



# P66shc and its role in ischemic cardiovascular diseases

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## Abstract

Oxidative stress caused by an imbalance in the formation and removal of reactive oxygen species (ROS) plays an important role in the development of several cardiovascular diseases. ROS originate from various cellular origins; however, the highest amount of ROS is produced by mitochondria. One of the proteins contributing to mitochondrial ROS formation is the adaptor protein p66shc, which upon cellular stresses translocates from the cytosol to the mitochondria. In the present review, we focus on the role of p66shc in longevity, in the development of cardiovascular diseases including diabetes, atherosclerosis and its risk factors, myocardial ischemia/reperfusion injury and the protection from it by ischemic preconditioning. Also, the contribution of p66shc towards cerebral pathologies and the potential of the protein as a therapeutic target for the treatment of the aforementioned diseases are discussed.

**Keywords** P66shc · Longevity · Diabetes · Atherosclerosis · Ischemia/reperfusion · Preconditioning · Mitochondria · Stroke

## The p66shc protein

P66shc is a member of the spontaneous human combustion (shc) family. The human shcA locus not only encodes p66shc but also the isoforms p46shc and p52shc, which derive from the same transcript via usage of two distinct ATG start codons. The three isoforms share functional domains, namely the phosphotyrosine binding (PTB) domain, the adjacent proline- and glycine-rich collagen-homology (CH1) domain, as well as the carboxyterminal src-homology (SH2) domain. P66shc differs from p46shc and p52shc in the way that it contains an additional aminoterminal collagen-homology domain (CH2) consisting of 110 amino acids [69]. The shc proteins are adaptor proteins lacking intrinsic enzymatic activity and they function in the transduction of cellular signals [1]. Here, phosphorylated conserved tyrosine residues in the CH1 domain (tyrosine 239–240 and tyrosine 317) represent binding sites for other proteins. The proline- and glycine-rich stretches in the CH1 and CH2 domains mediate the interaction with SH3 domain-containing proteins. Serine (S) 36, which represents an important phosphorylation site within p66shc, is present

in the p66shc-specific CH2 domain. At the carboxyterminal part of the CH2 domain, a region controlling the interaction with cytochrome *c* is localized [40]. Based on the differential structure of p46shc, p52shc and p66shc, the isoforms exert different functions: whereas p46shc and p52shc are involved in cell survival and the progression of the cell cycle [105], p66shc plays a role in apoptosis and contributes to oxidative stress [68]. In the present review, we will focus on the expression and function of p66shc.

## P66shc: localization, phosphorylation and mitochondrial translocation

The intracellular localization of p66shc has first been analyzed in mouse embryonic fibroblasts (MEFs). Here, a predominantly cytosolic localization of the protein is demonstrated with fractions of p66shc present in the endoplasmic reticulum as well as in the mitochondria, even under basal conditions [80]. Cardiomyocytes contain different subpopulations of mitochondria, which differ in form and function, namely the subsarcolemmal and the interfibrillar mitochondria, [83, 84]. The quantification of p66shc in these subtypes of mitochondria reveals equal amounts of p66shc in the two subgroups [55]. The isolation of interfibrillar mitochondria involves the use of proteases, which may hamper the exact quantification of proteins in this mitochondrial subtype;

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however, in case of p66shc the protease treatment for mitochondrial isolation does not interfere with the amount of the protein in IFM [55]. The analysis of the exact submitochondrial localization of p66shc shows that in liver mitochondria the protein is present in the fraction enriched with inner membrane proteins [80]. A more detailed analysis of subfractionated MEF mitochondria indicates that the highest amount of p66shc immunoreactivity is found within the intermembrane space [40]. Mitochondrial p66shc is part of a high molecular weight complex (approximately 670 kDa), which, among other proteins, contains mitochondrial heat shock protein 70 (mtHSP70) with which p66shc directly interacts [80].

The translocation of p66shc from the cytosol to the mitochondria is dependent on the phosphorylation status of the protein. Treatment with a protein kinase C (PKC) activator induces a phosphorylation of p66shc at S36 [87]. The use of the PKC $\beta$  isoform-specific inhibitor hispidin reduces such phosphorylation, thereby demonstrating the importance of this isoform for p66shc phosphorylation [87]. This initial observation in MEFs is confirmed in other cell types such as airway epithelial cells [113] or endothelial cells [59]. However, another study excludes S36 as a residue phosphorylated by PKC $\beta$  in MEFs; instead, S139 and S213 are proposed to function as PKC $\beta$ -targeted amino acids [44]. It appears that S36 within p66shc can also be phosphorylated by JNK1/2 (c-Jun N-terminal kinases 1 and 2) [49], an observation confirmed in endothelial cells [81]. Also, S54 and threonine (T) 386 within p66shc become phosphorylated, presumably by p38 mitogen-activated protein kinase [50]. In addition to PKC $\beta$ , also PKC $\delta$  contributes to p66shc phosphorylation [113]. Hydrogen sulfide—which exerts multiple functions in the cardiovascular system [6]—inhibits mitochondrial ROS production via the sulfhydration of the cysteine 59 residue at p66shc, which in turn prevents the phosphorylation of p66shc [66, 109] (for review, also see Ref. [108]).

In endothelial cells, increased expression of NADPH oxidase (NOX) 4, potentially through increased canonical Wnt signaling [103], increases mitochondrial ROS; this increase in ROS formation is prevented by silencing of NOX2 [52]. Mechanistically, NOX2-induced hydrogen peroxide increases S36 phosphorylation of p66shc, which is inhibited by silencing NOX2. Moreover, NOX2 or NOX4 knockdown or overexpression of S36 phosphorylation-defective mutant of p66shc inhibits mitochondrial ROS formation; thus, NOX4, NOX2 and p66shc might contribute to the ROS-induced ROS release [52, 100]. Increased microRNA (miR) 200c expression might contribute to the ROS-induced increase in S36 phosphorylation of p66shc [20].

P66shc interacts with prolyl isomerase 1 (Pin1), an enzyme isomerizing phosphorylated serine/threonine-proline bonds in substrate proteins, in a phosphorylation-dependent manner. In Pin1-deficient MEFs, the

mitochondrial amount of p66shc is reduced suggesting a contribution of this protein–protein interaction for the mitochondrial import of p66shc [87]. Also, the Pin1-inhibitor juglone decreases the mitochondrial translocation of p66shc in human umbilical vein endothelial cells (HUVECs) [112] and in intestinal cells [32]. Dimeric p66shc is imported into the mitochondria possibly via a disulfide relay system such as the mitochondrial intermembrane space import and assembly protein 40 (Mia40) [38]; however, the exact mechanism and pathway by which p66shc enters the mitochondria remain to be elucidated.

Other molecular targets of p66shc like the tumor suppressor p53, the kruppel like factor-2 (KLF2) transcription factor, or the forkhead box protein O (FOXO9) have been discussed in details recently [57]. Also, oxidation of protein tyrosine phosphatases is modified by p66shc, thereby controlling growth factor-induced signaling and migration of endothelial cells [35].

## The role of p66shc in affecting mitochondrial function

The inner mitochondrial membrane forms extensive folds called cristae, and cristae structure is affected by p66shc [88]. Once p66shc has entered the mitochondria, the protein affects the function of the organelle, especially ROS formation. Mitochondrial p66shc oxidizes cytochrome *c* and thereby catalyzes the reduction of oxygen to hydrogen peroxide [40]. Accordingly, reduced levels of ROS in response to different stimuli are demonstrated in different cell types/organs devoid of p66shc, including mouse embryonic and adult fibroblasts [102], endothelial cells [81, 107], and myocardial tissue [21]. Whereas the prooxidant function of mitochondrial of p66shc is well documented, a cytosolic fraction of the protein may also exert antioxidative function [71].

Elevated levels of ROS function as trigger molecules to open the mitochondrial permeability transition pore (MPTP), a large conductance pore in the inner mitochondrial membrane, which is largely closed under physiological conditions. During the last years, progress has been made regarding the identification of proteins involved in MPTP formation. Whereas it is discussed that dimers of the F<sub>0</sub>F<sub>1</sub>ATP synthase build up the MPTP [41], other data showed that permeability transition occurs upon the dissociation of ATP synthase dimers [72]. Upon dissociation of the F<sub>1</sub> and F<sub>0</sub> subunits, the *c* subunits of the F<sub>0</sub>F<sub>1</sub>ATP synthase are considered to form the lumen of the MPTP [3, 8]. Opening of the MPTP induces mitochondrial swelling with subsequent rupture of the outer mitochondrial membrane. As a consequence, the activities of the complexes of the electron transport chain protein decline and pro-apoptotic factors are released [72]. Therefore, enhanced ROS formation by

p66shc would favor MPTP opening and indeed mitochondrial swelling is observed upon the addition of recombinant p66shc to isolated mitochondria [40].

In addition, the absence of p66shc is associated with reduced mitochondrial oxygen consumption in mouse embryonic fibroblasts, whereas the reconstitution of p66shc expression in p66shc-deficient cells increases respiration [77]. However, in mitochondria isolated from brown adipose tissue mitochondrial respiration is higher in p66shc-deficient compared to wildtype mitochondria and the authors suggest that p66shc-deficient mitochondria are in an uncoupled state [11]. Also, mitochondria isolated from aged mouse brains display higher complex 1-mediated respiration upon knock-out of p66shc [86].

Mitophagy serves to eliminate dysfunctional mitochondria; in B cells, p66shc induces depolarization of the mitochondrial membrane potential and ubiquitination of outer mitochondrial membrane proteins inducing mitophagy. In addition, p66shc serves as a receptor for microtubule-associated protein 1A/1B-light chain 3 (LC3-II) and thereby contributes to the initiation of mitophagy [79].

Taken together, the expression of p66shc in a variety of cells/organs and its relevance for different aspects of mitochondrial function (including respiration, ROS formation and mitophagy) makes p66shc an interesting target to be studied in the context of cardiovascular diseases and we will highlight the role of the protein in this context in the following sections of the review.

## Influence of p66shc on cardiac function and life span

The deletion of exon2a of p66shc by Migliaccio and coworkers [68] resulted in a mouse line with a normal development and without effects on fertility. These p66shc knockout (p66shc KO) mice are comparable to wildtype mice in terms of body weight, food consumption, and histology of different organs. However, some lung abnormalities are detected, although lung function is not affected. Others report that p66shc KO mice are leaner than wildtypes [23, 101] and that the observed difference is related to a modification of the composition of gut microbiota and their response to diet [22] (for detailed review: see Ref. [24]). A more detailed analysis of cardiovascular parameters reveals no differences between wildtype and p66shc KO mice regarding systolic blood pressure, heart rate, weights of the right and left ventricles. However, an increase in the number of cardiomyocytes is observed which is associated with a reduced volume of the left ventricular chamber [42]. In our own colony of p66shc KO mice, in contrast to the previous work [42], left ventricular end-diastolic and end-systolic volumes are increased compared to wildtype mice without affecting

stroke volume or cardiac output (Fig. 1). In accordance, the length of cardiomyocytes isolated from p66shc KO mice is increased compared to the length of cardiomyocytes isolated from wildtype mice, while unloaded shortening is similar between both strains (Fig. 1).

In the context of the putative role of oxidative stress in mitochondria-dependent aging, p66shc represents an interesting target and the role of p66shc in life span is addressed in several studies. In wildtype hearts, the amount of p66shc increases with aging [110]. Initially, an increase in life span was shown in p66shc KO mice compared to wildtype mice [68], and others related the extended life span due to arginase II deficiency also to downregulation of p66shc [110]. However, this first report could not be confirmed when mice were housed in a large outdoor enclosure (with increased physical activity, temperature changes and food competition); here, even a deleterious effect of the p66shc knockout was described [39]. When life span is analyzed in p66shc KO mice on different genetic backgrounds, there is no indication that p66shc may function as a longevity protein [91]. However, when wildtype and p66shc KO mice are fed a calorie-restricted diet, the survival of p66shc KO mice early on is improved but without any difference in total life span compared to wildtype mice [91].

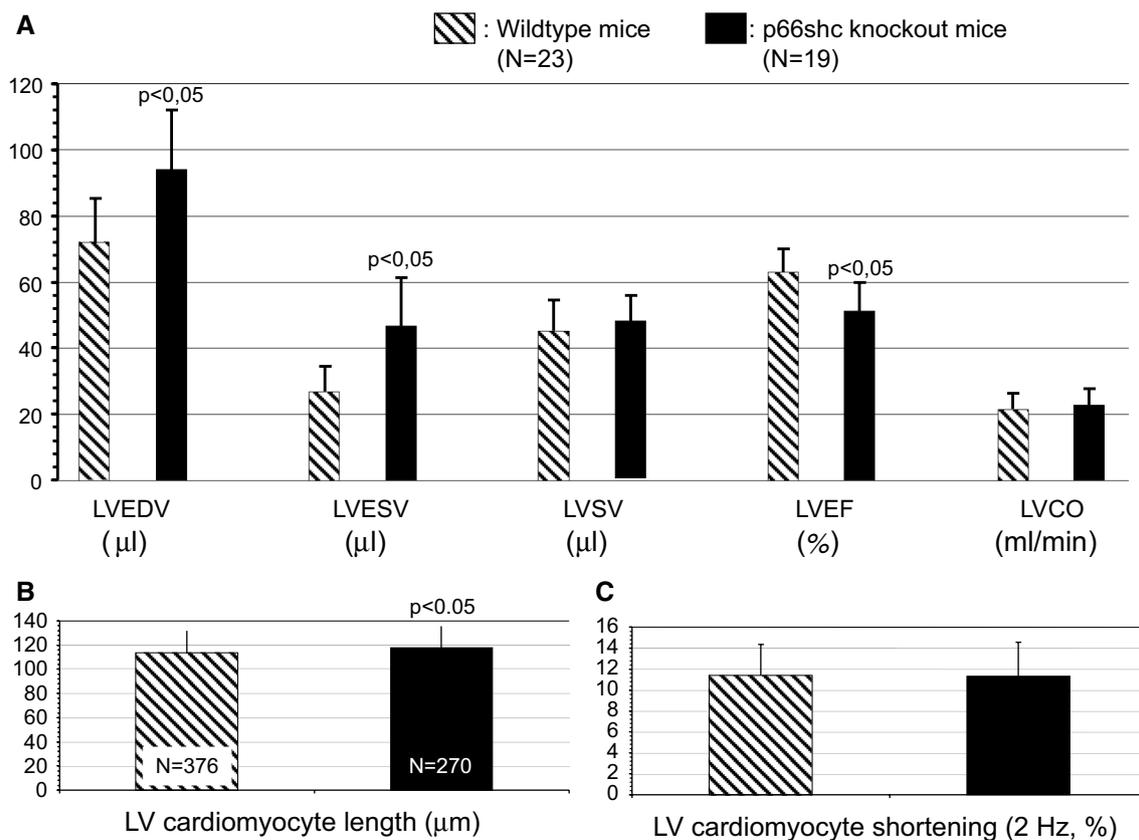
## P66shc and cardiovascular risk factors

The importance of aging on p66shc and vascular dysfunction has been reviewed extensively elsewhere [18].

### Hyperglycemia

High glucose induces acetylation of p66shc at lysine 81, which in turn promotes the phosphorylation of p66shc at S36 and thereby enhances the mitochondrial import of the protein, where ROS formation is stimulated [58]. A mouse line in which lysine 81 is not acetylatable is protected from hyperglycemia-induced oxidative stress [58]. Augmented p66shc phosphorylation in response to high glucose is also shown in osteoclasts [90] and HUVECs [112] as well as in ventricular cardiomyocytes [63]. Again, enhanced phosphorylation of p66shc is associated with increased mitochondrial translocation of the protein and with a concomitant increase in ROS [63, 70]. The high glucose-induced enhancement of ROS is abrogated by silencing p66shc [70].

Apart from increased phosphorylation and mitochondrial translocation of p66shc, hyperglycemia induces an increased expression of p66shc in macrophages from apolipoprotein E (ApoE)-deficient mice [95], in HUVECs [104], retinal [70] and aortic endothelial cells [85], in the rat retina [114], and also in mouse hearts [25]. The transcription of p66shc is controlled by epigenetic modifications, and in human aortic



**Fig. 1 a** Echocardiographic assessment of wildtype and p66shc knockout (KO) mice at rest. Both the left ventricular (LV) end-diastolic (LVEDV) and end-systolic (LVESV) volumes were higher in p66shc KO mice than in wildtype mice, while LV stroke volume (LVSV) remained unchanged. LV ejection fraction decreased in p66shc KO mice compared to wildtype mice while cardiac output

was similar between both strains of mice. **b** Cardiomyocytes isolated from p66shc KO mice hearts were somewhat longer than those isolated from wildtype mice hearts, while **c** unloaded cardiomyocyte shortening at 2 Hz pacing was identical. Statistical analysis was performed by unpaired Student's *t* test and a  $p < 0.05$  was considered to indicate a significant difference between genotypes

endothelial cells high glucose causes acetylation of histone 3, which leads to an open chromatin structure and, therefore, promotes transcription and increases expression of the p66shc protein [85].

## Diabetes

The overall role of ROS in the development of diabetes is reviewed in detail elsewhere [37, 78].

Sirtuin 1 (Sirt1, a member of the class III NAD<sup>+</sup>-dependent histone deacetylases) is downregulated in diabetic mouse hearts, involving micro RNAs such as miR-34a [61]—and this is accompanied by reduced Sirt1-dependent deacetylation of the p66shc promoter [25], potentially leading to increased p66shc transcription (for review, see Ref. [56]). The tRNA methyltransferase NSUN2 can subsequently methylate SHC mRNA, thereby enhancing the translation of p66shc and subsequently the levels of ROS—for example—during hyperglycemia [17].

Sirt1 not only impacts on the p66shc promoter region but also directly acts on lysine 81 within p66shc [58], which might promote p66shc phosphorylation (see above). Indeed, diabetes (induced by streptozotocin) is associated with increased phosphorylation of p66shc in mouse hearts [25], and it is also detected in rat hearts [115], where it is accompanied by enhanced amounts of phosphorylated PKC $\beta$ II. The mitochondrial amount of p66shc, its interaction with cytochrome *c*, and the amount of ROS are increased in hearts of diabetic mice; interestingly, glycemic control is unable to revert the increased translocation of p66shc into the mitochondria [25]. The *in vivo* silencing of p66shc during glycemic control, however, inhibits ROS formation and restores cardiac function. The finding that p66shc is of functional relevance in diabetes is confirmed in diabetic mice in which as a consequence of p66shc-mediated ROS formation a loss of viability occurs [31].

Streptozotocin-induced diabetic wildtype mice display a marked impairment of endothelium-dependent relaxations, increased peroxynitrite generation, nitrotyrosine expression,

and lipid peroxidation, all alterations being absent in p66shc KO mice [19].

Diabetes induced by streptozotocin also enhances the p66shc mRNA in the bone marrow [5]. Interestingly, the impairment of the mobilization of hematopoietic stem/progenitor cells from the bone marrow in diabetes is coupled to p66shc and oncostatin M [4] (for review, see Ref. [106]). In addition, an increased amount of p66shc mRNA is detected in peripheral blood mononuclear cells from diabetic patients and the increased p66shc expression correlates with a marker of oxidative stress [82].

Different from what has been described in diabetic hearts, in a prediabetic rat model the amount of p66shc is not affected [54].

### Hypercholesterolemia

Hypercholesterolemia is characterized by an elevation of low-density lipoprotein cholesterol (LDL-C) and represents a major risk factor for atherosclerotic vascular disease. In LDL-C stimulated HUVECs, the amount of p66shc increases both at the mRNA and at the protein level [53]. The upregulation of p66shc by LDL-C is mediated by hypomethylation of two CpG dinucleotides and acetylation of histone 3 in the p66shc promoter, thereby increasing its activity. In addition to enhanced expression of p66shc after treatment with LDL-C, the phosphorylation of p66shc at S36 is stimulated in human and mouse aortic endothelial cells after incubation with oxidized LDL-C (oxLDL), together with increased phosphorylation of PKC $\beta$ 2 [59, 96]. Such activation of p66shc is mediated by lectin-like oxLDL receptor-1, which is involved in oxLDL-induced ROS formation. In primary cultured HAEC treated with oxLDL, p66shc-mediated oxidative stress is derived from endothelial nitric oxide synthase (NOS) uncoupling and prevented by early treatment with tetrahydrobiopterin [97].

In visceral fat arteries (VFAs) isolated from obese subjects dysregulation of methyltransferase SUV39H1, demethylase JMJD2C and acetyltransferase SRC-1 occurs compared to VFAs from normal weight patients and these changes are associated with reduced di-(H3K9me2) and trimethylation (H3K9me3) as well as acetylation (H3K9ac) of histone 3 lysine 9 (H3K9) on p66shc promoter. Reprogramming SUV39H1, JMJD2C, and SRC-1 in isolated endothelial cells as well as in aortas from obese mice suppressed p66shc-derived ROS, restored nitric oxide levels, and rescued endothelial dysfunction [26].

There is also a link between hyperlipidemia and diabetes in that high concentration of LDL-C [7] or free fatty acids [73] induce pancreatic  $\beta$ -cell dysfunction and/or apoptosis. Free fatty acid-induced  $\beta$ -cell apoptosis is abrogated in islets from p66shcKO mice; by contrast, overexpression of p66shc, but not that of the phosphorylation-defective p66shc

mutant, enhances palmitate-induced apoptosis of pancreatic  $\beta$ -cells [76]. The underlying mechanism includes CD36, c-Jun-N-terminal kinase activation, and p66shc S36 phosphorylation causing beta-cell apoptosis via mitochondrial dysfunction [48].

### Hyperhomocysteinemia

Hyperhomocysteinemia represents a risk factor for atherosclerotic vascular disease and homocysteine is known to impact on DNA methylation. The p66shc promoter is hypomethylated in response to homocysteine and in turn the amount of the p66shc mRNA increases [51]. S-adenosylhomocysteine (SAH) is a precursor of homocysteine and the S-adenosylhomocysteine hydrolase (SAHH) catalyzes the breakdown of SAH to homocysteine. Inhibition of SAHH leads to hypomethylation of the p66shc promoter and subsequently enhances the expression of p66shc in the mouse aorta and in human endothelial cells [107]. SAHH inhibition is also accompanied by an induction of ROS formation, which is reduced after downregulation of p66shc by small interfering RNAs.

Taking into account that LDL-C and homocysteine induce the expression of p66shc, it is hypothesized that inhibition or deletion of p66shc would decrease the development of atherosclerosis (for review, also see Ref. [43]). Indeed, p66shc KO mice fed a high-fat diet not only demonstrate reduced levels of oxidative stress, but also develop less early atherosclerotic lesions than wildtype mice [75]. In addition, mice deficient for both ApoE and p66shc have smaller advanced atherosclerotic lesions compared to ApoE knockout mice [65].

In patients with coronary heart disease (CHD), expression of the p66shc mRNA in peripheral blood mononuclear cells positively correlates with the serum LDL-C and homocysteine levels and inversely with flow-mediated vasodilation, highlighting the pivotal role for the expression of p66shc in CHD and endothelial dysfunction [67]. P66shc might be most important for the transition of a stable coronary artery disease to an acute coronary syndrome patient [34]. The search for variants in the p66shc gene in patients with early-onset coronary artery disease indicates that variations appear to be rare and are presumably not linked to the genetic susceptibility of the disease [94]. Also, according to current databases (Online Mendelian Inheritance in Man, ClinVar, Human Genome Mutation Database), the gene encoding p66shc, *SHC1*, has not yet been linked to a cardiovascular disease condition.

Taken together, hyperglycemia induces the expression and phosphorylation of p66shc, which leads to an accumulation of the protein into the mitochondria, where it induces ROS formation leading to cell and/or tissue damage. The finding that p66shc-deficient cells or mice are protected

from hyperglycemia/diabetes-induced cellular/organ damage emphasizes the important role of the protein in the development of diabetes. LDL-C and homocysteine induce epigenetic modifications and lead to hypomethylation of the p66shc promoter, which stimulates the expression of p66shc. As a consequence, all risk factors increase oxidative stress through p66shc and finally result in endothelial dysfunction, inflammation and the development of atherosclerosis.

### **P66shc and myocardial ischemia/reperfusion injury**

During myocardial ischemia, ROS formation is initiated [14]; however, the majority of ROS is generated at the onset of reperfusion [36, 74, 118]. The detrimental effects of high amounts of ROS are mediated by oxidative modifications on proteins, lipids and on the histone-free mitochondrial DNA. Therefore, a reduction of ROS at the onset of reperfusion is proposed to decrease myocardial ischemia/reperfusion (I/R) injury and indeed anti-oxidative therapies exert cardioprotective effects (reviewed in Ref. [13]). However, ROS are not only causing myocardial damage; if present in low amounts they are important signaling molecules in the cardioprotection by ischemic conditioning strategies (for review see Refs. [15, 27, 30, 45]). Indeed, ROS scavenging during the preconditioning ischemia abrogates the cardioprotection by ischemic preconditioning (IPC, here, infarct size is reduced by short, non-lethal periods of I/R applied before a longer lasting phase of I/R) [98]. In this context, the ROS-generating protein p66shc represents an interesting protein to be studied in models of I/R injury and protection from it by preconditioning.

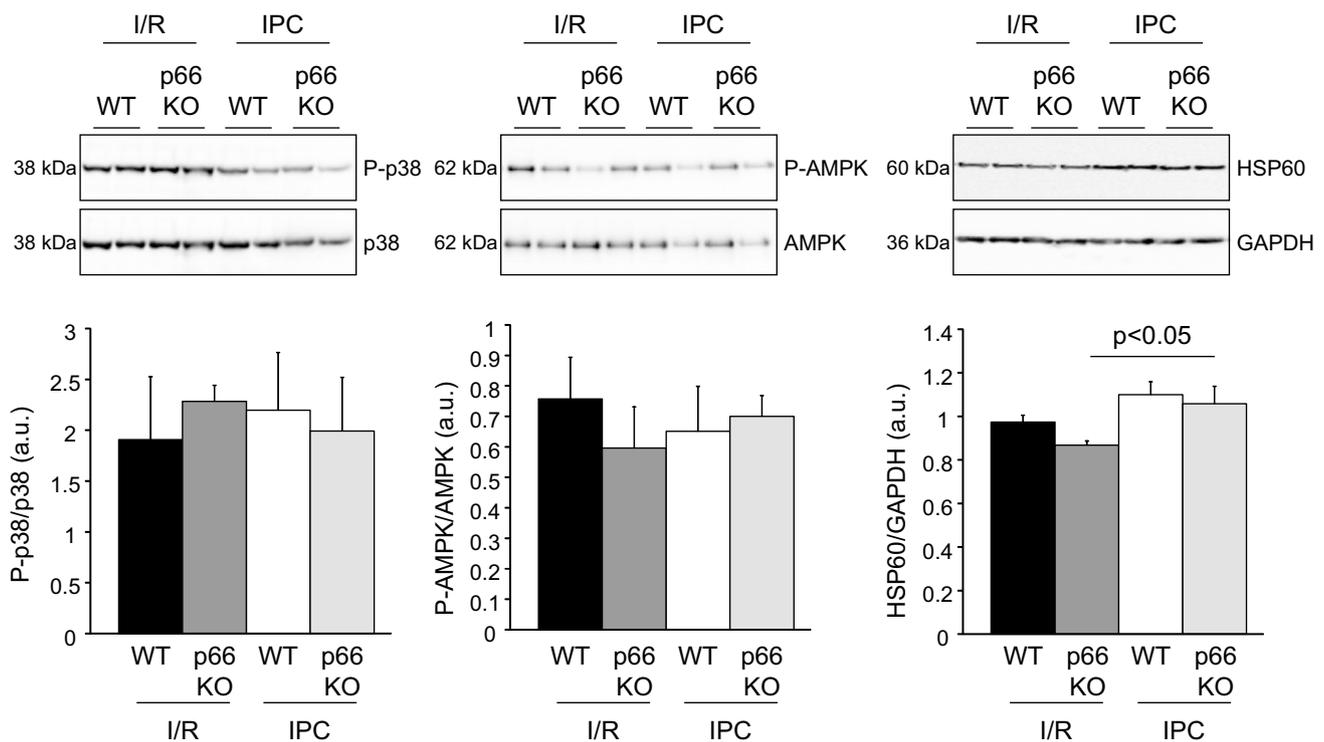
Indeed, the phosphorylation of p66shc at S36 increases in isolated guinea pig hearts undergoing I/R; however, the extent of phosphorylation of the protein depends on the duration of I/R. Whereas the p66shc phosphorylation is not altered after 20 or 30 min ischemia without reperfusion, 5 or 10 min ischemia followed by 20 min reperfusion increases p66shc phosphorylation. When 30 min of ischemia are followed by 10 min of reperfusion such enhanced phosphorylation is maintained for up to 1 h of reperfusion [111]. The enhanced phosphorylation of p66shc is accompanied by a translocation of the protein into the mitochondria and inhibition of PKC $\beta$ II diminishes such translocation of p66shc. Translocation of p66shc after 30 min ischemia and 10 min reperfusion, however, is enhanced only in SSM isolated from wildtype mice hearts [12]; such enhanced translocation of p66shc is associated with increased mitochondrial ROS formation in SSM compared to IFM. In contrast, ROS formation is comparable in SSM and IFM isolated after I/R from p66shc KO hearts

[12]. Interestingly, the I/R-induced increased mitochondrial translocation of p66shc into SSM is abrogated after IPC [12].

Malondialdehyde formation and tropomyosin oxidation—indicators of oxidative stress—as well as irreversible injury decreases following I/R in p66shc-deficient compared to wildtype hearts [21]. However, these *in vitro* results cannot easily be transferred to the *in vivo* situation, where myocardial infarct size after I/R is not affected [12] or even increased [2] by the ablation of p66shc. The authors of the aforementioned study also investigated the involvement of signaling pathways involved in I/R injury and in the protection from it, namely the RISK (reperfusion injury salvage kinase) and SAFE (survivor activating factor enhancement) pathway. In p66shc-deficient hearts, the phosphorylation of Akt kinase (also known as protein kinase B) at T308 and the phosphorylation of the signal transducer and activator of transcription 3 (STAT3) at S727 is blunted following 30 min ischemia and 5 min of reperfusion. Our own results demonstrate that neither the phosphorylation of the p38 mitogen-activated protein kinase (p38) nor the phosphorylation of the AMP-activated protein kinase (AMPK)—proteins suggested to be involved in I/R injury [46, 62, 89]—differs in wildtype and p66shc KO hearts after I/R without or with IPC *in vitro* (Fig. 2). Therefore, we hypothesize that the absence of reduced I/R injury in p66shc KO hearts in our model *in vitro* (30 min ischemia/10 min reperfusion) is due to a lacking activation of cardioprotective signaling pathways. In contrast, expression of heat shock protein 60 (HSP60) increased in p66shc KO hearts after IPC; however, since IPC was equally effective in reducing myocardial infarct size *in vitro* [21] and *in vivo* [12] in wildtype and p66shc KO hearts this upregulation of HSP60 is not a prerequisite for cardioprotection. Thus, it is unlikely that increased p66shc-mediated mitochondrial translocation and subsequent ROS formation are a prerequisite for IPC-induced cardioprotection (for review, also see Ref. [47]).

### **Post-myocardial infarction**

In mice with a coronary artery ligation, p66shc expression and phosphorylation increase transiently during the first week post-infarction. P66shc KO mice, despite a similar infarct size compared to wildtype mice, show improved survival and reduced occurrence of heart rupture post-myocardial infarction. In p66shc KO mice, the expression of cardiac matrix metalloproteinase 2 is reduced, fibroblast activation and collagen accumulation are facilitated and oxidative stress is attenuated early post-myocardial infarction resulting in reduced reactive fibrosis and left ventricular dilatation. Thus, p66shc activation is involved in adverse cardiac remodeling post-myocardial infarction [10].



**Fig. 2** Activation of signaling molecules in wildtype and p66shc KO hearts undergoing I/R injury or IPC. Wildtype or p66shc KO (p66 KO,  $n=4$  per group) hearts were Langendorff-perfused for 30 min under ischemic conditions and subsequently reperused for 10 min. IPC was performed by three preceding cycles of 3 min ischemia and 5 min reperfusion. The left ventricular tissue was homogenized and subjected to western blot analysis for total and phosphorylated p38

(Thr180, Tyr182), total and phosphorylated (Thr172) AMPK and the expression of HSP60. Immunoreactivities of the phosphorylated proteins were normalized to the total forms of the proteins, whereas the expression of HSP60 was normalized to that of the housekeeping protein GAPDH (glyceraldehyd-3-phosphate dehydrogenase). Statistical analysis was performed by two-way ANOVA and a  $p < 0.05$  was considered to indicate a significant difference between groups

### Drug-induced cardiotoxicity

Cancer patients treated with chemotherapy often suffer from cardiotoxicity of the drugs [33], which is induced by mitochondrial dysfunction and cardiomyocyte apoptosis leading to heart failure [60]. In the rat cardiomyoblast H9c2 cell line doxorubicin (Dox) treatment induces activation of p66shc [92] which is in part responsible for increased cellular oxidative stress. In rat cardiomyoblast, H9c2 cells as well as in rats in vivo, Dox treatment increases miR-34a-5p in the myocardium and plasma; similarly in patients with diffuse large B cell lymphoma miR-34a-5p is enhanced after epirubicin therapy. MiR-34a-5p modulates Sirt1 expression and enhances p66shc expression, accompanied by an increase of Bax and activation of caspase-3. MiR-34a-5p enhances cardiomyocyte apoptosis by targeting Sirt1 and activation of miR-34a-5p/Sirt1/p66shc pathway contributes to Dox-induced cardiotoxicity [116], which can be attenuated by endurance exercise training [64].

Taken together, p66shc becomes activated by I/R and translocates to mitochondria, most importantly the subsarcolemmal ones. Such activation and translocation can be

abolished by IPC. Despite increased translocation and subsequent ROS formation, p66shc does neither contribute to infarct size development during I/R nor to cardioprotection by IPC. However, p66shc activation appears to be important for post-myocardial infarction remodeling and cardiotoxicity elicited by cancer drugs. Here, abrogation of p66shc signaling might be of therapeutic interest.

### The contribution of p66shc towards brain injury

The role of p66shc is not restricted to the heart, since a contribution of the protein towards brain injury is also described. In Alzheimer's disease (AD), abnormally folded amyloid  $\beta$  proteins accumulate in the brain and induce cytotoxicity, e.g., via increased ROS formation. In C6 glioma cells, amyloid  $\beta$  induces the phosphorylation of p66shc at S36 whereas the knockdown of p66shc is associated with reduced amyloid  $\beta$ -induced ROS formation and subsequently less apoptotic cell death [9]. P66shc-ablated PSAPP mice (a double transgenic mouse line expressing mutant amyloid

precursor protein and presenilin-1, used as AD model) show improved survival and less cognitive defects, the latter being mediated by improved function of brain mitochondria (including enhanced respiration, adenosine triphosphate production as well as reduced ROS formation) [28]. Increased respiration and diminished ROS formation are also detected in brain mitochondria isolated from aged p66shc-KO mice compared to aged wildtype mice [86]. The induction of oxidative stress and apoptosis in mouse hippocampal HT22 cells by angiotensin II increases the amount of PKCβII, the phosphorylation of p66shc at S36 and the mitochondrial translocation of the protein, which is accompanied by enhanced ROS formation and cell death, effects which are reversed by propofol [117].

An involvement of p66shc on neuronal cell death is shown in p66shc KO mice, in which the development of experimental autoimmune encephalomyelitis is delayed, an effect suggested to be mediated by delayed MPTP opening [93].

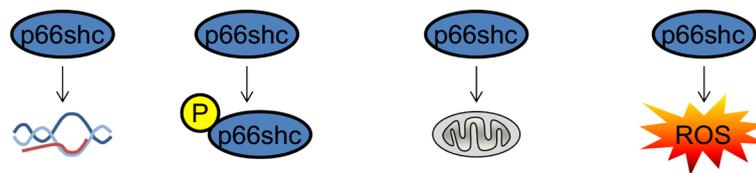
Post-ischemic silencing of p66shc in the brain of wildtype mice undergoing I/R injury by occlusion of the middle cerebral artery decreases neurological deficits, reduces stroke volume and finally increases survival 6 days after stroke [99]. In acute ischemic stroke patients, the amount of the

p66shc mRNA in peripheral blood monocytes increases 6 h after initial stroke symptoms and positively correlates with short-term neurological outcome [99].

Taken together, pathological conditions in the brain are often associated with activation of p66shc, and enhanced oxidative stress and consequently downregulation and/or inhibition of p66shc reduce or delay these pathologies and make the protein an interesting therapeutic target. However, preconditioning of cortical cells results in a phosphorylation and subsequent mitochondrial translocation of p66shc and, different from the heart, the cytoprotection afforded by preconditioning is blocked by inhibition of p66shc [16]. Alterations of p66shc expression, phosphorylation, translocation into mitochondria and ROS formation in aging, cardiovascular risk factors and pathologies as well as in brain injury are summarized in Fig. 3.

### Conclusion

Risk factors for the development of atherosclerosis increase the expression of p66shc, a process involving epigenetic modifications. The protein becomes phosphorylated, translocates into the mitochondria and contributes to



risk factor/ pathology	mRNA, protein	phosphorylation	mitochondrial translocation	ROS formation
aging	↑			
diabetes	↑	↑	↑	↑
hyperglycemia	↑	↑	↑	↑
hypercholesterolemia	↑	↑		↑
hyperhomocysteinemia	↑			↑
ischemia/ reperfusion		↑	↑	↑
post-myocardial infarction/heart failure	↑	↑		↑
cardiotoxicity	↑			↑
brain injury	↑	↑	↑	↑

**Fig. 3** P66shc and cardiovascular risk factors and pathologies. The figure summarizes the role of p66shc in relation to cardiovascular risk factors and pathologies, especially towards the expression (mRNA, protein), phosphorylation and translocation of the protein into the

mitochondria as well as reactive oxygen species (ROS) formation. ↑ Indicates a p66shc-dependent increase in the respective process. For further details, see text

ROS formation. Consequently, the inhibition or ablation of p66shc may represent a therapeutic target for the treatment of these diseases. The role of p66shc in myocardial I/R is less clear and further studies are required to establish whether p66shc increases, decreases or has no effect on I/R injury. A causative role for p66shc in ischemic brain injury is also suggested; however, more in vivo studies in the context of conditioning phenomena are required. Whereas the pharmacological modulation of p66shc activity is generally feasible [29], more specific inhibitors or activators of p66shc would help to elucidate the function of p66shc in cardiovascular diseases.

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### Compliance with ethical standards

**Conflict of interest** Rainer Schulz received honoraries for lectures provided to AstraZeneca, Recordati and Sanofi.

**Ethical approval** All applicable international, national, and/or institutional guidelines for the care and use of animals were followed. The study was approved by local authorities (“Regierungspräsidium Giessen” (G91-2017) and the animal welfare office of the Justus-Liebig-University Giessen). This article does not contain any studies with human participants performed by any of the authors.

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