Increased Arterial Blood Pressure and Vascular Remodeling in Mice Lacking Salt-Inducible Kinase 1 (SIK1)

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Rationale: In human genetic studies a single nucleotide polymorphism within the salt-inducible kinase 1 (SIKI) gene was associated with hypertension. Lower SIK1 activity in vascular smooth muscle cells (VSMCs) leads to decreased sodium-potassium ATPase activity, which associates with increased vascular tone. Also, SIK1 participates in a negative feedback mechanism on the transforming growth factor-β1 signaling and downregulation of SIK1 induces the expression of extracellular matrix remodeling genes.

Objective: To evaluate whether reduced expression/activity of SIK1 alone or in combination with elevated salt intake could modify the structure and function of the vasculature, leading to higher blood pressure.

Methods and Results: SIK1 knockout (sik1−/−) and wild-type (sik1+/+) mice were challenged to a normal- or chronic high-salt intake (1% NaCl). Under normal-salt conditions, the sik1−/− mice showed increased collagen deposition in the aorta but similar blood pressure compared with the sik1+/+ mice. During high-salt intake, the sik1−/− mice exhibited an increase in SIK1 expression in the VSMCs layer of the aorta, whereas the sik1+/+ mice exhibited upregulated transforming growth factor-β1 signaling and increased expression of endothelin-1 and genes involved in VSMC contraction, higher systolic blood pressure, and signs of cardiac hypertrophy. In vitro knockdown of SIK1 induced upregulation of collagen in aortic adventitial fibroblasts and enhanced the expression of contractile markers and of endothelin-1 in VSMCs.

Conclusions: Vascular SIK1 activation might represent a novel mechanism involved in the prevention of high blood pressure development triggered by high-salt intake through the modulation of the contractile phenotype of VSMCs via transforming growth factor-β1-signaling inhibition. (Circ Res. 2015;116:642-652. DOI: 10.1161/CIRCRESAHA.116.304529.)

Key Words: endothelin-1 ■ muscle, smooth, vascular ■ SIK1 protein, human ■ vascular remodeling

Salt-inducible kinase (SIK) is a member of the AMP-activated protein kinase family of serine/threonine kinases.1 SIK1 was demonstrated to be elevated in the adrenal glands from animals under a high-salt diet.2 In this tissue, it inhibits the production of aldosterone by modulating cAMP response element-binding activity directly or via transducer of regulated cAMP response element-binding phosphorylation.3 In addition, SIK1 regulates active sodium transport in renal and lung epithelia by increasing sodium–potassium ATPase (Na+,K+-ATPase) activity and mediates gene expression activation in cardiac myocytes on increase in intracellular sodium.4–6

SIK1 is also present in the vasculature and its activity in endothelial and vascular smooth muscle cells (VSMCs) seems to be relevant for controlling the vascular tone and arterial blood pressure by regulating Na+K+-ATPase activity in VSMCs.7 A polymorphism in SIK1 gene resulting in 1 amino acid change (Gly→Ser) in the protein enhances the kinase activity and is associated with lower blood pressure and reduced left ventricle (LV) mass index in humans.8 Overexpression of the rare allele (SIK1-15Ser) in VSMCs leads to higher Na+,K+-ATPase activity. An increase in Na+,K+-ATPase activity is associated with a decrease in intracellular Ca2+ concentration, which impairs contractility leading to reduced VSMCs tone; therefore, this may indicate a role of vascular SIK1 activity on vascular tone relaxation that could, in part, explain the lower arterial blood pressure observed in human genetic studies.8–9

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Elevated arterial blood pressure can occur as a consequence of increased vascular stiffness attributed to both extracellular matrix deposition/remodeling and enhanced contractility/stiffness of VSMCs.\textsuperscript{10–13} Transforming growth factor-β1 (TGF-β1) is a pleiotropic cytokine that mediates extracellular matrix remodeling processes within the vasculature in addition to promote VSMCs differentiation toward a contractile phenotype.\textsuperscript{14–18} SIK1 participates in a negative feedback mechanism on the TGF-β1 signaling pathway.\textsuperscript{19} We have reported that in epithelial cells the loss of SIK1 increased the expression of SNAI2 and TWIST1, known transcription factors involved in fibrosis and extracellular matrix remodeling.\textsuperscript{2}

Recently, brain SIK1 activity has been shown to be relevant for blood pressure regulation in rodents by regulating sympathoexcitatory activity and lower arterial blood pressure in rats after a high-salt diet and intra-cerebroventricular infusion of Na\textsuperscript{+}.\textsuperscript{20}

Because SIK1 is present in the vasculature and lower SIK1 activity was associated with elevated blood pressure in humans and rodents, we hypothesize that the lack of SIK1 could trigger vascular remodeling processes leading to increased vascular stiffness and consequently to higher blood pressure. Furthermore, these events alone or in combination with other risk factors (high-salt intake) may contribute to the development of high blood pressure.

Methods

**Generation of sik1\textsuperscript{-/-} Mice and Experimental**

The sik1\textsuperscript{-/-} mice has been previously described.\textsuperscript{3} All animals were maintained under standard conditions of light (7:00 Am, 7:00 Pm) and temperature (22\textdegree C, 55% humidity), with free access to chow diet and tap water. At 10-week old, the sik1\textsuperscript{-/-} and sik1\textsuperscript{+/+} mice remained on a chow diet but they were challenged to either normal-salt (NS, tap water) or high-salt (HS, 1% NaCl in tap water) intake for 14 weeks. A chow diet but they were challenged to either normal-salt (tap water) or high-salt (1% NaCl in tap water) intake for 14 weeks.

**Renal Function**

After the telemetry recording, mice were placed in metabolic cages (Tecniplast, Buguggiate, Italy) for a 24-hour urine collection. The urine samples were collected in vials that were subsequently stored at –80\degree C until assayed. After completion of this protocol, mice were anesthetized with sodium pentobarbital (60 mg/kg, IP). The animals were then euthanized by exsanguination using cardiac puncture and the blood collected into tubes containing K3 EDTA for later determination of plasma biochemical parameters. All biochemical assays were performed by Coba Mira Plus analyzer (ABX Diagnostics for Cobas Mira, Switzerland). Aldosterone measurement in plasma samples was performed by radioimmunoassay (Diagnostic Products Corporation; Los Angeles, CA).

**Cell Cultures and Transfection**

Human aortic adventitial fibroblasts (AFs; CC-7014) and human VSMCs (CC-2571) were obtained from Lonza (Lonza, Walkersville, MD) and maintained in SCGM or in SmGM (Lonza, Walkersville, MD), respectively. Transfections were performed using Lipofectamine RNAiMAX (Invitrogen, Carlshad, CA) according to the manufacturers’ instructions. The transfection efficiency, monitored by the expression of a fluorescent-labeled control small interfering RNA by flow cytometry, was >90% for both cell types. Cells (80,000) were plated on 96-well plates and transfected at 40% confluence for 24 hours, followed by incubation with or without 2.5 ng/mL of TGF-β1 (R&D Systems, Minneapolis, MN).
Minneapolis, MN) for 24 hours. Scrambled- (sc-37007) and human SIK1-small interfering RNA (sc-91428) were purchased from Santa Cruz Biotechnology (Santa Cruz Biotechnology, CA). Studies were performed between cell passages 3 to 6.

Protein Expression Analysis

Tissue samples and cell cultures were lysed as described elsewhere. Protein samples (20–50 μg) were run on SDS-PAGE and Western blot was performed. The membranes were probed with antibodies against: 1:500 COL1A1 (No. SAB1402151, Sigma-Aldrich), 1:500 COL3A1 (sc-28888, Santa Cruz Biotechnology), 1:500 COL6A1 (sc-377143, Santa Cruz Biotechnology) and β-actin or β-tubulin as loading controls (Sigma-Aldrich).

Determination of mRNA Expression

Aorta and heart tissue samples were directly incubated with RNAlater (Ambion, Austin, TX) and homogenized with a FastPrep using Lysing Matrix D tubes (MP Biomedicals, Germany). Reverse transcription and cDNA synthesis were performed as previously described. cDNA was amplified using StepOnePlus Real-Time PCR System (Applied Biosystems, Foster City, CA). The relative amount of the mRNA of interest was normalized against to ribosomal protein, large, P0 (RPLP0) and TATA box binding protein mRNAs using the comparative Ct-method.

Immunohistochemistry

Samples from the abdominal aorta were frozen in Tissue-Tek Oct medium (Sakura Finetek USA Inc, Torrance, CA) for histology analysis. Sections were fixed in acetone and stained with Mayer’s hematoxylin (Histolab Products, Göteborg, Sweden) for measurement of lumen diameter and intima/media thickness at ×20 or ×40 magnification. Immunodetection was performed using a monoclonal antibody against SIK1 (1:2000; No. SAB1402668, Sigma-Aldrich), a polyclonal antibody against endothelin-1 (EN1; 1:3000; sc-21625, Santa Cruz Biotechnology), a monoclonal antibody against TGF-β1 (40 μg/mL; No. MAB240, R&R Systems) and a polyclonal antibody against phospho-SMAD2/3 (1:50, No. 8828, Cell Signaling), respectively, and counterstained with Mayer’s hematoxylin as described previously. Picrosirius red staining was used for the assessment of collagen fibers in the vessels. Sections were stained for 1 hour in saturated picric acid containing 0.1% picrosirius red (Direct Red 80, Fluka, Buchs, Switzerland). This technique allowed for the discrimination of thick (red-orange staining) from thin (green staining) collagen fibers, which represent mature and immature collagen fibers. The total collagen content was measured using the Leica QWin software. All sections were analyzed under linear polarized light at ×40 magnification.

Statistics

Results are expressed as mean±SEM or box plots (t test or Mann–Whitney as appropriate) and plotted using GraphPad Prism software. P values <0.05 were considered statistically significant.

Results

Loss of SIK1 Triggers an Increase in Blood Pressure on a Chronic High-Salt Intake in Mice

Blood pressure measurements and cardiac parameters were assessed on the sik1−/− and sik1+/+ mice challenged to either a NS or a HS for 14 weeks. Body weight and heart rate (Figure 1A and 1B) were similar among all experimental groups. No differences in blood pressure levels were observed between the sik1−/− and sik1+/+ mice under NS. However, on a chronic HS intake systolic blood pressure was significantly greater in the sik1−/− mice (135.0±4.3 mm Hg) when compared with that in the sik1+/+ mice (122.1±1.9 mm Hg), whereas diastolic and mean arterial blood (Figure 1C–1E) pressure were similar in both groups. Systolic blood pressure relates more closely to vascular resistance; thus, this result might reflect an increased arterial stiffness in the sik1−/− mice.

Figure 1. Blood pressure in the SIK1 wild-type (WT) and SIK1 knockout (KO) mice under normal (NS) or high-salt (HS) intake. Body weight (A), heart rate (HR; B), and radiotelemetry recordings of (C) systolic blood pressure (SBP), (D) diastolic blood pressure (DBP), and (E) mean arterial blood pressure (MAP). Means±SEM; n=6 to 7.
The ultrasound examination of the hearts of these mice revealed that under HS the sik1−/− mice have an increased LV wall thickness and a decreased LV diameter (Online Figure II A; Figure 2A and 2B) when compared with the sik1+/+ mice. In addition, LV+septum weight/body weight ratio was significantly increased in the sik1−/− mice, whereas no changes were observed in right ventricle weight/body weight or heart weight/body weight (Figure 2C−2E), further confirming the presence of a hypertrophic heart in the sik1−/− mice. No changes were observed in the fractional shortening in neither diet nor genotype (Online Figure II B). At the molecular level, the mRNA expression of the transcription factor MEF2C, as well as structural components of the cardiomyocyte such as skeletal actin and β-myosin heavy chain (Online Figure II C−II E), was significantly elevated in the sik1−/− mice versus the sik1+/+ mouse group only under HS intake.

These results suggest that the lack of SIK1 renders the mice salt sensitive and demonstrate the relevance of SIK1 in blood pressure regulation on a HS intake.

Increased Natriuresis But Preserved Sympathetic Activity in the sik1−/− Mice

Increases in blood pressure can arise from an enhanced sympathetic drive or from an abnormal secretion of numerous hormones and peptides that participates in water and sodium homeostasis as a consequence of a deteriorated renal function.25 Renal function and sympathetic activity (plasma norepinephrine) were evaluated in the sik1−/− and sik1+/+ mice and the results are summarized in the Table and Online Table I, respectively. Water intake and urinary volume were similar between both genotypes under both NS and HS intakes. During HS intake water consumption increased significantly (≈50%) in both groups and this was accompanied by an increase in urinary volume. Plasma creatinine and creatinine clearance showed no differences between both genotypes under neither NS nor HS intake, indicating a preserved glomerular filtration rate in the knockout mice. Urinary protein concentration as well as fractional excretion of sodium and potassium was similar for both genotypes, indicating no signs of renal damage. The daily urinary excretion of Na+, K+ and Cl− was increased in the knockout mice under both treatments, despite this, their plasma electrolytes concentrations (Na+, K+, Cl−) were normal. Plasma aldosterone levels were similar between the sik1−/− and sik1+/+ mice under both NS and HS intake and decreased significantly during HS to a similar extent in both groups. Likewise, no differences were observed in plasmatic norepinephrine levels and heart rate between the sik1−/− and sik1+/+ mice under both NS and HS intake (Online Table I; Figure 1B). At the molecular level, the mRNA expression of SIK1 and SIK2 in kidney samples from the sik1−/− mice was significantly reduced on HS intake, whereas no variations in the expression of SIK2 and SIK3 isoforms were observed in the sik1−/− mice (Online Figure III). Apart from an enhanced urinary excretion of electrolytes, the loss of SIK1 does not significantly affect the normal function of the kidneys or the proximal tubule.

Table. Renal Function and Plasma Electrolytes in the sik1+/+ and sik1−/− Mice

<table>
<thead>
<tr>
<th></th>
<th>sik1+/+ Tap Water</th>
<th>sik1−/− Tap Water</th>
<th>sik1+/+ 1% NaCl</th>
<th>sik1−/− 1% NaCl</th>
</tr>
</thead>
<tbody>
<tr>
<td>Body weight, g</td>
<td>28.2±0.9</td>
<td>27.4±1.3</td>
<td>29.3±1.6</td>
<td>27.4±1.2</td>
</tr>
<tr>
<td>Kidney weight (weight/body weight)</td>
<td>12.2±0.8</td>
<td>12.9±1.1</td>
<td>13.0±0.8</td>
<td>13.8±0.6</td>
</tr>
<tr>
<td>Water intake, mL/24 h</td>
<td>2.58±0.31</td>
<td>3.32±0.61</td>
<td>3.98±0.28*</td>
<td>4.49±0.63*</td>
</tr>
<tr>
<td>Urinary volume, mL/24 h</td>
<td>1.00±0.21</td>
<td>0.71±0.07</td>
<td>1.40±0.20</td>
<td>0.94±0.13</td>
</tr>
<tr>
<td>Urinary creatinine, mg/24 h</td>
<td>0.71±0.06</td>
<td>0.56±0.05</td>
<td>0.70±0.07</td>
<td>0.57±0.04</td>
</tr>
<tr>
<td>Urinary urea, mg/24 h</td>
<td>118.1±16.3</td>
<td>103.8±7.9</td>
<td>129.9±14.1</td>
<td>118.7±9.4</td>
</tr>
<tr>
<td>Urinary protein, mg/24 h</td>
<td>6.0±1.0</td>
<td>4.1±1.0</td>
<td>5.9±1.4</td>
<td>4.1±0.9</td>
</tr>
<tr>
<td>Urinary Na+, μmol/24 h</td>
<td>38.3±8.2</td>
<td>93.9±21.4*</td>
<td>231.3±35.3</td>
<td>500.0±97.2†</td>
</tr>
<tr>
<td>Urinary K+, μmol/24 h</td>
<td>437.6±98.7</td>
<td>1054.1±222.0*</td>
<td>294.1±66.5</td>
<td>743.8±244.6</td>
</tr>
<tr>
<td>Urinary Cl−, μmol/24 h</td>
<td>261.3±55.3</td>
<td>596.8±120.3*</td>
<td>402.8±84.5</td>
<td>912.7±233.1</td>
</tr>
<tr>
<td>FE Na+</td>
<td>0.21±0.06</td>
<td>0.23±0.06</td>
<td>1.66±0.21</td>
<td>1.81±0.36</td>
</tr>
<tr>
<td>FE K+</td>
<td>47.2±7.0</td>
<td>57.9±5.9</td>
<td>50.2±4.5</td>
<td>54.7±4.7</td>
</tr>
<tr>
<td>Urinary sodium/potassium ratio</td>
<td>0.131±0.049</td>
<td>0.094±0.019</td>
<td>0.776±0.054</td>
<td>0.755±0.075</td>
</tr>
<tr>
<td>Creatinine clearance, mL/min</td>
<td>0.12±0.01</td>
<td>0.10±0.01</td>
<td>0.14±0.02</td>
<td>0.11±0.01</td>
</tr>
<tr>
<td>Plasma creatinine, mg/dL</td>
<td>0.4±0.0</td>
<td>0.4±0.0</td>
<td>0.4±0.0</td>
<td>0.4±0.0</td>
</tr>
<tr>
<td>Plasma Na+, mmol/L</td>
<td>143.1±6.7</td>
<td>147.2±5.4</td>
<td>143.9±0.6</td>
<td>143.7±2.8</td>
</tr>
<tr>
<td>Plasma K+, mmol/L</td>
<td>5.8±0.4</td>
<td>6.0±0.8</td>
<td>6.1±0.5</td>
<td>6.1±1.0</td>
</tr>
<tr>
<td>Plasma Cl−, mmol/L</td>
<td>115.7±2.9</td>
<td>113.4±2.0</td>
<td>110.7±1.4</td>
<td>109.0±1.7</td>
</tr>
<tr>
<td>Plasma aldosterone, ng/dL</td>
<td>16.9±4.3</td>
<td>24.7±6.0</td>
<td>4.6±1.0*</td>
<td>4.5±1.2*</td>
</tr>
</tbody>
</table>

Values are expressed as mean±SEM. Renal function studies and plasma electrolytes on the sik1+/+ and sik1−/− mice under normal (tap water) or high-salt (1% saline) intake. Mice were placed in metabolic cages for 24 hours and urine and blood samples were collected. Mean±SEM; n=6 to 7. FE indicates fractional excretion.

*P<0.05 vs sik1+/+ tap water; †P<0.05 vs sik1−/− 1% NaCl.
Figure 3. Histochemistry and gene expression analysis of aortas from young SIK1 wild-type (WT) and SIK1 knockout (KO) mice. Representative image (left) and the corresponding quantifications (right) of abdominal aorta sections from 8-week-old mice stained with (A and B) hematoxylin showing (A) lumen diameter (x20) and (B) intima/media thickness (x40) and (C) picrosirius red coupled to polarized light microscopy (x40) showing immature collagen fibers (thin fibers=green) and mature collagen fibers (thick fibers=red-orange). D, mRNA (left) and protein (right) expression in the sik1+/+ and sik1−/− mice aortas. Representative Western blots are shown. Optical density (OD) was calculated normalizing the specific signal against β-tubulin signal. Mean±SEM or box plots; n=6 to 7. *P<0.05; **P<0.01.
sympathetic activity suggesting that blood pressure variations are most probably because of an extrarenal action of SIK1.

**Loss of SIK1 Induces Vascular Remodeling Through the Modulation of Adventitial Fibroblasts and Smooth Muscle Cell Phenotype**

Histological analysis of abdominal aorta specimens from young mice (8 weeks old) showed no changes in vessel diameter but a significant increase in intima/media thickness (Figure 3A and 3B) in those from the sik1−/− mice. In addition, the loss of SIK1 resulted in a significant increase of immature collagen fibers (newly synthesized collagen) compared with the wild-type mice (Figure 3C). In the aortas of the sik1−/− mice there was a significant increase in the expression of SNAIL1 and TWIST1 mRNAs, together with a parallel upregulation of several collagen isoforms at the mRNA (Figure 3D, left) and at the protein level (Figure 3D, right). COL6A1 gene was not detected at the transcriptional level because of its low turn-over. Furthermore, matrix metalloproteinase-9, neural (N)- and vascular endothelial (VE)-cadherin mRNAs were also upregulated by the loss of SIK1 (Figure 3D, left). Thus, lacking SIK1 drives an advanced tissue remodeling process within the vasculature characterized by an increased fibrosis.

Vascular collagen deposition was further evaluated in adult mice (24 weeks old) after NS or chronic HS intake. Abdominal aorta diameter was similar among all experimental groups (Figure 4A). Under NS, collagen deposition was similar as observed in aortas from young mice; there was a significant increase in immature collagen fibers (Figure 4B), whereas no changes in mature collagen fibers content (Figure 4C) in the sik1−/− mice compared with the wild-type mice. This result is consistent with the gene expression data, where the transcription of collagen isoforms was increased in aortas from the sik1−/− mice (Figure 4D–4F). Interestingly, under HS intake the situation changes significantly. The loss of SIK1 in combination with a HS intake did not affect immature collagen fibers deposition (Figure 4B), meanwhile it decreased mature collagen fibers content (Figure 4C) when compared with wild-type mice aortas. This can be explained by the inhibition of collagen transcription in the knockout mice (Figure 4D–4F), in contrary to the observed under NS. Also, the decrease in mature collagen fibers indicates an enhanced collagen degradation process, which could be because of an increased activity of matrix metalloproteinases induced by HS. Furthermore, the loss of SIK1 significantly increased SNAIL1, and VE-cadherin expression under both NS and HS intake (Online Figure IV). Of note, the chronic HS intake did not modify the deposition of collagen in the aortas of the wild-type mice (mature collagen fibers, arbitrary units=3.72±1.42 versus 3.72±0.78; immature collagen fibers, arbitrary units=2.73±0.95 versus 3.07±0.59 versus wild-type-HS diet; Figure 4B and 4C).

Next, transient knockdown of SIK1 (using small interfering RNAs) in the presence of TGF-β1 in primary cell cultures of human AFs significantly enhanced the expression of collagen isoforms both at the mRNA and at the protein level (Figure 5A), consistent with the notion of SIK1 being a negative regulator of the TGF-β1 signaling. On the contrary, SIK1 knockdown in primary cell cultures of human VSMCs did not alter collagen expression (Figure 5B) but it did affect the expression of several genes involved in the acquisition of a differentiated contractile phenotype. The expression of myocardin, smoothelin, and N-cadherin was highly upregulated (≈3- to 4-fold increase) when compared to control small interfering RNA-transfected cells (Figure 5C). VSMCs are also an important source of the vasoconstrictor factor EN1. The mRNA expression of EN1, EN1 receptor type A, which mediates vasoconstriction via increasing intracellular calcium signaling, and EN-converting enzyme 1, one of the enzymes responsible for processing EN1 into the mature peptide, was significantly elevated in SIK1 knockdown cells. Moreover, the mRNA expression of genes involved in cell cycle progression such as forkhead box protein M1 and polo-like kinase 1 was significantly diminished (Figure 5C). TGF-β1 incubation in AFs and VSMCs in culture significantly induced the SIK1 isoform without major changes in SIK2 and SIK3 (Online Figure VA and VB). These results show that the loss of SIK1 apart from triggering collagen deposition by an increased activity of AFs, it also promotes the phenotypic switch of VSMCs from synthetic-proliferative to contractile.

We next evaluated whether SIK1 can modulate the expression of these genes in vivo. The mRNA levels of these genes in NS were similar in both genotypes, except for N-cadherin that was upregulated in the sik1−/− mice. Alpha-smooth muscle actin was upregulated by HS in both groups of mice, independently of SIK1 expression (Figure 6A). During HS intake there was a significant upregulation (≈50%) of myocardin, smoothelin, and N-cadherin in the sik1−/− mice (Figure 6B–6D). Immunohistochemistry analysis of aorta sections revealed

![Figure 4. Histochemistry and gene expression analysis of aortas from the SIK1 wild-type (WT) and SIK1 knockout (KO) mice under normal (NS) or high-salt (HS) intake. Quantitative measurement of abdominal aorta (A) lumen diameter, (B) immature and (C) mature collagen fibers from picrosirius red staining. D to F, mRNA expression in the sik1−/− and sik1−/− mice aortas. Means±SEM or box plots; n=6 to 7.](http://circres.ahajournals.org/)

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**SIK1, Hypertension, and Vascular Remodeling**

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increased EN1 expression throughout the media layer in the sik1−/− mice compared with the wild-type mice under HS, whereas high expression was observed in the endothelial cell layer in both mice (Figure 15E). SIK1 was highly expressed in the endothelial and adventitial layers and to a lesser extent in the media layer (subendothelium mainly) of the abdominal aorta of wild-type mice on NS (Figure 21A). In this tissue on chronic HS intake, SIK1 expression increased specifically throughout the media layer but more markedly in the subendothelium and remained high in endothelial and adventitial layers. SIK1 mRNA levels increased during HS, whereas no changes were observed for the other SIK isoforms at any condition (Figure 7B; Online Figure VC). In addition, during HS intake TGF-β1 mRNA and protein levels were higher in aorta sections from the sik1−/− mice compared with the wild-type mice, and similarly an increase of phospho-SMAD2/3 staining was observed (Figure 14C–14E).

Together these results suggest that the loss of SIK1 drives a tissue remodeling process within the vasculature as a consequence of a dysregulated fibrotic phenotype of AFs, as well as an increased contractile phenotype of VSMCs because of enhanced EN1 expression and TGF-β1 signaling.

Discussion

Many pathophysiologic and environmental factors have been implicated in the genesis of hypertension.27 Among these, HS intake contributes to the elevation of arterial blood pressure in humans and animal models.11,27–31 In human genetic studies, the identification of a single nucleotide polymorphism in the coding region of SIK1 gene that was associated with hypertension provided us an insight on the potential role of SIK1 in the development of hypertension.7 In the present study, we show that the loss of SIK1 contributes to the development of high blood pressure triggered by a chronic HS intake in mice. The negative impact on blood pressure was associated with alterations of the vasculature, for example, dysregulated collagen synthesis and increased contractile phenotype of VSMCs as well as increased EN1 expression. SIK1 was initially discovered in adrenal glands of rats fed with a HS diet and it has been shown to act as a mediator during the cellular adaptation to variations in intracellular sodium in a variety of cell types.4,6 In agreement with previous literature, we observed that the regulatory action of SIK1 on blood pressure levels is exerted specifically during abnormal salt intake. Furthermore, our results showed that within the vasculature SIK1 was induced in the VSMCs layer of the wild-type mice aorta in response to the chronic HS intake.

As mentioned previously, hypertension is the result of complex interactions between genetic and environmental factors. Despite this, it is thought that renal mechanisms play a primary role in blood pressure increase through impairment of sodium and water handling.25 SIK1 participates in sodium reabsorption in the proximal convoluted tubule via modulating Na+,K+-ATPase activity and is involved in the establishment of a polarized epithelium, which is essential for the vectorial transport of ions and solutes via controlling E-cadherin availability in the plasma membrane.4,5 The results presented here showed no differences in renal function between the sik1−/− and sik1+/+ mice after 14 weeks of NS or HS intake (glomerular filtration rate, fractional excretion of sodium, plasma electrolytes, and aldosterone levels were similar between both genotypes), except for urinary Na+ excretion. The knockout mice showed increased natriuresis during HS intake, effect that was also observed during NS where blood pressure levels were normal. This phenotype is consistent with decreased activity of the Na+,K+-ATPase and also possibly with downregulation of
E-cadherin in the renal epithelium as we previously showed. One possible explanation for the increase in urinary Na⁺ and K⁺ in the \textit{sik1}⁻⁻ mice without evidence of severe sodium depletion, as indicated by normal plasma Na⁺ and K⁺ levels, is that of a possible intestinal absorptive compensatory mechanism to keep electrolyte homeostasis.³²–³⁵ Although we cannot exclude the possibility that renal function is affected in the \textit{sik1}⁻⁻ mice during the first days/weeks of HS intake, it is unlikely that the loss of renal SIK1 is responsible for the mild hypertension given that increased urinary Na⁺ excretion, and not the opposite, is observed in these mice. Aldosterone levels did not differ in the \textit{sik1}⁻⁻ mice, therefore it is plausible to think that in the adrenal glands the other SIK isoforms could display compensatory mechanisms to maintain transducer of regulated cAMP response element–binding phosphorylation levels and indeed in vitro studies in adrenocortical cells showed that SIK2 and SIK3 also phosphorylate this cofactor.³³,³⁶

It has been described that HS intake increases endothelial production of TGF-β₁, which can act in a paracrine fashion on the vessel wall participating in VSMCs differentiation toward a contractile phenotype.¹⁸,³⁷–³⁹ Here, we showed that in the vasculature of the \textit{sik1}⁺⁺ mice the HS intake increased TGF-β₁ expression and downstream phospho-SMAD2/3 signaling compared with the wild-type mice, which suggests that the contractile phenotype of VSMCs should be favored in the \textit{sik1}⁻⁻ mice. Indeed, we found increased expression of contractile genes and of EN1 in the knockout compared with the wild-type mice aortas, only during HS intake. The role of SIK1 in VSMCs differentiation was further confirmed in vitro where SIK1 knockdown in VSMCs resulted in an enhanced expression of contractile genes as well as EN1, EN1 receptor type A, and EN-converting enzyme 1, whereas the expression of proliferative genes was diminished. However, in the aorta of the \textit{sik1}⁺⁺ mice the HS intake caused an increase of SIK1 expression in the VSMCs layer, which in turn negatively regulates TGF-β₁ signaling, therefore inhibiting VSMCs differentiation. Thus, these results suggest that the loss (or reduced activity) of SIK1 in combination with HS intake predispose to an active contractile phenotype of VSMCs, setting to a higher vascular tone, and thereby contributing to higher blood pressure. Therefore, SIK1 activation in the vasculature may function as a protective mechanism to maintain a relaxed VSMCs tone and ultimately a lower blood pressure.

It is well recognized that vascular changes are associated with cardiovascular diseases and hypertension.⁴⁰–⁴² Systolic blood pressure, in particular, increases with age and is related to arterial stiffness of large conduit arteries.⁴¹,⁴² We observed an increased collagen deposition in the aorta of young and adult NS-fed knockout mice compared with wild-type mice.
Similarly, SIK1 knockdown in AFs showed an enhanced expression of collagen isoforms compared with control cells. The increase in collagen deposition observed in the knockout mice under NS did not affect blood pressure levels, suggesting that collagen deposition per se is not sufficient to trigger high blood pressure, at least at the time points tested. We cannot exclude the possibility that these mice will develop hypertension in later stages of life because of the increased vascular fibrosis. Interestingly, on HS intake the knockout mice, which developed high blood pressure, showed significantly less mature collagen fibers in the aortic wall than the wild-type mice. Although contradictory, these results show that SIK1 can modulate collagen synthesis and degradation in a cell- and context-specific fashion. Whether a reduction in collagen fibers in the vasculature may favor an increase in blood pressure on HS intake deserves further studies, but we can speculate that modifications of the vascular extracellular matrix composition by modifying the availability or activity of salt-inducible vasoactive compounds could affect the vascular tone.

SIK1 is also present in the brain and it has been proposed that dysregulation of the SIK1-Na⁺,K⁺-ATPase network in neurons contributes to the salt-induced hypertension through enhanced angiotensinergic sympathetic hyperactivity by increasing intracellular Ca²⁺. Our results showed no differences in sympathetic activity between the knockout and wild-type mice as plasma norepinephrine levels remained unaffected. However, it should be noted that plasma norepinephrine values provide only limited assessment of sympathetic control of blood pressure in conscious animals. In addition, heart rate and locomotor activity were similar between both genotypes at any given condition. The reason for these differences could be because of differences in methodological approaches used in each study.

In this study, we demonstrate the importance of vascular SIK1 activity for blood pressure regulation under chronic HS intake; however, we cannot exclude the possibility that SIK1 present in other tissues could also be of relevance by affecting the release, availability, and the activity of unknown salt-inducible mediators. Ideally, a vascular specific SIK1 knockout mouse model would provide more accurate information on the relative contribution of vascular versus nonvascular SIK1 activity.

In conclusion, this study confirms and extends our previous observations in human genetic studies and highlights the relevance of SIK1 in blood pressure regulation in vivo. Vascular SIK1 activity is necessary to prevent the development of high blood pressure triggered by a chronic HS intake. Therefore, efforts aimed at increasing SIK1 expression or activity could
SIK1, Hypertension, and Vascular Remodeling


**What Is Known?**

- Salt-inducible kinase 1 (SIK1) is a serine/threonine kinase that is involved in the cellular adaptation to changes in intracellular sodium concentration by genomic and nongenomic effects.
- SIK1 controls expression/activity of transcription factors and increases the Na+, K+-ATPase activity.
- In addition, SIK1 negatively regulates transforming growth factor-β1 (TGF-β1) signaling pathway by facilitating TGF-β1 type I receptor turnover.
- A single nucleotide polymorphism within the SIK1 gene that results in increased kinase activity of the encoded protein is associated with lower blood pressure and reduced left ventricle mass index in humans.
- Increased arterial stiffness caused by extracellular matrix deposition or enhanced contractility of vascular smooth muscle cells (VSMCs), processes that are regulated by TGF-β1, play important roles in development of hypertension in humans and in animal models of hypertension.

**What New Information Does This Article Contribute?**

- Activation of vascular SIK1 maintains a dedifferentiated phenotype of VSMCs and is necessary for controlling blood pressure on a high-salt intake.
- Downregulation of SIK1 induces VSMCs differentiation toward a contractile phenotype through transcriptional upregulation of contractile genes and endothelin-1 and inhibition of genes involved in cell cycle progression. The latter effect depends on enhanced TGF-β1 expression/signaling in the vasculature.
- SIK1 controls collagen deposition within the vessel walls by modulating adventitial fibroblasts activity.

Despite advances in treatment strategies, hypertension remains one of the major risk factors for cardiovascular diseases. Therefore, there is a growing interest to develop novel therapies for the prevention and treatment of hypertension. Previous studies proposed a role of SIK1 in the development of hypertension in humans; however, the precise mechanism is not fully elucidated. In this study, we analyzed the cellular and physiological SIK1-dependent mechanisms involved in blood pressure regulation. We found that upregulation of SIK1 in the vasculature is required for controlling blood pressure on high-salt intake. Studies using SIK1 knockout mice challenged to chronic high-salt intake showed that the increase in blood pressure levels was associated with increased TGF-β1 expression and enhanced contractile phenotype of VSMCs within the aorta. On contrary, the salt-dependent increase in SIK1 expression in aortic VSMCs protected the wild-type mice against developing high blood pressure. In vitro studies demonstrated that the loss of SIK1 is required for the acquisition of a contractile phenotype of VSMCs in the presence of TGF-β1. These findings increase the knowledge of salt-dependent mechanisms leading to hypertension and suggest that therapeutic strategies targeting vascular SIK1 could be beneficial for the treatment of hypertension and other vascular fibrosis-related diseases.
Increased Arterial Blood Pressure and Vascular Remodeling in Mice Lacking Salt-Inducible Kinase 1 (SIK1)

Alejandro M. Bertorello, Nuno Pires, Bruno Igreja, Maria João Pinho, Emina Vorkapic, Dick Wågsäter, Johannes Wikström, Margareta Behrendt, Anders Hamsten, Per Eriksson, Patricio Soares-da-Silva and Laura Brion

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SUPPLEMENTAL MATERIAL

Increased arterial blood pressure and vascular remodeling in mice lacking Salt-Inducible kinase 1 (SIK1)

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†This study was initiated by Dr. Alejandro M. Bertorello. Unfortunately he passed away 23rd January 2013. All coauthors have agreed on the submission of the manuscript on his behalf.

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Running title: SIK1, hypertension and vascular remodeling.
Online Figure I: Typical 24h circadian rhythms blood pressure and heart rate in the sik1+/+ (WT) and sik1−/− (KO) mice under normal (NS) or high-salt (HS) intake. Radio-telemetry recordings of (A) systolic blood pressure (SBP), (B) diastolic blood pressure (DBP), (C) mean arterial pressure (MAP) and (D) heart rate (HR) for 3 consecutive days following implantation of the telemetry device. Plots represent mean values over each 4h in a 12:12h light-dark cycle. Gray segments indicate the dark period (7p.m. to 7a.m.). Mean±SEM; n=6-7.
Online Figure II: Cardiac parameters and gene expression analysis in the sik1+/+ (WT) and sik1−/− (KO) mice under normal (NS) or high-salt (HS) intake. (A) Representative ultrasound images of the hearts indicating left ventricular anterior and posterior wall thickness and left ventricular end diastolic diameter. (B) Fractional shortening (FS). (C-D) mRNA expression of Myocyte-specific Enhancer Factor 2C (MEF2C), skeletal actin (ACTA1) and β-myosin heavy chain (MHY7) in the sik1+/+ and sik1−/− mice hearts. Mean±SEM; n=6-7.
Online Figure III: Gene expression analysis in the kidney of the sik1<sup>+/+</sup> (WT) and sik1<sup>-/-</sup> (KO) mice under normal (NS) or high-salt (HS) intake. The mRNA expression of all SIK isoforms in the sik1<sup>+/+</sup> and sik1<sup>-/-</sup> mice kidney. Mean±SEM; n=6-7. *p<0.05, vs. WT-NS.

Online Figure IV: Gene expression analysis in the aorta of the sik1<sup>+/+</sup> (WT) and sik1<sup>-/-</sup> (KO) mice under normal (NS) or high-salt (HS) intake. (A-D) mRNA expression in the sik1<sup>+/+</sup> and sik1<sup>-/-</sup> mice aortas. Mean±SEM; n=6-7.
Online Figure V: Gene expression analysis in human aortic adventitial fibroblasts (AFs), human vascular smooth muscle cells (VSMCs) and in the aorta of the sik1+/+ (WT) and sik1−/− (KO) mice under normal (NS) or high-salt (HS) intake. Primary cultures of AFs (A) and VSMCs (B) were transfected with either SIK1- (si-SIK1) or scrambled- (si-SCR) siRNAs for 24h in the presence or absence of TGFβ1 for additional 24h and mRNA levels of all SIK isoforms were evaluated. (C) mRNA levels of SIK2 and SIK3 in the sik1+/+ and sik1−/− mice aortas upon NS or HS intake. Mean±SEM; n=6-7. *p<0.05, vs. si-scr-vehicle; †p<0.05, vs. si-scr-TGFβ1.

Online Table I. Plasma norepinephrine levels in the sik1+/+ and sik1−/− mice

<table>
<thead>
<tr>
<th></th>
<th>sik1+/+ tap water</th>
<th>sik1−/− tap water</th>
<th>sik1+/+ 1% NaCl</th>
<th>sik1−/− 1% NaCl</th>
</tr>
</thead>
<tbody>
<tr>
<td>Norepinephrine (pmol/ml)</td>
<td>6.99±0.51</td>
<td>8.09±0.68</td>
<td>6.58±0.55</td>
<td>6.98±0.73</td>
</tr>
</tbody>
</table>

Values are expressed as mean±SEM.

Online Table I: Sympathetic activity in the sik1+/+ and sik1−/− mice under normal (tap water) or high-salt (1% saline) intake. Blood samples were collected and plasma norepinephrine quantification was performed by HPLC with electrochemical detection. Mean±SEM; n=6-7.