Metabolomics in Angiotensin II–Induced Cardiac Hypertrophy

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Abstract—Angiotensin II (Ang II) induces mitochondrial dysfunction. We tested whether Ang II alters the “metabonomic” profile. We harvested hearts from 8-week-old double transgenic rats harboring human renin and angiotensinogen genes (dTGRs) and controls (Sprague-Dawley), all with or without Ang II type 1 receptor (valsartan) blockade. We used gas chromatography coupled with time-of-flight mass spectrometry to detect 247 intermediary metabolites. We used a partial least-squares discriminate analysis and identified 112 metabolites that differed significantly after corrections (false discovery rate q <0.05). We found great differences in the use of fatty acids as an energy source, namely, decreased levels of octanoic, oleic, and linoleic acids in dTGR (all P<0.01). The increase in cardiac hypoxanthine levels in dTGRs suggested an increase in purine degradation, whereas other changes supported an increased ketogenic amino acid tyrosine level, causing energy production failure. The metabonomic profile of valsartan-treated dTGRs more closely resembled Sprague-Dawley rats than untreated dTGRs. Mitochondrial respiratory chain activity of cytochrome C oxidase was decreased in dTGRs, whereas complex I and complex II were unaltered. Mitochondria from dTGR hearts showed morphological alterations suggesting increased mitochondrial fusion. Cardiac expression of the redox-sensitive and the cardioprotective metabolic sensor sirtuin 1 was increased in dTGRs. Interestingly, valsartan changed the level of 33 metabolites and induced mitochondrial biogenesis in Sprague-Dawley rats. Thus, distinct patterns of cardiac substrate use in Ang II–induced cardiac hypertrophy are associated with mitochondrial dysfunction. The finding underscores the importance of Ang II in the regulation of mitochondrial biogenesis and cardiac metabolomics, even in healthy hearts. (Hypertension. 2010;55[part 2]:508-515.)

Key Words: hypertrophy ■ metabolomics ■ angiotensin II ■ hypertension ■ oxidative stress

Hypertension-induced left ventricular hypertrophy (LVH) represents an adaptive and compensatory response to increased workload and represents an independent risk factor of cardiovascular events. Patients with LVH have more strokes, congestive heart failure, and sudden cardiac death compared with those without LVH.1 The mechanisms are unknown, although angiotensin (Ang) II contributes greatly to the process. Other than the regulatory effects on blood pressure, sodium excretion, and aldosterone secretion, Ang II also induces inflammatory responses and oxidative stress by blood pressure–independent mechanisms.2–4 Energy metabolism is deranged in LVH, with and without heart failure.5,6 All 3 of the components of cardiac energy metabolism, namely substrate use, oxidative phosphorylation, and high-energy phosphate metabolism, are affected. Mitochondria generate energy, regulate apoptosis, and produce reactive oxygen species (ROS). Doughan et al7 showed recently that Ang II induces mitochondrial dysfunction via a protein kinase C–dependent pathway that activates NADPH oxidase and formation of peroxynitrite. Several factors regulate mitochondrial function and biogenesis. ROS, NO, peroxisome proliferator-activated receptor-γ coactivator (PGC) 1α, and sirtuins are all potential links between metabolic diseases and mitochondrial dysfunction.8,9 Sirtuin 1 (SIRT1) is a redox-sensitive metabolic sensor exerting cardioprotective, antiapoptotic, and anti-inflammatory properties.8,9 SIRT1 is of particular interest because its expression is increased during heart failure.10 SIRT1 may also reduce mitochondrial ROS formation by increasing mitochondrial activity via an NO-dependent pathway.11 Metabolomics is a novel systems biology tool for the global study of metabolites and their dynamics, composition, interactions, and responses to different interventions.12 Metabolomic profiling is usually on the basis of the quantification of small molecules leaking from injured myocardial cells. We used a 2D gas chromatography (GC×GC-TOF) coupled with a time-of-flight mass spectrometry (MS) system.
to profile 247 intermediary metabolites directly from myocardial samples. Such a GC\times GC-TOF/MS-based platform offers high peak capacity without compromising sensitivity. We used this system to evaluate Ang II–dependent cardiac hypertrophy with preserved systolic function in a novel rat model harboring human renin and angiotensinogen transgenes. These rats generate large amounts of Ang II in the absence of Ang II type 1 (AT1) receptor blockade. Changes in cardiac metabolomics were interpreted with the relationship to Ang II–induced changes in mitochondrial morphology, respiratory chain enzyme activities, and mitochondrial biogenesis markers. Furthermore, we investigated whether Ang II–induced mitochondrial dysfunction and a shift in the metabolomic profiling were counteracted by upregulation of cardiac SIRT1.

**Methods**

We used fifty 4-week–old dTGRs and 14 age-matched SD rats. The animal experimentation committee of the University of Helsinki and the Provincial State Office of Southern Finland approved the study (STU 1187 A). All of the studies were conducted in accordance with the National Institutes of Health Guide for the Care and Use of Laboratory Animals. The rats had free access to chow (Harlan) and water. dTGRs and SD rats were divided into 4 groups to receive the following diet and drug regimens for 4 weeks: (1) dTGR controls (n=40); (2) dTGR + valsartan (30 mg/kg in the food; n=10); (3) SD controls (n=6); and (4) SD + valsartan (n=8).

Systolic blood pressure was measured weekly using a tail cuff (Apollo-2AB Blood Pressure Analyzer, model 179-2AB, ITTC Life Science). Transthoracic echocardiography (Toshiba Ultrasound) was performed under isoflurane anesthesia (AGA) in a blinded fashion by the same technician during the last study week, as described previously. At age 8 weeks, rats were anesthetized with CO\textsubscript{2}/O\textsubscript{2} (AGA) and decapitated. The hearts were excised, washed with ice-cold saline, blotted dry, weighed, and snap-frozen in liquid nitrogen. All of the samples were stored at −80°C.

The hearts were investigated in a blinded fashion. Light microscopy at X\times40 magnification was used to determine the cardiomyocyte cross-sectional area. The cross-sectional area was evaluated in a blinded fashion and was analyzed using the ISImaging software (Image Solutions, Inc). We used GC\times GC-TOF/MS to detect 247 intermediary metabolites. The instrument used was a GC\times GC-TOF mass spectrometer (Pegasus 4D, Leco) with an autosampler (6890N GC and Combi PAL, Agilent Technologies). The metabolites were identified using an in-house reference compound library, as well as by searching the reference mass spectral library. Mass spectra from the GC\times GC-TOF/MS analysis were searched against the Palisade Complete Mass Spectral Library, 600K Edition (Palisade Mass Spectrometry).

The respiratory chain activities of complex I (reduced nicotinamide-adenine dinucleotide dehydrogenase), complex II (succinate dehydrogenase), and complex IV (cytochrome C oxidase) were quantitated by measuring the oxygen consumption polarographically with a Clark-type electrode (Instech). Quantitative real-time RT-PCR was performed using the LightCycler instrument (Roche Diagnostics) for detection of atrial natriuretic peptide (ANP) and the mitochondrial biogenesis markers nuclear respiratory factor 1, transcription factor A mitochondrial, PGC-1α, and ribosomal 18S mRNA, as described elsewhere. Briefly, total RNA from the rat hearts was collected with TRIzol (Gibco, Invitrogen), treated with deoxyribonuclease 1 (Sigma Chemicals) and reverse transcribed to cDNA by reverse-transcription enzyme (Im-Prom-II reverse tran-
scription system, Promega). One microliter of cDNA was subjected to quantitative real-time PCR for the detection of ANP, as well as mitochondrial biogenesis markers nuclear respiratory factor 1, transcription factor A mitochondrial, PGC-1α, and ribosomal 18S mRNA. The following primers were used: ANP forward CCG-ATAGATTTGCGCCCTTGGA; reverse CCCGAAAGCAGTTC- GATCTCTC; nuclear respiratory factor 1 forward GCACCTG- GTGCTGCTAC; reverse GTGGCTGCTGCTGCTGAT; transcription factor A mitochondrial forward AGACCTCGGTCAGCATATA- CACA; reverse GCCAGGGATGAGACTCAT; and PGC-1α for- ward GGGCCCCAGGCTATG, reverse CTCCATATCCGCCCCG- CAG. The samples were amplified using FastStart DNA Master SYBR Green I (Roche Diagnostics) according to the protocol of the manufacturer. The quantities of the PCR products were quantified with an external standard curve amplified from purified PCR product. Electron microscopy from samples taken from left ventricle was performed as described in detail elsewhere.15

SIRT1 expression was analyzed by Western blot using polyclonal anti-SIRT1 (Abcam) as a primary antibody. Briefly, myocardial samples were electrophoretically separated by 8% SDS-PAGE (15 μg of total protein of the whole cell lysate per lane). Each lane corresponded with 1 rat, and all 4 of the groups were run on 1 gel. Proteins were transferred to a polyvinylidene fluoride membrane (Immobilon-P, Millipore) and blocked in 5% nonfat milk-Tris-buffered saline-0.01% Tween-20 buffer. The membranes were probed with the primary anti-SIRT1 antibody (Abcam). After being probed for SIRT1, the membranes were stripped and reprobed for tubulin (Antialpha tubulin, Abcam), which was used as the loading control. Horse radish peroxidase–conjugated antirabbit secondary antibody (Chemicon) was subjected to enhanced chemiluminescence solution (ECLplus, Amersham Biosciences). We quantified the relative protein expression in separate samples from the membranes with Fluorescent Image Analyzer (FUJIFILM Corp). The measurements were repeated 3 times, and the data were presented as mean±SEM of these experiments.

Statistically significant differences in mean values were tested by ANOVA and the Tukey post hoc test for comparisons of multiple groups. The differences were considered significant when P<0.05. For cardiac metabolic profiles, R statistical software (http://www.r-project.org/) was used for data analyses and visualization. The concentrations were compared using the Wilcoxon rank-sum test, with P values <0.05 considered significant. To account for multiple comparisons, false discovery rate was estimated as the maximum q value19 in the set of significant differences for the metabolomic data set. False discovery rates were computed using the R package q value. The significance of the group differences was evaluated by the P value for the fixed-effect parameter estimate of group differences.

**Results**

Untreated dTGR mortality at week 8 was 55% (Figure 1A). Systolic blood pressure in untreated dTGRs increased progressively to 205±2 mm Hg at week 8 (Figure 1B). Ejection fraction and fractional shortening were preserved, compared with SD rats. Details on all of the hemodynamic variables are available in the online Data Supplement (at http://hyper.ahajournals.org, Table S1). Untreated dTGRs showed pronounced cardiac hypertrophy expressed as the heart weight:body weight ratio (Figure 1C) and cardiomyocyte cross-sectional area (Figure 1D). Myocardial ANP mRNA expression was increased 20-fold in untreated dTGRs (Figure 1E). Cardiac damage score was markedly increased in dTGRs (Figure 1F). Valsartan treatment prevented hypertension, mortality, LVH, and increased ANP mRNA expression.

The GC×GC-TOF/MS data set consisted of 247 intermediary metabolites. Using multivariate analysis (partial least-squares discriminant analysis) for all of the metabolites detected, we identified 112 metabolites from myocardial samples that differed statistically significantly between the groups after correction for multiple comparisons (false discovery rate q <0.05; Figure 2 and Table S2); 64 cardiac metabolites differed significantly between dTGRs and SD rats (P<0.05), 32 metabolites differed between dTGR and valsartan treatment (P<0.05), and 34 metabolites differed between SD and SD+valsartan treatment (P<0.05). Figure 3 represents a heat map consisting of the top 40 metabolites after using a more strict statistical significance (P<0.001) that had the highest impact on the separation of the different treatment groups (P<0.01). Changes in cardiac metabolomics covered a wide range of metabolites from different functional classes (Figure 3 and Table S2). In general, the metabolomic profile of valsartan-treated dTGRs was closer to SD rats than to untreated dTGRs. Interestingly, partial least-squares discriminant analysis revealed that the metabolomic profile of valsartan-treated SD rats also clearly differed from untreated SD controls, although there were no differences between the groups in hemodynamic parameters (Figure 1).

Metabolomic profiling revealed several decreases in cardiac fatty acid concentrations in dTGRs (Figure 4A). In particular, we found lower myocardial octanoic acid, oleic acid, and linoleic acid levels (all parameters P<0.001). From the selected amino acids, we found markedly increased ketogenic amino acid tyrosine levels and decreased tryptophan levels in dTGRs; otherwise, drug effect dominated the amino acid changes (Figure 4B). dTGRs showed several changes in organic acid levels. We found decreased hippuric acid, malic acid, and γ-hydroxybutyric acid concentrations,
whereas the level of β-hydroxybutyric acid in dTGRs was increased (Figure 4C). The increase in cardiac hypoxanthine level found in dTGRs suggests an increase in purine degradation (Figure 4D). Interestingly, valsartan treatment decreased the cardiac hypoxanthine level by 70%.

We found that the activity of cytochrome c oxidase, an important enzyme in the mitochondrial adenosine triphosphate production, was lower in dTGRs than in SD rats (Figure 5A). AT1 antagonist valsartan partly reversed this change. The activities of other respiratory chain enzymes did not vary between groups (Figure 5B and 5C). Also, the yield of mitochondria was lower from dTGRs than from SD rats (data not shown). There was no difference between dTGR and SD rats in the mRNA expressions of mitochondrial biogenesis markers nuclear respiratory factor 1, transcription factor A mitochondrial, or PGC-1α (Figure 5D through 5F). Valsartan increased mitochondrial biogenesis markers in SD rats, whereas the expression of mitochondrial biogenesis markers in valsartan-treated dTGRs was slightly but significantly lower compared with control dTGRs.

Mitochondria are dynamic organelles that undergo continuous fusion and fission events that promote the exchange of metabolites, proteins, and nucleic acids between individual mitochondria.20 Changes in the cellular metabolic status influence the balance between fission and fusion leading to alterations in the mitochondrial morphology. We, therefore, investigated the ultrastructure of cardiac mitochondria in dTGRs. With electron microscopy, we found that cardiac mitochondria from dTGRs, but not from control animals, frequently formed interconnected tubes (Figure 6A and 6B). This finding suggests that alterations in the cardiac metabolism of dTGRs promote mitochondrial fusion. Finally, cardiac SIRT1 expression measured by Western blot was increased in dTGRs compared with SD controls (Figure 6C). Valsartan prevented an Ang II–induced increase in cardiac SIRT1 expression.

Discussion

Metabolomic approaches have been applied recently to cardiovascular biomarker and pathway discovery.21 We applied
Impaired cardiac substrate metabolism contributes to progression of left ventricular remodeling and to contractile dysfunction in heart failure. Although substrate use is relatively normal during the transition from compensatory LVH to heart failure, a downregulation in fatty acid oxidation, increased glycolysis, and glucose oxidation, as well as defects in mitochondrial respiratory chain function and oxidative phosphorylation, have been reported in advanced stages of heart failure. Metabolic profiling of low molecular weight biochemicals, such as lipids, sugars, and amino acids, that serve as substrates and products in metabolic pathways or regulatory signals with hormone-like functions has been used so far in the early detection of myocardial injury and, to a lesser extent, to cardiovascular biomarker discovery. Lewis et al recently reported changes in circulating metabolites participating in pyrimidine metabolism, the tricarboxylic acid cycle, and the pentose phosphate pathways in hypertrophic cardiomyopathy patients undergoing planned septal myocardial infarction. Turer et al profiled 63 intermediate metabolites from plasma in patients with coronary disease undergoing surgical cardioplegic arrest and ischemia/reperfusion and demonstrated global suppression of metabolic fuel uptake. Mayr et al used a combined metabolomic and proteomic approach to investigate the effects of atrial fibrillation. Metabolomic profiling of 24 metabolites from the atrial tissue revealed increased levels of β-hydroxybutyrate, ketogenic amino acids, and glycine, indicating metabolic adaptation to persistent atrial fibrillation. We avoided analytic problems related to plasma samples, such as rapid metabolism, excretion, wide distribution, and consequent dilution of the metabolites, by using a novel GC×GC-TOF/MS to detect 247 intermediate metabolites directly from samples taken from the left ventricle.

Previous gene expression profile analyses reported the downregulation of several genes encoding mitochondrial respiratory chain and lipid metabolism in dTGRs with terminal heart failure. Furthermore, distinct patterns in the expression profile of genes encoding transcription factors, coagulation, cardiac remodeling, immune system, and metabolic pathways were also found. We found a consistent decrease of medium-chain fatty acids in dTGRs, most notably octanoic, oleic, and linoleic acids, suggesting downregulation of fatty acid synthesis. In general, changes in cardiac metabolomics covered a wide range of metabolites from different functional classes. We detected 247 intermediate metabolites from cardiac tissue, of which 112 showed statistically significant differences among the treatment groups. We were interested to find that cardiac octanoic acid level was markedly decreased in dTGRs. Because octanoic acid acts as a precursor of lipoic acid, an endogenous sulfur-containing...
coenzyme required for the mitochondrial dehydrogenase reactions leading to adenosine triphosphate formation, our finding could also partially explain the beneficial effects of lipoic acid supplementation in dTGRs. The increase in cardiac hypoxanthine level found in dTGRs suggests an increase in purine degradation. Accordingly, we showed previously increased expression of xanthine oxidoreductase in dTGRs. We also noticed increased cardiac levels of some ketogenic amino acids, such as tyrosine, indicating derangement in glucose use in dTGRs. Finally, our metabolomic profile revealed that valsartan AT1 receptor blockade influenced cardiac metabolomics. The drug also induced the expression of cardiac biogenesis markers in healthy and normotensive SD rats. These effects on metabolomic profile were independent of changes in blood pressure and cardiac function. Similarly, Benigni et al reported recently that disruption of AT1 receptor promotes longevity in mice through attenuation of oxidative stress and induction of mitochondrial biogenesis.

Ang II induces mitochondrial oxidative damage and mitochondrial dysfunction largely via the NAPDH oxidase. We found that the dTGR heart showed an increased tendency toward mitochondrial fusion, suggesting that alterations in the cardiac metabolism of dTGRs promote mitochondrial fusion. Additional studies are warranted to investigate whether Ang II–induced derangements in mitochondrial dynamics are linked to ultrastructural abnormalities in cardiac mitochondria. Mitochondrial respiratory chain experiments revealed that cytochrome c oxidase (complex IV) activity was decreased in dTGRs and was partially corrected by valsartan. Because cytochrome C oxidase is an important enzyme in the mitochondrial adenosine triphosphate production, impaired cytochrome C oxidase activity found in untreated dTGRs would lead to diminished adenosine triphosphate production and would thereby contribute to the impairment of contractile activity in heart failure. Surprisingly, AT1 receptor blockade exerted distinct effects on mitochondrial biogenesis markers in dTGRs compared with SD rats. Whether this state of affairs is related to activation of mitochondrial biogenesis in dTGRs remains to be determined.

SIRT1 is a highly conserved oxidized nicotinamideadenine dinucleotide–dependent enzyme that regulates the life span in lower organisms and acts as a cellular metabolic sensor. SIRT1 increases cellular stress resistance and genomic stability and regulates cellular senescence and energy metabolism via deacetylation of the target proteins, such as p53, FOXO transcription factors, and PGC-1α. SIRT1 transgenic mice given a standard diet show phenotypes resembling caloric restriction, and during a high-fat diet, SIRT1 transgenic mice show lower inflammatory responses and improved glucose tolerance. In contrast, tumorigenesis, genomic instability, and impaired DNA damage responses have been reported in SIRT1 mutant mice. Alcendor et al provided the first evidence that SIRT1 plays a cardioprotective role in pathological hearts in vivo. They also demonstrated increased cardiac SIRT1 expression during heart failure. Recently, a tissue-specific transgenic approach showed that moderate cardiac SIRT1 overexpression (2.5- to

Figure 5. Bar graphs show mitochondrial respiratory chain activities (A through C) and cardiac gene expressions of mitochondrial biogenesis markers (D through F) in dTGRs and SD rats in the presence and absence of 4 weeks of valsartan treatment. For abbreviations, see Figure 1 legend. Mean±SEM are given, n=6 to 8 in each group. *P<0.05 vs dTGR VAL; #P<0.05 vs SD; ++P<0.05 vs SD VAL.
Ang II–induced target-organ damage. These findings suggest that the induction of the redox-sensitive SIRT1 may be cardioprotective and could counteract the detrimental effects of Ang II in the dTGR heart, an issue that will be singularly pursued. The insights here were garnered with a metabolomics approach that we believe will have increasing use in identifying additional hitherto fore unknown pathways.

Perspectives
Very recently, Zhang et al. showed that SIRT1 is essential in the maintenance for T-cell tolerance. We showed earlier that oxidative stress, inflammatory response, and protection against cellular senescence, whereas higher cardiac SIRT1 levels were associated with increased apoptosis, hypertrophy, and decreased cardiac function. We found that cardiac SIRT1 expression was moderately increased in untreated dTGRs compared with SD controls, with no differences in the cardiac SIRT1 mRNA expressions.

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Disclosures
None.

References


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Metabolomic profiling reveals distinct patterns of cardiac substrate utilization in angiotensin II-induced cardiac hypertrophy

Online Supplemental Methods and Data Tables

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1. Supplemental Materials and Methods

Experimental animals, blood pressure measurement and sample preparation
We used 30 4-week-old male double transgenic rats (dTGR) and 20 age-matched normotensive Sprague-Dawley (SD) rats described elsewhere. The protocols were approved by the Animal Experimentation Committee of the University of Helsinki, Finland, and the Provincial State Office of Southern Finland (approval number STU 1187 A), whose standards correspond to those of the American Physiological Society. The rats had free access to chow (Harlan) and drinking water. dTGR and normotensive SD control rats were divided into four groups to receive the following diet and drug regimens for 4 weeks: (1) dTGR controls (n = 20); (2) dTGR + valsartan (30 mg/kg mixed in the food) (n = 10); (3) SD controls (n = 10); (4) SD + valsartan (n = 10). This valsartan dosage have produced maximal pharmacological effects in our previous rat experiments. Systolic blood pressure was measured weekly using a tail cuff blood pressure analyzer (Apollo-2AB Blood Pressure Analyzer, Model 179-2AB, IITC Life Science, Woodland Hills, CA, USA). At the age of 7 weeks, rats were anesthetized with CO₂/O₂ (AGA, Riihimäki, Finland) and decapitated. Blood samples were collected for biochemical measurements using EDTA as an anticoagulant. The hearts were excised, washed with ice-cold saline, blotted dry, weighed, and snap-frozen in liquid nitrogen. All samples were stored at -80°C until assayed.

Echocardiography
Transthoracic echocardiography (Toshiba Ultrasound, Japan) was performed on all rats under isoflurane anesthesia (AGA, Riihimäki, Finland) in a blinded fashion by the same technician during the last study week as described previously.

Cardiac morphology and cardiomyocyte cross sectional area
The myocardial morphology was investigated in a blinded fashion as described in detail previously. Briefly, in the heart, the arteries and ventricular fibrous tissue formation were evaluated. Each sample was scored from 0 to 4 according to the morphological changes. Conventional light microscopy at x400 magnification was used to determine cardiomyocyte cross sectional area. Fifteen to 17 random fields were studied, and in each field the cell borders were measured from myocytes cut in the short axis with a visible nucleus. An average of 50 cardiomyocytes per animal was studied from each animal in the group. The cross-sectional area was evaluated in a blinded fashion and was analyzed using the ISImaging software (Image Solutions Inc., Whippany, New Jersey, USA).

Metabolomic analysis using the GCxGC-TOF/MS platform
20 µl of an internal standard-labeled palmitic acid (16:0-16,16,16d₃ ; 258 mg/l) and 400 µl of methanol solvent were added to 11-14 mg samples. Samples were ground and extracted with a Retsch Mixer Mill Type MM 301 for 5 min at 25 Hz. After incubating for 30 min at room temperature, the supernatant was separated by centrifugation at 10,000 rpm for 5 min. The sample was dried under constant flow of nitrogen gas. 25 µl MOX (2% methoxyamine HCl in pyridine) was added to the dried sample. The mixture was then incubated at 45 °C for 1 h and derivatized with 25 µl MSTFA (N-methyl-N-(trimethylsilyl)trifluoroacetamide) by incubating at 45 °C for 1 h. 5 µl of retention index standard mixture with five alkanes at 150 ppm was added to
the metabolite mixture. Sample order for analysis was established by randomization. The instrument was a GCxGC-TOF mass spectrometer (Pegasus 4D; Leco) with an autosampler (6890N GC and Combi PAL; Agilent Technologies). The instrument parameters were as follows: 1 µl split injection 1:20; first column, RTX-5, 10 m x 180 µm x 0.20 µm; second column, BPX-50, 1.50 m x 100 µm x 0.10 µm; helium 39.6 psig constant pressure; temperature programs, primary oven, Initial 50 °C, 1 min at 295 °C, 7 °C/min, 3 min, and secondary oven, 20 °C above primary oven temperature; second dimension separation time 5 s; MS measurement 45–700 amu, 100 spectra/s. Raw data were processed using ChromaTOF software (Leco) followed by alignment and normalization using the in house–developed software. Unwanted background peaks were eliminated using the classifications feature of ChromaTOF software. In house–developed software was used to perform additional filtering using compound identifications by ChromaTOF. The metabolites were identified using an in house reference compound library as well as by searching the reference mass spectral library. Mass spectra from the GCxGC-TOF/MS analysis were searched against The Palisade Complete Mass Spectral Library, 600K Edition (Palisade Mass Spectrometry). The matches to reference spectra are based on a weighted dot product of the two spectra, with higher m/z peaks having more weight than the lower. A similarity value is assigned between 0 and 999, with 999 being a perfect match and 750 generally considered as a reasonable match. We used the conservative cut-off criterion of 850 for identification.

Measurement of the activities of the mitochondrial respiratory chain
Rat heart mitochondria were isolated by differential centrifugation. Resulting pellet was washed once with medium containing 250mM sucrose, 5mM KH2PO4, 10mM KCl, 10 mM HEPES and 5mM MgCl2, pH 7.4. The washed mitochondria were used immediately after preparation. The respiratory chain activity was quantitated by measuring the oxygen consumption polarographically with a Clark-type electrode (Instech). The mitochondria were supplemented with appropriate substrates. The complex I (NADH dehydrogenase) activity was tested by using glutamate and malate as substrates. The complex II (succinate dehydrogenase) was tested by using succinate and the complex IV, cytochrome c oxidase (COX), was tested by using ascorbate and TMPD (tetrathylphénylendiamine). All activities were verified by using appropriate, specific respiratory chain inhibitors.

Cardiac mRNA expressions of ANP and mitochondrial biogenesis markers
Quantitative real-time RT-PCR was performed using the LightCycler® instrument (Roche diagnostics, Neuilly sur Seine, France) for detection of atrial natriuretic peptide (ANP), and the mitochondrial biogenesis markers NRF-1, TFAM, PGC-1α and ribosomal 18S mRNA as described elsewhere. Total RNA from the rat hearts were collected with Trizol® (Gibco, Invitrogen, Carlsbad, CA, USA), treated with DNase 1 (Deoxyribonuclease 1, Sigma Chemicals Co., St Louis, MO, USA) and reverse transcribed to cDNA by reverse transcription enzyme (Im-Prom-II reverse transcription system, Promega, Madison, WI, USA). One µl of cDNA was subjected to quantitative real time polymerase chain reaction for detection of atrial natriuretic peptide (ANP), mitochondrial biogenesis markers NRF-1, TFAM, PGC-1α and ribosomal 18S mRNA. The following primers were used: ANP forward CCGATAGATTCTGCCCTTTGAA, reverse CCCGAAGCAGCTTGATCTCTCC; NRF-1 forward GCACCGTGTTCGTTCAT, reverse GCTTGCCTGTCTCGGAT; TFAM forward AGACCTCGGTACGATATAACA, reverse
GCGACGGATGAGATCACTT; PGC-1? forward GGTCCCCACGGCAGTAG, reverse CTCCATCATCCCCGAG. The samples were amplified using FastStart DNA Master SYBR Green 1 (Roche diagnostics) according to the protocol of the manufacturer. The quantities of the PCR products were quantified with an external standard curve amplified from purified PCR product.

Transmission electronic microscopy
Tissue samples of approximately 1 mm were excised from the left ventricle and placed in a medium containing 250 mM sucrose, 10 mM Hepes-KOH, pH 7.40, 2% glutaraldehyde, 2% paraformaldehyde, and 2% DMSO. The samples were incubated at RT for 2 h, and then rinsed 4 times for 15 min with water. Postfixation with osmium tetroxide, dehydration, and embedding in epoxy resin was performed as described. Thin sections were stained with uranyl acetate and lead citrate, and viewed with a JEOL 1200 EX II electron microscope.

Cardiac SIRT1 expression by Western blot
Myocardial samples were electrophoretically separated by 8 % SDS-PAGE (15 µg total protein of the whole cell lysate per lane). Each lane corresponded to one rat and all 4 groups were run on one gel. Proteins were transferred to a PVDF membrane (Immobilon-P®, Millipore, Bedford, MA, USA) and blocked in 5% non-fat milk-TBS - 0.01% Tween-20® buffer. The membranes were probed with the primary anti-SIRT1 antibody (Abcam). After being probed for SIRT1 the membranes were stripped and re-probed for tubulin (Antialpha tubulin; Abcam) which was used as the loading control. Horseradish peroxidase-conjugated anti-rabbit secondary antibody (Chemicon, Temecula, CA, USA) was subjected to enhanced chemiluminescence solution (ECLplus, Amersham Biosciences, Buckinghamshire, UK). We quantified the relative protein expression in separate samples from the membranes with Fluorescent Image Analyzer (FUJIFILM Corp, Tokyo, Japan). The measurements were repeated three times, and the data values were presented as means±SEM of these experiments.

Statistical analyses
Data are presented as means ± SEM. Statistically significant differences in mean values were tested by analysis of variance (ANOVA) and the Tukey’s post-hoc test for comparisons of multiple groups. The differences were considered significant when p<0.05. For cardiac metabolomic profiles R statistical software (http://www.r-project.org/) was used for data analyses and visualization. The concentrations were compared using the Wilcoxon rank-sum test, with p-values < 0.05 considered significant. To account for multiple comparisons, false discovery rate was estimated as the maximum q –value in the set of significant differences for metabolomic dataset. False discovery rates were computed using the R package qvalue. The significance of the group differences was evaluated by the p-value for the fixed effect parameter estimate of group differences.
2. References


**Supplemental Table 1.** Cardiac functions measured by echocardiography in 8-week-old double transgenic rats harbouring human renin and angiotensinogen genes (dTGR) and normotensive Sprague Dawley (SD) controls. Valsartan was given orally at a daily dose of 30 mg/kg. s denotes systolic and d diastolic; IVST, interventricular septum; LVD, left ventricular diameter; LVW, left ventricular wall; EDV, end diastolic volume; ESV, end systolic volume; EF, ejection fraction; FS, fractional shortening; CO, cardiac output; HR, heart rate. Means ± SEM are given, n=7-14 in each group. * denotes p<0.05 compared to dTGR; † denotes p<0.05 compared to dTGR + VAL.

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<tr>
<th>Variable</th>
<th>dTGR (n=14)</th>
<th>dTGR+VAL (n=10)</th>
<th>SD (n=9)</th>
<th>SD + VAL (n=7)</th>
<th>ANOVA, p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>IVST (d), mm</td>
<td>2.45 ± 2.11 ± 0.09*</td>
<td>1.68 ± 1.73 ± &lt;0.0001</td>
<td>2.39 ± 2.01 ± 0.07*</td>
<td>1.86 ± 1.61 ± 0.08*</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>LVD (d), mm</td>
<td>6.94 ± 6.48 ± 0.15</td>
<td>7.54 ± 7.10 ± 0.23</td>
<td>0.002</td>
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<td></td>
</tr>
<tr>
<td>LVPWT (d), mm</td>
<td>2.39 ± 3.87 ± 0.09</td>
<td>1.86 ± 3.35 ± &lt;0.0001</td>
<td>0.0002</td>
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</tr>
<tr>
<td>IVST (s), mm</td>
<td>3.92 ± 3.06 ± 0.13*</td>
<td>3.80 ± 3.80 ± 0.28†</td>
<td>0.0001</td>
<td></td>
<td></td>
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<tr>
<td>LVD (s), mm</td>
<td>3.85 ± 3.46 ± 0.10</td>
<td>3.10 ± 2.95 ± 0.25*</td>
<td>0.0006</td>
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<tr>
<td>LVPWT (s), mm</td>
<td>0.77 ± 0.64 ± 0.04</td>
<td>0.96 ± 0.82 ± 0.07</td>
<td>0.001</td>
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<td></td>
</tr>
<tr>
<td>EDV, ml</td>
<td>0.09 ± 0.03 ± 0.15</td>
<td>0.10 ± 0.02 ± 0.0008</td>
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</tr>
<tr>
<td>ESV, ml</td>
<td>88.5 ± 2.3</td>
<td>95.1 ± 0.7</td>
<td>84.4 ± 3.1†</td>
<td>89.0 ± 1.9</td>
<td>0.006</td>
</tr>
<tr>
<td>EF (%)</td>
<td>67.2 ± 1.7*</td>
<td>49.8 ± 3.2†</td>
<td>56.9 ± 3.3†</td>
<td>0.0006</td>
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<tr>
<td>FS (%)</td>
<td>228.5 ± 210.5 ± 13.9</td>
<td>302.5 ± 262.2 ± 20.5</td>
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<td></td>
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<tr>
<td>CO (ml/min)</td>
<td>338 ± 6</td>
<td>348 ± 6</td>
<td>373 ± 12*</td>
<td>361 ± 12</td>
<td>0.03</td>
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Supplemental Table 2. Metabolomic analysis of cardiac tissue from dTGR and SD rats in the presence and absence of valsartan by GCxGC-TOF/MS.

<table>
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<tr>
<th>Name</th>
<th>p(ANOVA)</th>
<th>q(ANOVA)</th>
<th>p(dTGR/SD)</th>
<th>p(dTGR/dTGR+V)</th>
<th>p(SD/SD+V)</th>
<th>Mn(dTGR)</th>
<th>Mn(dTGR+V)</th>
<th>Mn(SD)</th>
<th>Mn(SD+V)</th>
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<td>Linoleic acid, TMS</td>
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<td>8.01</td>
<td>12.65</td>
<td>11.22</td>
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<td>8.69E-05</td>
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<td>2.90E-01</td>
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<td>5.67</td>
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<td>13.04</td>
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<td>9H-Purin-6-amine, N,O-bis(trimethylsilyl)</td>
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<td>8.36E-05</td>
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<td>1.48E-04</td>
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<tr>
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<td>Ribitol, 1,2,3,4,5pentakis-O(trimethylsilyl)-9,12-Octodecaenoic acid ([Z]-, 2-[(trimethylsilyloxyl)ox]-1-[[trimethylsilyloxyl]ox</td>
<td>9.80E-04</td>
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<td>Comp2</td>
<td>Comp3</td>
<td>Comp4</td>
<td>Comp5</td>
<td>Comp6</td>
<td>Comp7</td>
<td>Comp8</td>
<td>Comp9</td>
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<td>-----------------------------------------------------------</td>
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<tr>
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<td>(all-Z)</td>
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<td>3.98E-02</td>
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<td>Inositol, 1,2,4,5,6pentakis-O-(trimethylsilyl), biss(trimethylsilyl) phosphate</td>
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<td>3.60E-02</td>
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<td>Inositol, 1,2,4,5,6pentakis-O-(trimethylsilyl), biss(trimethylsilyl) phosphate</td>
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**HEPTADECYLGLYCEROL**

- **1,2-Ethanediame, N-ethyl**: 4.39E-02, 3.40E-02, 2.01E-01, 2.22E-01, 7.26E-01, 1.68, 2.28, 0.99, 1.15
- **2-(7-Methoxy-3-benzofuryl)ethylamine**: 4.47E-02, 3.40E-02, 3.98E-02, 4.40E-01, 9.17E-01, 0.42, 0.66, 1.01, 1.01
- **19,19-Dimethyl-eicosa-8,11-dienoic acid**: 4.67E-02, 3.51E-02, 8.89E-01, 9.86E-01, 3.66E-02, 14.75, 14.72, 14.94, 10.80
- **Inositol, 1,2,4,5,6pentakis-O-(trimethylsilyl), biss(trimethylsilyl) phosphate**: 4.94E-02, 3.60E-02, 9.22E-01, 8.29E-01, 9.48E-02, 71.30, 73.25, 72.69, 40.44
- **1-Butanamine, N,N-dimethyl**: 4.91E-02, 3.60E-02, 4.82E-03, 3.07E-01, 1.10E-01, 0.50, 0.30, 0.00, 0.20

**Additional Entries**

- **1,4-Methano-2H-cyclopent[d]oxepin-2,5(4H)-dione, 6-[(dimethylamino)methyl]hexahydro**: 4.96E-02, 3.60E-02, 1.26E-01, 5.94E-01, 2.98E-01, 1.61, 1.91, 1.03, 0.72
- **1,3-Dioxolane**: 5.34E-02, 3.84E-02, 4.87E-01, 9.60E-02, 5.81E-02, 1.04, 1.44, 1.23, 1.58
- **2-Tridecen-1-ol, (E)**: 5.47E-02, 3.84E-02, 2.02E-01, 3.39E-01, 2.22E-01, 17.00, 15.77, 15.15, 13.21
- **2-Butene-1-d, TMS**: 5.45E-02, 3.84E-02, 3.39E-02, 4.07E-02, 3.58E-01, 3.05, 6.20, 4.72, 4.16
- **1,3-Dimethyl-2-oxo-2-(2-dimethylamino-ethoxy)-1,3,2-diazaphopholidine**: 5.91E-02, 4.06E-02, 2.31E-01, 1.71E-01, NaN, 0.12, 0.51, 0.00, 0.00
- **5,8,11,14-Eicosatetraenoic acid, ethyl ester, (all-Z)**: 6.47E-02, 4.40E-02, 4.94E-01, 2.26E-01, 4.17E-01, 30.88, 37.48, 28.15, 24.78
- **3-(3'-Trimethylsiloxypropyl)-1,1,2-tris(trimethylsilyl)cyclopropane**: 6.61E-02, 4.45E-02, 6.72E-01, 4.88E-02, 2.88E-01, 2.06, 3.36, 1.73, 2.39
- **2-Monopalmitin trimethylsilyl ether**: 6.98E-02, 4.56E-02, 1.96E-02, 2.62E-01, 3.32E-02, 24.53, 22.09, 18.93, 23.22
- **6,7-DIHYDROXYCOUMARIN-á-D-GLUCOPYRANOSIDE, PENTA-TMS**: 7.61E-02, 4.87E-02, 5.98E-01, 1.12E-01, 3.11E-02, 1.20, 2.97, 3.43, 1.59
- **Acetic acid, [(trimethylsilyl)oxy]-, trimethylsilyl ester**: 8.28E-02, 4.94E-02, 6.59E-01, 3.92E-02, 2.19E-01, 66.31, 64.99, 70.42, 76.97
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<td>1.25E-01</td>
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