Patients with type 2 diabetes often present with cardiovascular complications; however, it is not clear how diabetes promotes cardiac dysfunction. In murine models, deletion of the gene encoding aryl hydrocarbon nuclear translocator (ARNT, also known as HIF1β) in the liver or pancreas leads to a diabetic phenotype; however, the role of ARNT in cardiac metabolism is unknown. Here, we determined that cardiac-specific deletion of Arnt in adult mice results in rapid development of cardiomyopathy (CM) that is characterized by accumulation of lipid droplets. Compared with hearts from ARNT-expressing mice, ex vivo analysis of ARNT-deficient hearts revealed a 2-fold increase in fatty acid (FA) oxidation as well as a substantial increase in the expression of PPARα and its target genes. Furthermore, deletion of both Arnt and Ppara preserved cardiac function, improved survival, and completely reversed the FA accumulation phenotype, indicating that PPARα mediates the detrimental effects of Arnt deletion in the heart. Finally, we determined that ARNT directly regulates Ppara expression by binding to its promoter and forming a complex with HIF2α. Together, these findings suggest that ARNT is a critical regulator of myocardial FA metabolism and that its deletion leads to CM and an increase in triglyceride accumulation through PPARα.
Cardiac-specific ablation of ARNT leads to lipotoxicity and cardiomyopathy

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Introduction

Diabetes mellitus is a common disorder, with approximately 300 million people worldwide believed to be affected (1). Type 2 diabetes is associated with cardiovascular complications, including an increased incidence of heart failure after myocardial infarction or even in the absence of coronary artery disease (2). The mechanism linking diabetes to heart dysfunction is not entirely clear, and several hypotheses have been proposed, including microvascular disease, glucose toxicity, mitochondrial dysfunction, and lipid toxicity. The latter mechanism is supported by studies showing that lipid accumulation and excessive fatty acid oxidation (FAO) contribute to cardiomyocyte dysfunction (3, 4). Furthermore, the hearts of diabetic animals and patients cannot fully utilize glucose, resulting in increased fatty acid uptake (FAU) and FAO and lipid deposition (3). The cardiomyopathy (CM) that is associated with these features is termed lipotoxic CM.

Aryl hydrocarbon nuclear translocator (ARNT), also known as hypoxia-inducible factor 1β (HIF1β), belongs to the basic helix-loop-helix (bHLH) family of transcription factors and heterodimerizes with several other bHLH family members, including HIF1α, HIF2α, and the aryl hydrocarbon receptor (AHR) (5–7). In response to hypoxia, ARNT binds to HIF1/2α and interacts with hypoxia response elements (HREs) to activate the transcription of genes needed for adaptation to oxygen deprivation and for cell survival under hypoxia. ARNT also dimerizes with AHR, and this heterodimer plays a role in the development and detoxification of a wide array of xenobiotics (8). The homozygous deletion of Arnt in mice leads to embryonic lethality due to defects in angiogenesis and an impaired response to glucose deprivation and hypoxia (9). Interestingly, reduced ARNT expression has been observed in the pancreas and liver of humans with type 2 diabetes, and Arnt deletion in the pancreas and liver of mice leads to a condition that mimics type 2 diabetes (10, 11). These studies suggest that ARNT deficiency plays an important role in the altered metabolic function associated with diabetes, however, the mechanism for this phenomenon is not well characterized. Furthermore, the role of ARNT in the metabolism of other insulin-responsive tissues, such as the heart, has not been studied.

 Peroxisome proliferator-activated receptors (PPARs) are ligand-activated transcription factors that belong to the nuclear receptor superfamily and play an important role in the regulation of cellular metabolism (12). PPARα controls the expression of a wide range of proteins involved in both the transport and β oxidation of free FAs in liver, kidney, heart, muscle, and adipose tissue (13, 14) and is activated by FA moieties and fibrates (15). In the vasculature, PPARα exerts antiinflammatory effects in addition to having a positive influence on vessel reactivity and remodeling and macrophage lipid handling within the plaque (16–18). PPARα is also known to play a role in the development of hypertension and the cardiac response to ischemia-reperfusion and pressure overload (12), and the levels of PPARαs and its target genes are elevated in the hearts of mouse models of diabetes (19). Ppara−/− mice are viable and have normal cardiac function at baseline; however, they exhibit lipid accumulation in their tissues in response to inhibition of mitochondrial FA import (20). Transgenic (Tg) mice that overexpress PPARα in their hearts display phenotypic features similar to those observed in diabetic hearts (19),
including increased myocardial FAU and FAO, reduced glucose utilization, and CM (21). They also exhibit FA deposits throughout their heart, which is believed to be due to an imbalance between FAU and FAO, both of which are increased to different degrees. Furthermore, the CM seen in PPARα Tg mice is exacerbated by a high-fat diet, suggesting that FA overload contributes to the lipotoxicity and cardiac dysfunction (22). However, it is not known whether an increase in PPARα through non-Tg models would still result in the same phenotype.

Here, we demonstrate that deletion of Arnt in the heart leads to CM and lipid accumulation. Our mechanistic studies determined that PPARα mediates the deleterious effects and metabolic changes of Arnt deletion in the heart, as deletion of PPARα reverses the phenotype associated with Arnt knockout. Furthermore, we demonstrate that ARNT regulates PPARα at the transcriptional level by binding to its promoter and by forming a complex with HIF2α. We believe that these findings provide the first evidence for a functional link between the HIF/ARNT pathway and PPARα in the heart and demonstrate that deletion of Arnt leads to CM and cardiac lipotoxicity through PPARα activation.

Results

Cardiac deletion of Arnt leads to CM. ARNT levels are reduced in the liver and pancreas in diabetes, and its deletion in those tissues leads to a diabetic phenotype (10, 11). However, the function of ARNT in the heart is not known. We first assessed the levels of ARNT in hearts from diabetic mice. The levels of ARNT were significantly decreased in db/db mice at 32 weeks of age compared with those detected in age-matched WT animals (Figure 1A). To study the role of ARNT in the heart, we generated tamoxifen-inducible cardiac-specific ARNT-knockout mice (csArnt−/−) by crossing mice withloxP sequences flanking exon 8 of Arnt (Arntfl/fl) (23) with mutated estrogen receptor (MER)-Cre-MER (MCM) Tg mice under the α-myosin heavy chain (Myh6) promoter (24) (Figure 1, B and C, and Supplemental Figure 1A; supplemental material available online with this article; doi:10.1172/JCI76737DS1). Intraperitoneal injection of tamoxifen in these mice resulted in transient but severe CM independent of Arnt deletion, consistent with previous work (25). Thus, we adopted a 2-week protocol of oral tamoxifen administration (Supplemental Figure 1B), which did not result in any changes in body weight (Supplemental Figure 1C). Deletion of Arnt in the heart was confirmed at the genomic DNA (Figure 1D), mRNA (Figure 1E and Supplemental Figure 2A), and protein levels (Figure 1F). We found that deletion of Arnt was specific to the heart, as its mRNA and protein levels in other tissues were comparable to those in the control mice (Supplemental Figure 2, B and C).

We then assessed the effects of Arnt deletion on cardiac function. A dilated left ventricle in csArnt−/− mice was observed at 4 weeks after tamoxifen treatment, while all control group mice displayed normal cardiac size and function (Figure 2A and Supplemental Figure 3, A–E). For subsequent studies, we used Arntfl/− mice treated with tamoxifen as controls. Echocardiographic analysis of the hearts of csArnt−/− mice revealed decreased fractional shortening (FS) and ejection fraction (EF) and increased left ventricular end-diastolic internal dimensions (LVID−d) as early as 2 weeks after tamoxifen treatment, with the reduction in FS and EF persisting at least up to 4 weeks (Figure 2, B–D). csArnt−/− mice also displayed a reduction in the early to late ventricular filling velocities (E/A) ratio that was measured across the mitral valve (Figure 2E). Invasive hemodynamic measurements revealed increased end-diastolic pressure (EDP), while the maximum and minimum rates of pressure change in the left ventricle (+dP/dt and −dP/dt) were significantly reduced with Arnt deletion (Figure 2, F and G), suggesting a combination of systolic and diastolic dysfunction in the hearts of csArnt−/− mice. Consistent with cardiac dysfunction, csArnt−/− mice also displayed higher heart and lung weights normalized to tibia length (Supplemental Figure 4, A–C). Finally, the levels of heart failure markers atrial natriuretic protein (ANP) and brain natriuretic protein (BNP) were significantly higher in csArnt−/− mice than in controls (Supplemental Figure 5, A and B). These results suggest that Arnt deletion in the heart leads to the development of spontaneous dilated CM.

Arnt deletion in the heart leads to excess lipid accumulation. We then studied the mechanism for the CM associated with Arnt deletion. H&E staining showed myofiber architectural distortion and markedly increased interstitial fibrosis in csArnt−/− hearts 4 weeks after tamoxifen administration (Figure 3A). We also noted evidence of enhanced apoptosis in csArnt−/− hearts compared with that seen in control hearts, as assessed by TUNEL staining of ventricular tissue (Figure 3B). Electron microscopic analysis revealed the presence of large vacuoles scattered throughout the heart tissue of csArnt−/− mice (Figure 3C), bearing structural similarity to lipid vacuoles (26). These results suggest that Arnt deletion in the heart may lead to lipid accumulation; thus, we performed further analysis of the lipid levels in csArnt−/− hearts 4 weeks after initiation of tamoxifen treatment. Oil red O staining revealed enhanced dye accumulation in csArnt−/− hearts (Figure 3, D and E), confirming increased lipid content. Moreover, we found that triacylglycerol (TAG) levels were higher in the hearts of csArnt−/− mice (Figure 3F), while serum TAG levels were similar compared with those in control mice (Supplemental Figure 6A). Consistent with these results, we also found an increase in TAG levels in isolated neonatal rat cardiomyocytes (NRCMs) in response to ARNT knockdown with siRNA (Supplemental Figure 6, B and C). Taken together, these results show that Arnt deletion causes significant lipid accumulation in the heart.

Arnt deletion in the heart leads to an increase in FA metabolism. We next assessed the effects of Arnt deletion on cardiac FA and glucose metabolism in isolated working hearts using radioisotope-labeled substrates. Deletion of Arnt in the heart resulted in an approximately 2-fold increase in FAO (as assessed by oxidation of 14C-palmitate) (Figure 4A). csArnt−/− mice also displayed a decrease in glucose oxidation (Supplemental Figure 7A) and a significant reduction in genes involved in glucose metabolism (Supplemental Figure 7B). To confirm that the observed changes in glucose and FA metabolism in the csArnt−/− hearts were specific to the absence of cardiac ARNT and not secondary to the CM associated with Arnt deletion, we performed in vitro studies in NRCMs. Consistent with the in vivo data, ARNT knockdown in NRCMs led to increased FA uptake (FAU) (Figure 4B) and FAO (Figure 4C). Knockdown of ARNT in NRCMs also resulted in a significant reduction in glucose uptake and the extracellular acidification rate (ECAR) (Supplemental Figure 7, C and D). These results suggest

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HIF binding sites) (Figure 5A) or a control plasmid into HEK293 cells, along with control or ARNT siRNA. ARNT siRNA resulted in effective knockdown in HEK293 cells (Supplemental Figure 9A) and led to a significant increase in luciferase activity (Figure 5B), suggesting that ARNT likely regulates PPARα at the mRNA level.

We then assessed which of the HREs is responsible for the inhibitory effects of ARNT on the Ppara promoter by making truncated forms of the promoter to sequentially remove HREs (Figure 5A). A truncated construct with removal of the second HRE upstream of the initiation site abolished the inhibitory effect of ARNT on the Ppara promoter, suggesting that this site is likely involved in the regulation of the gene (Figure 5B). To confirm this observation, we performed ChIP analysis on this HRE. Negative and positive controls for the ChIP are shown in Supplemental Figures 9, B and C, and ChIP analysis of the second HRE upstream of the Ppara initiation site confirmed that ARNT binds to this sequence (Figure 5C).

To determine which ARNT partner mediates its effects on PPARα expression, we then downregulated HIF1α, HIF2α, and AHR in NRCMs and assessed PPARα levels. A reduction in HIF1α or AHR did not alter the levels of PPARα significantly, while HIF2α knockdown, similar to the effects of ARNT reduction, resulted in an increase in PPARα levels (Supplemental Figure 10, A–D, and Figure 5D). These results suggest that the effects of Arnt deletion on PPARα are, at least partially, through its association with HIF pathway generally causes activation of genes; however, recent studies suggest that HIF may also inhibit promoter activity in certain genes (27–29). To assess whether ARNT regulates PPARα at the transcriptional level, we first transfected a plasmid construct of the human Ppara promoter luciferase reporter (which has 5 HIF binding sites) (Figure 5A) or a control plasmid into HEK293 cells, along with control or ARNT siRNA. ARNT siRNA resulted in effective knockdown in HEK293 cells (Supplemental Figure 9A) and led to a significant increase in luciferase activity (Figure 5B), suggesting that ARNT likely regulates PPARα at the mRNA level.

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Deletion of Ppara prevents cardiac metabolic derangements associated with Arnt deletion. We next assessed whether PPARα is increased in the hearts of diabetic mice and showed that its mRNA levels were higher in hearts from db/db mice (Supplemental Figure 13). These findings are consistent with studies by Finck et al., who demonstrated that PPARα mRNA and protein levels are increased in streptozotocin-treated hearts and that PPARα target genes (but not its own mRNA levels) are increased in db/db hearts (19). To better assess the role of PPARα in the metabolic effects of ARNT in the heart, we knocked down ARNT or PPARα individually or together in NRCMs, then measured the genes involved in FA metabolism. Deletion of Ppara either completely or partially reversed the effects of Arnt deletion on genes involved in FA metabolism (Figure 6A). Furthermore, we found that the increase in FAO (as assessed by oxygen consumption in the presence of palmitate) with ARNT knockdown was completely reversed with Ppara deletion (Figure 6B). Also, csArnt–/– hearts displayed higher levels of UCP2 and UCP3 (Supplemental Figure 14), suggesting that the hearts of these mice have more uncoupling and inefficient fuel use.

To confirm that myocardial lipid accumulation and FAO associated with Arnt deletion in the heart are PPARα dependent, we generated csArnt–/– and Ppara–/– double-knockout mice by crossing Myh6-MCM Arnt+/– mice with Ppara–/– mice, followed...
provide in vitro and in vivo data showing that PPARα mediates the lipid accumulation and increase in FAO associated with ARNT knockdown. Cardiac function is restored with Ppara deletion in csArnt–/– mice. Finally, we sought to determine whether the CM observed in csArnt–/– mice is due to PPARα activation. We assessed cardiac function by echocardiography in the csArnt–/– and csArnt–/–Ppara–/– double-knockout mice 1, 2, and 4 weeks after tamoxifen administration. While csArnt–/– mice displayed CM 4 weeks after tamoxifen treatment, csArnt–/–Ppara–/– double-knockout mice showed a complete reversal of CM, as determined by cardiac output, EF, and FS (Figure 7, A–D, and Supplemental Table 1). Moreover, the molecular markers of heart failure, ANP and BNP, were also reduced upon PPARα deletion (Supplemental Figure 16, A and B). Finally, Kaplan-Meier analysis showed that csArnt–/–Ppara–/– double-knockout mice had no mortality by 2 months of age, while csArnt–/– mice had approximately 15% mortality by that time (Figure 7E). These results suggest that Arnt deletion leads to cardiac dysfunction, which is mediated through PPARα-mediated lipid accumulation (Figure 7F).
Here, we showed that csArnt–/– mice display enlarged left ventricular size and reduced cardiac function, consistent with CM. csArnt–/– hearts also exhibited lipid accumulation, as assessed by electron microscopy, oil red O staining, and TAG measurements. Using an ex vivo working heart system, we demonstrated that csArnt–/– hearts have an approximately 2-fold increase in FAO and a decrease in glucose metabolism. In addition, we showed that PPARα and its target genes involved in FAU and FAO are significantly increased in the csArnt–/– hearts. To confirm that the effects of ARNT downregulation on cardiac metabolism are through PPARα, we crossed csArnt–/– with Ppara–/– mice and showed that knockout of Ppara reverses the pathologic changes associated with ARNT reduction. Finally, we showed that ARNT inhibits Ppara promoter activity by forming a complex with HIF2α. We conclude that ARNT is a critical regulator of myocardial FA metabolism and that a reduction in ARNT levels leads to cardiac dysfunction at baseline by increasing TAG accumulation through a PPARα-mediated pathway.

The mechanism for an increased incidence of heart dysfunction in diabetes is not totally clear, and several hypotheses have been proposed. Lipid toxicity has been suggested as a potential mechanism, an idea that is supported by studies showing that excessive FA accumulation and oxidation contribute to cardiomyocyte dysfunction. Furthermore, glucose uptake and utilization are reduced in diabetic hearts, while there is a concurrent increase in FAU and metabolism, leading to lipotoxic CM. Overexpression of PPARα results in a phenotype similar to that of diabetic cardiac dysfunction, and PPARα levels are increased in the hearts of diabetic mice (19), raising the possibility that PPARα plays a major role in the pathogenesis of lipotoxicity associated with diabetic CM. In our studies, we also noted an increase in PPARα with Arnt deletion, which was associated with lipid accumulation in the heart. It is important to point out that the extent of the PPARα increase in the csArnt–/– mice was only approximately 5- to 6-fold at the protein level (Figure 4E), which was associated with a significant reduction in cardiac function. This phenotype is not totally consistent with what was observed in PPARα Tg mice, which displayed a greater than 15-fold increase in PPARα levels in the heart and a milder form of CM compared with csArnt–/– mice (19). Thus, in addition to a PPARα-dependent pathway, other mechanisms (independent of PPARα) may contribute to the pathogenesis of CM associated with Arnt deletion. Nevertheless, our findings provide evidence that even an indirect increase in the levels of PPARα (as opposed to direct overexpression in Tg animals) contributes to lipotoxicity and CM, providing a further link between PPARα and the diabetic CM phenotype.

The active HIF complex is composed of 2 subunits: ARNT and either HIF1α or HIF2α. In the ischemic heart, the HIF/ARNT complex participates in the cardiomyocyte response to low oxygen tension by upregulating glucose transporters and glycolytic enzymes (30). Global Hif1α knockout results in embryonic leth-
ity with failure of neural tube closure, defective vascularization, and increased thickness of the heart in embryos (31, 32). Cardiac-specific Hif1α knockout leads to mild cardiac hypertrophy with reductions in contractility, vascularization, and high-energy phosphate content (33), but no evidence of lipid accumulation. However, inducible knockout of Hif1α after birth in the heart does not cause cardiac dysfunction (34), suggesting that baseline HIF1α function may be more important during development than in the maintenance of adult cardiac function. Mice with global Hif2a knockout display changes in different organs, including lipid accumulation in skeletal muscle, cardiac muscle, and liver (35). These mice also have cardiac hypertrophy, although cardiac function was not assessed directly (35). We showed that deletion of Arnt in the adult heart leads to spontaneous CM due to lipid accumulation, which is distinct from what is observed with HIF1α deletion, but is more similar to that of Hif2a-knockout mice. In the background of Arnt deletion, it is not technically possible to reconstitute the activity of each of its partners (i.e., HIF1α and -2α and AHR).

However, we assessed the effects of ARNT partners in PPARα regulation and demonstrated that a reduction in HIF2α increases PPARα levels in vitro and that ARNT forms a complex with HIF2α to inhibit the Ppara promoter. Although this effect is likely independent of HDACs and histone deacetylation, it is possible that the binding of ARNT/HIF2α to the Ppara promoter blocks the access of other transcription factors to their binding sites.

The link between the HIF pathway and PPARs was previously studied in the heart. Krishnan et al. showed that HIF1α activates PPARγ, which in turn, activates FAU, glucose-to-lipid conversion via the glycerol-3-phosphate pathway, apoptosis, and contractile dysfunction (36). They also demonstrated that HIF1α activates PPARγ by binding to its promoter and that deletion of Hif1α attenuates stress-induced cardiac hypertrophy. These studies focused on HIF1α, which is only one of the partners of ARNT and which was shown in our studies not to play a role in the CM associated with Arnt deletion. Furthermore, our studies focused on CM rather than the cardiac hypertrophy studied by Krishnan et al. (36).
In summary, our results demonstrate that deletion of Arnt in the heart leads to CM, lipid accumulation, and PPARα activation. The mechanism for PPARα activation occurs at the transcriptional level and through the regulation of its promoter by ARNT/HIF2α. These results demonstrate a functional link between the HIF/ARNT pathway and lipid metabolism in the heart through PPARα activation and provide a novel potential target for the treatment of cardiac lipotoxicity.

Methods

Animal models. csArnt−/− mice were generated by crossing Arntfl/fl mice with Myh6-MCM (tamoxifen-inducible heart-specific Cre) Tg mice (purchased from The Jackson Laboratory), followed by oral adminis-

Nevertheless, these 2 studies provide evidence for a link between the HIF pathway and FA metabolism in the heart in response to stress.

In addition to providing substrates for oxidative phosphorylation and ATP generation, FA and TAG stores serve as important signaling molecules in the cell. Importantly, free FAs are known to bind to nuclear receptors such as PPARα and stimulate their translocation into the nucleus. It is conceivable that the activation of PPARα signaling we observed with Arnt deletion was secondary to the binding of free FAs to PPARα and its subsequent activation. However, this mechanism is unlikely to explain all of our findings, since our luciferase studies of the Ppara promoter showed regulation of this receptor at the transcriptional level. Nevertheless, higher TAG levels in Arnt-knockout mice may further amplify PPARα signaling.

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tation of tamoxifen (30 mg/kg) for 2 weeks as described previously (37). Three sets of sex-matched littermate mice (Myh6-MCM with tamoxifen; Arnt\(^{−/−}\) with tamoxifen; and Myh6-MCM Arnt\(^{−/−}\) without tamoxifen) were used as controls. db/db mice were purchased from The Jackson Laboratory and studied at 32 weeks of age. All groups of mice included a mix of males and females.

**Genotyping.** Genomic DNA was prepared from tail clips using the PureGene DNA isolation kit (Gentra Systems) according to the manufacturer’s protocol. Approximately 10 ng of the genomic DNA was used for PCR. Genotyping of Myh6-MCM mice was performed using 2 sets of primers. The first primer set was designed to amplify the Cre Tg construct (forward, 5′-ATACCGGAGATCATGCC GCA-GC-3′; reverse, 5′-AGGTGGACCTGATCATGGAG-3′). The second primer set was used to amplify a mouse WT internal positive control (forward, 5′-CTAGGCCACAGAATTGAAAGATCT-3′; reverse, 5′-GTAGGTTGGACCTGATCATGGAG-3′). Genotyping of Arnt\(^{−/−}\) mice was performed by PCR amplification (forward, 5′-CACCTGAGCTTAAT TACCAGGCC-3′; reverse, 5′-GCATTTCGGTAGCAGGTAGTCTT-3′). The 2 sets of primers used for genotyping of Ppara\(^{−/−}\) mice were: forward, 5′-GAGAAGTTGAGGAGGGAGTTG-3′ (served as common); reverse: 5′-CCTATGCCGAGATGCAGTATTTC-3′ (WT); and reverse, 5′-GCCATTTCCGGAGATGCAGTATTTC-3′ (mutant).

**Primary cell culture.** NRCMs were isolated from 1- to 2-day-old Sprague–Dawley rats as previously described (38). Cardiomyocytes were cultured in DMEM/M199 (3:1), supplemented with 5% FBS, 1.5 mM vitamin B12, and 1 mM penicillin-streptomycin (Invitrogen). To prevent the proliferation of nonmyocytes, 100 μM BrdU was added to the culture media (Sigma-Aldrich).

**Echocardiography.** Cardiac function was noninvasively monitored by transthoracic echocardiography using a VisualSonics Vevo 770 high-resolution imaging system with a 30 MHz scanhead 1, 2, 3, and 4 weeks after oral administration of tamoxifen or normal chow. Parasternal short- and long-axis views were used to obtain 2D and M-mode images. At least 10 independent cardiac cycles per experiment were obtained.

**Cardiac hemodynamic measurement.** Hemodynamic studies were performed 2 weeks after tamoxifen treatment was completed, as described previously (39). A high-fidelity transducer-tipped pressure-volume catheter (Scisense Inc.) was introduced from the right carotid artery into the left ventricle of the anesthetized mouse to determine hemodynamics. Signals were digitized using a data translation series analog-digital converter and then stored and analyzed.

**Histological analysis.** Hearts were fixed in 10% formalin (PBS buffered), dehydrated, and embedded in paraffin. Heart architecture was determined using transverse 5-μm deparaffinized sections stained with H&E. Fibrosis was detected with Masson trichrome staining. TUNEL positivity in the hearts from csArnt\(^{−/−}\) and control mice were determined using an in situ detection kit according to the manufacturer’s instructions (Roche Diagnostics). Oil red O staining was performed on sections of unfixed, freshly frozen heart samples (6-μm in thickness).

**Electron microscopy.** Cardiac tissue from the left ventricle free wall was fixed with 2% glutaraldehyde in sodium cacodylate buffer at 4°C. Fixed tissues were embedded in epoxy resin, processed for thin (70-nm) cutting with a Leica UC6 ultramicrotome, and examined with a FEI Tecnai Spirit transmission electron microscope.

**Heart TAG content.** Heart TAG was extracted as previously reported (40) and quantified using a Triglyceride Quantification Kit (Abcam) following the manufacturer’s instructions. To measure TAG levels in isolated cells, NRCMs were homogenized in 5% NP-40 solution. Samples were solubilized by slowly heating to 80°C to 100°C for 5 minutes and then cooling down to room temperature. They were
centrifuged to remove insoluble material and then diluted 10-fold in ddH₂O. TAG levels were determined using the Triglyceride Quantification Kit from BioVision. All samples and standards were run in triplicate, and values were normalized to protein content.

**Measurement of cellular glycolysis (ECAR) and FAO.** Cellular glycolysis was determined by measuring the ECAR in NRCMs using a Seahorse Bioscience XF24 extracellular flux analyzer (Billericia) as described previously (41). An increased oxygen consumption rate (OCR) immediately following the addition of palmitate substrate to the cells was used as an indicator for FAO in the XF24 Analyzer. Sixty thousand cells were seeded per well, and 24 hours later were treated for 2 subsequent days with siRNA. Forty-eight hours later, cells were used for oxygen consumption studies using unbuffered DMEM plus 1 mM sodium pyruvate plus 1 g/l glucose. Oxygen consumption readings were normalized to total protein per well.

**2-Deoxyglucose uptake.** Neonatal cardiomyocytes were grown in 6-well plates. Following serum depletion, cells were rinsed with HEPES buffer and incubated with 1 μCi 2H-2-deoxy-glucose and 5 mM glucose per well for 10 minutes. Cells were then rinsed with ice-cold PBS and lysed in a buffer containing 0.1% SDS. 2-Deoxyglucose uptake was measured for 30 seconds. Nonspecific uptake was determined in the presence of 10 μM cytochalasin B, and this value was subtracted from all values. Cell-associated radioactivity was determined by lysing the cells with 0.05 M NaOH, followed by measuring radioactivity using a liquid scintillation counter. Total cellular protein was determined by the Bradford method.

**FAU.** BSA-conjugated palmitate was freshly prepared with Krebs-Henseleit buffer at a final concentration of 0.0425 mM for BSA and 0.25 mM for palmitate. Cells were plated in a 6-well plate, rinsed with PBS buffer with 1% BSA, and incubated with 2 ml BSA-palmitate in each well for 2 minutes at 37°C. After washing 5 times with ice-cold PBS, cells were lysed with RIPA buffer, followed by liquid scintillation counting. Total cellular protein was determined by the Bradford method and used for normalization.

**RNA isolation and quantitative real-time PCR.** Total RNA from cultured NRCMs was isolated using the RNA Stat-60 reagent (Tel-Test Inc.), and RNA from mouse heart was isolated using an RNeasy Fibrous Tissue Mini Kit from QIAGEN according to the manufacturer’s instructions. Samples of total RNA (500 ng) were reverse transcribed using the TaqMan reverse transcription reagents PCR Kit (Applied Biosystems), and the resulting cDNA was used as a PCR template. The mRNA levels of Arnt, Ppara, Pparg, Pparb, Cd36, Acs, Cpt1, Mcad, Hk2, Glut1, and Glut4 were determined by quantitative real-time PCR (qRT-PCR) with SYBR Green using the 7500 Fast Real-Time PCR system (Applied Biosystems) according to the manufacturer’s instructions. 18S RNA was amplified as an internal control. Relative gene expression levels were calculated using the comparative Ct method formula 2⁻ΔΔCt.

**siRNA treatment of NRCMs.** siRNA was transfected into NRCMs using a TransMessenger Transfection Kit (QIAGEN). Forty-eight hours later, cells were lysed and used for Western blot analysis or for RNA isolation by qRT-PCR.

**Western blot analysis.** For Western blotting of total protein, hearts were homogenized in a modified RIPA buffer containing protease and phosphatase inhibitors (Roche). Total protein lysates were isolated from NRCMs in RIPA buffer containing protease and phosphatase inhibitors. Antibodies against ARNT, PPARα, HDAC1, HDAC2, HDAC3, and HDAC4 were purchased from Cell Signaling Technology. GAPDH and tubulin antibodies were purchased from Santa Cruz Biotechnology Inc. Samples were run on an SDS-PAGE gel and transferred to a nitrocellulose membrane (Invitrogen). The protein bands were developed with an enhanced chemiluminescence substrate kit. Quantification of blots was performed using ImageJ software (NIH). (Full, uncut gels are shown in the Supplemental Material.)

**Heart isolation and perfusion conditions.** Hearts from C57BL/6J and littermate control mice were perfused in the working mode. Mice were anesthetized with an intraperitoneal injection of Avertin (400 mg/kg body weight), and the hearts were subsequently excised and immersed in ice-cold Krebs-Henseleit bicarbonate solution (118 mM NaCl, 25 mM NaHCO₃, 5.9 mM KCl, 5 mM EDTA [pH = 7.4], 1.2 mM MgSO₄·7H₂O, 2.5 mM CaCl₂·2H₂O, and 5 mM glucose). The aorta was cannulated and perfused with Krebs-Henseleit solution (37°C) initiated at a hydrostatic pressure of 60 mmHg. The hearts were trimmed of excess tissue, and the opening to the left atrium was cannulated. After equilibration in the Langendorff mode, the hearts were switched to the working mode by clamping off the aortic inflow line from the Langendorff reservoir and opening the left atrial inflow line. Oxygenated Krebs-Henseleit solution consisting of 0.4 mM palmitate bound to 3% FA-free BSA, 5 mM glucose, and 1 mM lactate in the presence of 100 μU/ml insulin was delivered to the left atrium at a preload pressure of 11.5 mmHg. Perfusate was ejected from spontaneously beating hearts into a compliance chamber and into the aortic outflow line against a hydrostatic afterload pressure of 50 mmHg. The perfusate was recirculated, and the pH was adjusted to 7.4 by gassing the perfusate in a glass oxygenator with a gas mixture containing 95% O₂ and 5% CO₂. At the end of perfusion, the hearts were immediately frozen in liquid N₂ with Wollenberger tongs and stored at −80°C.

**Determination of glucose and palmitate oxidation.** Glucose oxidation was measured by perfusing hearts with [U-¹³C] glucose and unlabeled lactate and palmitate (42, 43). Palmitate oxidation measurements were performed by perfusing the hearts with glucose and [9,10-³H]palmitate. The total myocardial ¹³CO₂ production and ¹⁴CO₂ production were determined at 10-minute intervals during the 40- to 60-minute aerobic perfusion period. To measure the rates of palmitate oxidation, ¹³H₂O in perfusate samples was separated from [¹H] palmitate hearts using a vapor transfer method (42, 43). This method consisted of adding 500 μl of water into a 5-ml scintillation vial, then placing a lidless 1.5-ml microcentrifuge tube inside the scintillation vial. A 200-μl perfusate sample was then added to the microcentrifuge tube, and the scintillation vial was capped. Scintillation vials were then stored initially at 50°C for 24 hours and then at 4°C for 24 hours. Following storage, the microcentrifuge tube was removed, scintillation fluid (EcoLite; Fisher Scientific) was added, and the radioactivity was counted in a liquid scintillation counter. The glucose oxidation rate was determined by quantitative measurement of ¹⁴CO₂ production from ¹³C-glucose–perfused hearts released as a gas in the oxygenation chamber and ¹⁴CO₂ dissolved as H⁺¹⁴CO⁻ in perfusate. The gaseous ¹⁴CO₂, which exits the perfusion system via an exhaust line, was trapped in hyamine hydroxide solution. The dissolved ¹⁴CO₂ as H⁺¹⁴CO⁻ was released and trapped on filter paper saturated with hyamine hydroxide in the central well of 25-ml stoppered flasks after perfusate samples were acidified by the addition of 1 ml 9N H₂SO₄.

**Luciferase studies.** H9EK293 cells were cotransfected using Lipofectamine Plus Reagent (Invitrogen) in a serum-free medium with both
the recombinant firefly luciferase plasmids containing a human PPARα promoter-luciferase reporter (200 ng) and the Renilla luciferase plasmid (25 ng), along with 25 nM of either ARNT siRNA or control siRNA. Forty-eight hours after transfection, cells were collected, and the luciferase signal intensity was measured with a dual-luciferase reporter assay kit (Promega) on a Berthold Lumat LB 9570 luminometer. Firefly luciferase expression was corrected by Renilla luciferase expression in the same well to normalize for transfection efficiency.

Mutagenesis of the HRE site was performed using PCR-based site-directed mutagenesis. Briefly, primers containing the desired mutations were used to amplify the Ppara promoter-luciferase reporter plasmid using the HiFi PCR Kit (Kapa Biosystems), followed by DpnI (New England Biolabs Inc.) digestion to remove the original template. The following primers were used for the HRE sequence, with the mutation indicated in bold letters: sense primer, GGGGCCAGGGGCGGTATGCTGGGCGGCGGCG; anti-sense primer, GCCGGCGCCCGGCGGACGATAACCGCCCTCGGCCC. The sequence of the resulting plasmid was verified before subsequent experiments.

ChIP studies. Confluent HepG2 culture was harvested with trypsin and cross-linked with 1.1% formaldehyde. ChIP was performed using anti-ARNT antibody (Cell Signaling Technology) as described previously (44). After reverse cross-linking and proteinase K and RNase A digestion, DNA was purified with a QIAGEN PCR purification kit. Purified DNA was used as input for qRT-PCR. For sequential ChIP, chromatin from the first IP was eluted with elution buffer containing 5 mM DTT and diluted 10-fold before being used as input for the second IP. The second IP was performed as described previously (44).

The positive control genes were identified in earlier studies, and the primer sequences for those genes have been validated as described previously (45). For ChIP against acetylated histones, sodium butyrate was added to all buffers. Anti-HIF2α antibody was purchased from Novus, and acetylated histone H3 and acetylated histone H4 antibodies were purchased from Millipore.

Statistics. Data are expressed as the mean ± SEM. Statistical significance was assessed with ANOVA. For multiple group comparisons, a post-hoc Tukey’s test was performed when ANOVA reached significance. A P value of less than 0.05 was considered statistically significant.

Study approval. All animal studies were reviewed and approved by the IACUC of Northwestern University.

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