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Perspective Emerging roles of SIRT1 in vascular endothelial homeostasis

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Key words: angiogenesis, endothelial cells, HDAC, sirtuins

Sir2 is a NAD⁺-dependent deacetylase, which regulates life span in multiple model organisms in response to caloric restriction. Mammalian homologues of Sir2 comprise a family of seven proteins termed sirtuins (SIRT1-SIRT7), which have gained considerable attention for their impact on several important physiological processes associated with metabolism and stress resistance. In addition, recent studies point to SIRT1 as a key regulator of vascular endothelial homeostasis controlling angiogenesis, vascular tone and endothelial dysfunction. Here, we review the emerging role of SIRT1 as an important modulator of signaling networks critical for maintaining vascular endothelial homeostasis and discuss SIRT1 as a potential therapeutic target for cardiovascular diseases in the adult.

Histone Deacetylases and Vascular Endothelial Homeostasis

Blood vessels form a highly organized and stereotyped vascular network, which is essential for the delivery of nutrients, gases, macromolecules and cells to all organs in the body. The formation and growth of blood vessels plays a fundamental role for organ growth and regeneration and the vascular network needs to expand significantly during both, embryonic and postnatal development.¹⁻³ When blood vessel growth is dysregulated, it is a key contributing factor for numerous malignant, ischemic and inflammatory diseases.¹⁻³ Endothelial cells line the inner surface of the vasculature and are essentially required for angiogenic blood vessel growth, which is the formation of new vessels from pre-existing ones by means of endothelial sprouting, migration and proliferation.¹⁻³ In addition to their role in angiogenesis, endothelial cells control vascular tone, blood coagulation, and are important mediators of inflammation.⁴ Precise control of endothelial cell functions is, thus, critical for the maintenance of blood vessel homeostasis.

The transcriptional regulation of vascular homeostasis requires the coordinated action of several transcription factors and their association with cofactors (coactivators amd corepressors), which allow for a precise time- and signal-dependent regulation of gene expression.⁵⁻⁷ Histone deacetylases (HDACs) act as critical transcriptional cofactors that are recruited to promoters by sequence-specific transcription

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Previously published online as a *Cell Cycle* E-publication: http://www.landesbioscience.com/journals/cc/article/6267 factors to regulate gene expression. By removing acetyl groups from nucleosomal histones, HDACs counteract the stimulatory effects of histone acetyltransferases (HATs) resulting in chromatin condensation with consequent transcriptional repression.^{8,9} In addition to chromatin remodeling, reversible acetylation has emerged as an important post-translational modification of several non-histone proteins, which are targeted and regulated by HDACs.¹⁰

HDACs can be classified into three classes based on their sequence homology with yeast proteins Rpd3 (class I), Hda1 (class II) and Sir2 (class III).¹¹ Class I and II HDACs have been shown to play important roles in vascular biology by controlling endothelial gene expression and vascular development.¹²⁻¹⁵ Amongst these enzymes, particularly class II HDACs appear to have a key function for the maintenance of vascular endothelial homeostasis.^{12,16} For example, deletion of the HDAC7 gene, which is expressed specifically in endothelial cells during embryonic development, resulted in embryonic lethality due to the loss of vascular integrity in mice.¹² In contrast, the role of members of the structurally and functionally distinct class III enzymes (sirtuins) in vascular endothelial homeostasis remains poorly defined.

The Sirtuin Gene Family

The evolutionary conserved silent information regulator (Sir2) protein is the founding member of class III enzymes, which controls longevity in response to caloric restriction in many organisms, including yeast, worms, flies and possibly mammals.¹⁷⁻²¹ In mammals there are 7 homologues of Sir2 termed sirtuins (SIRT1-SIRT7) among which SIRT1 is the closest human homologue of yeast Sir2.²² Each sirtuin familiy member is characterized by a highly conserved, NAD⁺-dependent catalytic core domain (sirtuin domain), first identified in the yeast Sir2 protein.²² Mammalian sirtuins have diverse cellular localizations, modify multiple substrates, and affect numerous cellular functions. Amongst these, SIRT1, SIRT6 and SIRT7 are classified as the nuclear sirtuins, although SIRT1 is not restricted to the nucleus and appears to have important non-nuclear functions.²³ SIRT3, SIRT4 and SIRT5 reside in the mitochondria, whereas SIRT2 is localized predominantly in the cytoplasm.²³ Sirtuins differ not only in their sub-cellular localization, but also in their enzymatic activity. SIRT1, SIRT2, SIRT3 and SIRT5 are NAD-dependent deacetylases, whereas SIRT4 and SIRT6 are primarily mono-ADP-ribosyl transferases with no apparent deacetylase activity on histone substrates in vitro.²³ The enzymatic activity of SIRT7 remains to be determined.

Sirtuin Functions in Physiology and Disease

While it is not clear whether sirtuins regulate lifespan in mammals, systematic analysis of sirtuin knockout mice has revealed that this group of proteins serves essential functions during embryonic and postnatal development. Amongst the published sirtuin knockout mice, SIRT1- and SIRT6-deficient mice display the most severe phenotypes and are characterized by complex developmental defects.²⁴⁻²⁶

SIRT1 knockout mice are early postnatal lethal and exhibit heart and retinal developmental defects. 24,25 In addition to the essential functions of SIRT1 during embryonic and early postnatal development, SIRT1 maintains its important regulatory role for several homeostatic programs during adulthood. Indeed, SIRT1 has been shown to be a key component in several stress-responsive pathways involved in apoptotic cell death and cellular senescence and to control metabolic processes such as fat and glucose homeostasis.^{23,27} The physiologic effects of SIRT1 are mediated by targeting a large number of substrates for deacetylation, including p53, Foxo, PPAR cofactors NCoR/SMRT, PGC1a or LXR proteins.²⁸⁻³⁴ SIRT3deficient mice, which do not have an obvious phenotype under basal conditions, are characterized by hyperacetylation of mitochondrial proteins suggesting that its main function is to control the acetylation levels of mitochondrial proteins.³⁵ Analysis of SIRT4 null mice revealed a role of SIRT4 in pancreatic beta cell mitochondria, in which SIRT4 inhibits insulin secretion in response to amino acids, thereby, opposing the effects of caloric restriction in these cells.³⁶ Although born at Mendelian ratios, SIRT6 deficiency is associated with a severe degenerative syndrome phenotype resembling some aspects of premature ageing leading to death at about 4 weeks of age.²⁶ Mechanistically, SIRT6 promotes resistance to DNA damage and suppresses genomic instability in association with a role in base excision repair (BER). Consequently, loss of SIRT6 leads to increased genomic instability associated with impaired cellular growth and increased sensitivity to genotoxic stresses.²⁶ Recently, SIRT7-deficient mice have been shown to undergo a reduction in mean and maximum lifespans and to develop heart hypertrophy and inflammatory cardiomyopathy suggesting roles for this particular sirtuin in stress resistance and apoptosis in cardiomyocytes.³⁷

Requirement of Endothelial SIRT1 for Postnatal Vascular Growth

In an effort to identify the functions of sirtuins in vascular endothelial cells, SIRT1 was recently identified as a critical regulator of sprouting angiogenesis during vascular growth.³⁸ Using a threedimensional assay of sprouting angiogenesis assay combined with RNA interference to specifically knock down individual SIRT family members as a model system, SIRT1 deacetylase activity was shown to be critical for the angiogenic activity of endothelial cells. Although endothelial cells expressed all sirtuin family members, knock down of SIRT1 was uniquely associated with a near total loss of sprouting angiogenesis in vitro.³⁸

The most remarkable function of SIRT1 in the endothelium was revealed by an aberrant neovascularization response of endothelialrestricted SIRT1 mutant mice, in which the deacetylase domain was removed by Cre-mediated excision. Although genetic deletion of SIRT1 activity in the endothelium failed to induce an overt

phenotype during embryonic development, analysis of postnatal neovascularization demonstrated that these SIRT1 mutant mice were characterized by an impaired ability to form new vessels in response to angiogenic signals such as ischemic stress.³⁸ Obviously, the lack of an overt phenotype during embryonic vascular development raises the question whether redundancy among the different sirtuins might compensate for each other's loss in vivo. While this issue needs to be addressed in future studies, these findings also suggest that the signaling pathways, which transduce postnatal angiogenic responses are not necessarily operational during embryonic development and imply that SIRT1 responds to specific signals postnatally to mediate its effects on vascular growth (e.g., upon ischemia). These results are consistent with a role of SIRT1 as a mediator of stress-induced signaling pathways as it has been shown for other cell types and tissues and identify SIRT1 as a signal-responsive regulator of vascular growth.

A clue to the mechanism of how SIRT1 modulates endothelial angiogenic functions came from the time-lapse analysis of segmental vessel formation in transgenic zebrafish embryos with fluorescently labeled endothelial cells in which segmental arteries emanate from the dorsal aorta to form the dorsal longitudinal anastomosing vessel. Compared to the highly organized process of blood vessel formation in the control embryos, SIRT1-deficient zebrafish were characterized by vascular patterning defects and hemorrhages due to dysregulated endothelial sprouting and vessel navigation.38 Consistent with these observations, loss of SIRT1 activity by either pharmacological inhibition, RNAi-mediated gene silencing or Cre-mediated excision of the floxed SIRT1 deacetylase domain blocked the ability of endothelial cells to form vascular-like sprouts and networks in vitro.38 Importantly, the reduced angiogenic activity was not a reflection of an overall reduced biological activity as apoptotic cell death or cell cycle arrest were not significantly altered in these cells under basal conditions. Taken together, these findings identify the NAD-dependent deacetylase SIRT1 as critical regulator of endothelial angiogenic functions and postnatal vascular growth. Although the usefulness of SIRT1 as a pharmacological target needs to be addressed in additional ischemia and tumor models, one may speculate that modulation of SIRT1 activity might provide novel opportunities to modulate angiogenesis and blood vessel homeostasis for regeneration and cancer treatment.

Role of SIRT1 in Vascular Tone and Stress-Induced Endothelial Dysfunction

In addition to its function as a regulator of angiogenesis, sirtuins may play a critical role in endothelial homeostasis by regulating the endothelial nitric oxide synthase (eNOS). Endothelial-derived nitric oxide (NO) regulates blood vessel relaxation and provides atheroprotective effects. Resveratrol, a polyphenolic activator of SIRT1, has been shown to increase the expression of eNOS³⁹ and the combination of resveratrol with the HMG-CoA reductase inhibitors (statins) increased the activation of eNOS resulting in increased functional recovery in a model of acute myocardial infarction.⁴⁰ Additionally, chronic resveratrol treatment improved endothelium-dependent relaxation in spontaneous hypertensive rats, however, it did not increase eNOS expression.⁴¹ A recent study by Mattagajashingh and colleagues might explain the mechanism underlying the posttranscriptional activation of eNOS. In this study, SIRT1 has been

shown to promote endothelial-dependent vasodilation by targeting endothelial nitric oxide synthase (eNOS) for deacetylation leading to enhanced nitric oxide production.⁴² Likewise, blocking SIRT1 function by transduction of endothelial cells with a deacetylasedefective SIRT1 mutant decreased NO-bioavailability and inhibited endothelium-dependent vasorelaxation. Interestingly, caloric restriction, which is known lo lower blood pressure, led to the deacetylation of eNOS suggesting that the caloric restriction-induced decrease in blood pressure might result from a SIRT1-dependent deacetylation of eNOS.⁴² Consistent with an important role of SIRT1 in maintaining endothelial function, a recent report demonstrated that blocking SIRT1 by either pharmacological inhibition or RNAi-mediated knock down induced premature senescence-like phenotypes in endothelial cells.⁴³ Conversely, overexpression of SIRT1 prevented hydrogen peroxide-induced endothelial senescence suggesting that activating SIRT1 might exert protective effects on the vascular endothelium by preventing stress-induced endothelial dysfunction, an early step in the pathogenesis of several cardiovascular diseases.⁴³

In addition to its cell-autonomous role in the vascular endothelial homeostasis, SIRT1 might also modulate vascular homeostasis by beneficially affecting several metabolic pathways involved in cardio-vascular disease progression such as cholesterol metabolism, glucose homeostasis and insulin resistance.²⁷ Recent reports have shown that SIRT1 deacetylates and thereby activates the nuclear receptor LXR, a central transcriptional regulator of reverse cholesterol transport.³⁴ By modulating the activity of this nuclear factor, SIRT1 might favor cholesterol removal from peripheral tissues and, thus, prevent the formation of age-associated atherosclerotic lesion formation.^{34,44}

SIRT1 has also been shown to improve insulin resistance,^{45,46} a key contributing factor for the development of type 2 diabetes. Whereas loss of SIRT1 activity induces insulin resistance, overexpression of SIRT1 or enhancing its activity by treatment with resveratrol improved insulin sensitivity especially under insulinresistant conditions.^{45,46} Taken together, these findings advance the knowledge of SIRT1 as a key regulator of tissue homeostasis by defining the vascular endothelium as an important target tissue for the direct and indirect actions of SIRT1.

Molecular Targets of SIRT1 in Endothelial Cells

Besides histones, several non-histone proteins are targeted by SIRT1 for deacetylation. Among these are several transcription factors, transcriptional cofactors and chromatin modifying enzymes, including p53, Foxo, NCoR/SMRT, PGC1 α or SUV39H1, which mediate specific SIRT1-dependent cellular responses.^{28-33,47}

Several studies highlight the importance of SIRT1 in mediating stress resistance by interfering with stress-responsive pathways (e.g., p53, Foxo or NBS1).^{28-31,48-50} For example, SIRT1 has been shown to promote cell survival in response to cellular stress by deacetylating the tumor suppressor protein p53, which downregulates p53 stability and activity.^{24,28,29,51} In addition, SIRT1 associates with forkhead transcription factors (Foxo) upon exposure to hydrogen peroxide (H₂O₂) to mediate Foxo deacetylation and target gene expression.^{30,48,52} This stress-responsive and evolutionary highly conserved interaction of SIRT1 and Foxo transcription factors has been adopted by the vascular endothelium to control its angiogenic activity. Indeed, Foxo family members have been identified as essential negative regulators of blood vessel formation among

which Foxo1 appears to be the physiologically most important repressor of endothelial integrity.53,54 Using gain- and loss-of-function approaches, it has been demonstrated that SIRT1 has the ability to repress Foxo1-dependent transcriptional activity in endothelial cells³⁸ and, thus, point to this transcription factor as an effector in the SIRT1-dependent angiogenic signaling pathway. However, the mode of Foxo regulation by SIRT1 remains controversial, with some data suggesting that deacetylation decreases^{31,38,55} and others that it increases Foxo activity.^{30,48,49,56} The molecular basis for these apparent differences is currently unclear. However, given the fact that Foxo1 is acetylated on several lysine residues,^{30,52,57} it is tempting to speculate that dependent on cofactor recruitment of Foxo1, SIRT1 might only have access to a subset of acetylated lysine residues leading to a signal-dependent acetylation pattern of Foxo1, thereby, modulating its biological activity. In addition, it is notable that acetylation of Foxo1 might compete with other posttranslational modifications such as ubiquitylation or sumoylation for the same lysine acceptor sites to regulate gene expression.⁵⁸ The transcriptional output might, thus, depend on the combination of distinct posttranslational modifications converging on Foxo lysine residues.

Although Foxo1 is an important deacetylation target of SIRT1 in the vascular endothelium, the data available so far point to the existence of additional molecular targets of SIRT1, as neither the dysregulated gene expression nor the loss of angiogenic sprouting could be fully attributed to an inhibition of Foxo1.38 Given the multitude of SIRT1 interacting partners described in other cells and tissues,²⁷ it is more than likely that SIRT1 has additional partners in vascular endothelial cells to mediate its specific effects. Intriguingly, SIRT1 has been shown to interact with eNOS,⁴² which plays a key role in maintaining vascular homeostais. SIRT1 has been shown to bind to eNOS and deacetylate lysines 496 and 506 in the calmodulin-binding domain of eNOS leading to enhanced NO production. ⁴² Given that eNOS-derived NO is not only essential for endothelial-dependent vasorelaxation,⁵⁹ but also for endothelial cell survival, migration and postnatal neovascularization,⁶⁰⁻⁶⁴ NO might contribute to the Foxo-independent effects of the SIRT1-dependent regulation of sprouting angiogenesis. Of note, the Foxo transcription factors Foxo1 and Foxo3a have been shown to repress eNOS expression⁵³ suggesting a crosstalk between SIRT1, Foxos and eNOS. However, eNOS mRNA was not significantly downregulated in SIRT1-silenced endothelial cells³⁸ implying that additional cofactors contribute to the Foxo-dependent regulation of eNOS expression.

In overexpression studies, Takata and colleagues reported that SIRT1 associated with the Hairy and Enhancer-of-split basic helix-loop-helix (bHLH) transcriptional repressor Hey2 to mediate transcriptional repression.⁶⁵ Hey2 is the human homologue of the zebrafish gridlock, which has been shown to be an important regulator of endothelial gene expression and mutant mice lacking *Hey1* and *Hey2* are embryonically lethal due to defects in vascular development.⁶⁶ While it needs to be proven whether such an interaction occurs in endothelial cells, Hey2 appears to be an attractive target, given its essential functions in the cardiovascular system and recent reports demonstrating the importance of the Delta-like 4/Notch/Hey signaling cascade for controlling tip cell formation and vascular patterning.⁶⁷⁻⁷¹ Thus, it is indeed tempting to hypothesize that SIRT1 modulates endothelial angiogenic activity by interfering with this pathway, e.g., by associating with Hey2.

It is well conceivable that in addition to the targets outlined here in brief (Fig. 1), SIRT1 has additional binding partners in endothelial cells and, thus, point to this deacetylase as a point of convergence of several signaling pathways critical for homeostatic endothelial functions. In the future, it will be interesting to identify these novel SIRT1-regulated factors and to investigate their involvement in vascular growth and disease.

Gene Targets of SIRT1 in Endothelial Cells

By associating with transcription factors and transcriptional cofactors, SIRT1 acts as an important modulator of gene expression. In endothelial cells, gene targets (direct and indirect) of SIRT1 have been assessed by RNA interference-mediated knock down of SIRT1. This expression screen revealed that loss of SIRT1 activity leads to the dysregulation of several genes with essential roles in cardiovascular development and homeostasis. Among the regulated genes were several transcription factors (e.g., *Fli1*, *Hex*), members of the TGF β signaling cascade (e.g., *SMAD7*, *Tak1*), cell surface receptors (e.g., *Flt1*, *CXCR4*) and important signaling molecules involved in angiogenesis and vascular remodeling.³⁸

Although the upstream mechanisms (direct and indirect) leading to the dysregulation of most of these genes remain to be determined, they provide interesting mechanistic insights of how SIRT1 might coordinate signaling networks and affects endothelial cell behavior. As such, the SIRT1 siRNA induced reduction of MMP14 (MT1-MMP), a membrane-anchored matrix metalloproteinase essential for tip cell activity during sprouting angiogenesis,^{72,73} suggests that it might contribute to the path-finding defects observed in the SIRT1deficient zebrafish.³⁸

In addition, the altered expression of genes involved in TGF β signaling suggests that SIRT1 might be a key modulator of this signaling pathway by interfering with an upstream regulator or even an TGF β transcriptional effector such as SMAD proteins.³⁸ Consistent with these considerations, SIRT1 has been reported to interact and deacetylate SMAD7, which is an auto-inhibitory downstream molecule of TGF β signaling.⁷⁴

A caveat to the identification of SIRT1-modulated genes is that SIRT1 appears to be a context/signal-dependent regulator of cellular responses. While the gene expression profile in SIRT1-deficient endothelial cells clearly support a role of SIRT1 in the transcriptional control of endothelial homeostatic functions, it remains to be determined whether the gene expression changes observed in the microarray analysis performed under basal conditions reflect the entire signaling network of SIRT1 in vascular homeostasis. It is, thus, tempting to speculate that the gene targets of SIRT1 will most likely depend on the activity and acetylation pattern of the signaling pathway targeted by SIRT1.

SIRT1 as a "Drugable" Target for Cardiovascular Disease

The important role of SIRT1 for vascular endothelial homeostasis in vivo as well as its obvious beneficial effects on metabolic pathways, which critically contribute to the progression of cardiovascular disease, suggest opportunities for therapeutically exploiting the function of SIRT1 in the setting of cardiovascular diseases. Because SIRT1 targets several proteins in distinct signaling pathways for deacetylation, modulation of SIRT1 activity could alter the biological activity of entire signaling networks and thereby modify complex disease



Figure 1. Signaling networks of SIRT1 involved in the maintenance of vascular homeostasis. In endothelial cells SIRT1 modulates the transcriptional activity of Foxo1 and p53 and activates the enzymatic activity of the endothelial nitric oxide synthase (eNOS). SIRT1 regulates cholesterol homeostasis by deacetylating the nuclear factor LXR in hepatocytes. By repressing the expression of the phosphatase PTP1B at the chromatin level, SIRT1 improves insulin sensitivity under insulin resistant conditions.

processes such as pathological angiogenesis or atherosclerosis. Indeed, recent studies reported that resveratrol mimicked the anti-ageing effects of calorie restriction in mice fed a high-fat diet and ameliorated insulin resistance and prolonged survival.75,76 Although it is still not clear, whether resveratrol acts directly or indirectly through SIRT1 in vivo,⁷⁷ the recently developed small molecule activators of SIRT1 that are structurally unrelated to, and 1.000-fold more potent than resveratrol, induce many of the beneficial metabolic changes observed after caloric restriction/resveratrol treatment, point to SIRT1 as a promising new therapeutic approach for treating diseases of ageing.46 Thus, the identification of an intrinsic function of SIRT1 in the endothelium suggests that diseases of the cardiovascular system might be particularly sensitive to SIRT1-modifiying drugs. Based on these considerations, one would predict that activation of SIRT1 would not only benefically affect established risk factors such type 2 diabetes or cholesterol homeostasis, but would also directly protect the endothelium by preventing endothelial dysfunction. Likewise, SIRT1 activation might ameloriate ischemic vascular diseases by promoting angiogenesis or by enhancing progenitor cellmediated neovascularization. As such, resveratrol was recently shown to increase the number of endothelial progenitor cells in vitro.78-80

The finding that SIRT1 acts as an important regulator of postnatal vascular growth suggests that strategies to inhibit SIRT1 activity could also provide an opportunity for anti-angiogenesis therapies. Dysregulation of angiogenic growth has been shown to contribute to numerous pathologies including malignant or inflammatory disorders and anti-angiogenic agents such as α -VEGF have been shown to prolong the survival of cancer patients.^{1,81}

While SIRT1 clearly plays a critical role in development, ageing and protection against cancer development, several tumors exhibit enhanced expression levels of SIRT1 and appear to be dependent on SIRT1 for proliferation and survival.⁸² Therefore, SIRT1-specific inhibitors may be useful and might evolve as additional chemotherapeutic agents for tumors that depend on SIRT1 activity. Current strategies for anti-angiogenic therapy target early steps in the signal transduction cascade such as ligands or their cognate receptors.^{1,81,83} Given the multitude of downstream factors targeted by SIRT1 for deacetylation, SIRT1 might act as a nexus of several pathways common to the growth and vascularization of tumors and might, thus, represent alternative approach for blocking tumor progression.

While these considerations imply that strategies to modulate the activity of SIRT1 might serve as a potential therapy for ageassociated cardiovascular diseases or cancer, the rather ubiquitous expression and broad effects of SIRT1 might also pose significant hurdles with regard to specificity and side-effects.

Outlook

In summary, the findings of the recent studies point to SIRT1 as a novel regulator of vascular endothelial homeostasis, which plays a key role in the maintenance of vessel function. However, many questions remain to be answered. For instance, is SIRT1 active in pathologic vessels in growing tumors or other vascular-related diseases? Is SIRT1 activity recruited by specific pathways such as VEGF/VEGFR2 signaling to mediate its cellular responses? Likewise, it will be interesting to investigate, how SIRT1 activity and expression is controlled in several physiologic and pathologic programs. Given the fact that most work so far focused on the biological actions of the closest Sir2 homologue, SIRT1, in the vascular system, further studies will be required to address the functions of the other sirtuin family members in the vasculature and to link their mode of action with specific vascular programs.

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