

Tyrosine Phosphorylation Modifies Protein Kinase C δ -dependent Phosphorylation of Cardiac Troponin I*

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Marius P. Sumandea[‡], Vitalyi O. Rybin[§], Aaron C. Hinken[¶], Chaojian Wang[§], Tomoyoshi Kobayashi[¶], Erin Harleton[§], Gail Sievert[‡], C. William Balke[‡], Steven J. Feinmark[§], R. John Solaro[¶], and Susan F. Steinberg^{§1}

From the [‡]Department of Internal Medicine, Cardiovascular Research Center, University of Kentucky, Lexington, Kentucky 40536, the [§]Department of Pharmacology, Columbia University, New York, New York 10032, and the [¶]Department of Physiology and Biophysics, Center for Cardiovascular Research, University of Illinois at Chicago, Chicago, Illinois 60612

Our study identifies tyrosine phosphorylation as a novel protein kinase C δ (PKC δ) activation mechanism that modifies PKC δ -dependent phosphorylation of cardiac troponin I (cTnI), a myofilament regulatory protein. PKC δ phosphorylates cTnI at Ser²³/Ser²⁴ when activated by lipid cofactors; Src phosphorylates PKC δ at Tyr³¹¹ and Tyr³³² leading to enhanced PKC δ autophosphorylation at Thr⁵⁰⁵ (its activation loop) and PKC δ -dependent cTnI phosphorylation at both Ser²³/Ser²⁴ and Thr¹⁴⁴. The Src-dependent acquisition of cTnI-Thr¹⁴⁴ kinase activity is abrogated by Y311F or T505A substitutions. Treatment of detergent-extracted single cardiomyocytes with lipid-activated PKC δ induces depressed tension at submaximum but not maximum [Ca²⁺] as expected for cTnI-Ser²³/Ser²⁴ phosphorylation. Treatment of myocytes with Src-activated PKC δ leads to depressed maximum tension and cross-bridge kinetics, attributable to a dominant effect of cTnI-Thr¹⁴⁴ phosphorylation. Our data implicate PKC δ -Tyr³¹¹/Thr⁵⁰⁵ phosphorylation as dynamically regulated modifications that alter PKC δ enzymology and allow for stimulus-specific control of cardiac mechanics during growth factor stimulation and oxidative stress.

Protein kinase C δ (PKC δ)² is a ubiquitous serine/threonine kinase implicated in a wide range of cellular responses (1, 2). PKC δ is conventionally viewed as a lipid-dependent enzyme that is anchored to membranes in close proximity to target substrates through interactions with lipid cofactors. However, there is recent evidence that PKC δ also is dynamically regulated through activation loop (Thr⁵⁰⁵) phosphorylation (3, 4). For other PKC isoforms, activation loop phosphorylation is a stable

“priming” phosphorylation completed during *de novo* enzyme synthesis (5). In the case of cPKCs, activation loop phosphorylations are mediated by phosphoinositide-dependent kinase-1 and are essential to generate a catalytically competent enzyme. Although newly synthesized PKC δ also undergoes maturational phosphoinositide-dependent kinase-1-dependent Thr⁵⁰⁵ phosphorylation, PKC δ differs from other PKC isoforms in that 1) PKC δ is a catalytically active enzyme even without Thr⁵⁰⁵ phosphorylation and 2) PKC δ -Thr⁵⁰⁵ phosphorylation is dynamically regulated through an autocatalytic mechanism (4). Although there are hints that Thr⁵⁰⁵ phosphorylation might contribute to the control of PKC δ enzymology, a PKC δ -Thr⁵⁰⁵ autophosphorylation mechanism that regulates the actions of PKC δ toward a physiologically relevant substrate in a differentiated cell has never been reported.

PKC δ also is regulated through tyrosine phosphorylation. However, the consequences of PKC δ tyrosine phosphorylation remain disputed, because PKC δ tyrosine phosphorylation is variably linked to increased, decreased, or unchanged PKC δ activity (1). Inconsistencies in the literature have been attributed to the presence of multiple tyrosine residues throughout the structure of PKC δ (including Tyr⁵², Tyr⁶⁴, Tyr¹⁵⁵, Tyr¹⁸⁷, Tyr³¹¹, Tyr³³², Tyr⁵¹², and Tyr⁵²³, numbering based upon rodent sequence) that are targets for independently regulated phosphorylations by Src family kinases, c-Abl, and potentially other tyrosine kinases. The general consensus in the literature is that PKC δ tyrosine phosphorylation patterns vary according to the nature of the inciting stimulus and dictate the functional properties of the enzyme in cells. Our recent studies show Tyr³¹¹ and Tyr³³² (residues in the hinge region of PKC δ that links the regulatory and kinase domains) are phosphorylated *in vivo* in H₂O₂-treated cardiomyocytes and *in vitro* in kinase assays performed with Src (4, 6). We also obtained unanticipated evidence that Src and PKC δ tyrosine phosphorylation promote PKC δ -Thr⁵⁰⁵ autophosphorylation in cells. These results run counter to the prevailing assumption that PKC δ tyrosine and Thr⁵⁰⁵ phosphorylations are independently regulated mechanisms and suggest that at least some of the dynamically regulated changes in PKC δ -Thr⁵⁰⁵ phosphorylation in cells can be attributed to tyrosine phosphorylation (*i.e.* PKC δ -Thr⁵⁰⁵ autophosphorylation constitutes a final common mechanism to control PKC δ activity, including during oxidative stress).

PKCs induce structural and functional ventricular remodeling both by activating signaling pathways that alter gene

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¹ To whom correspondence should be addressed: Dept. of Pharmacology, College of Physicians and Surgeons, Columbia University, 630 West 168 St., New York, NY 10032. Tel.: 212-305-4297; E-mail: sfs1@columbia.edu.

² The abbreviations used are: PKC, protein kinase C; cTnI, cardiac troponin I; GFP, green fluorescent protein; EGFP, enhanced GFP; PMA, phorbol 12-myristate 13-acetate; PKA, cAMP-dependent protein kinase; PS, phosphatidylserine; HPLC, high pressure liquid chromatography; MALDI-TOF, matrix-assisted laser desorption ionization time-of-flight; WT, wild type; PSSA, phospho site-specific antibody; DAG, diacylglycerol; PKD, protein kinase D.

expression and by directly phosphorylating myofilament proteins that control cardiac contraction (7). cTnI, the “inhibitory” subunit of the troponin complex, is an important PKC substrate that plays an indispensable role in Ca²⁺-dependent regulation of myofilament function (8). At low intracellular [Ca²⁺], cTnI is anchored to the actin filament via peptides (an inhibitory peptide ¹³⁸GKFKRPTLRRVR¹⁴⁹) and a second actin-binding site (residues 161–188) flanking a so-called switch peptide (9). This tethering of cTnI acts together with other regulatory proteins to prevent strong, force-generating interactions of myosin cross-bridges with thin filaments. At high intracellular [Ca²⁺], the switch peptide binds strongly to the cTnC regulatory domain and induces a movement of cTnI away from actin thereby releasing inhibition (for recent reviews see Refs. 10 and 11 and references within). Myofilament function is further regulated and fine-tuned to hemodynamic load, by cTnI phosphorylation. cTnI contains three phosphorylation clusters (Ser²³/Ser²⁴, Ser⁴³/Ser⁴⁵, and Thr¹⁴⁴) that exert distinct effects on cardiac function. Ser²³/Ser²⁴ phosphorylation desensitizes myofilaments to Ca²⁺ and leads to an enhanced rate of relaxation, augmented cross-bridge cycling, and accelerated unloaded shortening velocity. In contrast, Ser⁴³/Ser⁴⁵ phosphorylation leads to a decrease in maximal actomyosin Mg-ATPase, Ca²⁺-activated force, and cross-bridge cycling rate. Despite the fact that Thr¹⁴⁴ is critically positioned in the inhibitory peptide region, the functional impact of Thr¹⁴⁴ phosphorylation has been less intensively studied. Recent studies suggest that Thr¹⁴⁴ phosphorylation may influence myofilament Ca²⁺ sensitivity (12–14).

PKC-dependent cTnI phosphorylation is believed to be particularly important in the development of hypertrophy/failure syndromes, where coordinate increases in PKC isoform expression and cTnI phosphorylation have been linked to reduced actin-myosin interactions and depressed contractile function (7, 15, 16). However, conventional models of PKC δ activation, which attribute PKC isoform specificity entirely to translocation events that localize the enzyme to membranes, do not adequately explain PKC-dependent cTnI phosphorylation in the sarcomere. A role for tyrosine-phosphorylated PKC δ that is released from membranes and recovered as a constitutively active, lipid-independent enzyme in the soluble fraction of H₂O₂-treated cardiomyocytes would be more plausible (6). This study examines the role of PKC δ as a cTnI kinase, with a particular focus on the role of Src (and PKC δ tyrosine phosphorylation) to regulate PKC δ -dependent phosphorylation of cTnI and transduce physiologically relevant changes in contractile function.

EXPERIMENTAL PROCEDURES

Materials—Antibodies were from the following sources: PKC δ -Thr(P)⁵⁰⁵, PKC δ -Tyr(P)³¹¹, Src-Tyr(P)⁴¹⁶, troponin I-Ser(P)²³/Ser(P)²⁴, and anti-pTXR from Cell Signaling Technology; GFP (for immunoblot analysis), PKC δ , and PKC δ -Tyr(P)³³² from Santa Cruz Biotechnology; Src from Oncogene; anti-Tyr(P) from Upstate Biotechnology; and GFP (for immunoprecipitation) from Invitrogen. Recombinant human PKC δ was from Calbiochem; active Src kinase was from Invitrogen; c-Abl was from Upstate Biotechnology. PMA was from Sigma.

1,2-Dioleoyl-*sn*-glycerol was from Avanti Polar Lipids, Inc. The other chemicals were reagent grade.

cTnI Phosphorylation in Adult Ventricular Cardiomyocytes—Left ventricular myocytes enzymatically isolated from male Sprague-Dawley rats according to a modification of published methods were plated for 2 h on laminin-coated dishes (10 μ g/ml; Invitrogen) at a density of 5×10^4 rod-shaped cells/35-mm dish (27). The cells were washed with fresh media, pretreated with vehicle (Me₂SO), GF109203X (5 μ M), or PP1 (10 μ M) and then stimulated with H₂O₂ (5 mM) or PMA (100 nM) for 15 min. Cell lysis was in ice-cold radioimmune precipitation assay buffer (with protease/phosphatase inhibitor mixture) and was followed by centrifugation (16,000 \times g, 4 °C, 15 min) to pellet myofilament proteins, which were then resuspended in a urea/thiourea sample buffer and separated on 15% acrylamide gels. The gels were stained with Pro-Q Diamond (to detect phosphorylated proteins) followed by Sypro Ruby (to detect total protein), and analysis was by imaging on a Typhoon 9410 molecular imager (GE Healthcare) using ImageQuant TL software.

Cardiomyocyte Culture and PKC δ Immunoprecipitation for Kinase Assays—Cardiomyocytes were isolated from hearts of 2-day-old Wistar rats by a trypsin dispersion procedure that uses a differential attachment procedure followed by irradiation to enrich for cardiomyocytes (6). The cells were plated on protamine sulfate-coated culture dishes at a density of 5×10^6 cells/100-mm dish and grown in minimum essential medium (Invitrogen) supplemented with 10% fetal calf serum for 4 days and then serum-deprived for 24 h prior to experiments. The cells were treated with vehicle, 5 mM H₂O₂, or 100 nM PMA for 15 min and then lysed in homogenization buffer, and cell extracts were subjected to immunoprecipitation with anti-PKC δ (Santa-Cruz) and used in immunocomplex kinase assays modified only to include cTn complex as substrate according to methods described previously (4, 6, 12).

In Vitro Kinase Assays with Recombinant Enzymes—*In vitro* kinase assays were performed with 0.032 units (32.4 ng) of recombinant human PKC δ (Calbiochem) for assays of cTn complex phosphorylation (or 0.4 units for peptide mapping studies) or other serine/threonine kinases (0.083 units of PKC α , 0.063 units of PKC β II, 0.566 units of PKC ϵ , 0.026 units of PKD, or 3.84 units of PKA; all from Upstate Biotechnology) in 80 μ l of a reaction buffer containing 30 mM Tris-Cl, pH 7.5, 5 mM MgCl₂, 10 mM MnCl₂, 0.9 mM EDTA, 0.9 mM EGTA, 3 mM dithiothreitol, 0.1 mM sodium vanadate, 76 mM NaCl, 23.5% glycerol, 0.006% Brij-35, 0.023% Triton X-100, 0.04 mM phenylmethylsulfonyl fluoride, 0.2 mM benzamide, 83 μ g/ml phosphatidylserine (PS), 175 nM PMA, 4 μ g of troponin complex, and [γ -³²P]ATP (25 μ Ci, 97 μ M). Incubations were for 30 min at 30 °C in the absence or presence of Src or c-Abl (0.66 units) and lipid cofactors; PS-PMA was included in assays to allosterically activate PKC δ and render it a better substrate for Src-dependent tyrosine phosphorylation (4).

PKC δ Mutants—pPKC δ -EGFP (pGFP-PKC δ) was obtained as a generous gift from Dr. Mary Reyland (University of Colorado Health Sciences Center, Denver, CO). The pPKC δ -EGFP construct expresses PKC δ protein with enhanced GFP fused to its C terminus. The pPKC δ (T505A)-EGFP and pPKC δ (T505E)-

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EGFP were generated by site-directed mutagenesis according to the manual for the QuikChange site-directed mutagenesis kit (Stratagene). The PKC δ expression plasmids were introduced into COS-7 cells by Effectene transfection reagent (Qiagen) according to the instruction manual. The cells were grown for 24 h, lysed in homogenization buffer (20 mM Tris-Cl, pH7.5, 0.05 mM EDTA, 0.5 mM dithiothreitol, 0.2% Triton X-100, 5 μ g/ml aprotinin, 5 μ g/ml leupeptin, 5 μ g/ml benzamide, 1 mM phenylmethylsulfonyl fluoride, 5 μ M pepstatin A). Cell extracts were subjected to immunoprecipitation with mouse monoclonal anti-GFP antibody 3E6 (Invitrogen).

Peptide Mapping Studies—For peptide mapping studies, kinase reactions (see above) were stopped by adding 27 μ l of 4 \times SDS-PAGE sample buffer. The proteins were separated by SDS-PAGE and transferred to nitrocellulose, and the band corresponding to PKC δ was excised from the membrane, cut into small pieces, and treated for 30 min at 37 $^{\circ}$ C with polyvinylpyrrolidone (0.5%, w/v) in acetic acid (100 mM), followed by five water washes (to remove the acid) and a 10-min incubation at room temperature in the dark with 100 mM iodoacetate to carboxymethylate PKC δ . The membrane pieces were then washed three times with water and twice with 50 mM ammonium bicarbonate and incubated overnight at 37 $^{\circ}$ C in 60 μ l of a buffer containing 42 mM ammonium bicarbonate, 17 μ M HCl, and 10 μ g of sequencing grade trypsin. Digested peptides were eluted from the membrane by sonication and lyophilized, and the residue was reconstituted in 0.1% trifluoroacetic acid and fractionated by reverse phase-HPLC on a Vydac semimicro C₁₈ column (2.1 \times 250 mm). The peptides were eluted with a linear gradient from 0.1% trifluoroacetic acid in water to 0.1% trifluoroacetic acid in acetonitrile over 140 min at a flow rate of 1 ml/min. The eluant was monitored at 220 nm, and fractions were collected every 30 s for Cherenkov counting. Radioactive peptides of interest were submitted to the Howard Hughes Medical Institute/Columbia University Protein Chemistry Core Facility for sequencing by MALDITOF mass spectrometry.

Mechanical Measurements in Skinned Rat Ventricular Myocytes—Rat ventricular myocytes were mechanically isolated and mounted in the experimental set-up as described previously (20). Isometric force production and the rate constant of force redevelopment (k_{tr}) were assessed in single, skinned myocytes, as described previously (20), before and after PKC δ treatment alone (as described above) or in combination with Src kinase. All of the PKC δ treatments were in the presence of lipid cofactors (PS/PMA). Lipid cofactors and Src alone had no effect on mechanical parameters.

Statistical Analysis—All of the values are presented as the means \pm S.E., and the values of $p < 0.05$ were the criteria of statistical significance. Statistical evaluation was by Student *t* test (KaleidaGraph, Synergy Software).

RESULTS

cTnI Phosphorylation via a PKC δ /Src-dependent Mechanism in H₂O₂-treated Cardiomyocytes—Initial studies examined the mechanisms that control cTnI phosphorylation *in situ* in the myofilament lattice of cultured adult rat cardiomyocytes subjected to oxidative stress by H₂O₂ treatment. Fig. 1 shows that PMA (which directly activates PKCs) and H₂O₂ induce similar

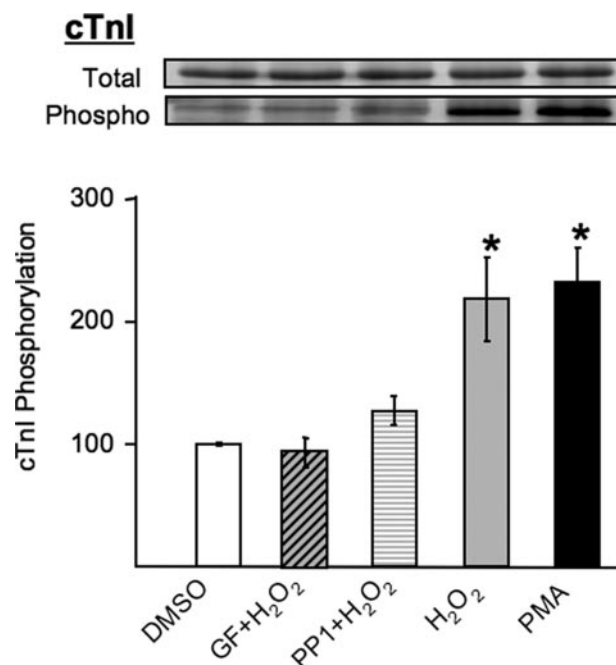


FIGURE 1. Stimulus-dependent cTnI phosphorylation in cardiomyocytes. Adult ventricular myocytes were treated with vehicle (dimethyl sulfoxide (DMSO)), GF109203X (5 μ M), or PP1 (10 μ M) followed by H₂O₂ (5 mM) or PMA (100 nM) for 15 min. The gels were stained with Pro-Q Diamond (phosphoproteins stain) followed by Sypro Ruby (total protein stain), and the phospho/total protein ratios were determined ($n = 4$, means \pm S.E.; *, $p < 0.05$). The results are normalized by setting the mean value for vehicle-treated samples to 100.

increases in cTnI phosphorylation. The H₂O₂-dependent increment in cTnI phosphorylation is completely abrogated by GF109203X (a relatively nonselective inhibitor of PKC isoforms), and it is markedly blunted by PP1 (an inhibitor of Src family kinases). The observation that H₂O₂ increases cTnI phosphorylation through a PKC-dependent mechanism that requires tyrosine kinase activity provided the rationale to consider a role for tyrosine-phosphorylated PKC δ .

PKC δ was immunopurified from vehicle-, PMA-, and H₂O₂-treated cardiomyocyte cultures and used in assays with cTn ternary complexes (consisting of equimolar cTnI, cTnN, and cTnT) as substrate to resolve the cellular actions of PKC δ from the actions of other PKC isoforms. Native PKC δ is recovered from quiescent cardiomyocyte cultures with only very low lipid-independent cTnI kinase activity; cTnI phosphorylation is markedly increased when lipid activators, PS/PMA, are added to the *in vitro* kinase assay (Fig. 2A). PMA treatment of cardiomyocyte cultures, prior to PKC δ immunoprecipitation, leads to a minor increase in basal and lipid-dependent cTnI kinase activity, in association with a trace increase in overall PKC δ tyrosine phosphorylation. Oxidative stress induced by H₂O₂ treatment results in a marked increase in PKC δ tyrosine phosphorylation and a dramatic increase in PKC δ -dependent phosphorylation of cTnI, including in assays without lipid cofactors (*i.e.* PKC δ is recovered from cardiomyocytes subjected to oxidative stress as a lipid-independent cTnI kinase). Although H₂O₂ treatment has been linked to the activation of an array of serine/threonine kinases that may potentially associate with PKC δ during immunoprecipitation, control experi-

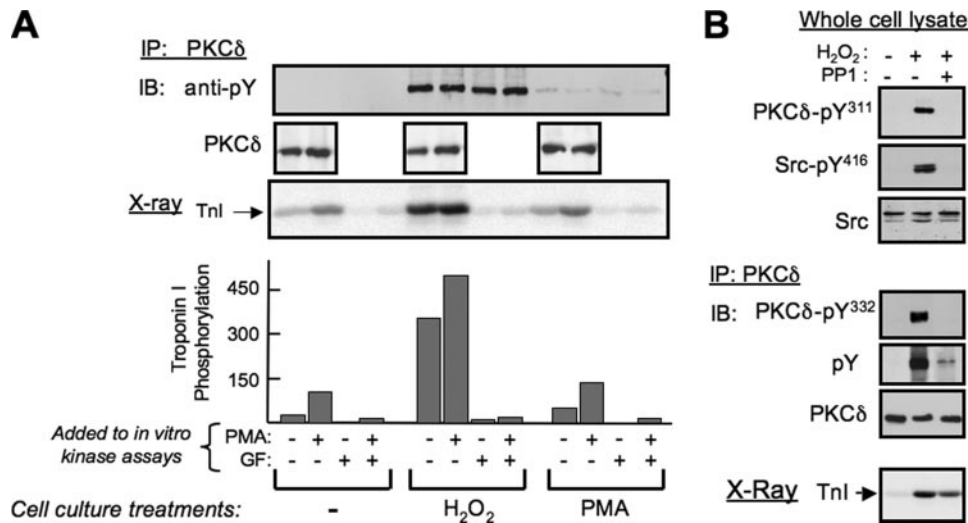


FIGURE 2. PKC δ is recovered as a lipid-independent kinase from H₂O₂-treated cardiomyocytes. *A*, PKC δ immunoprecipitated from cardiomyocytes treated with vehicle (Me₂SO), PMA (100 nM), or H₂O₂ (5 mM), each for 15 min, was used in immune complex kinase assays with cTn complex as substrate (with 100 nM PMA and 5 μ M GF109203X also included in kinase assays as indicated). Immunoblotting (IB) was used to validate equal PKC δ recovery from control and PMA- and H₂O₂-treated cultures and to show that PKC δ is tyrosine-phosphorylated in H₂O₂-treated cultures (and to a much lesser extent in PMA-treated cultures) but not in control cultures. The autoradiogram showing cTnI phosphorylation and quantification is from a representative experiment, with similar results obtained in separate experiments on four separate culture preparations. *B*, cardiomyocytes were treated with vehicle, 5 mM H₂O₂, or 5 mM H₂O₂ + 10 μ M PP1 (each for 15 min); cell extracts were subjected to immunoblotting for PKC δ -Tyr(P)³¹¹ and Src-Tyr(P)⁴¹⁶ (with Src protein as a loading control, *top right*), and PKC δ pull-downs were immunoblotted for PKC δ -Tyr(P)³³² and Tyr(P) (with PKC δ as a loading control; the anti-PKC δ -Tyr(P)³³² antibody displays too much nonspecific immunoreactivity to be used directly on cell extracts, *middle right*). PKC δ in immune complexes also was used in kinase assays with cTn complex as substrate; a representative autoradiogram of cTnI phosphorylation is illustrated (*bottom right*). IP, immunoprecipitation.

ments identify similar pharmacologic profiles for the cTnI kinase activity recovered from resting and H₂O₂-treated cultures; in both cases, cTnI phosphorylation is fully inhibited by 5 μ M GF109203X and 5 μ M Gö6983 (broad spectrum PKC inhibitors) but not by 10 μ M Gö6976 (a conventional PKC isoform-selective inhibitor that also directly inhibits the catalytic activity of PKD, another potential H₂O₂-activated cTnI kinase; Fig. 2 and data not shown). These results implicate PKC δ as a lipid-independent cTnI kinase in cardiomyocytes exposed to oxidative stress.

PKC δ kinase activity may be activated by H₂O₂ indirectly as a result of Src-dependent tyrosine phosphorylation or directly through cysteine oxidation (17). To assess the importance of tyrosine phosphorylation in H₂O₂-dependent changes in PKC δ activity, we compared cTnI phosphorylation by PKC δ recovered from myocytes treated with H₂O₂ alone or H₂O₂ + PP1 (to inhibit PKC δ tyrosine phosphorylation). Fig. 2*B* shows that H₂O₂ increases overall PKC δ tyrosine phosphorylation (tracked with a general anti-phosphotyrosine antibody) and PKC δ -Tyr³¹¹ and -Tyr³³² phosphorylation (tracked by phospho site-specific antibodies (PSSAs)); H₂O₂-dependent PKC δ tyrosine phosphorylation is blocked by PP1, under conditions that also block H₂O₂-dependent activation of Src (tracked by immunoblotting for Src activation loop Tyr⁴¹⁶ phosphorylation). PP1 attenuates (by 28.4 \pm 4%, n = 4, p < 0.05) but does not entirely block the H₂O₂-dependent increase in cTnI phosphorylation by PKC δ . These results indicate that H₂O₂ increases PKC δ phosphorylation of cTnI through at least two mechanisms that differ in their requirements for Src-depend-

ent tyrosine phosphorylation. The Src and tyrosine phosphorylation-dependent mechanisms that regulate PKC δ activity are the focus of the remainder of the studies in this manuscript.

Src Phosphorylates PKC δ at Tyr³¹¹ and Tyr³³², Leading to Enhanced PKC δ Phosphorylation of cTnI—We recently used PSSAs to identify Tyr³¹¹ and Tyr³³² as sites for Src-dependent PKC δ phosphorylation (4). Recombinant PKC δ (human sequence) was subjected to *in vitro* kinase assays without and with active Src in buffers containing [γ -³²P]ATP and PS/PMA, and radiolabeled PKC δ was subjected to peptide mapping analysis as an alternative method to map sites for Src-dependent PKC δ phosphorylation sites (without relying on available PSSAs). Fig. 3*A* shows that Src increases ³²P incorporation into PKC δ , leading to the appearance of a PKC δ species that migrates more slowly in SDS-PAGE and displays increased PKC δ -Tyr(P)³¹¹ and PKC δ -Tyr(P)³³² immunoreactivity. Src also increases PKC δ autophosphorylation at Thr⁵⁰⁵, consistent with our recent observation that the activation loop of PKC δ is the target of an autophosphorylation reaction that is augmented by Src (4).

PKC δ purified by SDS-PAGE and blotted to nitrocellulose was excised from the membrane and digested with trypsin, and peptide fragments were separated by reverse phase-HPLC (Fig. 3*B*). Radioactive peptide fragments detected in assays with PKC δ + Src (but not in assays with PKC δ alone) were sequenced by MALDI-TOF mass spectrometry to determine sites for Src-dependent PKC δ phosphorylation. Fig. 3*B* shows that three distinct radioactive peaks were detected in reverse phase-HPLC chromatograms of phospho-peptide fragments derived from *in vitro* kinase assays with PKC δ , Src, and [³²P]ATP (and not *in vitro* kinase assays with PKC δ alone).

Peaks 1 and 2 were identified by mass spectrometry analysis as the oxidized and reduced forms of a Tyr(P)³³²-containing fragment (note that differences in oxidation status arise during sample preparation and should not be construed as evidence that this modification occurs in cells). Peak 3 contained a Tyr(P)³¹¹ fragment, as well as nonphosphorylated forms of peptides containing Tyr⁶⁴ and Tyr⁵² (other sites on PKC δ that have been reported to be phosphorylated under certain stimulatory conditions). Collectively, these results identify Tyr³¹¹ and Tyr³³² as the major sites for *in vitro* Src-dependent PKC δ tyrosine phosphorylation.

Having identified Tyr³¹¹ and Tyr³³² as major targets for Src-dependent PKC δ phosphorylation *in vitro* and H₂O₂-dependent PKC δ phosphorylation *in vivo*, we performed *in vitro* kinase assays with PKC δ , active Src, a kinase buffer containing

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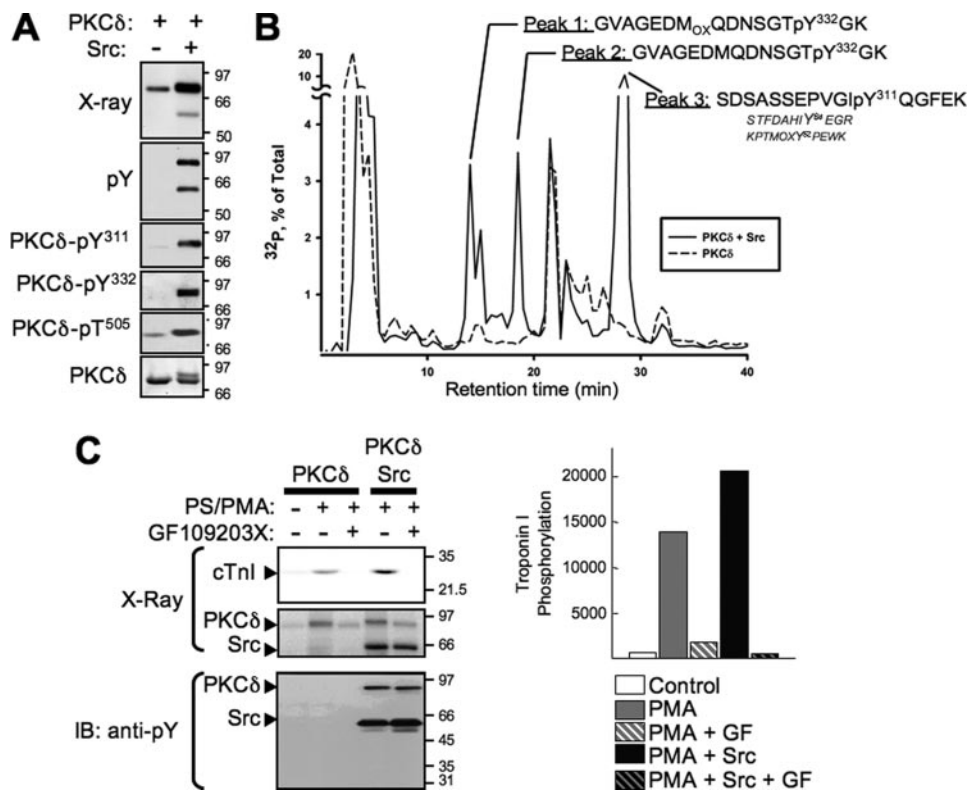


FIGURE 3. Src-dependent PKC δ phosphorylation maps to Tyr³¹¹ and Tyr³³² and leads to increased PKC δ -dependent cTnI phosphorylation. PKC δ was incubated in a kinase buffer containing [³²P]ATP without and with active Src and PKC δ phosphorylation was tracked by immunoblotting (A) and MALDI-TOF mass spectrometry (B) according to "Experimental Procedures." C, *in vitro* kinase assays were performed with PKC δ in the absence or presence of Src, 100 nM PMA + 112 μ M PS, and 5 μ M GF109203X as indicated. Autoradiograms showing ³²P incorporation into PKC δ , Src, and cTnI are depicted (top left) with results for cTnI phosphorylation quantified (right). Immunoblotting (IB) with anti-Tyr(P) antibody shows Src autophosphorylation and Src-dependent tyrosine phosphorylation of PKC δ , but no cTnI tyrosine phosphorylation.

[³²P]ATP and cTn complex (consisting of wild type (WT) cTnT, WT-cTnC, and WT-cTnI) to determine whether Src-dependent PKC δ tyrosine phosphorylation leads to a change in PKC δ -dependent phosphorylation of cTnI. PKC δ phosphorylates cTnI in a lipid-dependent fashion *in vitro*, with cTnI phosphorylation markedly increased in assays performed in the presence of active Src (under conditions that lead to PKC δ tyrosine phosphorylation; Fig. 3C). The Src-dependent increment in cTnI phosphorylation cannot be attributed to direct myofibrillar protein phosphorylation by Src, because 1) cTnI phosphorylation is completely blocked by GF109203X and 2) anti-Tyr(P) antibodies detect tyrosine-phosphorylated forms of PKC δ and Src, but no anti-Tyr(P) immunoreactivity comigrating with cTnI was detected. These results indicate that the Src-dependent increment in cTnI phosphorylation results from serine/threonine phosphorylation by PKC δ rather than direct cTnI tyrosine phosphorylation by Src.

In vitro kinase assays were extended to use cTn complexes containing WT-cTnI or substituted forms of cTnI (cTnI-S23D/S24D, cTnI-S23A/S24A, cTnI-S43E/S45E, cTnI-Thr¹⁴⁴E, or cTnI-S43E/S45E/T144E; see Fig. 4A) as substrate to 1) map the sites phosphorylated by allosterically activated PKC δ (in assays with PS/PMA) and 2) determine whether the Src-dependent increment in PKC δ activity is directed toward the same or different sites on cTnI. PhosphorImager analysis of PKC δ -dependent cTnI phosphorylation shows that PKC δ preferen-

tially radiolabels forms of cTnI that can be phosphorylated at Ser²³/Ser²⁴ (Fig. 4B, top panel, gray bars). PKC δ induces similar increases in ³²P incorporation into WT-cTnI and cTnI mutants harboring Ser \rightarrow Glu substitutions at Ser⁴³/Ser⁴⁵ or Thr¹⁴⁴ alone or in combination (*i.e.* cTnI-S43E/S45E, cTnI-T144E, and cTnI-S43E/S45E/T144E), whereas PKC δ -dependent phosphorylation of cTnI-S23D/S24D is markedly reduced in comparison. Quantification of data from three separate experiments shows the S23D/S24D substitution (making Ser²³/Ser²⁴ nonphosphorylatable) reduces PKC δ -dependent cTnI phosphorylation by 68.0 \pm 2.3% (relative to WT-cTnI; *n* = 3, *p* < 0.05). These results indicate that PS/PMA-activated PKC δ phosphorylates cTnI primarily at Ser²³/Ser²⁴; Ser⁴³/Ser⁴⁵ and Thr¹⁴⁴ are relatively poor substrates for allosterically activated PKC δ . A similar mutagenesis approach was used to map the Src-dependent increment in PKC δ -dependent cTnI phosphorylation to cTnI-Thr¹⁴⁴. Src increases PKC δ -dependent phosphorylation of WT-cTnI and forms of cTnI that can be

phosphorylated at Thr¹⁴⁴ (cTnI-S23D/S24D or cTnI-S43E/S45E), whereas the Src-dependent increment in PKC δ -dependent cTnI phosphorylation is abrogated by T144E or cTnI-S43E/S45E/T144E substitutions (Fig. 4B, top panel, black bars).

Conclusions derived from PhosphorImager studies were validated by immunoblot analysis (Fig. 4B, bottom panel). An anti-cTnI-Ser(P)²³/Ser(P)²⁴ PSSA that specifically recognizes the Ser²³/Ser²⁴-phosphorylated form of cTnI detects similar PKC δ -dependent phosphorylation of WT-cTnI and cTnI mutants harboring single residue substitutions at Ser⁴³/Ser⁴⁵ and Thr¹⁴⁴ (alone and in combination); this PSSA does not detect phosphorylation of the cTnI-S23D/S24D mutant. Importantly, radiolabeling studies show that Src increases overall WT-cTnI phosphorylation by PKC δ , but direct immunoblotting studies show that Src does not increase PKC δ -dependent cTnI-Ser²³/Ser²⁴ phosphorylation (compare Fig. 4B, top and bottom panels). We performed additional studies with an anti-pTXR phospho-motif antibody (Cell Signaling Technology; that recognizes phospho-threonines flanked by an arginine in the +2 position, which is predicted to recognize cTnI phosphorylation at KRPT¹⁴⁴LR, but not RS²³S²⁴AN or KIS⁴³AS⁴⁵RK) to localize the Src-dependent increment in PKC δ -dependent cTnI phosphorylation. The anti-pTXR PSSA does not recognize cTnI phosphorylation in assays with PKC δ alone (without Src), where PKC δ acts primarily as a cTnI-Ser²³/Ser²⁴ kinase. Rather, this antibody selectively recognizes phosphorylation of

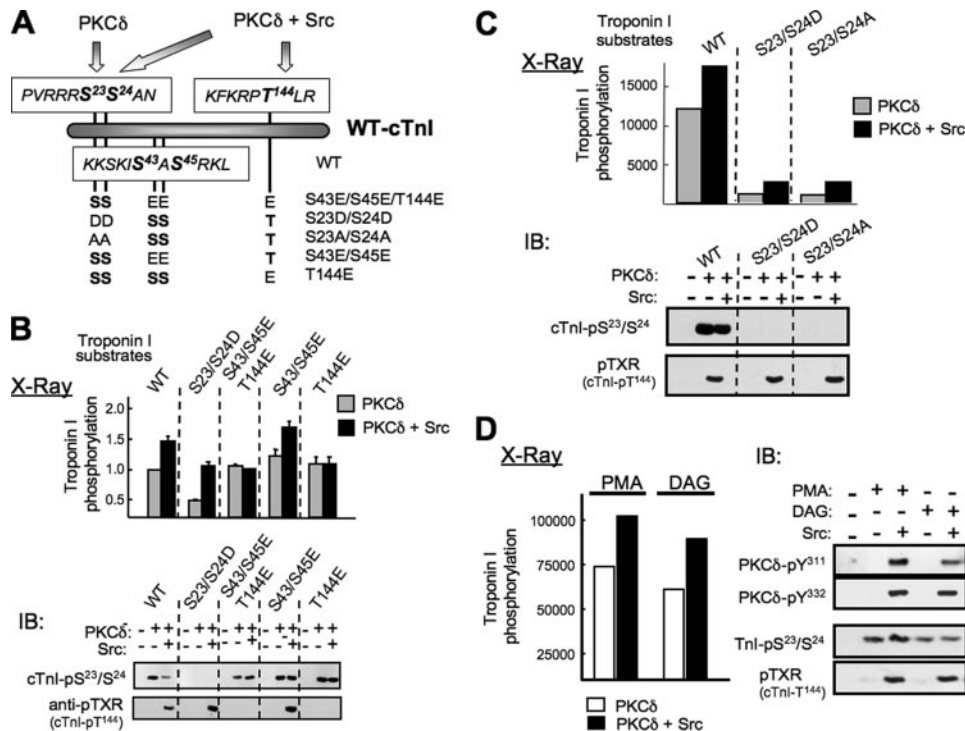


FIGURE 4. Lipid-activated PKC δ is a cTnI-Ser²³/Ser²⁴ kinase; tyrosine-phosphorylated-PKC δ is a cTnI-Ser²³/Ser²⁴ kinase that also phosphorylates cTnI at Thr¹⁴⁴. *A*, schematic of WT-cTnI and cTnI mutants used in this study. *B* and *C*, *in vitro* kinase assays with PKC δ alone or PKC δ + Src performed with 112 μ M PS + 175 nM PMA and cTnI complexes containing WT or mutant cTnIs as substrates. cTnI phosphorylation was quantified by PhosphorImager analysis (mean \pm S.E., $n = 3$ top) and immunoblotting (*B*) with anti-cTnI-Ser²³/Ser²⁴ and anti-pTXR (that recognizes cTnI-Thr¹⁴⁴ phosphorylation; representative experiment is depicted at the bottom). *D*, *in vitro* kinase assays with PKC δ alone or PKC δ + Src with complexes containing WT-cTnI and either 175 nM PMA or 7.2 μ M 1,2-DAG (each with 112 μ M PS) as lipid cofactor. PKC δ tyrosine (Tyr³¹¹ and Tyr³³²) was tracked by immunoblotting; cTnI phosphorylation was tracked by PhosphorImager analysis (top) and immunoblotting (bottom). Similar results were obtained in two additional separate experiments.

WT-cTnI, cTnI-S23D/S24D, and cTnI-S43E/S45E (*i.e.* forms of cTnI that can be phosphorylated at Thr¹⁴⁴) in assays performed with PKC δ + Src (Fig. 4*B*, bottom panel); the cTnI-S43E/S45E/T144E and cTnI-T144E mutants are not detected. These immunoblotting studies validate the use of the anti-pTXR PSSA to selectively track cTnI-Thr¹⁴⁴ phosphorylation and validate conclusions derived from radiolabeling experiments tracking overall cTnI phosphorylation (by PhosphorImager); both techniques identify an effect of Src to selectively increase PKC δ cTnI-Thr¹⁴⁴ kinase activity. Additional studies show that PKC δ functions as a cTnI-Thr¹⁴⁴ kinase in assays with Src having either cTnI-S23D/S24D or cTnI-S23/24A as substrate (Fig. 4*C*). These results argue that Thr¹⁴⁴ phosphorylation does not require prior phosphorylation (or negative charge) at Ser²³/Ser²⁴ (*i.e.* cTnI phosphorylation does not appear to be a hierarchical process). Collectively, these results provide surprising evidence that PKC δ acquires a new activity, directed toward a different site on cTnI (namely Thr¹⁴⁴), when it is tyrosine-phosphorylated by Src; Src does not increase PKC δ -dependent cTnI-Ser²³/Ser²⁴ phosphorylation.

In vitro kinase assays were performed in buffers containing PS/PMA, which is included both to activate PKC δ (in assays without Src) and to induce a conformational change required for Src-dependent PKC δ tyrosine phosphorylation (in assays with Src); our previous studies established that Src phosphorylates PKC δ only in assays performed with PS/PMA (4). Given

recent evidence that the PKC δ C1 domain is comprised of C1A and C1B domains with markedly different affinities for PMA and the natural lipid cofactor DAG (*i.e.* PMA binds with high affinity to the PKC δ -C1B domain, whereas DAG anchors full-length PKC δ to membranes via an interaction with the PKC δ -C1A domain (18)), it was important to determine whether the Src-dependent changes in PKC δ -dependent cTnI phosphorylation also are detected in assays with DAG. Fig. 4*D* shows that DAG effectively substitutes for PMA in these experiments. PS/DAG supports PKC δ -dependent cTnI-Ser²³/Ser²⁴ phosphorylation, in assays with PKC δ alone and mimics the effect of PMA to render PKC δ a substrate for Src, leading to PKC δ -Tyr³¹¹/Tyr³³² phosphorylation and PKC δ -dependent cTnI-Thr¹⁴⁴ phosphorylation in assays with Src.

cTnI is a substrate for several physiologically and pathophysiologically relevant serine/threonine kinases that control contractile function, including other PKC isoforms, PKA, and PKD. We performed *in vitro* kinase assays with PKA, PKD, PKC α , PKC β II, PKC δ , and PKC ϵ (under conditions calibrated to achieve similar levels of autophosphorylation) and used immunoblotting with anti-cTnI-Ser²³/Ser²⁴ and anti-pTXR (cTnI-Thr¹⁴⁴) PSSAs to determine whether Src regulates the cTnI kinase activity of these other enzymes. All of these enzymes increase ³²P incorporation into cTnI, tracked by PhosphorImager analysis; immunoblotting studies show that PKC δ , PKC α , PKC β II, PKA, and PKD are all effective cTnI-Ser²³/Ser²⁴ kinases (Fig. 5). In contrast, PKC ϵ promotes cTnI phosphorylation (detected by PhosphorImager), but PKC ϵ is a relatively poor cTnI-Ser²³/Ser²⁴ kinase. Rather, PKC ϵ and PKC β are weak cTnI-Thr¹⁴⁴ kinases; PKC α , PKD, PKA, and allosterically activated PKC δ (in assays without Src) do not phosphorylate cTnI at Thr¹⁴⁴. Of note, PKC ϵ - and PKC β II-dependent increases in cTnI-Thr¹⁴⁴ phosphorylation are modest in magnitude compared with the robust increase in cTnI-Thr¹⁴⁴ phosphorylation induced by Src-phosphorylated PKC δ . Moreover, the effect of Src to convert PKC δ into a cTnI-Thr¹⁴⁴ kinase is quite specific. Although Src also tyrosine phosphorylates PKC ϵ and PKD (but not PKC α or PKC β II), Src has no effect on (or actually decreases, in the case of PKC α) the cTnI kinase activities of these other enzymes (measured by PhosphorImager analysis or by immunoblotting with the anti-cTnI-pSer²³/Ser²⁴ PSSA). Src does not convert any of these other enzymes into effective cTnI-Thr¹⁴⁴ kinases. Finally, because PKD also is a known substrate for c-Abl (19), c-Abl-dependent

Cardiac Troponin I Phosphorylation by PKC δ

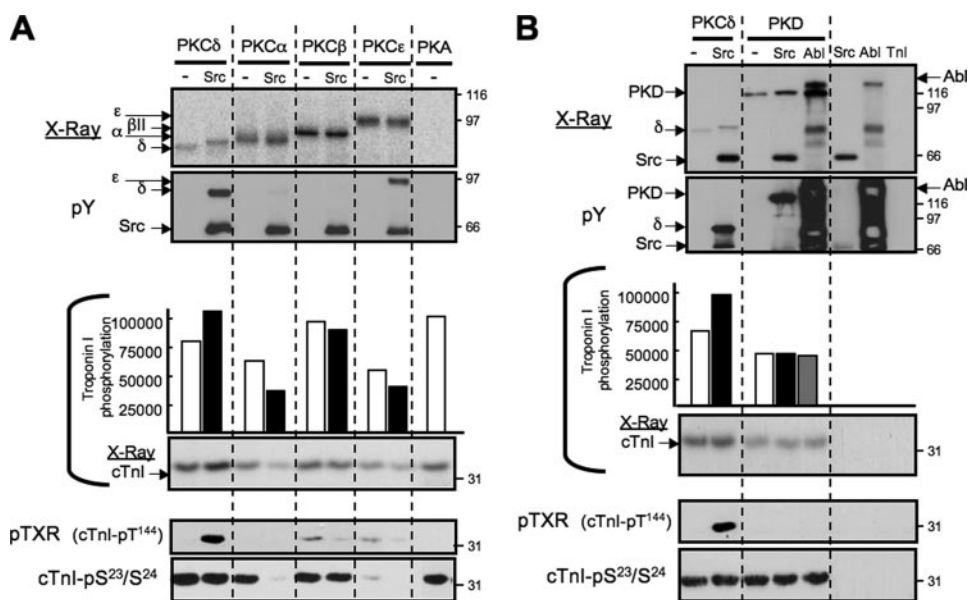


FIGURE 5. cTnI phosphorylation by PKC isoforms, PKA, and PKD. *In vitro* kinase assays performed with PKC δ , PKC α , PKC β , PKC ϵ , or PKA alone or with Src as indicated are depicted in A; assays with PKD (alone or with Src or c-Abl) and control assays with Src and c-Abl alone are depicted in B. All of the reactions contained PS/PMA. Autoradiograms and anti-Tyr(P) blots showing the positions of the various enzymes is on top; cTnI phosphorylation quantified by PhosphorImager analysis (with a representative autoradiogram depicted) and immunoblotting for cTnI-Ser²³/Ser²⁴ and Thr¹⁴⁴ (detected as anti-pTXR) from a single experiments are illustrated at the bottom; the results were replicated in separate experiments.

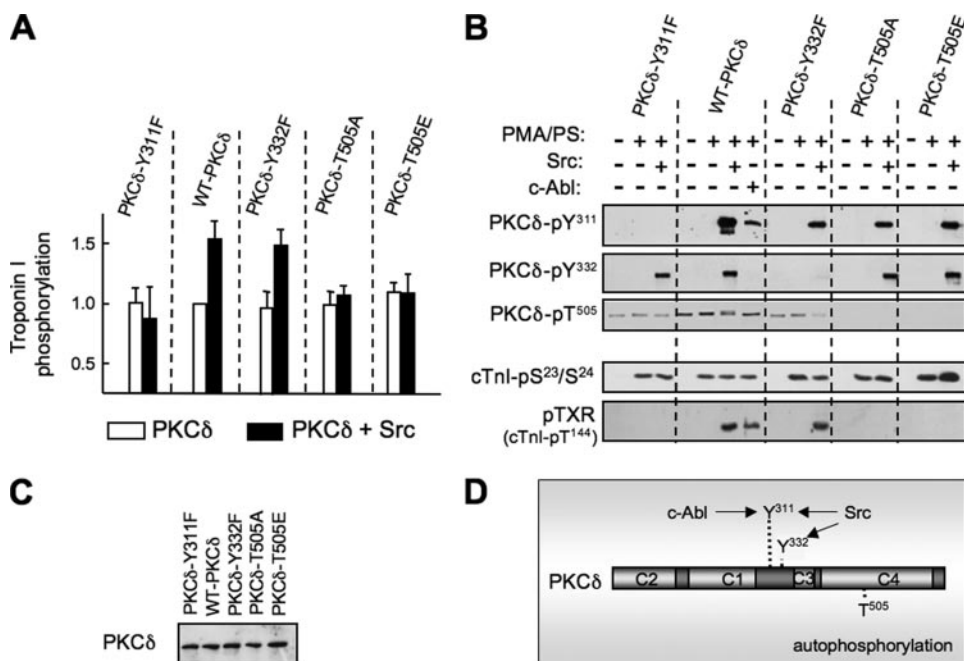


FIGURE 6. Tyr³¹¹ and Thr⁵⁰⁵ substitutions prevent Src-dependent changes in PKC δ substrate specificity. COS cells were transfected with plasmids that drive expression of WT and Y311F, Y332F, T505A, and T505E substituted forms of PKC δ fused to GFP. PKC δ was immunoprecipitated with anti-GFP, subjected to immunoblotting with anti-GFP to validate equal protein recovery (C), and subjected to immunocomplex kinase assays without and with lipid cofactor, Src, or c-Abl as indicated. cTnI phosphorylation was quantified by PhosphorImager (and is expressed relative to the basal level of phosphorylation for each PKC δ construct (A)). PKC δ -Tyr³¹¹, -Tyr³³², and -Thr⁵⁰⁵ phosphorylation and cTnI-Ser²³/Ser²⁴ and Thr¹⁴⁴ phosphorylation were detected by immunoblot analysis according to the legend for B. The results were replicated in two separate experiments. D, a schematic that marks the various phosphorylation sites of PKC δ and the main kinases implicated in phosphorylating each site.

modulation of PKD activity also was considered. Fig. 5B shows that PKD undergoes an autophosphorylation reaction; ³²P incorporation into PKD is increased slightly by Src (which pro-

motes PKD tyrosine phosphorylation) and to an even greater extent by c-Abl (although the very high nonspecific anti-Tyr(P) immunoreactivity in assays with c-Abl alone thwarted efforts to directly track c-Abl-dependent PKD tyrosine phosphorylation). PKD does not acquire cTnI-Thr¹⁴⁴ kinase activity when tyrosine-phosphorylated by Src or c-Abl.

Src-dependent Changes in PKC δ Substrate Specificity Require Tyr³¹¹ and Thr⁵⁰⁵—We used a mutagenesis approach to explore the structural basis for Src-dependent changes in PKC δ substrate specificity. Fig. 6 shows that Tyr → Phe substitutions at Tyr³¹¹ or Tyr³³² (that selectively abrogate Src-dependent PKC δ phosphorylation at the cognate tyrosine residues) have no effect on PKC δ -dependent cTnI-Ser²³/Ser²⁴ phosphorylation. However, the Tyr → Phe substitution at Tyr³¹¹ completely abrogates the Src-dependent increment in cTnI phosphorylation by PKC δ (detected by PhosphorImager) and cTnI-Thr¹⁴⁴ phosphorylation (detected by immunoblot analysis). In contrast, a Tyr → Phe substitution at Tyr³³² does not interfere with these activities.

We used a similar mutagenesis approach to examine the role of activation loop phosphorylation. Although recombinant PKC δ (which displays at most trace Thr⁵⁰⁵ phosphorylation prior to *in vitro* kinase assays) undergoes pronounced Thr⁵⁰⁵ autophosphorylation during *in vitro* kinase assays (particularly in the presence of Src), WT-PKC δ , PKC δ -Y311F, and PKC δ -Y332F enzymes recovered from COS-7 cells exhibit similar levels of basal Thr⁵⁰⁵ phosphorylation that do not increase during *in vitro* kinase assays (with or without Src; compare Figs. 3A and 6). Basal PKC δ -Thr⁵⁰⁵ phosphorylation (for WT and Tyr → Phe substituted enzymes heterologously overexpressed in COS-7 cells) is presumed to be

attributable to a phosphoinositide-dependent kinase-1-dependent mechanism that mediates activation loop phosphorylation *in trans* during *de novo* enzyme synthesis (and is not

prevented by Y311F or Y332F mutations). T505A or T505E substitutions prevent activation loop phosphorylation, but they do not interfere with Src-dependent PKC δ -Tyr³¹¹ (or Tyr³³²) phosphorylation; T505A or T505E substitutions also do not alter overall cTnI phosphorylation (detected by ³²P incorporation into cTnI) or cTnI-Ser²³/Ser²⁴ phosphorylation (detected by immunoblot analysis with the anti-cTnI-pSer²³/Ser²⁴ PSSA) in assays without Src. However, T505A and T505E substitutions abrogate the Src-dependent increment in PKC δ -depend-

ent overall cTnI phosphorylation (detected by Phosphor-Imager) and the Src-dependent acquisition of cTnI-Thr¹⁴⁴ kinase activity (detected with the anti-TXR PSSA). These results indicate that PKC δ is catalytically active without Thr⁵⁰⁵ phosphorylation, but that Thr⁵⁰⁵ phosphorylation is necessary (and that a phospho-mimetic substitution is not sufficient) for Src-dependent regulation of PKC δ substrate specificity. Collectively, these results indicate that Tyr³¹¹ and Thr⁵⁰⁵ cooperate in the Src-activated mechanism that alters the substrate specificity of PKC δ . The conclusion that the substrate specificity of PKC δ is influenced by a phosphorylation event at Tyr³¹¹, but not Tyr³³², is supported further by studies with c-Abl, which selectively increases PKC δ phosphorylation at Tyr³¹¹ (not Tyr³³²) and supports PKC δ -dependent cTnI-Thr¹⁴⁴ phosphorylation (Fig. 6).

TABLE 1

Summary of mechanical properties of detergent extracted (skinned) rat ventricular myocytes before and after kinase treatments

The data are presented as the means \pm S.E. Maximum tension and the rate constant of force redevelopment (k_{tr}) were measured at pCa 4.5 in myocytes before and after treatment with PKC δ alone ($n = 4$) or with PKC δ in the presence of Src kinase ($n = 5$). Submaximal tension and k_{tr} were measured at pCa 5.5.

	[Ca ²⁺]	PKC δ		Src + PKC δ	
		Before	After	Before	After
Tension (kN/m ²)	pCa 4.5	26.7 \pm 1.0	23.4 \pm 1.4	26.2 \pm 0.6	20.4 \pm 1.8 ^a
k_{tr} (s ⁻¹)	pCa 4.5	8.3 \pm 0.2	8.1 \pm 0.2	8.6 \pm 0.3	7.4 \pm 0.5 ^a
Tension (kN/m ²)	pCa 5.5	19.7 \pm 1.2	3.3 \pm 0.3 ^a	15.2 \pm 2.0	10.6 \pm 3.1
k_{tr} (s ⁻¹)	pCa 5.5	6.8 \pm 0.7	6.7 \pm 0.7	6.3 \pm 0.3	6.0 \pm 0.3

^a Significantly different from pre-treatment value as determined by paired Student *t*-test ($p < 0.05$).

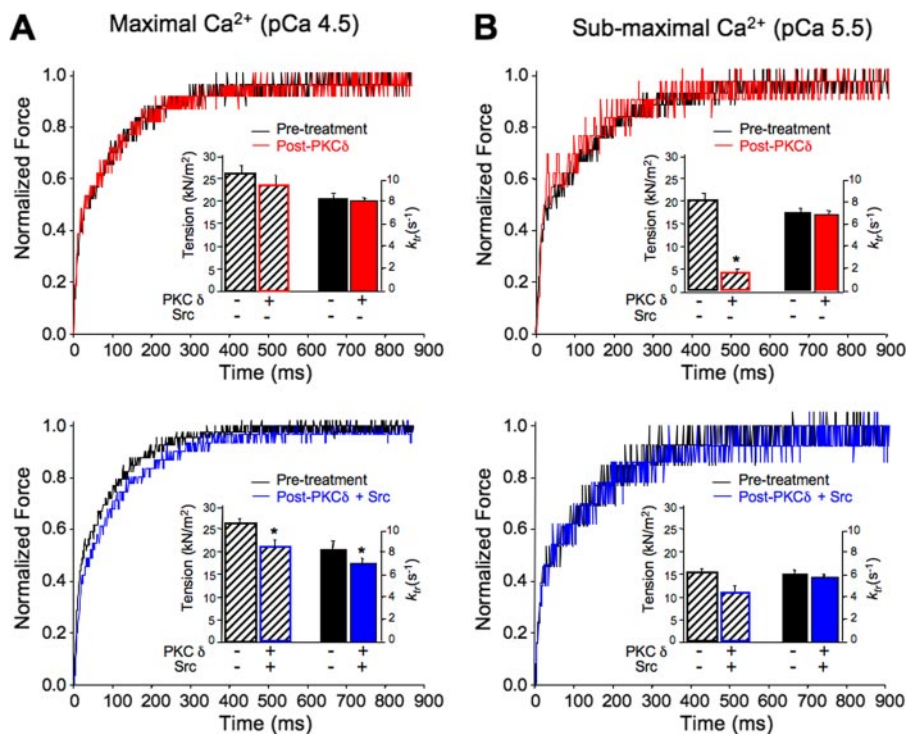


FIGURE 7. Mechanical properties of skinned cardiomyocyte preparations before and after PKC δ treatments at maximal and submaximal [Ca²⁺]. The traces show the recovery of force following a mechanical detachment of cross-bridges, to drop force to near-zero values. *A, top panel*, representative records used for the determination of k_{tr} rates before (black) and after (red) PKC δ treatment demonstrate no change in rate of force recovery. Histograms (inset) summarize lack of effect of PKC δ on maximum Ca²⁺-activated parameters. *A, bottom panel*, force tracings demonstrate that Src (tyrosine-phosphorylated) PKC δ (blue) decreases the rate of recovery of force (i.e. return to equilibrium more slowly) and therefore k_{tr} . Histograms of maximum Ca²⁺-activated tension and k_{tr} values demonstrate significant decreases in these parameters in myocytes treated with Src (tyrosine-phosphorylated) PKC δ . *B, top panel*, tracings show no difference between control (black) and PKC δ (red) on the rate of force recovery at submaximal Ca²⁺, although submaximal tension production was significantly low (histogram). *B, bottom panel*, force tracings reflect a minor (although nearly significant $p = 0.07$) shift in force recovery with PKC δ pretreated with Src kinase (blue). In contrast to PKC δ alone, no significant change in submaximal tension production was observed (histogram, bottom). All of the measurements were performed in the presence of lipid activators PS/PMA. The results are reported as the means \pm S.E. (* indicates $p < 0.05$).

PKC δ Regulates Cardiac Contractile Function in a Src-dependent Manner—We performed mechanical studies on skinned (detergent extracted) ventricular myocytes (20) to determine whether Src (and tyrosine phosphorylation) alters PKC δ -dependent regulation of contraction. PKC δ alone reduces submaximal Ca²⁺-activated isometric tension (force/cross-sectional area of the myocyte at pCa 5.5), without changing maximal Ca²⁺-activated tension (at pCa 4.5) in skinned myocytes (Table 1 and Fig. 7). However, PKC δ does not alter cross-bridge cycling kinetics as reflected in the rate constant of force redevelopment (k_{tr}) following a rapid release-restretch maneuver at either submaximum or maximum Ca²⁺ concentration. Control studies show that lipids (PS/PMA) and Src alone do not significantly alter mechanical function. These results are expected from previous data characterizing cTnI-Ser²³/Ser²⁴ phosphorylation as a modification that reduces submaximal tension but does not alter maximal Ca²⁺-activated tension or k_{tr} (21, 22).

The functional response to treatment with Src-phosphorylated PKC δ is quite different. PKC δ + Src lowers tension and the rate of force redevelopment at maximal but not submaximal Ca²⁺-activated tension in skinned myocytes (Table 1 and Fig. 7). These results are in agreement with previous studies linking cTnI-Thr¹⁴⁴ phosphorylation to a decrease in maximum Ca²⁺-activated tension (12, 23). The observation that Src-phosphorylated PKC δ does not mimic the effect of PKC δ alone to lower submaximal Ca²⁺-activated isometric tension suggests that a Ser²³/Ser²⁴ phosphorylation-

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induced effect is attenuated when cTnI is simultaneously phosphorylated at Ser²³/Ser²⁴ and Thr¹⁴⁴ (by Src-phosphorylated PKC δ). These mechanical studies provide a functional correlate to the *in vitro* biochemical studies and support the conclusion that when allosterically activated by PS/PMA PKC δ selectively phosphorylates cTnI at Ser²³/Ser²⁴ and leads to a fall in submaximal tension (without altering contractile function at maximal Ca²⁺) and that when it is prephosphorylated by Src PKC δ acquires an additional activity to phosphorylate cTnI at Thr¹⁴⁴ (which prevents the Ser²³/Ser²⁴ phosphorylation-dependent decrease in submaximal Ca²⁺-activated tension and results in a decrease in force and rate of force redevelopment at maximal Ca²⁺).

Other laboratories, conducting similar mechanical studies, considered analogous changes in tension and k_{tr} (as reported in Table 1) significant. Patel *et al.* (22) reported that PKA accelerates the rate of force development in murine skinned myocardium expressing α - or β -tropomyosin. They reported small but significant changes in the submaximal rate of force redevelopment after PKA treatments of non-transgenic myocardium with 100% α -tropomyosin (increased by 15%) and transgenic myocardium with 60% β -tropomyosin (increased by 18%) myocardium. Korte *et al.* (28) showed that loaded shortening, power output, and rate of force development (WT = $5.8 \pm 0.9 \text{ s}^{-1}$ versus MyBP-C^{-/-} = $7.7 \pm 1.7 \text{ s}^{-1}$) are increased with knock-out of cardiac myosin binding protein-C. Moreover similar shifts (to those presented here) in Ca²⁺ sensitivity of force are closely related to events common in fatal human cardiomyopathies.

DISCUSSION

This study provides novel evidence that cTnI phosphorylation by PKC δ is controlled by Src and tyrosine phosphorylation. These observations are highly significant for several reasons. First, previous studies have implicated tyrosine phosphorylation as a mechanism that alters the activity of PKC δ , but there is still no consensus as to the precise nature of this regulatory control. Tyrosine phosphorylation has variably been implicated as a mechanism that increases or decreases PKC δ activity. Although there have been isolated reports that link tyrosine phosphorylation to changes in PKC δ activity toward only selected substrates, studies of substrate specificity have been confined to assays with peptides or proteins with little-to-no physiologic significance. The results reported herein link a tyrosine phosphorylation-dependent change in PKC δ activity to a physiologically important event in the cell, namely the phosphorylation of cTnI. Second, this study is the first to map tyrosine phosphorylation sites that control PKC δ activity. Our experiments implicate Tyr³¹¹ (which is a major target for Src-dependent phosphorylation during both stimulation by PMA and oxidative stress) and Thr⁵⁰⁵ (a site that is phosphorylated via an autocatalytic reaction that is increased by Src) in this form of regulatory control. In contrast, Tyr³³² (which also is phosphorylated by Src during oxidative stress but is not a substrate for c-Abl and is not phosphorylated during stimulation with PMA) does not mediate Src-dependent changes in PKC δ substrate specificity. Third, an effect of PKC δ -Tyr³¹¹/Thr⁵⁰⁵ phosphorylation to regulate the phosphorylation of only

selected sites on a single substrate is unprecedented in the literature. Post-translational modifications typically induce more general changes in enzyme activity measured as a change in maximal catalytic activity (K_{cat}) or affinity for substrate or ATP (K_m). Although a recent study using a proteomic approach provided intriguing hints that activation loop phosphorylation can influence PKC δ substrate specificity (24), a post-translational modification that selectively regulates the phosphorylation of selected sites on a single substrate has not previously been identified.

The role of PKA-dependent cTnI phosphorylation at Ser²³/Ser²⁴ in the control of cardiac dynamics is well documented (10). Although PKC phosphorylation of cTnI was originally mapped to Ser⁴³/Ser⁴⁵ and Thr¹⁴⁴, recent studies also implicate Ser²³/Ser²⁴ as an alternate (and perhaps more important) phosphorylation site for certain PKC isoforms (and PKC-activated effectors). Our results also show that PKC α , PKC β , PKC δ , and PKD act in a similar manner to phosphorylate cTnI at Ser²³/Ser²⁴; only PKC ϵ is uniquely identified as a poor cTnI-Ser²³/Ser²⁴ kinase. We also link PKC δ -dependent cTnI-Ser²³/Ser²⁴ phosphorylation to a decrease in force development at submaximal Ca²⁺, but no change in maximal Ca²⁺-activated tension or cross-bridge cycling kinetics in skinned cardiomyocytes (the predicted response based upon studies examining the regulatory actions of PKA, the prototypical cTnI-Ser²³/Ser²⁴ kinase).

The data summarized in Table 1 show that at submaximal Ca²⁺ concentrations Ser²³/Ser²⁴ phosphorylation leads to an 83% fall in tension (from 19.7 ± 1.2 to $3.3 \pm 0.3 \text{ kN/m}^2$). This significant change in tension is in agreement with previous studies detailing the effect of PKA-dependent phosphorylation of cTnI-Ser²³/Ser²⁴ on cardiac muscle. The Ser²³/Ser²⁴ phosphorylation effect on tension ($3.3 \pm 0.3 \text{ kN/m}^2$) is largely reversed under oxidative stress conditions through additional phosphorylation of Thr¹⁴⁴ ($10.6 \pm 3.1 \text{ kN/m}^2$). This 68% increase in tension indicates improved sarcomeric Ca²⁺ responsiveness.

Allosterically activated PKC δ is not a cTnI-Thr¹⁴⁴ kinase. In fact, whereas cTnI-Thr¹⁴⁴ phosphorylation originally was attributed to PKCs, the physiologically relevant cTnI-Thr¹⁴⁴ kinase (and the functional consequences of cTnI-Thr¹⁴⁴ phosphorylation) remains uncertain. cTnI-Thr¹⁴⁴ phosphorylation mechanisms have largely been inferred from studies with T144A or T144E-substituted cTnI mutants, because a PSSA that directly tracks cTnI-Thr¹⁴⁴ phosphorylation (similar to the cTnI-pSer²³/Ser²⁴ PSSA) is not available. The identification of the anti-pTXR phospho-motif antibody as a reagent that can be used to track cTnI-Thr¹⁴⁴ phosphorylation in immunoblotting experiments allowed a comparison of cTnI-Thr¹⁴⁴ phosphorylation by individual PKC isoforms that was not previously possible. Our studies identify a low level of cTnI-Thr¹⁴⁴ phosphorylation by PKC β and PKC ϵ (consistent with recent studies that attribute cTnI-Thr¹⁴⁴ phosphorylation to PKC- β II (14)) but no cTnI-Thr¹⁴⁴ phosphorylation by related kinases such as PKC α , PKA, PKD, and allosterically activated PKC δ (*i.e.* the form of PKC δ that is anchored to membranes by lipid cofactors). In contrast, tyrosine-phosphorylated PKC δ is a robust cTnI-Thr¹⁴⁴ kinase. These results suggest that tyrosine-phosphoryl-

ated PKC δ is the most physiologically relevant cTnI-Thr¹⁴⁴ kinase and that cTnI-Thr¹⁴⁴ phosphorylation would be most prominent *in vivo* in conditions such as oxidative stress (where activation of Src leads to PKC δ tyrosine phosphorylation). Current concepts regarding the functional consequences of cTnI-Thr¹⁴⁴ phosphorylation are based largely on studies that use mutagenesis approaches or genetic models, with evidence that cTnI-Thr¹⁴⁴ phosphorylation accelerates myofilament relaxation in adult rat myocytes, decreases Ca²⁺ sensitivity in sliding filament assays, or sensitizes myofilaments to Ca²⁺ (without changing maximum tension) in skinned myocytes from transgenic mice that express the cTnI-Ser²³/Ser²⁴A mutant (12–14). Importantly, the studies reported herein examine the physiologic consequences of a coordinate increase in cTnI phosphorylation at Ser²³/Ser²⁴ and Thr¹⁴⁴ induced by Src-phosphorylated PKC δ . Here, the Ca²⁺-desensitizing effect of PKC δ alone is no longer detected. Rather, PKC δ + Src lowers tension and the rate of force redevelopment at maximal Ca²⁺, an effect that is predicted to contribute to oxidative stress-induced myocardial dysfunction. On the other hand, at submaximal Ca²⁺ concentrations, where the myocardium typically operates, oxidative stress events that activate Src-PKC δ signaling pathways could enhance cardiac function. This effect on one hand might be beneficial in maintaining systolic contractile function of the failing myocardium. On the other hand this might be detrimental during β -adrenergic stimulation hindering the expected increase of relaxation rate. These data underscore the importance of understanding events that modulate troponin I phosphorylation and ultimately fine-tune sarcomeric function.

Recent NMR data suggest that cTnI phosphorylation at Ser²³/Ser²⁴ weakens the interaction of the cTnI N-terminal residues 1–30 with cTnC, induces a lever-like bending around residues 33–42, and facilitates its repositioning to bind the inhibitory region of cTnI (9). This association between N-terminal and inhibitory regions of cTnI is stabilized by favorable electrostatic interactions between an acidic patch consisting of residues Asp³, Glu⁴, Asp⁷, Glu¹¹, and a basic patch Arg¹⁴², Arg¹⁴⁶, and Arg¹⁴⁹, surrounding Thr¹⁴⁴. Interestingly, the R146G mutation (linked to familial hypertrophic cardiomyopathy in humans) leads to myofilaments with increased Ca²⁺ sensitivity and lack of responsiveness to phosphorylation at Ser²³/Ser²⁴ (25, 26). In the case of the R146G mutant, replacement of an Arg with Gly presumably induces its effect by disrupting the electrostatic interactions between the acidic N terminus and the inhibitory region of cTnI. In our case, the addition of a bulky, negatively charged phosphate group to the basic patch, through Thr¹⁴⁴ phosphorylation, could induce a similar effect. Our mechanical data are consistent with this model, because Thr¹⁴⁴ phosphorylation alleviates the Ca²⁺-desensitizing effect of Ser²³/Ser²⁴ phosphorylation. Our data further suggest that phosphorylation at Thr¹⁴⁴ (on a Ser²³/Ser²⁴ phosphorylation background) prevents the cTnI inhibitory region from properly interacting with actin-tropomyosin, leading to a decrease in maximum force.

Collectively, our studies identify distinct signaling modes for PKC δ , a single PKC isoform whose substrate specificity can be

dynamically regulated through tyrosine phosphorylation. This study focuses on a dual role for PKC δ as both an allosterically activated and a tyrosine-phosphorylated enzyme leading to the phosphorylation of functionally distinct sites on cTnI, potentially underlying differences in PKC-dependent regulation of myofilament contraction in the normal heart and in the context of diseases associated with oxidative stress. This novel tyrosine phosphorylation-dependent change in PKC δ substrate specificity is likely to represent a general regulatory mechanism that also influences PKC δ phosphorylation of other cellular substrates and might be targeted in the future for therapeutic advantage.

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