Nitric oxide activates intradomain disulfide bond formation in the kinase loop of Akt1/PKBα after burn injury

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Abstract. Severe burn injury is an acute inflammatory state with massive alterations in gene expression and levels of growth factors, cytokines and free radicals. During the catabolic processes, changes in insulin sensitivity and skeletal muscle wasting (unintended loss of 5-15% of lean body mass) are observed clinically. Here, we reveal a novel molecular mechanism of Akt1/protein kinase Bα (Akt1/PKBα) regulated via cross-talking between dephosphorylation of Thr308 and S-nitrosylation of Cys296 post severe burn injury, which were characterized using nano-LC interfaced with tandem quadrupole time-of-flight mass spectrometry (Q-TOF) micro tandem mass spectrometry in both in vitro and in vivo studies. For the in vitro studies, Akt1/PKBα was S-nitrosylated with S-nitrosoglutathione and derivatized by three methods. The derivatives were isolated by SDS-PAGE, trypsinized and analyzed by the tandem MS. For the in vitro studies, Akt1/PKBα in muscle lysates from burned rats was immunoprecipitated, derivatized with HPDP-Biotin and analyzed as above. The studies demonstrated that the NO free radical reacts with the free thiol of Cys296 to produce a Cys296-SNO intermediate which accelerates interaction with Cys310 to form Cys296-Cys310 in the kinase loop. MS/MS sequence analysis indicated that the dipeptide, linked via Cys296-Cys310, underwent dephosphorylation at Thr308. These effects were not observed in lysates from sham animals. As a result of this dual effect of burn injury, the loose conformation that is slightly stabilized by the Lys297-Thr308 salt bridge may be replaced by a more rigid structure which may block substrate access. Together with the findings of our previous report concerning mild IRS-1 integrity changes post burn, it is reasonable to conclude that the impaired Akt1/PKBα has a major impact on FOXO3 subcellular distribution and activities.

Introduction

Metabolic alterations that are produced by critical illness such as burn trauma are associated with a hypermetabolic/inflammatory state, increased protein catabolism (with resulting muscle wasting) and insulin resistance. Muscle wasting can lead to muscle weakness that can result in hypoventilation, prolongation of dependence on mechanical ventilation, prolonged rehabilitation and even death (1-4). Insulin resistance is a well established state in critically ill patients and is considered to play a key role in the metabolic derangements and muscle wasting. Binding of insulin to its receptor (IR) activates IR tyrosine kinase, which then phosphorylates IR substrates (IRSs). Phosphorylation of IRS1 and IRS2 transduces the signal from IR to phosphatidylinositol-3-kinase (PI3-kinase) (4,5). Post-translational modifications (PTMs) of the insulin signaling system are considered to be major disease-dependent events that regulate glucose transport via GLUT-4 translocation and protein synthesis (6-12).

Akt1/PKBα is a critical downstream mediator of the IR/IRS/PI3-kinase pathway of the insulin signaling system (13-17). Akt1/PKBα consists of three structural features: the N-terminal pleckstrin homology (PH) domain, a large central kinase domain and a short C-terminal hydrophobic motif. High specific binding of the PH domain with membrane lipid products of PI3-kinase recruits Akt1/PKBα to the plasma membrane where phosphorylations of Thr308 (pThr308, kinase domain) and Ser473 (pSer473, hydrophobic motif) occur. Phosphorylation of Thr308 partially stimulates kinase activity; however, additional phosphorylation of Ser473 is required for full activity. Activation is associated with a disordered to ordered transition of a specific αC helix of Akt1/PKBα via an allosteric mechanism. A salt bridge between the side-chain of Lys297 and the phosphate group of pThr308 in this αC helix contributes to an ordered activation segment from DFG to APE18-21. Reversible dephosphorylations of Thr308 and Ser473 by protein phosphatase 2A (PP2A) and PH domain leucine-rich repeat protein phosphatase (PHLPPα) also occur in the Akt1/PKBα activation/deactivation cycle (22-25).

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Abbreviations: Akt1/PKBα, Akt1/protein kinase Bα; CAM, carboxamidomethyl cysteine; CMC, carboxymethyl cysteine; GSNO, S-nitrosoglutathione; PH, pleckstrin homology; PTM, post-translational modification; Q-TOF, tandem quadrupole time-of-flight mass spectrometry; TBSA, total body surface area

Key words: Akt1/protein kinase Bα, S-nitrosylation, disulfide bond, MS/MS
In addition to the role of reversible phosphorylation/dephosphorylation in the regulation of Akt1/PKBα activity, this kinase is also reversibly inactivated by S-nitrosylation under conditions that result in persistently increased production of nitric oxide; such as after burn injury (13,26-29). Thiol titration and NMR data indicate that a disulfide bond (Cys296-Cys310) exists in the kinase PH domain (30). A second disulfide bond in the critical kinase activation loop (Cys307-Cys313) has been reported to be associated with dephosphorylation under oxidative stress in vitro (31). In addition, it has been shown that when Cys224 of Akt1/PKBα is mutated to a Ser residue, the kinase becomes resistant to NO donor-induced S-nitrosylation and inactivation; suggesting that this residue is a major S-nitrosylation acceptor site (28). In vivo S-nitrosylations of the insulin receptor β and Akt1/PKBα result in reductions in their kinase activities (27). These data suggest that the redox status of Akt1/PKBα, regulated by NO, is a second factor in the PTM that modulates kinase activity (via dynamic conformational changes) and thus GLUT-4 trafficking and protein synthesis. Nevertheless, to date, published data on the reversible phosphorylation(s) and S-nitrosylation(s) relevant to Akt1/PKBα activation, conformation and regulation have not provided conclusive information concerning their interrelationships nor critical S-nitrosylation sites involved in the kinase activation/deactivation cycle.

Recent technical developments have made it feasible to study the molecular details of these important processes. These techniques include: i) sensitive and site-specific procedures for the detection of S-nitrosylation based upon nano-LC interfaced with tandem MS (32,33); ii) the Biotin-Switch method for qualitative discrimination of the thiol state between free, disulfide bonded and S-nitrolylated cysteine residues under carefully defined conditions (34-39). Potential problems related to quantification with this technique have been discussed previously (33); and iii) highly specific anti-Akt1/PKBα mAbs that can be used to immunoprecipitate quantities of protein that are sufficient to yield SDS-PAGE bands with Coomassie brilliant blue R-250 staining which are compatible with tandem MS analysis.

Burn injury-associated impairments in IRS1 signaling and attenuated IR-IRS-PI3K-Akt/PKB activation have been the major focuses of our research team (9,26,29,33). Significantly reduced phosphorylations of Ser473 and Thr308, as well as decreased Akt/PKB kinase activity were observed after burn injury [55% total body surface area (TBSA), day 3] and insulin stimulation (26). However, the interrelationship between impaired kinase activity and the loop disulfide bond (31) reported under oxidative stress remains unclear. In the present study we investigated the interaction between S-nitrosylation and phosphorylation at Cys296-Lys307 and Thr308-Phe309-Cys310 in the kinase loop at the proteomic level.

Specifically, the following issues need to be studied: i) the ability of Cys296 to chemically quench elevated levels of free radicals, mainly nitric oxide; ii) loop conformational changes associated with two types of PTMs; iii) quantitative proteomics of Akt1/PKBα by stable isotope labeling in mice. In this study, we obtained MS/MS sequence data to characterize the thiol states of Cys296 in the kinase activation loop of Akt1/PKB. These measurements were possible despite the extremely low level of nitrosylated protein (at the 10-15 pmol level, the chance of positive hits is ~25% with lysates prepared from 25 mg of soleus muscle). The biochemical role of S-nitrosylation at Cys296 was characterized as an intermediate state which reduces the kinetic barrier to form the disulfide bond with Cys310 within the activity loop. This occurs simultaneously with dephosphorylation of pThr308 after burn injury. The facts that no other disulfide bonds associated with Cys296 were detected suggest that they may be thermodynamically forbidden; due to geometry and/or dihedral strain. The data obtained with soleus muscle from burned and sham-treated rats indicates that NO-mediated formation of the Cys296-Cys310 disulfide bond (which likely downregulates kinase activity) plays a reciprocal role with formation of a Lys307-pThr308 salt bridge (which upregulates kinase activity) during disease-associated reversible activation/deactivation processes.

Materials and methods

Chemicals. Acetonitrile (ACN, LC-MS Chromasolv), formic acid (FA), glacial acetic acid, LC-MS grade water, dithiothreitol (DTT), iodoacetic acid, iodoacetamide, [Glu]-fibrinopeptide B, methyl methanethiosulfonate (MMTS), S-nitrosogluthathione (GSNO), sodium L-ascorbate, neocuproine, N,N-dimethylformamide (DMF), dimethyl sulfoxide (DMSO) were obtained from Sigma Chemical Co. (St. Louis, MO), SDS-PAGE Ready gels (4-15% Tris-HCl, cat. no. 161-1122), Laemmli sample buffer (cat. no. 161-0737) and Coomassie brilliant blue R-250 (no. 161-0436) were obtained from Bio-Rad. Trypsin profile IGD kits (cat. no. PP0100) were obtained from Sigma. Anti-Akt1/PKBα monoclonal antibody (cat. no. 05-798; lot, 26860) and inactive Akt1/PKBα (cat. no. 14-279) were purchased from Upstate (Charlottesville, VA, USA). Streptavidin agarose CL-4B (cat. no. 85881) was a product of Fluka (Milwaukee, WI, USA). HPDP-Biotin (cat. no. 21341) and Iodoacetyl-LC-Biotin (cat. no. 21333) were purchased from Pierce (Rockford, IL, USA).

Mapping of cysteine residues in inactive Akt1/PKBα. Inactive Akt1/PKBα (10 µg, 0.18 nmol, in 10 µl stock solution) was transferred to a siliconized Eppendorf tube (0.6 ml) containing Laemmli sample buffer (2X, 10 µl, pH was adjusted to 8.0) and DDT (2 µl, 20 nmol, PBS, pH 8.0), and the solution was kept at 95°C for 5 min. Freshly prepared Iodoacetyl-LC-Biotin (15 µl, 55 nmol, in DMF) was added to the denatured protein solution followed by stirring for an additional 15 min at room temperature. The resulting biotinylated Akt1/PKBα was purified by SDS-PAGE and stained with Coomassie brilliant blue R-250. The protein bands were excised (~1 mm size) and digested (Akt1/PKBα: trypsins 25, overnight at 37°C) with a Trypsin Profile IGD kit according to the manufacturer's instructions. The biotinylated peptide mixture was captured by gentle stirring with streptavidin agarose CL-4B (30 µl packed) at room temperature for 1 h (final vol, 100 µl). The streptavidin beads were washed with PBS (0.5 ml x3), followed by water/ acetonitrile (ACN 10%, 0.5 ml x3). Biotinylated peptides were released from the streptavidin beads with formic acid (70%, 100 µl) at room temperature for 15 min with brief vortexing. The supernatant containing biotinylated peptides was transferred to a new vial and the formic acid was evaporated with a SpeedVac. The biotinylated peptide mixture was resuspended.
in water/acetonitrile (ACN, 2%, with 0.1% FA, 70 µl), and the aliquots (10 µl) were injected into a Waters CapLC-tandem quadrupole time-of-flight mass spectrometry (Q-TOF) system.

**Identification of disulfide bonds in inactive Akt1/PKBα.** Inactive Akt1/PKBα (10 µg, 0.18 nmol, in 10 µl stock solution) was transferred into a siliconized Eppendorf tube (0.6 ml) containing Laemmli sample buffer (2X, 10 µl, pH 8.0) and iodoacetamide (2 µl, 20 nmol, PBS, pH 8.0). The mixture was maintained at 95˚C for 5 min and then stirred at room temperature for an additional 15 min. The Akt1/PKBα was purified by SDS-PAGE and stained with Coomassie brilliant blue R-250. The protein bands were processed as above.

**Identification of NO acceptor sites in inactive Akt1/PKBα.** Three samples of inactive Akt1/PKBα (10 µg, 0.18 nmol, in 10 µl stock solution) were treated with GSNO (250 nmol, 50 µl PBS, pH 8.0, 200-fold excess/thiol group) for 1 h at room temperature in the dark in siliconized Eppendorf tubes (0.6 ml). Separation of Akt1/PKBα and GSNO was achieved by two successive acetone/water precipitations (0.3 ml, 70% ACN) at -40˚C for 10 min. The supernatants (containing GSNO) were removed by centrifugation at 14,000 x g for 2 min. The kinase pellets were resuspended in blocking buffer (100 µl, 20 mM Tris- HCl, pH 7.7, 2.5% SDS, 20 mM MMTS, 1 mM EDTA, 0.1 mM neocuproine) at room temperature for 1 h with gentle stirring (1 mm ID x 5 mm bar). Excess MMTS was removed by acetone (100%, 0.3 ml) precipitation (as above), and the protein pellets were resuspended in PBS (50 µl, pH 8.0). Freshly prepared iodoacetic acid (5 µl, 2 mM in PBS, pH 8.0), HPDP-Biotin (5 µl, 2 mM in DMSO), Iodoacetyl-LC-Biotin (5 µl, 2 mM in DMF) and sodium ascorbate (20 µl, 5 mM, PBS) were added to the three vials containing nitrosylated Akt1/PKBα, respectively. The reaction mixtures were stirred at room temperature for 15 min (iodoacetic acid and Iodoacetyl-LC-Biotin) or 1 h for the thiol-disulfide exchange reaction. Aliquots of SDS sample buffer (2X, with 5% 2-mercaptoethanol, 50 µl) were added to the protein solutions, and the mixtures were incubated at 95˚C for 5 min. The derivatized proteins were processed as above. Carboxymethyl cysteine (CMC)-containing peptides, were neutralized with FA (5 µl) and sequenced via parent ion discovery triggered by the CMC immunion ion (134.02±0.05 mDa) as reported previously (33). Biotinylated peptides were sequenced with data-dependent LC-MS/MS analysis.

**LC-MS/MS analysis.** All experiments were performed using a Waters CapLC-Q-TOFmass system (Waters Corporation, Milford, MA, USA) as previously described (32,33). An analytical column (75 mm ID x150 mm, C18 PepMap300, 5 mm, LC Packings) was used to connect the stream select module of the CapLC with the voltage supply adapter for ESI. Peptide mixtures were loading onto the precolumn (C18 resin) at a flow rate of 15 µl/min. Dead volume from the CapLC injector to the precolumn was measured to be ~1.5 µl. After washing with mobile phase C (auxiliary pump, 0.1% formic acid in water/ACN, 2% ACN) for 2 min, the trapped peptides were back-washed from the precolumn onto the analytical column using the 10-position stream switching valve. Freshly prepared mobile phases A and C were sonicated under vacuum for ~25 min, and mobile phase B was treated in this way for 5 min. The mobile phases were degassed every week, and the CapLC pumps were wet primed for 20 cycles. A linear gradient was used to elute the peptide mixture from mobile phase A (0.1% FA in water/ACN, 2% ACN) to mobile phase B (0.1% FA in ACN). The gradient was segmented as follow: isocratic elution with 2% B for 3 min, increasing B from 2 to 70% (3-40 min), isocratic elution with 70% B (40-45 min) and decreasing B from 70 to 2% (over 2 min). The injector syringe (25 µl) was washed with degassed mobile phase A, and the injection volume was set as full loop mode (10 µl). The gradient flow rate was set at 1.5 µl/min before the 16/1 Nanotear splitter and the pressure drop from the analytical column was ~800 psi. The pressure drop (or the flow splitting ratio) was adjusted and maintained with 20 µm ID capillary tubing at the waste outlet position of the Nanotear splitter. The gradient flow rate was ~95 nl/min. The electrospray voltage was set to ~3,000 V to obtain an even ESI plume at the beginning of the gradient (high water content). As a routine sensitivity check, the PicoTip Emitter position and other
parameters were adjusted to achieve ~45 counts/sec for the capillary tubing background peak (m/z 429). Sample cone and extraction cone voltages were set at 45 and 3 V, respectively. The instrument was operated in positive ion mode with the electrospray source maintained at 90°C. The instrument was calibrated with synthetic human [Glu1]-fibrinopeptide B (100 fmol/µl in acetonitrile/water, 10:90, 0.1% formic acid, v/v) at an infusion rate of 1 µl/min in TOF MS/MS mode. The peptide was selected at m/z 785.8 and focused into the collision cell containing argon gas at ~3x10−4 Torr; the collision energy was set at 35 V. Instrument resolution for the [Glu1]-fibrinopeptide B parent ion, m/z 785.84, was found to be 5,250 FWHM. All data were acquired and processed using MassLynx 4.1 software. For parent ion discovery triggered by the CMC immonium ion (134.02±0.03 Da), the survey low and high collision energies were set at 5 and 30 V, respectively. MS survey data were collected in continuum mode over the m/z 100-1,200 range. Data-dependent acquisition (DDA) was set from 450 to 1,500 m/z for the biotinylated peptides. Scan time was in the range of 1.9-3.8 sec (depending upon sample conditions), and the inter-scan delay was 0.1 sec. MS to MS/MS switch criteria were dependent upon the reporter ion intensity (5 counts/sec) and detection window (2.3 Da, charge status). The instrument was switched from MS/MS back to MS after 5 sec without intensity restriction.

**Evaluation of the S-nitrosylated cysteine site.** Confirmations of the S-nitrosylation sites were performed by the following three step procedure. i) For parent ion discoveries by continuum MS survey, the peptide mass tolerance was 0.2 Da for the CMC immonium ion. Under these conditions, only a few false positive ions were observed and these were eliminated manually from the expected CMC parent ion list. ii) The positively discovered parent ions were analyzed with PepSeq of MassLynx V4.1 software; oxidation of methionine was searched as a variable modification. iii) For peptides, MS/MS scores <35, manual interpretations of candidate parent ions were performed with the following procedure: continuum MS/MS spectra were smoothed, the upper 80% was centroided and cysteine residues were confirmed with three different thiol-specifically derivatized y ions. Cysteine residue monoisotopic mass C6H5NOS = 103.01 Da was replaced with CMC residue monoisotopic mass C5H5NOS = 161.01 Da, HPDP-Biotin derivatized adduct residue monoisotopic mass C22H12N2O6S3 = 531.20 Da and Iodoacetyl-LC-Biotin derivatized adduct residue monoisotopic mass C23H16N6O3S2 = 485.21 Da, respectively.

**Results and Discussion**

It has been reported that NO production is elevated by stressors such as burn injury and in patients with type 2 diabetes (29-41). It has also been shown that the Cys378-Cys311 disulfide bond in the critical kinase activation loop of Akt1/PKBα may be formed in association with dephosphorylation under oxidative stress in vitro (31). Thus, we hypothesized that reversible S-nitrosylation at either Cys378 or Cys311 in the kinase active loop may be a second PTM factor which complements reversible phosphorylation at Thr308 in the regulation of kinase activity and we sought to determine how S-nitrosylation interacts with phosphorylation during the Akt1/PKBα activation cycle (22). To address these issues, GSNO was used as the only NO donor in a model S-nitrosylation system to randomly target the seven cysteine residues of the kinase at pH 8. Vicinal Cys296 and Cys310 take advantage of the pKa for dissociation of the thiol to thiolate, and these electron-rich thiolate groups can lead to formation of an intradomain disulfide bond. Under these conditions, intracellular free cysteine residues, and cysteines at the kinase surface without interactions or located in hydrophobic environments (i.e. high pKa), are unlikely to be affected by GSNO. In contrast, Cys308 and Cys310, which may have low pKa values due to weak interactions with vicinal residues inside the loop, are potential S-nitrosylation sites as predicted from the 3D structure of the kinase (19). NO donors, such as thiorredoxin and thiol/disulfide oxidoreductases were excluded from the system to prevent possible interferences (42,43); however, a small amount of 2-mercaptoethanol (~0.05% v/v) was necessary to prevent oxygen effects.

The simple, but well-defined, S-nitrosylation reaction model was used to probe for particular NO acceptor sites in human Akt1/PKBα (inactive, 89% pure containing 2-mercaptoethanol and EGTA; Upstate) in three steps. i) Mapping of all cysteine residues with DTT reduction, Iodoacetyl-LC-Biotin alkylation and affinity capture provided relative MS ionization efficacies and charge states. ii) Detection of disulfide bonds with and without GSNO, provided an understanding of NO-mediated disulfide bond formation. The concentrations of the NO donor used here were similar to the levels used in reported studies (35-37), iii) MS/MS pinpointed the S-nitrosylated sites with three different thiol-specific derivatives. As indicated above, false-negatives may occur with the Biotin-Switch method (33), whereas false-positives are more common with the other methods; however, thioether derivatives can be identified with MS/MS data. The findings of these studies were used to study the biological consequences of S-nitrosylation of Akt1/PKBα in soleus muscle from burned rats. This in vivo system was used because soleus muscle is an insulin-sensitive tissue with high levels of IRS-1.

A base peak intensity (BPI) nano-LC chromatogram of all seven affinity captured cysteine residues that were biotinylated with Iodoacetyl-LC-Biotin is shown (Fig. 1A). Cysteine residue monoisotopic mass of C6H5NOS = 103.01 Da was replaced with derivatized Cys residue monoisotopic mass of C6H5NOS = 161.01 Da, HPDP-Biotin derivatized adduct residue monoisotopic mass C22H12N2O6S3 = 531.20 Da and Iodoacetyl-LC-Biotin derivatized adduct residue monoisotopic mass C23H16N6O3S2 = 485.21 Da, respectively. Three predominate TOF MS tryptic parent ions were identified; m/z 674.29 (T41, M+2H+ = 368.83) eluting at 50.5 min, m/z 1088.49 (T9, M+CH3+2H+ = 1088.03) eluting at 51.5 min and m/z 924.67 (T44, M+3H+ = 924.43) eluting at 53 min are doubly and triply charged tryptic peptides containing Cys296, Cys310 and Cys311, respectively. Fig. 1B shows the parent ions co-eluting at ~53 min as well as the charge state assignments. Parent ions m/z 924.67 (T44, M+3H+ = 924.43) and m/z 1386.51 (T44, M+2H+ = 1386.14) are triply and doubly charged ions from the same tryptic peptide. 308TFCGTPEYLAPEVLEDNDYGR328, which contains Cys310. Parent ion m/z 1266.09 (T58, M+3H+ = 1266.41) is triply charged and derived from the peptide, 437YFDEEFTAQMTTIPPDQDSDMECVDSER465, which
contains Cys460. Parent ion m/z 815.87 (T11, M+2H⁺ = 815.93) is doubly charged from the tryptic peptide, 77CLQWTTVIER86, which contains Cys77. Parent ion m/z 1088.49 resulted from CH₄ neutral loss from m/z 1096.48 as shown in C. (B) TOF MS analysis of parent ions co-eluted at retention time of ~50.8 min. Parent ions m/z 731.33 and 1096.46 are triply and doubly charged ions from the same tryptic peptide, 99TFCGTPEYLAEVLEDNDYGR105, which contains Cys105. Parent ion m/z 1266.09 is a triply charged ion from the tryptic peptide, 43YFDEEFTAQMTITPQDSDMECVDSER145, which contains Cys145. Parent ion m/z 815.87 is a doubly charged ion derived from the tryptic peptide, 77CLQWTTVIER86, which contains Cys77. The parent ion at m/z 1088.49 results from CH₄ neutral loss from m/z 1096.46 as shown in C. (C) TOF MS analysis of parent ions co-eluting at retention time of ~50.8 min. Parent ions m/z 731.33 and 1096.46 are triply and doubly charged ions from the same tryptic peptide, 99ESPLNNFSVAQQLMK111, which contains Cys111. Parent ion m/z 1266.09 is triply charged and derived from tryptic peptide, 43TDDFGLCK137, which contains Cys137. (D) TOF MS analysis of parent ions co-eluting at retention time of ~53.5 min. Parent ion m/z 829.00 is triply charged and derived from tryptic peptide, 223AVDWGVLGVMYEMMCGR146, which contains Cys146. Parent ion m/z 872.70 is triply charged and derived from tryptic peptide, 223LCFVMEYANGGELFFHLSR241, which contains Cys241.

Figure 1. Mapping of cysteine residues in inactive Akt1/PKBα. (A) Base peak intensity (BPI) nano-LC chromatogram of affinity capture of all seven cysteine residues that were biotinylated with iodoacetyl-LC-Biotin. Sample preparation: see materials and methods section for details. Column conditions: 75 mm ID x150 mm, C18 PepMap300, 5 mm, under linear gradient conditions at a flow rate 90 nL/min. (B) TOF MS analysis of parent ions co-eluted at retention time of ~53 min. Parent ions m/z 924.67 and 1386.51 are triply and doubly charged ions from the same tryptic peptide, 309TFCGTPEYLAEVLEDNDYGR105, which contains Cys105. Parent ion m/z 1266.09 is a triply charged ion from the tryptic peptide, 43YFDEEFTAQMTITPQDSDMECVDSER145, which contains Cys145. Parent ion m/z 815.87 is a doubly charged ion derived from the tryptic peptide, 77CLQWTTVIER86, which contains Cys77. Parent ion m/z 1088.49 resulted from CH₄ neutral loss from m/z 1096.48 as shown in C. (C) TOF MS analysis of parent ions co-eluting at retention time of ~50.8 min. Parent ions m/z 731.33 and 1096.46 are triply and doubly charged ions from the same tryptic peptide, 99ESPLNNFSVAQQLMK111, which contains Cys111. Parent ion m/z 1266.09 is triply charged and derived from tryptic peptide, 43TDDFGLCK137, which contains Cys137. (D) TOF MS analysis of parent ions co-eluting at retention time of ~53.5 min. Parent ion m/z 829.00 is triply charged and derived from tryptic peptide, 223AVDWGVLGVMYEMMCGR146, which contains Cys146. Parent ion m/z 872.70 is triply charged and derived from tryptic peptide, 223LCFVMEYANGGELFFHLSR241, which contains Cys241.
When Akt1/PKBα was treated with GSNO without cleavage of disulfide bonds and the free cysteine residues were alkylated with iodoacetamide, two intradomain disulfide bonds were identified: Cys<sup>60</sup>-Cys<sup>77</sup> in the PH domain and Cys<sup>296</sup>-Cys<sup>310</sup> in the kinase active loop. The monoisotopic parent ion with m/z 821.35, shown in Fig. 2A, represents two tryptic peptides containing the Cys<sup>296</sup>-Cys<sup>310</sup> disulfide bond in the kinase loop. The isotopic peaks at m/z 821.61 and m/z 821.35 are attributed to the M+1 and M+0 ions. A mass difference of 0.26 Da (expected 0.25 Da) indicated four positive charges: two at N-terminals and two at side chains of the C-terminals of the dipeptides. The expected quadruply charged disulfide bond linked Cys<sup>296</sup> and Cys<sup>310</sup>-containing peptides (T41-SS-T44, M+4H<sup>+</sup>) were calculated to be m/z 821.38 [(894.45 + 2387.06 + 4)/4].

The monoisotopic parent ion with m/z 764.41, shown in Fig. 2B, represents the two tryptic peptides containing the Cys<sup>60</sup>-Cys<sup>77</sup> disulfide bond in the PH domain. The doubly charged m/z 816.35 ion is not from a Cys<sup>310</sup>-containing tryptic peptide (expected charge state 3), and quadruply charged m/z 821.33 occurs at the expense of diminished triply charged Cys<sup>310</sup> peptide. The free thiol of Cys<sup>310</sup> is completely converted into the disulfide bond with Cys<sup>296</sup>.

The impact of GSNO on Cys<sup>296</sup>-Cys<sup>310</sup> disulfide bond formation is demonstrated in Fig. 2C and D. The S-nitrosylation reaction...
Table I. Characterization of the thiol-specifically modified Akt1/PKBα peptide 269ITDFGLCK279.

<table>
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<tr>
<th>Chemical derivatives</th>
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<th>y2 ion calc.</th>
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</table>

Biotin-HPDP derivatized, 269ITDFGLCK279, was confirmed at m/z 678.29 (expected 678.32 = 531.20 + 145.10 + 2.02). The Cys Iodoacetyl-LC-Biotin adduct (Cys residue monoisotopic mass C₂H₅N₂O₃S = 103.01 Da was replaced with adduct residue monoisotopic mass C₂H₅N₂O₃S = 485.21 Da) was used for peptide sequence analysis. The corresponding y2 ion of Iodoacetyl-LC-Biotin derivatized, 269ITDFGLCK279 was confirmed at m/z 632.38 (expected 632.33 = 485.21 + 145.10 + 2.02). Since the y2 ions of 269Cys-Lys279 produced with the three different derivatization procedures were unambiguously observed it is likely that Cys296 is a favorable S-nitrosylation site under the conditions used. Although studies with mutated Akt1/PKBα (Cys224) indicated that Cys224 is a major S-nitrosylation acceptor site in vitro (28), the biological role of S-nitrosylated Cys224 in kinase regulation needs to be further explored. In the current study it was determined that significant S-nitrosylation of Cys224 is improbable, since using the three alkylation approaches and trypsin digestion, the levels of positive ionization of Cys224-containing peptides were below the level of detection. This failure in detection of S-nitrosylated Cys224 may be a false-negative under our experimental conditions and clearly warrants further investigation. Nevertheless, our findings clearly demonstrate that S-nitrosylated Cys296 is directly relevant to the kinase activation regulation cycle.

One possible explanation for the kinetics of Cys296-Cys310 disulfide bond formation in the kinase loop may be that there is a high kinetic barrier without GSNO. Due to its highly labile nature (44), S-nitrosylated Cys296, which forms rapidly in the presence of GSNO, may function as an intermediate state. Since this intermediate is likely to have a lower kinetic barrier for Cys296-Cys310 disulfide bond formation, the overall speed of the reaction should increase greatly. It has been reported that trans-nitrosylation reactions between vicinal thiols can occur and accelerate disulfide bond formation (45). The well characterized Cys296-Cys310 disulfide bond can be used as a signature peptide for detection of S-nitrosylation of Cys296 after immunoprecipitation. The separation of tryptic peptide mixtures with our nano-LC interfaced Q-TOFmass was demonstrated in Fig. 3 (bottom panel). The extracted mass ion peak m/z 821.62, as shown in Fig. 3 (top panel), is the M+1 isotopic peak of the quadruply charged dipeptides (the most intense nature (44), S-nitrosylated Cys296, which forms rapidly in the presence of GSNO, may function as an intermediate state. Since this intermediate is likely to have a lower kinetic barrier for Cys296-Cys310 disulfide bond formation, the overall speed of the reaction should increase greatly. It has been reported that trans-nitrosylation reactions between vicinal thiols can occur and accelerate disulfide bond formation (45). The well characterized Cys296-Cys310 disulfide bond can be used as a signature peptide for detection of S-nitrosylation of Cys296 after immunoprecipitation. The separation of tryptic peptide mixtures with our nano-LC interfaced Q-TOFmass was demonstrated in Fig. 3 (bottom panel). The extracted mass ion peak m/z 821.62, as shown in Fig. 3 (top panel), is the M+1 isotopic peak of the quadruply charged dipeptides (the most intense is improbable, since using the three alkylation approaches and trypsin digestion, the levels of positive ionization of Cys224-containing peptides were below the level of detection. This failure in detection of S-nitrosylated Cys224 may be a false-negative under our experimental conditions and clearly warrants further investigation. Nevertheless, our findings clearly demonstrate that S-nitrosylated Cys296 is directly relevant to the kinase activation regulation cycle.

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kinase activity conformation cycle (22); ii) kinase disulfide bond formation, Cys$^{297}$-Cys$^{311}$, and dephosphorylation at pThr$^{308}$ are induced simultaneously by H$_2$O$_2$ oxidative stress in vitro (31); iii) high levels of nitric oxide production occur both after burn injury (29,42) and in diabetic patients (43). Previous results from our laboratory have indicated that there is S-nitrosylation at Cys$^{296}$ in rat soleus muscle (33). A parent ion at m/z 690.83 containing Cys$^{296}$ (T41-T42: $^{290}$ITCFGLCKEGIK$^{301}$) was observed with CAM immionium triggered parent ion discovery; however, MS/MS sequencing data were not obtained. As a continuation of these studies to explore S-nitrosylation in the kinase active loop, large amounts of rat soleus muscle lysate (~3-5 mg/ml total proteins, 3 ml for each experiment, day 4 after 40% TBSA, 3rd degree burn) were used. In the present study, detailed MS/MS analyses of HPDP-biotinylated free Cys$^{296}$ peptide and Cys$^{296}$-Cys$^{310}$ disulfide bound dipeptides of Akt1/PKB$\alpha$ were performed with lysates of rat soleus muscle after burn injury. The tryptic
Ah, you've selected a page from the International Journal of Molecular Medicine. It seems to be discussing the derivatization of free Cys296 after burn injury, and the presence of Cys310-Cys296 intradomain disulfide bond formation, which is confirmed by MS/MS data. The authors note that the chance of obtaining an interpretable MS/MS outcome is only ~20-25%.

Figure 5 illustrates the MS/MS sequence analysis of the Cys296-Cys310 disulfide-linked peptide with dephosphorylated Thr308 in soleus muscle from burned rats. Partially sequenced Cys296-Cys310 disulfide-linked dipeptides: C-terminal y ion series (y3 to y9) of Cys310-containing peptide, TFCGTPEYLAPEVLEDNDYGR328, were observed from the quadruply charged parent ion (T41-SS-T44, M+4H+)

Figure 6 demonstrates the proposed mechanism for Akt1/PKBα kinase regulation by phosphorylation and S-nitrosylation in the muscle of burned rats. Phosphorylation of Thr308 stabilizes the disordered loop structure between DFG and APE via a salt bridge with Lys297, which upregulates Akt1/PKBα kinase activity. NO free radical production is increased after burn injury. A large portion of Cys296 undergoes S-nitrosylation at Cys296 (Peptide 2); however, some free Cys296 remains (Peptide 3). S-nitrosylation activates Cys296-Cys310 intradomain disulfide bond formation (Peptide 4). S-nitrosylation at Cys296 is associated with dephosphorylation of Thr308 and inaccessibility to the kinase site; which downregulates kinase activity.

Parent ion derivatized from free Cys296 after burn injury was observed at m/z 662.84 (M+2H+, expected 662.82) and the MS/MS sequence data are shown in Fig. 4. A low sequence score of 18 was obtained from the parent ion with S/N = 3. However, the critical diagnostic y2, y4 and y5 ions at m/z 678.29, 849.34 and 995.51 confirmed that trace amounts of free Cys296 are indeed present after intradomain disulfide bond formation induced by burn injury. In addition, partial sequencing data for Cys296-Cys310 disulfide-linked dipeptides are shown in Fig. 5. The C-terminal y ion series of Cys310-containing peptide, TFCGTPEYLAPEVLEDNDYGR328, was observed for the quadruply charged parent ion (T41-SS-T44, M+4H+). Cys296-Cys310 disulfide-linked dipeptides were not observed in muscle lysates from sham-treated animals (negative controls). The chance of obtaining the MS/MS sequence using our in vivo experimental conditions is only ~20-25%. This indicates that one interpretable MS/MS outcome (score >25) is expected in four or five independent experiments in which three successive injections are performed. Nevertheless, these MS/MS data for peptides containing free Cys296 and Cys296-Cys310-linked...
dipeptides are sufficient to verify our hypothesis that S-nitrosylation promotes intradomain disulfide bond formation and dephosphorylation at pThr\textsuperscript{110} after burn injury as illustrated in Fig. 6. Due to its high lability of Cys\textsuperscript{206}-SNO, direct identification of this species in vivo was not possible.

S-nitrosylation of Akt1/PKB\alpha is a key factor for understanding the regulation of glucose transport and downstream protein synthesis. A recent study demonstrated that blockade of iNOS prevents the S-nitrosylations of Akt and IRS-1 and results in insulin resistance in vivo (46). Although it is clear that two PTMs of Akt1/PKB\alpha: phosphorylation at Thr\textsuperscript{308} and S-nitrosylation at Cys\textsuperscript{206}, are critical for the regulation of Akt1/PKB\alpha activity under stress conditions, there are still many unanswered questions concerning how reversible phosphorylation/dephosphorylation and S-nitrosylation/denitrosylation modulate Akt1/PKB\alpha activity. For example, it has been reported that the Cys\textsuperscript{206}-Cys\textsuperscript{310} disulfide bond is present only when there is binding of substrate to the active kinase loop and phosphorylation at Thr\textsuperscript{308} (25); indicating that both disulfide bond formation as well as phosphorylation of Thr\textsuperscript{308} are important for kinase activity. In contrast, this disulfide bond was not observed under similar conditions in two studies of the ternary structure of the kinase (19,21); even though, oxidative stress was shown to induce dephosphorylation of pThr\textsuperscript{308} and disulfide bond formation in the kinase loop in an in vitro study (31).

In summary, our data establish that Cys\textsuperscript{206} is an important S-nitrosylation site in the kinase loop of Akt1/PKB\alpha under gentle reaction conditions: i) iodoacetic acid as previously described; ii) the HPDP-Biotin switch method; and iii) the Iodoacetyl-LC-Biotin method to ensure indirect capture of Cys\textsuperscript{206}-SNO which may be undetectable with HPDP-Biotin. The corresponding derivatized y2 ions (Cys\textsuperscript{206}-Lys\textsuperscript{297}) in the tryptic peptide (Ile-Thr-Asp-Phe-Gly-Leu-Cys-Lys) were obtained with mass sequences to eliminate false-positive discovery. Although no other S-nitrosylated cysteine residues were detected, it is possible that S-nitrosylations at Cys\textsuperscript{344} and Cys\textsuperscript{460} were missed due to very low ionizations (i.e., false-negative discoveries). As a consequence of S-nitrosylation at Cys\textsuperscript{206}, there is rapid disulfide bond formation with vicinal Cys\textsuperscript{310} in the kinase loop, which alters kinase substrate recognition (47) as well as Akt-FOXO switch (48). This affords a stable disulfide bond linked quadruply charged parent ion at m/z 821.35 (M+4H\textsuperscript{+}). Partial sequencing data for Cys\textsuperscript{206}-Cys\textsuperscript{310} linked dipeptides from soleus muscle lyses indicated that burn injury is associated with both dephosphorylation of pThr\textsuperscript{308} and disulfide bond formation. These two types of PTMs may provide insights for understanding negative cooperative effects on reduced Akt/PKB kinase activity after burn injury as previously reported by our laboratory (26). Although our results have provided important mechanistic information, quantitative measurements of Thr\textsuperscript{308}/pThr\textsuperscript{308} and free Cys\textsuperscript{206}/SNO-Cys\textsuperscript{206}/bound Cys\textsuperscript{206} in patients with burn injury and type 2 diabetes remain very challenging.

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References


