Activation of AKT by O-Linked N-Acetylglucosamine Induces Vascular Calcification in Diabetes Mellitus

Jack M. Heath, Yong Sun, Kaiyu Yuan, Wayne E. Bradley, Silvio Litovsky, Louis J. Dell’Italia, John C. Chatham, Hui Wu, Yabing Chen

Rationale: Vascular calcification is a serious cardiovascular complication that contributes to the increased morbidity and mortality of patients with diabetes mellitus. Hyperglycemia, a hallmark of diabetes mellitus, is associated with increased vascular calcification and increased modification of proteins by O-linked N-acetylglucosamine (O-GlcNAcylation).

Objective: We sought to determine the role of protein O-GlcNAcylation in regulating vascular calcification and the underlying mechanisms.

Methods and Results: Low-dose streptozotocin-induced diabetic mice exhibited increased aortic O-GlcNAcylation and vascular calcification, which was also associated with impaired aortic compliance in mice. Elevation of O-GlcNAcylation by administration of Thiamet-G, a potent inhibitor for O-GlcNAcase that removes O-GlcNAcylation, further accelerated vascular calcification and worsened aortic compliance of diabetic mice in vivo. Increased O-GlcNAcylation, either by Thiamet-G or O-GlcNAcase knockdown, promoted calcification of primary mouse vascular smooth muscle cells. Increased O-GlcNAcylation in diabetic arteries or in the O-GlcNAcase knockdown vascular smooth muscle cell upregulated expression of the osteogenic transcription factor Runx2 and enhanced activation of AKT. O-GlcNAcylation of AKT at two new sites, T430 and T479, promoted AKT phosphorylation, which in turn enhanced vascular smooth muscle cell calcification. Site-directed mutation of AKT at T430 and T479 decreased O-GlcNAcylation, inhibited phosphorylation of AKT at S473 and binding of mammalian target of rapamycin complex 2 to AKT, and subsequently blocked Runx2 transactivity and vascular smooth muscle cell calcification.

Conclusions: O-GlcNAcylation of AKT at 2 new sites enhanced AKT phosphorylation and activation, thus promoting vascular calcification. Our studies have identified a novel causative effect of O-GlcNAcylation in regulating vascular calcification in diabetes mellitus and uncovered a key molecular mechanism underlying O-GlcNAcylation–mediated activation of AKT. (Circ Res. 2014;114:1094-1102.)

Key Words: diabetes mellitus ■ myocytes, smooth muscle ■ vascular calcification

Diabetes mellitus has been strongly associated with chronic cardiovascular and renal complications, which leads to an increased morbidity and mortality in affected patients. Increased vascular calcification is commonly observed in diabetic arteries and in the intimal and medial layers of the vessel walls, which increases arterial stiffness, reduces compliance of the blood vessels, and increases the risk of cardiovascular events and mortality. Therefore, understanding of the molecular mechanisms underlying diabetic vascular calcification should provide important insights into overcoming these adverse clinical outcomes.

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Hyperglycemia, or elevated blood glucose, is a characteristic feature of diabetes mellitus. In addition to producing bioenergetic substrates via the tricarboxylic acid cycle, glucose metabolism through the hexosamine biosynthesis pathway generates UDP-GlcNAc, a substrate for protein O-linked β-N-acetylglucosaminyltransferase (O-GlcNAcylation). Hyperglycemia has also been associated with vascular calcification in vitro; however, the mechanistic function of hyperglycemia and O-GlcNAcylation in regulating diabetic vascular calcification is unknown. O-GlcNAcylation is a dynamic and reversible modification that regulates the activity and function of numerous cytoplasmic and nuclear proteins. Like protein phosphorylation, O-GlcNAcylation occurs on serine and threonine residues, and thus these two protein modifications cross-talk to regulate cellular signaling and function. Unlike phosphorylation, however, O-GlcNAcylation is tightly regulated by two specific enzymes: β-N-acetylglucosaminyltransferase and β-N-acetylglucosaminidase.
Protein O-GlcNAcylation regulates a variety of cellular functions in different tissues, including the cardiovascular system, related to diabetes mellitus and vascular injury. O-GlcNAcylation was found to serve as a cellular nutrient and stress sensor by modulating the function of specific proteins in response to glucose levels. In cardiomyocytes, O-GlcNAcylation is associated with cell survival in response to oxidative stress and preserves heart function in models of heart failure. In contrast, increased O-GlcNAcylation has been observed to influence contractility in left ventricular tissue from humans with heart failure negatively. In human diabetic carotid plaques, the overall O-GlcNAcylation level is increased. In addition, patients with diabetes mellitus have a higher incidence of calcified plaque. However, the contribution of elevated O-GlcNAcylation in the diabetic vasculature to vascular calcification is unknown.

The present studies investigate the function of O-GlcNAcylation in regulating vascular calcification and the underlying molecular mechanisms. We have demonstrated elevated O-GlcNAcylation and increased vascular calcification in arteries from diabetic mice, which was associated with impaired aortic compliance. Elevation of O-GlcNAcylation by Thiamet-G treatment, a potent inhibitor for OGA, further accelerated vascular calcification from diabetic mice, which was associated with impaired aortic compliance. Runx2

**Methods**

**Experimental Animals**

To induce hyperglycemia and diabetes mellitus, low-dose streptozotocin injection was performed as previously described. Briefly, C57BL/6 mice were intraperitoneally injected with streptozotocin (50 mg/kg) for 5 consecutive days, and blood glucose was monitored weekly for 4 months using the AlphaTrak glucose meter and strips (Abbott, Abbott Park, IL). For Thiamet-G treatment, mice were injected intravenously with Thiamet-G (20 mg/kg) for 5 consecutive days, and blood glucose was monitored weekly for 8 weeks. Both food and fluid intake were given ad libitum. All experimental protocols were approved by the Institutional Animal Care and Use Committee of the University of Alabama at Birmingham.

**Nonstandard Abbreviations and Acronyms**

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
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<tr>
<td>CA-AKT</td>
<td>constitutively activated AKT</td>
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<tr>
<td>mTOR</td>
<td>mammalian target of rapamycin</td>
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<tr>
<td>OGA</td>
<td>β-N-acetylglucosaminidase</td>
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<tr>
<td>OGT</td>
<td>β-N-acetylglucosaminyltransferase</td>
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<tr>
<td>O-GlcNAcylation</td>
<td>O-linked β-N-acetylglucosamine modification</td>
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<td>Runx2</td>
<td>runt-related transcription factor 2</td>
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<td>VSMC</td>
<td>vascular smooth muscle cells</td>
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**Tissue Harvest and Processing**

At the experimental end points, mice were euthanized, the aortic arch and descending aorta were dissected under a microscope and used for characterization of calcium content, RNA and protein expression, and immunostaining, as we previously described.

**Aortic Calcium Measurement**

Aortic calcium content was measured by Arsenazo III assay, as we previously described. Descending aortas were homogenized and digested by collagenase. Protein amount was determined by bicinchoninic acid assay, and calcium was extracted with 0.6 mmol/L HCl and quantified colorimetrically by Arsenazo III calcium measurement kit (StanBio). The amount of vascular calcium was normalized to the total protein amount in the tissues and expressed as fold change compared to corresponding control.

**Echocardiography and Measurement of Pulse Wave Velocity**

Pulse wave velocity was analyzed by echocardiography with the high-resolution imaging system VEVO 770 (Visual Sonics, Toronto, Canada). Detailed Methods are in the Online Data Supplement.

**In Vitro Calcification of VSMC**

Primary VSMC were isolated from the aortas of C57BL/6 mice, as we described. VSMC calcification was induced in osteogenic medium containing DMEM, supplemented with 20% fetal bovine serum, 1-ascorbic acid (0.25 mmol/L), β-glycerophosphate (10 mmol/L), and dexamethasone (10 μmol/L; Sigma Aldrich) for 3 weeks. Calcification was determined by Alizarin red staining, as we described. In parallel sets of dishes, cells were lysed with 0.5 N HCl and total calcium content was quantified with Arsenazo III calcium measurement kit (StanBio) and normalized to the amount of total proteins.

**Induction of O-GlcNAcylation in VSMC**

O-GlcNAcylation was induced by inhibition of OGA, using a pharmacological inhibitor, Thiamet-G, or OGA knockdown by lentivirus-mediated short hairpin RNA-specific targeting OGA (GenBank NC_000085.6; shRNA; Thermo Scientific, Waltham, MA), as we have described. OGA, OGT, and O-GlcNAcylation were determined by Western blot analysis using specific antibodies for OGA (Santa Cruz Biotechnology, Santa Cruz, CA), OGT (Sigma Aldrich, St. Louis, MO), and O-GlcNAcylation (RL-2; Abcam).

**O-GlcNAcylation of AKT**

To determine AKT O-GlcNAcylation and its effect on phosphorylation, immunoprecipitation was performed with AKT antibody (Cell Signaling). In brief, cell extracts were incubated with AKT antibody or isotope-matched IgG (as a negative control; Santa Cruz) at 4°C overnight and then mixed with protein G agarose beads (Sigma Aldrich) for 3 hours. Beads were washed, and proteins pulled down were analyzed by Western blotting using specific antibodies to detect O-GlcNAcylation (RL-2) and AKT phosphorylation (Cell Signaling, listed above).

**Dual-Luciferase Reporter Assay**

Transactivity of runt-related transcription factor 2 (Runx2) was determined as we described by Dual-Luciferase Reporter assay (Promega, Madison, WI) with the use of a luciferase reporter construct containing 6 Runx-binding elements (p6xRunx-Luc).

**Generation of AKT Mutants**

Constructs carrying cDNA-encoding wild-type and constitutively active AKT (CA-AKT) were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Constructs carrying cDNA-encoding wild-type AKT (CA-AKT) were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University). Point mutations in the sequence of the lentiviral CA-AKT were originally provided by Dr Wu (Tulane University).
their effects on AKT phosphorylation, Runx2 activity, and VSMC calcification. The effects of AKT mutants on the binding of AKT to its kinases and phosphatase were determined by immunoprecipitation followed by Western blot analysis of Rictor, mammalian target of rapamycin (mTOR), PKD1, PHLP with specific antibodies (Cell Signaling).

Statistical Analysis
Results are presented as the mean±SD. Differences between groups were determined with the use of Student t tests or 1-way ANOVA where appropriate. Significance was defined as P<0.05.

Results
Increased Vascular O-GlcNAcylation and Calcification in Diabetic Mice
Using low-dose streptozotocin injection-induced diabetic mouse model, we characterized O-GlcNAcylation and vascular calcification in mice. Blood glucose levels were monitored in the streptozotocin-injected mice and compared with those in the control mice (Figure 1A). Elevation of blood glucose levels was observed at 1 week in the streptozotocin-injected mice (Figure 1A). Severe hyperglycemia was observed after 3 weeks, which was sustained until the end of the experiments at 16 weeks after administration of streptozotocin. Echocardiography analysis demonstrated a significant increase in pulse wave velocity, an indicator for aortic stiffness, in the diabetic mice 16 weeks after administration of streptozotocin (Figure 1B), suggesting impaired aortic compliance in the diabetic mice. Therefore, streptozotocin-induced hyperglycemia was linked to impaired aortic function in the diabetic mice.

Because hyperglycemia has been linked to increased protein O-GlcNAc modification, we determined protein O-GlcNAcylation profile in the diabetic vasculature. Dramatic increases in O-GlcNAcylation were demonstrated in the aortas from streptozotocin-injected mice (Figure 1C, top). Increased O-GlcNAcylation in the diabetic arteries was associated with increased expression of the osteogenic transcription factor Runx2 (Figure 1C, middle). We have previously demonstrated that increased Runx2 determines vascular calcification.25,26 Consistently, increased calcification was also observed in the aortas from streptozotocin-injected mice (Figure 1D). In addition, increased O-GlcNAcylation was observed in the vasculature of mice 4 weeks after streptozotocin administration, but calcification was not significantly increased at this time point (Online Figure I), indicating that increased vascular O-GlcNAcylation may precede vascular calcification in diabetes mellitus.

Immunofluorescent staining further demonstrated increased vascular O-GlcNAcylation in the media of arteries from streptozotocin-injected diabetic mice when compared with those from controls (Figure 1E; O-GlcNAc). Increased O-GlcNAcylation was correlated with decreased smooth muscle–specific α-actin and increased Runx2 expression (Figure 1E). In addition, increased expression of Runx2 and osteogenic marker genes, including osteocalcin, collagen IA1, and osteopontin, was demonstrated in aortas from the diabetic mice (Figure 1F), further confirming an association of O-GlcNAcylation with VSMC dedifferentiation and calcification.

Increased O-GlcNAcylation in VSMC Induces Vascular Calcification
To determine a direct effect of increased O-GlcNAcylation on vascular calcification, we induced O-GlcNAcylation in cultured VSMC using Thiamet-G, a highly potent and selective inhibitor of OGA that has been shown to increase...
Increased O-GlcNAcylation Enhances Diabetic Vascular Calcification In Vivo

The effects of increased O-GlcNAcylation on vascular calcification were further determined in diabetic mice in vivo. Streptozotocin-induced vascular O-GlcNAcylation was dramatically enhanced by administration of Thiamet-G (Figure 4A). At 8 weeks after the streptozotocin injection, streptozotocin alone induced a significant increase in vascular calcification. Strikingly, administration of Thiamet-G further enhanced vascular calcification (Figure 4B). The effect of Thiamet-G on diabetic vascular calcification (Figure 4B) was well associated with increased expression of Runx2 and the osteogenic marker genes (Figure 4C). Consistently, administration of Thiamet-G further increased aortic stiffness and worsened aortic compliance, indicated by increased pulse wave velocity, in the diabetic mice (Figure 4D). Taken together, these data demonstrated a causative link between increased O-GlcNAcylation and vascular calcification in diabetic mice in vivo.

Figure 2. Inhibition of OGA increases O-GlcNAcylation and calcification in VSMC. A and B, Thiamet-G increased O-GlcNAcylation in VSMC. VSMC were treated with Thiamet-G for 6 hours at 0 to 10 μmol/L, and Western blot was performed to determine O-GlcNAcylation. Representative blots from 4 independent experiments are shown in A and B. The intensity of the bands in each condition in A was quantified by ImageJ (National Institutes of Health, Bethesda, MD) and compared with that in the control (Thiamet-G, 0), defined as 1. C and D, Thiamet-G-induced VSMC calcification. VSMC were treated with osteogenic medium alone (Control) or osteogenic medium with 10 μmol/L Thiamet-G for 3 weeks. Calcification was determined by Alizarin red staining (C) or quantified by Arsenazo III assay (D; n=3; *P<0.001). E and F, Thiamet-G increased the expression of Runx2 and osteogenic marker genes, as determined by Western blot (E) and real-time polymerase chain reaction analysis (F) in parallel experiments as described in C and D (n=3; *P<0.01 compared with control).

Figure 3. Knockdown of OGA increases VSMC calcification. A, Knockdown of OGA in VSMC by shRNA increased O-GlcNAcylation and Runx2. VSMC were infected with lentivirus containing scrambled shRNA (shScr) or shRNA for OGA (shOGA). Infected cells were selected using puromycin. The amount of OGA, β-N-acetylglucosaminyltransferase (OGT), Runx2, and O-GlcNAc was determined by Western blot analysis. Representative blots from 4 independent experiments are shown. B and C, OGA knockdown induced VSMC calcification. Control and OGA knockdown cells were cultured in osteogenic medium for 3 weeks. Calcification was determined by Alizarin red staining (B) or quantified by Arsenazo assay (C) in separate dishes (n=3; *P<0.001). D, OGA knockdown increased expression of Runx2 and osteogenic marker genes. Real-time polymerase chain reaction analysis was performed to determine the expression of Runx2 and osteogenic marker genes in parallel experiments as described in B and C (n=3; *P<0.005 compared with shScr).
Increased O-GlcNAcylation Enhances Activation of AKT

To determine the molecular mechanisms underlying O-GlcNAcylation on VSMC calcification, we characterized the activation of protein kinase AKT, a critical upstream kinase that we have previously determined to regulate Runx2 activity and VSMC calcification. Glucose-induced phosphorylation/activation of AKT at serine 473 (S473) and threonine 308 (T308) was demonstrated in the control VSMC (Figure 5A, shScr). Increased O-GlcNAcylation in the OGA knockdown VSMC (shOGA) resulted in basal activation of AKT by phosphorylation at S473 but not at T308. Furthermore, increased and sustained phosphorylation/activation at both S473 and T308 was demonstrated in OGA knockdown VSMC after stimulation with glucose (Figure 5A), suggesting a direct effect of O-GlcNAc modification on activation of AKT.

Consistently, increased phosphorylation of AKT at S473 but not T308 was observed in the vasculature of diabetic mice injected with streptozotocin for 16 weeks (Figure 5Ba). Furthermore, administration of Thiamet-G enhanced AKT phosphorylation at S473 (Figure 5Bb), suggesting the role of increased AKT activation in mediating the effect of increased O-GlcNAcylation on vascular calcification in diabetes mellitus. Using the AKT IV inhibitor, we demonstrated that inhibition of AKT activation blocked increased O-GlcNAcylation–induced VSMC calcification (Figure 5C and 5D), supporting a critical role of the AKT activation in mediating O-GlcNAcylation–induced VSMC calcification.

O-GlcNAcylation of AKT Directly Regulates Activation/Phosphorylation of AKT and Vascular Calcification

We further characterized whether AKT was directly modified by O-GlcNAcylation, and how the modification alters the AKT activation. O-GlcNAcylation of AKT was detected by Western blot analysis of the AKT immunoprecipitated complex using O-GlcNAc–specific antibody (Figure 6A). Four putative O-GlcNAc modification sites were predicted on AKT with the YinOYang 1.2 software (http://www.cbs.dtu.dk/services/YinOYang/): serine 122 (S122), threonine 430 (T430), serine 473 (S473), and threonine 479 (T479; Figure 6B). To determine the effect of O-GlcNAcylation on activation of AKT, a lentiviral CA-AKT vector was used to mutate the putative glycosylation sites to encode an alanine residue (A). Because S473 is a known site that determines AKT phosphorylation and activation, it was not targeted for mutagenesis. Mutations at both T430 and T479 inhibited O-GlcNAcylation of AKT, whereas mutation at S122 did not affect O-GlcNAcylation of AKT (Figure 6C).

Because phosphorylation of AKT is known to occur at S473 and T308, we characterized the effects of altered AKT O-GlcNAcylation on its activation with each AKT mutant. Decreased O-GlcNAcylation of AKT in either T430A or T479A mutant resulted in decreased phosphorylation of AKT.
AKT, significantly reduced VSMC calcification (Figure 7C). Consistently, CA-AKT–induced Runx2 transactivity was inhibited by AKT mutations of T430A and T479A but not of S122A (Figure 7D). Taken together, these data support a critical role of O-GlcNAcylation of AKT at T430/479 in regulating its phosphorylation/activation at S473, thus inducing Runx2 transactivity and promoting VSMC calcification.

**Discussion**

Vascular calcification is prevalent in diabetes mellitus and is correlated with adverse cardiovascular outcome; however, the molecular mechanisms underlying increased vascular calcification in diabetes mellitus are largely unknown. Elevation of O-GlcNAcylation is found in human diabetic carotid plaques and diabetic mouse vasculature. Cointcedly, increased vascular calcification has been identified in patients with both type I and type II diabetes mellitus and diabetic mouse models. Nevertheless, the role of O-GlcNAcylation in vascular calcification has not been previously determined. The present study has demonstrated a causative effect of O-GlcNAcylation on diabetic vascular calcification. Our studies revealed that the activation of AKT by O-GlcNAcylation in vasculature is a key to diabetic vascular calcification. Two novel O-GlcNAcylation sites on AKT play a crucial role in enhancing AKT phosphorylation at S473 to increase vascular calcification. Because O-GlcNAcylation is tightly regulated by two specific enzymes, the new findings have exciting implications for prevention and treatment of diabetic vascular calcification through therapies targeting O-GlcNAcylation and signaling.

We found that increased O-GlcNAcylation in response to chronic hyperglycemia induced vascular calcification in the low-dose streptozotocin-induced diabetic mouse model (Figure 1). Previous studies have demonstrated that acute increases in O-GlcNAcylation (<24 hours) protect cardiomyocytes from oxidative stress-induced calcium overload and structural damage in ischemia/reperfusion models of heart failure. However, few studies have examined the function of chronic increases in O-GlcNAcylation. This study and others indicate that chronic O-GlcNAcylation for an extended period of time, as observed in the later stages of diabetes mellitus, may cause adverse complications in the cardiovascular system. The distinct function of O-GlcNAcylation in chronic and acute disease model may be related to differential activation of unknown signaling cascades. Although the streptozotocin model has its limitation because of its toxicity in vitro and its inhibitory effect on OGA also; its diabetogenic mechanism of action has been shown to be independent of these side effects because streptozotocin has a very short half-life. Using Thiamet-G, a potent and selective OGA inhibitor, our studies have provided the first evidence that increased vascular O-GlcNAcylation enhanced vascular calcification in diabetic mice in vivo (Figure 4). Consistent with the clinical observations demonstrating an association between increased vascular calcification and other vascular complications in diabetes mellitus, our findings have demonstrated reduced aortic compliance in the streptozotocin-induced diabetic mice, which was further worsened by increased O-GlcNAcylation achieved by the Thiamet-G treatment (Figures 1 and 4). Together, our studies have revealed a causative link between increased O-GlcNAcylation and diabetic vascular calcification and impaired vascular compliance in vivo.
Using VSMC, we further demonstrated that increased O-GlcNAcylation by OGA inhibition or knockdown induced VSMC calcification. Previously considered a passive process by deposition of calcium, vascular calcification has now been recognized as a regulated dynamic process involving osteochondrogenic differentiation of vascular cells. Increased O-GlcNAcylation has been associated with osteogenesis and chondrogenesis; however, the underlying mechanisms are unknown. Our studies have revealed a direct effect of O-GlcNAcylation in regulating osteogenic differentiation of VSMC, which may also provide new insights into the function of O-GlcNAcylation in regulating differentiation of osteoblasts and chondrocytes. We have previously reported that oxidative stress induces AKT activation and vascular calcification. Both oxidative stress and high glucose induce vascular calcification and have been found to increase O-GlcNAcylation. Accordingly, it is also likely that hyperglycemia induces oxidative stress that further contributes to increased vascular calcification.

We found that increased activation of AKT was associated with increased vascular calcification in the streptozotocin-induced diabetic arteries (Figure 5B). These observations are consistent with previous studies showing that VSMC in diabetic models exhibit sustained activation of AKT after chronic hyperglycemia although other studies reported blunted AKT activation in diabetic cardiomyocytes and myotubes. Apparently, AKT may be differentially regulated depending on cell types, cellular environment, and disease status. Using Thiamet-G to induce O-GlcNAcylation in vivo, we demonstrated a direct effect of O-GlcNAcylation on AKT activation in the diabetic vasculature. Consistent with these findings, blockade of OGA in cultured VSMC increased O-GlcNAcylation and simultaneously increased and sustained activation of AKT (Figure 5). Furthermore, inhibition of AKT activation attenuated VSMC calcification, demonstrating an essential role of AKT activation in mediating O-GlcNAcylation–induced vascular calcification. Remarkably, CA-AKT was sufficient to induce VSMC calcification of VSMC (Figure 7), demonstrating that AKT activation is a key regulator of vascular calcification.

Importantly, the present studies have provided a novel mechanism, underlying the regulation of AKT phosphorylation and activation by O-GlcNAcylation. Although activation of AKT has been associated with altered O-GlcNAcylation in different cells, whether the AKT activation is regulated directly by O-GlcNAcylation is not clear. Our studies have identified that O-GlcNAcylation at T430 and T479 plays an important role in AKT phosphorylation at S473, which promotes vascular calcification. Recent studies suggested that O-GlcNAcylation of AKT at T305 and T312 inhibits AKT phosphorylation at T308 in COS-7 cells, which is in agreement with the prevailing belief that protein O-GlcNAcylation and phosphorylation reciprocally regulate protein activity. However, mutation at T305 and T312 did not affect AKT phosphorylation at S473 or VSMC calcification (Online Figure III). In addition, increased O-GlcNAcylation by the OGA knockdown in VSMC did not affect basal AKT phosphorylation at T308 (Figure 5). Furthermore, we found that inhibition of O-GlcNAcylation at T430 and T479 did not affect activation of AKT at T308 but only inhibited activation of AKT at S473, suggesting the selective effect of O-GlcNAcylation on the key residues. Therefore, we have identified a unique O-GlcNAc modification at two novel sites, T430/479 that are critical for AKT phosphorylation and its function to promote VSMC calcification.

Moreover, mechanistic studies further revealed that AKT O-GlcNAcylation at T430/479 is important for the binding of AKT to Rictor, a component of the mTOR complex 2 (Figure 7B). Because mTOR complex 2 is known to phosphorylate AKT at S473, disruption of AKT binding to Rictor by the T430A and T479A mutations may contribute to the inhibited phosphorylation of AKT at S473. Inhibition of O-GlcNAcylation–induced VSMC calcification by rapamycin (Online Figure II) further support a role of the mTOR signals in mediating O-GlcNAcylation–induced AKT activation and VSMC calcification. The precise mechanism of how O-GlcNAcylation at T430/479 affects its binding to Rictor remains to be determined. The T430, T479, and S473 residues lie in the hydrophobic motif of AKT, which plays a major role in AKT protein stability. It is possible that O-GlcNAc modifications at T430/479 may change the conformation of the hydrophobic motif so that it facilitates its binding to mTOR complex 2 and thus leading to its phosphorylation at S473 site.
Although S473 does not reside in the catalytic domain of AKT, phosphorylation of S473 may lead to a conformational change that modulates complete kinase activity and phosphorylation of downstream targets. This study revealed an essential role of AKT phosphorylation at S473 in regulating osteogenic transcription factor Runx2 and VSMC calcification.

The function of O-GlcNAcylation–induced phosphorylation/activation of AKT in promoting VSMC calcification seem to be independent of its regulation of cell proliferation and apoptosis because we found that increased O-GlcNAcylation, by the OGA knockdown, did not affect VSMC proliferation/ viability. Consistently, we have reported that AKT inhibition does not induces apoptosis of VSMC. Additional studies are warranted to dissect the precise signaling cascades that are responsible for AKT activation–induced Runx2 upregulation. Nevertheless, the novel regulation of AKT activation by O-GlcNAcylation uncovered in this study may not only have significant impact on the biological function of AKT activation but also provide novel mechanistic insights into pathogenesis of vascular disease featuring increased activation of AKT.

In summary, the present studies have demonstrated a novel causative link between chronic increases in vascular O-GlcNAcylation and vascular calcification in diabetes mellitus and uncovered a novel mechanism underlying the regulation of AKT activation by its O-GlcNAcylation, which induces Runx2 upregulation and promotes VSMC calcification (Online Figure IV). These findings have demonstrated O-GlcNAcylation as a novel contributor to the process of vascular calcification and identified O-GlcNAcylation of AKT as a possible target for the development of therapies for vascular calcification in diabetes mellitus.

Acknowledgments

We thank Dr Jay McDonald, University of Alabama at Birmingham, for critical review and helpful discussion.

Sources of Funding

This work was supported by grants from the National Institutes of Health (NIH) HL092215 and DK100847 and Veterans Affairs BX000369 and BX001591 (project 2) to Y. Chen. J.M. Heath was supported by grants from the National Institutes of Health (NIH) HL092215 and DK100847 and Veterans Affairs. This work was supported by grants from the NIH HL101192 and HL110192 and HL110366. J.C. Chatham was supported by grants from the NIH HL101192 and HL110366.

Disclosures

None.

References

Activation of AKT is important for oxidative stress-induced calcification

Increased O-GlcNAcylation in diabetic arteries or in the OGA knockdown

Inhibition of OGA in VSMC, either by Thiamet-G or the OGA knockdown, reduces O-GlcNAcylation, accelerated vascular calcification and worsened aortic compliance.

Hyperglycemia, a characteristic feature of diabetes mellitus, is associated with increased vascular calcification.

What Is Known?

- Patients with diabetes mellitus have increased prevalence of vascular calcification, which correlates with higher risk for adverse cardiovascular events.
- Hyperglycemia, a characteristic feature of diabetes mellitus, is associated with increased vascular calcification, as well as increased protein O-GlcNAcylation (O-GlcNAc).
- Protein O-GlcNAcylation is tightly regulated by 2 enzymes, β-N-acetylglucosaminyltransferase and β-N-acetylglucosaminidase (OGA).
- Activation of AKT is important for oxidative stress-induced calcification of vascular smooth muscle cells (VSMC).

What New Information Does This Article Contribute?

- Streptozotocin-induced diabetic mice in vivo shows increased O-GlcNAcylation and vascular calcification, which were associated with impaired aortic compliance.
- Inhibition of OGA in VSMC, either by Thiamet-G or the OGA knockdown, increases O-GlcNAcylation in VSMC, which promotes VSMC calcification.
- Administration of Thiamet-G in diabetic mice further enhances vascular O-GlcNAcylation, accelerated vascular calcification and worsened aortic compliance.
- Increased O-GlcNAcylation in diabetic arteries or in the OGA knockdown VSMC enhances activation of AKT that upregulates expression of runt-related transcription factor 2.

What Is New?

- AKT activation increased O-GlcNAcylation-induced VSMC calcification.
- Site-directed mutagenesis of AKT at T430 and T479 decreases O-GlcNAcylation that inhibits phosphorylation of AKT at S473 and binding of the mammalian target of rapamycin complex 2 to AKT, which leads to inhibition of the runt-related transcription factor 2 transactivity and subsequent VSMC calcification.
- O-GlcNAcylation of AKT at T430 and T479 promotes phosphorylation, which represents a novel mechanism underlying AKT activation and vascular calcification in diabetes mellitus.

Vascular calcification is often observed in diabetic arteries and is associated with increased frequency of cardiovascular events and mortality in patients with diabetes mellitus. O-GlcNAcylation is increased in response to stressors, such as hyperglycemia and oxidative stress. The present studies demonstrate a novel and causative link between protein O-GlcNAcylation and vascular calcification in diabetes mellitus and reveal that O-GlcNAcylation of AKT at 2 new sites enhances AKT phosphorylation and subsequently induces VSMC calcification. These findings suggest that O-GlcNAcylation is a novel regulator of vascular calcification and uncover a novel mechanism underlying AKT activation by O-GlcNAcylation. Thus, O-GlcNAcylation of AKT may be a potential new target for the development of therapies for vascular calcification in diabetes mellitus.
Activation of AKT by O-Linked N-Acetylglucosamine Induces Vascular Calcification in Diabetes Mellitus

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Circ Res. 2014;114:1094-1102; originally published online February 13, 2014; doi: 10.1161/CIRCRESAHA.114.302968

The online version of this article, along with updated information and services, is located on the World Wide Web at:
http://circres.ahajournals.org/content/114/7/1094

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SUPPLEMENTAL MATERIAL

DETAILED METHODS

**VSMC Culture** — Primary VSMC were isolated from the aortas of C57BL/6 mice and confirmed by flow cytometry with the use of α-SMA antibody as we described\(^1\). All experiments were performed with VSMC at passages 3–5. Cells were cultured in DMEM (Life Technologies) containing glucose (25 mM), L-glutamine (584 mg/L), and sodium pyruvate (110 mg/L), supplemented with 20% fetal bovine serum (Life Technologies).

**Western Blot Analysis** — Protein extracts were isolated and concentrations were measured as we previously described\(^1\). Proteins were subjected to sodium dodecyl sulfate–10% polyacrylamide gel electrophoresis. Immunoblotting was performed using specific antibodies and detected with a Western blot chemiluminescence detection kit (Millipore). Antibodies used were as follows: anti-phospho-AKT S473, anti-phospho-AKT T308, anti-AKT, anti-mTOR, anti-PHLPP, anti-PDK1 (Cell Signaling), anti-O-GlcNAc (RL-2, Abcam)\(^2\), and anti-OGT (Sigma-Aldrich). The expression of β-tubulin (Cell Signaling) was used as a loading control. The densities of Western blot bands were quantified using ImageJ analysis software (NIH).

**Real-time polymerase chain reaction (PCR)** — The expression of osteogenic factors in aortic tissues and VSMC was determined by real-time PCR. Total RNA was isolated using Trizol (Invitrogen) and reverse transcribed into cDNA. SYBR Green-based real-time PCR was performed using specific primers for Runx2, type I collagen (Col Ia1), osteocalcin (OC), and osteopontin (OPN), using iQ SYBR Green Supermix (Bio-Rad) on an iCycler Thermal Cycler (Bio-Rad).

**Dual-Luciferase Reporter Assay** — Runx2 transactivity was determined as we described by Dual-Luciferase Reporter assay (Promega, Madison, WI) with the use of a luciferase reporter construct containing six Runx binding elements (p6xRunx-Luc)\(^3\). VSMC were transiently transfected with p6xRunx-Luc and a Renilla reporter plasmid (control for transfection efficiency) using Lipofectamine 2000 transfection reagent (Invitrogen). Luciferase activities were determined 24 hours later with the Dual-Luciferase assay kit (Promega), and normalized to the activity of Renilla luciferase.

**Immunofluorescent staining** — For immunostaining, descending aortas were embedded in paraffin (Sakura Tissue-Tek, Torrance, CA) and serial sections (8μm in thickness) were collected. Immunofluorescent staining was performed as we described previously\(^4\). Anti-phospho-AKT S473 (Cell Signaling, Boston, MA), anti-O-GlcNAc (RL-2)\(^2\), anti-Runx2 (MBL, Woburn, MA), and anti-smooth muscle specific α-actin (α-SMA, Sigma-Aldrich, St. Louis, MO) antibodies were used. Slides were washed extensively before the addition of species-specific fluorescently labeled secondary antibody (Alexa Fluor® 488 or 594, Invitrogen). 4′, 6-diamidino-2-phenylindole (DAPI) was used for nuclear localization.

**Echocardiography and measurement of pulse wave velocity** — Analysis of pulse wave velocity (PWV) by echocardiography was performed with the high resolution imaging system VEVO 770 (Visual Sonics, Toronto, Canada). Animals were anesthetized with inhalation of 1-2% isoflurane, two Millar Mikro-tip 1.0F pressure transducers (0.47 mm; Millar Instruments) were introduced into the aortic arch just before the descending aorta and the bifurcation of the abdominal aorta. The propagation time for the pulse wave moving from the aortic arch to the
abdominal aorta was measured as the time interval between the upstroke (foot) of the pulse wave front recorded at each transducer. Measurements were performed by averaging at least 10 consecutive normal cardiac cycles. After euthanasia and without altering the position of the transducers, the aorta was exposed and the distance between the transducers (ie, the pulse-wave propagation distance) was determined *in situ* using a slide caliper. The PWV was obtained by dividing this distance by the time interval between the 2 pressure wave fronts.

**SUPPLEMENTAL FIGURES**

**Supplementary Figure I. STZ increases vascular O-GlcNAcylation at 4 weeks.** To determine whether STZ affects vascular O-GlcNAcylation and calcification at an earlier time point, we evaluated the O-GlcNAcylation of aortas from mice treated with STZ for 4 weeks. Increased O-GlcNAcylation was observed in the vasculature of mice treated with STZ for 4 weeks compared with control mice, as demonstrated by Western blot analysis (A, n=3 mice per group). At this time point, there was no significant difference in vascular calcification (n=3/per group, NS, not significant), suggesting that increased vascular O-GlcNAcylation precedes vascular calcification in the STZ treated mice.

**Supplementary Figure II. Rapamycin inhibits O-GlcNAcylation-induced VSMC calcification.** The effect of inhibition of mTOR signaling on O-GlcNAcylation-induced VSMC calcification was determined with the use of rapamycin, an mTOR signaling inhibitor. OGA knockdown VSMC, which exhibited increased O-GlcNAcylation (Fig 3), were grown in osteogenic media without (control) or with rapamycin (Rapamycin, 1 µM) for 3 weeks. Rapamycin markedly inhibited increased O-GlcNAcylation-induced VSMC calcification (A, Alizarin red staining, representative results of two experiments in duplicates), which was associated with inhibition of AKT phosphorylation/activation (B, pAKT) and decreased Runx2 (B, Runx2). The data suggest that mTOR signaling mediates increased O-GlcNAcylation-induced AKT activation and VSMC calcification.

**Supplementary Figure III. Mutation of AKT at T305 or T312 does not affect AKT activation and VSMC calcification.** VSMC were stably infected with lentiviruses expressing AKT constructs, including wild type (wt-AKT), constitutively active (CA-AKT) or CA-AKT with point mutations at S305A or T312A. A) Effect of AKT T305A or T312A mutation on AKT phosphorylation.
Immunoprecipitation was performed with AKT antibody, followed by Western blot analysis of O-GlcNAcylation (O-GlcNAc) of AKT. The expression and phosphorylation of AKT in cell lysates were determined by Western blot with antibodies for total AKT or AKT phosphorylation at S473 and T308. Representation blots from two independent experiments are shown. B) Effect of AKT T305A or T312A mutation on VSMC calcification. VSMC stably expressing wt-AKT, CA-AKT and the AKT mutants were cultured in osteogenic medium for 3 weeks. Calcification was quantified by Arsenazo III assay (n=3, *p<0.05 compared with wt-AKT).

Supplementary Figure IV. Increased AKT O-GlcNAcylation in VSMC promotes AKT phosphorylation and activation, which induces vascular calcification in diabetes. Increased protein O-GlcNAcylation and vascular calcification are demonstrated in diabetic vasculature. Elevation of O-GlcNAcylation in VSMC by OGA inhibition, using Thiamet-G or shRNA, promotes AKT phosphorylation, Runx2 upregulation, expression of osteogenic markers and VSMC calcification. Increased O-GlcNAcylation-induced VSMC calcification is blocked by AKT inhibition (AKT IV). Inhibition of AKT O-GlcNAcylation at T430 and T479 blocks its phosphorylation at S473 (P) but not T308 (P), which leads to inhibited Runx2 transactivity and reduced VSMC calcification.

SUPPLEMENTAL REFERENCES


2. Gao Y, Miyazaki J, Hart GW. The transcription factor PDX-1 is post-translationally modified by O-linked N-acetylglucosamine and this modification is correlated with its DNA binding activity and insulin secretion in min6 beta-cells. Arch. Biochem. Biophys. 2003;415:155-163

