

stem cells, which have a high level of telomerase activity and demonstrate consistent telomere length, most somatic cells including vascular cells show progressive telomere shortening due to low telomerase activity (Figure 1B). Critically short telomeres—those that cannot successfully complete replication—resemble damaged DNA and thus trigger cellular senescence via a p53-dependent pathway (Figure 1A).<sup>13</sup> Studies have demonstrated that nuclear foci containing markers of double-stranded DNA breaks form in cells with critically short or dysfunctional telomeres,<sup>14,15</sup> and that the number of such nuclear foci induced by telomere dysfunction increases in the fibroblasts of aging primates.<sup>16</sup>

Telomere shortening also occurs in human vessels and could be related to the development of atherosclerosis. The length of telomeres isolated from endothelial cells of human arteries shows a strong inverse correlation with age.<sup>17,18</sup> Interestingly, telomere shortening over time occurs faster in the endothelial cells of the iliac arteries than in those of the internal mammary arteries.<sup>17</sup> Thus, a high level of hemodynamic stress, such as that seen in the iliac arteries, could increase endothelial cell turnover to levels higher than those seen in vessels that are subject to less stress. Of note, telomeres are shorter in coronary artery endothelial cells from patients with coronary heart disease than in the same cells from healthy individuals.<sup>19</sup> Voghel *et al.* demonstrated that endothelial telomere length was shorter in patients with a long history of risk factors for cardiovascular disease than in those who had been at risk for less time.<sup>20</sup> These findings suggest that cardiovascular risk factors override the effects of chronological aging on endothelial cell turnover by accelerating stress-induced damage. Identification of factors that accelerate the attrition of endothelial telomere length will facilitate the development of targeted treatments for human atherosclerosis.

#### Role of telomeres in vascular senescence

Investigations have shown that disturbance of telomere integrity can lead to endothelial dysfunction *in vitro*.<sup>10</sup> Human endothelial cells and VSMCs demonstrate telomerase activity, which is markedly increased by mitogenic stimuli;<sup>21</sup> however, as the cells age this activity declines because of decreased expression of the catalytic component of telomerase, leading to telomere shortening and cellular senescence.<sup>22</sup> The introduction of telomerase into human

endothelial cells *in vitro* prevents progression to senescence-associated endothelial dysfunction, including the decrease in endothelial nitric oxide synthase activity and increase in monocyte adhesion to endothelial cells.<sup>10,23</sup> Introduction of telomerase has been used as a method to produce immortalized human endothelial cells, which seem to retain endothelial cell characteristics including various cell-surface markers.<sup>24</sup> When cultured in Matrigel® (BD Biosciences, San Jose, CA), these immortalized cells form capillary-like structures as efficiently as healthy, young endothelial cells.<sup>25</sup>

First-generation, telomerase-deficient mice have a normal phenotype, presumably because mice possess longer telomeres than humans.<sup>26,27</sup> With successive generations, however, the telomeres become shorter. By the sixth generation these mice become infertile due to impairment of their reproductive system.<sup>27</sup> Some of the abnormalities seen in later generations of telomerase-deficient mice mimic age-associated changes. For example, these animals have a shortened life span and a reduced capacity to respond to stresses such as wounds and hematopoietic ablation.<sup>28</sup> Later generations of telomerase-deficient mice also have impaired neovascularization,<sup>29</sup> which could be attributable to impairment of the function and replication of vascular endothelial cells by telomere shortening. In a mouse model of atherosclerosis, Poch *et al.* showed that telomere shortening decreased the size of atherosclerotic lesions, presumably due to reduced proliferation of macrophages.<sup>30</sup> Telomerase-deficient mice, however, develop atherosclerotic plaques with thin fibrous caps, indicating that shortening of vascular-cell telomeres could lead to plaque rupture in human atherosclerosis. First and third generation mice lacking telomerase develop hypertension as a result of an increase in levels of plasma endothelin 1 caused by overexpression of endothelin-converting enzyme. This upregulation is mediated by increased levels of reactive oxygen species and involves an activator-protein-1-dependent mechanism.<sup>31</sup>

#### Stress-induced premature senescence

In response to various stress signals, cells can develop a phenotype indistinguishable from that of senescent cells at the end of their replicative life span. For example, the constitutive activation of mitogenic stimuli by expression of the *ras* oncogene induces a senescent phenotype

in vascular cells.<sup>11</sup> Cellular senescence triggered by mitogenic stimuli is independent of replicative age, and mitogenic signals influence cell function before the replicative limit of a cell is reached. This form of senescence is apparently telomere-independent and thus termed 'stress-induced premature senescence'. Angiotensin II is a potent mitogen and one of the main effectors of *ras*. Arterial expression of angiotensin II increases with age, and this upregulation is thought to contribute to the pathogenesis of atherosclerosis. Inhibition of angiotensin II activity has been demonstrated to improve cardiovascular-related morbidity and mortality.<sup>32</sup> Angiotensin II has been reported to induce premature senescence of human VSMCs *in vitro* via the p53/p21-dependent pathway.<sup>33</sup> Furthermore, angiotensin II increased the proportion of senescent VSMCs and induced the expression of proinflammatory molecules, as well as p21, in aortic atherosclerotic lesions in a mouse model of atherosclerosis.<sup>33</sup> By knocking out p21 in these mice, the induction of proinflammatory molecules by angiotensin II was markedly reduced, thereby preventing the development of atherosclerosis.

Oxidative stress and DNA damage can induce premature senescence in vascular cells, and it has been theorized that both processes contribute to atherogenesis.<sup>33,34</sup> Evidence indicates that subjecting human endothelial cells to chronic oxidative stress, including exposure to oxidized LDL, enhances telomere shortening and accelerates the onset of senescence.<sup>35</sup> Conversely, treating endothelial cells isolated from patients with severe coronary heart disease with antioxidants can preserve telomere length and extend cell life, unless the oxidative stress-induced damage is severe and therefore irreversible.<sup>36</sup> Oxidative stress targets DNA among other cellular targets, and could induce DNA damage. Many different types of oxidative-stress-related DNA lesions have been described, ranging from base modifications to single-strand and double-strand breaks.<sup>37</sup>

To cope with DNA damage, cells have evolved DNA repair systems. Some strains of mice that lack components of these systems exhibit early onset of changes associated with aging, comparable to those seen in humans.<sup>37</sup> Fibroblasts from these mice also show accelerated senescence compared with normal counterparts.<sup>37</sup> In another set of mouse studies, constitutive activation of p53 caused premature aging

characterized by a reduced life span, osteoporosis, organ atrophy and diminished stress tolerance.<sup>38,39</sup> More importantly, phenotypic evidence of cellular senescence has been detected *in vivo* by studies of mice with premature aging disorders.<sup>40</sup> Considered together with the data from studies of telomerase-deficient mice, these results provide *in vivo* evidence that links cellular senescence to aging of the organism in question.

Although there are only a few reports indicating that mice with premature aging are prone to developing atherosclerosis, it is assumed that atherogenic stimuli such as oxidized LDL and angiotensin II increase cell turnover at sites of atherosclerosis and thus promote telomere shortening and possibly trigger oxidative stress-induced DNA damage. It is likely that senescence of vascular cells is triggered by both telomere-dependent and telomere-independent mechanisms, and that both mechanisms are involved in the development of human atherosclerosis.

#### SENESCENCE OF ENDOTHELIAL PROGENITOR CELLS

Maintenance of a healthy endothelium is essential for blood vessels to function properly and prevents the development of vascular diseases such as atherosclerosis. With increasing age, endothelial integrity becomes progressively impaired. Damaged endothelial cells can be replaced through replication of the surrounding endothelial cells, a process that induces senescence of the surrounding endothelium.

#### Effect of age on number and function of endothelial progenitor cells

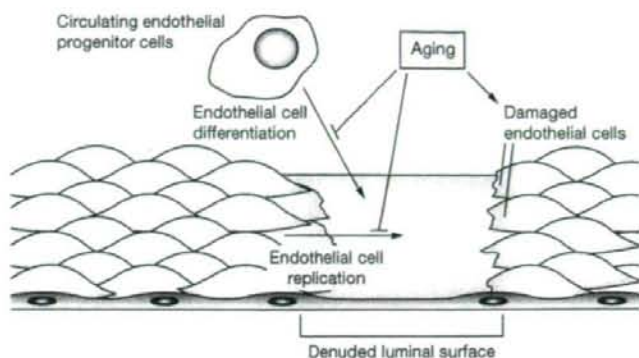
Bone-marrow-derived circulating endothelial progenitor cells (EPCs) have been identified in the peripheral blood in humans<sup>41,42</sup> and have been shown to contribute to both physiological and pathological vascularization in adults.<sup>43</sup> Accumulating evidence suggests that circulating EPCs also have a critical role in vascular repair,<sup>44</sup> although the precise role(s) of EPCs is still controversial.<sup>45</sup> Age-dependent impairment of vascular repair and neovascularization after tissue ischemia might be a consequence of reduced availability and impaired function of EPCs, as well as the limited regenerative capacity of mature endothelial cells (Figure 2).

Consistent with this notion, the number of EPCs in healthy individuals is reported to



reduce with increasing age.<sup>46</sup> Patients with coronary artery disease (CAD) have lower levels of EPCs than healthy controls, and the number of EPCs in patients with CAD also decreases with age, independent of any coronary risk factors.<sup>47</sup> Interestingly, reports suggest that the number of risk factors for cardiovascular disease is significantly correlated with the levels of circulating EPCs. Moreover, *in vitro* migration analysis has demonstrated that EPC function is severely impaired in patients with CAD and that this impairment becomes more serious with increasing age.<sup>47</sup> In patients undergoing CABG surgery, mobilization of EPCs was found to be impaired in older patients compared with younger individuals, suggesting that the responsiveness of EPCs declines with increasing age.<sup>48</sup> Hill *et al.* reported a strong correlation between number of EPCs and Framingham risk score in a population of individuals with no history of cardiovascular disease.<sup>49</sup> Moreover, flow-mediated vasodilation is significantly correlated with number of circulating EPCs.<sup>49</sup>

Transplantation of bone-marrow-derived mononuclear cells (BMCs) into ischemic tissues has been shown to improve perfusion in young mice (8 weeks), but the effect is markedly weaker when BMCs from older animals (18 months) are used.<sup>50</sup> Heeschen *et al.* transplanted BMCs into ischemic hind limbs of nude mice and found that blood flow recovery was significantly impaired in the group treated with BMCs from subjects with CAD compared with those who received BMCs from healthy subjects.<sup>51</sup> Likewise, incorporation of BMCs from subjects with CAD into vascular structures of ischemic limbs was markedly reduced. Consistent with the results of animal studies, recent clinical trials have reported limited benefit of autologous cell therapy in patients with CAD.<sup>52</sup> Conversely, age-associated impairment of cardiac angiogenesis in mice can be reversed by implantation of bone-marrow-derived EPCs from young animals.<sup>53</sup> Moreover, chronic treatment with bone-marrow-derived EPCs from young mice deficient in apolipoprotein E (apoE) prevents the progression of atherosclerosis in apoE-deficient recipients, but the effectiveness of this therapy is reduced when the donor is older.<sup>54</sup> In apoE-deficient recipients, this treatment seems to prevent endothelial senescence and vascular inflammation, as analysis of treated animals shows that they have longer telomeres in vascular cells and lower plasma levels of



**Figure 2** Endothelial repair. Replacement of damaged endothelial cells could occur through replication of surrounding endothelial cells. Bone-marrow-derived circulating endothelial progenitor cells also have a crucial role in endothelial repair. The number drops and the function of these cells become progressively impaired with age, while an age-associated increase of endothelial damage causes exhaustion of the endothelial repair system, thereby inducing cardiovascular aging.

cytokines. Likewise, systemic transfusion of splenic mononuclear cells can ameliorate endothelial dysfunction in apoE-deficient mice.<sup>55</sup> These results suggest that age-associated deterioration of EPCs contributes to the impairment of vascular repair in elderly subjects, thereby increasing the morbidity caused by cardiovascular disease. This impairment needs to be considered when elderly patients are treated with autologous EPCs.

#### Potential mechanisms of age-associated dysfunction of endothelial progenitor cells

Various factors seem to be involved in age-associated deterioration of EPC number and function. Reports suggest that cardiovascular risk factors such as dyslipidemia, hypertension and diabetes mellitus affect the number and function of circulating EPCs,<sup>6</sup> and that a reduced level of circulating EPCs can predict the occurrence of cardiovascular events.<sup>56</sup> EPC dysfunction could result from accelerated senescence (caused by CAD risk factors) and subsequent exhaustion of the pool of progenitor cells. Although the definition and role of EPCs remains to be determined, we believe that aging of stem and/or progenitor cells contributes to the pathology of age-associated disease. As with mature vascular cells, EPCs seem to undergo senescence via both telomere-dependent and telomere-independent mechanisms.

#### Effect of senescence on function of endothelial progenitor cells

The telomere length of white blood cells has been shown to decline with advancing age in healthy individuals and more-rapid telomere shortening occurs in white blood cells from patients with CAD,<sup>57</sup> implying that age and coronary risk factors could influence telomere length in EPCs. Consistent with this notion, elderly individuals have a higher number of senescent EPCs than young subjects.<sup>46</sup> EPCs from individuals at high risk of cardiovascular events show a higher rate of senescence *in vitro* than do EPCs from individuals with a low cardiovascular risk, possibly because EPCs 'age' at a faster rate in patients at risk of cardiovascular events and these individuals therefore have a proportionally greater number of senescent EPCs than healthy persons.<sup>49</sup>

Progressive shortening of EPC telomeres in CAD patients with the metabolic syndrome is associated with increased oxidative stress rather than age.<sup>58</sup> Likewise, early onset of senescence and activation of the p53/p21 signaling pathway have been detected in EPCs from patients with diabetes.<sup>59</sup> Deletion of p53 inhibits senescence of EPCs from individuals with diabetes and restores the ability of these cells to form tube-like structures.<sup>59</sup> A number of *in vitro* experiments have suggested that senescence has a potential role in age-associated impairment of EPC function. Exposure of cultured EPCs to oxidized LDL induces dose-dependent functional impairment and accelerates EPC senescence, possibly by inactivation of telomerase.<sup>60</sup> An increase in angiotensin II levels also diminishes telomerase activity and accelerates the onset of EPC senescence through an increase in oxidative stress.<sup>60</sup> Both angiotensin-II-induced senescence and angiotensin-II-induced inhibition of telomerase activity could be blocked by antioxidants. Homocysteine is another powerful coronary risk factor that can inhibit telomerase activity, thereby accelerating the senescence of EPCs.<sup>61</sup>

Conversely, introduction of telomerase has been shown to enhance the regenerative and angiogenic ability of EPCs, increasing the therapeutic efficiency of these cells in a murine model of hind limb ischemia.<sup>62</sup> Statin therapy is reported to reduce senescence of isolated human EPCs by modulating cell-cycle regulators and telomere binding protein.<sup>63,64</sup> Estrogen also increases telomerase activity and thus inhibits EPC senescence.<sup>6</sup>

#### Role of cytokines in regulating function of endothelial progenitor cells

Humans exhibit an age-dependent decline in the production of angiogenic cytokines and growth factors that is related to age-associated impairment of EPC function. This decline in angiogenic stimuli is partly attributable to an impaired response to ischemic injury. For example, aging decreases the stability of hypoxia-inducible factor 1 $\alpha$  (HIF-1 $\alpha$ )—a transcription factor that mediates the adaptive response to hypoxia—resulting in decreased expression of stromal-cell-derived factor and vascular endothelial growth factor.<sup>65,66</sup> Introduction of a constitutively activated form of HIF-1 $\alpha$  restores the response to hypoxia in aged animals and actually increases the number of circulating EPCs.<sup>65</sup> These angiogenic factors might have a key role in promoting the mobilization, migration and proliferation of EPCs, as well as in inhibiting senescence in these cells. Indeed, levels of insulin-like growth factor 1 are considerably reduced in elderly men compared with younger individuals, and this decline is associated with an increase in EPC dysfunction and in the proportion of senescent EPCs.<sup>46</sup> Treatment of elderly people with growth hormone increases the levels of insulin-like growth factor 1 and reduces EPC senescence, presumably via telomerase activation. Inhibition of EPC senescence by administration of growth factors could, therefore, be a novel therapeutic strategy for age-related vascular disorders.

#### PREMATURE AGING SYNDROMES

The term 'progeroid syndrome' includes a range of inherited disorders characterized by features of rapid aging. Among the human progeroid syndromes, Werner syndrome (WRN) and Hutchinson–Gilford progeria syndrome (HGPS) are two of the best characterized disorders and those that most closely mimic the features of human aging, including the cardiovascular changes.<sup>67,68</sup> Recently, major progress has been made in understanding the genetic, biochemical and cellular basis of these syndromes. Accumulating evidence indicates that the senescence of adult somatic cells and stem cells has a crucial role in the premature aging phenotype.

#### Hutchinson–Gilford progeria syndrome

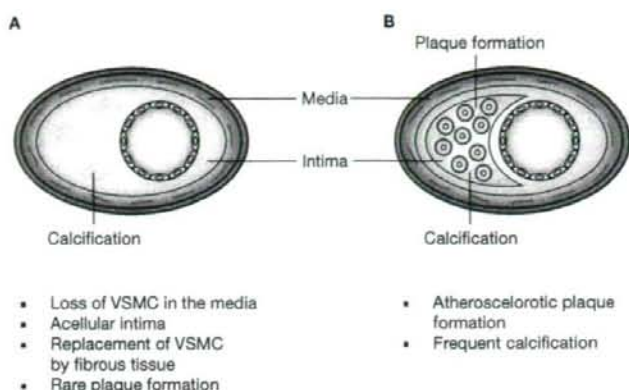
HGPS is referred to as 'childhood progeria' to differentiate the disorder from WRN, which is referred to as 'adult progeria'. Initially, patients do



not have any cardiovascular problems, but gradually develop shortness of breath with exertion between 6 years and 8 years of age.<sup>69</sup> Mortality in patients with HGPS is frequently a result of myocardial infarction or cerebrovascular events, which occur at an average age of 13 years.<sup>69</sup> At autopsy, the major finding in the cardiovascular system is extensive loss of VSMCs from the medial layer of the aorta and other great vessels, as well as smaller arteries (Figure 3A).<sup>69,70</sup> Most strikingly, unlike normal human aging, atherosclerotic plaques are very rare.

The genetic basis of HGPS was discovered in 2003, when it was found that most children with the disease have a single-nucleotide substitution in the lamin A gene (*LMNA*)—encoding A-type nuclear lamins—that leads to aberrant splicing.<sup>71,72</sup> Lamin A is synthesized as a precursor protein (prolamin A), which is cleaved twice by specific enzymes, including CAAX prenyl protease 1 homolog (also known as zinc metalloproteinase Ste24 homolog [*ZMPSTE24*]), during which the farnesyl modification is removed. The most frequent HGPS-associated mutation, Gly608Gly, is a silent base-substitution that results in internal deletion of 50 amino acid residues from the C terminus of lamin A. The resulting protein cannot be processed by CAAX prenyl protease 1 homolog. The mutant lamin A—called progerin—remains farnesylated and anchored to the nuclear envelope.<sup>72</sup> Consequently, patients with HGPS display various cellular changes such as irregular nuclear morphology and disorganization of heterochromatin, both associated with abnormal regulation of gene expression.

Several murine models of HGPS have been developed and provide insight into the mechanism of this disease. Mounkes *et al.* created a mouse model expressing mutant *Lmna*, which causes Emery–Dreifuss muscular dystrophy in humans, and found that these mutant mice displayed a severe HGPS-like phenotype.<sup>73</sup> Another mouse model of HGPS, generated by transgenic expression of human *LMNA* that contained the Gly608Gly mutation, showed changes that were largely restricted to the vascular system.<sup>74</sup> These mice exhibited progressive loss of VSMCs in the media of large arteries, which is very similar to the changes seen in patients with HGPS. Such structural changes in these mice were associated with vascular dysfunction exemplified by a lack of vasodilator response. By contrast, *Zmpste24*-knockout



**Figure 3** Histological features of progeroid vascular tissues. (A) Histological features of Hutchinson–Gilford progeria syndrome include extensive loss of VSMCs in the medial layer. Intimal thickening is present, but the intima is also acellular. Medial and intimal VSMCs are replaced by fibrous tissue and plaques rarely form. (B) Atherosclerotic plaque formation is common in individuals with Werner syndrome, and the plaques frequently show signs of calcification. Abbreviation: VSMCs, vascular smooth muscle cells.

mice have a broader progeria-like phenotype with severe growth retardation, skin defects and increased mortality.<sup>75</sup> Deletion of *Lmna* in mice results in a muscular-dystrophy-like phenotype that differs from mouse models of HGPS; therefore, permanent farnesylation of progerin seems to be implicated in the pathogenesis of HGPS.<sup>68</sup> This hypothesis is further supported by the finding that *Zmpste24*-knockout mice with reduced levels of farnesylated progerin have a normal phenotype.<sup>76</sup> Moreover, inhibiting farnesylation of prelamin A improves considerably the growth and survival of murine models of HGPS, and the shape of fibroblast nuclei is restored to normal.<sup>68,77</sup> Earlier this year, Varela *et al.* reported that prelamin A undergoes alternative prenylation by geranylgeranyltransferase upon inhibition of farnesyltransferase, which compromises the effects of farnesyltransferase inhibitors.<sup>78</sup> Consequently, inhibition of both farnesylation and geranylgeranylation of prelamin A with a combination of statins and aminobisphosphonates improves the aging-like phenotypes of *Zmpste24*-knockout mice.

Although the precise mechanisms by which progerin produces a progeria-like phenotype remain unclear, it seems likely that accumulation of progerin induces progressive changes to the nuclear architecture and exerts epigenetic control over the expression of genes that induce

premature aging.<sup>79</sup> In fact, progerin accumulates at later passages of HGPS fibroblasts and its accumulation is associated with loss of heterochromatin as well as progressive deformation of the nucleus.<sup>80</sup> Interestingly, fibroblasts from HGPS mice and fibroblasts from *Zmpste24*-knockout mouse embryos undergo premature cellular senescence as a consequence of increased DNA damage and exhibit genomic instability as a result of defects in the checkpoint response and DNA repair.<sup>81</sup> Deletion of p53 in *Zmpste24*-knockout mice improves some of the progeroid changes and extends life span,<sup>82</sup> suggesting that these cellular abnormalities are linked to the etiology of HGPS. Earlier this year, Scaffidi and Misteli demonstrated that expression of progerin activates downstream effectors of the Notch signaling pathways.<sup>83</sup> This activation causes dysregulation of stem-cell differentiation and possibly reduces cell life span. As lamin A mutations stimulate early apoptosis, it has also been suggested that high apoptotic cell death could deplete stem-cell pools, leading to impaired tissue regeneration.<sup>84</sup> These alterations could be involved in the development of vascular abnormalities; however, further studies are required to elucidate whether senescence of cardiovascular cells, including stem cells, accounts for the progeroid phenotype in patients with HGPS.

#### Werner syndrome

Patients with WRN are characterized by short stature, early graying and hair loss, an increased frequency of cancer, bilateral cataracts, scleroderma-like skin changes, type 2 diabetes, and atherosclerosis.<sup>67,68</sup> In contrast with individuals affected by HGPS, a considerable amount of atherosclerotic plaque accumulates in the coronary arteries and the aorta of patients with WRN, and calcium deposits are also observed in the aortic valve and mitral annulus (Figure 3B).<sup>85</sup> Patients with this syndrome usually die during middle age, with myocardial infarction and stroke being the two main causes. The mutation that causes WRN affects a member of the RecQ family of helicases called the *WRN* gene.<sup>86</sup> The *WRN* protein has helicase, exonuclease and single-stranded DNA annealing activities and is involved in DNA recombination, replication, repair and transcription, as well as in maintaining telomere integrity.<sup>87</sup>

Three different animal models of WRN have been developed to date: one has complete

knockout of the *WRN* protein;<sup>88</sup> another transgenic expression of a human mutant *WRN* protein that lacks helicase activity;<sup>89</sup> and the third has in-frame deletion of the helicase domain.<sup>90</sup> *WRN*-protein-knockout mice develop normally and do not exhibit premature aging.<sup>88</sup> By contrast, *WRN*-protein-knockout mice that have shorter telomeres representative of the length in humans have similar phenotypic changes to those seen in patients with WRN, including graying and loss of hair, osteoporosis, diabetes and cataracts.<sup>91,92</sup> Telomere attrition is, therefore, a key element in the pathology of WRN. Fibroblasts from patients with WRN are known to undergo premature senescence.<sup>67</sup> Consistent with results obtained in *WRN*-protein-deficient mice with short telomeres, introduction of telomerase can extend the life span and reduce the genomic instability of these fibroblasts.<sup>93,94</sup>

Although the *in vivo* changes in the transgenic mouse model of WRN have not been completely described, cells derived from these mice grow less readily and are more sensitive to agents that cause DNA damage than are normal mice cells.<sup>89</sup> The third model of WRN, in which the helicase domain is deleted, exhibits increased genomic instability, telomere attrition, and an increased incidence of tumors.<sup>90</sup> Cells from these mice show premature loss of proliferative activity. When this model is backcrossed to an inbred strain, the resulting mice have abnormal increases in visceral fat with high fasting triglyceride and cholesterol levels, and subsequently develop insulin resistance and high blood glucose levels.<sup>95</sup> Although atherosclerosis has not been observed, back-crossed adult mice develop severe cardiac fibrosis and show an increase in reactive oxygen species, as well as oxidative DNA damage in cardiac tissues. These findings imply that in the absence of functional *WRN* protein, cells accumulate toxic DNA intermediates or undergo telomere shortening. These changes could trigger genetic instability and DNA damage, which in turn could increase the DNA mutation rate or cellular senescence. Accumulation of dysfunctional cells may underlie the pathology of WRN.

#### TREATMENT OF VASCULAR AGING: FUTURE PERSPECTIVES

Recent studies on human progeroid syndromes have provided considerable insight into the treatment of age-associated vascular disease.

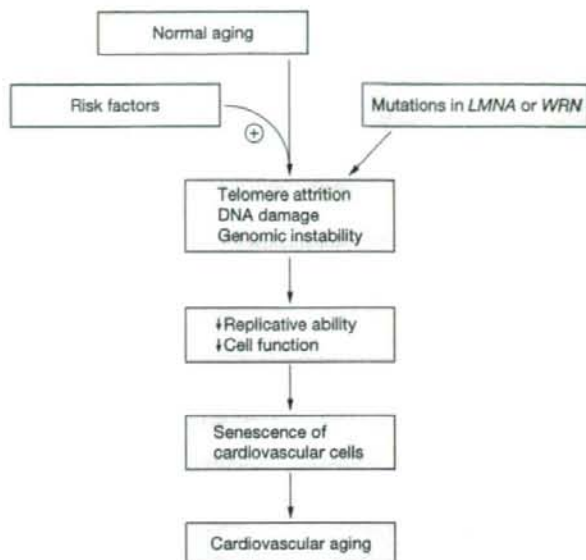


Cellular aging signals are potential targets for the treatment of atherosclerosis, as a single gene mutation that induces premature cellular senescence could cause vascular abnormalities. Specific individualized therapies could be developed for each patient with premature vascular disease by searching for reagents that improve the senescence-like phenotype at the cellular level, similar to the action of farnesylation inhibitors.

Several lines of evidence suggest that telomere-dependent senescence underlies age-associated vascular pathophysiology, thus one candidate for antisenescence therapy of atherosclerosis is telomerase. In addition to telomerase itself, all molecules involved in regulating telomerase activity could be used as therapeutic tools. For example, estrogen increases expression of the catalytic component of telomerase, thereby inducing telomerase activity. A number of reports have demonstrated that telomerase is activated by medications known to exert a beneficial effect on cardiovascular disease, such as statins,<sup>64</sup> thiazolidinediones<sup>96</sup> and aspirin.<sup>97</sup> Treatment with these medications or with humoral factors could prevent progressive telomere shortening in vascular cells and delay the onset of age-associated vascular dysfunction. Angiotensin II type 1 receptor antagonists could also be useful for the treatment of vascular aging by suppressing angiotensin-II-induced senescence.<sup>33</sup> Antagonists to p53 are available,<sup>98</sup> but systemic inhibition of p53 activity could induce tumorigenesis. Vascular-specific regulation of cellular aging signals would, therefore, be required. Recent studies indicate that tissue-specific inhibition of the signaling pathways for senescence increases longevity in a non-cell-autonomous manner.<sup>99</sup> Consequently, it would be interesting to investigate whether cellular aging signals in certain tissues regulate those in the vasculature.

## CONCLUSIONS

Cell division is essential for the survival of multicellular organisms that contain renewable tissues, but places the organism at risk of developing cancer. Thus, complex organisms have evolved at least two cellular mechanisms to prevent oncogenic transformation—apoptosis and cellular senescence. In this regard, aging and age-associated diseases can be viewed as by-products of the tumor suppressor mechanism known as cellular senescence. Consistent with this idea, the number of senescent fibroblasts



**Figure 4** Potential common pathways for normal aging and age-associated cardiovascular disease. Telomere attrition, DNA damage and genomic instability are increased in the elderly and in patients with progeroid syndromes, thereby inducing senescence of cardiovascular cells including stem and/or progenitor cells. Risk factors for cardiovascular disease override the effect of chronological aging on cell turnover by accelerating stress-induced damage. Senescence of cardiovascular cells is associated with decreased replication and cellular dysfunction that contribute to the development of cardiovascular aging. Abbreviations: LMNA, lamin A gene; WRN, Werner syndrome gene.

increases exponentially in the skin of aging primates.<sup>16</sup> Conversely, extension of life span by calorie restriction decreases biomarkers of cellular senescence *in vivo*.<sup>160</sup> In human progeroid syndromes, DNA damage signaling pathways are activated, thereby promoting premature senescence and apoptosis; accumulation of senescent cells and excessive cell death is thought to contribute to the pathogenesis of these syndromes. As discussed, the features of premature aging (including cardiovascular changes) in patients with progeroid syndromes are markedly different to those of normal aging. Indeed, it is not clear whether WRN and HGPS polymorphisms are associated with human aging or age-associated cardiovascular disease. Features common to progeroid syndromes and normal aging are, however, likely to exist (Figure 4), particularly at the cellular level. Identification of such traits could lead to new treatment strategies for cardiovascular disease as well as for aging.

## KEY POINTS

- Cellular senescence probably contributes to the pathogenesis of cardiovascular disease
- Telomere integrity is impaired with advancing age, which leads to vascular dysfunction
- The number and function of cardiovascular stem cells and/or progenitor cells shows a progressive decline with age
- Telomere attrition, DNA damage, and genomic instability might be common features of both normal aging and progeroid syndromes

## References

- 1 Lakatta EG and Levy D (2003) Arterial and cardiac aging: major shareholders in cardiovascular disease enterprises: Part I: aging arteries: a "set up" for vascular disease. *Circulation* **107**: 139–146
- 2 Lakatta EG (2003) Arterial and cardiac aging: major shareholders in cardiovascular disease enterprises: Part III: cellular and molecular clues to heart and arterial aging. *Circulation* **107**: 490–497
- 3 Reed MJ and Edelberg JM (2004) Impaired angiogenesis in the aged. *Sci Aging Knowledge Environ* **7**: pe7
- 4 Gennaro G et al. (2003) Age-dependent impairment of reendothelialization after arterial injury: role of vascular endothelial growth factor. *Circulation* **107**: 230–233
- 5 Minamino T and Komuro I (2007) Vascular cell senescence: contribution to atherosclerosis. *Circ Res* **100**: 15–26
- 6 Ballard VL and Edelberg JM (2007) Stem cells and the regeneration of the aging cardiovascular system. *Circ Res* **100**: 1116–1127
- 7 Thompson KV and Holliday R (1983) Genetic effects on the longevity of cultured human fibroblasts: II. DNA repair deficient syndromes. *Gerontology* **29**: 83–88
- 8 Buring KF (1991) The endothelium of advanced arteriosclerotic plaques in humans. *Arterioscler Thromb* **11**: 1878–1889
- 9 Ross R et al. (1984) Human atherosclerosis: I. cell constitution and characteristics of advanced lesions of the superficial femoral artery. *Am J Pathol* **114**: 79–93
- 10 Minamino T et al. (2002) Endothelial cell senescence in human atherosclerosis: role of telomere in endothelial dysfunction. *Circulation* **106**: 1541–1544
- 11 Minamino T et al. (2003) Ras induces vascular smooth muscle cell senescence and inflammation in human atherosclerosis. *Circulation* **108**: 2264–2269
- 12 Blasco MA (2005) Telomeres and human disease: ageing, cancer and beyond. *Nat Rev Genet* **6**: 611–622
- 13 Herbig U et al. (2004) Telomere shortening triggers senescence of human cells through a pathway involving ATM, p53, and p21(CIP1), but not p16(INK4a). *Mol Cell* **14**: 501–513
- 14 d'Adda di Fagagna F et al. (2003) A DNA damage checkpoint response in telomere-initiated senescence. *Nature* **426**: 194–198
- 15 Takai H et al. (2003) DNA damage foci at dysfunctional telomeres. *Curr Biol* **13**: 1549–1556
- 16 Herbig U et al. (2006) Cellular senescence in aging primates. *Science* **311**: 1257
- 17 Chang E and Harley CB (1995) Telomere length and replicative aging in human vascular tissues. *Proc Natl Acad Sci USA* **92**: 11190–11194
- 18 Aviv H et al. (2001) Age dependent aneuploidy and telomere length of the human vascular endothelium. *Atherosclerosis* **159**: 281–287
- 19 Ogami M et al. (2004) Telomere shortening in human coronary artery diseases. *Arterioscler Thromb Vasc Biol* **24**: 546–550
- 20 Voghel G et al. (2007) Cellular senescence in endothelial cells from atherosclerotic patients is accelerated by oxidative stress associated with cardiovascular risk factors. *Mech Ageing Dev* **128**: 662–671
- 21 Minamino T and Kourembanas S (2001) Mechanisms of telomerase induction during vascular smooth muscle cell proliferation. *Circ Res* **89**: 237–243
- 22 Minamino T et al. (2001) Hypoxia extends the life span of vascular smooth muscle cells through telomerase activation. *Mol Cell Biol* **21**: 3336–3342
- 23 Matsushita H et al. (2001) eNOS activity is reduced in senescent human endothelial cells: preservation by hTERT immortalization. *Circ Res* **89**: 793–798
- 24 Yang J et al. (1999) Human endothelial cell life extension by telomerase expression. *J Biol Chem* **274**: 26141–26148
- 25 Yang J et al. (2001) Telomerized human microvasculature is functional in vivo. *Nat Biotechnol* **19**: 219–224
- 26 Blasco MA et al. (1997) Telomere shortening and tumor formation by mouse cells lacking telomerase RNA. *Cell* **91**: 25–34
- 27 Lee HW et al. (1998) Essential role of mouse telomerase in highly proliferative organs. *Nature* **392**: 569–574
- 28 Rudolph KL et al. (1999) Longevity, stress response, and cancer in aging telomerase-deficient mice. *Cell* **96**: 701–712
- 29 Franco S et al. (2002) Decreased B16F10 melanoma growth and impaired vascularization in telomerase-deficient mice with critically short telomeres. *Cancer Res* **62**: 552–559
- 30 Poch E et al. (2004) Short telomeres protect from diet-induced atherosclerosis in apolipoprotein E-null mice. *FASEB J* **18**: 418–420
- 31 Perez-Rivero G et al. (2006) Mice deficient in telomerase activity develop hypertension because of an excess of endothelin production. *Circulation* **114**: 309–317
- 32 Najjar SS et al. (2005) Arterial aging: is it an immutable cardiovascular risk factor? *Hypertension* **46**: 454–462
- 33 Kunieda T et al. (2006) Angiotensin II induces premature senescence of vascular smooth muscle cells and accelerates the development of atherosclerosis via a p21-dependent pathway. *Circulation* **114**: 953–960
- 34 Matthews C et al. (2006) Vascular smooth muscle cells undergo telomere-based senescence in human atherosclerosis: effects of telomerase and oxidative stress. *Circ Res* **99**: 156–164
- 35 Kurz DJ et al. (2004) Chronic oxidative stress compromises telomere integrity and accelerates the onset of senescence in human endothelial cells. *J Cell Sci* **117**: 2417–2426
- 36 Voghel G et al. (2008) Chronic treatment with N-acetyl-cysteine delays cellular senescence in endothelial cells isolated from a subgroup of atherosclerotic patients. *Mech Ageing Dev* **129**: 261–270
- 37 Hasty P et al. (2003) Aging and genome maintenance: lessons from the mouse? *Science* **299**: 1355–1359
- 38 Tyner SD et al. (2002) p53 mutant mice that display early ageing-associated phenotypes. *Nature* **415**: 45–53



- 39 Maier B *et al.* (2004) Modulation of mammalian life span by the short isoform of p53. *Genes Dev* **18**: 306–319
- 40 Cao L *et al.* (2003) Senescence, aging, and malignant transformation mediated by p53 in mice lacking the Brca1 full-length isoform. *Genes Dev* **17**: 201–213
- 41 Asahara T *et al.* (1997) Isolation of putative progenitor endothelial cells for angiogenesis. *Science* **275**: 964–967
- 42 Shi Q *et al.* (1998) Evidence for circulating bone marrow-derived endothelial cells. *Blood* **92**: 362–367
- 43 Rafii S and Lyden D (2003) Therapeutic stem and progenitor cell transplantation for organ vascularization and regeneration. *Nat Med* **9**: 702–712
- 44 Walter DH *et al.* (2002) Statin therapy accelerates reendothelialization: a novel effect involving mobilization and incorporation of bone marrow-derived endothelial progenitor cells. *Circulation* **105**: 3017–3024
- 45 Puhonen S *et al.* (2008) Bone marrow-derived circulating endothelial precursors do not contribute to vascular endothelium and are not needed for tumor growth. *Proc Natl Acad Sci USA* **105**: 6620–6625
- 46 Thum T *et al.* (2007) Age-dependent impairment of endothelial progenitor cells is corrected by growth-hormone-mediated increase of insulin-like growth-factor-1. *Circ Res* **100**: 434–443
- 47 Vasa M *et al.* (2001) Number and migratory activity of circulating endothelial progenitor cells inversely correlate with risk factors for coronary artery disease. *Circ Res* **89**: E1–E7
- 48 Scheibel RJ *et al.* (2003) Age-dependent depression in circulating endothelial progenitor cells in patients undergoing coronary artery bypass grafting. *J Am Coll Cardiol* **42**: 2073–2080
- 49 Hill JM *et al.* (2003) Circulating endothelial progenitor cells, vascular function, and cardiovascular risk. *N Engl J Med* **348**: 593–600
- 50 Sugihara S *et al.* (2007) Age-related BM-MNC dysfunction hampers neovascularization. *Mech Ageing Dev* **128**: 511–516
- 51 Heeschen C *et al.* (2004) Profoundly reduced neovascularization capacity of bone marrow mononuclear cells derived from patients with chronic ischemic heart disease. *Circulation* **109**: 1615–1622
- 52 Ward M R *et al.* (2007) Endothelial progenitor cell therapy for the treatment of coronary disease, acute MI, and pulmonary arterial hypertension: current perspectives. *Catheter Cardiovasc Interv* **70**: 983–998
- 53 Edelberg JM *et al.* (2002) Young adult bone marrow-derived endothelial precursor cells restore aging-impaired cardiac angiogenic function. *Circ Res* **90**: E89–E93
- 54 Rauscher FM *et al.* (2003) Aging, progenitor cell exhaustion, and atherosclerosis. *Circulation* **108**: 457–463
- 55 Wassmann S *et al.* (2006) Improvement of endothelial function by systemic transfusion of vascular progenitor cells. *Circ Res* **99**: e74–e83
- 56 Werner N *et al.* (2005) Circulating endothelial progenitor cells and cardiovascular outcomes. *N Engl J Med* **353**: 999–1007
- 57 Samani NJ *et al.* (2001) Telomere shortening in atherosclerosis. *Lancet* **358**: 472–473
- 58 Satoh M *et al.* (2008) Association between oxidative DNA damage and telomere shortening in circulating endothelial progenitor cells obtained from metabolic syndrome patients with coronary artery disease. *Atherosclerosis* [doi:10.1016/j.atherosclerosis.2007.09.040]
- 59 Rosso A *et al.* (2006) p53 Mediates the accelerated onset of senescence of endothelial progenitor cells in diabetes. *J Biol Chem* **281**: 4339–4347
- 60 Shantsila, E *et al.* (2007) Endothelial progenitor cells in cardiovascular disorders. *J Am Coll Cardiol* **49**: 741–752
- 61 Zhu JH *et al.* (2006) Homocysteine accelerates senescence and reduces proliferation of endothelial progenitor cells. *J Mol Cell Cardiol* **40**: 648–652
- 62 Murasawa S *et al.* (2002) Constitutive human telomerase reverse transcriptase expression enhances regenerative properties of endothelial progenitor cells. *Circulation* **106**: 1133–1139
- 63 Spyridopoulos I *et al.* (2004) Statins enhance migratory capacity by upregulation of the telomere repeat-binding factor TRF2 in endothelial progenitor cells. *Circulation* **110**: 3136–3142
- 64 Assmus B *et al.* (2003) HMG-CoA reductase inhibitors reduce senescence and increase proliferation of endothelial progenitor cells via regulation of cell cycle regulatory genes. *Circ Res* **92**: 1049–1055
- 65 Bosch-Marce M *et al.* (2007) Effects of aging and hypoxia-inducible factor-1 activity on angiogenic cell mobilization and recovery of perfusion after limb ischemia. *Circ Res* **101**: 1310–1318
- 66 Chang EI *et al.* (2007) Age decreases endothelial progenitor cell recruitment through decreases in hypoxia-inducible factor 1 $\alpha$  stabilization during ischemia. *Circulation* **116**: 2818–2829
- 67 Martin GM (2005) Genetic modulation of senescent phenotypes in *Homo sapiens*. *Cell* **120**: 523–532
- 68 Capell B C *et al.* (2007) Mechanisms of cardiovascular disease in accelerated aging syndromes. *Circ Res* **101**: 13–26
- 69 Hennekam RC (2006) Hutchinson–Gilford progeria syndrome: review of the phenotype. *Am J Med Genet A* **140**: 2603–2624
- 70 Stehens WE *et al.* (1999) Histological and ultrastructural features of atherosclerosis in progeria. *Cardiovasc Pathol* **8**: 29–39
- 71 De Sandre-Giovannoli A *et al.* (2003) Lamin A truncation in Hutchinson–Gilford progeria. *Science* **300**: 2055
- 72 Eriksson M *et al.* (2003) Recurrent de novo point mutations in lamin A cause Hutchinson–Gilford progeria syndrome. *Nature* **423**: 293–298
- 73 Mounkes LC *et al.* (2003) A progeroid syndrome in mice is caused by defects in A-type lamins. *Nature* **423**: 298–301
- 74 Varga R *et al.* (2006) Progressive vascular smooth muscle cell defects in a mouse model of Hutchinson–Gilford progeria syndrome. *Proc Natl Acad Sci USA* **103**: 3250–3255
- 75 Bergo MO *et al.* (2002) Zmpste24 deficiency in mice causes spontaneous bone fractures, muscle weakness, and a prelamin A processing defect. *Proc Natl Acad Sci USA* **99**: 13049–13054
- 76 Fong LG *et al.* (2004) Heterozygosity for Lamin A deficiency eliminates the progeria-like phenotypes in Zmpste24-deficient mice. *Proc Natl Acad Sci USA* **101**: 18111–18116
- 77 Yang SH *et al.* (2005) Blocking protein farnesyltransferase improves nuclear blebbing in mouse fibroblasts with a targeted Hutchinson–Gilford progeria syndrome mutation. *Proc Natl Acad Sci USA* **102**: 10291–10296
- 78 Varela I *et al.* (2006) Combined treatment with statins and aminobisphosphonates extends longevity in a mouse model of human premature aging. *Nat Med* **14**: 767–772
- 79 Shumaker DK *et al.* (2006) Mutant nuclear lamin A leads to progressive alterations of epigenetic control in premature aging. *Proc Natl Acad Sci USA* **103**: 8703–8708

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**Competing interests**

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- 80 Goldman RD *et al.* (2004) Accumulation of mutant lamin A causes progressive changes in nuclear architecture in Hutchinson–Gilford progeria syndrome. *Proc Natl Acad Sci USA* **101**: 8963–8968
- 81 Liu B *et al.* (2005) Genomic instability in laminopathy-based premature aging. *Nat Med* **11**: 780–785
- 82 Varela I *et al.* (2005) Accelerated ageing in mice deficient in Zmpste24 protease is linked to p53 signalling activation. *Nature* **437**: 564–568
- 83 Scaffidi P and Misteli T (2008) Lamin A-dependent misregulation of adult stem cells associated with accelerated ageing. *Nat Cell Biol* **10**: 452–459
- 84 Halaschek-Wiener J and Brooks-Wilson A (2007) Progeria of stem cells: stem cell exhaustion in Hutchinson–Gilford progeria syndrome. *J Gerontol A Biol Sci Med Sci* **62**: 3–8
- 85 Cohen JL *et al.* (1987) Cardiovascular features of the Werner syndrome. *Am J Cardiol* **59**: 493–495
- 86 Yu CE *et al.* (1996) Positional cloning of the Werner's syndrome gene. *Science* **272**: 258–262
- 87 Opreško PL *et al.* (2004) Junction of RecQ helicase biochemistry and human disease. *J Biol Chem* **279**: 18099–18102
- 88 Lombard DB *et al.* (2000) Mutations in the WRN gene in mice accelerate mortality in a p53-null background. *Mol Cell Biol* **20**: 3286–3291
- 89 Wang L *et al.* (2000) Cellular Werner phenotypes in mice expressing a putative dominant-negative human WRN gene. *Genetics* **154**: 357–362
- 90 Leibel M and Leder P (1998) A deletion within the murine Werner syndrome helicase induces sensitivity to inhibitors of topoisomerase and loss of cellular proliferative capacity. *Proc Natl Acad Sci USA* **95**: 13097–13102
- 91 Chang S *et al.* (2004) Essential role of limiting telomeres in the pathogenesis of Werner syndrome. *Nat Genet* **36**: 877–882
- 92 Du X *et al.* (2004) Telomere shortening exposes functions for the mouse Werner and Bloom syndrome genes. *Mol Cell Biol* **24**: 8437–8446
- 93 Wyllie FS *et al.* (2000) Telomerase prevents the accelerated cell ageing of Werner syndrome fibroblasts. *Nat Genet* **24**: 16–17
- 94 Crabbe L *et al.* (2007) Telomere dysfunction as a cause of genomic instability in Werner syndrome. *Proc Natl Acad Sci USA* **104**: 2205–2210
- 95 Massip L *et al.* (2006) Increased insulin, triglycerides, reactive oxygen species, and cardiac fibrosis in mice with a mutation in the helicase domain of the Werner syndrome gene homologue. *Exp Gerontol* **41**: 157–168
- 96 Ogawa D *et al.* (2006) Activation of peroxisome proliferator-activated receptor gamma suppresses telomerase activity in vascular smooth muscle cells. *Circ Res* **98**: e50–e59
- 97 Bode-Boger SM *et al.* (2005) Aspirin reduces endothelial cell senescence. *Biochem Biophys Res Commun* **334**: 1226–1232
- 98 Komarov PG *et al.* (1999) A chemical inhibitor of p53 that protects mice from the side effects of cancer therapy. *Science* **285**: 1733–1737
- 99 Russell SJ and Kahn CR (2007) Endocrine regulation of ageing. *Nat Rev Mol Cell Biol* **8**: 681–691
- 100 Krishnamurthy J *et al.* (2004) Ink4a/Arf expression is a biomarker of aging. *J Clin Invest* **114**: 1299–1307



# Role of Heat Shock Transcriptional Factor 1 and Heat Shock Proteins in Cardiac Hypertrophy

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*Cardiac hypertrophy is an independent risk factor for cardiovascular disease. Initially, cardiac hypertrophy is an adaptive response to increased wall stress, but sustained stress leads to heart failure. It remains unclear how the transition from adaptive cardiac hypertrophy to maladaptive cardiac hypertrophy occurs. It has been postulated that there are two forms of cardiac hypertrophy, which are physiologic and pathologic cardiac hypertrophy. Unlike pathologic cardiac hypertrophy caused by chronic pressure or volume overload, cardiac hypertrophy induced by exercise is associated with less fibrosis and better systolic function, suggesting that adaptive mechanisms may be involved in exercise-induced cardiac hypertrophy. Therefore, elucidation of the molecular differences between these two types of cardiac hypertrophy may provide insights into the mechanisms underlying the transition from adaptive cardiac hypertrophy to heart failure. By comparing the two types of cardiac hypertrophy, we have identified heat shock transcription factor 1 and its target heat shock proteins as key factors involved in the adaptive mechanism of cardiac hypertrophy. In this review, we summarize the protective role of heat shock transcription factor 1 and heat shock proteins in cardiovascular disease. (Trends Cardiovasc Med 2008;18:88-93) © 2008, Elsevier Inc.*

## • Introduction

Heart failure is the final outcome of various heart diseases, and cardiac hyper-

trophy is one of the main causes of heart failure. The Framingham Heart Study revealed that there is a relationship between the severity of cardiac hypertrophy and the incidence of cardiovascular events, and that cardiac hypertrophy is an independent risk factor for heart failure, arrhythmia, myocardial infarction, and sudden death (Levy et al. 1990, Behar et al. 1992, Haider et al. 1998, Verdecchia et al. 2001). Therefore, it is important to develop therapeutic strategies for this condition, but the precise mechanisms underlying the transition from cardiac hypertrophy to heart failure are still largely unknown.

Cardiac hypertrophy is induced by various pathologic or physiologic stimuli. For example, acute pressure overload initially induces adaptive cardiac hypertrophy that is associated with normal cardiac function, but systolic and diastolic dysfunction occur in the setting

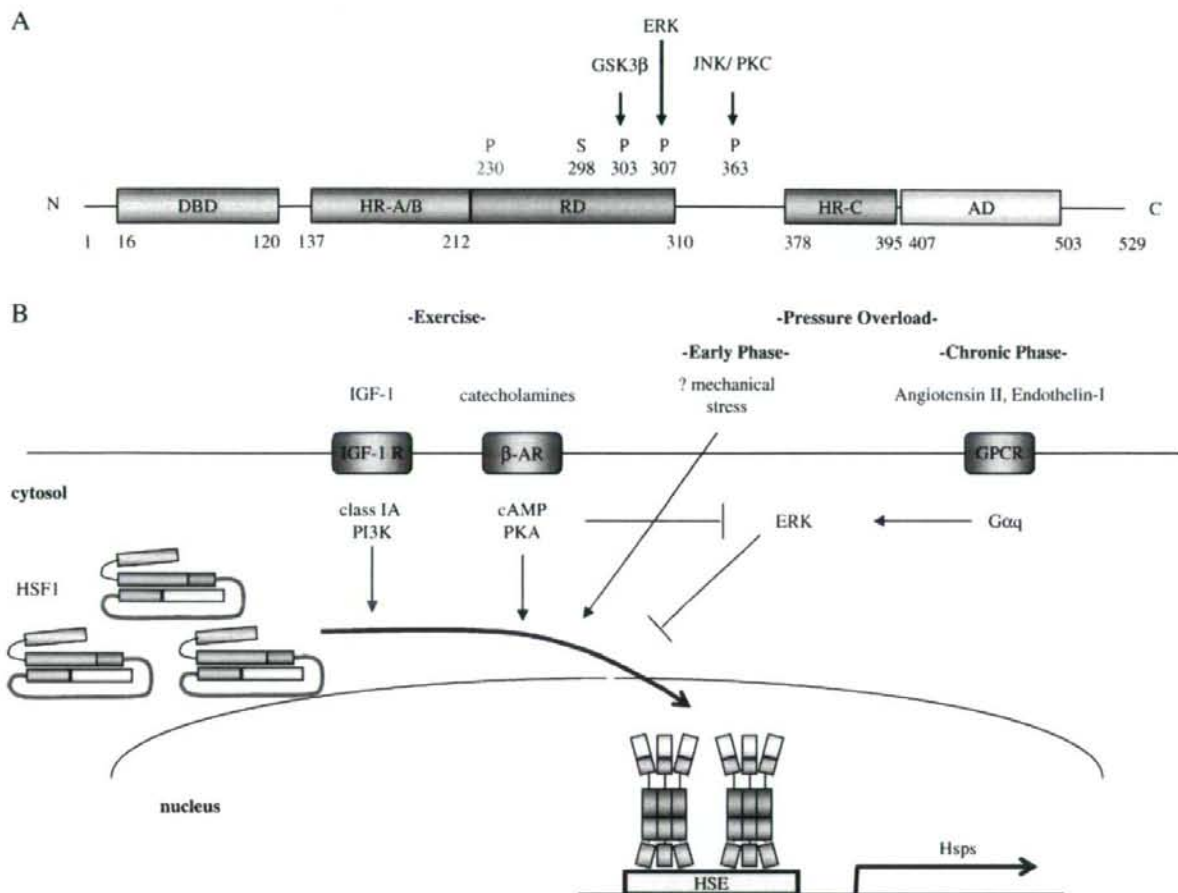
of chronic pressure overload, resulting in heart failure. Thus, chronic pressure overload is thought to cause pathologic or maladaptive cardiac hypertrophy. On the other hand, regular exercise can induce cardiac hypertrophy without causing systolic or diastolic dysfunction (Pluim et al. 2000). Because exercise-induced cardiac hypertrophy does not progress to heart failure, it is thought to be physiologic or adaptive cardiac hypertrophy. Although it has been reported that these two types of cardiac hypertrophy are morphologically (Richey and Brown 1998, Iemitsu et al. 2001, McMullen and Jennings 2007), functionally, and molecularly distinct from each other, the precise mechanism underlying these differences remains unclear. What are the exact differences between pathologic and physiologic cardiac hypertrophy? Why is cardiac function preserved in physiologic cardiac hypertrophy? Why does sustained pressure overload cause heart failure? Answering these questions will provide insights into novel therapeutic options for both cardiac hypertrophy and heart failure.

## • Pathologic and Physiologic Cardiac Hypertrophy

The differences between these two conditions include the stimuli inducing cardiac hypertrophy, their duration of action, and the signaling pathways involved. Pathologic cardiac hypertrophy is induced by persistent stress, such as pressure overload and volume overload caused by hypertension or valvular heart disease. On the other hand, physiologic cardiac hypertrophy is induced by intermittent stress such as exercise. Thus, the manifestations of cardiac hypertrophy caused by various stimuli may depend on their duration and intensity. In a recent study, Perrino et al. (2006) applied intermittent pressure overload to the heart and investigated the role of the duration of stress in the development of cardiac failure. Despite only developing mild cardiac hypertrophy, the hearts exposed to intermittent pressure overload displayed various pathologic changes, including diastolic dysfunction and histologic abnormalities.

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**Figure 1.** Potential regulators of HSF1 in cardiac hypertrophy. (A) Structure of HSF1. DBD indicates DNA-binding domain; HR, hydrophobic repeat; RD, regulatory domain; AD, transcriptional activation domain; P, phosphorylated site (the activating site is indicated in red); S, sumoylated site. (B) Potential regulatory mechanism of HSF1. Under nonstressful conditions, HSF1 exists as a monomer whose transcriptional activity is repressed by phosphorylation of the repressing sites (Ser303, Ser307, and Ser363). Upon stress, phosphorylation of the activating site (Ser230) is enhanced, thereby promoting the transcriptional activity of the trimerized and DNA-bound HSF1. The ratio of phosphorylation between the activating and repressing sites may be influenced by various stimuli, such as IGF-1, catecholamine, and angiotensin II, and determine the magnitude of the transcriptional activity. IGF-1R indicates IGF-1 receptor;  $\beta$ -AR,  $\beta$  adrenergic receptor; GPCR, G-protein-coupled receptor.

Thus, the nature of the stress acting on the heart, rather than its duration, may be a key determinant of the maladaptive phenotype.

A number of studies have shown that various signaling pathways contribute to the development of pathologic and physiologic cardiac hypertrophy by using mice that overexpress or lack specific genes (Richey and Brown 1998, Selvetella et al. 2004, Heineke and Molkenin 2006, Shiojima and Walsh 2006, McMullen and Jennings 2007). Endocrine factors such as angiotensin II and endothelin 1 induce pathologic cardiac hypertrophy (Yamazaki et al. 1995, Yamazaki et al.

1996), whereas inhibition of angiotensin II by angiotensin-converting enzyme inhibitors or angiotensin II receptor type 1 blockers can lead to regression of cardiac hypertrophy (Okin et al. 2003). Overexpression of  $G\alpha_q$  in the heart, which is activated by these factors, also induces cardiac hypertrophy associated with cardiac dysfunction (D'Angelo et al. 1997), whereas overexpression of an inhibitory peptide that interferes with  $G\alpha_q$  coupling prevents the onset of maladaptive cardiac hypertrophy (Akhter et al. 1998). These findings suggest that the  $G\alpha_q$ -mediated pathway is important for the development of pathologic cardiac hypertrophy.

The calcium/calmodulin-dependent phosphatase calcineurin has also been suggested to have a role in pathologic cardiac hypertrophy. Transgenic mice that overexpress active forms of calcineurin or its downstream transcription factor (NFAT3) develop cardiac hypertrophy and heart failure (Molkenin et al. 1998). Calcineurin inhibitors, such as cyclosporin A and FK506, suppress angiotensin II-induced cardiomyocyte hypertrophy in vitro and inhibit pressure overload-induced cardiac hypertrophy in vivo (Molkenin et al. 1998, Shimoyama et al. 2000). Overexpression of a dominant-negative mutant of calcineurin in



the heart also suppresses the induction of pathologic cardiac hypertrophy by pressure overload (Zou et al. 2001).

On the other hand, it has been reported that the insulin-like growth factor-1 (IGF-1)/class I<sub>A</sub> phosphoinositide 3-kinase (PI3K) pathway is activated in physiologic cardiac hypertrophy. Cardiac production of IGF-1 is significantly higher in athletes than in control subjects (Neri Serneri et al. 2001, Melling et al. 2006), and serum levels of IGF-1 increase in response to training (Koziris et al. 1999). Transgenic mice overexpressing the IGF-1 receptor or a constitutively active form of class I<sub>A</sub> PI3K in the heart develop cardiac hypertrophy without cardiac dysfunction or an increase of fibrosis (Shioi et al. 2000, McMullen et al. 2004). In contrast, transgenic mice with reduced cardiac class I<sub>A</sub> PI3K activity have smaller hearts and show a blunted hypertrophic response to exercise training, but not to pressure overload (McMullen et al. 2003, Luo et al. 2005). These results suggest that the IGF-1/class I<sub>A</sub> PI3K pathway is involved in the regulation of cardiac growth during postnatal development, and that this pathway plays a crucial role in inducing physiologic cardiac hypertrophy.

Although there have been a number of previous reports about the stimuli and signaling pathways involved in the regulation of physiologic or pathologic cardiac hypertrophy, the target genes and molecules of these pathways remain unclear. To answer these questions, various research groups have compared the pattern of cardiac gene expression between physiologic and pathologic cardiac hypertrophy (Richey and Brown 1998, Iemitsu et al. 2001, McMullen and Jennings 2007). These studies have shown that an array of genes display differential expression, suggesting that such differences might be involved in producing the two distinct phenotypes of cardiac hypertrophy. However, it remains to be determined whether these gene products actually promote different types of cardiac hypertrophy. Recently, we examined gene expression patterns in the heart and found differences in the expression of about 100 genes between physiologic and pathologic cardiac hypertrophy. Among them, we examined the role of heat shock proteins (HSPs) and heat shock transcription factor 1 (HSF1) in cardiac

hypertrophy because the expression of *Hsp70* and *Hsp27* was only elevated in physiologic cardiac hypertrophy.

#### • Role of Heat Shock Transcriptional Factor 1/HSPs in Cardiovascular Disease

Heat shock proteins are ubiquitously expressed, and their expression is enhanced by various acute and chronic stimuli, such as heat shock, heavy metals, low molecular weight toxins, infection, and oxidative stress (Li and Laszlo 1985, Benjamin and McMillan 1998, Morimoto 1998, Pockley 2002, Westerheide and Morimoto 2005). Heat shock proteins act to ensure the proper protein folding, as well as to prevent protein misfolding and assist in protein refolding to the correct state. Expression of HSPs is mainly regulated by HSF1 at the transcriptional level. In the unstressed state, HSF1 exists as a latent monomer, with repressed DNA binding and transcriptional activity. Upon activation, HSF1 undergoes multiple processes that include a monomer-to-trimer transition, nuclear accumulation, binding to the heat shock element located in the promoter region of each HSP gene, and transcriptional activation (Figure 1). Heat shock transcription factor 1-heat shock element DNA binding is not sufficient to elicit maximal transcription of the HSP genes, and it is necessary for HSF1 to be modified by phosphorylation and sumoylation to increase its transcriptional activity (Holmberg et al. 2002, Westerheide and Morimoto 2005). It has been suggested that HSF1 is repressed by GSK-3 $\beta$  (Ser303), ERK (Ser307), and JNK (Ser363) under normal conditions, whereas it is activated by hyperphosphorylation (Ser-230) upon exposure to various stresses (Figure 1A) (Chu et al. 1996, Chu et al. 1998, Morimoto 1998, Holmberg et al. 2002). However, the mechanisms underlying the activation of HSF1, particularly its regulation by phosphorylation, remain unclear.

A number of studies have shown that HSF1 and HSPs confer protection against cardiovascular disease. Induction of HSF1 and HSP expression by various stimuli, such as heat shock, reduces the size of infarcts after ischemia/reperfusion (Donnelly et al. 1992, Marber et al. 1993, Bannani et al. 1998). Transgenic mice overexpressing a constitutively active

form of HSF1 or inducible Hsp70 in the heart show more resistance to ischemia/reperfusion injury compared with wild-type mice (Marber et al. 1995, Plumier et al. 1995, Zou et al. 2003). In contrast, the cardiac function of inducible Hsp70 knockout mice is markedly impaired by ischemia/reperfusion injury (Kim et al. 2006). In addition to a protective effect against ischemia/reperfusion injury, it has been reported that HSPs have a beneficial role in myocardial infarction, doxorubicin-induced cardiomyopathy, and atrial fibrillation (Baljinnayam et al. 2006, Brundel et al. 2006, Venkatakrishnan et al. 2006, Liu et al. 2007, Wakisaka et al. 2007).

Our recent study identified HSF1 as a critical transcription factor that regulates cardiac hypertrophy (Sakamoto et al. 2006). Heat shock transcription factor 1 was only activated in exercise-induced cardiac hypertrophy, but not in chronic pressure overload-induced cardiac hypertrophy. When heterozygous HSF1<sup>+/-</sup> mice (Inouye et al. 2004) were forced to exercise (which is thought to induce physiologic cardiac hypertrophy), significant systolic dysfunction occurred. In contrast, when transgenic mice that expressed a constitutively active form of HSF1 (Nakai et al. 2000) were exposed to chronic pressure overload (which is thought to induce pathologic cardiac hypertrophy), their systolic function was preserved. These results indicate that HSF1 is a key molecule for preservation of systolic function during the development of cardiac hypertrophy under both pathologic and physiologic conditions. Accumulation and aggregation of unfolded proteins are associated with an increase of protein synthesis in hypertrophied hearts and induce cardiomyocyte death that eventually leads to systolic dysfunction (Okada et al. 2005). Thus, the protective effects of HSF1 may be attributable to the functions of HSPs in protein folding and degradation. In addition to such well-known functions, accumulating evidence indicates that different HSPs directly act on the cell death machinery and inhibit the signaling pathway for cell death at various points (Sreedhar and Csermely 2004). For example, Hsp27 binds to cytochrome c and prevents it from binding to Apaf-1 (Bruey et al. 2000), whereas Hsp70 prevents Apaf-1 from recruiting procaspase-9 (Beere et al. 2000), thereby inhibiting apoptotic cell death. It is



conceivable that sustained activation of HSF1 prevents the onset of cardiac dysfunction in hypertrophic hearts through the mechanisms involving a direct action of HSPs on the cell death machinery as well as their functions in protein degradation.

#### • Potential Regulators of HSF1 in Cardiac Hypertrophy

Heat shock transcription factor 1 and HSPs are upregulated by exercise (Taylor et al. 1999, Hamilton et al. 2001, Sakamoto et al. 2006), but the mechanisms involved are not fully understood. As mentioned above, the IGF-1/class I<sub>A</sub> PI3K pathway is thought to play an important role in inducing physiologic cardiac hypertrophy (McMullen et al. 2004). Interestingly, expression of HSPs is increased in the hearts of transgenic mice, with enhancement of cardiac IGF-1 or class I<sub>A</sub> PI3K, suggesting a potential relationship between this signaling pathway and HSF1 activity. Consistent with this notion, the IGF-1/class I<sub>A</sub> PI3K pathway is known to inhibit GSK-3 $\beta$  (Shiojima and Walsh 2006), which is a negative regulator of HSF1. It could be assumed that IGF-1-induced inhibition of GSK-3 $\beta$  contributes to the activation of HSF1 in exercise-induced cardiac hypertrophy (Figure 1B).

Another possibility is that catecholamines may upregulate HSF1 and HSPs after exercise, because circulating levels of catecholamines are increased by exercise. Isoproterenol (a  $\beta$ -adrenergic agonist) increases cardiac expression of HSP70 (White and White 1986), whereas inhibition of protein kinase A (PKA), a downstream kinase of the  $\beta$ -adrenergic receptor, suppresses exercise-induced upregulation of *Hsp70* (Melling et al. 2004). Moreover, exercise-induced activation of PKA attenuates the phosphorylation of ERK, which is a negative regulator of HSF1 (Melling et al. 2006). Taken together, these findings suggest that exercise may upregulate HSF1 by activating the  $\beta$ -adrenergic signaling pathway that induces PKA-mediated inactivation of ERK (Figure 1B). Although activation of protein kinase C in the heart during exercise is thought to have a protective role, it remains unclear whether this pathway is involved in the upregulation of HSF1 and HSPs after exercise (Yamashita et al. 2001, Melling

et al. 2004). Moreover, posttranslational modifications rather than phosphorylation may regulate the transcriptional activity of HSF1 during exercise.

Our findings showed that HSF1 was only activated in the early phase of pressure overload (the adaptive phase), but not in the chronic phase (the maladaptive phase) (Sakamoto et al. 2006). Other groups have also demonstrated that acute pressure overload activates HSF1 and increases the expression of HSPs (Delcayre et al. 1988, Izumo et al. 1988, Nishizawa et al. 2002). Why is HSF1 downregulated during the chronic phase of pressure overload? Production of autocrine/paracrine factors such as angiotensin II and endothelin 1 is increased by pathologic stimuli and plays a critical role in inducing pathologic cardiac hypertrophy. These factors bind to G-protein-coupled receptors, leading to dissociation of the G $\alpha$ q subunit and activation of downstream signaling molecules, which include negative regulators of HSF1 such as ERK and JNK. Accordingly, this signaling pathway may induce pathologic cardiac hypertrophy partly via the inactivation of HSF1 (Figure 1B), although there is a conflicting report that angiotensin II does not influence the activity of HSF1 (Nishizawa et al. 2002). Further studies are necessary to elucidate precisely how HSF1 activity is regulated as cardiac hypertrophy develops.

#### • Conclusion and Future Prospects

Because there have been many reports that induction of HSF1 and HSPs has a beneficial effect in animal models of cardiovascular disease, activation of HSF1 and HSPs could be a novel therapeutic strategy for various cardiovascular diseases. Geranylgeranylacetone, an anti-ulcer agent, has been reported to upregulate HSF1 and HSPs, and shows a protective effect against ischemia/reperfusion injury and atrial fibrillation (Yamanaka et al. 2003, Brundel et al. 2006, Wakisaka et al. 2007). Exercise also upregulates HSF1 and HSPs, and it ameliorates cardiac dysfunction in hypertensive animals (Schauer et al. 1982, Schaible et al. 1986, Moreno Junior et al. 1995, Emter et al. 2005). Moreover, recent studies have further demonstrated the protective effect of exercise on cardiac func-

tion in animal models of myocardial infarction and ischemia/reperfusion injury (Hoshida et al. 2002). However, conflicting data also suggest that any increase of HSPs in the heart after exercise is not necessary for protection against ischemia/reperfusion injury and that moderate exercise does not improve cardiac dysfunction in hypertensive rats (Taylor et al. 1999, Hamilton et al. 2001). Moreover, excessive exercise accelerates the rate of progression from cardiac hypertrophy to heart failure in untreated hypertensive rats (Sarma and Schulze 2007). To develop a novel therapeutic strategy targeting the HSF1/HSP system for patients with cardiovascular disease, one is required to perform further studies of elucidating the protective mechanisms involved.

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#### References

- Akhter SA, Luttrell LM, Rockman HA, et al: 1998. Targeting the receptor-Gq interface to inhibit in vivo pressure overload myocardial hypertrophy. *Science* 280:574-577.
- Baljinnyam E, Hasebe N, Morihira M, et al: 2006. Oral pretreatment with ebselen enhances heat shock protein 72 expression and reduces myocardial infarct size. *Hypertens Res* 29:905-913.
- Beere HM, Wolf BB, Cain K, et al: 2000. Heat-shock protein 70 inhibits apoptosis by preventing recruitment of procaspase-9 to the Apaf-1 apoptosome. *Nat Cell Biol* 2: 469-475.
- Behar S, Reicher-Reiss H, Abinader E, et al: 1992. Long-term prognosis after acute myocardial infarction in patients with left ventricular hypertrophy on the electrocardiogram. SPRINT Study Group. *Am J Cardiol* 69:985-990.
- Benjamin IJ, McMillan DR: 1998. Stress (heat shock) proteins: molecular chaperones in



- cardiovascular biology and disease. *Circ Res* 83:117-132.
- Bennani YL, Marron KS, Mais DE, et al: 1998. Synthesis and characterization of a highly potent and selective isotopically labeled retinoic acid receptor ligand, ALRT1550. *J Org Chem* 63:543-550.
- Bruey JM, Ducasse C, Bonniaud P, et al: 2000. Hsp27 negatively regulates cell death by interacting with cytochrome c. *Nat Cell Biol* 2:645-652.
- Brundel BJ, Shiroshita-Takeshita A, Qi X, et al: 2006. Induction of heat shock response protects the heart against atrial fibrillation. *Circ Res* 99:1394-1402.
- Chu B, Soncin F, Price BD, et al: 1996. Sequential phosphorylation by mitogen-activated protein kinase and glycogen synthase kinase 3 represses transcriptional activation by heat shock factor-1. *J Biol Chem* 271:30847-30857.
- Chu B, Zhong R, Soncin F, et al: 1998. Transcriptional activity of heat shock factor 1 at 37 degrees C is repressed through phosphorylation on two distinct serine residues by glycogen synthase kinase 3 and protein kinases Calpha and Czeta. *J Biol Chem* 273:18640-18646.
- D'Angelo DD, Sakata Y, Lorenz JN, et al: 1997. Transgenic Galpha overexpression induces cardiac contractile failure in mice. *Proc Natl Acad Sci U S A* 94:8121-8126.
- Delcayre C, Samuel JL, Marotte F, et al: 1988. Synthesis of stress proteins in rat cardiac myocytes 2-4 days after imposition of hemodynamic overload. *J Clin Invest* 82:460-468.
- Donnelly TJ, Sievers RE, Vissern FL, et al: 1992. Heat shock protein induction in rat hearts. A role for improved myocardial salvage after ischemia and reperfusion? *Circulation* 85:769-778.
- Ermter CA, McCune SA, Sparagna GC, et al: 2005. Low-intensity exercise training delays onset of decompensated heart failure in spontaneously hypertensive heart failure rats. *Am J Physiol Heart Circ Physiol* 289: H2030-H2038.
- Haider AW, Larson MG, Benjamin EJ, et al: 1998. Increased left ventricular mass and hypertrophy are associated with increased risk for sudden death. *J Am Coll Cardiol* 32:1454-1459.
- Hamilton KL, Powers SK, Sugiura T, et al: 2001. Short-term exercise training can improve myocardial tolerance to I/R without elevation in heat shock proteins. *Am J Physiol Heart Circ Physiol* 281: H1346-H1352.
- Heineke J, Molkenin JD: 2006. Regulation of cardiac hypertrophy by intracellular signaling pathways. *Nat Rev Mol Cell Biol* 7:589-600.
- Holmberg CI, Tran SE, Eriksson JE, et al: 2002. Multisite phosphorylation provides sophisticated regulation of transcription factors. *Trends Biochem Sci* 27:619-627.
- Hoshida S, Yamashita N, Otsu K, et al: 2002. Repeated physiologic stresses provide persistent cardioprotection against ischemia-reperfusion injury in rats. *J Am Coll Cardiol* 40:826-831.
- Iemitsu M, Miyauchi T, Maeda S, et al: 2001. Physiological and pathological cardiac hypertrophy induce different molecular phenotypes in the rat. *Am J Physiol Regul Integr Comp Physiol* 281:R2029-R2036.
- Inoue S, Izu H, Takaki E, et al: 2004. Impaired IgG production in mice deficient for heat shock transcription factor 1. *J Biol Chem* 279:38701-38709.
- Izumo S, Nadal-Ginard B, Mahdavi V: 1988. Protooncogene induction and reprogramming of cardiac gene expression produced by pressure overload. *Proc Natl Acad Sci U S A* 85:339-343.
- Kim YK, Suarez J, Hu Y, et al: 2006. Deletion of the inducible 70-kDa heat shock protein genes in mice impairs cardiac contractile function and calcium handling associated with hypertrophy. *Circulation* 113:2589-2597.
- Koziris LP, Hickson RC, Chatterton RT, et al: 1999. Serum levels of total and free IGF-I and IGFBP-3 are increased and maintained in long-term training. *J Appl Physiol* 86:1436-1442.
- Levy D, Garrison RJ, Savage DD, et al: 1990. Prognostic implications of echocardiographically determined left ventricular mass in the Framingham Heart Study. *N Engl J Med* 322:1561-1566.
- Li GC, Laszlo A: 1985. Amino acid analogs while inducing heat shock proteins sensitize CHO cells to thermal damage. *J Cell Physiol* 122:91-97.
- Liu L, Zhang X, Qian B, et al: 2007. Overexpression of heat shock protein 27 attenuates doxorubicin-induced cardiac dysfunction in mice. *Eur J Heart Fail* 9:762-769.
- Luo J, McMullen JR, Sobkiw CL, et al: 2005. Class IA phosphoinositide 3-kinase regulates heart size and physiological cardiac hypertrophy. *Mol Cell Biol* 25: 9491-9502.
- Marber MS, Latchman DS, Walker JM, et al: 1993. Cardiac stress protein elevation 24 hours after brief ischemia or heat stress is associated with resistance to myocardial infarction. *Circulation* 88:1264-1272.
- Marber MS, Mestrl R, Chi SH, et al: 1995. Overexpression of the rat inducible 70-kD heat stress protein in a transgenic mouse increases the resistance of the heart to ischemic injury. *J Clin Invest* 95:1446-1456.
- McMullen JR, Jennings GL: 2007. Differences between pathological and physiological cardiac hypertrophy: novel therapeutic strategies to treat heart failure. *Clin Exp Pharmacol Physiol* 34:255-262.
- McMullen JR, Shioi T, Huang WY, et al: 2004. The insulin-like growth factor 1 receptor induces physiological heart growth via the phosphoinositide 3-kinase(p110alpha) pathway. *J Biol Chem* 279:4782-4793.
- McMullen JR, Shioi T, Zhang L, et al: 2003. Phosphoinositide 3-kinase(p110alpha) plays a critical role for the induction of physiological, but not pathological, cardiac hypertrophy. *Proc Natl Acad Sci U S A* 100:12355-12360.
- Melling CW, Krause MP, Noble EG: 2006. PKA-mediated ERK1/2 inactivation and hsp70 gene expression following exercise. *J Mol Cell Cardiol* 41:816-822.
- Melling CW, Thorp DB, Noble EG: 2004. Regulation of myocardial heat shock protein 70 gene expression following exercise. *J Mol Cell Cardiol* 37:847-855.
- Molkentin JD, Lu JR, Antos CL, et al: 1998. A calcineurin-dependent transcriptional pathway for cardiac hypertrophy. *Cell* 93: 215-228.
- Moreno Junior H, Cezareti ML, Picarro IC, et al: 1995. The influence of isotonic exercise on cardiac hypertrophy in arterial hypertension: impact on cardiac function and on the capacity for aerobic work. *Comp Biochem Physiol A Physiol* 112: 313-320.
- Morimoto RI: 1998. Regulation of the heat shock transcriptional response: cross talk between a family of heat shock factors, molecular chaperones, and negative regulators. *Genes Dev* 12:3788-3796.
- Nakai A, Suzuki M, Tanabe M: 2000. Arrest of spermatogenesis in mice expressing an active heat shock transcription factor 1. *EMBO J* 19:1545-1554.
- Neri Serneri GG, Boddi M, Modesti PA, et al: 2001. Increased cardiac sympathetic activity and insulin-like growth factor-I formation are associated with physiological hypertrophy in athletes. *Circ Res* 89: 977-982.
- Nishizawa J, Nakai A, Komeda M, et al: 2002. Increased preload directly induces the activation of heat shock transcription factor 1 in the left ventricular overloaded heart. *Cardiovasc Res* 55:341-348.
- Okada K, Minamoto T, Kitakaze M: 2005. Role of endoplasmic reticulum stress in hypertrophic and failing hearts. *Nippon Yakurigaku Zasshi* 126:385-389.
- Okin PM, Devereux RB, Jern S, et al: 2003. Regression of electrocardiographic left ventricular hypertrophy by losartan versus atenolol: the Losartan Intervention for Endpoint reduction in Hypertension (LIFE) Study. *Circulation* 108:684-690.
- Perrino C, Naga Prasad SV, Mao L, et al: 2006. Intermittent pressure overload triggers hypertrophy-independent cardiac dysfunction and vascular rarefaction. *J Clin Invest* 116:1547-1560.



- Pluim BM, Zwinderman AH, van der Laarse A, et al: 2000. The athlete's heart. A meta-analysis of cardiac structure and function. *Circulation* 101:336-344.
- Plumley JC, Ross BM, Currie RW, et al: 1995. Transgenic mice expressing the human heat shock protein 70 have improved post-ischemic myocardial recovery. *J Clin Invest* 95:1854-1860.
- Pockley AG: 2002. Heat shock proteins, inflammation, and cardiovascular disease. *Circulation* 105:1012-1017.
- Richey PA, Brown SP: 1998. Pathological versus physiological left ventricular hypertrophy: a review. *J Sports Sci* 16:129-141.
- Sakamoto M, Minamino T, Toko H, et al: 2006. Upregulation of heat shock transcription factor 1 plays a critical role in adaptive cardiac hypertrophy. *Circ Res* 99:1411-1418.
- Sarma S, Schulze PC: 2007. Exercise as a physiologic intervention to counteract hypertension: can a good idea go bad? *Hypertension* 50:294-296.
- Schaible TF, Malhotra A, Ciambone GJ, et al: 1986. Chronic swimming reverses cardiac dysfunction and myosin abnormalities in hypertensive rats. *J Appl Physiol* 60:1435-1441.
- Scheuer J, Malhotra A, Hirsch C, et al: 1982. Physiologic cardiac hypertrophy corrects contractile protein abnormalities associated with pathologic hypertrophy in rats. *J Clin Invest* 70:1300-1305.
- Selvetella G, Hirsch E, Notte A, et al: 2004. Adaptive and maladaptive hypertrophic pathways: points of convergence and divergence. *Cardiovasc Res* 63:373-380.
- Shimoyama M, Hayashi D, Zou Y, et al: 2000. Calcineurin inhibitor attenuates the development and induces the regression of cardiac hypertrophy in rats with salt-sensitive hypertension. *Circulation* 102:1996-2004.
- Shioi T, Kang PM, Douglas PS, et al: 2000. The conserved phosphoinositide 3-kinase pathway determines heart size in mice. *EMBO J* 19:2537-2548.
- Shiojima I, Walsh K: 2006. Regulation of cardiac growth and coronary angiogenesis by the Akt/PKB signaling pathway. *Genes Dev* 20:3347-3365.
- Sreedhar AS, Csermely P: 2004. Heat shock proteins in the regulation of apoptosis: new strategies in tumor therapy: a comprehensive review. *Pharmacol Ther* 101: 227-257.
- Taylor RP, Harris MB, Starnes JW: 1999. Acute exercise can improve cardioprotection without increasing heat shock protein content. *Am J Physiol* 276:H1098-H1102.
- Venkatakrishnan CD, Tewari AK, Moldovan L, et al: 2006. Heat shock protects cardiac cells from doxorubicin-induced toxicity by activating p38 MAPK and phosphorylation of small heat shock protein 27. *Am J Physiol Heart Circ Physiol* 291:H2680-H2691.
- Verdecchia P, Porcellati C, Reboldi G, et al: 2001. Left ventricular hypertrophy as an independent predictor of acute cerebrovascular events in essential hypertension. *Circulation* 104:2039-2044.
- Wakisaka O, Takahashi N, Shinohara T, et al: 2007. Hyperthermia treatment prevents angiotensin II-mediated atrial fibrosis and fibrillation via induction of heat-shock protein 72. *J Mol Cell Cardiol* 43:616-626.
- Westerheide SD, Morimoto RI: 2005. Heat shock response modulators as therapeutic tools for diseases of protein conformation. *J Biol Chem* 280:33097-33100.
- White FP, White SR: 1986. Isoproterenol induced myocardial necrosis is associated with stress protein synthesis in rat heart and thoracic aorta. *Cardiovasc Res* 20:512-515.
- Yamanaka K, Takahashi N, Ooie T, et al: 2003. Role of protein kinase C in geranylgeranyl-lactone-induced expression of heat-shock protein 72 and cardioprotection in the rat heart. *J Mol Cell Cardiol* 35:785-794.
- Yamashita N, Baxter GF, Yellon DM: 2001. Exercise directly enhances myocardial tolerance to ischemia-reperfusion injury in the rat through a protein kinase C mediated mechanism. *Heart* 85:331-336.
- Yamazaki T, Komuro I, Kudoh S, et al: 1995. Angiotensin II partly mediates mechanical stress-induced cardiac hypertrophy. *Circ Res* 77:258-265.
- Yamazaki T, Komuro I, Kudoh S, et al: 1996. Endothelin-1 is involved in mechanical stress-induced cardiomyocyte hypertrophy. *J Biol Chem* 271:3221-3228.
- Zou Y, Hiroi Y, Uozumi H, et al: 2001. Calcineurin plays a critical role in the development of pressure overload-induced cardiac hypertrophy. *Circulation* 104:97-101.
- Zou Y, Zhu W, Sakamoto M, et al: 2003. Heat shock transcription factor 1 protects cardiomyocytes from ischemia/reperfusion injury. *Circulation* 108:3024-3030.

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TCM

## Understanding Proteasome Assembly and Regulation: Importance to Cardiovascular Medicine

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*The cardiac proteasome is increasingly recognized as a complex, heterogeneous, and dynamic organelle contributing to the modulation of cardiac function in health and diseases. The emerging picture of the proteasome system reveals a highly regulated and organized molecular machine integrated into multiple biologic processes of the cell. Full appreciation of its cardiovascular relevance requires an understanding of its proteolytic function as well as its underlying regulatory mechanisms, of which assembly, stoichiometry, posttranslational modification, and the role of the associating partners are increasingly poignant. (Trends Cardiovasc Med 2008;18:93-98) Published by Elsevier Inc.*

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### • Introduction

The mammalian protein degradation machinery is dominated by the proteasome, as it endoproteolytically cleaves more than 70% of intracellular proteins (Rock et al. 1994). The core of this multimeric protease is a duplex of two sets of 14 subunits, housing duplicate sites of trypsin-like, caspase-like, and chymotrypsin-like peptidase activities. Termed the 20S proteasome, its gated pores maintain the complex in a latently active state, enabling only limited



## A crucial role of a high mobility group protein HMGA2 in cardiogenesis

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The high mobility group (HMG) of nuclear proteins regulates expression of many genes through architectural remodelling of the chromatin structure, and formation of multiprotein complexes on promoter/enhancer regions. This leads to the active transcription of their target genes<sup>1-3</sup>. Here we show that HMGA2, a member of the HMGA sub-family of HMG proteins, has a critical function in cardiogenesis. Overexpression of *HMGA2* enhanced, whereas siRNA-mediated knockdown of *HMGA2* blocked, cardiomyocyte differentiation of the embryonal carcinoma cell line P19CL6. Moreover, overexpression of a dominant-negative HMGA2 or morpholino-mediated knockdown of *HMGA2* expression blocked normal heart formation in *Xenopus laevis* embryos, suggesting that HMGA2 has an important role in cardiogenesis both *in vitro* and *in vivo*. Mechanistically, HMGA2 associated with Smad1/4 and showed synergistic trans-activation of the gene for a cardiac transcription factor *Nkx2.5*; a conserved HMGA2 binding site was required for the promoter activity of *Nkx2.5* gene, both in P19CL6 cells and in transgenic *Xenopus* embryos. Thus, HMGA2 is a positive regulator of *Nkx2.5* gene expression and is essential for normal cardiac development.

The process of vertebrate heart development is regulated by a network of multiple transcription factors and signalling proteins<sup>4,5</sup>. Congenital heart malformations occur in approximately 1% of the population<sup>6</sup>; this high susceptibility of the developing heart to diseases may be in part due to the complexity of the molecular framework that controls cardiogenesis. A precise understanding of the causes of heart malformations is therefore imperative for establishing therapeutic strategies for congenital heart diseases. Molecules involved in the early stage of cardiac development are of particular interest because they may also function in repair or regeneration of the injured heart<sup>7</sup>. In this regard, cardiac transcription factors

such as *Nkx2.5* (A001667), *GATA-4* (A001029) and *MEF2C* (A001503) have been investigated extensively, because they are essential for normal heart development and they are also encoded by early cardiac marker genes expressed in the heart-forming region, when cardiac precursors are specified in the anterior lateral mesoderm<sup>8</sup>. Signalling molecules such as bone morphogenetic proteins (BMPs), fibroblast growth factors, Wnts and soluble Wnt inhibitors have also been characterized as inducers or inhibitors of cardiac mesoderm specification<sup>5,7</sup>. However, it is not clear how these signalling molecules and transcription factors regulate the commitment of undifferentiated mesodermal cells into cardiac precursors.

To further investigate the regulatory mechanisms that control the early stage of cardiomyocyte differentiation, we used P19CL6 cells, which are derived from P19 murine embryonal carcinoma cell lines and differentiate into beating cardiomyocytes in the presence of 1% dimethyl sulphoxide (DMSO)<sup>9</sup>. Differential mRNA display was performed to isolate mRNA species whose expression was upregulated in the early stage (day 6) of P19CL6 differentiation into cardiomyocytes, when early cardiac marker genes, such as *Nkx2.5*, start to be expressed. Among the 50 clones isolated, five were confirmed by northern blotting to be upregulated at day 6 of differentiation and one of these five clones was found to be a cDNA encoding the HMG protein HMGA2. Northern blot analysis revealed that the expression of *HMGA2* mRNA was detected from day 2 and peaked at day 6 after DMSO treatment (Fig. 1a), indicating that the expression of *HMGA2* precedes those of early cardiac marker genes during cardiomyocyte differentiation.

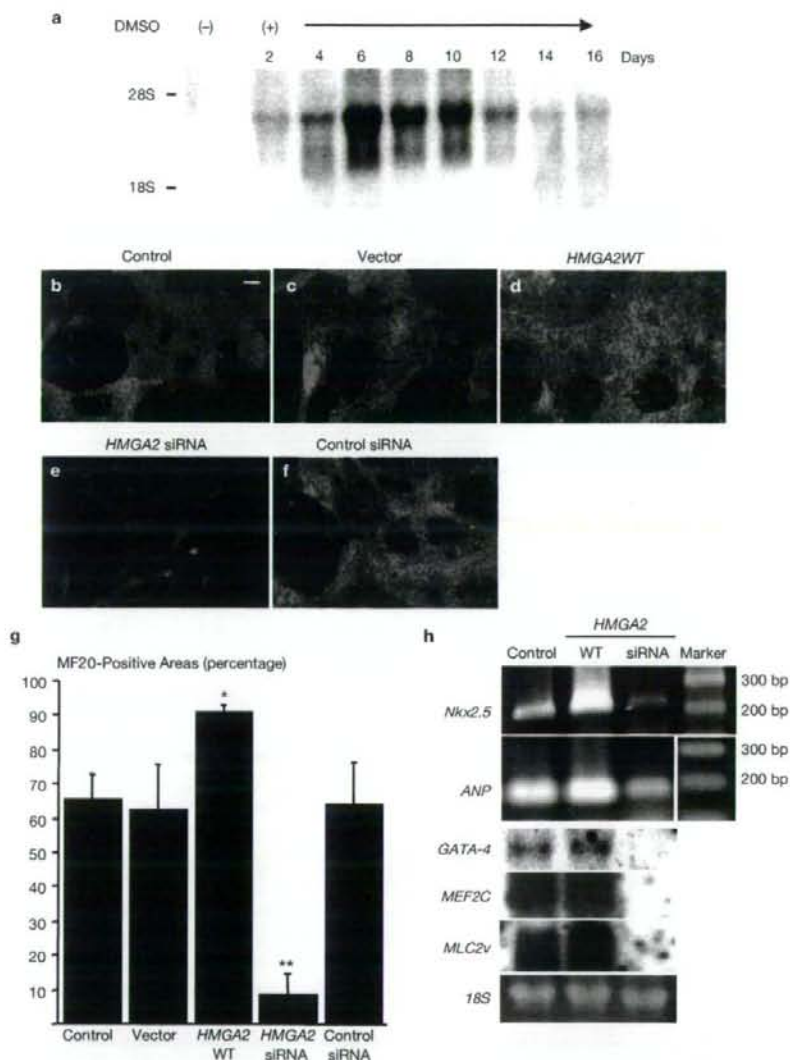
HMGA2 is a member of the HMG superfamily of non-histone chromatin proteins, which consists of three sub-families, HMGA, HMGB and HMGN<sup>1,2</sup>. HMG proteins modulate the expression of many genes by remodelling the chromatin architecture and promoting the formation of multiprotein complexes on the promoter/enhancer region, leading to the active transcription of their target genes. The HMGA sub-family consists of four members, HMGA1a-c,

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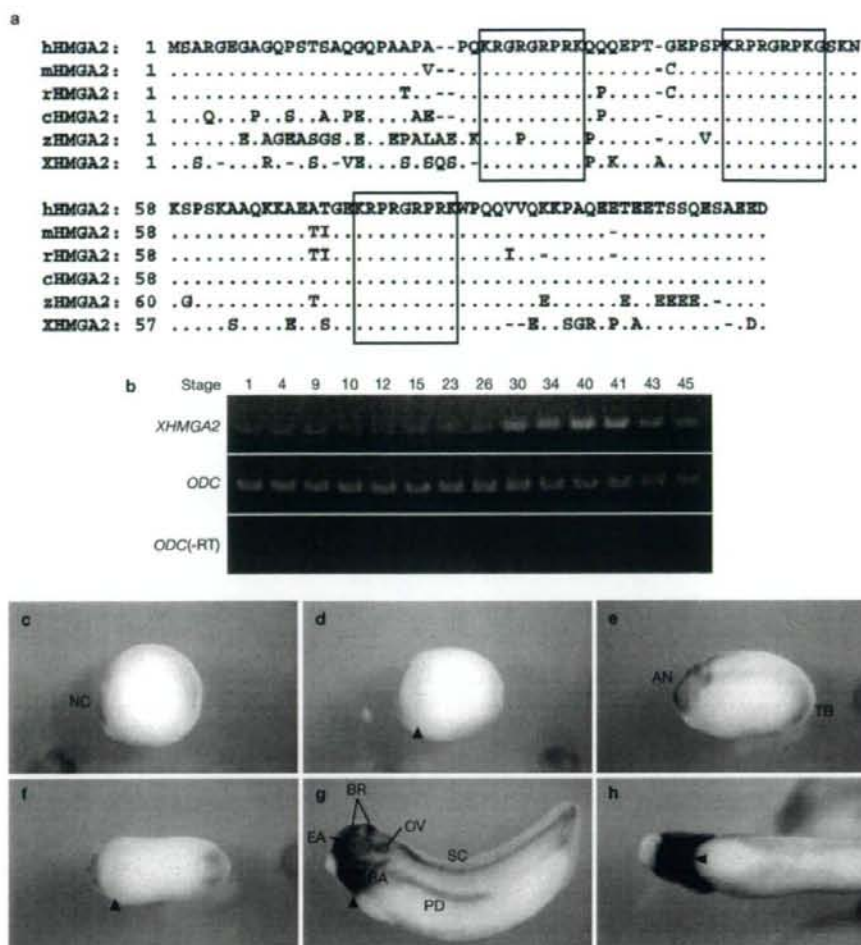
**Figure 1** *HMGGA2* is an essential positive regulator of cardiomyocyte differentiation. **(a)** Expression of *HMGGA2* mRNA during P19CL6 differentiation into cardiomyocytes was assessed by northern blot analysis. **(b–f)** The effect of *HMGGA2* overexpression or *HMGGA2* knockdown on cardiomyocyte differentiation was assessed with MF20 staining in control **(b)**, empty vector-transfected **(c)**, *HMGGA2* overexpressing **(d)**, *HMGGA2* siRNA-transfected **(e)** and control siRNA-transfected **(f)** P19CL6 cells. Scale bar is

100  $\mu$ m. **(g)** Quantification of MF20-positive area. The results are shown as mean  $\pm$  s. d. \* $P < 0.05$ , compared with control or vector-transfected cells, \*\* $P < 0.01$  compared with control or irrelevant siRNA-transfected cells (one-way ANOVA, followed by Fisher's PLSD test;  $n = 6$ ) **(h)** The effect of *HMGGA2* overexpression or *HMGGA2* knockdown on cardiac marker gene expression was assessed by RT-PCR (for *Nkx2.5* and atrial natriuretic peptide (*ANP*)) and northern blot (for *GATA-4*, *MEF2C* and myosin light chain 2v (*MLC2v*)).

generated by alternative splicing of *HMGGA1* gene transcripts, and *HMGGA2*, encoded by the *HMGGA2* gene. All HMGGA proteins except *HMGGA1c* contain three short basic repeats called AT-hooks, which bind to the minor groove of AT-rich DNA stretches<sup>1</sup>. HMGGA proteins are also able to associate with multiple transcription factors and regulate the expression of their target genes. For example, expression of the interferon- $\beta$  gene is regulated by a multiprotein complex

containing NF- $\kappa$ B, interferon regulatory factor, activating transcription factor-2/c-Jun and *HMGGA1a*<sup>9</sup>. HMGGA proteins also participate in the regulation of the genes for interleukin-2 receptor  $\alpha$  and the insulin receptor<sup>10,11</sup>. HMGGA proteins are expressed ubiquitously and abundantly during embryogenesis, whereas their expression is low or undetectable in fully differentiated adult tissues<sup>12</sup>. This suggests that HMGGA proteins regulate normal cell growth and differentiation.





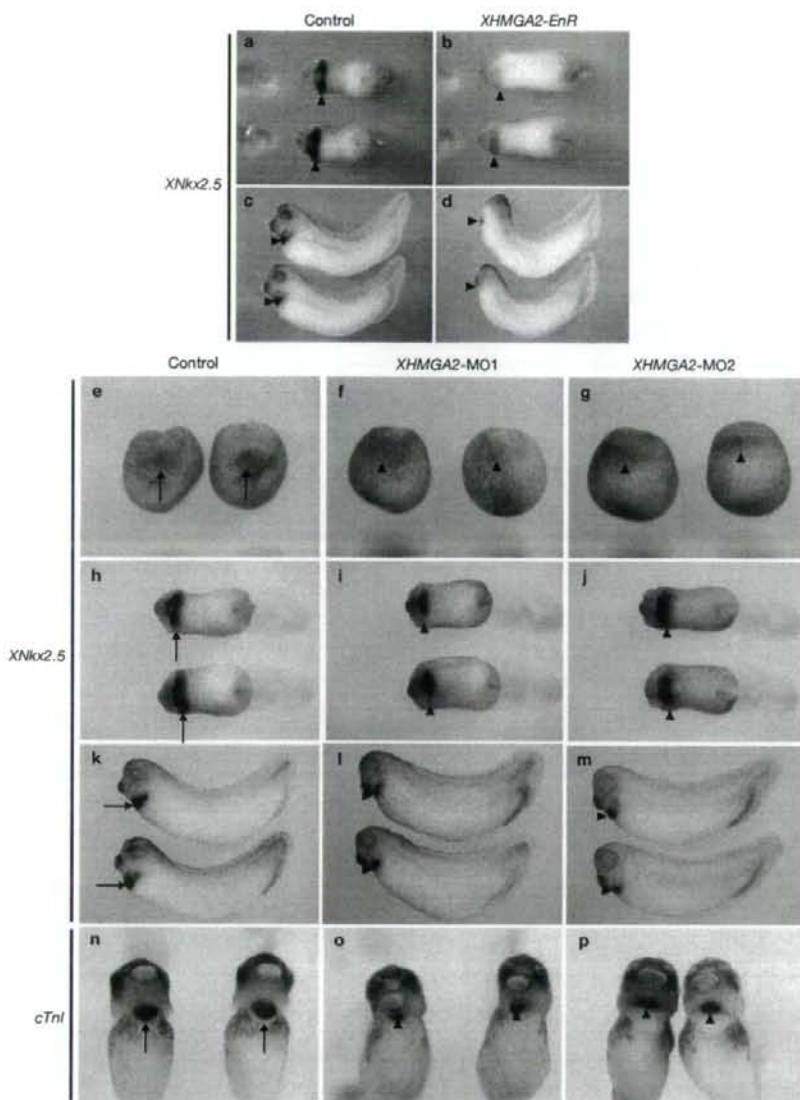
**Figure 2** cDNA sequence and expression pattern of *XHMGA2*. (a) Amino acid sequences of *XHMGA2* protein were compared with those of human (NM\_001094371), mouse (NM\_010441), rat (NM\_032070), chicken (NM\_205001) and zebrafish (NM\_212680) *HMGA2*. Dots indicate identities and dashed lines are introduced to maximize the alignment. Boxes represent the three AT-hooks. (b) Expression of *XHMGA2* mRNA during embryogenesis analysed by RT-PCR. *Omitine decarboxylase* (*ODC*) represents internal controls. (c-h) Expression of *XHMGA2* mRNA during embryogenesis analysed by *in situ*

hybridization. Lateral (c) and ventral (d) view of stage-15 embryo. *XHMGA2* expression was detected in neural crest (NC) and weakly in precardiac region (arrowhead). Lateral (e) and ventral (f) view of stage-23 embryo. *XHMGA2* was expressed in anterior neural tissue (AN), tailbud (TB) and weakly in precardiac region (arrowhead). Lateral (g) and ventral (h) view of stage-32 embryo. *XHMGA2* was detected in brain (BR), spinal cord (SC), eye anlage (EA), otic vesicle (OV), branchial arch (BA), pronephric duct (PD) and heart anlage (arrowhead). Anterior is left and dorsal is top for c, e, g, and anterior is left for d, f, h.

To examine whether *HMGA2* regulates cardiomyocyte differentiation, we analysed the ability of P19CL6 clones stably overexpressing wild-type *HMGA2* (P19CL6-*HMGA2*) to differentiate into cardiomyocytes. The extent of cardiomyocyte differentiation was assessed by the area positive for an anti- $\alpha$ -myosin heavy chain antibody (MF20). In response to DMSO, P19CL6-*HMGA2* differentiated into beating cardiomyocytes more efficiently than the parental P19CL6 cells (Fig. 1b-d, g), and there was a positive correlation between the extent of cardiomyocyte differentiation and the level of *HMGA2* expression in multiple P19CL6-*HMGA2* clones (Supplementary Information, Fig. S1a). On the other hand, siRNA-mediated knockdown of *HMGA2* blocked cardiomyocyte

differentiation of P19CL6 cells without altering the expression of mesodermal marker genes such as *Brachyury* and *Flk-1*, whose expressions precede those of early cardiac marker genes such as *Nkx2.5* (Fig. 1e-g; Supplementary Information, Fig. S1b). The expression levels of cardiac marker genes was upregulated in response to *HMGA2* overexpression, whereas they were downregulated by knockdown of *HMGA2* expression (Fig. 1h). Together, these results suggest that *HMGA2* is an essential positive regulator of cardiomyocyte differentiation.

To investigate the role of *HMGA2* in cardiogenesis *in vivo*, we performed experiments using *Xenopus* embryos. We first cloned *XHMGA2*, a *Xenopus* orthologue of *HMGA2*. *XHMGA2* encodes a protein of 105



**Figure 3** XHMGA2 is essential for cardiogenesis. (a–d) Overexpression of a dominant-negative XHMGA2 mutant in *Xenopus* embryos blocked *XNkx2.5* expression. Ventral view of stage-23 (a, b) and lateral view of stage-34 (c, d) embryos. Expression of *XNkx2.5* mRNA was decreased in XHMGA2-EnR mRNA-injected embryos (b, d, arrowheads), compared with that of control embryos (a, c, arrowheads). (e–p) MO-mediated XHMGA2 knockdown results in impaired cardiogenesis. Whole-mount *in situ* hybridization analysis was

performed sequentially for *Xenopus* embryos at stage 15 (e–g), stage 23 (h–j) and stage 34 (k–m) for *XNkx2.5*, and at stage 41 for *cardiac troponin I* (*cTnl*) (n–p). Expression of *XNkx2.5* mRNA was detected in uninjected control embryos (e, h, k, arrows), whereas it was attenuated in both XHMGA2-MO1 (f, i, l) and XHMGA2-MO2 (g, j, m)-injected embryos (arrowheads). *In situ* hybridization analysis for *cardiac troponin I* revealed that the heart size in MO-injected embryos (o, p, arrowheads) was smaller than that of control embryos (n, arrows).

amino acids that contains three highly conserved AT-hooks and is 60–70% homologous with HMGA2 proteins in other species (Fig. 2a). Reverse transcriptase-polymerase chain reaction (RT-PCR) analysis revealed that XHMGA2 was maternally transcribed in the early stage of embryogenesis and its expression levels increased at stage 30 (Fig. 2b). *In situ* hybridization analysis revealed that XHMGA2 was

expressed in neural crest cells and the precardiac region at the neurula stage (Fig. 2c, d), and in anterior neural tissue, tailbud and precardiac region at the early tailbud stage (Fig. 2e, f). At the late tailbud stage, a strong signal was detected in brain, spinal cord, eye anlage, otic vesicle, branchial arch, pronephric duct and heart anlage (Fig. 2g, h). To examine whether XHMGA2 regulates cardiogenesis *in vivo*, we injected