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Identification of genes related to heart failure using global gene expression profiling of human failing myocardium

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ABSTRACT

Although various management methods have been developed for heart failure, it is necessary to investigate the diagnostic or therapeutic targets of heart failure. Accordingly, we have developed different approaches for managing heart failure by using conventional microarray analyses. We analyzed gene expression profiles of myocardial samples from 12 patients with heart failure and constructed datasets of heart failure-associated genes using clinical parameters such as pulmonary artery pressure (PAP) and ejection fraction (EF). From these 12 genes, we selected four genes with high expression levels in the heart, and examined their novelty by performing a literature-based search. In addition, we included four G-protein-coupled receptor (GPCR)-encoding genes, three enzyme-encoding genes, and one ion-channel protein-encoding gene to identify a drug target for heart failure using *in silico* microarray database. After the *in vitro* functional screening using adenovirus transfections of 12 genes into rat cardiomyocytes, we generated gene-targeting mice of five candidate genes, namely, *MYLK3*, *GPR37L1*, *GPR35*, *MMP23*, and *NBC1*. The results revealed that systolic blood pressure differed significantly between *GPR35*-KO and *GPR35*-WT mice as well as between *GPR37L1*-Tg and *GPR37L1*-KO mice. Further, the heart weight/body weight ratio between *MYLK3*-Tg and *MYLK3*-WT mice and between *GPR37L1*-Tg and *GPR37L1*-KO mice differed significantly. Hence, microarray analysis combined with clinical parameters can be an effective method to identify novel therapeutic targets for the prevention or management of heart failure.

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Introduction

Heart failure is a multi-factorial condition with increasing prevalence worldwide; further, a significant increase has been observed in the mortality rate and economic impact associated with this condition. In the last 20 years, substantial development of treatment for heart failure, including angiotensin-converting-enzyme inhibitors [1] and beta-blockers [2,3], has greatly improved the

prognosis of the patients with heart failure. However, despite these rapid advancements in the management of heart failure, effective treatment of end-stage heart failure without providing ventricular assistance or heart transplantation is still difficult. Investigation of new and unexplored targets for the prevention or treatment of heart failure is warranted. Global gene expression analysis using microarray technique has been used in the last decade to identify biomarkers or drug targets for heart failure [4–10]. Several gene expression signatures of heart failure have been identified by analyzing independent microarray datasets [11,12]. However, most of these analyses did not consider the severity of heart failure. Because the severity of heart failure may quantitatively reflect the expression levels of genes such as the natriuretic

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peptide-encoding gene, expression analysis combined with the severity of heart failure could be an appropriate method to identify heart failure-related genes. However, microarray analysis of genes expressed in failing myocardium while considering the severity of heart failure has not yet been reported.

Hence, we investigated the genes whose expression level correlated with clinical parameters such as pulmonary artery pressure (PAP), left ventricular ejection fraction (EF), and brain natriuretic peptide (BNP) mRNA level. Using this approach, we identified cardiac myosin light chain kinase as a novel heart failure-related gene [13]. Here, we describe newly identified several genes whose expression correlated with clinical parameters and additional genes encoding G-protein-coupled receptor genes (GPCRs), other enzymes and ion-channel proteins, and performed the functional analysis of these heart failure-related genes. This novel strategy involving the use of clinical parameters might find potential applications for the identification of disease-associated genes that could not be detected using conventional microarray techniques.

Materials and methods

Patient characteristics. We recruited 12 patients (11 males and 1 female) with heart failure and obtained written informed consent from them. The patients were diagnosed with severe chronic heart failure due to various cardiac diseases such as dilated cardiomyopathy and myocardial infarction [13]. The average age of patients was 55 ± 13 years. The plasma level of BNP, which is the best marker for the severity of heart failure, ranged from 80 to 2710 pg/ml. The mean PAP measured using a Swan–Ganz catheter 1–4 weeks before the operation varied between 16 and 59 mmHg. The average of EF determined by echocardiography on the day before the operation was $32.5\% \pm 12.4\%$.

Microarray analysis and subsequent in silico functional analysis. RNA was extracted from myocardium samples of 12 heart failure patients who had undergone either Batista or Dor surgeries. RNA samples of non-failing hearts were purchased from Biochain, Inc. Complementary RNA (cRNA) was prepared from RNA samples and hybridized to HG-U95 Affymetrix GeneChip (Affymetrix, US). The expression data were analyzed using Microarray Analysis Suite version 5.0 software. Among all the genes detected on the microarray, we selected the genes whose expression was significantly different in the failing and non-failing myocardial samples ($p < 0.005$). From these genes, we selected genes whose expression was correlated with PAP, EF, and BNP mRNA level, with 0.7 being the cutoff value of the correlation coefficient. The values of PAP, EF, and BNP mRNA level used for the correlation analysis were normalized to their median during the measurements. Subsequently, the functional analysis of datasets was performed using Ingenuity Pathway Analysis (Ingenuity® Systems; www.ingenuity.com), and the biological functions most significant to the dataset were identified.

Cell culture. Cardiomyocytes were harvested before the experiments from 2- to 3-day-old neonatal rats and cultured as described in previous studies [14]. Briefly, primary cardiomyocytes isolated from neonatal rats were grown in Dulbecco's modified Eagle medium/F12 (Gibco) supplemented with 10% fetal calf serum for 72 h, and then cultured in a serum-free condition for 24 h.

Adenovirus generation and transfection. Adenovirus constructs encoding the genes of interest were generated using the ViraPower Adenoviral Expression System (Invitrogen, US) according to the manufacturer's method. Adenovirus vectors were transfected to cultured cardiomyocytes for 12 h according to the published protocol.

In vitro functional analysis of genes. Cultured rat cardiomyocytes were infected by adenovirus vectors. After 24 h, hypertrophic

reaction, cell viability, and cellular morphology were assessed. Hypertrophic reaction was determined by estimating the incorporation of [³H]phenylalanine. In brief, [³H]phenylalanine was added to the culture medium at the final concentration of 0.1 μCi/ml, and the cells were incubated for an additional 24 h. Then, the incorporation of [³H]phenylalanine was determined by counting the radioactivity of each sample with a liquid scintillation counter. The viability of cardiomyocytes was evaluated by the Alamar blue assay according to the manufacturer's method. The morphology of cardiomyocytes was evaluated 24 h after adenovirus transfections.

Generation of transgenic and knockout mice. To generate transgenic mice, open reading frame of each gene, namely, *Mylk3*, *Gpr3711*, or *Nbc1* was amplified from mouse cDNA by PCR, with Sal I site linker on each end, and cloned into Sal I site of alpha-MHC clone 26 vector. Then the DNAs used in the microinjections were released from the vector by digestion with NotI and were microinjected into fertilized eggs of mouse. Founder mice were identified by PCR analysis with appropriate primers. To develop *Gpr3711* knockout mice, the targeting vector was assembled to replace the exon 1 and 2 by neomycin selection cassette resulting in the absence of *Gpr3711* protein. W9.5 ES cells were electroporated with linearized targeting vector. ES cell clones with successful homologous recombination was determined by the PCR and subsequent direct sequence. From these targeted ES cells, the chimera mice were bred to C57 BL/6 females to generate F1 and F2 offsprings were obtained. The *Gpr3711* null mice were determined by PCR genotyping of F2 offsprings. The knockout mice of *Gpr35* and *Mmp23* (the mouse ortholog of MMP23B) were purchased from Deltagen, Inc. (California, US).

Invasive blood pressure measurement. The phenotype of the gene-targeted mice was examined. Before sacrificing the mice, their hemodynamic parameters were evaluated. The mice were anesthetized and ventilated, and a Millar catheter was inserted via right carotid artery. The left-ventricular systolic and end-diastolic pressures were measured. Then, the mice were sacrificed and the weight of the whole body and heart was determined.

Statistical analysis. Unpaired Student's *t*-test was used for comparing the two groups. Results are expressed as means \pm SEM, and *p* value less than 0.05 was considered statistically significant.

Results

Identification of heart failure-related genes by expression analysis using clinical parameters

We performed microarray analysis of the genes expressed in failing myocardium obtained from 12 patients with heart failure and the genes expressed in non-failing myocardium from two normal objects whose characteristics were reported in the previous study [13]. Although all patients were diagnosed with chronic heart failure, the plasma BNP level, which is an index of the severity of heart failure, ranged from 80 to 2710 pg/ml, suggesting that the severity of heart failure varied extensively among the patients. This marked difference in the severity of heart failure reflects the fact that the gene expression patterns in the 12 patients were not uniform, as shown in Fig. 1A. Thus, we analyzed gene expression profiles of failing myocardium using clinical parameters representing the severity of heart failure. We identified 166 and 194 genes whose expressions were correlated with PAP and BNP mRNA level, respectively (Fig. 1B and Supplementary Tables S1, S2). Among these, 49 genes correlated with both PAP and BNP mRNA level (Fig. 1C). The expression of only two genes, namely, *FMO2* and *LMAN1L*, correlated with the EF. We investigated the functional categories of these genes by performing Ingenuity Pathway Analysis. The number of genes in each group, functional categories, and

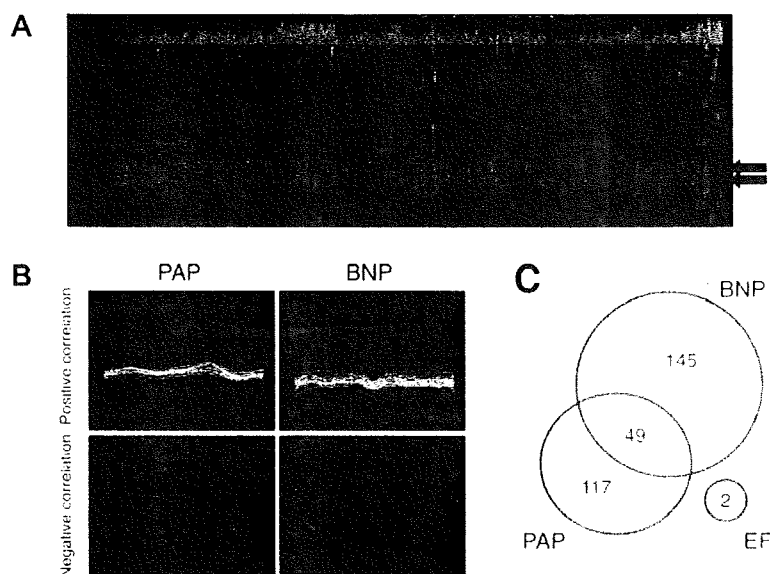


Fig. 1. The gene expression profile of human failing or non-failing myocardium. Gene expression levels of myocardial samples from 12 patients with severe heart failure and from two normals were analyzed using microarray. (A) Heat maps showing the genes with differential expression between the 12 failing myocardial samples and the two non-failing myocardial samples. Red color indicates upregulated gene expression. Green color indicates downregulated gene expression. Arrows indicate non-failing samples. (B) Expression profile of positively or negatively correlated genes to pulmonary artery pressure (PAP) or brain natriuretic peptide (BNP) mRNA level ($r > 0.7$). (C) Venn diagram of genes correlated with PAP, BNP, and ejection fraction.

Table 1
Datasets of genes whose expressions were correlated to clinical parameters.

	PAP	EF	BNP mRNA level
<i>Positive correlation</i>			
Number	124	1	175
Function	Cardiovascular system development and function Cell death	-	Cardiovascular system development and function Cell cycle
Representative genes	<i>ARNT, MYOCD, SMARCA4</i> <i>BGN, CFLAR, EEF2, MTPN</i>	<i>LMAN1L</i>	<i>BTG1, NPPA, NPPB, SERPNI</i> <i>CKS1B, DDR2, FCGR2B, FN1</i>
<i>Negative correlation</i>			
Number	42	1	19
Function	Skeletal and muscular system development and function Cellular assembly and organization	-	Skeletal and muscular system development and function Cellular assembly and organization
Representative genes	<i>PIK3R1, PRKARIA, SLMAP</i> <i>C19ORF20, RAB9A, SYNGAPI, TTN</i>	<i>FMO2</i>	<i>ACTC1, RBBP4, TTN</i>

The function of gene sets was analyzed by Ingenuity Pathway Analysis.
PAP, pulmonary artery pressure; EF, ejection fraction; BNP, brain natriuretic peptide.

representative genes are shown in Table 1. Interestingly, both gene sets correlated positively with PAP and BNP mRNA level were most associated with the same functional category of "cardiovascular system development and function", although the included genes were different. Similarly, the gene sets correlated negatively with both PAP and BNP mRNA level had most association with common functional categories of "skeletal and muscular system development and function" and "cellular assembly and organization".

Selection of 12 genes for *in vitro* screening

Among the genes selected using clinical parameters, we selected those genes that showed high expression levels in the heart by performing microarray analysis. On the basis of their novelty determined by a literature-based search, we selected four genes for further investigation (Table 2). Concurrently, to identify possible drug targets, we included four orphan GPCRs and four additional genes (three enzyme-encoding genes and one ion-channel protein-encoding gene) in the further analysis. The *RHOQ* and

STK38 genes were selected based on their correlation with BNP mRNA level and PAP, respectively. *GPR161* and *NBC1* were selected owing to their high expression level in the heart. *GPR37L1*, *GPR35*, *F2RL2*, and *MMP23B* were selected because of their high expression level in the heart, and their association with the cardiac diseases-related genes listed in the database was determined by *in silico* analysis.

Functional analysis of genes on the basis of adenovirus-mediated overexpression of proteins in neonatal rat cardiomyocytes

To determine which of the selected genes were associated with the physiological functions of the heart, we first generated adenovirus vectors for each gene listed in Table 2 and transfected these vectors into neonatal rat cardiomyocytes. Next, we evaluated the hypertrophic reaction, viability, and morphology of the transfected cardiomyocytes. Among the 12 selected genes, three adenovirus-mediated genes decreased the incorporation of [^3H]phenylalanine in neonatal rat cardiomyocytes (Table 2); the expression of one

Table 2
In vitro functional screening of the 12 candidate genes.

Probe set ID	Gene symbol	Gene name	Criteria for selection	<i>p</i> value	[³ H]PA intake	Fluorescence of Alamar blue	Cellular morphology
<i>Genes relevant to clinical parameters</i>							
75678_at	MYLK3	Myosin light chain kinase 3	Correlation with PAP (<i>r</i> = 0.792)	0.00262	No change	No change	Spiking
49333_at	XPR1	Xenotropic and polytropic retrovirus receptor	Correlation with PAP (<i>r</i> = 0.765), GPCR, change in CHF	0.00045	No change	No change	No change
38435_at	PRDX4	Peroxisiredoxin 4	Correlation with BNP (<i>r</i> = 0.863)	0.00024	Increased	Decreased	No change
45314_at	SMOC2	SPARC related modular calcium binding 2	Correlation with both PAP and BNP (<i>r</i> = 0.715 and 0.758, respectively)	0.00444	No change	No change	No change
<i>Genes encoding orphan GPCRs</i>							
35544_at	GPR37L1	G-protein-coupled receptor 37 like 1	Orphan GPCR, downregulated in CVD	>0.005	Decreased	Decreased	Apoptosis
31700_at	GPR35	G-protein-coupled receptor 35	Orphan GPCR, upregulated in MI	0.00216	Decreased	Decreased	Hypertrophy
45204_at	F2RL2	Coagulation factor II (thrombin) receptor-like 2	GPCR, change in CVD	>0.005	Increased	No change	No change
40299_at	GPR161	G-protein-coupled receptor 161	GPCR, expression in heart	>0.005	Decreased	Decreased	No change
<i>Genes encoding interesting enzymes or ion-channels</i>							
38950_at	MMP23B	Matrix metalloproteinase 23B	Family of MMP, change in CHF	>0.005	No change	Decreased	No change
35285_at	NBC1	Na ⁺ -HCO ₃ ⁻ cotransporter 1	Expression in heart	>0.005	No change	Decreased	No change
87788_at	RHOQ	Ras homolog gene family, member Q	Expression in DCM, correlation with BNP (<i>r</i> = 0.711)	>0.005	No change	No change	No change
78801_at	STK38	Serine/threonine kinase 38	Kinase activity, correlation with PAP (<i>r</i> = 0.736)	>0.005	No change	No change	No change

PAP, pulmonary artery pressure; GPCR, G-protein-coupled receptor; CHF, congestive heart failure; BNP, brain natriuretic peptide; CVD, cardiovascular disease; MI, myocardial infarction; DCM, dilated cardiomyopathy; PA, phenylalanine. *p* value indicates the significance of the difference between the gene expression level of failing and non-failing myocardium.

gene promoted [³H]phenylalanine incorporation; and the overexpression of six genes lowered the viability of cardiomyocytes, which was evaluated by Alamar blue assay. We also evaluated the phenotype of transfected cardiomyocytes. Unlike control cells, MYLK3-adenovirus-transfected cardiomyocytes were spike shaped. The overexpression of GPR37L1 induced apoptosis of cardiomyocytes. The transfection of NBC1-adenoviral vectors modified the beating rate of cardiomyocytes (data not shown). Then, we analyzed each gene that encoded a distinct cardiomyocyte phenotype by developing gene-targeted mouse models.

In vivo analysis using transgenic and knockout mice

To study the *in vivo* role of the selected genes, we developed genetically modified mice: three transgenic (Tg) mice for *Mylk3*, *Gpr37l1*, or *Nbc1* and three knockout (KO) mice for *Gpr37l1*, *Gpr35*, or *Mmp23*. We estimated hemodynamic parameters using Miller catheter and the heart weight (HW)/body weight (BW). As shown in Fig. 2A, we found that the blood pressure of *Gpr37l1*-KO mice was significantly higher than that of *Gpr37l1*-Tg mice by 61.7 mmHg (*p* < 0.01). Further, the blood pressure of *Gpr35*-KO mice was higher than that of wild type (WT) littermate by 37.5 mmHg (*p* < 0.01). Overexpression with or knockout of *Mylk3*, *Mmp23*, or *Nbc1* did not result in a significant change in the systolic blood pressure. The HW/BW of *Mylk3*-Tg mice was lower than that of *Mylk3*-WT mice (Fig. 2B). The HW/BW was higher in *Gpr37l1*-KO mice than in *Gpr37l1*-Tg mice. The HW/BW in mice with *Nbc1*, *Gpr35*, or *Mmp23* manipulations did not show any difference. These data showed that modification of *Gpr37l1*, *Gpr35*, or *Mylk3* can produce a distinct cardiovascular phenotype *in vivo*.

Discussion

The present study identified heart failure-related genes using a novel strategy that was different from the conventional microarray analysis approach. Firstly, we constructed global gene expression profiles to analyze the gene expression in 12 human samples of failing myocardium and two samples of non-failing myocardium. Secondly, we prepared datasets of heart failure-related genes asso-

ciated with the severity of heart failure; this approach is unique to our study and has not been published before. Thirdly, we selected four genes from these datasets by microarray analysis and a literature-based search. We also included four orphan GPCR genes and four other genes with high expression in the heart as possible drug targets for heart failure treatment. Fourthly, we screened the *in vitro* functions of these 12 genes by achieving adenovirus-mediated overexpression of these genes in rat cardiomyocytes. Finally, we generated gene-targeted mouse models of the five selected genes and screened the *in vivo* functions of these genes. Our novel strategy using a microarray analysis revealed three potential targets, namely, MYLK3, GPR37L1, and GPR35 for diagnosing and managing heart failure.

End-stage heart failure caused by a variety of cardiovascular diseases including hypertension, cardiomyopathy, and ischemic heart disease features a common phenotype of reduced cardiac function and dilated cardiac chamber. This result strongly suggested the existence of common genes during the development of heart failure, including the genes encoding natriuretic peptides. To identify novel diagnostic or therapeutic targets for heart failure, such as natriuretic peptides, several microarray analyses of genes expressed in failing myocardium have been performed in the last decade by comparing the gene expression levels between different pairs of samples, such as non-failing versus failing hearts [4–6], failing hearts before versus after placement of left-ventricular assisting device [7,8], hypertrophic versus failing hearts [9], ischemic versus non-ischemic hearts [10]. However, the severity of heart failure is not fixed, but varies from mild to severe heart failure in these studies. To identify the therapeutic targets for heart failure effectively, we believe that it is important to consider the severity of heart failure with microarray data analysis. In this study, we prepared new datasets of heart failure-associated genes that were selected from gene expression profiles of 12 human failing myocardial samples using clinical parameters. A number of genes were associated with PAP, which is an index for the severity of heart failure, whereas only two genes correlated with EF, which is an index for cardiac contractility. This result implies that the stress caused to the heart, and not the ability of cardiac contraction, regulates gene expression in heart failure. We also selected heart failure-related genes whose expression correlated to

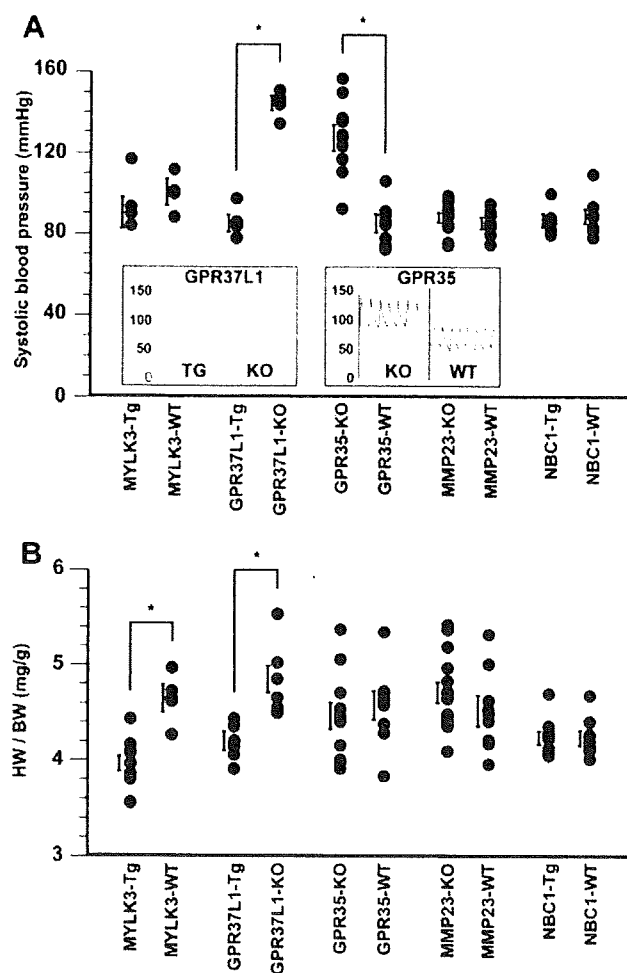


Fig. 2. *In vivo* functional analysis using gene-targeting mice of the *Mylk3*, *Gpr37l1*, *Gpr35*, *Mmp23*, and *Nbc1* genes. Blood pressure and heart weight (HW)/body weight (BW) of transgenic (Tg), knockout (KO) and their wild type (WT) littermate mice of each gene were investigated. Values are means \pm SEM. * $p < 0.01$. (A) Systolic blood pressure measured using Millar catheter inserted via right carotid artery. The monitoring chart shows representative data of *Gpr37l1*- and *Gpr35*-manipulated mice. (B) HW/BW ratio of each gene-targeting mouse.

the BNP mRNA level, which is the best known indicator of heart failure. The approach used in our study can help in efficient identification of the diagnostic or therapeutic targets for heart failure rather than only comparing two types of samples such as failing versus non-failing myocardium. Among the genes from these new datasets, we focused on the genes exhibiting high expression in heart tissues and finally selected four genes for performing the screening of functional analysis *in vitro*. The expression level of *MYLK3* gene was highly correlated to PAP, and this gene was detected only in the heart tissue. Recently, we reported that *MYLK3* plays a crucial role in sarcomere assembly via phosphorylation of myosin regulatory light chain 2V (MLC2v) [13]. We also showed that the knockdown of *MYLK3* by using a morpholino oligo caused immature sarcomere formation leading to ventricular dilation in zebrafish. These results indicate that *MYLK3* is strongly associated with the pathophysiology of heart failure. Chan et al. also reported that *MYLK3* phosphorylates MLC2v and regulates sarcomere organization [15]. These reports affirm the reliability of our original strategy that involves the microarray analysis of failing myocardium. Among these genes, most genes including *XPR1*, *PRDX4*, and *SMOC2* have not been reported to link with cardiovascular

phenotypes and were not included in many gene expression profiles published previously.

Next, we performed *in vivo* functional analysis of five selected genes, and we found that gene-targeted mouse models of *Mylk3*, *Gpr37l1*, or *Gpr35* showed the cardiovascular phenotype. As described above, *Mylk3* plays a crucial role in failing heart. In this study, we identified two GPCRs, namely, *Gpr37l1* and *Gpr35*, whose modification affects systolic blood pressure or HW/BW. To our knowledge, this is the first report about the role of these genes in cardiovascular system.

GPCRs constitute one of the largest protein families, but many GPCRs remain to be orphaned. GPR35 is now known to have some ligands such as kynurenic acid (KYNA) [16], zaprinast [17], and 5-nitro-2-(3-phenylpropylamino) benzoic acid [18]. These agonists mobilize intracellular calcium concentration. Therefore, lowering systolic blood pressure in *Gpr35*-KO mice can be induced by modulating calcium release from calcium-storing organelles. Among the three agonists, only KYNA is produced endogenously as a metabolite of tryptophan. Although GPR35 gene expression is supposed to be specific to immune cells and gastrointestinal tract, we found that GPR35 gene expression increased in failing myocardium. In an inflammatory state, interferon γ induces indoleamine 2,3-dioxygenase, a rate-limiting enzyme involved in tryptophan degradation, resulting in a substantial increase in KYNA. Inflammation is thought to be involved in the pathogenesis of dilated cardiomyopathy as well as myocardial infarction. Hence there is a possibility that a KYNA-GPR35 signaling plays a role in the pathogenesis of cardiovascular diseases.

Unlike GPR35, GPR37L1 is still orphaned. However, we found that *Gpr37l1*-KO mice showed significant high blood pressure and high HW/BW as compared to Tg mice, which implies the existence of cardiovascular-related function of *Gpr37l1*. Identification of the ligand and the function of this orphan receptor are awaited.

Although no significant phenotype was observed in *Mmp23* and *Nbc1*-Tg mice, we have been investigating their cardiac function in pathological condition such as myocardial infarction or hypertension and determined their detrimental effect on heart failure (data not shown).

In the present study, we determined 12 novel heart failure-related genes by integrating an original method with parameters that indicated disease severity. Further, we assessed these possible targets of drug discovery. *MYLK3*, *GPR37L1*, and *GPR35* were the newly identified targets that play an interesting role in the cardiovascular system.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.bbrc.2010.01.076.

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Natriuretic Peptides Enhance the Production of Adiponectin in Human Adipocytes and in Patients With Chronic Heart Failure

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Objectives	We investigated the functional relationship between natriuretic peptides and adiponectin by performing both experimental and clinical studies.
Background	Natriuretic peptides are promising candidates for the treatment of congestive heart failure (CHF) because of their wide range of beneficial effects on the cardiovascular system. Adiponectin is a cytokine derived from adipose tissue with various cardiovascular-protective effects that has been reported to show a positive association with plasma brain natriuretic peptide (BNP) levels in patients with heart failure.
Methods	The expression of adiponectin messenger ribonucleic acid (mRNA) and its secretion were examined after atrial natriuretic peptide (ANP) or BNP was added to primary cultures of human adipocytes in the presence or absence of HS142-1 (a functional type A guanylyl cyclase receptor antagonist). Changes of the plasma adiponectin level were determined in 30 patients with CHF who were randomized to receive intravenous ANP (0.025 $\mu\text{g}/\text{kg}/\text{min}$ human ANP for 3 days, $n = 15$) or saline ($n = 15$).
Results	Both ANP and BNP dose-dependently enhanced the expression of adiponectin mRNA and its secretion, whereas such enhancement was inhibited by pre-treatment with HS142-1. The plasma adiponectin level was increased at 4 days after administration of human ANP compared with the baseline value (from $6.56 \pm 0.40 \mu\text{g}/\text{ml}$ to $7.34 \pm 0.47 \mu\text{g}/\text{ml}$, $p < 0.05$), whereas there was no change of adiponectin in the saline group (from $6.53 \pm 0.57 \mu\text{g}/\text{ml}$ to $6.55 \pm 0.56 \mu\text{g}/\text{ml}$).
Conclusions	Natriuretic peptides enhance adiponectin production by human adipocytes in vitro and even in patients with CHF, which might have a beneficial effect on cardiomyocytes in patients receiving recombinant natriuretic peptide therapy for heart failure. (J Am Coll Cardiol 2009;53:2070-7) © 2009 by the American College of Cardiology Foundation

Plasma natriuretic peptide levels are increased in patients with congestive heart failure (CHF), and the measurement of these peptides is used widely to assess the presence,

severity, and prognosis of CHF (1,2). Both atrial natriuretic peptide and brain natriuretic peptide (ANP and BNP, respectively) have a beneficial effect in patients with heart failure because of their various biological actions (3-5).

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Adiponectin is a circulating cytokine derived from adipose tissue that has attracted considerable interest because of its identification as a risk factor for cardiovascular disease (6,7) and CHF (8). Adiponectin production is down-regulated in patients with coronary risk factors that are associated with the development of heart failure (9,10).

Recently, adiponectin was reported to have a cardioprotective effect against ischemia-reperfusion injury (11) and hemodynamic stress (12,13) in mice. Interestingly, it has been reported that the level of N-terminal pro-brain natriuretic peptide shows a positive correlation with the plasma adiponectin concentration in patients with chronic heart failure (14).

Given these experimental and clinical observations, we hypothesized that natriuretic peptides might increase adiponectin production in patients with heart failure to protect the cardiovascular system. Accordingly, in the present study, we investigated whether natriuretic peptides could directly increase adiponectin production by these adipocytes (and the cellular mechanisms involved) and confirmed this effect on adiponectin in the clinical setting.

Methods

Agents. Both human ANP and BNP were purchased from Sigma-Aldrich (St. Louis, Missouri). HS142-1, a functional guanylyl cyclase-A type receptor antagonist, was provided by Kyowa Hakko Kogyo Co., Ltd. (Mishima, Japan). A cGMP analog (8-pCPT-cGMP) and a selective cGMP-dependent protein kinase G (PKG) inhibitor (R_p -8-Br-PET-cGMP-S) were obtained from Biolog Life Science Institute (Bremen, Germany). An antibody directed against mouse adiponectin (MAB3608) was purchased from Chemicon International, Inc.

Primary culture and in vitro study of human adipocytes. Subcutaneous adipocytes derived from the adipose tissue of 6 women were obtained commercially together with culture medium from Zen-Bio, Inc. (Research Triangle Park, North Carolina). The donors were nonsmokers with a mean body mass index of 27.0 kg/m² (range 25.9 to 29.1 kg/m²) and an average age of 47 years (range 29 to 63 years). Cells were maintained in adipocytes maintenance medium (i.e., AM-1) containing Dulbecco's modified Eagle medium/Ham's F-12 (1:1, v/v), 3% fetal calf serum, 15 mmol/l HEPES (pH 7.4), biotin, pantothenate, human insulin, 1 μ mol/l dexamethasone, 100 U/ml penicillin, 100 μ g/ml streptomycin, and 0.25 μ g/ml amphotericin B at 37°C in a humidified atmosphere of 95% air/5% CO₂. The medium was changed every 2 days. Primary cultures of the adipocytes were used to examine the effects of natriuretic peptides (ANP or BNP) on the expression of adiponectin.

Before these experiments, the cells were plated in adipocyte basal medium (i.e., BM-1) containing Dulbecco's modified Eagle medium/Ham's F-12 (1:1, volume/volume), 15 mmol/l 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid (pH 7.4), biotin, and pantothenate for 24 h. Then the indicated concentrations of either natriuretic peptide (from 10⁻¹¹ to 10⁻⁹ mol/l) were added to the BM-1 medium. After 24 h of incubation, the medium was harvested for Western blotting to measure the secretion of adiponectin, and the cells were also harvested for ribonucleic acid (RNA) analysis. The effect of each natriuretic peptide on adiponectin messenger ribonucleic acid (mRNA) levels

was determined by quantitative real-time polymerase chain reaction (PCR).

Measurement of adiponectin. In patients with CHF, the plasma adiponectin concentration was measured by the use of an ELISA kit (Otsuka Pharmaceutical Co., Ltd., Tokyo, Japan) according to the manufacturer's protocol. Adiponectin secretion by primary cultured human adipocytes was assessed by Western blotting of the culture medium, as previously described (15), and the immunoreactive bands were quantified by densitometry (Molecular Dynamics, Sunnyvale, California).

Reverse transcriptional-PCR. Total RNA was extracted from adipocytes derived from human white fat with the use of RNA-Bee-RNA Isolation Reagent (Tel-Test, Inc., Gainesville, Florida). Then, 200 ng of total RNA was reversed transcribed and amplified by the use of an Omniscript RT kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol. The forward primers for type A guanylyl cyclase receptor (GC-A) and natriuretic peptide receptor (NPR)-C were 5'-CCAGTTCCAAGTCTTTGCCAA-GACAGCA and 5'-GGAAGACATCGTGCGCAATA, respectively, and the reverse primers for GC-A and NPR-C were 5'-CATTGTGTAGAAACAGCATGCCCTTGACGA and 5'-TGCTCCGGATGGTGTCACT, respectively. As a positive control, we used the samples of human cardiac tissue under the protocol approved by the institutional review board of the National Cardiovascular Center (No. 14-18) (16).

Quantitative real-time PCR analysis. Quantitative real-time PCR was performed as described previously (17). Oligonucleotide primers and TaqMan probes for human adiponectin and glyceraldehyde 3-phosphate dehydrogenase were purchased from Applied Biosystems (Foster City, California).

Subjects and design of the clinical study. We prospectively studied 30 consecutive CHF patients who were admitted to the emergency department of the National Cardiovascular Center between April and July 2006. The exclusion criteria were as follows: age >80 years, cardiogenic shock or hypotension (systolic blood pressure <100 mm Hg), and renal failure (serum creatinine >2.0 mg/dl). This study was approved by the Committee on Human Investigation of the National Cardiovascular Center, and all patients who participated gave informed consent. The 30 patients were randomized to 2 groups, a human atrial natriuretic peptide (hANP) group consisting of 15 patients who received administration of hANP and a control group consisting of 15 patients who were administered saline. In the hANP group, from immediately after the diagnosis of

Abbreviations and Acronyms

ANP = atrial natriuretic peptide

BNP = brain natriuretic peptide

CHF = congestive heart failure

GC-A = type A guanylyl cyclase receptor

hANP = human atrial natriuretic peptide

NPR = natriuretic peptide receptor

PKG = protein kinase G

acute exacerbation of CHF, hANP (0.025 $\mu\text{g}/\text{kg}/\text{min}$) was infused intravenously for 3 days. The study protocol did not restrict or specify any other diagnostic or therapeutic strategies. Blood for measuring the plasma adiponectin level was sampled before and 1 and 7 days after finishing the administration of hANP or saline (days 1, 4, and 10, respectively) (Fig. 3A).

Statistical analysis. For analysis of differences between the various treatments of adipocytes, analysis of variance was performed, followed by the appropriate post-hoc test. The differences in adiponectin levels between days 1 and 4 in each group were tested with a paired *t* test. The changes in adiponectin levels from day 1 to 4 between ANP group and saline group was tested with an unpaired *t* test. Results are expressed as the mean \pm SEM, and *p* values of <0.05 were considered significant.

Results

Effect of natriuretic peptides on the expression and secretion of adiponectin by primary cultured human adipocytes. First, we checked the expression of GC-A and NPR-C mRNA by using reverse transcriptional-PCR. As shown in Figure 1A, both GC-A and NPR-C mRNA was detectable in primary cultured human adipocytes. To investigate the effects of natriuretic peptides on the regulation of adiponectin production in adipocytes, we incubated primary cultured human adipocytes with recombinant ANP. When ANP was used at a concentration of 10^{-10} mol/l (pathological plasma concentration), it increased adiponectin mRNA expression after 6 h of incubation and reached a maximum after 12 h (Fig. 1B). Next, we incubated human adipocytes with ANP at the concentration of 10^{-11} mol/l (normal plasma concentration) to 10^{-9} mol/l (pharmacological plasma concentrations) and demonstrated enhanced adiponectin mRNA expression and adiponectin secretion into the medium in a dose-dependent manner, whereas these changes were completely inhibited by pretreatment with HS142-1 (Figs. 1C and 1D). Incubation of adipocytes with BNP also increased the expression of adiponectin mRNA in a dose-dependent manner and this effect was completely blocked by pretreatment with HS142-1 (Figs. 1E and 1F).

Involvement of cGMP/PKG signaling in natriuretic peptide-induced synthesis of adiponectin. Because both ANP and BNP exert their biological effects by promoting cGMP production, to investigate the role of the GC-A/cGMP/PKG signaling pathway in adiponectin production, we measured the changes of cGMP in ANP-treated primary cultured human adipocytes. We found that incubation with ANP increased the cGMP level and that this effect was blunted by co-treatment with HS142-1 (data not shown). Next, we treated human adipocytes with the cGMP analog 8-pCPT-cGMP and the PKG inhibitor (R_p)-8-Br-PET-cGMP-S. The activation of PKG by 8-pCPT-cGMP (50 $\mu\text{mol}/\text{l}$ for 12 h) produced an increase of adiponectin

mRNA expression similar to that observed after incubation with ANP. The effect of ANP on adiponectin mRNA expression was abolished in the presence of (R_p)-8-Br-PET-cGMP-S (100 nmol/l) (Fig. 2A). Consistent with these findings, adiponectin secretion into the culture medium also was increased by stimulation of the cGMP/PKG-dependent pathway (Fig. 2B). These results suggested that natriuretic peptides promote adiponectin synthesis via the GC-A/cGMP/PKG-dependent pathway.

Increase of plasma adiponectin levels in CHF patients treated with hANP. To confirm the effect of natriuretic peptides on the production of adiponectin, we conducted the clinical study. Thirty consecutive patients who met the inclusion criteria were enrolled in this clinical study. Fifteen patients were randomized to the ANP group, and 15 were assigned to the saline group. Baseline variables and treatments of the 2 groups are shown in Table 1. There were no differences in baseline clinical characteristics, hemodynamics, biochemical data, or medications. There was also no significant difference in the baseline plasma level of adiponectin between the 2 groups. As shown in Figure 3B, the plasma level of adiponectin did not change throughout the study in the saline group. On the other hand, the plasma adiponectin level at 1 day after finishing the administration of hANP (day 4) was significantly increased compared with the baseline value (day 1) in the ANP group, and it returned to baseline by 7 days after the completion of hANP infusion (day 10). These results suggested that hANP infusion led to an increase of the plasma adiponectin level in patients with CHF.

Discussion

In the present study, we demonstrated a novel effect of natriuretic peptides (ANP and BNP) on the production of adiponectin by adipocytes in both experimental and clinical studies. First, we clearly demonstrated that pathophysiological and pharmacological concentrations of either ANP or BNP increased adiponectin synthesis by primary cultured human adipocytes. Second, we showed that administration of recombinant ANP increased the plasma adiponectin level in patients with CHF.

ANP and BNP play an important role in the regulation of cardiovascular homeostasis. Their actions are primarily mediated via GC-A, which is expressed in various tissues and organs, including the kidneys, blood vessels, adrenal glands, and heart (18). Consistent with a previous report (19), we demonstrated that GC-A and NPR-C are expressed by human adipocytes. In the present study, we demonstrated a novel effect of both ANP and BNP on primary cultured human adipocytes, which was that pathophysiological or pharmacological concentrations of both peptides augmented adiponectin production by human adipocytes, with this effect being inhibited by treatment with HS142-1. Furthermore, we demonstrated that natriuretic peptides augment the production of adiponectin via a cGMP-dependent

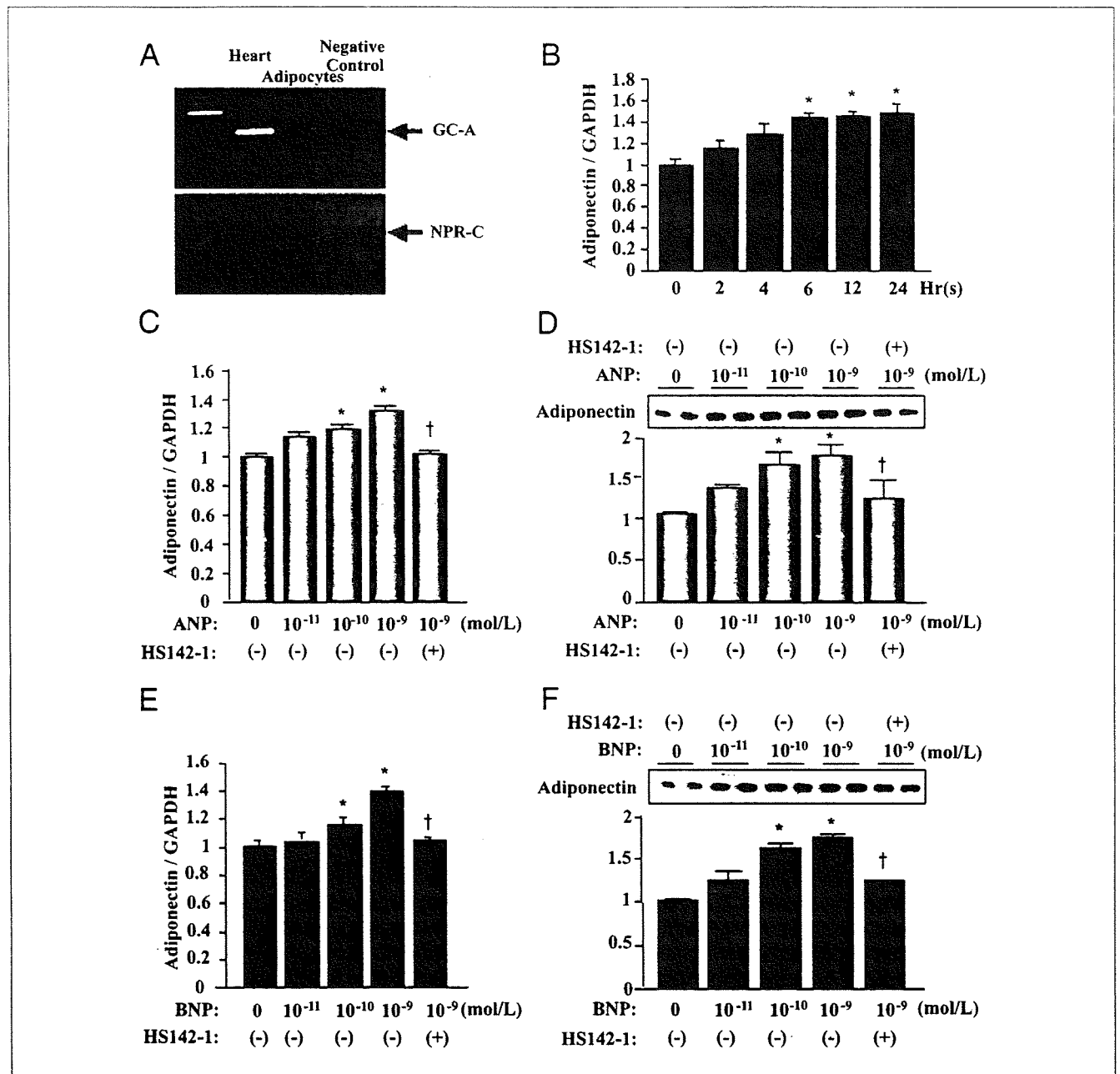


Figure 1 Effect of Natriuretic Peptides on the Expression and Secretion of Adiponectin by Primary Human Adipocytes

(A) Expression of GC-A receptors (top) and NPR-C (bottom) mRNA by primary cultured human adipocytes. Reverse-transcription PCR revealed expression of both GC-A receptors and NPR-C by human adipocytes. (B) Effect of ANP (10⁻¹⁰ mol/l) on the expression of adiponectin mRNA as determined by quantitative real-time PCR. (C) Dose-dependent effect of ANP on adiponectin mRNA expression, as determined by quantitative real-time PCR. Human adipocytes were treated with the indicated concentrations of ANP for 24 h. (D) Dose-dependent effect of ANP on adiponectin secretion into the culture medium. (Top) A representative Western blot of adiponectin. (Bottom) Quantitative analysis of adiponectin by densitometry. Values are normalized to the control. *p < 0.05 versus control, †p < 0.05 versus ANP 10⁻⁹ mol/l. (E) Dose-dependent effect of BNP on adiponectin mRNA expression, as determined by quantitative real-time PCR. (F) Dose-dependent effect of BNP on adiponectin secretion into the culture medium as determined by Western blotting. (Top) Representative Western blot of adiponectin. (Bottom) Quantitative analysis of adiponectin by densitometry. Values are normalized to the control. *p < 0.05 versus control, †p < 0.05 versus BNP 10⁻⁹ mol/l. ANP = atrial natriuretic peptide; BNP = brain natriuretic peptide; GC-A = type A guanylyl cyclase receptor; mRNA = messenger ribonucleic acid; NPR-C = natriuretic peptide receptor C; PCR = polymerase chain reaction.

pathway. These findings are important evidence that ANP and BNP regulate adiponectin production by human adipocytes.

Intravenous infusion of nesiritide (recombinant human BNP) has been reported to have beneficial hemodynamic

effects in patients with CHF (4,5). The use of ANP also has been reported to have beneficial effects in patients with acute myocardial infarction (20,21). These beneficial effects have been attributed to the cardiovascular-protective actions of natriuretic peptides, including diuresis, natriuresis, vaso-

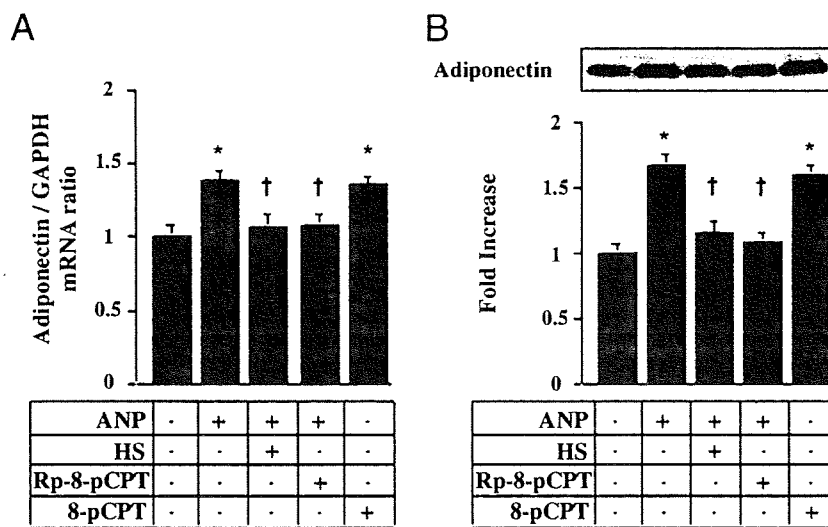


Figure 2 Involvement of the cGMP/PKG Signaling Pathway in the Induction of Adiponectin Synthesis by ANP

(A, B) Involvement of PKG was assessed by the treatment of primary cultured human adipocytes with 8-pCPT-cGMP (8-pCPT) and (Rp)-8-Br-PET-cGMP-S (Rp-8-pCPT). Adiponectin mRNA levels were determined by quantitative real-time PCR (A) and secretion of adiponectin into the culture medium was determined by Western blotting. Quantitative analysis of adiponectin secretion into the culture medium was done by densitometry (B). Values are normalized to the control. *p < 0.05 versus control. †p < 0.05 versus ANP. HS = HS142-1; other abbreviations as in Figure 1.

dilation, and reduction of activity of the sympathetic nervous system and the renin-angiotensin-aldosterone system (3-5). In the present study, we administered recombinant ANP to patients with CHF and observed the changes of plasma adiponectin. The plasma adiponectin level of the ANP group was increased at 1 day after the finish of ANP administration compared with that in the control group, and then returned to baseline by 7 days after the completion of administration in patients with CHF.

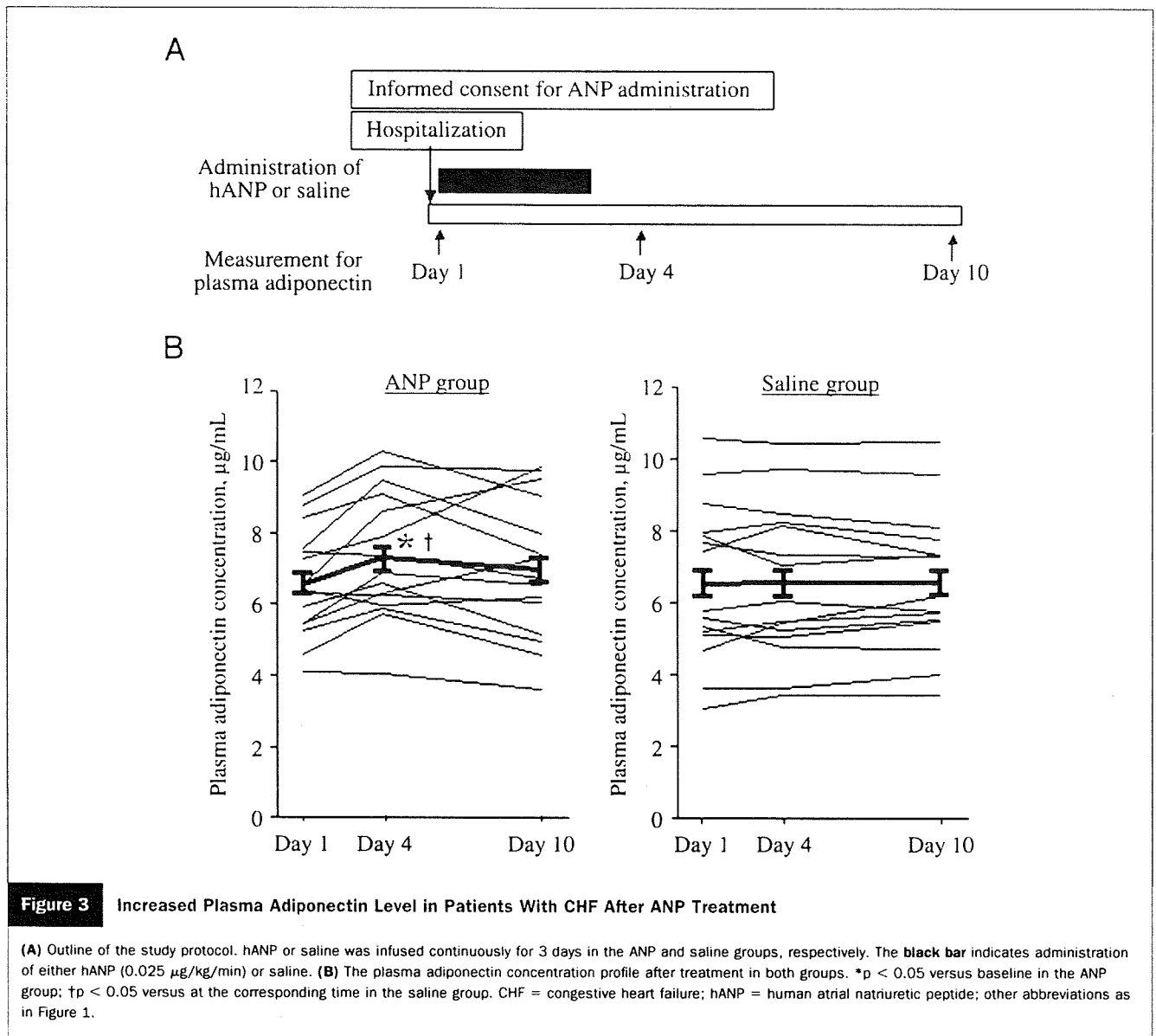
Importantly, Moro et al. (22) showed that ANP did not affect the secretion of adiponectin in human abdominal

adipose tissue from overweight women. This result may appear contradict ours, but we believe that is not the case. First, the concentration of ANP they used (10^{-6} mol/l) in the experiment of cultured adipocytes was greater than our concentration. Second, our data that recombinant ANP increased the plasma adiponectin levels were drawn from patients with heart failure, whereas the data of Moro et al. (22) were from cultured fat tissues of overweight women who underwent plastic surgery. However, they also demonstrated the potential stimulatory effect of ANP on adiponectin production from human adipose tissue in the presence of

Table 1 Clinical Characteristics of the 2 Groups

	hANP Group (n = 15)	Saline Group (n = 15)	p Value
Age (yrs)	60 ± 19	59 ± 19	NS
Sex (male/female)	9/6	10/5	NS
Heart rate (beats/min)	62 ± 11	66 ± 7	NS
Body mass index (kg/m ²)	21.4 ± 1.1	21.1 ± 1.7	NS
Systolic blood pressure (mm Hg)	116 ± 9	113 ± 9	NS
Diastolic blood pressure (mm Hg)	76 ± 12	74 ± 6	NS
NYHA functional class (II/III)	14/1	10/5	NS
LVEF by echocardiography (%)	32 ± 2	31 ± 8	NS
Plasma BNP (pg/ml)	506 ± 39	537 ± 33	NS
Other medications n (%)			
Loop diuretics	9 (60)	10 (67)	NS
Spironolactone	5 (33)	8 (53)	NS
ACEI or ARB	12 (80)	11 (80)	NS
Beta-blockers	13 (86)	12 (80)	NS

ACEI = angiotensin-converting enzyme inhibitors; ARB = angiotensin II receptor blockers; BNP = brain natriuretic peptide; hANP = human atrial natriuretic peptide; LVEF = left ventricular ejection fraction; NS = not significant; NYHA = New York Heart Association.



hormone-sensitive lipase inhibitor, which inhibits the formation of lipolysis-derived byproducts by ANP-induced lipolysis (22).

Recently, Yu et al. (23) demonstrated the increased ANP-induced lipolysis rates in large adipocytes compared with small adipocytes. Thus, the difference of adipocyte size between patients with CHF and obesity might contribute to the different pattern of adiponectin secretion. Finally, catecholamines also are involved in the control of lipolysis in humans (24). Thus, the prolonged exposure of high plasma level of catecholamines or the treatment with beta-adrenergic receptor blockers in patients with CHF also might affect the distinct pattern of adiponectin secretion from adipocytes. Although precise mechanisms are unknown, the human adipocytes could secrete adiponectin when the certain stress was loaded. However, it remains possible that factors such as tumor necrosis factor-alpha (25)

and alpha-adrenergic stimulation (26), both of which are increased in patients with CHF, may influence the expression of adiponectin or that adiponectin levels are affected by medical treatment, so further investigations are needed.

It is not clear whether ANP augments the plasma adiponectin levels in healthy subjects because of the ethical problems. However, we have reported that the plasma adiponectin level increased along with an increase of plasma BNP levels in 1,538 healthy subjects (27). These results suggest that an increase of natriuretic peptides augments the plasma adiponectin levels and exerts a cardioprotective effect in clinical settings.

Under normal conditions the adult heart utilizes predominantly fatty acids to derive the majority of its energy (28). However, metabolic remodeling such as a marked shift in substrate preference away from fatty acids toward glucose is observed in hypertrophic and failing hearts and the decrease

in fatty acid oxidation is not fully compensated for by an increase in glucose oxidation (29). Thus, the failing heart suffers from chronic energy starvation (30). Insulin resistance also is common in patients with heart failure (31). Adiponectin improves both glucose metabolism and insulin resistance via the AMPK signaling pathway (32). Therefore, we believe that the administration of recombinant natriuretic peptide has beneficial effects on cardiac energy metabolism via adiponectin in patients with CHF.

Interestingly, the plasma adiponectin level was reported to be decreased in patients with risk factors for heart failure (9,33-35) and increased along with BNP after the onset of heart failure (14). Although approximately 10% increase in adiponectin levels in the ANP group seems relatively small, this would not be the case because there was about a 20% reduction in plasma adiponectin levels in patients with coronary artery disease compared with those in control subjects (35), which leads us to believe that the 10% increase in adiponectin is important from the viewpoint of pathophysiology of heart diseases. Therefore, we hypothesized that ANP and/or BNP regulates the plasma level of adiponectin in patients with CHF and conducted this study.

Conclusions

We demonstrated that natriuretic peptides increase the production of adiponectin by human adipocytes, as well as in patients with CHF. These findings may help to shed more light on the pathophysiology of heart failure.

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Key Words: adiponectin ■ natriuretic peptides ■ heart failure ■ adipose tissue.

Metformin Prevents Progression of Heart Failure in Dogs

Role of AMP-Activated Protein Kinase

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Background—Some studies have shown that metformin activates AMP-activated protein kinase (AMPK) and has a potent cardioprotective effect against ischemia/reperfusion injury. Because AMPK also is activated in animal models of heart failure, we investigated whether metformin decreases cardiomyocyte apoptosis and attenuates the progression of heart failure in dogs.

Methods and Results—Treatment with metformin (10 $\mu\text{mol/L}$) protected cultured cardiomyocytes from cell death during exposure to H_2O_2 (50 $\mu\text{mol/L}$) via AMPK activation, as shown by the MTT assay, terminal deoxynucleotidyl transferase-mediated dUTP nick-end labeling staining, and flow cytometry. Continuous rapid ventricular pacing (230 bpm for 4 weeks) caused typical heart failure in dogs. Both left ventricular fractional shortening and left ventricular end-diastolic pressure were significantly improved in dogs treated with oral metformin at 100 $\text{mg} \cdot \text{kg}^{-1} \cdot \text{d}^{-1}$ ($n=8$) ($18.6 \pm 1.8\%$ and 11.8 ± 1.1 mm Hg, respectively) compared with dogs receiving vehicle ($n=8$) ($9.6 \pm 0.7\%$ and 22 ± 0.9 mm Hg, respectively). Metformin also promoted phosphorylation of both AMPK and endothelial nitric oxide synthase, increased plasma nitric oxide levels, and improved insulin resistance. As a result of these effects, metformin decreased apoptosis and improved cardiac function in failing canine hearts. Interestingly, another AMPK activator (AICAR) had effects equivalent to those of metformin, suggesting the primary role of AMPK activation in reducing apoptosis and preventing heart failure.

Conclusions—Metformin attenuated oxidative stress-induced cardiomyocyte apoptosis and prevented the progression of heart failure in dogs, along with activation of AMPK. Therefore, metformin may be a potential new therapy for heart failure. (*Circulation*. 2009;119:2568-2577.)

Key Words: AMP-activated protein kinase ■ heart failure ■ metformin ■ nitric oxide

Metformin is widely used as an antidiabetic drug with an insulin-sensitizing effect. A large-scale clinical trial (the UK Prospective Diabetes Study [UKPDS] 34) has shown that metformin therapy decreased the risk of cardiovascular death and the incidence of myocardial infarction associated with diabetes mellitus,¹ suggesting that this drug may be useful for patients who have both cardiovascular disease and diabetes mellitus. Eurich and colleagues² recently reported the results of a meta-analysis showing that metformin was the only antidiabetic agent to reduce all-cause mortality without causing any harm in patients who had heart failure and diabetes mellitus. These results suggest that a tight link exists between cardiovascular disease and diabetes mellitus and that metformin has a cardioprotective effect. Metformin is known

to activate AMP-activated protein kinase (AMPK),³⁻⁵ which is expressed in various tissues, including the myocardium, and plays a central role in the regulation of energy metabolism under stress conditions.⁶ AMPK is activated by ischemia/reperfusion,⁷⁻⁹ as well as in hearts with pressure overload hypertrophy¹⁰ and subsequent heart failure.^{11,12} In addition, Russell et al⁹ have demonstrated that isolated hearts of AMPK-deleted mice show increased apoptosis and dysfunction after ischemia/reperfusion. Activation of AMPK by adiponectin also has been reported to protect cardiomyocytes against apoptosis and to attenuate myocardial ischemia/reperfusion injury in mice.⁸ Furthermore, metformin has been reported to increase the production of nitric oxide (NO),¹³⁻¹⁵ which is known to have various beneficial cardiovascular

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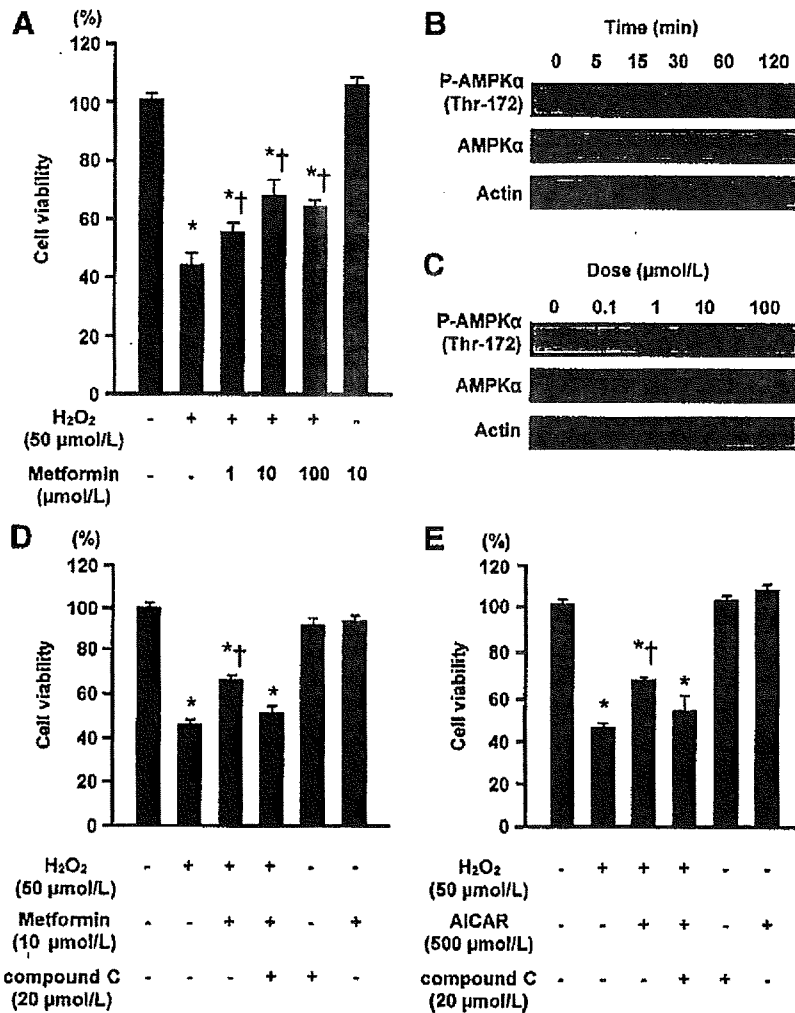


Figure 1. Effect of metformin on oxidative stress-induced cell death via AMPK activation in cultured rat cardiomyocytes. **A**, Cardiomyocyte viability after treatment with metformin (1, 10, or 100 μmol/L) and exposure to H₂O₂ (50 μmol/L). **B**, Time (0, 5, 15, 30, 60, 120 minutes)-dependent changes in AMPK phosphorylation in cardiomyocytes after treatment with metformin (10 μmol/L). **C**, Dose-dependent changes in AMPK phosphorylation in cardiomyocytes after treatment with metformin (0.1, 1, 10, or 100 μmol/L). **D**, Effect of an AMPK inhibitor (compound C; 20 μmol/L) on cardiomyocyte viability after treatment with metformin (10 μmol/L). **E**, Effect of an AMPK activator (AICAR; 500 μmol/L) on cardiomyocyte viability after treatment with metformin (10 μmol/L). Values are mean±SEM. P-AMPKα indicates phosphorylation of AMPKα. *P<0.05 vs no treatment; †P<0.05 vs H₂O₂ (50 μmol/L) treatment.

effects¹⁶ and may alleviate mechanical or neurohormonal stress on the heart.

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These findings led us to hypothesize that activation of AMPK by metformin may exert a cardioprotective effect under stress conditions. Accordingly, metformin might be a potential new treatment for cardiac failure because it activates AMPK and increases NO production. Therefore, we investigated the influence of metformin on apoptosis, an important feature of heart failure, using cultured neonatal cardiomyocytes exposed to H₂O₂ and the effect of metformin on the progression of pacing-induced heart failure in dogs, along with activation of AMPK.

Methods

Experimental procedures are described in the online-only Data Supplement.

Statistical Analysis

Results are expressed as mean±SEM. Comparison of changes between groups over time was performed by 2-way repeated-measures ANOVA. Other data were compared between groups by

1-way fractional ANOVA. The Tukey-Kramer test was used to correct for multiple comparisons. In all analyses, values of P<0.05 were considered to indicate statistical significance.

The authors had full access to and take full responsibility for the integrity of the data. All authors have read and agree to the manuscript as written.

Results

Metformin Attenuates Oxidative Stress-Induced Cell Death and Apoptosis in Cultured Cardiomyocytes via AMPK Activation

Cell viability was decreased in the presence of H₂O₂, as shown by the MTT assay, but this change was blunted by treatment with metformin in a dose-dependent manner (Figure 1A). Treatment with metformin (10 μmol/L) stimulated phosphorylation of AMPK in cultured cardiomyocytes in a time- and dose-dependent manner (Figure 1B and 1C). The effect of metformin on cell viability was blunted by cotreatment with compound C, an AMPK inhibitor (20 μmol/L) (Figure 1D). 5-Amino-4-imidazole-1-β-D-carboxamide ribofuranoside (AICAR; another AMPK activator) had an effect similar to metformin on cardiomyocyte viability after exposure to H₂O₂ (Figure 1E). These results suggested that

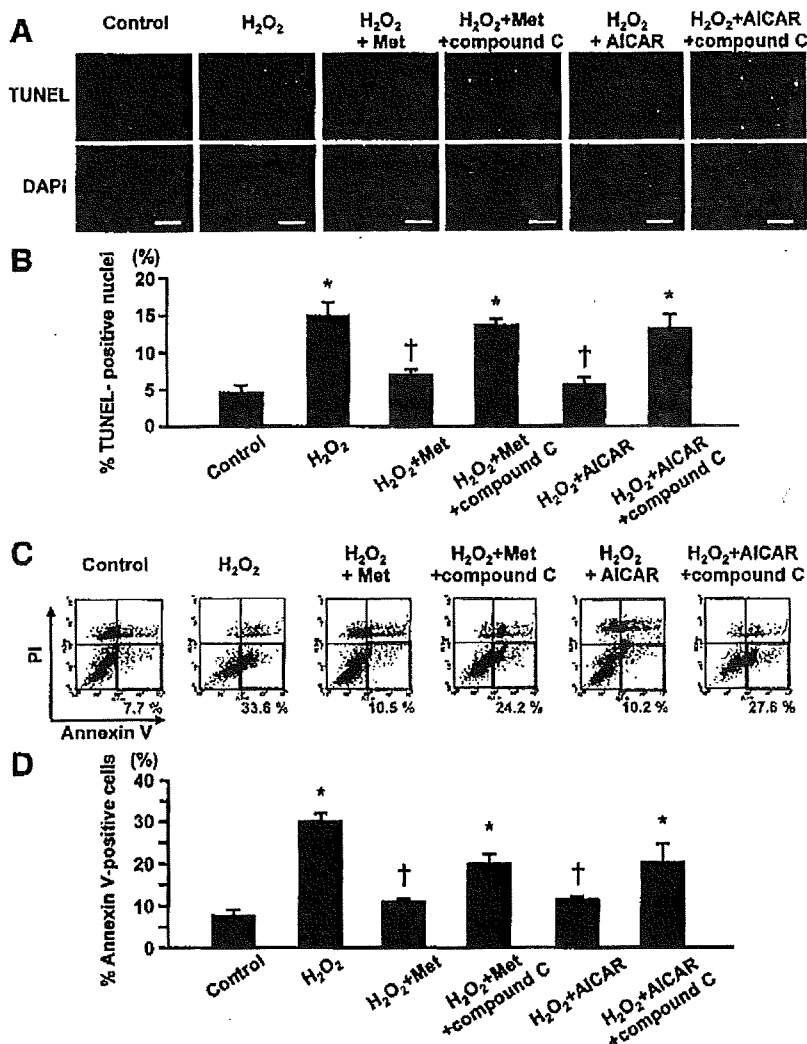


Figure 2. Effect of metformin on oxidative stress-induced apoptosis via AMPK activation in cultured rat cardiomyocytes. Representative (A) and quantitative (B) data on cardiomyocyte apoptosis obtained by TUNEL staining (n=3 in each experiment). Representative (C) and quantitative (D) data on cardiomyocyte apoptosis obtained by flow cytometry (n=3 in each experiment). Values are mean±SEM. PI indicates propidine iodide. *P<0.05 vs control; †P<0.05 vs H₂O₂ (50 μmol/L) treatment.

activation of AMPK protected cardiomyocytes against damage caused by H₂O₂.

H₂O₂ also increased cardiomyocyte apoptosis, as shown by the terminal deoxynucleotidyl transferase-mediated dUTP nick-end labeling (TUNEL) staining and flow cytometry (annexin V-positive and propidine iodide-negative cells) (Figure 2A through 2D). Metformin pretreatment significantly reduced the extent of cardiomyocyte apoptosis compared with that in untreated control cells (Figure 2A through 2D). Treatment with compound C inhibited the effects of metformin and AICAR (which was similar to that of metformin) on apoptosis in cardiomyocytes exposed to H₂O₂ (Figure 2A through 2D). These results suggested that the activation of AMPK by metformin could prevent apoptosis of cardiomyocytes induced by H₂O₂.

Effect of Metformin on Cardiac Function in Dogs With Pacing-Induced Heart Failure

Cardiac Physiological and Pathophysiological Parameters
Four weeks after the rapid right ventricular (RV) pacing, left ventricular (LV) end-diastolic dimension, LV end-systolic

dimension, LV fractional shortening, and LV ejection fraction of the pacing group showed significant deterioration compared with the sham group (Figure 3A and 3B). Treatment with metformin significantly reduced both LV dimensions and increased both LV fractional shortening and LV ejection fraction compared with the pacing group (Figure 3A and 3B). Before RV pacing, both mean aortic pressure and heart rate were similar in all groups, and these parameters did not change throughout the study (Table). Four weeks after the RV pacing, pulmonary capillary wedge pressure, mean pulmonary artery pressure, and LV end-diastolic pressure were all significantly higher in the pacing group compared with the sham group (Figure 4A and 4B). Metformin treatment significantly reduced pulmonary capillary wedge pressure, mean pulmonary artery pressure, and LV end-diastolic pressure compared with the pacing group (Figure 4A and 4B). Furthermore, cardiac output was decreased and systemic vascular resistance was increased in the pacing group compared with the sham group, whereas metformin increased cardiac output and decreased systemic vascular resistance compared with the levels in the pacing group (the Table).