 1). Although, there is an increase in left ventricular wall thickness with age, this reflects an increase in size, and not number, of cardiomyocytes. In fact, aging is associated with a decrease in regenerative capacity, which may be compounded by an increase in cell death. This in turn may be related to an age-dependent decline in mitochondrial function and accumulation of senescent cells. At the same time, elevated inflammatory activity likely drives the increase in myocardial fibrosis with age. The following sections will discuss new insights into the cellular processes that contribute to cardiac deterioration with aging. While some of these are systemic processes that affect a range of organ systems, we will concentrate on the cardiac manifestations of these systemic processes.



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### Figure 1. Schematic of processes and pathways contributing to age-related cardiac disease.

As we age, multiple processes likely contribute to cardiac dysfunction, including fibrosis, inflammation, mechanical stiffening and diastolic dysfunction, mitochondrial dysfunction, and a growing imbalance between loss and birth of cardiomyocytes (**center**). These processes are driven by molecular mechanisms (some of which are depicted at **right**) such as telomere shortening, senescence-associated secreted factors, accumulation of somatic mutations, epigenetic changes, and alterations in noncoding RNAs regulating gene expression. Some of these may represent targets for new therapeutic strategies to mitigate both age-related and other forms of heart failure. Since exercise mitigates many effects of aging (**left, bottom**), it may provide a useful tool by enabling us to prioritize candidate cardiac pathways exacerbated by aging and mitigated by exercise. Illustration by Nicole Wolf, MS, ©2019. Printed with permission.

## Cardiomyocyte Death and Regeneration

While neonatal mammals can regenerate myocardial tissue following damage, the adult mammalian heart does not regenerate after injury and has traditionally been understood to lack the capacity for cardiomyogenesis.<sup>30</sup> However, studies in mice and humans have revealed that adult cardiomyocytes renew at a rate of 0.5% to 2% per year, indicating that the adult heart has some, albeit limited, endogenous regenerative potential.<sup>31–33</sup> This renewal was found to decline with age implying a diminished ability to compensate for cardiomyocyte loss.<sup>31–33</sup> The consequences of this decline in regenerative potential could be serious as even very low levels of experimentally induced cardiomyocyte loss have been shown to result in cardiomyopathy and death.<sup>34</sup> Elevated rates of cardiomyocyte apoptosis may pose an additional challenge to cardiac homeostasis,<sup>35</sup> although the evidence for this is mixed, with recent human studies failing to detect a correlation.<sup>36</sup> Given the aging heart's declining regenerative potential, therapeutic interventions to promote endogenous regenerative capacity may be able to favorably tilt the homeostatic balance and improve performance in aging hearts.

Adult cardiomyocyte regeneration has been the subject of intense investigation and debate. Although there have been reports of cardiomyogenesis from bone marrow-derived and tissue-resident putative cardiac progenitors, many of the original reports have been discredited and some retracted.<sup>37–39</sup> In particular, cell fate-mapping studies have demonstrated that cells expressing the hematopoietic stem cell marker c-kit, once proposed as resident cardiac stem cells, give rise to remarkably few cardiomyocytes and do not appear to contribute to myocardial regeneration in a meaningful way.<sup>40–43</sup> Even these small numbers of labeled cardiomyocytes were further determined to be present independent of the ability of c-kit<sup>+</sup> cell progeny to adopt a cardiomyocyte fate, reflecting the fusion of preexisting cardiomyocytes with labeled leukocytes, but not cardiomyogenesis.<sup>44</sup> The consensus that has emerged from these studies is that cardiomyogenesis in the adult heart results from division of preexisting cardiomyocytes and not from differentiation of stem cells.<sup>31,37,45,46</sup> Investigation into the cardiomyocyte populations mediating endogenous cardiomyocyte renewal and the factors regulating their proliferative activity over time will likely lead to new therapeutic targets relevant to aging. Indeed, several molecular mechanisms implicated in regulation of cardiomyocyte proliferation are now being investigated as potential therapeutic targets, some of which will be discussed in later sections. Interestingly, mechanical strain induced by hemodynamic forces has been shown to modulate the activity of yes-associated protein and transcriptional co-activator with PDZ-binding motif (TAZ), transcriptional co-activators implicated in proliferation, with implications for the development of atherosclerosis.<sup>47</sup> The potential impact of this mechanosignaling pathway in the age-related decline in cardiomyocyte proliferation is an intriguing topic for future investigation.

## Mitochondrial Dysfunction

Mitochondria are not only the primary source of energy in the heart, in the form of ATP, but are also key regulators of cardiomyocyte survival. Mitochondrial dysfunction is a core feature of cardiac aging and is at the crossroads of multiple key pathways related to senescence.<sup>48</sup> Cardiac aging is accompanied by a general decline in mitochondrial function and the resulting increase in reactive oxygen species (ROS) production appears to be a major contributing factor in HF (Figure 1).

Recent studies of mitochondrial dysfunction in the aging heart are consistent with the oxidative stress hypothesis of aging, which posits that oxidative stress induced by excessive mitochondrial ROS generation damages mitochondrial DNA (mtDNA) and redox-sensitive mitochondrial proteins, leading to mitochondrial dysfunction and further increasing ROS production. This self-perpetuating cycle of oxidative damage is hypothesized to result in cellular and organ functional decline, limiting lifespan and healthspan. The direct role of mitochondrial oxidative damage in cardiac aging has been demonstrated using mitochondria-specific overexpression of human catalase, an antioxidant enzyme, in mice (mCAT). mCAT mice exhibited prolonged lifespan and displayed attenuated cardiac aging phenotypes including reduced cardiac hypertrophy, improved diastolic function, and improved myocardial performance. On the molecular level, these improvements were accompanied by reduced mitochondrial protein oxidative damage, mtDNA mutations, and deletion frequencies.<sup>49,50</sup>

Mitochondrial dysfunction is also sufficient to induce deterioration of cardiac function. In mice, knock-out of PGC-1 $\alpha$  (proliferator-activated receptor  $\gamma$  coactivator 1 $\alpha$ ), a key regulator of mitochondrial biogenesis, resulted in suppression of mitochondrial gene expression within the heart and development of cardiac dysfunction at 7 to 8 months old.<sup>51</sup> Notably, the same PGC-1 $\alpha$  knockout mouse line exhibited accelerated cardiac dysfunction when subjected to transverse aortic constriction (TAC).<sup>52</sup> This indicates a protective role of PGC-1 $\alpha$  in cardiac function and highlights the increased vulnerability of the heart to insult once mitochondrial biogenesis is compromised.

Taken together, these findings suggest that mitochondrial dysfunction and the resulting ROS generation could contribute to age-associated cardiac dysfunction. Consequently, mitochondrial-targeted antioxidant therapies may have therapeutic value. However, the effects of mitochondrial ROS seem to be context-dependent, limiting the therapeutic potential of antioxidant therapy. In healthy young men, a 4-week intervention of physical exercise improved insulin sensitivity and induced endogenous ROS defenses as well as PGC-1 $\alpha$ , but counterintuitively, these beneficial effects were blocked by antioxidant supplementation, demonstrating that under some conditions ROS production can be beneficial perhaps through induction of adaptive responses that mediate chronic benefit.<sup>53</sup> Indeed, small increases in mitochondrial ROS have been shown to increase cellular defenses<sup>54</sup> and in some cases extend lifespan.<sup>55</sup> Further evidence for the context-dependent effects of mitochondrial manipulations comes from experiments showing that upregulating mitochondrial biogenesis through cardiac-specific overexpression of PGC-1 $\alpha$  has protective effects in young mice but accelerates cardiac aging in old mice.<sup>56</sup> Perhaps because of these complexities, multiple attempts to exploit antioxidant treatments for a range of cardiovascular diseases have thus far failed to demonstrate clinical benefits.

Recent research has suggested other possible approaches to targeting mitochondrial dysfunction and/or metabolic remodeling in heart failure. For example, complementary metabolomic and proteomic analyses in advanced human heart failure and animal models, respectively, suggest a reduction in fatty acid oxidation and an increased use of ketones and ketone bodies as fuel in heart failure.<sup>57,58</sup> While the pathophysiological consequences of this shift in substrate utilization remain incompletely understood,<sup>59,60</sup> prior work in murine models suggests ketone metabolism may be important in mitigating cardiac dysfunction.<sup>61</sup> In these studies, lineage-specific deletion of SCOT (succinyl-CoA:3-oxoacid CoA transferase), the enzyme mediating terminal oxidation of ketone bodies, in cardiomyocytes accelerated adverse remodeling and increased ROS production after

TAC.<sup>61</sup> Collectively, these studies raise the intriguing hypothesis that altering substrate availability through dietary interventions in patients could improve energy homeostasis in the failing heart.

Another approach to metabolic remodeling has focused on the NADH/NAD<sup>(+)</sup> ratio, as a critical determinant of electron transport, oxidative stress, and intracellular signaling.<sup>62</sup> In both experimental pathological hypertrophy and failing human hearts, NADH/NAD<sup>(+)</sup> ratios were increased.<sup>62</sup> Experimental models suggest NAD<sup>(+)</sup> may exert its functional effects in part through mitochondrial NAD<sup>(+)</sup>-dependent deacetylases Sirtuin 3 (Sirt3) and Sirt4, which regulate cell survival and the mitochondrial permeability transition pore, important determinants of cardiomyocyte survival and function.<sup>63,64</sup> Importantly, normalizing NADH/NAD<sup>(+)</sup> ratios through either genetic or pharmacological interventions had important metabolic and functional benefits in murine models.<sup>62</sup> Since NADH/NAD<sup>(+)</sup> ratios can be modified through dietary nicotinamide riboside supplementation,<sup>65</sup> translation of preclinical findings to clinical trials to test this hypothesis in humans seems feasible.

## Cellular Senescence and Inflammation

Cellular senescence is a state triggered by telomere attrition due to repeated replication,<sup>66</sup> or by other forms of cellular stress,<sup>67</sup> in which cells undergo permanent cell cycle arrest, functional decline, and take on a proinflammatory phenotype. Senescent cells progressively accumulate in tissues during life and confer deleterious paracrine effects on neighboring cells and systemic effects on other tissues/organs. These effects are mediated by secretion of proinflammatory cytokines, proteases, and insoluble extracellular matrix components, known as the senescence-associated secretory phenotype (SASP).<sup>67</sup> SASP signaling promotes inflammation as well as cell death and senescence in other cells, and growing evidence suggests that senescent cells contribute to cardiac remodeling and dysfunction during aging (Figure 1).<sup>68,69</sup>

Consistent with a role for cellular senescence in cardiac aging, there is evidence that senescent cells in the heart contribute to functional decline including decreased contractility and impaired mitochondrial function.<sup>70,71</sup> Furthermore, promoting senescence can accelerate the development of cardiac aging phenotypes. Cardiomyocyte death, hypertrophy, and HF were increased in mice with accelerated senescence resulting from a deficiency of telomerase, an enzyme that prevents senescence by combating the loss of telomeres during replication.<sup>72</sup> Similarly, in senescence-accelerated mice fed a high-fat, high-salt diet for 24 weeks, senescent endothelial cells were increased in the heart and this was associated with diastolic dysfunction and left ventricular hypertrophy,<sup>73</sup> suggesting a role for endothelial cell senescence in cardiac dysfunction in aged hearts.

Complementary findings suggest that reducing senescence can have cardioprotective effects. Elimination of cells expressing the senescence marker p16<sup>Ink4a</sup> inhibited aging phenotypes in the heart (eg, reduced cardiomyocytes size, preserved cardioprotective K<sub>ATP</sub> channels, reduced cardiac fibrosis) and extended lifespan.<sup>74</sup> Similarly, clearance of p16<sup>Ink4a</sup>-positive senescent cells in aged mice reduced cardiac hypertrophy and fibrosis and induced cardiomyocyte proliferation manifested as elevated EdU and Ki-67 positive cardiomyocytes.<sup>75,76</sup>

The beneficial effects of eliminating senescent cells suggest that these cells may be actively suppressing the function of otherwise healthy heart cells. In line with this, Anderson et al showed that during aging, human and murine cardiomyocytes exhibited a senescent-like phenotype, including secretion of nontypical SASP signals (Edn3 [endothelin 3]; Tgf $\beta$ 2 [transforming growth factor  $\beta$  2]; and GDF15 [growth differentiation factor-15]), and incubation of neonatal fibroblasts with conditioned culture medium from cardiomyocytes isolated from old mice resulted in fibroblast activation and senescence. This implies an interaction between senescent cardiomyocytes and fibroblasts during cardiac aging and dysfunction.<sup>70</sup>

These observations support a model in which, during aging, cellular stress induced by oxidative stress and inflammation leads to cardiomyocyte senescence. These senescent cardiomyocytes undergo functional decline, including decreased contractility, increased cell size, and mitochondrial dysfunction, negatively affecting cardiac performance. As aging progresses, senescent cardiomyocytes accumulate, interfere with intercellular communication, compromise cardiac function, and further induce chronic inflammation, resulting in cell death, and eventual cardiac dysfunction.<sup>77</sup>

Our current understanding of what drives senescence may not be sufficient to enable therapeutic strategies to prevent it. However, it may be possible to intervene further downstream. The dramatic beneficial effects seen with genetic elimination of senescent cells, described above, have prompted efforts to develop senolytics, small molecules capable of reducing or eradicating these cells.<sup>78-81</sup> While these approaches are novel and exciting, the clinical benefits will obviously need to be demonstrated in realistic clinical contexts where multiple cardiometabolic comorbidities coexist. A complementary strategy would be to target the downstream effectors mediating the adverse consequences of senescent cells. As noted, secreted proteins likely contribute to these adverse effects in many settings and in cases where the principal culprits can be identified, a variety of strategies could be used to mitigate the effects of these secreted proteins. Activin and the closely related family of growth/differentiation factors are senescence-associated secreted proteins that provide one example of this strategy. As detailed below, we recently described an increase in activin signaling in age-related heart failure that could be dramatically mitigated by either antibodies directed to the dominant activin receptors or a soluble-receptor acting as a ligand trap.<sup>15</sup>

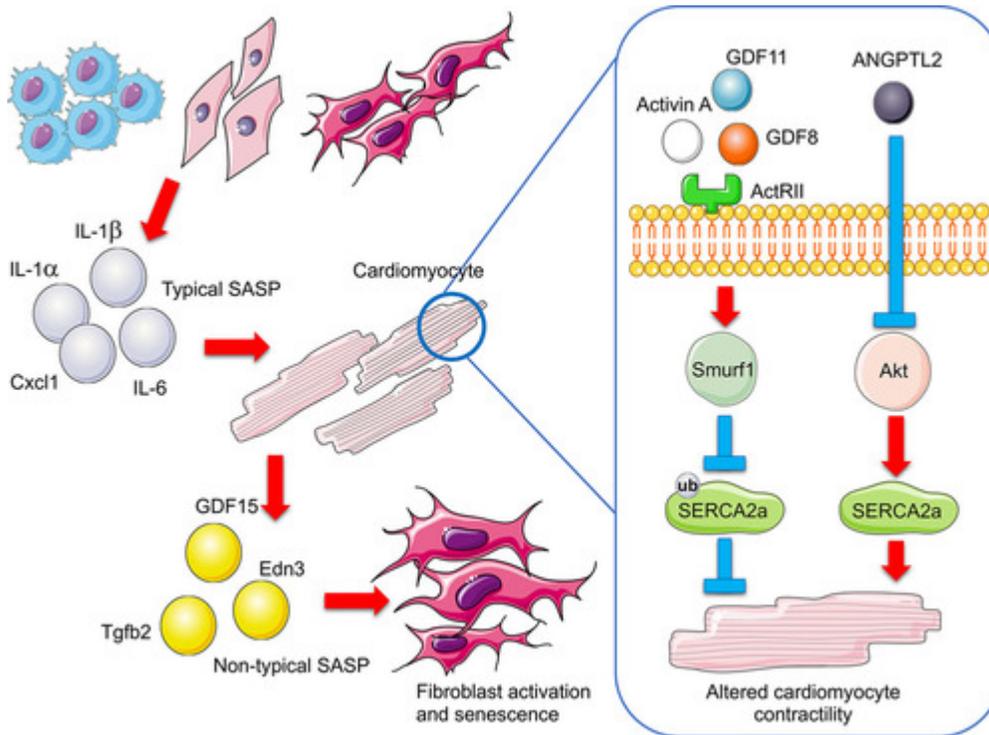
Another consideration is that, although the findings described strongly indicate a mechanistic role of cellular senescence in the development of cardiac disease during aging, cellular senescence in specific cell lineages and conditions may actually be beneficial to the heart. In neonatal mice subjected to apical resection, a model for cardiac regeneration, senescent cells were identified in the peri-resected regions at several time points after apical resection but disappeared when the hearts were fully restored. Elimination of the senescent fibroblasts by fibroblast-targeted genetic deletion of Trp53 (tumor protein 53) inhibited regeneration after apical resection, indicating that senescent fibroblasts promote neonatal heart regeneration.<sup>82</sup> The regenerative activity of senescent fibroblasts is not limited to the neonatal heart. Meyer et al found that senescent fibroblasts accumulated in fibrotic regions of hearts subjected to TAC, and inactivation of cardiac senescent cells by double knockout of Trp53 and cyclin-dependent kinase inhibitor 2a genes further increased fibrosis and fibroblast proliferation leading to severe cardiac dysfunction. In contrast, activation of premature senescence by cardiac-specific overexpression of cellular communication network factor

1 reduced perivascular fibrosis after TAC and improved cardiac function.<sup>75</sup> These results indicate that, in contrast to the deleterious effects of senescence in the aging heart, fibroblast senescence in the apically resected neonatal heart and in TAC is actually beneficial. Thus, while there is strong evidence implicating cellular senescence in age-related cardiac deterioration, the effect of senescence on cardiac regeneration and disease may be complex and context-specific, perhaps varying depending on cell type, age, health, and other factors.

## **Exercise Counteracts Age-Related Pathophysiological Changes**

Exercise is associated with improved cardiac function and may even partially reverse pathological cardiac remodeling in the elderly (Figure 1).<sup>21</sup> In one study, for instance, 3 to 6 months' aerobic exercise training improved peak oxygen consumption and exercise efficiency in elderly subjects (65–79 years).<sup>83</sup> While these benefits likely derive in part from peripheral conditioning, there is also evidence of cardiac remodeling through exercise training in the elderly. For example, 1 year of progressive and vigorous endurance exercise training in previously inactive individuals over age 65 induced physiological left ventricular remodeling, increasing left ventricular mass without affecting left ventricular mass-volume ratio.<sup>26</sup> These cardiovascular benefits have been attributed, in part, to antioxidant effects. Consistent with this, a 6-month exercise training regimen increased the activity of ROS scavenging enzymes in the skeletal muscle of HF patients relative to sedentary controls in a randomized controlled study.<sup>84</sup>

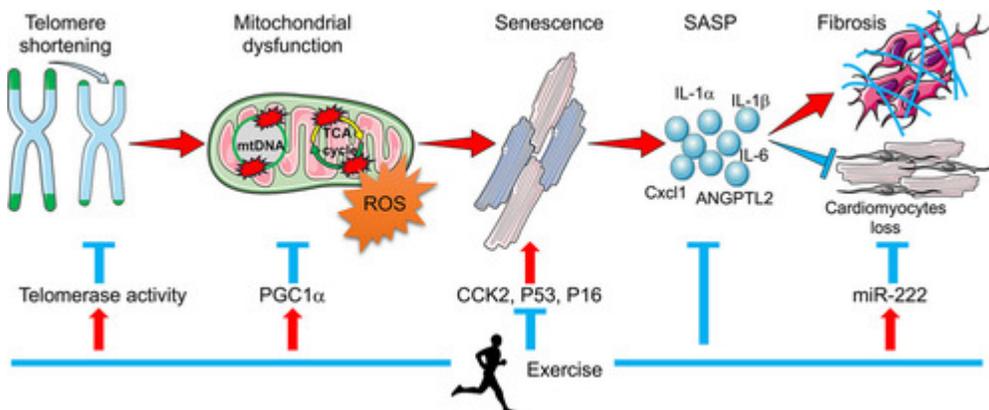
In line with its reported therapeutic effects in humans, experiments in animal models show that exercise has the potential to counteract many pathological processes thought to contribute to age-related HF, including senescence, inflammation, mitochondrial dysfunction, and declining cardiomyocyte regeneration (Figure 3). In mice, voluntary running for 21 days downregulated senescence gene markers in the heart including cell-cycle Chk2 (checkpoint kinase 2), p53, and p16, and upregulated cardiac telomerase activity by 2-fold.<sup>22,23</sup> These effects were abolished in TERT (telomerase reverse transcriptase) deficiency mice, suggesting an antisenescent effect of exercise on the heart. In line with this, exercise reduced age-related cardiac inflammation and fibrosis,<sup>85</sup> increased left ventricular mitochondrial number and volume<sup>86</sup> and induced expression of genes involved in mitochondrial biogenesis and antioxidant response.<sup>87,88</sup> Exercise also reduced cardiomyocyte apoptosis in aging animals<sup>89</sup> and in both young and old animals subjected to ischemia-reperfusion injury.<sup>90</sup> Furthermore, we demonstrated that exercise can promote cardiomyogenesis in young adult mice. We found that 2 weeks of swimming induced cell proliferation markers (eg, BrdU, phosphorylated histone H3, Aurora B kinase, etc) in young (12 weeks old) adult mouse hearts compared with sedentary controls.<sup>91</sup> Exercise also induced cell proliferation in adult cardiomyocytes, measured with multiphoton ionization mass spectrometry<sup>92</sup> based imaging using the stable isotope tracer <sup>15</sup>N-thymidine,<sup>93</sup> and expanded the proliferative zone after myocardial ischemia reperfusion injury.<sup>94</sup>



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**Figure 2. Schematic of secreted factors contributing to age-related cardiac disease.**

Accumulating senescent cells adversely affect other cells (eg, cardiomyocytes and fibroblasts) through a senescence-associated secretory phenotype (SASP) which promotes inflammation, cell death and senescence. While systemic increases in senescent cells lead to increasing secretion of typical SASP proteins with age (eg, IL-1 $\alpha$ , IL-1 $\beta$ , IL-6, Cxcl1), senescent cardiomyocytes secrete nontypical SASP (eg, GDF15, Tgfb2, and Edn3). Circulating activin and ANGPTL2 are also increased with age. Elevated activin, through binding to its receptor ActRIIb, triggers Smurf1-mediated ubiquitination and subsequent degradation of SERCA2a, while increased ANGPTL2 inactivates Akt and thereby degrades SERCA2a. All of these processes contribute to cardiac aging and cardiac dysfunction.



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### **Figure 3. Schematic of telomere shortening contributing to age-related cardiac disease.**

Telomeres shorten with cell division and aging is associated with reduced telomere length. Mitochondria are particularly vulnerable. Critically short telomeres lead to mitochondrial DNA damage, ultimately disrupting mitochondrial function and inducing senescence. Through secretion of senescence-associated secretory phenotype (SASP) factors, senescent cells induce fibrosis and promote cardiomyocyte loss, eventually leading to cardiac dysfunction. Exercise has been shown to protect the heart against cardiac aging and cardiac dysfunction by modulating each step in this sequence.

Interestingly, the cardiac response to exercise and pathological growth stimuli appear to involve distinct molecular pathways.<sup>91</sup> Thus, the study of exercise models is likely to yield different candidates for intervention than those identified through studies of disease models. Moreover, with remarkable consistency, pathways identified as functionally important in the cardiac response to exercise also protect the heart against pathological stress.<sup>21,95</sup> Examples include PI3-kinase,<sup>96,97</sup> Akt1,<sup>98–100</sup> eNOS,<sup>101</sup> PGC1 $\alpha$ ,<sup>52,102</sup> C/EBP $\beta$ ,<sup>91</sup> CITED4,<sup>103</sup> and miR-222.<sup>94</sup> Thus, we suggest that exercise models provide platforms for discovery of new therapeutic target candidates likely to complement those gleaned from disease models. Below, we will discuss recent developments in our understanding of the molecular mechanisms underlying cardiac aging and the cardioprotective effects of exercise.

## **Molecular Mechanisms of Heart Failure During Aging**

Our understanding of the fundamental mechanisms underlying cardiac aging, and aging in general, is limited. However, recent studies have begun to elucidate the molecular basis for cardiac decline as well as potentially protective molecular pathways. Molecular mechanisms underlying cardiac aging are multifactorial and interactive. Here, we will discuss important findings in recent years concerning the roles of telomere shortening and damage, circulating factors, epigenetic alterations, noncoding RNAs, and somatic mutations in cardiac aging, and insights into the protective effects of exercise (Figure 1).

### **Telomere Shortening and Damage**

Telomeres are DNA repeats serving as protective caps at the end of chromosomes. Telomeric DNA is bound by the shelterin protein complex, which is essential for telomere structure maintenance. Telomeres are synthesized by telomerase, an enzyme composed of an RNA component (TERC) and a catalytic subunit (TERT).<sup>104</sup> Telomeres shorten with cell division and aging, or in response to stressors such as inflammation and oxidative stress. Critically short telomeres destabilize the shelterin complex, thereby disrupting the telomeric DNA structure, leading to DNA damage, cell cycle arrest, cellular senescence, and cell death.<sup>105</sup>

Telomere length is perhaps the best-known cellular marker of aging. Although rates of cardiomyocyte division are extremely low in adults,<sup>33</sup> resulting in minimal end-replication-associated telomere shortening, animal studies have consistently pointed to a key role for telomere shortening in cardiac aging and disease.<sup>106</sup> The wild mouse strain *Mus musculus castaneus* (CAST), which

bears short telomeres from birth, shows a premature cardiac aging phenotype.<sup>107</sup> Similarly, Wong et al<sup>108</sup> showed that breeding multiple generations of TERC-deficient mice induced critical telomere shortening, leading to cardiac dysfunction and myocardial remodeling, similar to the effects of aging. In cardiomyocytes from TERC-deficient mice, Aix et al<sup>109</sup> showed that critically short telomeres marked by  $\gamma$ H2AX, a DNA double strand break biomarker, induced p21-dependent cardiomyocyte cell cycle arrest, consistent with senescence and an aging and diseased cardiac profile. In addition, accelerated telomere shortening has been linked to several hereditary cardiomyopathies in humans, including Duchenne muscular dystrophy,<sup>110</sup> with animal models supporting a causal relationship.<sup>111</sup> Together, these results suggest that accelerated telomere shortening phenocopies the effects of aging on the heart.

Conversely, slowing telomere shortening can protect the heart against pathological stress. Biomechanical stress induced by partial aortic constriction in mice caused reduction in TRF2 (telomeric repeat-binding factor 2), one of the shelterin proteins, leading to activation of the DNA damage response protein Chk2, a reduction in telomere length and cardiomyocyte apoptosis, and these changes were attenuated by cardiac-specific overexpression of TERT or overexpression of TRF2.<sup>112</sup> Cardiac-specific overexpression of telomerase also decreased cardiomyocyte apoptosis during myocardial ischemia reperfusion in vivo or serum-free insulin-free challenge in vitro.<sup>113</sup> Telomere shortening may affect the heart in part by triggering mitochondrial dysfunction. In the third generation TERC<sup>-/-</sup> telomerase-deficient premature aging mouse model, accelerated cardiac aging is associated with p53 mediated suppression of PGC-1 $\alpha$ , leading to mitochondrial dysfunction. Furthermore, cardiac-specific overexpression of PGC-1 $\alpha$  in TERC<sup>-/-</sup> mice partially rescued cardiac function, delayed the onset of age-related cardiac symptoms and extend healthspan.<sup>56</sup> It is worth noting, however, that the value of TERC deficient mice as a model for telomere-associated cardiac aging has been questioned as the degree of telomere shortening in late-generation TERC mice far exceeds the shortening experienced during normal aging.<sup>114</sup> Although there are some caveats to consider, overall results from animal models point to a critical role for telomere length in cardiac cells in mitochondrial function, cardiac aging and HF.

The role of telomere shortening in human cardiac aging and HF, however, is controversial. Terai et al reported that human myocardial telomere length is reduced at a rate of 20 base pairs per year.<sup>115</sup> Compared with cardiac tissues from age- and sex- matched normal or hypertrophic obstructive cardiomyopathy patients without pump failure, cardiac tissues from end-stage HF patients showed shorter telomeres and less TRF2, associated with increased cardiac apoptosis.<sup>112</sup> Similar results were observed in cardiac tissue from end-stage genetic hypertrophic cardiomyopathy and dilated cardiomyopathy patients as well as cardiomyocytes derived from patient-derived induced pluripotent stem cells.<sup>110</sup> These results were confirmed by a recent study showing that, compared with nonfailing controls, HF patients exhibited shorter telomeres specifically in cardiomyocytes but not in cardiac smooth muscle cells from the same hearts.<sup>116</sup> Further, this telomere shortening in HF patients was associated with extensive DNA damage in cardiomyocytes.<sup>116</sup> However, the authors did not observe any difference in cardiomyocyte telomere length between young and old nonfailing controls.<sup>116</sup> These results not only highlight the important role of telomere length in HF but also raise the possibility that telomere shortening does not reflect normal (physiological) cardiac aging. Indeed, most recently, Anderson et al demonstrated that in response to oxidative stress induced by mitochondrial dysfunction during cardiac aging, persistent telomere-associated foci, which contain

DNA damage response proteins and trigger cellular senescence and cell cycle arrest, increased in cardiomyocytes but not in other cell types. This suggests telomere damage in cardiomyocytes occurs independently of telomere length during cardiac aging.<sup>70</sup>

## Secreted Factors

Given the progressive functional decline in multiple organ systems seen with aging, it has long been hypothesized that secreted or circulating factors might contribute to the systemic phenotypes seen with aging. The role of pro-inflammatory SASP factors, such as IL-1 $\alpha$ , IL-1 $\beta$ , IL-6, Cxcl1, have been extensively studied in the context of chronic systemic inflammation leading to HF, but an increasing number of secreted proteins or RNAs other than traditional SASP factors are now also being found to contribute to the development of aging-related disease (Figure 2).<sup>117</sup> An interesting experimental approach to explore the role of circulating factors in aging phenotypes has been the use of the heterochronic parabiosis model, in which animals of different chronological ages are surgically sewn together to develop a shared circulatory system.<sup>118</sup> Indeed, a recent series of studies utilizing this approach in mice found that introducing youthful blood into the circulation of old animals improved age-related neurological, skeletal muscle, and cardiac phenotypes.<sup>119–121</sup> Aptamer-based proteomic analyses of plasma samples from these mice identified 13 differentially expressed proteins, of which circulating levels of growth differentiation factor-11 (GDF11), a secreted member of the TGF $\beta$  superfamily, was reported to be significantly lower in aged mice. Subsequent experiments suggested that increasing circulating levels of GDF11 was sufficient to improve neurogenesis, skeletal muscle regeneration, cardiac hypertrophy regression, and overall fitness in old mice, suggesting the exciting possibility that an age-related decline in a secretory factor like GDF11 might be causal in the systemic functional decline seen in aging.

Numerous follow-up studies, however, have questioned some of these results. More extensive validation of the GDF11 aptamer used in the proteomics analyses revealed that it recognizes not only GDF11, but also the closely homologous protein GDF8 (also known as myostatin), which is likely responsible for the decrease reported in the initial studies.<sup>122</sup> Of note, myostatin knockout mice have better preservation of cardiac function and less cardiac fibrosis as they age, arguing against an age-related reduction in myostatin being detrimental.<sup>123</sup> Interestingly, myostatin is a catabolic protein best known for inducing muscle atrophy and dysfunction, and subsequent work investigating the role of GDF11 overexpression in aged animals demonstrated that both GDF11 and myostatin have similar effects in the skeletal muscle and the heart.<sup>15,124,125</sup> This has raised a number of important questions, including whether this secretory pathway changes with age, and if so, what its functional effects are in aged cardiac and skeletal muscle. Most recently, our group conducted an extensive investigation of this pathway in humans and animal models of aging and HF.<sup>15</sup> We confirmed that circulating GDF8 levels indeed decline with age. However, we found that overall systemic activation of this secreted pathway is actually upregulated in aging and HF, and that its activation appears to be largely driven by an age-related increase in secreted activin, another TGF $\beta$  family member that binds the same receptors as GDF8 and GDF11. We further showed that activation of the ActRIIb receptor downstream of activin triggers Smurf1-mediated ubiquitination and subsequent degradation of the SERCA2a, a Ca<sup>2+</sup> ATPase critical for normal cardiomyocyte contractility (Figure 2). Importantly, targeted inhibition of ActRIIb receptor signaling improved the

function and adverse remodeling of aged or failing hearts, confirming that these secreted factors likely play important roles in cardiac aging and HF.

ANGPTL2 (angiopoietin-like protein 2) is a glycoprotein that has recently been shown to be secreted by cardiomyocytes and adipocytes and to play a role in age-related HF in animal models. Cardiac ANGPTL2 is increased in mice subjected to TAC, angiotensin II-induced HF, and in HF patients. ANGPTL2 is also increased in hearts from aged mice compared with young mice,<sup>126</sup> and in senescent fibroblasts from patients with adult progeria Werner syndrome.<sup>127</sup> Overexpression of ANGPTL2 in the mouse heart induced inactivation of Akt and sarcoplasmic reticulum Ca<sup>2+</sup>-ATPase signaling, leading to cardiac dysfunction, while knockdown of ANGPTL2 protected the heart against HF.<sup>126</sup> Interestingly, the same group further showed that, while circulating ANGPTL2 was increased both in dilated cardiomyopathy patients and in mice subjected to TAC-induced HF, experimentally increasing circulating ANGPTL2 did not induce cardiac dysfunction. Thus, cardiomyocyte-secreted ANGPTL2 may require other signaling mechanism to induce HF or could work through an autocrine/paracrine signaling mechanism not recapitulated with ectopic expression.<sup>128</sup> Interestingly, ANGPTL2 was decreased in exercised hearts,<sup>126</sup> indicating that exercise may protect against HF in part through lowering ANGPTL2 (Figure 3).

In nonpurified cardiomyocytes isolated from old mice compared with those from young mice, significant differences in gene expression of traditional SASP components (eg, IL-6 and Cxcl1) were observed. However, such differences in SASP were not observed in purified cardiomyocytes isolated from old and young mice, indicating that traditional SASP may be secreted from noncardiomyocytes.<sup>70</sup> Interestingly, in the purified cardiomyocytes isolated from old mice, three nontypical SASP signals were identified including Edn3, Tgfb2 and GDF15. Induction of Edn3, Tgfb2 and GDF15 induced neonatal fibroblast activation and senescence, while induction of Edn3 or Tgfb2 but not GDF15 increased neonatal cardiomyocyte size,<sup>70</sup> suggesting that senescent cardiomyocytes can induce senescence in neighboring cells through secretion of nontypical SASP. While these studies provide compelling evidence for a role of secreted factors in aging, further investigations are needed to better define this group of secreted factors and determine how to best target them therapeutically.

Given the antioxidant and anti-inflammatory effects of exercise, it is likely that exercise counteracts the age-related upregulation of some or all of these secretory signaling pathways. Consistent with this, twelve weeks of exercise training resulted in a reduction of myostatin levels in skeletal muscle of chronic HF patients.<sup>129</sup> In rats with chronic HF induced by coronary ligation, four weeks of treadmill training also reduced myostatin protein expression both in the skeletal muscle and the myocardium, and this was associated with improvement of cardiac function.<sup>130</sup> These data are consistent with our observation that cardiac structure and function are better preserved in aged myostatin knockout mice.<sup>123</sup> Other ligands in this family, including GDF11 and activin, were not investigated in these studies but would be of great interest given more recent findings cited above. Future investigation of the effects of exercise on age-related secretory signaling pathways may suggest new therapeutic approaches.

## Epigenetic Alterations

Epigenetics refers to somatically-acquired and/or inherited modifications in gene function that occur, not as a consequence of changes in DNA sequence, but rather as a result of changes in DNA methylation, histone modifications, or chromatin remodeling.<sup>131</sup> Epigenetic changes are a hallmark of aging,<sup>106</sup> and likely contribute to cardiac aging and cardiovascular disease more generally.<sup>132</sup>

DNA methylation, which mainly occurs through attachment of methyl groups to the carbon-5 position in CpG dinucleotide sequences, generally represses gene activity by preventing transcription factors from binding to gene promoters, favoring instead the recruitment of chromatin modifying enzymes.<sup>133</sup> DNA methylation patterns are maintained by DNMT (DNA methyltransferase) 1, while *de novo* DNA methylation is typically mediated by DNMT3a and DNMT3b.<sup>133</sup> Global differences in DNA methylation patterns were observed in patients with two cardiomyopathy-prone premature aging syndromes, Hutchinson-Gilford Progeria and Werner syndrome.<sup>134</sup> DNA methylation increases with age and is negatively correlated with lifespan in mice and humans, and the gradual accumulation of this difference in DNA methylation with age constitutes an “epigenetic clock”, serving as a biomarker for chronological age, or even biological age.<sup>135</sup>

DNA methylation also appears to play a role in HF. In a community-based study involving 1568 residents over the age of 65, significant differences in methylation state at CpG sites were observed in peripheral blood from patients with left ventricular HF with preserved ejection fraction compared with controls.<sup>136</sup> Differential methylation patterns were also found in large genomic regions in cardiomyocytes from neonatal, adult healthy, and adult failing hearts.<sup>137</sup> Similarly, genome-wide DNA methylation profiling revealed significant differences in promoter CpG islands, intragenic CpG islands, and gene bodies in left ventricle tissue from HF patients compared with healthy controls. Among these, the DUX4 locus was associated with differential DNA methylation, which was responsive to DNA methylation inhibition. Gene knockdown of DUX4 in a mouse HL1 cardiac cell line led to a decrease in cell viability, suggesting a possible causal role for DUX4 methylation in cardiac dysfunction.<sup>138</sup> Further supporting a causal role for DNA hypermethylation in HF, hypermethylation was found in hearts from rats with norepinephrine-induced cardiac hypertrophy, associated with elevated ROS production in the heart. Inhibition of DNMT reduced norepinephrine-induced cardiac ROS level and reversed both norepinephrine-induced cardiac hypertrophy and HF.<sup>139</sup> Most recently, Dorn et al showed that enhancement of METTL3-mediated N<sup>6</sup>-Methyladenosine methylation induced compensated cardiac hypertrophy, whereas its diminishment induced cardiac dysfunction,<sup>140</sup> pointing to the importance of methylation in cardiac disease.

Histone proteins are responsible for maintaining chromatin structure and mediating dynamic and long-term gene regulation. Reduction of histone expression, maturation or deposition during replication leads to histone depletion, a feature of cellular aging.<sup>141</sup> Telomere attrition-induced DNA damage triggers global histone depletion, chromatin disorganization and genomic instability, thereby inducing cellular senescence.<sup>142</sup> This, along with the fact that telomere attrition is a hallmark of aging that may contribute to HF in aging hearts, suggests a possible link between histone levels and HF during aging.

In addition to histone levels, post-translational histone modifications, particularly acetylation, are also implicated in the regulation of chromatin structure and cardiac function in aging. Histones are

acetylated by histone acetyltransferases and deacetylated by HDACs (histone deacetylases). The roles of HDACs in regulating cardiac homeostasis and longevity have been examined in various HDAC deletion or overexpression mouse models, which have led to the conclusion that loss of specific HDAC isoforms promotes cardiac hypertrophy, dysfunction and vulnerability to cardiac injury, in some cases mimicking the effects of aging.<sup>143-145</sup> Cardiac-specific knockout of Sirt1 (an NAD<sup>(+)</sup>-dependent histone deacetylase) in young mice (4-6 months) recapitulates the exacerbated response to ischemia reperfusion normally observed in older mice (24-26 months), including cardiac dysfunction, cardiac metabolic phenotypes and mitochondrial dysfunction (increase in mitochondria fission, reduction in mitochondrial density, and increase in mitochondrial DNA damage) in response to ischemia reperfusion.<sup>146</sup> Mechanistically, cardiac specific Sirt1 knockout leads to mitochondrial biogenesis defects in which liver kinase B1 (LKB1) hyperacetylation compromises AMPK activation and acetyl-CoA carboxylase phosphorylation, resulting in cardiac dysfunction that can be reversed by Sirt1 overexpression.<sup>146</sup> Age-related chromatin modifications have also been linked to changes in DNA damage repair, potentially contributing to senescence and loss of functional cardiomyocytes. In aged mice, loss of histone 4 lysine 20 trimethylation disrupts DNA damage repair and causes TGF- $\beta$ /miR-29-induced cardiac dysfunction, whereas disruption of TGF- $\beta$  signaling restores histone 4 lysine 20 trimethylation and improves cardiac function. These findings are consistent with a role for histone modification in cardiac dysfunction during aging.<sup>147</sup>

Although loss of specific HDACs causes cardiac dysfunction in animal models, pharmacological HDAC inhibition appears to protect against age-related heart dysfunction. While cardiac diastolic function progressively declined in aged mice fed with normal chow, it was preserved out to 20 months of age in aged mice fed with ITF2357, an HDACs inhibitor currently in a phase 3 trial for treating patients with Duchenne muscular dystrophy, and this was associated with improved myofibril relaxation.<sup>16</sup> The apparently conflicting outcomes of targeted elimination of specific HDACs versus pharmacological HDAC inhibition likely reflects the broad isoform specificity of pharmacological intervention. Interestingly, studies of exercise have revealed dynamic regulation of specific HDAC isoforms in the heart. High volume swimming exercise in rats induced physiological cardiac growth that was associated with down regulated HDAC3 and 4 but up regulated HDAC1.<sup>148</sup> Moreover, in aged mice (18-month-old) with myocardial infarction, eight weeks of swimming training improved cardiac function and mitochondrial biogenesis, which was associated with increased cardiac Sirt3.<sup>149</sup> Gain- and loss-of-function studies have yielded some insight into the specific mechanisms of action of different HDACs in the heart.<sup>150</sup> However, further investigation is needed to clarify their functional roles in exercise-mediated beneficial effects on the aging heart.

Bromodomain and extraterminal domain (BET) proteins are histone acetylation “readers” that recognize acetyl-lysine labels on histones and nonhistone proteins and serve to interpret and transmit the signals initiated by histone acetylation.<sup>151</sup> The BET family consists of BRD2, BRD3, BRD4, and testis-specific BRDT, with BRD4 being the most abundant isoform in the heart.<sup>152</sup> BET inhibition by the selective inhibitor JQ1 or siRNA reduced cardiac fibrosis and apoptosis and attenuated cardiac hypertrophy and pathological gene induction in phenylephrine-treated neonatal rat cardiomyocytes in vitro or in mice subjected to TAC or phenylephrine infusion in vivo. Further molecular analysis showed that BETs serve as co-activators for transcription factors implicated in HF, including NFAT (nuclear factor of activated T cells); NF- $\kappa$ B (nuclear factor- $\kappa$ B); and GATA4.<sup>152</sup> This effect of BET inhibition was confirmed by the same group in human induced pluripotent stem

cell-derived cardiomyocytes, where the BET inhibitor JQ1 blocked agonist-induced hypertrophy.<sup>153</sup> They further showed that BET inhibition confers this protective effect by blocking NF- $\kappa$ B and TGF- $\beta$ -mediated innate inflammatory and profibrotic gene networks. Given the contributions of inflammatory and profibrotic genes to the pathogenesis of age-related HF, it is possible that pharmacological BET inhibition could also protect against cardiac aging phenotypes and age-related HF.

## Noncoding RNAs

Noncoding RNAs (ncRNAs) are functional RNA molecules that are transcribed from DNA but not translated into proteins. In general, ncRNAs can be classified into two categories based on their length as small ncRNAs (< 200 nucleotides) and long ncRNAs (lncRNAs). ncRNAs have been increasingly recognized as important regulators and biomarkers of cardiac aging and disease.

MicroRNAs (miRNAs) are endogenous small ncRNAs, approximately 22 nucleotides long that work as post-transcriptional regulators by binding to complementary sequences of messenger RNAs (mRNAs) to inhibit mRNA translation or to promote mRNA degradation.<sup>154</sup> A number of miRNAs have been found to have pathophysiological roles in HF. In a screen for 380 miRNAs in cardiomyocytes, miRNA (miR)-22 was identified as an abundant and strong inhibitor of cardiac autophagy, whose expression level increased during aging in mice *in vivo* and in cardiomyocytes *in vitro* by a p53-dependent mechanism.<sup>155</sup> Pharmacological inhibition of miR-22 in mice prevented post-infarction cardiac remodeling and improved cardiac function by activating autophagy in old mice. Moreover, circulating miR-22 was increased in patients with systolic HF associated with early mortality.<sup>155</sup> miR-34a is predominantly expressed in cardiomyocytes, and is upregulated in aging mouse hearts and in biopsies from aging human hearts. Silencing of miR-34a reduced cardiomyocyte cell death in aged hearts and improved recovery of cardiac infarction. Phosphatase-1 nuclear targeting subunit (PNUTS) was identified as downstream target of miR-34a.<sup>156</sup> More recently, Lyu et al demonstrated that miR-29a and -29c mediated TGF- $\beta$ /Smad-induced senescence by suppressing Suv4-20h. This reduces histone 4 lysine 20 trimethylation, which compromises DNA damage repair and genome maintenance, contributing to cardiac aging and cardiac dysfunction.<sup>147</sup> Moreover, miR-128 has been showed to increase progressively in cardiomyocytes during the postnatal switching from proliferation to terminal differentiation. Deletion of miR-128 promoted cell cycle re-entry in adult cardiomyocytes, reduced cardiac fibrosis and improved cardiac function after myocardial infarction.<sup>157</sup> Identification of noncoding RNA pathways where inhibition has cardiac benefits could have important practical implications given that modified oligonucleotide antisense approaches appear highly effective in both animal models and clinical trials.<sup>158,159</sup>

In contrast to these pathological miRNA-dependent pathways, other miRNAs promote cardiac health. The miRNAs miR-18 and miR-19 were down regulated in HF-prone but up regulated in HF-resistant aged hearts, where they regulated aging cardiomyopathy through targeting profibrotic pathways involving TGF- $\beta$  and thrombospondin-1 signaling.<sup>160</sup> Eulalio et al found that induction of miR-199 and miR-590 promoted cell cycle re-entry of adult cardiomyocytes *ex vivo*, and that overexpression of these miRNAs in adult mice undergoing myocardial ischemia reperfusion can induce cardiac regeneration and improve cardiac function.<sup>161</sup>

We and others have also identified miRNAs that act as important mediators of exercise-induced cardiac growth and cardiomyogenesis, further expanding the repertoire of potential therapeutic targets of cardiac aging and cardiac disease. Cardiac miR-222 is upregulated in mice after swimming or voluntary wheel running exercise training, and this was associated with physiological cardiac growth and birth of new cardiomyocytes.<sup>93,94</sup> This effect was abolished by inhibition of miR-222, indicating miR-222 is necessary for exercise-induced physiological cardiac growth (Figure 3). Molecular studies further indicated that miR-222 acts through downregulation of HIPK1, p27, and HMBOX1.<sup>93,94</sup> Interestingly, the exercise-induced downregulation of the pathophysiological secreted signaling protein ANGPTL2 was also blocked by miR-222 inhibition.<sup>126</sup> An area of growing interest concerns the role of exercise-induced exosomes in cardiac health. Exosomal miR-342-5p was increased in plasma from volunteers who had been on a rowing team for over 1 year and in rats with 4 weeks of swimming training. Increase miR-342-5p protected cardiomyocytes against hypoxia reoxygenation-induced cell apoptosis via Jnk2/Caspase 9 and Ppm1f/Akt signaling.<sup>162</sup> All of these data point to miRNAs as important mediators of the beneficial effects of exercise on the heart. However, whether or not miRNAs play a role in the beneficial effects of exercise in the aging heart needs further investigation. Moreover, given that a single miRNA may have over 100 predicted targets, additional studies delineating miRNA biology, and identifying the relevant downstream targets in cardiac aging, are needed.

Unlike miRNAs, lncRNAs are poorly conserved across species, and most known lncRNAs are tissue- and developmental stage-specific. lncRNAs regulate cardiac development, cardiac aging, and disease through multiple mechanisms including epigenetic regulation, transcriptional regulation, nuclear compartmentalization, and post-transcriptional gene regulation, and by acting as competing RNA sponges. Zhang and colleagues found that lncRNA H19 is down regulated in D-galactose-induced senescence in neonatal rat cardiomyocytes associated with loss of cardioprotection of ischemic postconditioning. Furthermore, H19 gene silencing exacerbated post-hypoxic cell injury in senescent cardiomyocytes by releasing miR-29b-3p, thereby down-regulating cIAP1.<sup>163</sup> lncRNA metastasis-associated lung adenocarcinoma transcript 1 is decreased in aged hearts and in senescent hearts induced by D-galactose. Infusion of umbilical cord mesenchymal stem cell-derived exosomes from young mice into D-galactose-induced senescent hearts improved cardiac function and increased telomere length by downregulating TNF $\alpha$  and p65, while these effects were reduced by silencing metastasis-associated lung adenocarcinoma transcript 1 in umbilical cord mesenchymal stem cell-derived exosomes. This suggests that the age-related decline in exosomal metastasis-associated lung adenocarcinoma transcript 1 may contribute to cardiac dysfunction in aged hearts, and that combating this decline could have beneficial effects.<sup>164</sup>

By microarray screening, lncRNA ENSMUST00000134285 was found to be upregulated in aged mouse hearts (18 months) compared with young mice (8 weeks). Interestingly, lncRNA ENSMUST00000134285 knockdown increased while overexpression decreased post-hypoxic cell apoptosis in neonatal mice cardiomyocytes through miR-760/MAPK11 signaling.<sup>165</sup> This suggests a protective role for the aging-dependent increase in lncRNA ENSMUST00000134285, which is somewhat counterintuitive given the evidence of increased cardiomyocyte loss in aging.

Circular RNAs are a newly identified subtype of lncRNAs, which are generated from back-splicing of premRNA. Specific circular RNAs have recently been shown to have a role in cardiac regenerative

repair. circNfix was upregulated in adult heart under the regulation of a super enhancer. Knockout of circNfix promoted cardiomyocyte proliferation and angiogenesis and improved post-infarction cardiac functional recovery through suppression of Ybx1 ubiquitin-dependent degradation and enhancement of miR-214 activity.<sup>166</sup> In separate studies, cardiac circFndc3b was found to decrease after ischemia-reperfusion injury in animals and in ischemic cardiomyopathy patients. Induction of circFndc3b through FUS/VEGF-A axis promoted cardiac repair after ischemia reperfusion injury.<sup>167</sup> Interestingly, circFndc3b was also downregulated in hearts from 22-month-old as compared with 1-month-old mice,<sup>168</sup> raising the possibility that downregulation of circFndc3b contributes to cardiac aging and that overexpression of circFndc3b may provide cardiac protective effects in aging hearts. However, research determining the role of lncRNA in cardiac aging is still in its infancy. Further investigation is needed to unveil fully the role of lncRNAs in cardiac aging.

## Somatic DNA Mutations

Somatic DNA mutations accumulate over time in many tissues, representing not only a hallmark of the aging process but also a potential cause of cardiac aging and diseases.<sup>169,170</sup> Due to the high rate of mutation and limited repair capacity of mitochondrial DNA, mtDNA mutation is a common feature in cellular aging and cardiac disease.<sup>170</sup> Mitochondrial DNA mutations compromise the integrity of the mitochondrial genome, thereby impairing mitochondrial biogenesis and increasing mitochondrial ROS production, and are perhaps the best-studied somatic DNA mutations in cardiac aging and disease.<sup>104</sup> The direct roles of mtDNA mutations in cardiac aging and disease have been supported by evidence from several mouse models. In “mutator” mice with homozygous mutation of mitochondrial polymerase gamma ( $\text{Polg}^{\text{m/m}}$ ), and in mice with disruption of the mitochondrial DNA helicase Twinkle ( $\text{Twnk}$ ), mitochondrial function was compromised, leading to oxidative damage as well as accelerated cardiac aging and cardiac dysfunction.<sup>171–173</sup> As early as 8 weeks old, the accumulation rate of mtDNA mutations is 3 to 5 times higher in mutator mice compared with wild-type controls in multiple tissues including the heart. By 6 months, mutator mice develop premature aging phenotypes. Within the first year after birth, mutator mice exhibit cardiac hypertrophy and dilated cardiomyopathy as well as cardiac fibrosis, with an average lifespan of 12 months.<sup>171,173</sup> Although ROS markers were normal in  $\text{Polg}^{\text{m/m}}$  mice, the accelerated cardiac aging and HF phenotypes in these animals were partially rescued by crossing with mCAT antioxidant overexpressing mice, suggesting a role for oxidative damage.<sup>174–176</sup> Similarly, in mice overexpressing dominant-negative Twnk helicase in the myocardium, mtDNA deletions accumulated at an accelerated rate in cardiomyocytes, and this was paralleled by mitochondrial deficiency and the development of arrhythmias, a common correlate of aging.<sup>172</sup> In contrast, mice with targeted mutation of the  $\text{p66}^{\text{Shc}}$  gene involved in mitochondrial ROS production display prolonged lifespan, reduced ROS production and resistance to ROS-mediated apoptosis.<sup>177</sup> Moreover, disruption of  $\text{p66}^{\text{Shc}}$  protected against angiotensin-II induced cardiac hypertrophy and cardiomyocyte apoptosis as well as reducing oxidative damage in multiple cardiovascular lineages in diabetic mice.<sup>178–180</sup> All of these observations highlight the importance of mtDNA mutations in cardiac aging and diseases. Notably, in mutator mice, 6 months of treadmill exercise training reduced mtDNA mutation, attenuated mitochondrial dysfunction and extended lifespan,<sup>181</sup> indicating a protective role of exercise in mtDNA repair during aging.

In another example of the detrimental effects of somatic mutations, using whole-genome sequencing of blood-derived DNA in humans, Jaiswal and colleagues demonstrated that clonal expansion of hematopoietic cells with somatic mutations in leukemogenic genes increased with age and correlated with increased mortality. They termed this phenomenon clonal hematopoiesis of indeterminate potential (CHIP).<sup>182</sup> They further showed that CHIP in peripheral blood cells was associated with a nearly doubled risk of coronary heart disease or early-onset myocardial infarction.<sup>183</sup> This was supported by mouse models with CRISPR-mediated inactivation of ten-eleven translocation enzymes 2 (Tet2) or DNA Methyltransferase 3a (Dnmt3a), the two commonly mutated genes in CHIP. Inactivation of Tet2 or Dnmt3a in hematopoietic stem/progenitor cells also worsened cardiac function in mice infused with angiotensin-II, and this was mediated by elevated inflammation.<sup>184</sup> Similar effects of Tet2 inactivation in hematopoietic cells were observed in two other heart failure mice models. Sano et al showed that Tet2 inactivation in hematopoietic cells worsened late-stage cardiac remodeling through effects on IL-1 $\beta$ /NLRP3 inflammasome activity, and reduced cardiac function in mice with HF induced by permanent left anterior descending artery ligation or TAC.<sup>185</sup> Given that CHIP has been found to be relatively common in asymptomatic, cancer-free older individuals,<sup>183,186</sup> the association between CHIP and cardiac disease in the elderly provides a potential causal link between somatic mutation and aging-related cardiovascular disease. CHIP-associated mutations may provide useful markers for assessing cardiovascular risk in aging populations independent of traditional cardiometabolic risk factors. Moreover the link to inflammatory signaling raises the possibility that therapies directed at specific mediators of inflammation, such as antibodies to IL-1 $\beta$ ,<sup>187</sup> might be particularly beneficial in subjects with a high burden of CHIP.

While all organs are subject to accumulation of somatic mutations over time, the cells of the cardiovascular system may be particularly prone to DNA damage due to the hemodynamic forces and mechanical strain these cells experience. In a process known as mechanosignaling, physical stresses can modulate intracellular signaling pathways, including pathways that protect the cell from DNA damage, and the activity of these mechanosensitive protective pathways may change over time. Lamin A is a mechanosensitive nuclear structural protein that promotes DNA damage control in cardiomyocytes by preventing strain-induced breaches in the nuclear membrane.<sup>188</sup> Genetic perturbations of lamin A in human patients result in dilated cardiomyopathy, likely reflecting excessive activation of the platelet-derived growth factor pathway, and are also associated with a premature aging phenotype similar to that resulting from disruption of DNA repair enzymes.<sup>189,190</sup> Lamin A levels are greatest in cell types that experience a high degree of physical strain, and physical strain is required to maintain lamin A levels in cardiomyocytes by blocking its MMP-dependent degradation.<sup>190</sup> Notably, accumulation of the lamin A precursor, prelamin A, increases with age in arterial vascular smooth muscle cells, and results in DNA damage and senescence in these cells, suggesting that this protective mechanosignaling mechanism may become pathologically dysregulated in the aging cardiovascular system.<sup>191</sup> In addition to its protective structural role, lamin A levels also regulate histone methylation in lamin A-associated domains near the nuclear membrane in iPSC-derived cardiomyocytes, raising the interesting possibility that declining lamin A may also contribute to epigenetic changes observed with age.<sup>190</sup>

## Conclusions and Perspectives

Given the aging of populations around the world and the associated increase in HF prevalence, there is a compelling need to develop therapeutic interventions that mitigate age-related HF. New candidates for intervention have emerged as our knowledge of the biology of aging and HF has progressed in recent years. Moreover, exercise studies have provided complementary insights in the search for new targets.<sup>21,52,91,94,96–100,102,103,192–194</sup> We can anticipate that as a deeper understanding of the fundamental biology of aging develops, there will be additional opportunities for translation in the future. Since biological aging and HF are complex and multifactorial systemic processes, it seems unlikely that any single pathway or intervention will fully mitigate age-related cardiac phenotypes. However, we are optimistic that insights gained through studies of aging biology and its interplay with cardiovascular pathophysiology will lay a foundation for new therapeutic strategies that can at least mitigate some features of age-related heart disease and may even be generalizable to other forms of heart failure.

## **Nonstandard Abbreviations And Acronyms**

<b>ANGPTL2</b>	<b>angiopoietin-like protein 2</b>
<b>BET</b>	<b>bromodomain and extraterminal domain</b>
<b>CHIP</b>	<b>clonal hematopoiesis of indeterminate potential</b>
<b>Chk2</b>	<b>checkpoint kinase 2</b>
<b>DNMT</b>	<b>DNA methyltransferase</b>
<b>Edn3</b>	<b>endothelin 3</b>
<b>GDF</b>	<b>growth/differentiation factor</b>
<b>HDACs</b>	<b>histone deacetylases</b>
<b>HF</b>	<b>heart failure</b>

<b>lncRNA</b>	<b>long noncoding RNA</b>
<b>mtDNA</b>	<b>mitochondrial DNA</b>
<b>ncRNAs</b>	<b>noncoding RNAs</b>
<b>PGC-1<math>\alpha</math></b>	<b>proliferator-activated receptor <math>\gamma</math> coactivator 1<math>\alpha</math></b>
<b>Pol<math>\gamma</math></b>	<b>polymerase <math>\gamma</math></b>
<b>ROS</b>	<b>reactive oxygen species</b>
<b>SASP</b>	<b>senescence-associated secretory phenotype</b>
<b>SCOT</b>	<b>succinyl-CoA:3-oxoacid CoA transferase</b>
<b>TAC</b>	<b>transverse aortic constriction</b>
<b>TERT</b>	<b>telomerase reverse transcriptase</b>
<b>Tgf<math>\beta</math>2</b>	<b>transforming growth factor <math>\beta</math> 2</b>
<b>TRF2</b>	<b>telomeric repeat-binding factor 2</b>

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## Disclosures

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## Footnotes

For Sources of Funding and Disclosures, see page 546.

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