Research Article

PKCε Phosphorylates and Mediates the Cell Membrane Localization of RhoA

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Protein kinase Cε (PKCε) signals through RhoA to modulate cell invasion and motility. In this study, the multifaceted interaction between PKCε and RhoA was defined. Phosphopeptide mapping revealed that PKCε phosphorylates RhoA at T127 and S188. Recombinant PKCε bound to recombinant RhoA in the absence of ATP indicating that the association between PKCε and RhoA does not require an active ATP-docked PKCε conformation. Activation of PKCε resulted in a dramatic coordinated translocation of PKCε and RhoA from the cytoplasm to the cell membrane using time-lapse fluorescence microscopy. Stoichiometric FRET analysis revealed that the molecular interaction between PKCε and RhoA is a biphasic event, an initial peak at the cytoplasm and a gradual prolonged increase at the cell membrane for the entire time-course (12.5 minutes). These results suggest that the PKCε-RhoA complex is assembled in the cytoplasm and subsequently recruited to the cell membrane. Kinase inactive (K437R) PKCε is able to recruit RhoA to the cell membrane indicating that the association between PKCε and RhoA is proximal to the active catalytic site and perhaps independent of a PKCε-RhoA phosphorylation event. This work demonstrates, for the first time, that PKCε phosphorylates and modulates the cell membrane translocation of RhoA.

1. Introduction

Numerous publications have clearly defined the role of PKCε as transforming oncogene in fibroblasts and epithelial cells. Overexpression of PKCε in NIH3T3 fibroblasts and FRC/TEX cells in rat colonic epithelial cells was shown to increase cell proliferation, enhance anchorage-independent colony formation, and induce a highly tumorigenic in vivo phenotype with tumor incidence of 100% [1, 2]. In addition, NIH3T3 fibroblasts with PKCε overexpression were invasive and displayed a polarized morphology with extended long cellular membrane protrusions [3]. Epidermis-specific PKCε transgenic mice developed highly malignant and metastatic squamous cell carcinomas in response to 12-O-tetradecanoylphorbol-13-acetate stimulation [4]. PKCε was demonstrated to transform androgen-dependent LNCaP prostate cancer cells into an androgen-independent variant [5]. Moreover, transgenic mice with selective overexpression of PKCε in the prostate epithelium developed prostate hyperplasia and prostate intraepithelial neoplasia [6]. Our laboratory demonstrated that inhibition of PKCε in MDA-MB231 cells, a highly metastatic breast cancer cell line with elevated PKCε levels, was sufficient to dramatically decrease in vivo tumor growth and reduce the incidence of lung metastasis [7]. Subsequently, PKCε was shown to promote an invasive and
motile phenotype in HNSCC through modulation of RhoA presumably through posttranslation phosphorylation [8].

RhoA, a member of the Rho GTPase family, has been implicated to be involved in the development and/or progression of numerous cancers. A recent report showed that overexpression of RhoA is sufficient to immortalize human mammary epithelial cells [9]. Elevated RhoA is associated with invasive breast cancer progression [10]. Moreover, miR-31 was reported to be inversely associated with metastasis through inhibition of RhoA in breast cancer patients [11]. Multivariate analysis revealed that elevated RhoA is an independent prognostic biomarker of poorer overall survival in pancreatic adenocarcinoma [12]. High levels of RhoA correlated with venous invasion, advanced pTNM stage, and prognosis in hepatocellular carcinoma [13, 14]. Increased RhoA is associated with tumor progression in ovarian carcinoma and lymph node metastasis and overall survival in bladder carcinoma [15, 16]. Similarly, RhoA was shown to be biomarker for lymph node metastasis and overall survival in esophageal squamous cell carcinoma [17]. RhoA, Rac2, and Cdc42 were found to be elevated in premalignant dysplastic and HNSCC cell lines in comparison to normal keratinocytes [18]. Furthermore, based on their immunohistochemistry analyses, RhoA was suggested to be a promising biomarker of malignancy and/or aggressiveness in head and neck squamous cell carcinoma (HNSCC) [18].

Our previous work provided the initial evidence linking two proteins, PKCe and RhoA, intimately involved in metastasis. PKCe was shown to signal through RhoA to modulate cell invasion and motility in HNSCC [8]. In this study, we further studied the interaction between PKCe and RhoA. PKCe was shown to phosphorylate RhoA at T127 and S188. Interestingly, an active ATP-docked PKCe conformation is not required for PKCe to bind to RhoA indicating that the PKCe-RhoA complex is assembled independently of the transient substrate-kinase interaction at the catalytic site of PKCe. Stoichiometric FRET analysis with HEK293 cells overexpressing mCherry-PKCe and eGFP-RhoA revealed that the PKCe-RhoA complex is assembled in the cytoplasm and subsequently translocates to the cell membrane. Our work revealed that PKCe phosphorylates RhoA but, intriguingly, also has a kinase-independent action to function as a chaperone to traffic RhoA to the cell membrane.

2. Materials and Methods

2.1. Plasmid Constructs. Human PKCe cDNA was cloned into pENTR/D-TOPO vector (Invitrogen, Carlsbad, CA) by PCR from a human cDNA library (Clontech, Mountain View, CA). The N-mCherry-tagged PKCe was made by inserting PKCe open reading frame into BglII/XbaI site of mCherry-C1 vector (Clontech, Mountain View, CA). mCherry-PKCe/K437R mutant was generated using the QuickChange Lightning kit (Agilent Technologies, Inc., Santa Clara, CA). The positive control plasmid mCherry-linker-eGFP for stoichiometric FRET analysis was made by inserting mCherry DNA fragment into NheI/BglII sites and followed by eliminating the sequence between BamH1 and BglII sites within the multiple cloning site in vector eGFP-C1 (Clontech), resulting in a 10 amino acid long in-frame linker SGLKDPPVAT.

2.2. Cell Line. HEK293 cells were purchased from ATCC (Rockville, MD) and cultured in Dulbecco’s modified Eagle’s medium supplemented with penicillin (100 units/mL), streptomycin (100 μg/mL), and 10% fetal bovine serum.

2.3. In Vitro Kinase Assay. Recombinant PKCe was incubated with recombinant RhoA in kinase buffer (24 mM Tris (pH 7.4), 0.5 mM EDTA, 0.5 mM EGTA, 10 mM β-mercaptoethanol, 1 μg/mL leupeptin, 1 μg/mL aprotinin, and 50 μg/mL PMSF) containing PKC activators, phosphatidylserine and diacylglycerol, and [32P]ATP for 30 minutes at 25°C. Subsequently, termination buffer consisting of 7.5 M guanidine-HCl was added to stop the reaction. The incubation reaction was separated by SDS-PAGE and visualized using autoradiography.

2.4. Phosphopeptide Mapping. RhoA was phosphorylated by PKCe in vitro and then subjected to digestion by trypsin, chymotrypsin, or Glu-C. Following enzyme digestion the sample was acidified to 0.5% trifluoroacetic acid concentration and stored at −20°C until further analyzed. The digested RhoA protein was analyzed by reverse-phase nanoscale LC-MS using a Waters QTof Premier mass spectrometry system. Prior to analysis EDTA and diammonium phosphate were added to sample for a final concentration of 25 mM each, and 11–25 ng of digested protein was analyzed. Peptides were separated using acetonitrile/water mobile phases containing 0.1% formic acid on a Waters NanoAcquity UPLC system employing a 300 μm ID × 20 mm C-18 5 μm particle Symmetry trap column and a 75 μm ID × 150 mm C-18 1.7 μm BEH analytical column. Peptides were trapped for 15 minutes at 3 μL/min followed by gradient elution using 0–28% acetonitrile in 40 minutes through the analytical column at 300 nL/min. ESI was conducted at approximately 3.3 kV using in-house prepared spray emitters. Emitters were constructed by sleeving a 7 cm piece of 20 μm ID × 90 OD FSC into a 3 cm piece of 100 μm ID × 360 OD FSC and gluing the junction with epoxy. The polyimide coating on the terminal end of the emitter was burned off using a microtorch, and the emitter was used with a Waters NanoEase ESI mount. The QToF Premier mass spectrometer was programmed to collect alternate scan MS² data as previously described [19, 20]. Briefly, MS² data collection was performed by a low collision energy acquisition of 0.8 seconds followed by a high collision energy acquisition for 0.8 seconds without quadrupole mass filtering across a 50–1990 m/z mass range. This was performed in an alternating fashion during a 65-minute run and termed LC-MS² analysis. Low collision energy acquisition records all peptide precursor mass data, while the high collision energy portion of the acquisition collected peptide fragmentation data. Following the low collision energy acquisition set at 10 volts, collision energy was ramped from 10 volts to 40 volts over the 0.8 second high collision energy acquisition to accommodate peptides requiring different collision energy for fragmentation. Glu-fibrinopeptide at a concentration...
of 200 fmol/µL in 25% acetonitrile/water/0.1% formic acid was introduced as a lockspay calibrant through a second ESI probe at 0.5 µL/min using an auxiliary UPLC pump. Lockspay data was collected for 1 second every 30 seconds over a 65-minute analysis.

Following an LC-MS analysis, data processing was performed using Waters PLGS software version 2.3 build 23 using the following parameters: low-energy threshold 100 counts, high-energy threshold 10 counts, and an intensity threshold of 1000 counts. Data processing combined the signal intensity of all charge states generated from a given peptides into singly charged MH⁺ values and determined the peak apex for both low-energy precursors and all fragment ions within the vicinity of the precursor. This lockmass corrected, accurate mass data was used in two ways. First, the data was used to search Human RefSeq database version 17 within PLGS software using the following search parameters: peptide and fragment tolerance was automatic, the minimum fragment ion matches per peptide were 3, the minimum fragment ions per protein were 7, the minimum peptides matches per protein were 1, missed cleavages were 2, the false positive rate was 4%, and modifications allowed were Acetyl N-term, Carbamidomethyl-C, Carbamyl N-term, and phosphorylation at STY. Second, low-energy precursor MH⁺ data was copied into Excel and compared to MH⁺ values calculated for predicted RhoA trypsin, chymotrypsin, or Glu-C protease peptides bearing up to 4 phosphate groups. (Light-house Data, GPMAW version 8.00sr1, Odense, Denmark). Experimental MH⁺ masses that matched within 0.03 Da of GPMAW calculated values were evaluated manually in PLGS or Masslynx Protein/Peptide Editor software. Possible phosphopeptide assignment was made when the measured mass was within 0.03 Da of the calculated phosphopeptide mass and greater than 3 accurate mass product ions could be assigned to a peptide sequence. Confident site-specific phosphorylation also used this criteria but further required fragment ions including phosphorylated serine or threonine amino acids.

2.5. Immunoprecipitation. Recombinant PKCe (GenWay Inc., San Diego, CA) was incubated with recombinant RhoA (Cytoskeleton, Denver, CO) in PKC kinase buffer for 30 minutes at 25°C. The binding reaction was immunoprecipitated using agarose-conjugated anti-PKCε antibody or IgG (Abcam, Cambridge, MA) at 4°C with gentle agitation overnight. The suspension was centrifuged at 1,000 x g for 1 minute, and the agarose beads were washed three times with ice-cold PBS and resuspended in SDS sample buffer. The same procedure was performed to immunoprecipitate the binding reaction containing His-tagged PKCe-kinase domain (BioBasic Inc., Markham, Canada), and RhoA except agarose-conjugated anti-His antibody (Abcam) was used. The immunoprecipitated samples were boiled in SDS sample buffer, resolved by SDS-PAGE, and transferred to Immobilon membrane. The membranes were incubated with anti-RhoA (Cytoskeleton) or anti-His (Millipore, Billerica, MA) antibodies and visualized by ECL using the Fast Western kit (Pierce, Rockford, IL).

2.6. Fluorescence Microscopy and Quantitative Stoichiometric FRET Analysis. HEK293 cells were seeded on 35 mm glass-bottomed dishes one day prior to transfection with mCherry-PKCe and eGFP-RhoA. Fluorescence microscopy experiments were performed in the Center for Live-Cell Imaging (CLCI) at the University of Michigan Medical School using an Olympus IX70 inverted microscope (Olympus, Center Valley, PA). Experiments involving live-cell imaging employed a heated stage (Harvard Apparatus, Inc., Holliston, MA) in combination with HEPES-buffered medium to maintain cell viability and activity for several hours of microscopic observation. Illumination was provided from a 100 W halogen lamp for phase-contrast microscopy and by an X-Cite 120 metal halide light source (EXFO, Mississauga, Canada) for fluorescent microscopy. The microscope was equipped with 100x (oil immersion; UPlan FL, NA = 1.30), 40x (LCP LanFL, NA = 0.6), and 10x (CPlan, NA = 0.25) objectives. Excitation and emission filter sets (Chroma Technology Corp., Rockingham, VT) were used for fluorescence imaging; in particular set number 8601v2 includes filters used for GFP (excitation 492 nm/BP18, emission 535 nm/BP40) and mCherry (excitation 572 nm/BP23, emission 630 nm/BP60). The excitation and emission filters were mounted in a Lambda 10-3 automatic filter wheels (Sutter Instrument Co., Novato, CA) allowing rapid filter switching. Images were collected using a CoolSNAP HQ2 14-bit CCD camera (Photometrics, Tucson, AZ). All devices were controlled through Metamorph Premier v7.7 software (Molecular Devices, Downingtown, PA). Quantitative analysis of the imaging data and the preparation of presentation quality images were performed using Metamorph v7.7 software. Quantitative stoichiometric FRET analysis of the data was performed with proprietary software created by the CLCI staff using MATLAB R2009a (The Mathworks, Natick, MA), and this FRETcalc software can be obtained from the University of Michigan Tech Transfer. The methods and algorithms used in FRET stoichiometry have been previously described [21, 22].

3. Results and Discussion

3.1. Results

3.1.1. PKCe Phosphorylates and Binds to RhoA. Our laboratory reported that PKCe modulates RhoA activity in HNSCC presumably through posttransformation phosphorylation [8]. In silico prediction of phosphorylation sites identified multiple serine and threonine residues that are putative PKC phosphorylation sites on RhoA suggesting that direct phosphorylation of RhoA through PKCe may be a possibility. To determine if PKCe can directly phosphorylate RhoA, we performed an in vitro kinase reaction and incubated recombinant PKCe with RhoA in the presence of PKC activators, phosphatidylserine and diacylglycerol, and 32P-ATP. As shown in Figure I(a), PKCe directly phosphorylated RhoA. Pro-Q Diamond, a phosphoprotein staining reagent, confirmed RhoA as a substrate for PKCe (Figure I(b)). Next, we identified the phosphorylation sites on RhoA using phosphopeptide mapping.
PKC\(\varepsilon\) phosphorylates and binds to RhoA. (a) PKC\(\varepsilon\) phosphorylates RhoA. Recombinant RhoA was incubated with or without recombinant PKC\(\varepsilon\) in kinase buffer containing PKC activators, phosphatidylserine and diacylglycerol, and \([32^P]\)ATP for 30 minutes at 25°C. Subsequently, the incubation reaction was terminated, separated by SDS-PAGE and visualized using autoradiography. (b) Pro-Q Diamond staining of phosphorylated RhoA. Recombinant RhoA was incubated with or without recombinant PKC\(\varepsilon\) in kinase buffer containing PKC activators, phosphatidylserine and diacylglycerol, and ATP for 30 minutes at 25°C. Subsequently, the incubation reaction was terminated, separated by SDS-PAGE and visualized using a stain specific to phosphoproteins. (c) PKC\(\varepsilon\) binds to RhoA. Recombinant PKC\(\varepsilon\) was incubated with recombinant RhoA in kinase buffer containing PKC activators, phosphatidylserine and diacylglycerol, for 30 minutes at 25°C. The binding reaction was immunoprecipitated using agarose-conjugated anti-PKC\(\varepsilon\) or nonspecific IgG antibody. The immunoprecipitated proteins were visualized by western blot analysis using an anti-RhoA antibody. Two independent immunoprecipitation experiments are presented. (d) The kinase domain of PKC\(\varepsilon\) binds to RhoA. Recombinant His-tagged PKC\(\varepsilon\)-kinase domain was incubated with recombinant GST tagged-RhoA in kinase buffer containing PKC activators, phosphatidylserine and diacylglycerol, for 30 minutes at 25°C. The binding reaction was immunoprecipitated using agarose-conjugated anti-His, anti-RhoA, or nonspecific IgG antibody. The immunoprecipitated proteins were visualized by western blot analysis using an anti-His and anti-RhoA antibody.

with liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS). Phosphorylated RhoA was digested with trypsin, chymotrypsin, or Glu-C. LC-MS\(^6\) analysis of peptides resulting from trypsin digested RhoA showed about 83% coverage, whereas the combined data from trypsin and Glu-C digested RhoA showed 100% coverage of the serine and threonine residues on RhoA. Thus, it is reasonable to conclude that a comprehensive phosphopeptide map of RhoA was generated using trypsin and Glu-C. Phosphopeptide analysis revealed T127 and S188 as the confident PKC\(\varepsilon\)-mediated phosphorylation sites on RhoA. Our results provide the first evidence that RhoA is a direct substrate for PKC\(\varepsilon\) phosphorylation.

3.1.2. PKC\(\varepsilon\) Associates with RhoA. There is limited, although intriguing, literature demonstrating that a kinase preassembles with its substrate prior to a kinase phosphorylation event. The preassembled kinase-substrate complex not only increases specificity but also shortens the time between kinase activation and phosphorylation of the substrate [23, 24]. To determine if PKC\(\varepsilon\) preassembles with RhoA without an active ATP-docked PKC\(\varepsilon\) conformation, recombinant PKC\(\varepsilon\) and
RhoA were incubated in ATP-free in vitro kinase buffer. As shown in Figure 1(c), PKCε was able to bind to RhoA under this condition. Moreover, the kinase domain of PKCε was sufficient to bind to RhoA demonstrating that the RhoA docking site is within the PKCε kinase domain (Figure 1(d)). These results indicate that the binding between PKCε and RhoA does not require an active ATP-docked PKCε kinase conformation, and thus, the interaction between these two proteins is more complex than a transient substrate-kinase intermediate state.

3.1.3. PKCε Colocalizes with RhoA at the Cell Membrane in Response to PMA. There is evidence that a preassembled kinase-substrate complex not only enhances phosphorylation specificity and efficiency but also plays a role in cellular localization [25]. To determine if PKCε mediates the localization of RhoA, HEK293 cells were transfected with mCherry-PKCε or eGFP-RhoA or cotransfected with mCherry-PKCε and eGFP-RhoA. Subcellular localization of PKCε and RhoA was visualized in living cells using fluorescence microscopy in the presence or absence of phorbol 12-myristate 13-acetate (PMA). Activation of PKCs with PMA is associated with the translocation of PKCs to the cell membrane. As expected, PKCε was translocated from the cytoplasm to the cell membrane following PMA stimulation in HEK293 cells overexpressing mCherry-PKCε and eGFP-RhoA with spatiotemporal resolution, HEK293 cells overexpressing mCherry-PKCε and eGFP-RhoA were stimulated with PMA, and images collected over a 12.5 minute time course were subjected to quantitative stoichiometric FRET analysis. PMA treatment induced an obvious reorganization of mCherry-PKCε and eGFP-RhoA in the cell from the cytoplasm to the cell membrane as evidenced by comparing the IA and ID images at 0 min and 12.5 min after PMA stimulation, respectively (Figure 3). Furthermore, PMA treatment resulted in an overall increase in ED, a measure of the FRET efficiency of the interaction between mCherry-PKCε and eGFP-RhoA. The initial increase and peak in ED occurred in the cytoplasm followed by an elevation of the PKCε-RhoA interaction at the cell membrane for the entire time course. Recruitment of RhoA and the increase in FRET activity was especially robust in the actively ruffling regions of the cell (upper and bottom right corners of the cell). Taken together, FRET analysis demonstrated that in response to PMA stimulation, the PKCε-RhoA complex is recruited to the cell membrane over time, and furthermore, the PKCε-RhoA complex may be preassembled in the cytoplasm prior to translocation to the cell membrane.

3.1.4. Dynamic Interaction between PKCε and RhoA in Live Cells. To better define the interaction between PKCε and RhoA at the cell membrane. Our in vitro protein binding experiments indicate that an active ATP-docked PKCε confirmation is not required for PKCε to bind to RhoA. The kinase-inactive PKCε mutant (K437R) contains a point mutation in the ATP binding pocket to prevent ATP occupancy. Interestingly, PKCε/K437R is localized to the cell membrane in unstimulated HEK293 cells overexpressing mCherry-PKCε/K437R (Figure 4(a)). HEK293 cells cotransfected with mCherry-PKCε/K437R and eGFP-RhoA showed colocalization of these two proteins at the cell membrane without PMA stimulation. In support of these observations, quantitative stoichiometric
The accepted model of PMA-mediated activation of PKCs is that PMA changes PKCs from a closed to an open conformation. Additionally, the substrate-docking sites for JNK2 and Csk were identified to be within the kinase domain and in proximity, within 50 amino acids, to the catalytic loop of the kinase [29, 30]. The substrate-docking sites for [NK2 and Csk were identified to be within the kinase domain and in proximity, within 50 amino acids, to the catalytic loop of the kinase [29, 30]. Consistent with these results, the kinase domain of PKCe is sufficient to bind to RhoA. Our work showed that PKCe binds to RhoA within the kinase domain and without the requirement of ATP.

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conformation resulting in translocation of PKCs to the cell membrane. FRET results showed that the initial response to PMA is an increase in the molecular interaction between PKCε and RhoA in the cytoplasm. This observation indicates that the active PKCε conformation is required to expose the RhoA docking site and thus allow RhoA to complex with PKCε. The interaction between PKCε and RhoA showed an early peak at the cytoplasm and then decreased to basal levels for the remainder of the time course. In contrast, a gradual but prolonged increase in FRET intensity was observed at the cell membrane, in particular the actively ruffling regions of the cell, over the entire time course. A plausible explanation is that, following a PKC activation signal, PKCε and RhoA are assembled in the cytoplasm, and the resulting complex is subsequently trafficked to the cell membrane. It is important to point out that PMA does not induce translocation of RhoA to the cell membrane without the presence of PKCε. Therefore, the recruitment of the PKCε-RhoA complex to the cell membrane is completely dependent on the cellular localization of PKCε in response to a stimulus.

Fluorescence microscopy showed that kinase-inactive PKCε is predominantly localized to the cell membrane under basal conditions. This result suggests that the PKCε/K437R is in an open conformation capable to interact with chaperone proteins involved in PKCε translocation. The cellular localization of RhoA is concentrated at the cell membrane in cells cotransfected with mCherry-PKCε/K437R and eGFP-RhoA. Similarly, FRET analysis showed that the interaction

**Figure 4:** Kinase-inactive PKCε colocalizes with RhoA at the cell membrane. (a) Colocalization of kinase-inactive PKCε and RhoA. HEK293 cells were cotransfected with mCherry-PKCε/K437R and eGFP-RhoA. Fluorescence images were captured prior to and 15 minutes after PMA (100 nM) stimulation. (b) Stoichiometric FRET analysis of kinase-inactive PKCε and RhoA interaction. HEK293 cells were cotransfected with mCherry-PKCε/K437R and eGFP-RhoA. Fluorescence images were captured prior to and every 15 seconds after PMA (100 nM) stimulation for 12.5 minutes and then subjected to quantitative FRET analysis. The images presented at each time point represent mCherry-PKCε/K437R (acceptor image, IA), eGFP-RhoA (donor image, ID), and the FRET interaction between mCherry-PKCε/K437R and eGFP-RhoA (ED). The color bars at the end of the panels indicate the scaling of the ED images with warmer colors representing higher values. Time course of normalized ED for the cell membrane and cytoplasm is presented. ED was normalized to the ED of the cytoplasm at the 0 minute time point. Cell membrane is defined as ±1 μm from the cell membrane border. Cytoplasm is defined as all intracellular space, including the nucleus, 1 μm from the cell membrane border.
between PKCe/K437R and RhoA is concentrated at the cell membrane rather than at the cytoplasm in unstimulated cells. Furthermore, PMA did not alter the extent of the molecular interaction between PKCe/K437R and RhoA at the cell membrane. FRET analysis with PKCe/K437R confirmed our in vitro observations and showed that PKCe is able to recruit RhoA to the cell membrane without a PKCe-RhoA phosphorylation event. Taken together, these findings support a kinase independent role of PKCe as a chaperone to traffic RhoA to the cell membrane.

4. Conclusions

Work from our laboratory provided the initial evidence linking two proteins, PKCe and RhoA, intimately involved in metastasis. The PKCe-RhoA signaling module was shown to modulate cancer cell invasion and motility. However, the molecular mechanism of PKCe regulation of RhoA remains to be elucidated. In this study, our results revealed that PKCe has both kinase-dependent and kinase-independent functions to regulate RhoA; PKCe directly phosphorylates RhoA and, moreover, serves as a chaperone to translocate RhoA to the cell membrane.

Authors’ Contribution

Tizhi Su designed and conducted most of the experiments and analyzed and interpreted data. Samuel Straight assisted with the FRET experiments and analysis. Liwei Bao and Xiujie Xie assisted with the experiments and analyzed and interpreted data. Caryn L. Lehner and Greg S. Cavey performed the phosphopeptide mapping of RhoA. Theodoros N. Teknos analyzed and interpreted data. Quintin Pan conceived and supervised the project, designed experiments, analyzed and interpreted data, and wrote the paper. All authors read and approved the final paper.

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