MicroRNA-181b Improves Glucose Homeostasis and Insulin Sensitivity by Regulating Endothelial Function in White Adipose Tissue

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Rationale: The pathogenesis of insulin resistance involves dysregulated gene expression and function in multiple cell types, including endothelial cells (ECs). Post-transcriptional mechanisms such as microRNA-mediated regulation of gene expression could affect insulin action by modulating EC function.

Objective: To determine whether microRNA-181b (miR-181b) affects the pathogenesis of insulin resistance by regulating EC function in white adipose tissue during obesity.

Methods and Results: MiR-181b expression was reduced in adipose tissue ECs of obese mice, and rescue of miR-181b expression improved glucose homeostasis and insulin sensitivity. Systemic intravenous delivery of miR-181b robustly accumulated in adipose tissue ECs, enhanced insulin-mediated Akt phosphorylation at Ser473, and reduced endothelial dysfunction, an effect that shifted macrophage polarization toward an M2 anti-inflammatory phenotype in epididymal white adipose tissue. These effects were associated with increased endothelial nitric oxide synthase and FoxO1 phosphorylation as well as nitric oxide activity in epididymal white adipose tissue. In contrast, miR-181b did not affect insulin-stimulated Akt phosphorylation in liver and skeletal muscle. Bioinformatics and gene profiling approaches revealed that Pleckstrin homology domain leucine-rich repeat protein phosphatase, a phosphatase that dephosphorylates Akt at Ser473, is a novel target of miR-181b. Knockdown of Pleckstrin homology domain leucine-rich repeat protein phosphatase increased Akt phosphorylation at Ser473 in ECs, and phenocopied miR-181b’s effects on glucose homeostasis, insulin sensitivity, and inflammation of epididymal white adipose tissue in vivo. Finally, ECs from diabetic subjects exhibited increased Pleckstrin homology domain leucine-rich repeat protein phosphatase expression.

Conclusions: Our data underscore the importance of adipose tissue EC function in controlling the development of insulin resistance. Delivery of miR-181b or Pleckstrin homology domain leucine-rich repeat protein phosphatase inhibitors may represent a new therapeutic approach to ameliorate insulin resistance by improving adipose tissue endothelial Akt–endothelial nitric oxide synthase–nitric oxide signaling. (Circ Res. 2016;118:810-821. DOI: 10.1161/CIRCRESAHA.115.308166.)

Key Words: adipose tissue ■ endothelial cells ■ insulin resistance ■ microRNA ■ obesity ■ PHLPP2

A dipose tissue dysfunction, characterized by low-grade inflammation, is considered to play a primary role in obesity-associated insulin resistance, which predisposes the majority of obese patients to the development of important chronic metabolic diseases including, type 2 diabetes mellitus and cardiovascular diseases.1–4 Excessive caloric intake may expose tissues such as white adipose tissue to superphysiological levels of metabolic substrates types, including endothelial cells (ECs). Post-transcriptional mechanisms such as microRNA-mediated regulation of gene expression could affect insulin action by modulating EC function.

and promote the development of low-grade inflammation.5 Inflamed white adipose tissue contains a range of leukocyte subsets including monocytes that preferentially differentiate toward M1 macrophages, and they are associated with increased expression

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of proinflammatory cytokines. Accumulating studies support the concept that chronic inflammation in white adipose tissue is critically involved in the pathogenesis of obesity-associated insulin resistance. White adipose tissue is composed of multiple cell types including not only adipocytes and leukocytes but also endothelial cells (ECs). Cellular interactions emanating from white adipose tissue may control local and systemic homeostasis of cardiometabolic function. However, our understanding of the basic mechanisms linking EC dysfunction with the adipocyte response in insulin-resistant states remains incompletely understood.

EC dysfunction is a common feature of type 2 diabetes mellitus and cardiovascular disease, and a hallmark of insulin resistance. The reciprocal relationships between insulin resistance and endothelial dysfunction are experimentally and clinically established. In both rodents and primates, EC activation is an early event that occurs before or in parallel with the development of impaired insulin signaling. ECs of inflamed adipose tissue from obese subjects have adverse effects on insulin signaling in adipocytes, such as reduced expression of phospho-Akt at Ser473, increased endoplasmic reticulum stress, and release of inflammatory mediators. However, EC function is subjected to the regulation by insulin-mediated signaling. For example, transient activation of endothelial PI3K/Akt signaling inhibits the expression of adhesion molecules involved in leukocyte rolling and adhesion to the vascular luminal wall. Insulin resistance also leads to EC dysfunction through increased circulating free fatty acids and hyperglycemia. Indeed, ECs from visceral adipose tissue of obese mice or human subjects exhibit a marked inflammatory state with increased expression of chemokines, cytokines, and adhesion molecules. Several studies have shown insulin signaling in ECs protect endothelial function and attenuates the progression of atherosclerosis. However, it remains unknown whether enhancing endothelial insulin signaling in adipose tissue may improve systemic insulin resistance.

Akt phosphorylation regulates many fundamental biological processes, such as the insulin signaling cascade. Dysregulation of Akt phosphorylation is often involved in heart disease and diabetes mellitus. Full Akt activity depends on the phosphorylation of residues Thr308 and Ser473, which can be repressed by the lipid phosphatase—phosphatase and tensin homolog (PTEN) and the protein phosphatase—PH domain leucine-rich repeat phosphatases isoform 2 (PHLPP2). PHLPP2 inactivates Akt signaling by specifically dephosphorylating Ser473 but not Thr308 of Akt. It remains unknown whether altering the expression of PHLPP2 in ECs regulates Akt signaling, downstream substrates, insulin sensitivity, and glucose homeostasis.

MicroRNAs (miRNAs) are evolutionarily conserved small noncoding RNAs, which post-transcriptionally regulate gene expression by promoting mRNA degradation or inhibiting translation. It has been reported that miRNAs are differentially expressed in adipose tissue between lean and obese mice, as well as lean and obese human subjects. We have shown that miRNA-181b (miR-181b) ameliorates nuclear factor (NF)-κB—mediated EC activation and vascular inflammation in mouse models of endotoxemia and atherosclerosis. However, it remains unknown whether miR-181b expression is dysregulated in ECs of adipose tissue and (2) increasing miR-181b expression in adipose tissue will ameliorate obesity-associated insulin resistance and inflammatory responses.

In this study, we examined the expression of miR-181b in adipose tissue ECs of obese mice and the role of miR-181b and PHLPP2 in modulating glucose homeostasis and insulin sensitivity. Our findings reveal that miR-181b improves insulin signaling and reduces inflammation and EC dysfunction in white adipose tissue by targeting endothelial PHLPP2 without altering hepatic steatosis or lipid profiles.

Methods

Methods are available in the Online Data Supplement.

Results

MiR-181b Is Reduced by Diabetic Stimuli in ECs

Differential expression of miRNAs has been observed in adipose tissue from lean and obese mice as well as humans, although miRNA expression in adipose tissue ECs has not been previously explored. To examine the expression of miR-181b, an anti-inflammatory microRNA that we previously identified in the macrovasculature, ECs or adipocytes were isolated as described from epididymal white adipose tissue (eWAT) of C57BL/6 mice fed a 60% high-fat diet (HFD) for 0, 3, 7, or 14 days followed by quantitative polymerase chain reaction analysis (Figure 1A). We found miR-181b is the most dominantly expressed among miR-181 family members in adipose tissue ECs as demonstrated that its expression is 3.6-fold higher than that of miR-181a. MiR-181b expression was reduced by 33% and 36% after HFD for 7 and 14 days, respectively, whereas the expression of miR-181a and miR-181c was reduced by 53% and 67% after HFD for 14 days (Figure 1A). In contrast, the expression of miR-181 family members was not significantly changed in adipocytes after HFD for the indicated days (Figure 1A), and miR-181b expression was not reduced in liver or skeletal muscle ECs (Online Figure 1A). However, miR-181b expression was reduced by 24%, 32%, 31%, and 33% in ECs in vitro after treatment with glucose, phorbol myristate acetate, tumor necrosis factor (TNF)-α, or palmitate (Figure 1B). In addition, we examined miR-181b expression in ECs of eWAT during the period of 12 weeks of HFD. MiR-181b expression was decreased by 42%, 84%, and 66% in ECs isolated from eWAT of mice fed a HFD for 2, 6, and 12 weeks, respectively (Online Figure IB). Although the ratios of phosphorylated Akt total Akt were not changed under basal conditions (Online Figure IC), insulin responsiveness was blunted as indicated by reduced phosphorylation of Akt in ECs.
miR-181b expression may delay the progression of inflammation in the macrovasculature. On the basis of the reduced expression of miR-181b in the microvasculature of white adipose tissue, we hypothesize that rescue of miR-181b expression may serve as an anti-inflammatory regulator in the macrovasculature. Our previous observations indicate that miR-181b serves as an anti-inflammatory regulator in the macrovasculature. On the basis of the reduced expression of miR-181b in the microvasculature of white adipose tissue, we hypothesize that rescue of miR-181b expression may delay the progression of inflammation and insulin resistance, and improve insulin sensitivity. To examine the effect of miR-181b systemic delivery on glucose homeostasis and insulin sensitivity, C57BL/6 mice were fed a 60% HFD for 12 weeks. After 6 weeks HFD, mice were treated with miR-181b mimics (181b-m) or miRNA-negative control (NS-m) for 6 weeks (twice a week, 1 nmol/injection intravenously [IV]; Figure 2A). Insulin tolerance test and glucose tolerance test (GTT) were performed at weeks 5 and 6, respectively, after miR-181b treatment (Figure 2A). The body weights were significantly increased in HFD-fed mice, which were independent of miRNA treatments (Figure 2B). However, miR-181b treatment markedly improved glucose tolerance (Figure 2C and 2D) and insulin sensitivity (Figure 2E and 2F) compared with NS-m treatment. MiR-181b reduced the area under curves for insulin tolerance test and GTT by 57% and 38%, respectively, compared with control mice (Figure 2D and 2F). These beneficial effects occurred independent of any changes in lipid profiles, fat mass, or plasma levels of insulin and free fatty acids (Online Table I). Taken together, these data demonstrate that miR-181b delivery is able to improve glucose homeostasis and insulin sensitivity.
MiR-181b Reduces Inflammation in eWAT

We have shown that miR-181b ameliorates NF-κB–mediated EC activation and vascular inflammation in mouse models of endotoxemia and atherosclerosis. This prompted us to examine the effect of miR-181b delivery on inflammation and EC dysfunction in obese mice. First, paraffin sections of eWAT or liver were stained for the macrophage marker Mac2. Macrophage content indicated by Mac2 staining was significantly increased in eWAT of mice after 12 weeks of HFD. However, macrophage accumulation in eWAT of miR-181b–treated mice was reduced by 60% compared with NS ctrl-treated mice (Figure 3A). The macrophage content in liver was not reduced by miR-181b delivery. Second, macrophage M1 and M2 markers were examined by quantitative polymerase chain reaction. MiR-181b delivery reduced the expression of the macrophage M1 markers Tnfa, Il1b, and Il12 by 48%, 51%, and 39%, respectively, and increased the expression of M2 markers Mrc2, Mgl2, Fizz1, and Ym1 by 43%, 33%, 60%, and 21%, respectively, in eWAT; whereas it exerted minimal effects on M1 and M2 markers of macrophage in liver (Figure 3B). Third, we observed that miR-181b delivery reduced ICAM-1 and VCAM-1 expression in eWAT from obese mice (Figure 3C), suggesting that EC dysfunction in eWAT in obese mice was ameliorated by miR-181b delivery. These effects of miR-181b treatment are associated with a 1.5-fold overexpression of miR-181b in eWAT and a 15-fold overexpression in ECs of eWAT (Online Figure IIA). Systemic delivery of miR-181b could lead to more pronounced exogenous miR-181b expression in specific cell types within eWAT, such as adipocytes or adipose tissue ECs. To test this, the expression of miR-181b in eWAT or ECs isolated from eWAT was examined after 3 consecutive injections of NS-m or miR-181b. Three daily injections of miR-181b resulted in 105-fold expression of miR-181b in adipose tissue ECs, and 29-fold expression in eWAT (Online Figure IIB). These data suggest that systemic delivery of miR-181b leads to predominant accumulation of exogenous miR-181b in adipose tissue ECs within eWAT, and reduces EC activation, macrophage accumulation, and inflammatory phenotype in white adipose tissue.

MiR-181b Does Not Directly Inhibit the Cell-Intrinsic Capacity of Monocytes/Macrophages to Migrate, Proliferate, or Be Activated

Macrophage infiltration, proliferation, and activation are all involved in the pathogenesis of obesity-induced insulin resistance. Reduced macrophage content in eWAT could result from the direct effect of miR-181b on migratory and proliferative ability of monocytes/macrophages or by directly reducing EC activation and dysfunction. To explore any direct effects of miR-181b on monocyte migration, adoptive transfer of monocytes was conducted as previously described. Monocytes were isolated from HFD-fed mice treated with miR-181b or NS-m, labeled with PKH26, and injected into HFD-fed obese mice. Stromal vascular fractions were isolated from eWAT of the recipient mice 2 days later, and subjected to FACS (fluorescence-activated cell sorting) analysis. As shown in Figure 4A, miR-181b overexpression (25-fold, data not shown) in monocytes does not significantly inhibit their migration into eWAT revealed by the percentage of PKH26-positive cells among CD11b and F4/80 double-positive cells (NS-m: [22.1±5.1] %; 181b-m: [19.2±4.0] %). To examine the effect of miR-181b on macrophage proliferation, staining for Ki67 (cell division marker), F4/80 (macrophage marker), and DAPI (nuclear marker) was performed on paraffin sections of eWAT from mice. The percentages of proliferating macrophages are (13.9±1.9) % and (12.5±1.1) % in NS-m or miR-181b–treated mice, respectively, suggesting systemic delivery of miR-181b did not affect macrophage proliferation in eWAT (Figure 4B). We previously showed that miR-181b does not inhibit NF-κB activation in macrophages and NF-κB target gene expression in peripheral blood mononuclear cells. Consistently, miR-181b did not affect TNF-α, interleukin (IL)-1β, and COX-2 gene expression in peripheral blood mononuclear cells isolated from insulin-resistant mice (Figure 4C). Collectively, these data indicate that miR-181b does not directly regulate cell-intrinsic monocytes/macrophage function, including migration, proliferation, and activation.

MiR-181b Expression Promotes Glucose Uptake in Adipocytes in a Paracrine Manner

Because miR-181b does not directly regulate cell-intrinsic functions of monocytes/macrophages, the protective effects

Figure 3. Systemic delivery of miR-181b reduces inflammation in epididymal fat. A. Paraffin sections of epididymal white adipose tissue (eWAT) or liver were stained with Mac2, and the positive areas were quantified. B. Quantitative polymerase chain reaction (qPCR) of gene expression in eWAT and liver; results were presented relative to those of miRNA-negative control mimics (NS-m)–treated mice. C. qPCR and Western blot analysis of vascular cell adhesion molecule 1 (VCAM-1) and intracellular adhesion molecule 1 (ICAM-1) in eWAT. Mean±SEM, n=6 to 9; *P<0.05, 181b-m indicates miR-181b.
of miR-181b delivery on insulin signaling in eWAT may result from the direct effects of miR-181b on adipocytes or ECs. To assess this, glucose uptake experiments were performed in differentiated, mature 3T3-L1 adipocytes. Consistent with our hypothesis, miR-181b overexpression in 3T3-L1 adipocytes did not promote glucose uptake (Figure 5A). ECS of inflamed adipose tissue may have adverse effects on insulin signaling in adipocytes, possibly via paracrine effects.17 Because miR-181b attenuates endothelial inflammation in adipose tissues (Figure 3C), we reasoned that miR-181b improves insulin signaling in a paracrine manner by exerting protective effects in ECs. Indeed, the conditioned medium (supernatant) from ECs overexpressing miR-181b markedly improved glucose uptake in adipocytes (Figure 5B). These data suggest that miR-181b overexpression in ECs may improve glucose uptake via paracrine mechanisms with adipocytes.

**MiR-181b Delivery Improves Insulin Signaling by Increasing Akt Phosphorylation in eWAT**

Because Akt phosphorylation is a central event in insulin signaling cascade, we examined the expression of phospho-Akt (Ser473 and Thr308) in eWAT, skeletal muscle, and liver. HFD mice were treated with miR-181b or NS ctrl mimics in an analogous manner as shown in Figure 2 and stimulated in the presence or absence of insulin for an additional 10 minutes before tissue harvest. In insulin-stimulated miR-181b--treated mice, phospho-Akt (Ser473) was significantly increased by 2.2-fold in eWAT, whereas there were no significant differences in skeletal muscle or liver (Figure 6A). Phospho-Akt (Thr308) was not changed by miR-181b delivery compared with controls in all the tissues examined. Moreover, the effect of miR-181b delivery on upstream insulin signaling was examined in eWAT. Because inflammatory stimuli can blunt insulin action by affecting the phosphorylation of mediators in upstream insulin signaling, such as insulin receptor-β and insulin receptor substrate 1,42–45 their phosphorylation status was examined by immunoprecipitation assays from eWAT lysates (Figure 6B). MiR-181b delivery did not

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**References and Data**

- [Figure 4](#): miR-181b does not inhibit the proliferation, migration, and activation of monocytes/macrophages. A, Paraffin sections of epididymal white adipose tissue (eWAT) were stained with F4/80, DAPI, and Ki67. The percentages of Ki67 among F4/80-positive cells were calculated. Mean±SEM, n=7 to 10 mice per group. B, Adoptive transfer of PKH26-labeled monocytes from obese mice overexpressing miRNA-negative control mimics (NS-m) or miR-181b, and fluorescence-activated cell sorting (FACS) analysis of PKH26-positive cells were calculated. Mean±SEM, n=7 to 10 mice per group. C, Peripheral blood mononuclear cells (PBMCs) were isolated from NS-m or miR-181b--treated mice fed on a high-fat diet for 14 weeks and stimulated in the presence of medium from adipocytes or endothelial cells (ECs). Cox-2 expression was determined by quantitative polymerase chain reaction (qPCR) analysis. Data show mean±SEM, n=6 mice per group. HFD indicates high-fat diet; IL, interleukin; N.S., nonsignificant; SSC, side scatter; and TNF-α, tumor necrosis factor-α.

- [Figure 5](#): Glucose uptake in 3T3-L1 adipocytes is promoted by conditioned medium from endothelial cells overexpressing miR-181b. A, Adipocytes were transfected with miRNA-negative control mimics (NS-m) or miR-181b, and glucose uptake was quantified. B, Adipocytes were cultured with conditioned medium from endothelial cells (ECs) overexpressing NS-m or miR-181b, and glucose uptake was quantified. Mean±SEM, n=4; *P<0.05. N.S. indicates nonsignificant; and Supe, supernatant.
affect the expression of phospho-insulin receptor-β (Tyr1162) and phospho-receptor substrate 1 (Ser307) in eWAT, suggesting upstream insulin signaling was not changed by miR-181b. Both FoxOs and endothelial nitric oxide synthase (eNOS) are important molecules mediating insulin signaling events downstream of phospho-Akt in ECs.46–48 We found phospho-FoxO1 (Ser 256) is increased ≤1.7-fold (Figure 6D) and NO activity by 1.5-fold (Online Figure 6E) and reduced ICAM-1 expression in eWAT of miR-181b–treated mice compared with controls after insulin stimulation (Figure 6B). Consistently, miR-181b overexpression increased Akt phosphorylation at Ser473 and reduced nuclear accumulation of FoxO1 at 10 minutes after insulin stimulation in ECs (Figure 6C). Similarly, miR-181b increased phospho-eNOS (Ser1176) by 1.7-fold (Figure 6D) and NO activity by 1.5-fold (Online Figure III) in eWAT compared with controls after insulin stimulation. In a separate experiment, obese mice were treated with miR-181b using the same dosing regimen as outlined in Figure 2, and ECs were isolated from eWATs to examine the effects of miR-181b delivery on insulin signaling and inflammation. Consistent with the effects of miR-181b on insulin signaling and inflammation in eWATs, we found miR-181b increased the phosphorylation of Akt by ≈1.6-fold (Figure 6E) and reduced ICAM-1 expression by 43% in ECs isolated from eWATs (Online Figure IV). These data indicate that miR-181b delivery reduced insulin resistance and inflammation in ECs within eWATs. We also examined the expression of genes involved in thermogenesis and hepatic glucose production. The mRNA expression of UCP-1, PRDM16, and PGC-1α genes were not changed in brown fat and eWAT by miR-181b, suggesting that the thermogenic program is not affected by miR-181b delivery (Online Figure VA). To exclude any effects of miR-181b on hepatic glucose production, we examined miR-181b delivery on the expression of key metabolic enzymes involved in maintaining hepatic glucose homeostasis in liver from mice described in Figure 2. MiR-181b had no effect on mRNA expression for glycogen synthase, glucokinase, pyruvate kinase, glycogen phosphorylase, FBP1 (fructose1,6-biphosphatase), G6P (glucose-6-phosphatase), and phosphoenolpyruvate carboxykinase (Online Figure VB). Finally, miR-181b delivery had no effect on regulating lipid homeostasis in liver revealed by Oil Red O staining (Online Figure VC). These data suggest that systemic delivery of miR-181b improves glucose homeostasis and insulin sensitivity in a tissuespecific manner by promoting Akt phosphorylation and sensitizing insulin action in eWAT independent of any effects on insulin signaling in the liver and skeletal muscle, or lipid accumulation in the liver.

The reduction of endogenous miR-181b by inflammatory stimuli such as TNF-α could affect insulin signaling in ECs. Indeed, TNF-α treatment reduced insulin-induced Akt phosphorylation in ECs (Online Figure VIA) as previously described.49 MiR-181b inhibition reduced insulin-induced Akt phosphorylation, which was potentiated in the presence of TNF-α treatment (Online Figure VIA). Furthermore, miR-181b overexpression rescued the reduction of insulin-induced Akt phosphorylation by TNF-α treatment (Online Figure VIB). The data imply that the early reduction of endogenous miR-181b in ECs of eWAT is likely involved in the pathogenesis of endothelial insulin resistance in eWATs during the development of obesity.

**MiR-181b Targets PHLP2** MiR-181b could improve insulin signaling by directly regulating a target intrinsic to this pathway or by suppressing
target genes of other inter-related signaling pathways. Our previous studies demonstrated that miR-181b can repress importin-α3, a protein involved in the nuclear translocation of NF-κB (p65/p50), by binding to its 3′-untranslated region (UTR). 13,34 MiR-181b could inhibit adipose tissue inflammation by reducing importin-α3 expression in ECs. We examined NF-κB p65 nuclear accumulation in adipose tissue ECs. Surprisingly, nuclear p65 expression was not significantly induced by HFD feeding, and miR-181b delivery did not reduce p65 nuclear accumulation in adipose tissue ECs (Online Figure VII). A combined strategy using bioinformatics and microarray gene chip profiling was taken to identify potential miR-181b direct targets. Genes reduced by miR-181b overexpression identified by microarray gene chip analysis (GEO database accession no. GSE35030)34 that are also pre-

Figure 7. MicroRNA-181b targets Pleckstrin homology domain leucine-rich repeat protein phosphatase (PHLPP2). A, Bioinformatic approach predicts miR-181b direct targets among genes reduced by miR-181b overexpression in endothelial cells (ECs) identified by microarray gene chip profiling. B, Gene ontology analysis of 306 genes identified in A. C, Western blot analysis of ECs transfected with 10 nmol/L miRNA-negative control mimics (NS-m) or 181b-m. D, micro sirnucleoprotein IP analysis of enrichment of PHLPP2 mRNA in human umbilical vein endothelial cells (HUVECs) transfected with NS-m or 181b-m, n=2 independent experiments. E, Luciferase reporter assay of PHLPP2 3′ untranslated region (UTR) in the presence of pcdNA3.1(+) and pcdNA3.1-miR-181b, and pcdNA3.1-miR-181b mutant in HUVECs, n=3 independent experiments. F, Pharmacological inhibition or siRNA knockdown of PHLPP2 increases pSer473-Akt in ECs in response to 100 nmol/L insulin at 10 minutes. G, Western blot analysis of PHLPP2 expression in epidymal white adipose tissue (eWAT), n=3 to 5. H, PHLPP2 expression was detected in ECs isolated from eWAT of obese mice treated with NS-m or miR-181b using the dosing regimen as outlined in Figure 2, n=6 mice per group. All values show mean±SEM; *P<0.05. DMSO indicates dimethyl sulfoxide; FC, fold-change; GO, gene ontology; and PITA, probability of interaction by target accessibility.
we found miR-181b reduced PHLPP2 protein expression in ECs (Figure 7C). To verify that miR-181b directly targets PHLPP2, we performed Argonaute2 microribonucleoprotein IP studies to assess whether PHLPP2 mRNA is enriched in the RNA-induced silencing complex after miR-181b overexpression. An ≈4-fold enrichment of PHLPP2 mRNA was observed after Argonaute2 microribonucleoprotein IP in the presence of miR-181b, when compared with that with the miRNA-negative control (Figure 7D). Furthermore, miR-181b reduced the PHLPP2 3′-UTR activity by 54% (Figure 7E). To show the specificity of miR-181b on PHLPP2 3′-UTR, the seed sequence in pcDNA3.1-miR-181b construct was mutated. MiR-181b mutant lost the ability to inhibit the activity of PHLPP2 3′-UTR as shown in Figure 7E. Importantly, pharmacological inhibition53 or siRNA knockdown of PHLPP2 promoted insulin-induced Akt phosphorylation in ECs (Figure 7F). To examine whether miR-181b targets PHLPP2 in vivo, PHLPP2 expression was examined in lysates of eWAT, skeletal muscle, and liver from obese mice treated with miR-181b (twice a week for 6 weeks). Systemic delivery of miR-181b reduced PHLPP2 protein expression in eWAT, but not in skeletal muscle or liver (Figure 7G; Online Figure VIII-A). Because PHLPP2 expression is significantly lower in liver (nearly undetectable) than in eWAT and skeletal muscle, PHLPP2 may play a minimal role in regulating insulin signaling in liver (Online Figure VIII-B). Moreover, miR-181b treatment (twice a week for 6 weeks) reduced PHLPP2 expression by 55% in ECs isolated from eWAT of obese mice (Figure 7H). These results identify PHLPP2 as a bona fide direct target of miR-181b. PHLPP2 expression was significantly increased in ECs of eWAT from mice fed an HFD for 2, 6, or 12 weeks (Online Figure VIIIC), suggesting a counter-regulation of the miR-181b target PHLPP2 during the development of insulin resistance. In addition to PHLPP2, we examined the effects of miR-181b on other potential phosphatases, including INPPL5E, PPM1A, CTDSPL, and PPAR2B, which are predicted as miR-181b targets among 306 genes. MiR-181b overexpression reduced the expression of CTDSPL and PPAR2B by 41% and 56%, respectively, in human umbilical vein endothelial cells (Online Figure VIIID). In contrast, miR-181b overexpression had no effects on the expression of PPM1A and INPPL5E. However, siRNA-mediated knockdown of CTDSPL or PPAR2B did not promote the phosphorylation of Akt at Serine 473 in response to insulin in human umbilical vein endothelial cells (Online Figure VIIIE), suggesting CTDSPL and PPAR2B did not mediate miR-181b’s effect on insulin-Akt phosphorylation. It has been reported that miR-181b reduces insulin-like growth factor (IGF)-1R expression in tumor cells, and inhibits VEGF (vascular endothelial growth factor)-induced PI3K-Akt signaling42; in contrast, in T cells it may reduce PTEN expression, thereby promoting PI3K-Akt signaling.55 Therefore, we examined whether miR-181b regulates Akt phosphorylation by reducing IGF-1R and PTEN expression in ECs. As shown in Online Figure VIIIF, miR-181b overexpression did not reduce PTEN and IGF-1R expression in ECs, and also had no effect on PTEN expression in eWAT. These data suggest a cell-specific regulation of PTEN and IGF-1R expression by miR-181b. Collectively, these results identify PHLPP2 as a direct target of miR-181b that may mediate miR-181b’s effects on the insulin signaling pathway.

PHLPP2 Knockdown Improves Glucose Tolerance and Insulin Sensitivity in Diet-Induced Diabetic Mice

To examine whether PHLPP2 knockdown will phenocopy miR-181b’s effects to improve glucose homeostasis, insulin sensitivity, and reduce adipose tissue dysfunction in vivo, C57BL/6 obese mice were therapeutically treated with PHLPP2 siRNAs or negative control siRNAs for 6 weeks (twice a week, 1 nmol/injection IV; Figure 8A). PHLPP2 siRNAs injection did not affect the body weights of mice compared with control siRNAs (Figure 8B). However, GTT and insulin tolerance test studies revealed that PHLPP2 knockdown significantly improved glucose tolerance (Figure 8C and 8D) and insulin sensitivity (Figure 8E and 8F) by 19% and 20%, respectively, compared with mice treated with control siRNAs controls (Figure 8D and 8F). The effect of PHLPP2 knockdown on insulin tolerance test and GTT was associated with ≈1.5-fold increase of Akt phosphorylation at Ser473 in eWAT but not in liver (Figure 8G). Macrophage content indicated by Mac2 staining was also reduced by 58% in eWAT of PHLPP2 siRNA–treated mice (Figure 8H). In a separate experiment, 3 daily injections of PHLPP2 siRNA lead to a 72% and 12% reduction of PHLPP2 mRNA expression in adipose tissue ECs and adipocytes, respectively, suggesting that the majority of systemically delivered siRNAs accumulate in adipose tissue ECs (Figure 8I). Interestingly, PHLPP2 expression revealed by immunostaining was increased by 33% in ECs isolated from diabetic patients compared with control subjects (Figure 8J; Online Figure IX). PHLPP2 inhibition may represent a new therapeutic approach to reduce insulin resistance by improving vascular EC function within eWAT. These data suggest that knockdown of PHLPP2 improves glucose tolerance and insulin sensitivity, reduces adipose tissue endothelial inflammation, and inhibits macrophage accumulation.

Discussion

Several miRNAs have been identified as regulators of obesity-induced insulin resistance. For example, miR-802, miR-143, and miR-103/7 all regulate glucose metabolism and insulin sensitivity in obesity.56–58 It remains unknown whether miRNAs affect insulin sensitivity by regulating EC function within eWAT. In this study, we have discovered that (1) the expression of miR-181b is reduced in white adipose tissue ECs of HFD mice, which can be rescued by miR-181b systemic delivery; (2) miR-181b delivery improves glucose homeostasis and insulin sensitivity associated with reduced EC activation, macrophage infiltration, and inflammatory phenotype in eWAT; (3) miR-181b had no direct effects on regulating monocyte/macrophage activation, proliferation, or recruitment in vivo; (3) miR-181b targets PHLPP2, a phosphatase that dephosphorylates Akt at Ser473 in ECs; and (4) siRNA-mediated knockdown of PHLPP2 phenocopies miR-181b’s effect on glucose homeostasis, insulin sensitivity, and eWAT macrophage accumulation. We demonstrated that enhanced insulin signaling in adipose ECs exerts beneficial effects and promotes glucose...
uptake in adipocytes in a paracrine manner, and importantly, improves systemic glucose homeostasis and insulin sensitivity without altering hepatic steatosis or lipid profiles.

Several studies have been performed by other groups to uncover the causal relationships among vascular endothelial function, inflammation, and metabolic insulin resistance. For example, vascular inflammation (increased phosphorylation of IκBα and ICAM-1 expression) and insulin resistance (reduction of miR-181b in ECs of eW AT) are detectable in aortas of mice fed an HFD for 1 week,15 which precedes the onset of peripheral insulin resistance in liver, skeletal muscle, and adipose tissue. Another group showed systemic insulin resistance occurred in mice fed an HFD for 3 days revealed by GTT and hyperinsulinemic-euglycemic clamp studies.59 These data suggest that ECs Adipocytes

Figure 8. Systemic delivery of Pleckstrin homology domain and leucine-rich repeat protein phosphatase 2 (PHLPP2) siRNA improves glucose tolerance and insulin sensitivity in diet-induced obese mice. A, Schema of experimental procedure. C57BL/6J mice were fed a 60% high-fat diet (HFD) for 12 weeks. Six weeks after HFD, mice were treated with negative control siRNA or PHLPP2 siRNA for the subsequent 6 weeks as indicated (0.6 mg/kg IV). B, Body weights over time of mice injected with control siRNAs or PHLPP2 siRNAs, respectively. C and D, Blood glucose levels were measured on week 11 for the insulin tolerance test (ITT) and week 12 for the glucose tolerance test (GTT). Values were compared with basal glucose levels that were set as 100% for ITT. D and E, Area under the curves (AUC) for ITT and GTT were quantified. G, Western blot analysis of Akt and pSer473-Akt in epidymal white adipose tissue (eWAT) and liver. H, Paraffin sections of eWAT were stained with Mac2, and the positive areas were quantified. B-H, n=6 to 7. I, Mice were injected with negative control or PHLPP2 siRNAs 3× on consecutive days, and the expression of PHLPP2 was examined in endothelial cells (ECs) or adipocytes isolated from eWAT, n=3 mice per group. J, Quantification of PHLPP2 protein expression in ECs freshly isolated from control and diabetic subjects, n=11 subjects each group. All data show mean±SEM; *P<0.05.

by activated eNOS inhibits NF-κB activity, decreases cytokine-induced endothelial activation, and shifts macrophage polarization toward an M2 anti-inflammatory phenotype.62,64 MiR-181b delivery increased the phosphorylation of Akt and eNOS, increased NO activity (Online Figure III), and decreased FoxO activity and ICAM-1 expression in eWATs (Figure 6). In ECs of eWATs, miR-181b also increased Akt phosphorylation and decreased ICAM-1 expression (Figure 6E; Online Figure IV). In contrast, miR-181b delivery had no intrinsic effects on macrophage activation, infiltration, and proliferation (Figure 4). However, miR-181b delivery reduced macrophage accumulation and shifted M1 macrophages to an M2 anti-inflammatory phenotype in eWATs (Figure 3A). These data indicate that miR-181b improved insulin resistance in eWATs by primarily improving endothelial Akt--eNOS--NO signaling through targeting PHLPP2, an effect reducing endothelial ICAM-1 expression, EC-leukocyte interactions, and favorably shifting M1 to M2 macrophages thereby generating an anti-inflammatory milieu in eWAT. This anti-inflammatory milieu in eWATs generated by miR-181b may also promote glucose uptake in adipocytes through a paracrine manner (Figure 5).

Our results demonstrate that miR-181b delivery improves insulin signaling in epididymal fat but not in liver or skeletal muscle. There are at least 2 reasons that may account for this tissue-specific effect: (1) miRNAs may confer target and functional specificity in different cell types or tissues.65,66 MiR-181b may target PHLPP2 in eWAT but not liver and skeletal muscle (Figure 7G; Figure VIII A) and (2) tissue- and cell-specific accumulation of exogenous miR-181b. Although...
miR-181b delivery leads to its highest overexpression in liver, exogenous miR-181b is enriched higher in adipose ECs than in liver or skeletal muscle ECs (Online Figure III B). A fenestrated, discontinuous endothelium in liver may cause this differential accumulation of exogenous miR-181b. Furthermore, expression of the miR-181b target PHLPP2 is minimally expressed in liver compared with eWAT, a finding that may account for the lack of miR-181b’s effects on insulin signaling in liver. Interestingly, improved insulin signaling in liver ECs potentiated hepatic insulin resistance, suggesting potential phenotypic differences of liver ECs versus eWAT ECs.

NF-κB–mediated vascular inflammation participates in the pathogenesis of obesity-associated insulin resistance. We previously demonstrated that miR-181b reduces acute expression (or inhibition of PHLPP2 expression) in adipose tissue ECs in eW AT because miR-181b overexpression improves insulin sensitivity. MiR-181b–mediated effects were selective for ECs of eW AT because miR-181b overexpression is significantly induced in white adipose tissue ECs after 12 weeks of HFD, and miR-181b delivery had no inhibitory effect (Online Figure VII), suggesting that miR-181b targets different gene(s) than importin-α3 in adipose tissue ECs. Indeed, using a combination of bioinformatics and gene microarray profiling studies, our studies revealed that miR-181b directly targets PHLPP2 in ECs. Because miRNAs are known to regulate several targets, our study cannot rule out the possibility that miR-181b targets additional gene(s) that mediate its beneficial effects on insulin sensitivity and glucose homeostasis.

In our study, epididymal fat mass in miR-181b–treated HFD mice was not reduced, an effect suggesting that miR-181b delivery does not reduce the capacity of white adipocytes/adipose tissue to store lipids in the context of overnutrition. Consistent with this, the level of circulating triglycerides and liver lipid content were not significantly different between conditions. Furthermore, adipocytes incubated with conditioned medium from ECs overexpressing miR-181b exhibited markedly improved insulin resistance, an effect highlighting the potential importance of EC–adipocyte interactions in regulating the insulin-resistant state. Our data also suggest that miR-181b is able to reduce adipose tissue EC inflammation, leukocyte accumulation, and improve systemic glucose homeostasis and insulin sensitivity without potentiating the development of hepatic steatosis.

In conclusion, our study in HFD mice demonstrates that miR-181b expression is reduced in response to HFD-induced obesity and that rescue of miR-181b in the microvasculature of eWAT is sufficient to improve glucose homeostasis and insulin sensitivity. MiR-181b delivery decreases inflammation in adipose tissue ECs in eWAT by targeting the phosphatase PHLPP2, an effect that increases phospho-AKT (Ser473) to improve insulin signaling. MiR-181b–mediated effects were selective for ECs of eWAT because miR-181b overexpression in adipocytes did not promote glucose uptake. These data indicate that strategies aimed at improving microvascular EC function in visceral fat in general and restoring miR-181b expression (or inhibition of PHLPP2 expression) in adipose tissue ECs, in particular, may provide the basis for the rationale design of novel therapies for insulin resistance and its attendant cardiovascular complications.

Acknowledgments

We thank Dr Alexandra Newton (University of California, San Diego) for providing the PHLPP2 inhibitors.

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Disclosures

None.

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MicroRNA-181b Improves Glucose Homeostasis and Insulin Sensitivity by Regulating Endothelial Function in White Adipose Tissue

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Supplemental Material

MicroRNA-181b improves glucose homeostasis and insulin sensitivity by regulating endothelial function in white adipose tissue

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Reagents and cell culture

Pre-miR™ miRNA precursor molecules negative (non-silencing) control #1 (AM17110) and Hsa-miR-181b-5p Pre-miR™ miRNA precursor (PM12442) were ordered from Ambion. The mature miR-181b sequence is 5'-AACAUUCAUUGCUGUGGUGGUU-3', and its miRBase Accession# is MIMAT0000257. For in vivo studies, oligomers with the same sequence were synthesized on a larger scale by Ambion. Anti-miR miRNA inhibitors-negative control #1 (AM17010), and miR-181b inhibitor (AM12442) were from Ambion. Lipofectamine™ 2000 reagent was from Invitrogen.

Human umbilical vein endothelial cells (HUVECs) (cc-2159) was obtained from Lonza and cultured in endothelial cell growth medium EGM®-2 (cc-4176). Cells were treated with free fatty acid as previously described,1 or other stimuli. Silencer® Select siRNA against INPP5E, PPM1A, CTDSPL, PPAR2B, and PHLPP2 were ordered from Ambion.

Real-time quantitative PCR

Tissues were homogenized using TissueLyser II (QIAGEN). Total RNA was isolated from tissues or cells using TRizol® Reagent (Invitrogen) according to the manufacturer’s instructions. Briefly, samples were mixed with chloroform (5:1 v/v sample/chloroform) and centrifuged at 12,000 x g for 15 minutes at 4°C. The aqueous phase containing total RNA was collected, diluted 1:1 (v/v) in isopropanol, and precipitated by centrifugation at 12,000 x g for 15 minutes at 4°C. Pellets were washed with 75% ethanol, dried, and resuspended in nuclease-free water.

QuantiTect Reverse Transcription Kit (QIAGEN) was used to generate cDNA synthesized from 1 μg of total RNA and QuantiTect SYBR Green PCR Kit was used for real-time qPCR with the Mx3000P Real-time PCR system (Stratagene). For primer sequences, refer to Online Table II. Synthesis of stem-loop miRNA cDNAs was achieved by using TaqMan® MicroRNA Reverse Transcription Kit (PN4366596). To detect mature miRNA sequences, TaqMan® MicroRNA Assays hsa-miR-181b (Assay ID 001098), TaqMan® MicroRNA Assays hsa-miR-181a (Assay ID 000480), TaqMan® MicroRNA Assays hsa-miR-181c (Assay ID 000482), U6 snRNA (Assay ID 001973), and TaqMan® Universal PCR Master Mix No AmpErase® UNG (PN4324018) were used. The Delta-Delta CT method with formula: 2^[(-delta)(delta)Ct] was used to calculate relative gene expression values.

Western blot assay

Cells or mouse tissues were lysed in RIPA buffer (Boston BioProducts, Inc.). Protein concentration of tissue extracts or cell lysates was determined by using Pierce BCA Protein Assay Kit (Pierce). Proteins were separated by a 4–15% Mini-PROTEAN® TGX™ Precast Gel (Bio-Rad) and transferred to a methanol-activated PVDF membrane (Bio-Rad). The membrane was blocked in TBST containing 5% nonfat milk at room temperature for 1 hour and subsequently incubated with primary antibodies overnight at 4 °C. After wash, the membrane was incubated with HRP-conjugated secondary antibodies (Pierce) for 1 hour. Proteins were detected using Amersham ECL Prime Western Blotting Detection Reagent (GE Healthcare). Primary antibodies used were anti-pan-Akt (#2920, Cell Signaling), anti-phospho-Akt (Ser473; #4060, Cell Signaling), anti-phospho-Akt (Thr308; #2965, Cell Signaling), anti-IRS1 (#2382, Cell Signaling), anti-insulin receptor beta (sc-711, Santa Cruz), anti-phospho-IRS1 (Ser307; 05-1087, EMD Millipore), anti-phospho-insulin receptor beta (Tyr1162/1163; sc-25103, Santa Cruz), anti-FoxO1 (#9454, Cell Signaling), anti-phospho-FoxO1 (Ser256; #9461, Cell Signaling), polyclonal Rabbit Anti-eNOS (610298, BD Transduction Laboratories), anti-phospho-eNOS (Ser1177; #9571, Cell Signaling), anti-PTEN (#9188, Cell Signaling), anti-IGF-1R (#9750, Cell Signaling), anti-GAPDH (#2118, Cell Signaling), anti-ICAM-1 (AF-796, R&D Systems), and anti-PHLPP2
Quantitation was performed using the software Image J. Protein expression was normalized by a loading control.

Diet-induced obesity, glucose and insulin tolerance tests

C57BL/6J WT mice were purchased from the Jackson Laboratory. All mice were males and were maintained on a 12-hour light/dark cycle in a pathogen-free animal facility. Mice were kept on a standard chow diet or on a high-fat diet containing 60 kcal% fat (Research Diets, D12492) for 12 weeks. Mice had free access to food and water. Six weeks after HFD, mice were treated with miRNAs or siRNAs for 6 weeks (twice or once a week, i.v. 0.6 mg/kg). Systemic delivery of miRNAs or siRNAs was performed as described in our previous study.2 ITT and GTT were performed at week 5 and 6 respectively after miR-181b treatment. All protocols concerning animal use were approved by the Institutional Animal Care and Use Committee at Harvard Medical School, Boston, MA and conducted in accordance with the National Institutes of Health Guide for the Care and Use of Laboratory Animals.

For glucose tolerance tests (GTTs), mice were fasted for 12 hours, and then injected i.p. with d-glucose (Sigma, 1.0 g per kg of body weight). Insulin tolerance tests (ITTs) were performed on mice after 6 hours fasting. Recombinant human regular insulin (0.75 U per kg of body weight, Humulin R, Eli Lilly) was given to mice by i.p. injection. Blood glucose levels were measured before injection and at 15, 30, 60, 90, and 120 minutes after glucose or insulin injection using One Touch Ultra glucometer (LifeScan).

Luciferase activity assay and cell culture transfection

PHLPP2 3’-UTR sequences were PCR-amplified with specific primers, followed by purification and restriction enzyme digestion. Sequences were cloned into the pMIR-REPORT™-Luciferase vector between SpeI and MluI restriction sites. HUVECs cultured in 12-well plates were transfected in triplicates using Lipofectamine 2000 (Invitrogen) with 200 ng of the final construct per well. The next day, cells were transfected with 10nmol of either a miRNA non-silencing control or miR-181b. Cells were collected 36–48 hours after transfection and assayed using the Luciferase Reporter Assay System (Promega). Cells were co-transfected with pcDNA3.1(+), pcDNA3.1(+)-miR-181b, or pcDNA3.1(+)-miR-181b mutant. The seed sequence of miR-181b was mutated using QuikChange II XL Site-Directed Mutagenesis Kit from Agilent Technologies. Results were normalized to the amounts of protein and expressed relative to the average value of the control.

Blood chemistry

Plasma insulin was measured using the Ultra Sensitive Rat Insulin ELISA Kit (90080, Crystal Chem). Mouse Cytokine 32-Plex Discovery Assay was performed by Eve Technologies. Triglyceride levels were determined using Infinity™ Triglycerides Liquid Stable Reagent (Thermo Scientific) as described by the protocol. Total cholesterol was measured using the Infinity™ Cholesterol Reagent (Thermo Scientific). Cholesterol and triglyceride standard were from Pointe Scientific, Inc. Plasma free fatty acid was measured using Free Fatty Acid Quantification Kit (ab65341, Abcam).

Glucose uptake

Mouse mature adipocytes were serum-starved for 3–6 hours in DMEM and then incubated with KRH buffer (121 mM NaCl, 5 mM KCl, 0.33 mM CaCl2, 1.2 mM MgSO4, 12 mM Hapes, pH 7.4) with 25 nM insulin at 37 °C for 20 minutes and 2-deoxy-D-[2,6-3H]glucose (0.33 μCi ml⁻¹) for an additional 10 minutes. Uptake was stopped by three rapid washes on ice with KRH containing cytochalasin B (Sigma), the cells were solubilized with KRH buffer containing 0.1% SDS, and radioactivity was measured by liquid scintillation counting.
Histological and immunohistological examinations

For immunohistology, tissues were fixed with neutral buffered 10% formalin solution (HT501128, Sigma), embedded in paraffin wax, cut into sections, and then deparaffinized. Mac-2 staining was performed on the Leica Bond III autostainer. Antigen retrieval was performed using Bond ER1 (AR9961, Leica) for 30 minutes. Sections was incubated with anti-Mac-2 (CL8942AP, Cedarlane Labs) in 1:50,000 dilutions for 30 minutes at RT. Primary antibodies binding to tissue sections was visualized using Bond Polymer Refine Detection kit (DS9800, Leica), and counterstained with hematoxylin. Images were captured by a digital system, and the staining area was measured using computer-assisted image quantification (Image-Pro Plus software, Media Cybernetics). For immunofluorescence staining, antigen retrieval was performed by boiling the slides for 10 minutes in 10mM sodium citrate pH6.0 with a pressure cooker. The sections were then incubated with 1mg/ml sodium borohydride for 5 minutes at room temperature. After three washes with TBS, the sections were incubated with 5% normal donkey serum (Jackson ImmunoResearch Lab Inc.) for 1 hr at room temperature. Slides were then incubated with Rabbit anti-Ki-67 (1:200; RM-9106-S1, Thermo Scientific) and Rat anti-F4/80 (1:100; 14-4801-85, eBioscience) overnight at 4 °C. The slides were washed three times and incubated with Alexa647 conjugated Donkey anti-rabbit and Dylight549 conjugated Donkey anti-rat secondary antibodies. Sections were then washed three times with TBS and counterstained with Hoechst (H21492, Life technology) before mounting with Prolong Gold anti-fade mounting media (P36930, Life technology). Images were acquired on an upright Carl Zeiss LSM 510 confocal microscope equipped with Plan-Neofluar 40×/1.3 oil-immersion objective using the 405 nm diode laser, the 543 nm line of a HeNe543 laser, and the 633 nm line of a HeNe633 laser. Data were analyzed in a blinded fashion, by two independent observers.

Adoptive cell transfer, Isolation of stromal-vascular fraction and ECs, and flow cytometry

Adoptive transfer of monocytes was conducted as previously described. Monocytes were isolated from miR-181b- or control miRNA-treated obese mice, labeled with PKH26 in vitro, and injected into HFD-fed obese mice. Stromal vascular fractions were isolated from eWAT of the recipient mice, and subjected to FACS analysis, or EC isolation. Briefly, the perigonadal adipose tissues were isolated, minced into small pieces with scissors (1 x 2 mm2), digested with collagenase type II and dispase (1mg/ml each in DMEM/F12). Digested tissues were neutralized with DMEM/F12 medium containing 10% FBS, centrifuged at 500 xg for 10 minutes at 4 °C. Anti-Mouse CD11b Alexa Fluor® 488 (53-0112-80, eBioscience) and Anti-Mouse F4/80 Antigen APC (17-4801-80, eBioscience) were used for FACS analysis, which was performed on an LSR-II (Beckton-Deckinson, San Diego, CA) and analyzed with BD CellQuest software. For EC isolation, stromal-vascular fractions were incubated with sheep anti-rat IgG Dynabeads coated with PECAM-1 antibodies (557355, BD). The bead-bound cells were collected using a magnet and washed 3 times.

Isolation of fresh human endothelial cells and immunostaining

Isolation of EC from a forearm vein of human subjects was described previously. Briefly, ECs were captured by spring-wires from cannulated forearm veins of human subjects. Wires were cut, and cells were collected from wires by centrifugation in a dissociation buffer. Isolated cells were plated on slides, and fixed for staining. Anti-PHLPP2 (ab153918), anti-vWF (#M061601, Dako), and DAPI were used for staining and quantitative immunofluorescence was used to determine protein expression relative to control staining of cultured human aortic ECs. All human subject protocols were approved by BUMC IRB and subjects provided written informed consent.

Measurement of total nitric oxide levels
To measure total NO production, the concentration of nitrate and nitrite was determined in the lysates of eWAT using a total NO detection kit (ADI-917-020, Enzo Life Sciences). Fat tissues were harvested, immediately flash frozen, and homogenized in a buffer containing 1 mM protease inhibitor cocktail. Nitrate was converted to nitrite using nitrate reductase, and total nitrite was measured according to the manufacturer's instruction.

**Statistical analysis**

Results were expressed as mean ± SEM. We used a paired or unpaired Student t tests as appropriate for statistical comparison between two groups, and ANOVA for the comparison of 3 or more groups. Differences were considered significant when \( P<0.05 \).

**References**


Online Figure I

A. C57BL/6 mice were fed a HFD as indicated (0, 3, 7, or 14 days). Endothelial cells (ECs) were isolated from liver and skeletal muscle for qPCR. The expression of miR-181b was normalized to small RNA U6 expression and compared to its expression in mice on chow that was subsequently set to a value of one, n=5 – 6 per group. B. C57BL/6 mice were fed a HFD as indicated (0, 2, 6, or 12 weeks). ECs were isolated from epididymal white adipose tissue (eWAT) for qPCR. The expression of miR-181 was normalized to small RNA U6 expression and compared to the expression of miR-181b in mice on chow that was set to 100%, n=6 – 10 per group. C. C57BL/6 mice were fed a HFD for 0 or 2 weeks. ECs were isolated from eWAT for western blot analysis, n=6 – 9 mice per group. D. C57BL/6 mice were fed a HFD for 0 or 2 weeks. ECs were isolated from eWAT for western blot analysis, n=8 – 10 mice per group. Mice were fasted for 6 hours and administered with insulin 0.75 U/kg at 10 minutes before harvesting. E. C57BL/6 mice were fed a HFD for 0 or 2 weeks. ECs were isolated from eWAT for qPCR, n=6 – 9 mice per group. All data show mean ± SEM; *, P < 0.05.
Online Figure II

**A.** MiR-181b expression was detected in epididymal white adipose tissue (eWAT), skeletal muscle (SM), liver, and endothelial cells (ECs) isolated from eWAT of obese mice treated with NS-m or miR-181b using the dosing regimen as outlined in Figure 2, n=8–10 mice per group.

**B.** Mice were injected with NS-m or 181b-m three times on consecutive days. The expression of miR-181b was examined by qPCR analysis in eWAT and ECs isolated from eWAT, n=3 mice per group. Data show mean ± SEM; *, P < 0.05.

Online Figure II. A, MiR-181b expression was detected in epididymal white adipose tissue (eWAT), skeletal muscle (SM), liver, and endothelial cells (ECs) isolated from eWAT of obese mice treated with NS-m or miR-181b using the dosing regimen as outlined in Figure 2, n=8–10 mice per group. B, Mice were injected with NS-m or 181b-m three times on consecutive days. The expression of miR-181b was examined by qPCR analysis in eWAT and ECs isolated from eWAT, n=3 mice per group. Data show mean ± SEM; *, P < 0.05.
Online Figure III. Nitric oxide activity in epididymal white adipose tissue (eWAT). Obese mice were treated with NS-m or miR-181b using the dosing regimen as outlined in Figure 2 and stimulated with insulin (0.75 U per kg of body weight) before tissue harvesting, n=11 (NS-m) or n=12 (miR-181b) mice per group. Data show mean ± SEM; *, P < 0.05.
Online Figure IV. ICAM-1 expression was detected by qPCR in endothelial cells isolated from epididymal white adipose tissue of obese mice treated with NS-m or miR-181b using the dosing regimen as outlined in Figure 2, n=6 mice per group. Data show mean ± SEM; *, P < 0.05.
Online Figure V

A, qPCR analysis of genes involved in thermogenesis in brown adipose tissue (BAT) and epididymal white adipose tissue (eWAT) from mice described in Figure 2. GS: Glycogen synthase; GK: Glucokinase; PK: Pyruvate Kinase; G6P: Glucose-6-phosphatase; GP: Glycogen phosphorylase; FBP1: Fructose1,6-biphosphatase; PEPCK: Phosphoenolpyruvate carboxykinase. B, qPCR analysis of gene expression in liver from mice described in Figure 2. C, Frozen sections of liver from mice described in Figure 2 were stained with Oil Red O, and positive areas were quantified. All values show mean ± SEM, n=6 – 9 mice per group; *, P < 0.05. N.S., non-significant.
Online Figure VI

A

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**Online Figure VI.** A, HUVECs were transfected with 50 nM miRNA inhibitor negative control (NS-i), or miR-181b inhibitor (181b-i) for 24 hours. Cells were starved and treated with 10 ng/ml TNF-α or PBS for 8 hours followed by 100 nM insulin for 10 minutes, and harvested for western blot analysis, n=3 independent experiments. B, HUVECs were transfected with 10 nM miRNA non-specific negative control (NS-m), or miR-181b (181b-m) for 24 hours. Cells were starved and treated with 10 ng/ml TNF-α or PBS for 8 hours followed by 100 nM insulin for 10 minutes, and harvested for western blot analysis, n=3 independent experiments. Data show mean ± SEM; *, P < 0.05.
Online Figure VII. Paraffin sections of epididymal white adipose tissue (eWAT) from mice described in Figure 2 were stained with antibodies against CD31 and p65, and nuclear accumulation of p65 was quantified in ECs reflecting vehicle (n = 39 cells), NS-m (n= 73 cells) and 181b-m (n= 94 cells). Mean ± SEM, n=6 – 9 mice per group. N.S., non-significant.
Online Figure VIII

A

NS-m 181b-m

PHLPP2

GAPDH

Skeletal muscle

PHLPP2

1 min Exp

GAPDH

Liver

PHLPP2

15 min Exp

GAPDH

B

skeletal muscle eWAT liver

PHLPP2

GAPDH

C

Fold change (qPCR)

PHLPP2 in ECs of eWAT

Fold change (qPCR)

HFD (weeks)

0 2 6 12

D

INPP5E mRNA

Fold change (qPCR)

NS-m 181b-m

PPM1A mRNA

Fold change (qPCR)

NS-m 181b-m

CTDSPL mRNA

Fold change (qPCR)

NS-m 181b-m

PPAP2B mRNA

Fold change (qPCR)

NS-m 181b-m

E

Ctl siRNA CTDSPL siRNA Insulin

pSer473-Akt Akt

F

NS-m 181b-m Insulin

PTEN GAPDH

eWAT

NS-m 181b-m Insulin

PTEN IGF-1R

HUVECs

GAPDH

Figure legend is on the next page.
Online Figure VIII. **A** and **B**, Western blot analysis of PHLPP2 expression in skeletal muscle, liver, and epididymal white adipose tissue (eWAT). **C**, C57BL/6 mice were fed a HFD as indicated (0, 2, 6, or 12 weeks). Endothelial cells (ECs) were isolated from eWAT for qPCR. The expression of PHLPP2 was normalized to GAPDH expression and compared to the expression of PHLPP2 in chow-fed mice that was set to a value of 100%, n=6 –10 per group. **D**, HUVECs were transfected with 10 nM miRNA non-specific negative control (NS-m), or miR-181b (181b-m) for 36 hours, and harvested for qPCR analysis, n=3 per group. **E**, Ctl siRNA, CTDSPL siRNA, PPAP2B siRNA-transfected HUVECs were starved and treated with 100 nM insulin for 10 minutes. Cells were collected for western blot analysis of pSer473-Akt and total Akt. **F**, PTEN expression was examined in eWAT of obese mice treated with NS-m or miR-181b using the dosing regimen as outlined in Figure 2, n=6 mice per group (upper panel). Western blot analysis of PTEN and IGF-1R in HUVECs transfected with 10 nM miRNA non-specific control or miR-181b (lower panel). Data show mean ± SEM; *, P < 0.05.
Online Figure IX

Representative images show PHLPP2 staining in endothelial cells (ECs) freshly isolated from control and diabetic subjects.
Online Table I. Systemic delivery of miR-181b does not affect lipid profile, FFAs, insulin, fat mass, or body weight of obese C57BL/6 mice.

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<tr>
<th></th>
<th>Units</th>
<th>Ctl mimics</th>
<th>miR-181b</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total cholesterol</td>
<td>mg/dl</td>
<td>231.5 ± 22.4</td>
<td>231.3 ± 8.9</td>
</tr>
<tr>
<td>Triglycerides</td>
<td>mg/dl</td>
<td>95.5 ± 4.63</td>
<td>106.4 ± 4.65</td>
</tr>
<tr>
<td>FFAs</td>
<td>nmol/ml</td>
<td>236.8 ± 16.7</td>
<td>264.1 ± 18.4</td>
</tr>
<tr>
<td>Insulin</td>
<td>ng/ml</td>
<td>1.17 ± 0.11</td>
<td>0.91 ± 0.18</td>
</tr>
<tr>
<td>Body weight</td>
<td>g</td>
<td>43.3 ± 4.3</td>
<td>40.3 ± 4.8</td>
</tr>
<tr>
<td>Brown fat mass</td>
<td>mg</td>
<td>109.1 ± 14.5</td>
<td>113.1 ± 14.8</td>
</tr>
<tr>
<td>Epididymal fat mass</td>
<td>g</td>
<td>2.43 ± 0.11</td>
<td>2.57 ± 0.14</td>
</tr>
</tbody>
</table>

All values Ctl mimics vs. miR-181b, P=N.S., Mean ± SEM, n=6-10.
### Online Table II. Primers for real-time qPCR

<table>
<thead>
<tr>
<th>Name</th>
<th>Sequence (5' → 3')</th>
</tr>
</thead>
<tbody>
<tr>
<td>mouse VCAM-1 forward:</td>
<td>GTTCCAGCGAGGATCTACCA</td>
</tr>
<tr>
<td>mouse VCAM-1 reverse:</td>
<td>AACTCTTGACAACTATGCTG</td>
</tr>
<tr>
<td>mouse ICAM-1 forward:</td>
<td>GTGATGCTCAGGTATCCCATCCA</td>
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<td>mouse ICAM-1 reverse:</td>
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</tr>
<tr>
<td>mouse TNF-alpha forward:</td>
<td>CACAGTGACAGGCTGACC</td>
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<td>mouse IL-1beta forward:</td>
<td>GCAACTGTTCTCAGTGACTCAG</td>
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<td>mouse IL-1beta reverse:</td>
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<td>CACCGCACTTTTTTACGAG</td>
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<tr>
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<td>GACAGGTGAGGTTCACTGCCTTTCT</td>
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<tr>
<td>mouse NOS2 forward:</td>
<td>GTTCTCAGGCAAACAATACCAAGA</td>
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<td>mouse Mrc2 forward:</td>
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<tr>
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</tr>
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<tr>
<td>Gene</td>
<td>Forward Primer</td>
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<td>-----------------------------------------------------</td>
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<td>mouse GAPDH</td>
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<td>mouse SELE</td>
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<tr>
<td>mouse INPP5E</td>
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</tr>
<tr>
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<td>human PPM1A</td>
<td>AGGGGCAGGGTAATGGGTT</td>
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<td>human CTDSPL</td>
<td>GTGGCTGACCTCAGATGACCC</td>
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<td>human PPAP2B</td>
<td>CTCATGTTGACACTCAGTATAA</td>
</tr>
<tr>
<td>human PHLPP2</td>
<td>ATGGAGCAGACACTCAGAATGCA</td>
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</table>